Discovery Proteomics Identifies a Molecular Link between the Coatomer Protein Complex I and Androgen Receptor-dependent Transcription

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Supplemental:

Supplemental Table 1. Proteins identified in the proteomic screen

Subgroup	Entry Name	Minus	Plus	Ratio	Fold Change	Adjusted Values (max and min)	Ln(AS/AD)	Accession Number	Gene Name
3184.1	NAD-dependent protein deacet	0.00E+00	1.25E+03	1.25E+03	1.25E+03	NULL	AS	Q8IXJ6	SIRT2
1989.1	Kelch domain-containing protei	0.00E+00	1.70E+03	1.70E+03	1.70E+03	NULL	AS	Q8IXV7	KLHDC8B
2276.1	Ig lambda chain V-VI region SUT	0.00E+00	1.79E+03	1.79E+03	1.79E+03	NULL	AS	P06317	LV603
3101.1	FYVE, RhoGEF and PH domain-c	0.00E+00	1.80E+03	1.80E+03	1.80E+03	NULL	AS	Q6ZV73	FGD6
2199.1	Endonuclease V	0.00E+00	2.26E+03	2.26E+03	2.26E+03	NULL	AS	E5RII5	ENDOV
824.1	Isoform 2 of Lysine-specific dem	0.00E+00	2.29E+03	2.29E+03	2.29E+03	NULL	AS	Q8NHM5-	KDM2B
2160.1	T-cell activation inhibitor, mitoc	0.00E+00	2.33E+03	2.33E+03	2.33E+03	NULL	AS	Q8N3R3	TCAIM
2756.1	Olfactory receptor 5AR1	0.00E+00	2.39E+03	2.39E+03	2.39E+03	NULL	AS	Q8NGP9	OR5AR1
2767.1	Protein ALEX	0.00E+00	3.52E+03	3.52E+03	3.52E+03	NULL	AS	P84996	GNAS
2300.1	Chondroitin sulfate proteoglyca	0.00E+00	3.55E+03	3.55E+03	3.55E+03	NULL	AS	Q6UVK1	CSPG4
1092.1	Amidophosphoribosyltransferas	0.00E+00	3.95E+03	3.95E+03	3.95E+03	NULL	AS	Q06203	PPAT
1986.1	Cancer-associated gene 1 protei	0.00E+00	4.32E+03	4.32E+03	4.32E+03	NULL	AS	Q8TC20	CAGE1
2590.1	Ras-interacting protein 1	0.00E+00	4.82E+03	4.82E+03	4.82E+03	NULL	AS	Q5U651	RASIP1
1758.1	Ras-related protein Rab-11B	0.00E+00	4.96E+03	4.96E+03	4.96E+03	NULL	AS	Q15907	RAB11B
2912.1	Parafibromin	0.00E+00	4.98E+03	4.98E+03	4.98E+03	NULL	AS	Q6P1J9	CDC73
2772.1	Protein Shroom4	0.00E+00	5.08E+03	5.08E+03	5.08E+03	NULL	AS	Q9ULL8	SHROOM4
2153.1	mRNA-decapping enzyme 1A	0.00E+00	5.10E+03	5.10E+03	5.10E+03	NULL	AS	Q9NPI6	DCP1A
2123.1	Vacuolar protein sorting-associa	0.00E+00	5.17E+03	5.17E+03	5.17E+03	NULL	AS	O75436	VPS26A
1913.1	Peptidyl-alpha-hydroxyglycine a	0.00E+00	5.23E+03	5.23E+03	5.23E+03	NULL	AS	F8W8D9	PAM
3249.1	Zinc finger protein with KRAB ar	0.00E+00	5.38E+03	5.38E+03	5.38E+03	NULL	AS	Q63HK3	ZKSCAN2
1289.1	Hepatocyte cell adhesion molec	0.00E+00	5.67E+03	5.67E+03	5.67E+03	NULL	AS	Q14CZ8	HEPACAM
2583.1	Rab-like protein 5	0.00E+00	5.71E+03	5.71E+03	5.71E+03	NULL	AS	Q9H7X7	RABL5
1317.1	Rabenosyn-5	0.00E+00	6.09E+03	6.09E+03	6.09E+03	NULL	AS	Q9H1K0	ZFYVE20
3108.1	Myristoylated alanine-rich C-kin	0.00E+00	6.14E+03	6.14E+03	6.14E+03	NULL	AS	P29966	MARCKS
2853.1	Tumor protein p63-regulated ge	0.00E+00	6.20E+03	6.20E+03	6.20E+03	NULL	AS	Q5T0D9	TPRG1L
3054.1	BTB/POZ domain-containing pro	0.00E+00	6.23E+03	6.23E+03	6.23E+03	NULL	AS	Q6ZWB6	KCTD8
1757.1	Isoform 3 of PCNA-interacting p	0.00E+00	6.24E+03	6.24E+03	6.24E+03	NULL	AS	Q9NWS1-	PARPBP
1716.1	Isoform 2 of Cysteine-rich with	0.00E+00	6.28E+03	6.28E+03	6.28E+03	NULL	AS	Q96HD1-2	CRELD1
1675.1	TRAF family member-associate	0.00E+00	6.31E+03	6.31E+03	6.31E+03	NULL	AS	Q92844	TANK
2193.1	T-cell leukemia homeobox prote	0.00E+00	6.55E+03	6.55E+03	6.55E+03	NULL	AS	P31314	TLX1

3158.1	Complement receptor type 1	0.00E+00	6.64E+03	6.64E+03	6.64E+03	NULL	AS	E9PDY4	CR1
2252.1	Isoform 6 of Protein WWC2	0.00E+00	6.76E+03	6.76E+03	6.76E+03	NULL	AS	Q6AWC2-	WWC2
2410.1	WASH complex subunit strumpe	0.00E+00	6.85E+03	6.85E+03	6.85E+03	NULL	AS	Q12768	KIAA0196
1878.1	Protocadherin beta-11	0.00E+00	7.24E+03	7.24E+03	7.24E+03	NULL	AS	Q9Y5F2	PCDHB11
2094.1	Anoctamin-4	0.00E+00	7.24E+03	7.24E+03	7.24E+03	NULL	AS	Q32M45	ANO4
2516.1	Isoform 2 of Nucleolysin TIAR	0.00E+00	7.24E+03	7.24E+03	7.24E+03	NULL	AS	Q01085-2	TIAL1
3257.1	Beta-galactosidase	0.00E+00	7.29E+03	7.29E+03	7.29E+03	NULL	AS	P16278	GLB1
906.1	Zinc finger protein 598	0.00E+00	7.46E+03	7.46E+03	7.46E+03	NULL	AS	Q86UK7	ZNF598
2942.1	Protein disulfide-isomerase A5	0.00E+00	7.79E+03	7.79E+03	7.79E+03	NULL	AS	Q14554	PDIA5
1697.1	C-C motif chemokine 19	0.00E+00	7.89E+03	7.89E+03	7.89E+03	NULL	AS	Q5VZ75	CCL19
2164.1	Protein C15orf38-AP3S2	0.00E+00	7.89E+03	7.89E+03	7.89E+03	NULL	AS	Q7Z6K5	C15orf38
2975.1	Sorting nexin-27	0.00E+00	8.00E+03	8.00E+03	8.00E+03	NULL	AS	Q96L92	SNX27
2689.1	Vacuolar protein sorting-associa	0.00E+00	8.23E+03	8.23E+03	8.23E+03	NULL	AS	Q96QK1	VPS35
2619.1	Zinc finger protein 248	0.00E+00	8.77E+03	8.77E+03	8.77E+03	NULL	AS	Q8NDW4	ZNF248
1705.1	Serine/arginine-rich splicing fact	0.00E+00	8.79E+03	8.79E+03	8.79E+03	NULL	AS	P84103	SRSF3
2296.1	Ig gamma-4 chain C region	0.00E+00	9.08E+03	9.08E+03	9.08E+03	NULL	AS	P01861	IGHG4
2638.1	Survival of motor neuron-relate	0.00E+00	9.14E+03	9.14E+03	9.14E+03	NULL	AS	O75940	SMNDC1
3142.1	Werner syndrome ATP-depende	0.00E+00	9.15E+03	9.15E+03	9.15E+03	NULL	AS	Q14191	WRN
1487.1	Zinc finger protein 469	0.00E+00	9.29E+03	9.29E+03	9.29E+03	NULL	AS	H3BS19	ZNF469
2361.1	Isoform 4 of Kinesin-like protein	0.00E+00	9.39E+03	9.39E+03	9.39E+03	NULL	AS	O60333-4	KIF1B
2552.1	Phospholipase DDHD1	0.00E+00	9.46E+03	9.46E+03	9.46E+03	NULL	AS	Q8NEL9	DDHD1
2871.1	Short transient receptor potenti	0.00E+00	9.56E+03	9.56E+03	9.56E+03	NULL	AS	Q8TEL6	TRPC4AP
2980.1	U4/U6 small nuclear ribonucleo	0.00E+00	9.56E+03	9.56E+03	9.56E+03	NULL	AS	Q8WWY3	PRPF31
1889.1	Leucine-rich repeats and immu	0.00E+00	9.64E+03	9.64E+03	9.64E+03	NULL	AS	Q6UXM1	LRIG3
4.2	Acetyl-CoA carboxylase 2	0.00E+00	9.82E+03	9.82E+03	9.82E+03	NULL	AS	O00763	ACACB
1278.1	Cleavage and polyadenylation s	0.00E+00	9.90E+03	9.90E+03	9.90E+03	NULL	AS	Q9UKF6	CPSF3
1061.1	Isoform 2 of Isochorismatase d	0.00E+00	1.01E+04	1.01E+04	1.01E+04	NULL	AS	Q96AB3-2	ISOC2
2658.1	Isoform 2 of Protein KIBRA	0.00E+00	1.01E+04	1.01E+04	1.01E+04	NULL	AS	Q8IX03-2	WWC1
1679.1	Putative 60S ribosomal protein	0.00E+00	1.02E+04	1.02E+04	1.02E+04	NULL	AS	A6NKH3	RPL37L
1306.1	E3 ubiquitin-protein ligase LRSA	0.00E+00	1.03E+04	1.03E+04	1.03E+04	NULL	AS	Q6UWE0	LRSAM1
2478.1	Methyl-CpG-binding domain pr	0.00E+00	1.03E+04	1.03E+04	1.03E+04	NULL	AS	Q96DN6	MBD6
781.2	Isoform 3 of Zinc finger and SCA	0.00E+00	1.06E+04	1.06E+04	1.06E+04	NULL	AS	Q8TBC5-3	ZSCAN18
3049.1	Histone-lysine N-methyltransfer	0.00E+00	1.06E+04	1.06E+04	1.06E+04	NULL	AS	O96028	WHSC1
2541.1	Olfactory receptor 52H1	0.00E+00	1.07E+04	1.07E+04	1.07E+04	NULL	AS	Q8NGJ2	OR52H1
1933.1	Ankyrin repeat domain-containi	0.00E+00	1.14E+04	1.14E+04	1.14E+04	NULL	AS	E9PIL2	ANKRD42

2202.1	Zinc finger protein 555	0.00E+00	1.15E+04	1.15E+04	1.15E+04	NULL	AS	Q8NEP9	ZNF555
1246.1	Abnormal spindle-like microcep	0.00E+00	1.16E+04	1.16E+04	1.16E+04	NULL	AS	Q8IZT6	ASPM
3181.1	Ankyrin repeat domain-containi	0.00E+00	1.16E+04	1.16E+04	1.16E+04	NULL	AS	Q8N283	ANKRD35
3085.1	Beta-galactoside alpha-2,6-sialy	0.00E+00	1.17E+04	1.17E+04	1.17E+04	NULL	AS	P15907	ST6GAL1
3018.1	Isoform 5 of Oxysterol-binding	0.00E+00	1.18E+04	1.18E+04	1.18E+04	NULL	AS	Q9BZF3-5	OSBPL6
1925.1	TNF receptor-associated factor	0.00E+00	1.22E+04	1.22E+04	1.22E+04	NULL	AS	Q13077	TRAF1
1005.1	FAST kinase domain-containing	0.00E+00	1.23E+04	1.23E+04	1.23E+04	NULL	AS	Q53R41	FASTKD1
2934.1	Mitochondrial ribonuclease P pr	0.00E+00	1.23E+04	1.23E+04	1.23E+04	NULL	AS	Q7L0Y3	TRMT10C
1958.1	Diamine acetyltransferase 2	0.00E+00	1.24E+04	1.24E+04	1.24E+04	NULL	AS	Q96F10	SAT2
3200.1	BTB/POZ domain-containing pr	0.00E+00	1.24E+04	1.24E+04	1.24E+04	NULL	AS	B4DIP9	KCTD20
1037.1	Fructosamine-3-kinase	0.00E+00	1.25E+04	1.25E+04	1.25E+04	NULL	AS	Q9H479	FN3K
3090.1	Isoform 4 of Probable helicase s	0.00E+00	1.25E+04	1.25E+04	1.25E+04	NULL	AS	Q7Z333-4	SETX
1335.1	Isoform 2 of MOB kinase activat	0.00E+00	1.26E+04	1.26E+04	1.26E+04	NULL	AS	Q7L9L4-2	MOB1B
2661.1	Rho guanine nucleotide exchan	0.00E+00	1.29E+04	1.29E+04	1.29E+04	NULL	AS	Q9NZN5	ARHGEF12
1874.1	Olfactory receptor 51A7	0.00E+00	1.31E+04	1.31E+04	1.31E+04	NULL	AS	Q8NH64	OR51A7
1429.1	Sec1 family domain-containing	0.00E+00	1.33E+04	1.33E+04	1.33E+04	NULL	AS	Q8WVM8	SCFD1
2803.1	Chromosome 9 open reading fra	0.00E+00	1.33E+04	1.33E+04	1.33E+04	NULL	AS	Q5SQD6	C9orf47
1601.1	GTP:AMP phosphotransferase,	0.00E+00	1.36E+04	1.36E+04	1.36E+04	NULL	AS	Q9UIJ7	AK3
2782.1	Son of sevenless homolog 1	0.00E+00	1.37E+04	1.37E+04	1.37E+04	NULL	AS	Q07889	SOS1
1303.1	Hyaluronan synthase 3	0.00E+00	1.39E+04	1.39E+04	1.39E+04	NULL	AS	O00219	HAS3
3043.1	Serine/arginine repetitive matri	0.00E+00	1.44E+04	1.44E+04	1.44E+04	NULL	AS	E9PCT1	SRRM1
927.1	Diacylglycerol kinase eta	0.00E+00	1.45E+04	1.45E+04	1.45E+04	NULL	AS	Q86XP1	DGKH
2070.1	Glycine amidinotransferase, mit	0.00E+00	1.45E+04	1.45E+04	1.45E+04	NULL	AS	P50440	GATM
3102.1	Retinal dehydrogenase 2	0.00E+00	1.47E+04	1.47E+04	1.47E+04	NULL	AS	O94788	ALDH1A2
2246.1	Proteasome assembly chaperon	0.00E+00	1.52E+04	1.52E+04	1.52E+04	NULL	AS	Q969U7	PSMG2
1011.1	UBX domain-containing protein	0.00E+00	1.54E+04	1.54E+04	1.54E+04	NULL	AS	O94888	UBXN7
2129.1	E3 ubiquitin-protein ligase UHR	0.00E+00	1.54E+04	1.54E+04	1.54E+04	NULL	AS	Q96PU4	UHRF2
2075.1	Isoform 7 of Protein MTO1 hom	0.00E+00	1.55E+04	1.55E+04	1.55E+04	NULL	AS	Q9Y2Z2-6	MTO1
2671.1	Homeobox protein BarH-like 1	0.00E+00	1.55E+04	1.55E+04	1.55E+04	NULL	AS	Q9HBU1	BARX1
1718.1	Isocitrate dehydrogenase [NAD]	0.00E+00	1.57E+04	1.57E+04	1.57E+04	NULL	AS	O43837	IDH3B
1031.1	Adenosine receptor A2b	0.00E+00	1.58E+04	1.58E+04	1.58E+04	NULL	AS	P29275	ADORA2B
1950.1	CUB and sushi domain-containi	0.00E+00	1.58E+04	1.58E+04	1.58E+04	NULL	AS	Q7Z407	CSMD3
2053.1	THO complex subunit 6 homolo	0.00E+00	1.58E+04	1.58E+04	1.58E+04	NULL	AS	Q86W42	THOC6
1497.1	Porphobilinogen deaminase	0.00E+00	1.62E+04	1.62E+04	1.62E+04	NULL	AS	P08397	HMBS
1802.1	Ankyrin repeat and LEM domai	0.00E+00	1.62E+04	1.62E+04	1.62E+04	NULL	AS	Q86XL3	ANKLE2

2939.1	Homeobox protein SIX6	0.00E+00	1.62E+04	1.62E+04	1.62E+04	NULL	AS	O95475	SIX6
2353.1	IQ domain-containing protein E	0.00E+00	1.65E+04	1.65E+04	1.65E+04	NULL	AS	Q6IPM2	IQCE
1754.1	Rho guanine nucleotide exchang	0.00E+00	1.66E+04	1.66E+04	1.66E+04	NULL	AS	Q5VV41	ARHGEF16
3027.1	Guanine nucleotide-binding pro	0.00E+00	1.67E+04	1.67E+04	1.67E+04	NULL	AS	Q14344	GNA13
3215.1	E3 ubiquitin-protein ligase RNF1	0.00E+00	1.67E+04	1.67E+04	1.67E+04	NULL	AS	B7Z3J5	RNF14
2588.1	Ras-specific guanine nucleotide-	0.00E+00	1.68E+04	1.68E+04	1.68E+04	NULL	AS	Q13972	RASGRF1
2392.1	Spermatogenesis-associated prc	0.00E+00	1.69E+04	1.69E+04	1.69E+04	NULL	AS	P0DKV0	SPATA31C1
1713.1	Ankyrin repeat and SAM domair	0.00E+00	1.75E+04	1.75E+04	1.75E+04	NULL	AS	Q92625	ANKS1A
2559.1	Lysine-specific histone demethy	0.00E+00	1.75E+04	1.75E+04	1.75E+04	NULL	AS	F6S0T5	KDM1A
2154.1	GRIP and coiled-coil domain-cor	0.00E+00	1.79E+04	1.79E+04	1.79E+04	NULL	AS	Q8IWJ2	GCC2
2543.1	60S ribosomal protein L39-like	0.00E+00	1.87E+04	1.87E+04	1.87E+04	NULL	AS	Q96EH5	RPL39L
2501.1	Centrosomal protein of 89 kDa	0.00E+00	1.91E+04	1.91E+04	1.91E+04	NULL	AS	K7EJF0	CEP89
1665.1	Plexin-A4	0.00E+00	1.92E+04	1.92E+04	1.92E+04	NULL	AS	Q9HCM2	PLXNA4
1805.1	Nitric oxide synthase-interactin	0.00E+00	1.93E+04	1.93E+04	1.93E+04	NULL	AS	Q9Y314	NOSIP
1655.1	Isoform 3 of Neurabin-1	0.00E+00	1.94E+04	1.94E+04	1.94E+04	NULL	AS	Q9ULJ8-3	PPP1R9A
2960.1	Protein canopy homolog 3	0.00E+00	1.94E+04	1.94E+04	1.94E+04	NULL	AS	Q9BT09	CNPY3
1991.1	Synaptojanin-1	0.00E+00	2.05E+04	2.05E+04	2.05E+04	NULL	AS	J3KQV8	SYNJ1
1131.1	GTP-binding protein 1	0.00E+00	2.08E+04	2.08E+04	2.08E+04	NULL	AS	O00178	GTPBP1
1774.1	Arf-GAP with GTPase, ANK repe	0.00E+00	2.09E+04	2.09E+04	2.09E+04	NULL	AS	E7ESL9	AGAP3
1937.1	SH2 domain-containing adapter	0.00E+00	2.09E+04	2.09E+04	2.09E+04	NULL	AS	Q15464	SHB
2973.1	Beta-2-syntrophin	0.00E+00	2.09E+04	2.09E+04	2.09E+04	NULL	AS	Q13425	SNTB2
2120.1	Transmembrane protein FLJ373	0.00E+00	2.11E+04	2.11E+04	2.11E+04	NULL	AS	Q8N1W0	YF005
2857.1	Rab11 family-interacting proteir	0.00E+00	2.11E+04	2.11E+04	2.11E+04	NULL	AS	Q6WKZ4	RAB11FIP1
1948.1	Oligophrenin-1	0.00E+00	2.12E+04	2.12E+04	2.12E+04	NULL	AS	O60890	OPHN1
2904.1	Protein-L-isoaspartate O-methyl	0.00E+00	2.12E+04	2.12E+04	2.12E+04	NULL	AS	Q96MG8	PCMTD1
744.1	Zinc finger protein 287	0.00E+00	2.14E+04	2.14E+04	2.14E+04	NULL	AS	Q9HBT7	ZNF287
1615.1	Actin-related protein 2/3 compl	0.00E+00	2.16E+04	2.16E+04	2.16E+04	NULL	AS	Q9BPX5	ARPC5L
2747.1	Glutamine--fructose-6-phospha	0.00E+00	2.16E+04	2.16E+04	2.16E+04	NULL	AS	O94808	GFPT2
1659.1	Aldo-keto reductase family 1 me	0.00E+00	2.17E+04	2.17E+04	2.17E+04	NULL	AS	A6NHU4	AKR1C1
2429.1	Isoform SOLAT of Threonine syn	0.00E+00	2.19E+04	2.19E+04	2.19E+04	NULL	AS	Q86YJ6-5	THNSL2
308.2	Serine/arginine-rich splicing fact	0.00E+00	2.22E+04	2.22E+04	2.22E+04	NULL	AS	Q08170	SRSF4
1759.1	Isoform 1 of Ena/VASP-like prot	0.00E+00	2.22E+04	2.22E+04	2.22E+04	NULL	AS	Q9UI08-2	EVL
1980.1	Wolframin	0.00E+00	2.24E+04	2.24E+04	2.24E+04	NULL	AS	O76024	WFS1
2832.1	Thyrotropin-releasing hormone-	0.00E+00	2.26E+04	2.26E+04	2.26E+04	NULL	AS	Q9UKU6	TRHDE
3075.1	NACHT, LRR and PYD domains-c	0.00E+00	2.28E+04	2.28E+04	2.28E+04	NULL	AS	Q86W24	NLRP14

2668.1	Helicase SRCAP	0.00E+00	2.33E+04	2.33E+04	2.33E+04	NULL	AS	Q6ZRS2	SRCAP
1466.1	Nuclear fragile X mental retarda	0.00E+00	2.35E+04	2.35E+04	2.35E+04	NULL	AS	Q7Z417	NUFIP2
2872.1	Protein CMSS1	0.00E+00	2.35E+04	2.35E+04	2.35E+04	NULL	AS	Q9BQ75	CMSS1
1808.1	Coiled-coil domain-containing p	0.00E+00	2.36E+04	2.36E+04	2.36E+04	NULL	AS	Q567U6	CCDC93
1671.1	E3 ubiquitin-protein ligase NED	0.00E+00	2.38E+04	2.38E+04	2.38E+04	NULL	AS	P46934	NEDD4
2322.1	Neurexin-2-alpha	0.00E+00	2.38E+04	2.38E+04	2.38E+04	NULL	AS	Q9P2S2	NRXN2
966.1	MKL/myocardin-like 2, isoform	0.00E+00	2.44E+04	2.44E+04	2.44E+04	NULL	AS	B4DGT8	MKL2
2824.1	Clathrin heavy chain linker dom	0.00E+00	2.44E+04	2.44E+04	2.44E+04	NULL	AS	Q8NHS4	CLHC1
2024.1	RUN and FYVE domain-containi	0.00E+00	2.47E+04	2.47E+04	2.47E+04	NULL	AS	Q8WXA3	RUFY2
886.1	DnaJ homolog subfamily C mem	0.00E+00	2.50E+04	2.50E+04	2.50E+04	NULL	AS	Q96KC8	DNAJC1
2885.1	Pancreas/duodenum homeobo	0.00E+00	2.50E+04	2.50E+04	2.50E+04	NULL	AS	P52945	PDX1
2290.1	Mitochondrial import inner mer	0.00E+00	2.57E+04	2.57E+04	2.57E+04	NULL	AS	O43615	TIMM44
3211.1	Isoform 2 of Suppressor of IKBK	0.00E+00	2.67E+04	2.67E+04	2.67E+04	NULL	AS	Q9BRV8-2	SIKE1
3214.1	DNA-directed RNA polymerase I	0.00E+00	2.69E+04	2.69E+04	2.69E+04	NULL	AS	Q9NVU0	POLR3E
2060.1	ATP-sensitive inward rectifier p	0.00E+00	2.72E+04	2.72E+04	2.72E+04	NULL	AS	Q15842	KCNJ8
2355.1	Isoform 2 of Voltage-dependent	0.00E+00	2.73E+04	2.73E+04	2.73E+04	NULL	AS	Q13936-2	CACNA1C
2550.1	Ras-related protein Rab-5B	0.00E+00	2.73E+04	2.73E+04	2.73E+04	NULL	AS	P61020	RAB5B
1658.1	Structural maintenance of chro	0.00E+00	2.74E+04	2.74E+04	2.74E+04	NULL	AS	Q9UQE7	SMC3
1638.1	Bone morphogenetic protein 4	0.00E+00	2.78E+04	2.78E+04	2.78E+04	NULL	AS	P12644	BMP4
2371.1	Platelet-derived growth factor r	0.00E+00	2.78E+04	2.78E+04	2.78E+04	NULL	AS	P09619	PDGFRB
866.1	Asparagine synthetase [glutami	0.00E+00	2.79E+04	2.79E+04	2.79E+04	NULL	AS	P08243	ASNS
1430.1	Coiled-coil domain-containing p	0.00E+00	2.80E+04	2.80E+04	2.80E+04	NULL	AS	Q0VFZ6	CCDC173
1213.1	Isoform 3 of Ataxin-2-like protei	0.00E+00	2.82E+04	2.82E+04	2.82E+04	NULL	AS	Q8WWM7	ATXN2L
2130.1	Nuclear pore complex-interacti	0.00E+00	2.83E+04	2.83E+04	2.83E+04	NULL	AS	C9JG80	NPIPL3
1920.1	Poliovirus receptor-related prot	0.00E+00	2.89E+04	2.89E+04	2.89E+04	NULL	AS	Q15223	PVRL1
1928.1	Deleted in bladder cancer prote	0.00E+00	2.93E+04	2.93E+04	2.93E+04	NULL	AS	O60477	DBC1
2581.1	Integrator complex subunit 5	0.00E+00	2.93E+04	2.93E+04	2.93E+04	NULL	AS	Q6P9B9	INTS5
1326.1	Lys-63-specific deubiquitinase B	0.00E+00	2.94E+04	2.94E+04	2.94E+04	NULL	AS	P46736	BRCC3
2377.1	Cysteine/serine-rich nuclear pr	0.00E+00	2.94E+04	2.94E+04	2.94E+04	NULL	AS	Q9H175	CSRNP2
2707.1	Ankyrin repeat domain-containi	0.00E+00	2.96E+04	2.96E+04	2.96E+04	NULL	AS	H7C425	ANKRD36C
1499.1	Rho guanine nucleotide exchan	0.00E+00	2.98E+04	2.98E+04	2.98E+04	NULL	AS	Q96PE2	ARHGEF17
2151.1	THO complex subunit 7 homolo	0.00E+00	2.99E+04	2.99E+04	2.99E+04	NULL	AS	Q6I9Y2	THOC7
2395.1	Apoptotic chromatin condensat	0.00E+00	3.00E+04	3.00E+04	3.00E+04	NULL	AS	Q9UKV3	ACIN1
3236.1	SLAIN motif-containing protein	0.00E+00	3.03E+04	3.03E+04	3.03E+04	NULL	AS	Q9P270	SLAIN2
2561.1	RNA-binding protein 26	0.00E+00	3.04E+04	3.04E+04	3.04E+04	NULL	AS	Q5T8P6	RBM26

1291.1	FCH and double SH3 domains pr	0.00E+00	3.05E+04	3.05E+04	3.05E+04	NULL	AS	E9PG19	FCHSD2
2082.1	Protein FAM216A	0.00E+00	3.07E+04	3.07E+04	3.07E+04	NULL	AS	Q8WUB2	FAM216A
2627.1	Isoform 2 of WNT1-inducible-sig	0.00E+00	3.10E+04	3.10E+04	3.10E+04	NULL	AS	O95389-2	WISP3
1170.1	Dynein heavy chain 11, axonem	0.00E+00	3.12E+04	3.12E+04	3.12E+04	NULL	AS	Q96DT5	DNAH11
1826.1	G protein-activated inward recti	0.00E+00	3.12E+04	3.12E+04	3.12E+04	NULL	AS	P48051	KCNJ6
2709.1	Protein bassoon	0.00E+00	3.12E+04	3.12E+04	3.12E+04	NULL	AS	Q9UPA5	BSN
1764.1	Spectrin beta chain, non-erythr	0.00E+00	3.17E+04	3.17E+04	3.17E+04	NULL	AS	Q01082	SPTBN1
2066.1	Histone-lysine N-methyltransfer	0.00E+00	3.17E+04	3.17E+04	3.17E+04	NULL	AS	Q86TU7	SETD3
2336.1	RNA-binding motif protein, X ch	0.00E+00	3.17E+04	3.17E+04	3.17E+04	NULL	AS	P38159	RBMX
3183.1	Interferon-induced protein with	0.00E+00	3.20E+04	3.20E+04	3.20E+04	NULL	AS	Q13325	IFIT5
1760.1	3-ketoacyl-CoA thiolase, peroxis	0.00E+00	3.21E+04	3.21E+04	3.21E+04	NULL	AS	P09110	ACAA1
3093.1	Dual adapter for phosphotyrosi	0.00E+00	3.28E+04	3.28E+04	3.28E+04	NULL	AS	Q9UN19	DAPP1
1373.1	Leucine-rich repeat-containing	0.00E+00	3.34E+04	3.34E+04	3.34E+04	NULL	AS	B4DJ72	LRRC27
3240.1	Acetoacetyl-CoA synthetase	0.00E+00	3.36E+04	3.36E+04	3.36E+04	NULL	AS	F5GYW2	AACS
1814.1	ADNP homeobox protein 2	0.00E+00	3.42E+04	3.42E+04	3.42E+04	NULL	AS	Q6IQ32	ADNP2
2497.1	Endonuclease 8-like 2	0.00E+00	3.43E+04	3.43E+04	3.43E+04	NULL	AS	Q969S2	NEIL2
2970.1	Prickle-like protein 2	0.00E+00	3.46E+04	3.46E+04	3.46E+04	NULL	AS	H3BNU0	PRICKLE2
1668.1	Protein DENND6B	0.00E+00	3.48E+04	3.48E+04	3.48E+04	NULL	AS	Q8NEG7	DENND6B
1331.1	Chloride channel CLIC-like prote	0.00E+00	3.50E+04	3.50E+04	3.50E+04	NULL	AS	Q96S66	CLCC1
3227.1	Noggin	0.00E+00	3.57E+04	3.57E+04	3.57E+04	NULL	AS	Q13253	NOG
1286.1	Translation initiation factor eIF-	0.00E+00	3.62E+04	3.62E+04	3.62E+04	NULL	AS	P49770	EIF2B2
2085.1	Protein FAM149B1	0.00E+00	3.64E+04	3.64E+04	3.64E+04	NULL	AS	Q96BN6	FAM149B1
2622.1	Inhibitor of Bruton tyrosine kina	0.00E+00	3.64E+04	3.64E+04	3.64E+04	NULL	AS	Q9P2D0	IBTK
2277.1	Heat shock 70 kDa protein 4	0.00E+00	3.65E+04	3.65E+04	3.65E+04	NULL	AS	P34932	HSPA4
2312.1	Coiled-coil domain-containing p	0.00E+00	3.66E+04	3.66E+04	3.66E+04	NULL	AS	Q9NQR7	CCDC177
2352.1	Zinc finger protein 678	0.00E+00	3.71E+04	3.71E+04	3.71E+04	NULL	AS	F5GXA7	ZNF678
2203.1	Spermatogenesis-associated pr	0.00E+00	3.74E+04	3.74E+04	3.74E+04	NULL	AS	Q5VX52	SPATA1
2466.1	Peroxisome proliferator-activat	0.00E+00	3.76E+04	3.76E+04	3.76E+04	NULL	AS	Q86YN6	PPARGC1B
372.2	Nucleosome assembly protein 1	0.00E+00	3.78E+04	3.78E+04	3.78E+04	NULL	AS	F5HFY4	NAP1L4b
2472.1	Protein AKNAD1	0.00E+00	3.78E+04	3.78E+04	3.78E+04	NULL	AS	F2Z2Q7	AKNAD1
1873.1	Isoform 4 of Coiled-coil domain-	0.00E+00	3.79E+04	3.79E+04	3.79E+04	NULL	AS	Q6ZUS6-4	CCDC149
1782.1	Zinc finger protein 33A	0.00E+00	3.82E+04	3.82E+04	3.82E+04	NULL	AS	F6TH33	ZNF33A
2427.1	CD2 antigen cytoplasmic tail-bi	0.00E+00	3.85E+04	3.85E+04	3.85E+04	NULL	AS	O95400	CD2BP2
3116.1	Dimethylaniline monooxygenas	0.00E+00	3.85E+04	3.85E+04	3.85E+04	NULL	AS	P49326	FMO5
2673.1	Zinc finger protein GLI1	0.00E+00	3.87E+04	3.87E+04	3.87E+04	NULL	AS	P08151	GLI1

2930.1	Serine/threonine-protein kinase	0.00E+00	3.93E+04	3.93E+04	3.93E+04	NULL	AS	Q8IYT8	ULK2
2161.1	Polymerase delta-interacting pr	0.00E+00	4.00E+04	4.00E+04	4.00E+04	NULL	AS	Q9Y2S7	POLDIP2
2485.1	Isoform 3 of Epithelial-stromal i	0.00E+00	4.00E+04	4.00E+04	4.00E+04	NULL	AS	Q96J88-3	EPSTI1
2899.1	Zinc finger protein 564	0.00E+00	4.01E+04	4.01E+04	4.01E+04	NULL	AS	Q8TBZ8	ZNF564
3008.1	Podocan-like protein 1	0.00E+00	4.06E+04	4.06E+04	4.06E+04	NULL	AS	Q6PEZ8	PODNL1
2189.1	Membrane-associated phospha	0.00E+00	4.08E+04	4.08E+04	4.08E+04	NULL	AS	Q9BZ72	PITPNM2
1369.1	General transcription factor II-I	0.00E+00	4.13E+04	4.13E+04	4.13E+04	NULL	AS	P78347	GTF2I
810.1	Isoform 6 of Dynamin-1-like pro	0.00E+00	4.15E+04	4.15E+04	4.15E+04	NULL	AS	O00429-6	DNM1L
2217.1	Protein MCM10 homolog	0.00E+00	4.18E+04	4.18E+04	4.18E+04	NULL	AS	Q7L590	MCM10
1673.1	Isoform 3 of Zinc finger protein	0.00E+00	4.20E+04	4.20E+04	4.20E+04	NULL	AS	Q5VV52-3	ZNF691
638.1	YTH domain family protein 2	0.00E+00	4.27E+04	4.27E+04	4.27E+04	NULL	AS	Q9Y5A9	YTHDF2
1069.1	Pinin	0.00E+00	4.27E+04	4.27E+04	4.27E+04	NULL	AS	Q9H307	PNN
3167.1	Coiled-coil domain-containing p	0.00E+00	4.28E+04	4.28E+04	4.28E+04	NULL	AS	Q8IYE0	CCDC146
1837.1	Transcription factor Sp2	0.00E+00	4.31E+04	4.31E+04	4.31E+04	NULL	AS	Q02086	SP2
1898.1	WD repeat-containing protein 6	0.00E+00	4.32E+04	4.32E+04	4.32E+04	NULL	AS	Q8WVS4	WDR60
2103.1	Isoform 2 of TGF-beta receptor	0.00E+00	4.32E+04	4.32E+04	4.32E+04	NULL	AS	P37173-2	TGFBR2
3132.1	Fibronectin type-III domain-cont	0.00E+00	4.33E+04	4.33E+04	4.33E+04	NULL	AS	F2Z333	C1orf233
1116.1	Testis-specific Y-encoded-like pr	0.00E+00	4.34E+04	4.34E+04	4.34E+04	NULL	AS	Q9H0U9	TSPYL1
1749.1	Beta-catenin-interacting protein	0.00E+00	4.41E+04	4.41E+04	4.41E+04	NULL	AS	Q9NSA3	CTNNBIP1
2345.1	Cyclin-dependent kinase 7	0.00E+00	4.41E+04	4.41E+04	4.41E+04	NULL	AS	P50613	CDK7
2526.1	Thimet oligopeptidase	0.00E+00	4.41E+04	4.41E+04	4.41E+04	NULL	AS	P52888	THOP1
2959.1	A disintegrin and metalloprotein	0.00E+00	4.41E+04	4.41E+04	4.41E+04	NULL	AS	Q8TE58	ADAMTS15
2845.1	Zinc finger protein ZFPM2	0.00E+00	4.51E+04	4.51E+04	4.51E+04	NULL	AS	Q8WW38	ZFPM2
1174.1	Ornithine decarboxylase antizym	0.00E+00	4.55E+04	4.55E+04	4.55E+04	NULL	AS	P54368	OAZ1
2651.1	Protein phosphatase 1 regulator	0.00E+00	4.55E+04	4.55E+04	4.55E+04	NULL	AS	Q7Z4L9	PPP1R42
2482.1	Transcriptional activator protein	0.00E+00	4.56E+04	4.56E+04	4.56E+04	NULL	AS	Q00577	PURA
2521.1	Collagen alpha-1(XXII) chain	0.00E+00	4.61E+04	4.61E+04	4.61E+04	NULL	AS	Q8NFW1	COL22A1
2412.1	Transcription elongation factor	0.00E+00	4.63E+04	4.63E+04	4.63E+04	NULL	AS	Q14241	TCEB3
2165.1	Exportin-T	0.00E+00	4.65E+04	4.65E+04	4.65E+04	NULL	AS	O43592	XPOT
2910.1	Zinc finger protein 253	0.00E+00	4.73E+04	4.73E+04	4.73E+04	NULL	AS	O75346	ZNF253
2741.1	Fumarate hydratase, mitochond	0.00E+00	4.74E+04	4.74E+04	4.74E+04	NULL	AS	P07954	FH
2998.1	Coiled-coil domain-containing p	0.00E+00	4.76E+04	4.76E+04	4.76E+04	NULL	AS	J3KNW7	CCDC41
2071.1	Dihydropyrimidinase-related pr	0.00E+00	4.77E+04	4.77E+04	4.77E+04	NULL	AS	O14531	DPYSL4
3036.1	RUN domain-containing protein	0.00E+00	4.81E+04	4.81E+04	4.81E+04	NULL	AS	Q59EK9	RUNDC3A
2238.1	Lysine-specific demethylase 4D	0.00E+00	4.82E+04	4.82E+04	4.82E+04	NULL	AS	Q6B0I6	KDM4D

1635.1	Proteasomal ubiquitin receptor	0.00E+00	4.83E+04	4.83E+04	4.83E+04	NULL	AS	Q16186	ADRM1
2459.1	Isoform 2 of AF4/FMR2 family m	0.00E+00	4.83E+04	4.83E+04	4.83E+04	NULL	AS	P51826-2	AFF3
2049.1	Caspase recruitment domain-co	0.00E+00	4.87E+04	4.87E+04	4.87E+04	NULL	AS	Q9BWT7	CARD10
2879.1	Putative unconventional myosi	0.00E+00	4.90E+04	4.90E+04	4.90E+04	NULL	AS	Q96JP2	MYO15B
2372.1	Cornifin-B	0.00E+00	4.93E+04	4.93E+04	4.93E+04	NULL	AS	P22528	SPRR1B
3199.1	E3 ubiquitin-protein ligase TRIM	0.00E+00	4.96E+04	4.96E+04	4.96E+04	NULL	AS	G8JLN1	TRIM31
2091.1	Coiled-coil domain-containing p	0.00E+00	4.98E+04	4.98E+04	4.98E+04	NULL	AS	E9PKB1	CCDC15
2943.1	Signal transducer and activator	0.00E+00	4.98E+04	4.98E+04	4.98E+04	NULL	AS	Q14765	STAT4
1559.1	SAFB-like transcription modulat	0.00E+00	5.03E+04	5.03E+04	5.03E+04	NULL	AS	Q9NWH9	SLTM
1264.1	Echinoderm microtubule-associ	0.00E+00	5.05E+04	5.05E+04	5.05E+04	NULL	AS	Q6ZMW3	EML6
2462.1	Ubiquilin-3	0.00E+00	5.06E+04	5.06E+04	5.06E+04	NULL	AS	Q9H347	UBQLN3
2647.1	Receptor tyrosine-protein kinas	0.00E+00	5.06E+04	5.06E+04	5.06E+04	NULL	AS	Q15303	ERBB4
2524.1	Signal recognition particle 72 kD	0.00E+00	5.08E+04	5.08E+04	5.08E+04	NULL	AS	O76094	SRP72
1201.1	POC1 centriolar protein homolo	0.00E+00	5.10E+04	5.10E+04	5.10E+04	NULL	AS	F8VV91	POC1B
521.2	Transducin-like enhancer protei	0.00E+00	5.12E+04	5.12E+04	5.12E+04	NULL	AS	H0YL70	TLE3
1608.1	Cold shock domain containing E	0.00E+00	5.14E+04	5.14E+04	5.14E+04	NULL	AS	G5E9Q2	CSDE1
1685.1	Kinesin-like protein KIF15	0.00E+00	5.17E+04	5.17E+04	5.17E+04	NULL	AS	Q9NS87	KIF15
1746.1	Arf-GAP domain and FG repeat-	0.00E+00	5.17E+04	5.17E+04	5.17E+04	NULL	AS	O95081	AGFG2
2799.1	PRKC apoptosis WT1 regulator	0.00E+00	5.17E+04	5.17E+04	5.17E+04	NULL	AS	Q96IZ0	PAWR
1589.1	60S ribosomal protein L17	0.00E+00	5.20E+04	5.20E+04	5.20E+04	NULL	AS	P18621	RPL17
1719.1	Mitogen-activated protein kinas	0.00E+00	5.25E+04	5.25E+04	5.25E+04	NULL	AS	Q02779	MAP3K10
2966.1	Arginyl-tRNA--protein transfera	0.00E+00	5.25E+04	5.25E+04	5.25E+04	NULL	AS	O95260	ATE1
2692.1	Dermokine	0.00E+00	5.28E+04	5.28E+04	5.28E+04	NULL	AS	Q6E0U4	DMKN
2640.1	PTB-containing, cubilin and LRP	0.00E+00	5.31E+04	5.31E+04	5.31E+04	NULL	AS	Q7Z2X4	PID1
1890.1	Ubiquitin-like-conjugating enzy	0.00E+00	5.38E+04	5.38E+04	5.38E+04	NULL	AS	Q9NT62	ATG3
1941.1	Golgi integral membrane protei	0.00E+00	5.38E+04	5.38E+04	5.38E+04	NULL	AS	O00461	GOLIM4
1257.1	Nuclear receptor-binding factor	0.00E+00	5.44E+04	5.44E+04	5.44E+04	NULL	AS	B4DWS0	NRBF2
2431.1	Ephrin type-B receptor 1	0.00E+00	5.46E+04	5.46E+04	5.46E+04	NULL	AS	P54762	EPHB1
1356.1	Arrestin domain-containing prot	0.00E+00	5.49E+04	5.49E+04	5.49E+04	NULL	AS	Q8TBH0	ARRDC2
1517.1	Armadillo repeat-containing pr	0.00E+00	5.53E+04	5.53E+04	5.53E+04	NULL	AS	Q5W041	ARMC3
2225.1	Isoform 2 of Secernin-1	0.00E+00	5.53E+04	5.53E+04	5.53E+04	NULL	AS	Q12765-2	SCRN1
2949.1	Biotinidase	0.00E+00	5.53E+04	5.53E+04	5.53E+04	NULL	AS	F8WCU5	BTD
1823.1	EMILIN-1	0.00E+00	5.57E+04	5.57E+04	5.57E+04	NULL	AS	Q9Y6C2	EMILIN1
2710.1	Adenosine deaminase-like prote	0.00E+00	5.68E+04	5.68E+04	5.68E+04	NULL	AS	Q6DHV7	ADAL
3222.1	REST corepressor 1	0.00E+00	5.73E+04	5.73E+04	5.73E+04	NULL	AS	J3KN32	RCOR1

1305.1	Transforming growth factor-bet	0.00E+00	5.75E+04	5.75E+04	5.75E+04	NULL	AS	Q8WUH2	TGFBRAP1
5.2	Keratin, type I cuticular Ha5	0.00E+00	5.77E+04	5.77E+04	5.77E+04	NULL	AS	C4AM86	KRT35
2347.1	Transcription factor E4F1	0.00E+00	5.81E+04	5.81E+04	5.81E+04	NULL	AS	Q66K89	E4F1
3056.1	PHD finger protein 6	0.00E+00	5.84E+04	5.84E+04	5.84E+04	NULL	AS	E9PC97	PHF6
2730.1	Type I inositol 1,4,5-trisphospha	0.00E+00	5.86E+04	5.86E+04	5.86E+04	NULL	AS	Q14642	INPP5A
2768.1	Isoform Beta of Apoptosis regul	0.00E+00	5.86E+04	5.86E+04	5.86E+04	NULL	AS	Q07812-2	BAX
2922.1	Kinesin-like protein KIF24	0.00E+00	5.87E+04	5.87E+04	5.87E+04	NULL	AS	Q5T7B8	KIF24
2764.1	Retinol dehydrogenase 11	0.00E+00	5.88E+04	5.88E+04	5.88E+04	NULL	AS	G3V3K0	RDH11
2138.1	Semaphorin-3F	0.00E+00	5.90E+04	5.90E+04	5.90E+04	NULL	AS	Q13275	SEMA3F
2646.1	Coiled-coil domain-containing p	0.00E+00	5.90E+04	5.90E+04	5.90E+04	NULL	AS	C9JGU1	CCDC66
2829.1	Isoform 2 of Peroxisomal acyl-c	0.00E+00	5.90E+04	5.90E+04	5.90E+04	NULL	AS	Q15067-2	ACOX1
2006.1	PHD finger protein 21A	0.00E+00	5.96E+04	5.96E+04	5.96E+04	NULL	AS	Q96BD5	PHF21A
2149.1	Isoform 2 of Tapasin	0.00E+00	6.01E+04	6.01E+04	6.01E+04	NULL	AS	O15533-2	TAPBP
2335.1	Calcium-binding protein 5	0.00E+00	6.01E+04	6.01E+04	6.01E+04	NULL	AS	Q9NP86	CABP5
2967.1	EH domain-binding protein 1	0.00E+00	6.02E+04	6.02E+04	6.02E+04	NULL	AS	Q8NDI1	EHBP1
1740.1	WD repeat-containing protein 7	0.00E+00	6.04E+04	6.04E+04	6.04E+04	NULL	AS	Q9NW82	WDR70
1600.1	Protein SMIM12	0.00E+00	6.06E+04	6.06E+04	6.06E+04	NULL	AS	E5RH51	SMIM12
1026.1	Progesterone-induced-blocking	0.00E+00	6.09E+04	6.09E+04	6.09E+04	NULL	AS	Q8WXW3	PIBF1
2394.1	Serine/threonine-protein kinase	0.00E+00	6.11E+04	6.11E+04	6.11E+04	NULL	AS	Q9BVS4	RIOK2
3092.1	Isoform 2 of Perilipin-4	0.00E+00	6.15E+04	6.15E+04	6.15E+04	NULL	AS	Q96Q06-2	PLIN4
1558.1	Zinc finger and SCAN domain-co	0.00E+00	6.16E+04	6.16E+04	6.16E+04	NULL	AS	Q96SZ4	ZSCAN10
2723.1	Isoform 2 of TGF-beta receptor	0.00E+00	6.23E+04	6.23E+04	6.23E+04	NULL	AS	P36897-2	TGFBR1
2781.1	Lethal(3)malignant brain tumor-	0.00E+00	6.23E+04	6.23E+04	6.23E+04	NULL	AS	Q8NA19	L3MBTL4
3035.1	Protein GREB1	0.00E+00	6.24E+04	6.24E+04	6.24E+04	NULL	AS	Q4ZG55	GREB1
2994.1	Isoform 3 of F-box only protein	0.00E+00	6.32E+04	6.32E+04	6.32E+04	NULL	AS	O75426-3	FBXO24
2126.1	G antigen family E member 1	0.00E+00	6.33E+04	6.33E+04	6.33E+04	NULL	AS	Q96GU1	PAGE5
1720.1	Melanoma-associated antigen B	0.00E+00	6.34E+04	6.34E+04	6.34E+04	NULL	AS	A8MXT2	MAGEB17
2582.1	Isoform 6 of A-kinase anchor pr	0.00E+00	6.34E+04	6.34E+04	6.34E+04	NULL	AS	Q99996-6	AKAP9
3231.1	Poly [ADP-ribose] polymerase 4	0.00E+00	6.34E+04	6.34E+04	6.34E+04	NULL	AS	Q9UKK3	PARP4
2147.1	Zinc finger protein with KRAB ar	0.00E+00	6.40E+04	6.40E+04	6.40E+04	NULL	AS	Q9BRR0	ZKSCAN3
1135.1	Eukaryotic translation initiation	0.00E+00	6.42E+04	6.42E+04	6.42E+04	NULL	AS	Q13347	EIF3I
1410.1	Methionine--tRNA ligase, mitoc	0.00E+00	6.42E+04	6.42E+04	6.42E+04	NULL	AS	Q96GW9	MARS2
1562.1	Unconventional myosin-Id	0.00E+00	6.42E+04	6.42E+04	6.42E+04	NULL	AS	O94832	MYO1D
1856.1	C-X-C motif chemokine 2	0.00E+00	6.42E+04	6.42E+04	6.42E+04	NULL	AS	P19875	CXCL2
2007.1	Histone-lysine N-methyltransfer	0.00E+00	6.44E+04	6.44E+04	6.44E+04	NULL	AS	Q9UMN6	KMT2B

1848.1	Centrosome-associated protein	0.00E+00	6.48E+04	6.48E+04	6.48E+04	NULL	AS	Q9BV73	CEP250
2255.1	Eukaryotic translation initiation	0.00E+00	6.51E+04	6.51E+04	6.51E+04	NULL	AS	P60228	EIF3E
1946.1	Quinone oxidoreductase	0.00E+00	6.55E+04	6.55E+04	6.55E+04	NULL	AS	Q08257	CRYZ
2220.1	Transcription cofactor HES-6	0.00E+00	6.58E+04	6.58E+04	6.58E+04	NULL	AS	Q96HZ4	HES6
2706.1	Sodium/potassium-transporting	0.00E+00	6.60E+04	6.60E+04	6.60E+04	NULL	AS	Q13733	ATP1A4
2473.1	Integrin alpha-V	0.00E+00	6.61E+04	6.61E+04	6.61E+04	NULL	AS	P06756	ITGAV
2286.1	Speriolin	0.00E+00	6.63E+04	6.63E+04	6.63E+04	NULL	AS	Q76KD6	SPATC1
985.1	Ig kappa chain V-III region HIC	0.00E+00	6.64E+04	6.64E+04	6.64E+04	NULL	AS	P18136	KV313
2682.1	B-cell CLL/lymphoma 7 protein f	0.00E+00	6.65E+04	6.65E+04	6.65E+04	NULL	AS	F8WDZ4	BCL7B
793.1	Protein quaking	0.00E+00	6.67E+04	6.67E+04	6.67E+04	NULL	AS	Q96PU8	QKI
1915.1	Guanine nucleotide-binding pro	0.00E+00	6.78E+04	6.78E+04	6.78E+04	NULL	AS	Q03113	GNA12
1793.1	Zinc finger protein 485	0.00E+00	6.79E+04	6.79E+04	6.79E+04	NULL	AS	Q8NCK3	ZNF485
921.1	ADP-ribosylation factor-like prot	0.00E+00	6.80E+04	6.80E+04	6.80E+04	NULL	AS	P36405	ARL3
1598.1	Splicing factor 45	0.00E+00	6.82E+04	6.82E+04	6.82E+04	NULL	AS	Q96I25	RBM17
2303.1	Proline-rich protein 7	0.00E+00	6.82E+04	6.82E+04	6.82E+04	NULL	AS	Q8TB68	PRR7
2330.1	cAMP-responsive element-bindi	0.00E+00	6.82E+04	6.82E+04	6.82E+04	NULL	AS	O60519	CREBL2
3129.1	Inositol 1,4,5-trisphosphate rece	0.00E+00	6.83E+04	6.83E+04	6.83E+04	NULL	AS	Q14643	ITPR1
2454.1	Myosin-15	0.00E+00	6.84E+04	6.84E+04	6.84E+04	NULL	AS	Q9Y2K3	MYH15
997.1	Methylosome protein 50	0.00E+00	6.88E+04	6.88E+04	6.88E+04	NULL	AS	Q9BQA1	WDR77
2500.1	Isoform 2 of Protein TANC2	0.00E+00	6.92E+04	6.92E+04	6.92E+04	NULL	AS	Q9HCD6-2	TANC2
3162.1	Cholecystokinin receptor type A	0.00E+00	6.95E+04	6.95E+04	6.95E+04	NULL	AS	P32238	CCKAR
509.1	Alpha/beta hydrolase domain-c	0.00E+00	6.97E+04	6.97E+04	6.97E+04	NULL	AS	Q8NFV4	ABHD11
1500.1	Whirlin	0.00E+00	7.08E+04	7.08E+04	7.08E+04	NULL	AS	Q9P202	DFNB31
1539.1	SH2 domain-containing protein	0.00E+00	7.09E+04	7.09E+04	7.09E+04	NULL	AS	A6NKC9	SH2D7
910.1	Microsomal triglyceride transfe	0.00E+00	7.14E+04	7.14E+04	7.14E+04	NULL	AS	E9PBP6	MTTP
935.1	RNA-binding protein 25	0.00E+00	7.18E+04	7.18E+04	7.18E+04	NULL	AS	P49756	RBM25
2515.1	Coiled-coil domain-containing p	0.00E+00	7.19E+04	7.19E+04	7.19E+04	NULL	AS	B8ZZV3	CCDC148
1570.1	Large neutral amino acids trans	0.00E+00	7.21E+04	7.21E+04	7.21E+04	NULL	AS	Q9UHI5	SLC7A8
2023.1	Isoform 2 of Probable gluconoki	0.00E+00	7.23E+04	7.23E+04	7.23E+04	NULL	AS	Q5T6J7-2	IDNK
2343.1	Phosphatidylinositol 4,5-bispho	0.00E+00	7.27E+04	7.27E+04	7.27E+04	NULL	AS	Q15735	INPP5J
1419.1	Isoform 3 of Protein PRRC2A	0.00E+00	7.29E+04	7.29E+04	7.29E+04	NULL	AS	P48634-3	PRRC2A
667.1	Metallothionein-1G	0.00E+00	7.31E+04	7.31E+04	7.31E+04	NULL	AS	P13640	MT1G
1628.1	Transgelin-3	0.00E+00	7.35E+04	7.35E+04	7.35E+04	NULL	AS	Q9UI15	TAGLN3
1953.1	Rho guanine nucleotide exchan	0.00E+00	7.37E+04	7.37E+04	7.37E+04	NULL	AS	Q8N1W1	ARHGEF28
2218.1	Tankyrase-2	0.00E+00	7.44E+04	7.44E+04	7.44E+04	NULL	AS	Q9H2K2	TNKS2

2725.1	Aldose reductase	0.00E+00	7.47E+04	7.47E+04	7.47E+04	NULL	AS	P15121	AKR1B1
1094.1	Pre-mRNA-splicing factor RBM2	0.00E+00	7.48E+04	7.48E+04	7.48E+04	NULL	AS	Q9NW64	RBM22
2744.1	Actin filament-associated protei	0.00E+00	7.51E+04	7.51E+04	7.51E+04	NULL	AS	Q8TED9	AFAP1L1
1253.1	Maleylacetoacetate isomerase	0.00E+00	7.55E+04	7.55E+04	7.55E+04	NULL	AS	O43708	GSTZ1
2166.1	Isoform 3 of Deleted in lung anc	0.00E+00	7.61E+04	7.61E+04	7.61E+04	NULL	AS	Q9Y238-3	DLEC1
3107.1	Zinc finger protein 221	0.00E+00	7.63E+04	7.63E+04	7.63E+04	NULL	AS	Q9UK13	ZNF221
2624.1	Pre-mRNA-splicing factor SYF1	0.00E+00	7.66E+04	7.66E+04	7.66E+04	NULL	AS	Q9HCS7	XAB2
1524.1	Protein SFI1 homolog	0.00E+00	7.67E+04	7.67E+04	7.67E+04	NULL	AS	A8K8P3	SFI1
1553.1	ADP/ATP translocase 3	0.00E+00	7.67E+04	7.67E+04	7.67E+04	NULL	AS	P12236	SLC25A6
2808.1	Calcium-binding protein 39	0.00E+00	7.67E+04	7.67E+04	7.67E+04	NULL	AS	Q9Y376	CAB39
3237.1	rRNA-processing protein UTP23	0.00E+00	7.67E+04	7.67E+04	7.67E+04	NULL	AS	Q9BRU9	UTP23
2674.1	2-oxoisovalerate dehydrogenas	0.00E+00	7.72E+04	7.72E+04	7.72E+04	NULL	AS	P21953	BCKDHB
2869.1	Transmembrane protease serin	0.00E+00	7.73E+04	7.73E+04	7.73E+04	NULL	AS	Q7Z410	TMPRSS9
1346.1	GTP-binding protein SAR1b	0.00E+00	7.76E+04	7.76E+04	7.76E+04	NULL	AS	Q9Y6B6	SAR1B
2602.1	HAUS augmin-like complex subu	0.00E+00	7.77E+04	7.77E+04	7.77E+04	NULL	AS	Q9H6D7	HAUS4
1828.1	Cyclin-dependent kinase inhibit	0.00E+00	7.83E+04	7.83E+04	7.83E+04	NULL	AS	J3KQV0	CDKN1A
987.1	Perilipin-3	0.00E+00	7.86E+04	7.86E+04	7.86E+04	NULL	AS	O60664	PLIN3
1767.1	Eukaryotic translation initiation	0.00E+00	7.87E+04	7.87E+04	7.87E+04	NULL	AS	B0QY89	EIF3L
1845.1	Isoform 2 of Eukaryotic translati	0.00E+00	7.87E+04	7.87E+04	7.87E+04	NULL	AS	P55884-2	EIF3B
2259.1	Dimethyladenosine transferase	0.00E+00	7.93E+04	7.93E+04	7.93E+04	NULL	AS	Q9H5Q4	TFB2M
2381.1	Protein LOC100652824	0.00E+00	7.98E+04	7.98E+04	7.98E+04	NULL	AS	F5H626	LOC100652824
1709.1	Acidic leucine-rich nuclear phos	0.00E+00	7.99E+04	7.99E+04	7.99E+04	NULL	AS	O95626	ANP32D
2972.1	Putative ATP-dependent RNA he	0.00E+00	7.99E+04	7.99E+04	7.99E+04	NULL	AS	Q9H6R0	DHX33
2882.1	Beta-crystallin A3	0.00E+00	8.00E+04	8.00E+04	8.00E+04	NULL	AS	P05813	CRYBA1
2801.1	Laminin subunit alpha-4	0.00E+00	8.08E+04	8.08E+04	8.08E+04	NULL	AS	Q16363	LAMA4
1585.1	Zinc finger protein 616	0.00E+00	8.09E+04	8.09E+04	8.09E+04	NULL	AS	Q08AN1	ZNF616
1854.1	Lamina-associated polypeptide	0.00E+00	8.09E+04	8.09E+04	8.09E+04	NULL	AS	P42166	TMPO
2804.1	MICAL C-terminal-like protein	0.00E+00	8.11E+04	8.11E+04	8.11E+04	NULL	AS	Q6ZW33	MICALCL
1813.1	60S ribosomal protein L14	0.00E+00	8.15E+04	8.15E+04	8.15E+04	NULL	AS	P50914	RPL14
2374.1	TBC1 domain family member 26	0.00E+00	8.16E+04	8.16E+04	8.16E+04	NULL	AS	Q86UD7	TBC1D26
1104.1	HIV Tat-specific factor 1	0.00E+00	8.37E+04	8.37E+04	8.37E+04	NULL	AS	O43719	HTATSF1
2491.1	Unconventional myosin-XVIIIb	0.00E+00	8.39E+04	8.39E+04	8.39E+04	NULL	AS	F5GXR6	MYO18B
2270.1	Isoform 3 of Tyrosine-protein ki	0.00E+00	8.43E+04	8.43E+04	8.43E+04	NULL	AS	P06239-3	LCK
1886.1	Calcium-dependent secretion ac	0.00E+00	8.54E+04	8.54E+04	8.54E+04	NULL	AS	Q86UW7	CADPS2
1744.1	Bone morphogenetic protein 3	0.00E+00	8.55E+04	8.55E+04	8.55E+04	NULL	AS	P12645	BMP3

1960.1	Cleavage stimulation factor sub	0.00E+00	8.58E+04	8.58E+04	8.58E+04	NULL	AS	Q05048	CSTF1
2061.1	Isoform Mitochondrial of Lysine	0.00E+00	8.61E+04	8.61E+04	8.61E+04	NULL	AS	Q15046-2	KARS
2908.1	snRNA-activating protein compl	0.00E+00	8.61E+04	8.61E+04	8.61E+04	NULL	AS	O75971	SNAPC5
2486.1	Homeobox protein ARX	0.00E+00	8.62E+04	8.62E+04	8.62E+04	NULL	AS	Q96QS3	ARX
1695.1	AP2-associated protein kinase 1	0.00E+00	8.69E+04	8.69E+04	8.69E+04	NULL	AS	Q2M2I8	AAK1
1689.1	Dual specificity tyrosine-phosph	0.00E+00	8.78E+04	8.78E+04	8.78E+04	NULL	AS	Q13627	DYRK1A
2791.1	Protein FAM118A	0.00E+00	8.79E+04	8.79E+04	8.79E+04	NULL	AS	Q9NWS6	FAM118A
2728.1	Reelin	0.00E+00	8.85E+04	8.85E+04	8.85E+04	NULL	AS	J3KQ66	RELN
2022.1	72 kDa type IV collagenase	0.00E+00	8.87E+04	8.87E+04	8.87E+04	NULL	AS	P08253	MMP2
1609.1	Anamorsin	0.00E+00	8.91E+04	8.91E+04	8.91E+04	NULL	AS	Q6FI81	CIAPIN1
1471.1	WD repeat-containing protein 3	0.00E+00	8.96E+04	8.96E+04	8.96E+04	NULL	AS	Q8NI36	WDR36
2540.1	Nucleoside diphosphate-linked	0.00E+00	8.96E+04	8.96E+04	8.96E+04	NULL	AS	P0C025	NUDT17
2388.1	Ankyrin repeat domain-containi	0.00E+00	9.00E+04	9.00E+04	9.00E+04	NULL	AS	Q8IVF6	ANKRD18A
1798.1	Methionine aminopeptidase 2	0.00E+00	9.06E+04	9.06E+04	9.06E+04	NULL	AS	P50579	METAP2
3256.1	HCG1818442, isoform CRA_a	0.00E+00	9.06E+04	9.06E+04	9.06E+04	NULL	AS	I3L4Q0	FAM195B
2076.1	Protein fantom	0.00E+00	9.08E+04	9.08E+04	9.08E+04	NULL	AS	Q68CZ1	RPGRIP1L
2299.1	Coiled-coil domain-containing p	0.00E+00	9.29E+04	9.29E+04	9.29E+04	NULL	AS	Q2M329	CCDC96
2242.1	Protein Wnt	0.00E+00	9.32E+04	9.32E+04	9.32E+04	NULL	AS	D6RF47	WNT8A
2884.1	Alpha-1D adrenergic receptor	0.00E+00	9.32E+04	9.32E+04	9.32E+04	NULL	AS	P25100	ADRA1D
3139.1	Prostaglandin F2-alpha receptor	0.00E+00	9.32E+04	9.32E+04	9.32E+04	NULL	AS	P43088	PTGFR
1527.1	Wee1-like protein kinase 2	0.00E+00	9.36E+04	9.36E+04	9.36E+04	NULL	AS	P0C1S8	WEE2
1245.1	AP-2 complex subunit alpha-1	0.00E+00	9.40E+04	9.40E+04	9.40E+04	NULL	AS	O95782	AP2A1
1112.1	Plexin-A1	0.00E+00	9.41E+04	9.41E+04	9.41E+04	NULL	AS	Q9UIW2	PLXNA1
2471.1	Nucleolar and spindle-associate	0.00E+00	9.43E+04	9.43E+04	9.43E+04	NULL	AS	Q9BXS6	NUSAP1
2950.1	B-cell CLL/lymphoma 6 member	0.00E+00	9.48E+04	9.48E+04	9.48E+04	NULL	AS	Q8N143	BCL6B
1428.1	Isoform 4 of Nitrilase homolog	0.00E+00	9.52E+04	9.52E+04	9.52E+04	NULL	AS	Q86X76-3	NIT1
2315.1	Thiosulfate sulfurtransferase	0.00E+00	9.57E+04	9.57E+04	9.57E+04	NULL	AS	Q16762	TST
1555.1	Insulin receptor-related protein	0.00E+00	9.59E+04	9.59E+04	9.59E+04	NULL	AS	P14616	INSRR
2984.1	Ceramide synthase 3	0.00E+00	9.62E+04	9.62E+04	9.62E+04	NULL	AS	Q8IU89	CERS3
741.1	Prefoldin subunit 3	0.00E+00	9.64E+04	9.64E+04	9.64E+04	NULL	AS	P61758	VBP1
1204.1	Ubiquitin-conjugating enzyme E	0.00E+00	9.66E+04	9.66E+04	9.66E+04	NULL	AS	P49459	UBE2A
2033.1	Glycerol kinase	0.00E+00	9.69E+04	9.69E+04	9.69E+04	NULL	AS	F8WC39	GK
1436.1	Probable allantoicase	0.00E+00	9.75E+04	9.75E+04	9.75E+04	NULL	AS	Q8N6M5	ALLC
1084.1	Centrosomal protein POC5	0.00E+00	9.82E+04	9.82E+04	9.82E+04	NULL	AS	Q8NA72	POC5
1611.1	La-related protein 6	0.00E+00	9.83E+04	9.83E+04	9.83E+04	NULL	AS	Q9BRS8	LARP6

2206.1	Exonuclease 3'-5' domain-conta	0.00E+00	9.83E+04	9.83E+04	9.83E+04	NULL	AS	B7Z839	EXD1
3078.1	Macrophage erythroblast attac	0.00E+00	9.83E+04	9.83E+04	9.83E+04	NULL	AS	E7ESC7	MAEA
2408.1	Dimethylaniline monooxygenas	0.00E+00	9.93E+04	9.93E+04	9.93E+04	NULL	AS	B7Z3P4	FMO1
2198.1	Bifunctional methylenetetrahyd	0.00E+00	1.00E+05	1.00E+05	1.00E+05	NULL	AS	P13995	MTHFD2
2724.1	Growth arrest-specific protein 7	0.00E+00	1.01E+05	1.01E+05	1.01E+05	NULL	AS	O60861	GAS7
2839.1	Polycystic kidney disease protei	0.00E+00	1.01E+05	1.01E+05	1.01E+05	NULL	AS	Q8TDX9	PKD1L1
2915.1	Isoform 3 of Forkhead-associate	0.00E+00	1.01E+05	1.01E+05	1.01E+05	NULL	AS	B1AJZ9-3	FHAD1
3083.1	DENN domain-containing protei	0.00E+00	1.01E+05	1.01E+05	1.01E+05	NULL	AS	Q9ULE3	DENND2A
1123.1	Glutaryl-CoA dehydrogenase, m	0.00E+00	1.02E+05	1.02E+05	1.02E+05	NULL	AS	Q92947	GCDH
1819.1	SH3 and cysteine-rich domain-c	0.00E+00	1.02E+05	1.02E+05	1.02E+05	NULL	AS	Q96MF2	STAC3
2301.1	Kinesin-like protein KIF27	0.00E+00	1.02E+05	1.02E+05	1.02E+05	NULL	AS	Q86VH2	KIF27
3020.1	Isoform 5 of Afadin	0.00E+00	1.02E+05	1.02E+05	1.02E+05	NULL	AS	P55196-5	MLLT4
3069.1	Grancalcin	0.00E+00	1.03E+05	1.03E+05	1.03E+05	NULL	AS	P28676	GCA
1199.1	Isoform 2 of Splicing factor U2A	0.00E+00	1.04E+05	1.04E+05	1.04E+05	NULL	AS	Q01081-2	U2AF1
1568.1	V-type proton ATPase 116 kDa s	0.00E+00	1.05E+05	1.05E+05	1.05E+05	NULL	AS	Q9HBG4	ATP6V0A4
2810.1	Nucleolar protein of 40 kDa	0.00E+00	1.05E+05	1.05E+05	1.05E+05	NULL	AS	E7EPF0	ZCCHC17
2953.1	Arf-GAP with dual PH domain-c	0.00E+00	1.05E+05	1.05E+05	1.05E+05	NULL	AS	Q2V6Q1	CENTA2
996.1	Janus kinase and microtubule-in	0.00E+00	1.06E+05	1.06E+05	1.06E+05	NULL	AS	Q5VZ66	JAKMIP3
1421.1	C-C motif chemokine 5	0.00E+00	1.06E+05	1.06E+05	1.06E+05	NULL	AS	P13501	CCL5
2167.1	Dopamine beta-hydroxylase	0.00E+00	1.06E+05	1.06E+05	1.06E+05	NULL	AS	P09172	DBH
1188.1	Transmembrane protein 131	0.00E+00	1.07E+05	1.07E+05	1.07E+05	NULL	AS	Q92545	TMEM131
2488.1	Laminin subunit alpha-3	0.00E+00	1.07E+05	1.07E+05	1.07E+05	NULL	AS	Q16787	LAMA3
2596.1	Periostin	0.00E+00	1.07E+05	1.07E+05	1.07E+05	NULL	AS	Q15063	POSTN
717.1	Histone H1.5	0.00E+00	1.08E+05	1.08E+05	1.08E+05	NULL	AS	P16401	HIST1H1B
1189.1	T-cell surface protein tactile	0.00E+00	1.08E+05	1.08E+05	1.08E+05	NULL	AS	P40200	CD96
1614.1	Cancer/testis antigen 75	0.00E+00	1.08E+05	1.08E+05	1.08E+05	NULL	AS	Q6PK30	CT75
1622.1	Cytoplasmic polyadenylation ele	0.00E+00	1.08E+05	1.08E+05	1.08E+05	NULL	AS	Q17RY0	CPEB4
2038.1	Podoplanin	0.00E+00	1.08E+05	1.08E+05	1.08E+05	NULL	AS	D6RH07	PDPN
2093.1	Inositol polyphosphate-5-phosp	0.00E+00	1.08E+05	1.08E+05	1.08E+05	NULL	AS	B1ARF3	INPP5B
2775.1	Protein NipSnap homolog 2	0.00E+00	1.08E+05	1.08E+05	1.08E+05	NULL	AS	O75323	GBAS
2889.1	Zinc finger protein 608	0.00E+00	1.08E+05	1.08E+05	1.08E+05	NULL	AS	Q9ULD9	ZNF608
3153.1	Protein FAM83G	0.00E+00	1.08E+05	1.08E+05	1.08E+05	NULL	AS	A6ND36	FAM83G
1864.1	ATP-dependent DNA helicase Q	0.00E+00	1.09E+05	1.09E+05	1.09E+05	NULL	AS	O94762	RECQL5
2333.1	Phakinin	0.00E+00	1.09E+05	1.09E+05	1.09E+05	NULL	AS	Q13515	BFSP2
3053.1	Thiosulfate sulfurtransferase/rh	0.00E+00	1.09E+05	1.09E+05	1.09E+05	NULL	AS	Q5T7W7	TSTD2

1224.1	HCF N-terminal chain 5	0.00E+00	1.10E+05	1.10E+05	1.10E+05	NULL	AS	A6NEM2	HCFC1
1629.1	F-box/LRR-repeat protein 14	0.00E+00	1.11E+05	1.11E+05	1.11E+05	NULL	AS	Q8N1E6	FBXL14
2446.1	Lipolysis-stimulated lipoprotein	0.00E+00	1.11E+05	1.11E+05	1.11E+05	NULL	AS	B4DKL4	LSR
2778.1	Probable global transcription ac	0.00E+00	1.11E+05	1.11E+05	1.11E+05	NULL	AS	P28370	SMARCA1
3201.1	Serpin B8	0.00E+00	1.11E+05	1.11E+05	1.11E+05	NULL	AS	P50452	SERPINB8
908.1	AP-2 complex subunit mu	0.00E+00	1.12E+05	1.12E+05	1.12E+05	NULL	AS	E9PFW3	AP2M1
1179.1	Isoform 3 of Serine/threonine-p	0.00E+00	1.12E+05	1.12E+05	1.12E+05	NULL	AS	Q96PY6-3	NEK1
1686.1	Exportin-6	0.00E+00	1.12E+05	1.12E+05	1.12E+05	NULL	AS	Q96QU8	XPO6
756.1	Coproporphyrinogen-III oxidase,	0.00E+00	1.13E+05	1.13E+05	1.13E+05	NULL	AS	P36551	CPOX
1895.1	Filamin A-interacting protein 1-l	0.00E+00	1.13E+05	1.13E+05	1.13E+05	NULL	AS	Q4L180	FILIP1L
1906.1	Sonic hedgehog protein	0.00E+00	1.13E+05	1.13E+05	1.13E+05	NULL	AS	Q15465	SHH
2401.1	Isoform 2 of Bromodomain-cont	0.00E+00	1.13E+05	1.13E+05	1.13E+05	NULL	AS	O95696-2	BRD1
1234.1	Prolow-density lipoprotein rece	0.00E+00	1.14E+05	1.14E+05	1.14E+05	NULL	AS	Q07954	LRP1
2649.1	Protein polybromo-1	0.00E+00	1.14E+05	1.14E+05	1.14E+05	NULL	AS	Q86U86	PBRM1
3.7	Keratin, type II cytoskeletal 1b	0.00E+00	1.16E+05	1.16E+05	1.16E+05	NULL	AS	Q7Z794	KRT77
787.1	Probable ATP-dependent RNA h	0.00E+00	1.16E+05	1.16E+05	1.16E+05	NULL	AS	Q9BUQ8	DDX23
3190.1	CAP-Gly domain-containing link	0.00E+00	1.16E+05	1.16E+05	1.16E+05	NULL	AS	P30622	CLIP1
1337.1	Ubiquitin carboxyl-terminal hyd	0.00E+00	1.17E+05	1.17E+05	1.17E+05	NULL	AS	Q70EL4	USP43
1448.1	Activated CDC42 kinase 1	0.00E+00	1.17E+05	1.17E+05	1.17E+05	NULL	AS	C9J1X3	TNK2
1498.1	Vesicle transport through intera	0.00E+00	1.17E+05	1.17E+05	1.17E+05	NULL	AS	Q9UEU0	VTI1B
2609.1	Protein kinase C theta type	0.00E+00	1.17E+05	1.17E+05	1.17E+05	NULL	AS	Q04759	PRKCQ
2806.1	Pleckstrin homology domain-co	0.00E+00	1.17E+05	1.17E+05	1.17E+05	NULL	AS	Q8IVE3	PLEKHH2
1518.1	Protein unc-13 homolog C	0.00E+00	1.18E+05	1.18E+05	1.18E+05	NULL	AS	F5H090	UNC13C
1780.1	Serine/threonine-protein kinase	0.00E+00	1.18E+05	1.18E+05	1.18E+05	NULL	AS	Q7L7X3	TAOK1
2390.1	VPS10 domain-containing recep	0.00E+00	1.18E+05	1.18E+05	1.18E+05	NULL	AS	Q96PQ0	SORCS2
2584.1	Isoform 2 of C-type lectin doma	0.00E+00	1.18E+05	1.18E+05	1.18E+05	NULL	AS	A5D8T8-2	CLEC18A
2251.1	Beta-ureidopropionase	0.00E+00	1.19E+05	1.19E+05	1.19E+05	NULL	AS	Q9UBR1	UPB1
1212.1	Isoform 2 of mRNA cap guanine	0.00E+00	1.20E+05	1.20E+05	1.20E+05	NULL	AS	O43148-2	RNMT
2505.1	Histone acetyltransferase p300	0.00E+00	1.20E+05	1.20E+05	1.20E+05	NULL	AS	Q09472	EP300
2919.1	Pro-epidermal growth factor	0.00E+00	1.20E+05	1.20E+05	1.20E+05	NULL	AS	P01133	EGF
1194.1	Protein PML	0.00E+00	1.21E+05	1.21E+05	1.21E+05	NULL	AS	P29590	PML
2440.1	Isoform 2 of Plexin-A2	0.00E+00	1.21E+05	1.21E+05	1.21E+05	NULL	AS	O75051-2	PLXNA2
1425.1	Glycogen [starch] synthase, mus	0.00E+00	1.23E+05	1.23E+05	1.23E+05	NULL	AS	F5H1N8	GYS1
1717.1	Isoform 2 of Acid-sensing ion ch	0.00E+00	1.23E+05	1.23E+05	1.23E+05	NULL	AS	Q16515-2	ASIC2
3136.1	Tektin-5	0.00E+00	1.23E+05	1.23E+05	1.23E+05	NULL	AS	Q96M29	TEKT5

839.1	26S protease regulatory subunit	0.00E+00	1.24E+05	1.24E+05	1.24E+05	NULL	AS	P62191	PSMC1
944.1	Serine racemase	0.00E+00	1.24E+05	1.24E+05	1.24E+05	NULL	AS	Q9GZT4	SRR
1605.1	Ribosome-recycling factor, mito	0.00E+00	1.24E+05	1.24E+05	1.24E+05	NULL	AS	Q96E11	MRRF
1735.1	Limbic system-associated memb	0.00E+00	1.24E+05	1.24E+05	1.24E+05	NULL	AS	F5H5G1	LSAMP
2452.1	Isoform 3 of CD99 antigen-like p	0.00E+00	1.24E+05	1.24E+05	1.24E+05	NULL	AS	Q8TCZ2-3	CD99L2
3080.1	Protein transport protein Sec31	0.00E+00	1.24E+05	1.24E+05	1.24E+05	NULL	AS	D6RAB3	SEC31A
1372.1	Ubiquitin carboxyl-terminal hyd	0.00E+00	1.25E+05	1.25E+05	1.25E+05	NULL	AS	Q8NB14	USP38
1208.1	Glycerophosphocholine phosph	0.00E+00	1.26E+05	1.26E+05	1.26E+05	NULL	AS	Q9NPB8	GPCPD1
1902.1	Transcription factor 25	0.00E+00	1.27E+05	1.27E+05	1.27E+05	NULL	AS	Q9BQ70	TCF25
2310.1	Copine-9	0.00E+00	1.27E+05	1.27E+05	1.27E+05	NULL	AS	Q8IYJ1	CPNE9
2664.1	26S proteasome non-ATPase re	0.00E+00	1.27E+05	1.27E+05	1.27E+05	NULL	AS	O00232	PSMD12
2887.1	Rho guanine nucleotide exchan	0.00E+00	1.27E+05	1.27E+05	1.27E+05	NULL	AS	Q12774	ARHGEF5
2932.1	Arginine and glutamate-rich pro	0.00E+00	1.27E+05	1.27E+05	1.27E+05	NULL	AS	Q9NWB6	ARGLU1
690.1	Ester hydrolase C11orf54	0.00E+00	1.28E+05	1.28E+05	1.28E+05	NULL	AS	Q9H0W9	C11orf54
1926.1	Isoform 2 of Zinc finger protein	0.00E+00	1.28E+05	1.28E+05	1.28E+05	NULL	AS	Q8NEA6-2	GLIS3
2574.1	Probable lipid phosphate phosp	0.00E+00	1.28E+05	1.28E+05	1.28E+05	NULL	AS	Q8NBV4	PPAPDC3
2079.1	RNA-binding E3 ubiquitin-protei	0.00E+00	1.29E+05	1.29E+05	1.29E+05	NULL	AS	Q5U5Q3	MEX3C
2418.1	Protein FAM184A	0.00E+00	1.29E+05	1.29E+05	1.29E+05	NULL	AS	Q8NB25	FAM184A
2433.1	Kelch-like protein 22	0.00E+00	1.29E+05	1.29E+05	1.29E+05	NULL	AS	Q53GT1	KLHL22
1464.1	Phenylalanine-4-hydroxylase	0.00E+00	1.30E+05	1.30E+05	1.30E+05	NULL	AS	P00439	PAH
1474.1	Small nuclear ribonucleoprotein	0.00E+00	1.30E+05	1.30E+05	1.30E+05	NULL	AS	P62318	SNRPD3
1538.1	PHD finger protein 10	0.00E+00	1.30E+05	1.30E+05	1.30E+05	NULL	AS	Q8WUB8	PHF10
2796.1	Microcephalin	0.00E+00	1.30E+05	1.30E+05	1.30E+05	NULL	AS	Q8NEM0	MCPH1
1726.1	Isoform 3 of FLYWCH-type zinc f	0.00E+00	1.31E+05	1.31E+05	1.31E+05	NULL	AS	Q4VC44-3	FLYWCH1
2256.1	Calcium-transporting ATPase ty	0.00E+00	1.31E+05	1.31E+05	1.31E+05	NULL	AS	E7ES94	ATP2C2
2545.1	Hydroxylysine kinase	0.00E+00	1.31E+05	1.31E+05	1.31E+05	NULL	AS	A2RU49	AGPHD1
2601.1	Dystrophin	0.00E+00	1.32E+05	1.32E+05	1.32E+05	NULL	AS	P11532	DMD
3137.1	Isoform 4 of DNA topoisomeras	0.00E+00	1.32E+05	1.32E+05	1.32E+05	NULL	AS	P11388-4	TOP2A
1118.1	Lysosomal alpha-glucosidase	0.00E+00	1.34E+05	1.34E+05	1.34E+05	NULL	AS	P10253	GAA
1972.1	Sodium channel protein type 9 s	0.00E+00	1.34E+05	1.34E+05	1.34E+05	NULL	AS	E9PBA5	SCN9A
736.1	RNA-binding protein PNO1	0.00E+00	1.35E+05	1.35E+05	1.35E+05	NULL	AS	Q9NRX1	PNO1
1664.1	Beta-taxilin	0.00E+00	1.35E+05	1.35E+05	1.35E+05	NULL	AS	Q8N3L3	TXLNB
2558.1	Malcavernin	0.00E+00	1.35E+05	1.35E+05	1.35E+05	NULL	AS	Q9BSQ5	CCM2
2567.1	Protein FAM133B	0.00E+00	1.35E+05	1.35E+05	1.35E+05	NULL	AS	Q5BKY9	FAM133B
2718.1	Alpha-(1,6)-fucosyltransferase	0.00E+00	1.35E+05	1.35E+05	1.35E+05	NULL	AS	Q9BYC5	FUT8

2634.1	Protein LOC642778	0.00E+00	1.36E+05	1.36E+05	1.36E+05	NULL	AS	E9PJ88	LOC642778
1153.1	Dedicator of cytokinesis protein	0.00E+00	1.37E+05	1.37E+05	1.37E+05	NULL	AS	A6NIW2	DOCK11
1739.1	DNA endonuclease RBBP8	0.00E+00	1.37E+05	1.37E+05	1.37E+05	NULL	AS	I6L8A6	RBBP8
1938.1	Catenin beta-1	0.00E+00	1.37E+05	1.37E+05	1.37E+05	NULL	AS	P35222	CTNNB1
2432.1	Zinc finger protein 398	0.00E+00	1.37E+05	1.37E+05	1.37E+05	NULL	AS	B4DXA9	ZNF398
2685.1	Alpha-mannosidase 2	0.00E+00	1.37E+05	1.37E+05	1.37E+05	NULL	AS	Q16706	MAN2A1
3219.1	Vasohibin-1	0.00E+00	1.37E+05	1.37E+05	1.37E+05	NULL	AS	G3V4N9	VASH1
2948.1	Protein FAM3D	0.00E+00	1.38E+05	1.38E+05	1.38E+05	NULL	AS	Q96BQ1	FAM3D
1352.1	Glycine cleavage system H prote	0.00E+00	1.39E+05	1.39E+05	1.39E+05	NULL	AS	P23434	GCSH
3066.1	WD repeat-containing protein K	0.00E+00	1.39E+05	1.39E+05	1.39E+05	NULL	AS	A6NE52	KIAA1875
1452.1	Cystic fibrosis transmembrane c	0.00E+00	1.40E+05	1.40E+05	1.40E+05	NULL	AS	P13569	CFTR
2219.1	ATP-dependent RNA helicase DI	0.00E+00	1.40E+05	1.40E+05	1.40E+05	NULL	AS	Q9NVP1	DDX18
2342.1	Olfactory receptor 1A2	0.00E+00	1.40E+05	1.40E+05	1.40E+05	NULL	AS	Q9Y585	OR1A2
1100.1	Ribonuclease P protein subunit	0.00E+00	1.40E+05	1.40E+05	1.40E+05	NULL	AS	P78346	RPP30
945.1	Zinc finger protein 709	0.00E+00	1.42E+05	1.42E+05	1.42E+05	NULL	AS	Q8N972	ZNF709
1492.1	Isoform 3 of Leucine-rich repeat	0.00E+00	1.42E+05	1.42E+05	1.42E+05	NULL	AS	Q8ND23-3	LRRC16B
1209.1	Isoform 2 of Ubiquitin carboxyl-	0.00E+00	1.44E+05	1.44E+05	1.44E+05	NULL	AS	Q14694-2	USP10
1344.1	Pyruvate dehydrogenase E1 con	0.00E+00	1.44E+05	1.44E+05	1.44E+05	NULL	AS	P11177	PDHB
2385.1	Arf-GAP with coiled-coil, ANK re	0.00E+00	1.44E+05	1.44E+05	1.44E+05	NULL	AS	Q15027	ACAP1
2807.1	Olfactory receptor 2C3	0.00E+00	1.44E+05	1.44E+05	1.44E+05	NULL	AS	Q8N628	OR2C3
1756.1	Isoform 9 of Multidrug resistanc	0.00E+00	1.45E+05	1.45E+05	1.45E+05	NULL	AS	P33527-9	ABCC1
2233.1	Alstrom syndrome protein 1	0.00E+00	1.45E+05	1.45E+05	1.45E+05	NULL	AS	Q8TCU4	ALMS1
2320.1	Isoform 3 of Granulocyte colony	0.00E+00	1.45E+05	1.45E+05	1.45E+05	NULL	AS	Q99062-3	CSF3R
2917.1	Serine/threonine-protein kinase	0.00E+00	1.45E+05	1.45E+05	1.45E+05	NULL	AS	D6RBG5	NEK1
2907.1	Geranylgeranyl transferase type	0.00E+00	1.46E+05	1.46E+05	1.46E+05	NULL	AS	Q92696	RABGGTA
1809.1	NEDD4-binding protein 2	0.00E+00	1.48E+05	1.48E+05	1.48E+05	NULL	AS	Q86UW6	N4BP2
1077.1	ATP-binding cassette sub-family	0.00E+00	1.49E+05	1.49E+05	1.49E+05	NULL	AS	C9JQE6	ABCA8
2662.1	Isoform 2 of Cactin	0.00E+00	1.49E+05	1.49E+05	1.49E+05	NULL	AS	Q8WUQ7-	CACTIN
1985.1	Acid trehalase-like protein 1	0.00E+00	1.50E+05	1.50E+05	1.50E+05	NULL	AS	E7EMA9	ATHL1
2194.1	Olfactory receptor 2M2	0.00E+00	1.51E+05	1.51E+05	1.51E+05	NULL	AS	Q96R28	OR2M2
2503.1	Ryanodine receptor 1	0.00E+00	1.52E+05	1.52E+05	1.52E+05	NULL	AS	P21817	RYR1
3218.1	Meiosis arrest female protein 1	0.00E+00	1.52E+05	1.52E+05	1.52E+05	NULL	AS	Q9Y4F3	KIAA0430
854.1	High mobility group nucleosome	0.00E+00	1.53E+05	1.53E+05	1.53E+05	NULL	AS	O00479	HMGN4
1386.1	Zinc finger protein 622	0.00E+00	1.53E+05	1.53E+05	1.53E+05	NULL	AS	Q969S3	ZNF622
1528.1	Serine incorporator 4	0.00E+00	1.53E+05	1.53E+05	1.53E+05	NULL	AS	A6NM42	SERINC4

1579.1	SEC14-like protein 4	0.00E+00	1.53E+05	1.53E+05	1.53E+05	NULL	AS	Q9UDX3	SEC14L4
2443.1	RNA-binding protein 20	0.00E+00	1.53E+05	1.53E+05	1.53E+05	NULL	AS	Q5T481	RBM20
1454.1	Potassium voltage-gated channe	0.00E+00	1.54E+05	1.54E+05	1.54E+05	NULL	AS	Q14721	KCNB1
1626.1	Ribosomal RNA processing prot	0.00E+00	1.54E+05	1.54E+05	1.54E+05	NULL	AS	Q14684	RRP1B
2069.1	Testosterone 17-beta-dehydrog	0.00E+00	1.54E+05	1.54E+05	1.54E+05	NULL	AS	P37058	HSD17B3
2570.1	snRNA-activating protein compl	0.00E+00	1.54E+05	1.54E+05	1.54E+05	NULL	AS	Q16533	SNAPC1
2593.1	Isoform 2 of Kynurenine/alpha-a	0.00E+00	1.54E+05	1.54E+05	1.54E+05	NULL	AS	Q8N5Z0-2	AADAT
3161.1	Retinoblastoma-like protein 2	0.00E+00	1.54E+05	1.54E+05	1.54E+05	NULL	AS	Q08999	RBL2
1196.1	Isoform 4 of Thiosulfate sulfurtr	0.00E+00	1.55E+05	1.55E+05	1.55E+05	NULL	AS	Q8NFU3-4	TSTD1
2297.1	Interferon-induced guanylate-bi	0.00E+00	1.55E+05	1.55E+05	1.55E+05	NULL	AS	P32455	GBP1
2672.1	Lipoyltransferase 1, mitochondr	0.00E+00	1.55E+05	1.55E+05	1.55E+05	NULL	AS	Q9Y234	LIPT1
2321.1	ATPase, Ca++ transporting, type	0.00E+00	1.55E+05	1.55E+05	1.55E+05	NULL	AS	P98194	ATP2C1
2175.1	E3 UFM1-protein ligase 1	0.00E+00	1.56E+05	1.56E+05	1.56E+05	NULL	AS	O94874	UFL1
2439.1	Glucagon-like peptide 2 recepto	0.00E+00	1.56E+05	1.56E+05	1.56E+05	NULL	AS	O95838	GLP2R
2666.1	Transcriptional repressor NF-X1	0.00E+00	1.56E+05	1.56E+05	1.56E+05	NULL	AS	Q12986	NFX1
632.1	CLIP-associating protein 2	0.00E+00	1.57E+05	1.57E+05	1.57E+05	NULL	AS	F5H3X0	CLASP2
1911.1	Cystatin-F	0.00E+00	1.57E+05	1.57E+05	1.57E+05	NULL	AS	O76096	CST7
1971.1	REST corepressor 2	0.00E+00	1.57E+05	1.57E+05	1.57E+05	NULL	AS	Q8IZ40	RCOR2
2293.1	Isoform 2 of Cytochrome P450 4	0.00E+00	1.57E+05	1.57E+05	1.57E+05	NULL	AS	P13584-2	CYP4B1
3115.1	Arf-GAP with GTPase, ANK repe	0.00E+00	1.57E+05	1.57E+05	1.57E+05	NULL	AS	E7EUN2	AGAP1
2633.1	Meckel syndrome type 1 protei	0.00E+00	1.58E+05	1.58E+05	1.58E+05	NULL	AS	Q9NXB0	MKS1
1113.1	Retinoblastoma-like protein 1	0.00E+00	1.59E+05	1.59E+05	1.59E+05	NULL	AS	P28749	RBL1
2926.1	Glutamate--cysteine ligase regu	0.00E+00	1.60E+05	1.60E+05	1.60E+05	NULL	AS	P48507	GCLM
3045.1	DNA polymerase beta	0.00E+00	1.60E+05	1.60E+05	1.60E+05	NULL	AS	P06746	POLB
1957.1	Low-density lipoprotein recepto	0.00E+00	1.61E+05	1.61E+05	1.61E+05	NULL	AS	H0YMD1	LDLR
2084.1	Serine/arginine-rich splicing fact	0.00E+00	1.61E+05	1.61E+05	1.61E+05	NULL	AS	O75494	SRSF10
2996.1	NADH dehydrogenase [ubiquinc	0.00E+00	1.61E+05	1.61E+05	1.61E+05	NULL	AS	O43678	NDUFA2
2997.1	N-terminal kinase-like protein	0.00E+00	1.61E+05	1.61E+05	1.61E+05	NULL	AS	Q96KG9	SCYL1
2055.1	Retinol dehydrogenase 14	0.00E+00	1.62E+05	1.62E+05	1.62E+05	NULL	AS	Q9HBH5	RDH14
1707.1	Isoform 4 of Putative ribosomal	0.00E+00	1.63E+05	1.63E+05	1.63E+05	NULL	AS	P46087-4	NOP2
1769.1	DNA-binding protein A	0.00E+00	1.63E+05	1.63E+05	1.63E+05	NULL	AS	P16989	YBX3
2699.1	Major vault protein	0.00E+00	1.63E+05	1.63E+05	1.63E+05	NULL	AS	Q14764	MVP
2262.1	Homeobox protein goosecoid	0.00E+00	1.64E+05	1.64E+05	1.64E+05	NULL	AS	P56915	GSC
3041.1	HCG2008157	0.00E+00	1.64E+05	1.64E+05	1.64E+05	NULL	AS	Q96NP5	hCG_2008157
1844.1	ZNF507 protein	0.00E+00	1.65E+05	1.65E+05	1.65E+05	NULL	AS	B9EGE7	ZNF507

2170.1	IQ calmodulin-binding motif-cor	0.00E+00	1.65E+05	1.65E+05	1.65E+05	NULL	AS	Q15051	IQCB1
2334.1	HCG1780554	0.00E+00	1.65E+05	1.65E+05	1.65E+05	NULL	AS	Q5T4B6	TMSB4XP4
1678.1	Isoform 3 of MAM domain-cont	0.00E+00	1.66E+05	1.66E+05	1.66E+05	NULL	AS	Q7Z553-3	MDGA2
1998.1	Oxysterol-binding protein	0.00E+00	1.66E+05	1.66E+05	1.66E+05	NULL	AS	J3KPA3	OSBPL9
2836.1	Inositol-trisphosphate 3-kinase	0.00E+00	1.66E+05	1.66E+05	1.66E+05	NULL	AS	P27987	ITPKB
3203.1	Protein diaphanous homolog 3	0.00E+00	1.66E+05	1.66E+05	1.66E+05	NULL	AS	Q9NSV4	DIAPH3
1564.1	Carnitine O-palmitoyltransferas	0.00E+00	1.67E+05	1.67E+05	1.67E+05	NULL	AS	P23786	CPT2
1954.1	Phospholipase A-2-activating pr	0.00E+00	1.67E+05	1.67E+05	1.67E+05	NULL	AS	Q9Y263	PLAA
2423.1	Protein FAM71A	0.00E+00	1.68E+05	1.68E+05	1.68E+05	NULL	AS	Q8IYT1	FAM71A
1117.1	DnaJ homolog subfamily B mem	0.00E+00	1.69E+05	1.69E+05	1.69E+05	NULL	AS	P25685	DNAJB1
1508.1	DnaJ homolog subfamily C mem	0.00E+00	1.69E+05	1.69E+05	1.69E+05	NULL	AS	Q13217	DNAJC3
1704.1	Isoform 7 of Ras-specific guanin	0.00E+00	1.69E+05	1.69E+05	1.69E+05	NULL	AS	Q5JS13-7	RALGPS1
1328.1	Extracellular matrix protein FRA	0.00E+00	1.69E+05	1.69E+05	1.69E+05	NULL	AS	Q86XX4	FRAS1
2490.1	Cell division cycle-associated pr	0.00E+00	1.70E+05	1.70E+05	1.70E+05	NULL	AS	Q99618	CDCA3
2483.1	Isoform 6 of Tyrosine-protein p	0.00E+00	1.71E+05	1.71E+05	1.71E+05	NULL	AS	Q4JDL3-6	PTPN20A
1243.1	Isoform 2 of Merlin	0.00E+00	1.72E+05	1.72E+05	1.72E+05	NULL	AS	P35240-2	NF2
1868.1	GRAM domain-containing prote	0.00E+00	1.72E+05	1.72E+05	1.72E+05	NULL	AS	Q8IYS0	GRAMD1C
1244.1	Phosphorylase b kinase regulat	0.00E+00	1.73E+05	1.73E+05	1.73E+05	NULL	AS	P46019	PHKA2
1392.1	Carboxypeptidase E	0.00E+00	1.74E+05	1.74E+05	1.74E+05	NULL	AS	P16870	CPE
799.1	L-xylulose reductase	0.00E+00	1.75E+05	1.75E+05	1.75E+05	NULL	AS	Q7Z4W1	DCXR
1882.1	REST corepressor 3	0.00E+00	1.76E+05	1.76E+05	1.76E+05	NULL	AS	B4DV59	RCOR3
2204.1	28S ribosomal protein S18b, mit	0.00E+00	1.76E+05	1.76E+05	1.76E+05	NULL	AS	Q9Y676	MRPS18B
2683.1	WD repeat-containing protein 2	0.00E+00	1.76E+05	1.76E+05	1.76E+05	NULL	AS	Q64LD2	WDR25
657.1	Isoform 4 of PCI domain-contair	0.00E+00	1.77E+05	1.77E+05	1.77E+05	NULL	AS	Q5JVF3-4	PCID2
2536.1	Prefoldin subunit 4	0.00E+00	1.79E+05	1.79E+05	1.79E+05	NULL	AS	E9PQY2	PFDN4
1561.1	Pregnancy zone protein	0.00E+00	1.80E+05	1.80E+05	1.80E+05	NULL	AS	P20742	PZP
2720.1	Syntaxin-4	0.00E+00	1.80E+05	1.80E+05	1.80E+05	NULL	AS	Q12846	STX4
1109.1	Receptor-type tyrosine-protein	0.00E+00	1.81E+05	1.81E+05	1.81E+05	NULL	AS	Q15256	PTPRR
2936.1	ATP-binding cassette sub-family	0.00E+00	1.81E+05	1.81E+05	1.81E+05	NULL	AS	E7ETD3	ABCA5
2444.1	ADAMTS-like 2	0.00E+00	1.82E+05	1.82E+05	1.82E+05	NULL	AS	B1B0D4	ADAMTSL2
1682.1	Leucine-rich repeat-containing	0.00E+00	1.84E+05	1.84E+05	1.84E+05	NULL	AS	Q8IWT6	LRRC8A
1846.1	Protein EFR3 homolog B	0.00E+00	1.84E+05	1.84E+05	1.84E+05	NULL	AS	Q9Y2G0	EFR3B
2068.1	Liprin-alpha-3	0.00E+00	1.84E+05	1.84E+05	1.84E+05	NULL	AS	O75145	PPFIA3
674.1	Protein NipSnap homolog 3A	0.00E+00	1.85E+05	1.85E+05	1.85E+05	NULL	AS	Q9UFN0	NIPSNAP3A
3172.1	Isoform 5 of Serine/threonine-p	0.00E+00	1.85E+05	1.85E+05	1.85E+05	NULL	AS	Q8IWQ3-5	BRSK2

1505.1	Cyclin-dependent kinase 5	0.00E+00	1.86E+05	1.86E+05	1.86E+05	NULL	AS	Q00535	CDK5
2604.1	GC-rich sequence DNA-binding f	0.00E+00	1.86E+05	1.86E+05	1.86E+05	NULL	AS	P16383	GCFC2
2031.1	Isocitrate dehydrogenase [NAD]	0.00E+00	1.87E+05	1.87E+05	1.87E+05	NULL	AS	P50213	IDH3A
2589.1	Zinc finger matrin-type protein	0.00E+00	1.87E+05	1.87E+05	1.87E+05	NULL	AS	Q5H9K5	ZMAT1
2945.1	Isoform 2 of SWI/SNF-related m	0.00E+00	1.87E+05	1.87E+05	1.87E+05	NULL	AS	Q9H4L7-2	SMARCAD1
1322.1	Elongator complex protein 3	0.00E+00	1.88E+05	1.88E+05	1.88E+05	NULL	AS	Q9H9T3	ELP3
1406.1	A disintegrin and metalloprotei	0.00E+00	1.90E+05	1.90E+05	1.90E+05	NULL	AS	O75173	ADAMTS4
3052.1	Zinc finger protein 672	0.00E+00	1.90E+05	1.90E+05	1.90E+05	NULL	AS	Q499Z4	ZNF672
2143.1	Isoform 3 of Polypyrimidine trac	0.00E+00	1.91E+05	1.91E+05	1.91E+05	NULL	AS	P26599-3	PTBP1
2902.1	RCC1 domain-containing protei	0.00E+00	1.91E+05	1.91E+05	1.91E+05	NULL	AS	A6NED2	RCCD1
1396.1	Fanconi anemia group M protei	0.00E+00	1.92E+05	1.92E+05	1.92E+05	NULL	AS	Q8IYD8	FANCM
1566.1	E3 SUMO-protein ligase CBX4	0.00E+00	1.94E+05	1.94E+05	1.94E+05	NULL	AS	O00257	CBX4
2607.1	Isoform 3 of Trinucleotide repea	0.00E+00	1.96E+05	1.96E+05	1.96E+05	NULL	AS	Q8NDV7-3	TNRC6A
3151.1	Spindle and kinetochore-associa	0.00E+00	1.96E+05	1.96E+05	1.96E+05	NULL	AS	Q8IX90	SKA3
767.1	Ribosome-binding protein 1	0.00E+00	1.97E+05	1.97E+05	1.97E+05	NULL	AS	Q9P2E9	RRBP1
1951.1	Ig-like V-type domain-containin	0.00E+00	1.97E+05	1.97E+05	1.97E+05	NULL	AS	A6NFU0	FAM187A
2021.1	Calcyphosin-2	0.00E+00	1.97E+05	1.97E+05	1.97E+05	NULL	AS	B9A061	CAPS2
2569.1	Isoform 13 of Dysferlin	0.00E+00	1.97E+05	1.97E+05	1.97E+05	NULL	AS	O75923-1	DYSF
1205.1	COP9 signalosome complex sub	0.00E+00	1.99E+05	1.99E+05	1.99E+05	NULL	AS	Q7L5N1	COPS6
1800.1	Growth factor receptor-bound	0.00E+00	1.99E+05	1.99E+05	1.99E+05	NULL	AS	Q13322	GRB10
1066.1	Cyclin-I	0.00E+00	2.00E+05	2.00E+05	2.00E+05	NULL	AS	Q14094	CCNI
1832.1	NADH dehydrogenase (ubiquino	0.00E+00	2.00E+05	2.00E+05	2.00E+05	NULL	AS	B4DW83	NDUFAF6
3058.1	Isoform 7 of Histone deacetylas	0.00E+00	2.00E+05	2.00E+05	2.00E+05	NULL	AS	Q9UKV0-7	HDAC9
2063.1	Mitochondrial calcium uniporte	0.00E+00	2.01E+05	2.01E+05	2.01E+05	NULL	AS	Q96AQ8	MCUR1
3121.1	GTPase IMAP family member 6	0.00E+00	2.01E+05	2.01E+05	2.01E+05	NULL	AS	Q6P9H5	GIMAP6
2088.1	Sterile alpha motif domain-cont	0.00E+00	2.02E+05	2.02E+05	2.02E+05	NULL	AS	Q8IVG5	SAMD9L
2197.1	Putative short-chain dehydroge	0.00E+00	2.02E+05	2.02E+05	2.02E+05	NULL	AS	A6NKP2	SDR42E2
2715.1	POU domain, class 4, transcripti	0.00E+00	2.02E+05	2.02E+05	2.02E+05	NULL	AS	Q01851	POU4F1
3026.1	Tripartite motif-containing prot	0.00E+00	2.03E+05	2.03E+05	2.03E+05	NULL	AS	Q14142	TRIM14
847.1	Lupus La protein	0.00E+00	2.04E+05	2.04E+05	2.04E+05	NULL	AS	P05455	SSB
1017.1	39S ribosomal protein L37, mito	0.00E+00	2.04E+05	2.04E+05	2.04E+05	NULL	AS	Q9BZE1	MRPL37
2891.1	Lysosomal alpha-mannosidase	0.00E+00	2.04E+05	2.04E+05	2.04E+05	NULL	AS	O00754	MAN2B1
1183.1	Forkhead box protein C2	0.00E+00	2.05E+05	2.05E+05	2.05E+05	NULL	AS	Q99958	FOXC2
1597.1	Transcription elongation factor	0.00E+00	2.05E+05	2.05E+05	2.05E+05	NULL	AS	Q7KZ85	SUPT6H
2927.1	Isoform 4 of RNA-binding protei	0.00E+00	2.06E+05	2.06E+05	2.06E+05	NULL	AS	P49756-4	RBM25

1956.1	Neural cell expressed, developm	0.00E+00	2.07E+05	2.07E+05	2.07E+05	NULL	AS	G3V3F1	NEDD1
2564.1	SH3 and multiple ankyrin repeat	0.00E+00	2.07E+05	2.07E+05	2.07E+05	NULL	AS	A6NHU9	SHANK2
1336.1	Golgin subfamily B member 1	0.00E+00	2.08E+05	2.08E+05	2.08E+05	NULL	AS	Q14789	GOLGB1
1167.1	TP53-regulating kinase	0.00E+00	2.09E+05	2.09E+05	2.09E+05	NULL	AS	Q96S44	TP53RK
3072.1	TATA-binding protein-associate	0.00E+00	2.09E+05	2.09E+05	2.09E+05	NULL	AS	O14981	BTAF1
1374.1	Protein monoglycylase TTLL8	0.00E+00	2.10E+05	2.10E+05	2.10E+05	NULL	AS	A6PVC2	TTLL8
2686.1	Inactive N-acetylated-alpha-link	0.00E+00	2.10E+05	2.10E+05	2.10E+05	NULL	AS	Q58DX5	NAALADL2
2875.1	Alpha-N-acetylgalactosaminide	0.00E+00	2.11E+05	2.11E+05	2.11E+05	NULL	AS	Q9NSC7	ST6GALNAC1
1052.1	HESB like domain containing 2, i	0.00E+00	2.12E+05	2.12E+05	2.12E+05	NULL	AS	B4DJI5	ISCA1
2492.1	Myosin light chain kinase 3	0.00E+00	2.12E+05	2.12E+05	2.12E+05	NULL	AS	Q32MK0	MYLK3
2470.1	Rho GTPase-activating protein 6	0.00E+00	2.14E+05	2.14E+05	2.14E+05	NULL	AS	O43182	ARHGAP6
3163.1	Putative FAM120A opposite stra	0.00E+00	2.14E+05	2.14E+05	2.14E+05	NULL	AS	Q5T036	FAM120AOS
1514.1	Butyrophilin subfamily 3 membe	0.00E+00	2.16E+05	2.16E+05	2.16E+05	NULL	AS	O00478	BTN3A3
813.1	Serine/arginine-rich splicing fact	0.00E+00	2.18E+05	2.18E+05	2.18E+05	NULL	AS	Q16629	SRSF7
2549.1	Cannabinoid receptor 2	0.00E+00	2.18E+05	2.18E+05	2.18E+05	NULL	AS	P34972	CNR2
1748.1	Nucleolar complex protein 4 ho	0.00E+00	2.19E+05	2.19E+05	2.19E+05	NULL	AS	Q9BVI4	NOC4L
1804.1	tRNA selenocysteine 1-associate	0.00E+00	2.19E+05	2.19E+05	2.19E+05	NULL	AS	Q9NX07	TRNAU1AP
684.1	Protein ABHD14A-ACY1	0.00E+00	2.21E+05	2.21E+05	2.21E+05	NULL	AS	C9JMV9	ABHD14A-ACY1
737.1	Kinesin-associated protein 3	0.00E+00	2.21E+05	2.21E+05	2.21E+05	NULL	AS	Q92845	KIFAP3
1101.1	Isoform 6 of Spermine oxidase	0.00E+00	2.21E+05	2.21E+05	2.21E+05	NULL	AS	Q9NWM0-	SMOX
2247.1	Centriolin	0.00E+00	2.21E+05	2.21E+05	2.21E+05	NULL	AS	Q7Z7A1	CNTRL
3099.1	Zinc finger protein 425	0.00E+00	2.21E+05	2.21E+05	2.21E+05	NULL	AS	Q6IV72	ZNF425
8.4	Heat shock 70 kDa protein 1A/1	0.00E+00	2.23E+05	2.23E+05	2.23E+05	NULL	AS	E7EP94	HSPA1A
648.1	N-alpha-acetyltransferase 10	0.00E+00	2.23E+05	2.23E+05	2.23E+05	NULL	AS	P41227	NAA10
814.1	Muscleblind-like protein 1	0.00E+00	2.23E+05	2.23E+05	2.23E+05	NULL	AS	Q9NR56	MBNL1
2448.1	Enhancer of rudimentary homol	0.00E+00	2.24E+05	2.24E+05	2.24E+05	NULL	AS	P84090	ERH
2393.1	SH3 and PX domain-containing	0.00E+00	2.28E+05	2.28E+05	2.28E+05	NULL	AS	Q5TCZ1	SH3PXD2A
3171.1	Plexin-D1	0.00E+00	2.28E+05	2.28E+05	2.28E+05	NULL	AS	Q9Y4D7	PLXND1
3226.1	Matrix metalloproteinase-20	0.00E+00	2.28E+05	2.28E+05	2.28E+05	NULL	AS	O60882	MMP20
1006.1	Nucleolar protein 58	0.00E+00	2.29E+05	2.29E+05	2.29E+05	NULL	AS	Q9Y2X3	NOP58
1468.1	Mitogen-activated protein kinas	0.00E+00	2.29E+05	2.29E+05	2.29E+05	NULL	AS	Q8IVH8	MAP4K3
2294.1	Ribonuclease H2 subunit C	0.00E+00	2.29E+05	2.29E+05	2.29E+05	NULL	AS	E9PN81	RNASEH2C
1604.1	ATP-dependent RNA helicase DH	0.00E+00	2.30E+05	2.30E+05	2.30E+05	NULL	AS	Q14562	DHX8
1887.1	Dynein heavy chain domain-con	0.00E+00	2.30E+05	2.30E+05	2.30E+05	NULL	AS	Q96M86	DNHD1
2030.1	Surfeit 4, isoform CRA_c	0.00E+00	2.30E+05	2.30E+05	2.30E+05	NULL	AS	B7Z6A4	SURF4

2137.1	RNA-binding protein 5	0.00E+00	2.30E+05	2.30E+05	2.30E+05	NULL	AS	P52756	RBM5
563.1	Nuclear inhibitor of protein pho	0.00E+00	2.31E+05	2.31E+05	2.31E+05	NULL	AS	Q12972	PPP1R8
1627.1	Protein FAM188B2	0.00E+00	2.33E+05	2.33E+05	2.33E+05	NULL	AS	A8MYZ0	FAM188B2
1512.1	Headcase protein homolog	0.00E+00	2.34E+05	2.34E+05	2.34E+05	NULL	AS	Q9UBI9	HECA
2273.1	M-phase phosphoprotein 9	0.00E+00	2.34E+05	2.34E+05	2.34E+05	NULL	AS	Q99550	MPHOSPH9
2077.1	Centrosomal protein of 290 kDa	0.00E+00	2.35E+05	2.35E+05	2.35E+05	NULL	AS	J3KNF5	CEP290
2195.1	Kinesin-like protein KIF12	0.00E+00	2.35E+05	2.35E+05	2.35E+05	NULL	AS	Q96FN5	KIF12
2511.1	E3 ubiquitin-protein ligase pelli	0.00E+00	2.35E+05	2.35E+05	2.35E+05	NULL	AS	Q96FA3	PELI1
1018.1	Dpy-30-like protein, isoform CR	0.00E+00	2.36E+05	2.36E+05	2.36E+05	NULL	AS	B4DIS3	LOC84661
1510.1	Ataxin-2	0.00E+00	2.36E+05	2.36E+05	2.36E+05	NULL	AS	Q99700	ATXN2
2999.1	Isoform 4 of Ankyrin repeat and	0.00E+00	2.36E+05	2.36E+05	2.36E+05	NULL	AS	Q9P2R3-4	ANKFY1
2403.1	Rho GTPase-activating protein 2	0.00E+00	2.37E+05	2.37E+05	2.37E+05	NULL	AS	Q5T5U3	ARHGAP21
595.1	Phosphatidylinositol-binding cla	0.00E+00	2.39E+05	2.39E+05	2.39E+05	NULL	AS	Q13492	PICALM
802.1	Lactotransferrin	0.00E+00	2.39E+05	2.39E+05	2.39E+05	NULL	AS	P02788	LTF
2965.1	Pecanex-like protein 1	0.00E+00	2.39E+05	2.39E+05	2.39E+05	NULL	AS	Q96RV3	PCNX
1371.1	WD repeat-containing and plan	0.00E+00	2.41E+05	2.41E+05	2.41E+05	NULL	AS	O95876	WDPCP
2258.1	Ribonuclease P protein subunit	0.00E+00	2.41E+05	2.41E+05	2.41E+05	NULL	AS	Q8N5L8	RPP25L
2694.1	Transient receptor potential cat	0.00E+00	2.42E+05	2.42E+05	2.42E+05	NULL	AS	E9PGK7	TRPM2
3267.1	GPI transamidase component PI	0.00E+00	2.42E+05	2.42E+05	2.42E+05	NULL	AS	Q969N2	PIGT
1042.1	Ribosome-releasing factor 2, mi	0.00E+00	2.43E+05	2.43E+05	2.43E+05	NULL	AS	Q969S9	GFM2
2769.1	Isoform 3 of Ran-binding protei	0.00E+00	2.43E+05	2.43E+05	2.43E+05	NULL	AS	Q86VV4-3	RANBP3L
1592.1	Isoform 3 of Acyl-coenzyme A sy	0.00E+00	2.44E+05	2.44E+05	2.44E+05	NULL	AS	Q6P461-3	ACSM6
1435.1	60S ribosomal protein L18a	0.00E+00	2.45E+05	2.45E+05	2.45E+05	NULL	AS	Q02543	RPL18A
2003.1	Disabled homolog 1	0.00E+00	2.45E+05	2.45E+05	2.45E+05	NULL	AS	O75553	DAB1
3103.1	Unconventional myosin-IXa	0.00E+00	2.45E+05	2.45E+05	2.45E+05	NULL	AS	H3BMM1	MYO9A
420.2	Long-chain-fatty-acid--CoA ligas	0.00E+00	2.46E+05	2.46E+05	2.46E+05	NULL	AS	D6RER0	ACSL1
2539.1	ADP-ribose pyrophosphatase, m	0.00E+00	2.46E+05	2.46E+05	2.46E+05	NULL	AS	Q9BW91	NUDT9
3051.1	Collagen alpha-1(VIII) chain	0.00E+00	2.47E+05	2.47E+05	2.47E+05	NULL	AS	P27658	COL8A1
3007.1	Signal transducer and activator	0.00E+00	2.48E+05	2.48E+05	2.48E+05	NULL	AS	P52630	STAT2
3229.1	Tetratricopeptide repeat protei	0.00E+00	2.50E+05	2.50E+05	2.50E+05	NULL	AS	Q8N584	TTC39C
2078.1	LIM/homeobox protein Lhx4	0.00E+00	2.51E+05	2.51E+05	2.51E+05	NULL	AS	Q969G2	LHX4
2453.1	Coenzyme Q-binding protein CC	0.00E+00	2.51E+05	2.51E+05	2.51E+05	NULL	AS	Q96MF6	COQ10A
781.1	Isoform 2 of Zinc finger and SCA	0.00E+00	2.52E+05	2.52E+05	2.52E+05	NULL	AS	Q8TBC5-2	ZSCAN18
2231.1	Protein GDF5OS, mitochondrial	0.00E+00	2.52E+05	2.52E+05	2.52E+05	NULL	AS	Q5U4N7	GDF5OS
2340.1	Isoform L' of Protein patched h	0.00E+00	2.52E+05	2.52E+05	2.52E+05	NULL	AS	Q13635-2	PTCH1

940.1	Calcium homeostasis endoplasn	0.00E+00	2.53E+05	2.53E+05	2.53E+05	NULL	AS	J3QK89	CHERP
1115.1	1-phosphatidylinositol 4,5-bisph	0.00E+00	2.53E+05	2.53E+05	2.53E+05	NULL	AS	Q9P212	PLCE1
1240.1	FERM domain-containing protei	0.00E+00	2.53E+05	2.53E+05	2.53E+05	NULL	AS	A2A2Y4	FRMD3
1274.1	Isoform 4 of Sterol regulatory el	0.00E+00	2.53E+05	2.53E+05	2.53E+05	NULL	AS	P36956-4	SREBF1
1983.1	Melanoma-associated antigen E	0.00E+00	2.53E+05	2.53E+05	2.53E+05	NULL	AS	Q9HCI5	MAGEE1
2228.1	DNA-directed RNA polymerase I	0.00E+00	2.53E+05	2.53E+05	2.53E+05	NULL	AS	P05423	POLR3D
2230.1	Beta-nerve growth factor	0.00E+00	2.53E+05	2.53E+05	2.53E+05	NULL	AS	P01138	NGF
1310.1	Insulin-like growth factor 2 mRN	0.00E+00	2.54E+05	2.54E+05	2.54E+05	NULL	AS	F8W930	IGF2BP2
1779.1	Contactin-2	0.00E+00	2.54E+05	2.54E+05	2.54E+05	NULL	AS	Q02246	CNTN2
140.2	Rab GDP dissociation inhibitor a	0.00E+00	2.55E+05	2.55E+05	2.55E+05	NULL	AS	P31150	GDI1
1577.1	Neuroligin-2	0.00E+00	2.55E+05	2.55E+05	2.55E+05	NULL	AS	Q8NFZ4	NLGN2
2544.1	Interleukin-12 receptor subunit	0.00E+00	2.55E+05	2.55E+05	2.55E+05	NULL	AS	Q99665	IL12RB2
3010.1	Cyclin-dependent kinase-like 4	0.00E+00	2.55E+05	2.55E+05	2.55E+05	NULL	AS	Q2NME9	CDKL4
2774.1	Nucleolar GTP-binding protein 1	0.00E+00	2.56E+05	2.56E+05	2.56E+05	NULL	AS	Q9BZE4	GTPBP4
758.1	Myelin expression factor 2	0.00E+00	2.57E+05	2.57E+05	2.57E+05	NULL	AS	Q9P2K5	MYEF2
806.1	Nuclear pore complex protein N	0.00E+00	2.57E+05	2.57E+05	2.57E+05	NULL	AS	P57740	NUP107
1630.1	Beta-crystallin B2	0.00E+00	2.57E+05	2.57E+05	2.57E+05	NULL	AS	P43320	CRYBB2
1266.1	Unconventional myosin-Vc	0.00E+00	2.58E+05	2.58E+05	2.58E+05	NULL	AS	Q9NQX4	MYO5C
3082.1	Proprotein convertase subtilisin	0.00E+00	2.58E+05	2.58E+05	2.58E+05	NULL	AS	Q8NBP7	PCSK9
3032.1	Putative olfactory receptor 4A8	0.00E+00	2.60E+05	2.60E+05	2.60E+05	NULL	AS	P0C604	OR4A8P
3144.1	Multidrug resistance protein 3	0.00E+00	2.60E+05	2.60E+05	2.60E+05	NULL	AS	P21439	ABCB4
1866.1	Protein spire homolog 2	0.00E+00	2.62E+05	2.62E+05	2.62E+05	NULL	AS	Q8WWL2	SPIRE2
3029.1	BAH and coiled-coil domain-con	0.00E+00	2.62E+05	2.62E+05	2.62E+05	NULL	AS	F8WBW8	BAHCC1
901.1	ADP-ribosylation factor-like prot	0.00E+00	2.64E+05	2.64E+05	2.64E+05	NULL	AS	Q96BM9	ARL8A
1184.1	Dipeptidyl peptidase 2	0.00E+00	2.64E+05	2.64E+05	2.64E+05	NULL	AS	Q9UHL4	DPP7
1999.1	DmX-like protein 1	0.00E+00	2.65E+05	2.65E+05	2.65E+05	NULL	AS	F5H269	DMXL1
2621.1	Isoform 2 of Neuronal tyrosine-p	0.00E+00	2.66E+05	2.66E+05	2.66E+05	NULL	AS	Q6ZVC0-2	NYAP1
2913.1	ATP-binding cassette sub-family	0.00E+00	2.66E+05	2.66E+05	2.66E+05	NULL	AS	Q86UK0	ABCA12
2116.1	Isoform MOP3 of Aryl hydrocarb	0.00E+00	2.67E+05	2.67E+05	2.67E+05	NULL	AS	O00327-7	ARNTL
3233.1	Clarin-2	0.00E+00	2.68E+05	2.68E+05	2.68E+05	NULL	AS	A0PK11	CLRN2
2632.1	Disheveled-associated activator	0.00E+00	2.71E+05	2.71E+05	2.71E+05	NULL	AS	Q9Y4D1	DAAM1
3059.1	Isoform 4 of Tensin-like C1 dom	0.00E+00	2.71E+05	2.71E+05	2.71E+05	NULL	AS	Q63HR2-4	TENC1
3213.1	Collagen alpha-1(XXV) chain	0.00E+00	2.71E+05	2.71E+05	2.71E+05	NULL	AS	Q9BXS0	COL25A1
2181.1	Leucine-rich repeat and fibrone	0.00E+00	2.72E+05	2.72E+05	2.72E+05	NULL	AS	Q9ULH4	LRFN2
3148.1	RNA-binding protein 28	0.00E+00	2.72E+05	2.72E+05	2.72E+05	NULL	AS	Q9NW13	RBM28

1150.1	Mannosyl-oligosaccharide 1,2-a	0.00E+00	2.73E+05	2.73E+05	2.73E+05	NULL	AS	P33908	MAN1A1
2087.1	Prolyl 4-hydroxylase subunit alp	0.00E+00	2.73E+05	2.73E+05	2.73E+05	NULL	AS	P13674	P4HA1
549.1	Isoform 2 of Catenin alpha-1	0.00E+00	2.74E+05	2.74E+05	2.74E+05	NULL	AS	P35221-2	CTNNA1
2323.1	Cell division cycle protein 123 h	0.00E+00	2.74E+05	2.74E+05	2.74E+05	NULL	AS	O75794	CDC123
1376.1	Chromosome transmission fidel	0.00E+00	2.75E+05	2.75E+05	2.75E+05	NULL	AS	E7EXA6	CHTF18
1221.1	Centromere/kinetochore protei	0.00E+00	2.77E+05	2.77E+05	2.77E+05	NULL	AS	O43264	ZW10
2186.1	Fibronectin type III domain-cont	0.00E+00	2.78E+05	2.78E+05	2.78E+05	NULL	AS	Q53EP0	FNDC3B
2657.1	Isoform 2 of Testis-expressed se	0.00E+00	2.79E+05	2.79E+05	2.79E+05	NULL	AS	Q8IWB9-2	TEX2
2222.1	Zinc finger protein 700	0.00E+00	2.80E+05	2.80E+05	2.80E+05	NULL	AS	Q9H0M5	ZNF700
2413.1	Zinc finger protein 664	0.00E+00	2.80E+05	2.80E+05	2.80E+05	NULL	AS	Q8N3J9	ZNF664
1258.1	Serine-rich coiled-coil domain-c	0.00E+00	2.81E+05	2.81E+05	2.81E+05	NULL	AS	Q9C0I3	CCSER1
1988.1	Small nuclear ribonucleoprotein	0.00E+00	2.81E+05	2.81E+05	2.81E+05	NULL	AS	P62304	SNRPE
2415.1	MICAL-like protein 1	0.00E+00	2.82E+05	2.82E+05	2.82E+05	NULL	AS	Q8N3F8	MICALL1
2981.1	Ral-GDS-related protein	0.00E+00	2.82E+05	2.82E+05	2.82E+05	NULL	AS	E9PH21	RGL4
2735.1	HLA class II histocompatibility a	0.00E+00	2.82E+05	2.82E+05	2.82E+05	NULL	AS	P04440	HLA_DPB1
1383.1	Structural maintenance of chro	0.00E+00	2.83E+05	2.83E+05	2.83E+05	NULL	AS	Q14683	SMC1A
1698.1	HCG2002594, isoform CRA_c	0.00E+00	2.83E+05	2.83E+05	2.83E+05	NULL	AS	G3XAH0	SEPT5
2200.1	B-cell linker protein	0.00E+00	2.83E+05	2.83E+05	2.83E+05	NULL	AS	Q8WV28	BLNK
3264.1	Nance-Horan syndrome protein	0.00E+00	2.83E+05	2.83E+05	2.83E+05	NULL	AS	Q6T4R5	NHS
1515.1	Tektin-4	0.00E+00	2.84E+05	2.84E+05	2.84E+05	NULL	AS	Q8WW24	TEKT4
2183.1	Isoform 2 of Ubiquitin thioester	0.00E+00	2.84E+05	2.84E+05	2.84E+05	NULL	AS	Q96FW1-2	OTUB1
2278.1	Cyclin C	0.00E+00	2.84E+05	2.84E+05	2.84E+05	NULL	AS	Q5JV82	CCNC
2040.1	Thyroid receptor-interacting pr	0.00E+00	2.85E+05	2.85E+05	2.85E+05	NULL	AS	Q15643	TRIP11
3261.1	Isoform H7 of Myeloperoxidase	0.00E+00	2.85E+05	2.85E+05	2.85E+05	NULL	AS	P05164-3	MPO
2962.1	Kinesin-like protein KIF17	0.00E+00	2.86E+05	2.86E+05	2.86E+05	NULL	AS	Q9P2E2	KIF17
3251.1	Kelch repeat and BTB domain-c	0.00E+00	2.87E+05	2.87E+05	2.87E+05	NULL	AS	Q8NFY9	KBTBD8
1519.1	Ubiquinone biosynthesis monoo	0.00E+00	2.91E+05	2.91E+05	2.91E+05	NULL	AS	G3V4A6	COQ6
963.1	Isoform 4 of Kinesin-like protein	0.00E+00	2.92E+05	2.92E+05	2.92E+05	NULL	AS	O00139-4	KIF2A
1377.1	3-hydroxyisobutyrate dehydrog	0.00E+00	2.92E+05	2.92E+05	2.92E+05	NULL	AS	P31937	HIBADH
2698.1	Four and a half LIM domains pr	0.00E+00	2.93E+05	2.93E+05	2.93E+05	NULL	AS	Q13642	FHL1
3258.1	Ankyrin-2	0.00E+00	2.93E+05	2.93E+05	2.93E+05	NULL	AS	Q01484	ANK2
3255.1	ER degradation-enhancing alph	0.00E+00	2.95E+05	2.95E+05	2.95E+05	NULL	AS	Q9BV94	EDEM2
281.2	High mobility group protein B2	0.00E+00	2.96E+05	2.96E+05	2.96E+05	NULL	AS	P26583	HMGB2
2026.1	Zinc finger protein 41	0.00E+00	2.96E+05	2.96E+05	2.96E+05	NULL	AS	P51814	ZNF41
2523.1	Acyl-coenzyme A thioesterase 8	0.00E+00	2.97E+05	2.97E+05	2.97E+05	NULL	AS	E9PIS4	ACOT8

1897.1	Mitotic checkpoint serine/threo	0.00E+00	2.98E+05	2.98E+05	2.98E+05	NULL	AS	O43683	BUB1
2802.1	Recombining binding protein su	0.00E+00	2.98E+05	2.98E+05	2.98E+05	NULL	AS	Q9UBG7	RBPJL
96.3	Far upstream element-binding	0.00E+00	3.00E+05	3.00E+05	3.00E+05	NULL	AS	Q96I24	FUBP3
1529.1	Zinc finger protein 292	0.00E+00	3.03E+05	3.03E+05	3.03E+05	NULL	AS	O60281	ZNF292
1790.1	Double-strand-break repair prot	0.00E+00	3.03E+05	3.03E+05	3.03E+05	NULL	AS	O60216	RAD21
2894.1	Receptor-transporting protein 1	0.00E+00	3.04E+05	3.04E+05	3.04E+05	NULL	AS	P59025	RTP1
1230.1	Acyl-coenzyme A thioesterase 1	0.00E+00	3.07E+05	3.07E+05	3.07E+05	NULL	AS	Q9NPJ3	ACOT13
2704.1	Proline-rich protein PRCC	0.00E+00	3.07E+05	3.07E+05	3.07E+05	NULL	AS	Q92733	PRCC
960.1	SH3 domain-binding glutamic ac	0.00E+00	3.08E+05	3.08E+05	3.08E+05	NULL	AS	Q9H299	SH3BGRL3
1747.1	Isoform 2 of Lysine-specific dem	0.00E+00	3.09E+05	3.09E+05	3.09E+05	NULL	AS	Q9UGL1-2	KDM5B
2028.1	Paired immunoglobulin-like typ	0.00E+00	3.09E+05	3.09E+05	3.09E+05	NULL	AS	Q9UKJ1	PILRA
2702.1	Isoform 2 of EVI5-like protein	0.00E+00	3.10E+05	3.10E+05	3.10E+05	NULL	AS	Q96CN4-2	EVI5L
3187.1	1-acyl-sn-glycerol-3-phosphate	0.00E+00	3.10E+05	3.10E+05	3.10E+05	NULL	AS	Q9NUQ2	AGPAT5
663.1	mRNA export factor	0.00E+00	3.11E+05	3.11E+05	3.11E+05	NULL	AS	P78406	RAE1
1173.1	Isoform 3 of Cyclin-Y	0.00E+00	3.12E+05	3.12E+05	3.12E+05	NULL	AS	Q8ND76-3	CCNY
1290.1	SRSF protein kinase 3	0.00E+00	3.14E+05	3.14E+05	3.14E+05	NULL	AS	E7ETV6	SRPK3
897.1	E3 ubiquitin-protein ligase TRIM	0.00E+00	3.15E+05	3.15E+05	3.15E+05	NULL	AS	Q8WV44	TRIM41
1542.1	Cullin-3	0.00E+00	3.15E+05	3.15E+05	3.15E+05	NULL	AS	Q13618	CUL3
2663.1	THUMP domain-containing prot	0.00E+00	3.17E+05	3.17E+05	3.17E+05	NULL	AS	J3KQB0	THUMPD1
1307.1	Protein SERAC1	0.00E+00	3.20E+05	3.20E+05	3.20E+05	NULL	AS	Q96JX3	SERAC1
3067.1	Isoform 2 of Roundabout homol	0.00E+00	3.20E+05	3.20E+05	3.20E+05	NULL	AS	Q9Y6N7-2	ROBO1
729.1	Heterogeneous nuclear ribonuc	0.00E+00	3.21E+05	3.21E+05	3.21E+05	NULL	AS	Q9BUJ2	HNRNPUL1
2128.1	Protein naked cuticle homolog 1	0.00E+00	3.21E+05	3.21E+05	3.21E+05	NULL	AS	Q969G9	NKD1
3197.1	Mitogen-activated protein kinas	0.00E+00	3.21E+05	3.21E+05	3.21E+05	NULL	AS	Q99683	MAP3K5
2954.1	Bromodomain-containing prote	0.00E+00	3.22E+05	3.22E+05	3.22E+05	NULL	AS	O60885	BRD4
1829.1	YY1-associated protein 1	0.00E+00	3.23E+05	3.23E+05	3.23E+05	NULL	AS	Q9H869	YY1AP1
2235.1	Isoform 2 of Rho guanine nucle	0.00E+00	3.25E+05	3.25E+05	3.25E+05	NULL	AS	Q9NR81-2	ARHGEF3
2848.1	Protein kinase C alpha type	0.00E+00	3.25E+05	3.25E+05	3.25E+05	NULL	AS	P17252	PRKCA
2740.1	Cerebellin-2	0.00E+00	3.26E+05	3.26E+05	3.26E+05	NULL	AS	Q8IUK8	CBLN2
2257.1	Myelin-associated oligodendroc	0.00E+00	3.27E+05	3.27E+05	3.27E+05	NULL	AS	G5E945	MOBP
1161.1	Coiled-coil-helix-coiled-coil-heli	0.00E+00	3.28E+05	3.28E+05	3.28E+05	NULL	AS	Q8N8C4	CHCHD5
3225.1	Transmembrane protease serin	0.00E+00	3.29E+05	3.29E+05	3.29E+05	NULL	AS	O60235	TMPRSS11D
2818.1	52 kDa repressor of the inhibito	0.00E+00	3.32E+05	3.32E+05	3.32E+05	NULL	AS	O43422	PRKRIR
2064.1	Isoform 2 of INO80 complex sub	0.00E+00	3.34E+05	3.34E+05	3.34E+05	NULL	AS	Q53TQ3-2	INO80D
2754.1	N-acetylated-alpha-linked acidic	0.00E+00	3.34E+05	3.34E+05	3.34E+05	NULL	AS	Q9Y3Q0	NAALAD2

1755.1	Leucine-rich PPR motif-containi	0.00E+00	3.36E+05	3.36E+05	3.36E+05	NULL	AS	P42704	LRPPRC
2528.1	Isoform 3 of Engulfment and cel	0.00E+00	3.37E+05	3.37E+05	3.37E+05	NULL	AS	Q92556-3	ELMO1
1807.1	Putative zinc finger protein 726	0.00E+00	3.38E+05	3.38E+05	3.38E+05	NULL	AS	Q15940	ZNF726P1
1086.1	Probable G-protein coupled rec	0.00E+00	3.41E+05	3.41E+05	3.41E+05	NULL	AS	O15354	GPR37
1320.1	Isoform 2 of A disintegrin and m	0.00E+00	3.42E+05	3.42E+05	3.42E+05	NULL	AS	Q8TE60-2	ADAMTS18
2419.1	Histone deacetylase 7	0.00E+00	3.42E+05	3.42E+05	3.42E+05	NULL	AS	J3KPH8	HDAC7
1916.1	Advanced glycosylation end pro	0.00E+00	3.42E+05	3.42E+05	3.42E+05	NULL	AS	Q15109	AGER
1144.1	Alpha-N-acetylglucosaminidase	0.00E+00	3.44E+05	3.44E+05	3.44E+05	NULL	AS	P54802	NAGLU
1753.1	Lamin-B1	0.00E+00	3.44E+05	3.44E+05	3.44E+05	NULL	AS	P20700	LMNB1
1861.1	Insulin gene enhancer protein I	0.00E+00	3.44E+05	3.44E+05	3.44E+05	NULL	AS	Q96A47	ISL2
1432.1	Sorbin and SH3 domain-contain	0.00E+00	3.44E+05	3.44E+05	3.44E+05	NULL	AS	O94875	SORBS2
3.5	Keratin, type II cuticular Hb4	0.00E+00	3.46E+05	3.46E+05	3.46E+05	NULL	AS	Q9NSB2	KRT84
1228.1	Synaptojanin-2	0.00E+00	3.47E+05	3.47E+05	3.47E+05	NULL	AS	O15056	SYNJ2
1226.1	Sentan	0.00E+00	3.48E+05	3.48E+05	3.48E+05	NULL	AS	C9JXY5	SNTN
3247.1	Ankyrin repeat domain-containi	0.00E+00	3.49E+05	3.49E+05	3.49E+05	NULL	AS	Q5CZ79	ANKRD20A8P
1588.1	Zinc finger protein 524	0.00E+00	3.50E+05	3.50E+05	3.50E+05	NULL	AS	Q96C55	ZNF524
2298.1	Hemoglobin subunit alpha	0.00E+00	3.50E+05	3.50E+05	3.50E+05	NULL	AS	P69905	HBA1
2903.1	Armadillo repeat protein delete	0.00E+00	3.50E+05	3.50E+05	3.50E+05	NULL	AS	O00192	ARVCF
3047.1	Versican core protein	0.00E+00	3.50E+05	3.50E+05	3.50E+05	NULL	AS	P13611	VCAN
1195.1	Probable E3 ubiquitin-protein li	0.00E+00	3.51E+05	3.51E+05	3.51E+05	NULL	AS	Q15751	HERC1
1940.1	Sorcin	0.00E+00	3.52E+05	3.52E+05	3.52E+05	NULL	AS	P30626	SRI
2734.1	Protocadherin beta-1	0.00E+00	3.52E+05	3.52E+05	3.52E+05	NULL	AS	Q9Y5F3	PCDHB1
3135.1	Protein Z-dependent protease i	0.00E+00	3.52E+05	3.52E+05	3.52E+05	NULL	AS	G3V2W1	SERPINA10
3243.1	Eukaryotic translation initiation	0.00E+00	3.53E+05	3.53E+05	3.53E+05	NULL	AS	Q9P2K8	EIF2AK4
1351.1	HERV-K_5q33.3 provirus ancest	0.00E+00	3.54E+05	3.54E+05	3.54E+05	NULL	AS	P10266	POK10
1185.1	Cyclin-D1-binding protein 1	0.00E+00	3.55E+05	3.55E+05	3.55E+05	NULL	AS	O95273	CCNDBP1
1909.1	Methyltransferase-like protein	0.00E+00	3.55E+05	3.55E+05	3.55E+05	NULL	AS	Q9BUU2	METTL22
1051.1	Kelch domain-containing protei	0.00E+00	3.59E+05	3.59E+05	3.59E+05	NULL	AS	Q9Y2U9	KLHDC2
1360.2	Isoform 2 of Myosin phosphata	0.00E+00	3.59E+05	3.59E+05	3.59E+05	NULL	AS	Q6WCQ1-	MPRIP
3110.1	Isoform 3 of Protein shisa-6 ho	0.00E+00	3.60E+05	3.60E+05	3.60E+05	NULL	AS	Q6ZSJ9-3	SHISA6
849.1	Cathepsin Z	0.00E+00	3.61E+05	3.61E+05	3.61E+05	NULL	AS	Q9UBR2	CTSZ
2931.1	NXPE family member 3	0.00E+00	3.61E+05	3.61E+05	3.61E+05	NULL	AS	Q969Y0	NXPE3
981.1	Adenylate kinase isoenzyme 4,	0.00E+00	3.63E+05	3.63E+05	3.63E+05	NULL	AS	P27144	AK4
1646.1	Enoyl-CoA delta isomerase 1, m	0.00E+00	3.63E+05	3.63E+05	3.63E+05	NULL	AS	P42126	ECI1
789.1	Small EDRK-rich factor 2	0.00E+00	3.64E+05	3.64E+05	3.64E+05	NULL	AS	P84101	SERF2

942.1	Protein SZT2	0.00E+00	3.64E+05	3.64E+05	3.64E+05	NULL	AS	Q5T011	SZT2
1218.1	Isoform 2 of MAX gene-associat	0.00E+00	3.66E+05	3.66E+05	3.66E+05	NULL	AS	Q8IWI9-2	MGA
2124.1	Telomeric repeat-binding factor	0.00E+00	3.66E+05	3.66E+05	3.66E+05	NULL	AS	Q15554	TERF2
1141.1	N-alpha-acetyltransferase 25, N	0.00E+00	3.68E+05	3.68E+05	3.68E+05	NULL	AS	Q14CX7	NAA25
1786.1	FYVE, RhoGEF and PH domain cc	0.00E+00	3.68E+05	3.68E+05	3.68E+05	NULL	AS	G3XA97	FGD4
1456.1	Leucine-rich repeat and WD rep	0.00E+00	3.74E+05	3.74E+05	3.74E+05	NULL	AS	Q9UFC0	LRWD1
2852.1	Histone deacetylase 2	0.00E+00	3.74E+05	3.74E+05	3.74E+05	NULL	AS	J3KPW7	HDAC2
2971.1	Ubiquinone biosynthesis proteir	0.00E+00	3.74E+05	3.74E+05	3.74E+05	NULL	AS	O75208	COQ9
1193.1	Potassium/sodium hyperpolariz	0.00E+00	3.76E+05	3.76E+05	3.76E+05	NULL	AS	Q9Y3Q4	HCN4
678.1	Protein flightless-1 homolog	0.00E+00	3.80E+05	3.80E+05	3.80E+05	NULL	AS	Q13045	FLII
2458.1	Dual specificity mitogen-activat	0.00E+00	3.80E+05	3.80E+05	3.80E+05	NULL	AS	P36507	MAP2K2
2888.1	Tetratricopeptide repeat proteir	0.00E+00	3.81E+05	3.81E+05	3.81E+05	NULL	AS	Q6PGP7	TTC37
1992.1	Unconventional myosin-Ic	0.00E+00	3.82E+05	3.82E+05	3.82E+05	NULL	AS	O00159	MYO1C
3127.1	Testican-3	0.00E+00	3.83E+05	3.83E+05	3.83E+05	NULL	AS	Q9BQ16	SPOCK3
974.1	Isoform 3 of Importin-5	0.00E+00	3.84E+05	3.84E+05	3.84E+05	NULL	AS	O00410-3	IPO5
2987.1	DEP domain-containing protein	0.00E+00	3.84E+05	3.84E+05	3.84E+05	NULL	AS	Q5TB30	DEPDC1
841.1	U6 snRNA-associated Sm-like pr	0.00E+00	3.86E+05	3.86E+05	3.86E+05	NULL	AS	Q9Y4Z0	LSM4
2212.1	Isoform 2 of Janus kinase and m	0.00E+00	3.87E+05	3.87E+05	3.87E+05	NULL	AS	Q96N16-2	JAKMIP1
2350.1	Protein atonal homolog 1	0.00E+00	3.88E+05	3.88E+05	3.88E+05	NULL	AS	Q92858	ATOH1
2133.1	Transmembrane and TPR repeat	0.00E+00	3.91E+05	3.91E+05	3.91E+05	NULL	AS	Q6ZXV5	TMTC3
1151.1	Protein Dom3Z	0.00E+00	3.92E+05	3.92E+05	3.92E+05	NULL	AS	O77932	DOM3Z
1451.1	Isoform 3 of Twinfilin-1	0.00E+00	3.93E+05	3.93E+05	3.93E+05	NULL	AS	Q12792-3	TWF1
836.1	Eukaryotic translation initiation	0.00E+00	3.97E+05	3.97E+05	3.97E+05	NULL	AS	P55010	EIF5
2370.1	Semenogelin-1	0.00E+00	3.99E+05	3.99E+05	3.99E+05	NULL	AS	P04279	SEMG1
3154.1	Protein phosphatase 1F	0.00E+00	3.99E+05	3.99E+05	3.99E+05	NULL	AS	A8MX49	PPM1F
917.1	Neuron navigator 3	0.00E+00	4.00E+05	4.00E+05	4.00E+05	NULL	AS	Q8IVL0	NAV3
2866.1	Tudor and KH domain-containin	0.00E+00	4.04E+05	4.04E+05	4.04E+05	NULL	AS	Q9Y2W6	TDRKH
1586.1	DNA polymerase subunit gamm	0.00E+00	4.07E+05	4.07E+05	4.07E+05	NULL	AS	Q9UHN1	POLG2
3228.1	Ras-related GTP-binding protein	0.00E+00	4.13E+05	4.13E+05	4.13E+05	NULL	AS	Q5VZM2	RRAGB
795.1	Cleavage stimulation factor sub	0.00E+00	4.14E+05	4.14E+05	4.14E+05	NULL	AS	Q9H0L4	CSTF2T
1503.1	RNA polymerase-associated pro	0.00E+00	4.14E+05	4.14E+05	4.14E+05	NULL	AS	Q6PD62	CTR9
2375.1	Biorientation of chromosomes i	0.00E+00	4.15E+05	4.15E+05	4.15E+05	NULL	AS	Q8NFC6	BOD1L1
572.2	Adenine phosphoribosyltransfe	0.00E+00	4.18E+05	4.18E+05	4.18E+05	NULL	AS	H3BQZ9	APRT
2594.1	Serine/threonine-protein kinase	0.00E+00	4.22E+05	4.22E+05	4.22E+05	NULL	AS	Q9P0L2	MARK1
2145.1	Kinesin-like protein KIF3A	0.00E+00	4.26E+05	4.26E+05	4.26E+05	NULL	AS	E9PES4	KIF3A

2157.1	Transmembrane protein 199	0.00E+00	4.26E+05	4.26E+05	4.26E+05	NULL	AS	E9PBQ3	TMEM199
2398.1	Cyclin-dependent kinase 6	0.00E+00	4.26E+05	4.26E+05	4.26E+05	NULL	AS	Q00534	CDK6
745.1	Pre-rRNA-processing protein TSI	0.00E+00	4.31E+05	4.31E+05	4.31E+05	NULL	AS	Q2NL82	TSR1
1768.1	Isoform 3 of Cytosolic carboxype	0.00E+00	4.32E+05	4.32E+05	4.32E+05	NULL	AS	Q9UPW5-3	AGTPBP1
1418.1	ATP-binding cassette sub-family	0.00E+00	4.33E+05	4.33E+05	4.33E+05	NULL	AS	Q9NUQ8	ABCF3
2127.1	Isoform 7 of Aryl hydrocarbon r	0.00E+00	4.33E+05	4.33E+05	4.33E+05	NULL	AS	Q8WYA1-7	ARNTL2
613.1	60S ribosomal protein L12	0.00E+00	4.34E+05	4.34E+05	4.34E+05	NULL	AS	P30050	RPL12
1544.1	Leucine-rich repeat-containing p	0.00E+00	4.35E+05	4.35E+05	4.35E+05	NULL	AS	Q9BTT6	LRRC1
1944.1	5-azacytidine-induced protein 1	0.00E+00	4.35E+05	4.35E+05	4.35E+05	NULL	AS	Q9UPN4	AZI1
1745.1	Isoform B3 of Smoothelin	0.00E+00	4.38E+05	4.38E+05	4.38E+05	NULL	AS	P53814-6	SMTN
1251.1	Collagen alpha-3(VI) chain	0.00E+00	4.40E+05	4.40E+05	4.40E+05	NULL	AS	P12111	COL6A3
3198.1	Integrator complex subunit 7	0.00E+00	4.40E+05	4.40E+05	4.40E+05	NULL	AS	Q9NVH2	INTS7
676.1	Protein Red	0.00E+00	4.41E+05	4.41E+05	4.41E+05	NULL	AS	Q13123	IK
1486.1	Serine/threonine-protein kinase	0.00E+00	4.43E+05	4.43E+05	4.43E+05	NULL	AS	Q9C098	DCLK3
1034.1	Dynamin-like 120 kDa protein, r	0.00E+00	4.44E+05	4.44E+05	4.44E+05	NULL	AS	E5KLJ5	OPA1
1147.1	Isoform 2 of Calmodulin-regulat	0.00E+00	4.44E+05	4.44E+05	4.44E+05	NULL	AS	Q9P1Y5-2	CAMSAP3
1165.1	Eukaryotic translation initiation	0.00E+00	4.46E+05	4.46E+05	4.46E+05	NULL	AS	Q9UBQ5	EIF3K
826.1	Biliverdin reductase A	0.00E+00	4.47E+05	4.47E+05	4.47E+05	NULL	AS	P53004	BLVRA
1358.1	Synaptonemal complex protein	0.00E+00	4.47E+05	4.47E+05	4.47E+05	NULL	AS	Q8IZU3	SYCP3
1677.1	Transmembrane protein 168	0.00E+00	4.47E+05	4.47E+05	4.47E+05	NULL	AS	Q9H0V1	TMEM168
1776.1	Armadillo repeat-containing X-li	0.00E+00	4.47E+05	4.47E+05	4.47E+05	NULL	AS	Q7L311	ARMCX2
2302.1	Lysozyme g-like protein 1	0.00E+00	4.48E+05	4.48E+05	4.48E+05	NULL	AS	Q8N1E2	LYG1
1557.1	Protein FAM110D	0.00E+00	4.49E+05	4.49E+05	4.49E+05	NULL	AS	Q8TAY7	FAM110D
3096.1	ATP synthase subunit s-like prot	0.00E+00	4.53E+05	4.53E+05	4.53E+05	NULL	AS	Q9NW81	ATP5SL
1714.1	Interferon-induced helicase C d	0.00E+00	4.54E+05	4.54E+05	4.54E+05	NULL	AS	Q9BYX4	IFIH1
2957.1	Transcription factor HES-5	0.00E+00	4.54E+05	4.54E+05	4.54E+05	NULL	AS	Q5TA89	HES5
1216.1	Leucine-rich repeat serine/threo	0.00E+00	4.55E+05	4.55E+05	4.55E+05	NULL	AS	Q5S007	LRRK2
2958.1	F-box only protein 27	0.00E+00	4.55E+05	4.55E+05	4.55E+05	NULL	AS	Q8NI29	FBXO27
1772.1	Zinc finger protein 236	0.00E+00	4.57E+05	4.57E+05	4.57E+05	NULL	AS	J9JID5	ZNF236
650.1	Apoptosis-inducing factor 1, mit	0.00E+00	4.59E+05	4.59E+05	4.59E+05	NULL	AS	O95831	AIFM1
2636.1	Isoform 3 of Receptor-type tyro	0.00E+00	4.62E+05	4.62E+05	4.62E+05	NULL	AS	P23467-3	PTPRB
2812.1	Ankyrin repeat domain-containi	0.00E+00	4.62E+05	4.62E+05	4.62E+05	NULL	AS	C9JTQ0	ANKRD63
3157.1	Death-associated protein kinase	0.00E+00	4.63E+05	4.63E+05	4.63E+05	NULL	AS	Q5T8F1	DAPK1
1465.1	Sorting nexin-5	0.00E+00	4.64E+05	4.64E+05	4.64E+05	NULL	AS	Q9Y5X3	SNX5
1149.1	Alpha-mannosidase 2C1	0.00E+00	4.65E+05	4.65E+05	4.65E+05	NULL	AS	Q9NTJ4	MAN2C1

715.1	Coiled-coil domain-containing p	0.00E+00	4.67E+05	4.67E+05	4.67E+05	NULL	AS	Q16204	CCDC6
1163.1	Katanin p80 WD40 repeat-conta	0.00E+00	4.67E+05	4.67E+05	4.67E+05	NULL	AS	Q9BVA0	KATNB1
1381.1	Polyadenylate-binding protein-i	0.00E+00	4.67E+05	4.67E+05	4.67E+05	NULL	AS	Q9BPZ3	PAIP2
656.1	Peptidyl-prolyl cis-trans isomera	0.00E+00	4.68E+05	4.68E+05	4.68E+05	NULL	AS	P30405	PPIF
1427.1	Isoform 2 of HLA class I histocor	0.00E+00	4.69E+05	4.69E+05	4.69E+05	NULL	AS	P13746-2	HLA-A
1702.1	Tumor necrosis factor receptor	0.00E+00	4.69E+05	4.69E+05	4.69E+05	NULL	AS	Q969Z4	RELT
1313.1	E3 ubiquitin-protein ligase HECT	0.00E+00	4.72E+05	4.72E+05	4.72E+05	NULL	AS	Q5T447	HECTD3
3004.1	SLIT and NTRK-like protein 4	0.00E+00	4.72E+05	4.72E+05	4.72E+05	NULL	AS	Q8IW52	SLITRK4
2842.1	KAT8 regulatory NSL complex su	0.00E+00	4.73E+05	4.73E+05	4.73E+05	NULL	AS	A0AUZ9	KANSL1L
1473.1	Nuclear pore complex protein N	0.00E+00	4.76E+05	4.76E+05	4.76E+05	NULL	AS	Q8N1F7	NUP93
636.1	Serine/arginine-rich splicing fact	0.00E+00	4.79E+05	4.79E+05	4.79E+05	NULL	AS	Q13242	SRSF9
2880.1	RING finger protein 113A	0.00E+00	4.80E+05	4.80E+05	4.80E+05	NULL	AS	O15541	RNF113A
2610.1	Phytanoyl-CoA hydroxylase-inte	0.00E+00	4.83E+05	4.83E+05	4.83E+05	NULL	AS	Q96FC7	PHYHIPL
1140.1	Ubiquitin-associated protein 2	0.00E+00	4.84E+05	4.84E+05	4.84E+05	NULL	AS	E7EWG4	UBAP2
1422.1	Signal peptide, CUB and EGF-like	0.00E+00	4.86E+05	4.86E+05	4.86E+05	NULL	AS	Q8IWY4	SCUBE1
752.1	Probable ATP-dependent RNA h	0.00E+00	4.89E+05	4.89E+05	4.89E+05	NULL	AS	Q7L014	DDX46
2264.1	Zinc/RING finger protein 4	0.00E+00	4.90E+05	4.90E+05	4.90E+05	NULL	AS	Q8WWF5	ZNRF4
1947.1	Kappa-type opioid receptor	0.00E+00	4.91E+05	4.91E+05	4.91E+05	NULL	AS	P41145	OPRK1
735.1	Peptidyl-prolyl cis-trans isomera	0.00E+00	4.93E+05	4.93E+05	4.93E+05	NULL	AS	Q5VVH2	FKBP1C
727.1	Hydroxysteroid dehydrogenase-	0.00E+00	4.94E+05	4.94E+05	4.94E+05	NULL	AS	Q6YN16	HSDL2
2860.1	Anion exchange protein 2	0.00E+00	4.94E+05	4.94E+05	4.94E+05	NULL	AS	P04920	SLC4A2
1434.1	C-type lectin domain family 4 m	0.00E+00	4.95E+05	4.95E+05	4.95E+05	NULL	AS	Q8N1N0	CLEC4F
3241.1	Galectin-3	0.00E+00	5.00E+05	5.00E+05	5.00E+05	NULL	AS	G3V3R6	LGALS3
1083.1	Sel1 repeat-containing protein 1	0.00E+00	5.02E+05	5.02E+05	5.02E+05	NULL	AS	Q96BR5	SELRC1
2221.1	Isoform 2 of Coiled-coil domain-	0.00E+00	5.02E+05	5.02E+05	5.02E+05	NULL	AS	Q8NEF3-2	CCDC112
2493.1	A disintegrin and metalloprotei	0.00E+00	5.02E+05	5.02E+05	5.02E+05	NULL	AS	Q9UNA0	ADAMTS5
878.1	Leucine--tRNA ligase, cytoplasm	0.00E+00	5.03E+05	5.03E+05	5.03E+05	NULL	AS	Q9P2J5	LARS
2542.1	Tsukushin	0.00E+00	5.03E+05	5.03E+05	5.03E+05	NULL	AS	Q8WUA8	TSKU
1458.1	Semaphorin-3A	0.00E+00	5.04E+05	5.04E+05	5.04E+05	NULL	AS	Q14563	SEMA3A
2313.1	Phytanoyl-CoA dioxygenase, pe	0.00E+00	5.08E+05	5.08E+05	5.08E+05	NULL	AS	O14832	PHYH
1003.1	General transcription factor IIF	0.00E+00	5.09E+05	5.09E+05	5.09E+05	NULL	AS	P35269	GTF2F1
1142.1	Amine oxidase [flavin-containin	0.00E+00	5.10E+05	5.10E+05	5.10E+05	NULL	AS	P21397	MAOA
3079.1	Protein SOX-15	0.00E+00	5.13E+05	5.13E+05	5.13E+05	NULL	AS	O60248	SOX15
3262.1	Isoform 4 of Brain-derived neur	0.00E+00	5.13E+05	5.13E+05	5.13E+05	NULL	AS	P23560-4	BDNF
521.1	Transducin-like enhancer protei	0.00E+00	5.14E+05	5.14E+05	5.14E+05	NULL	AS	Q04724	TLE1

1399.1	Pleckstrin homology-like domai	0.00E+00	5.15E+05	5.15E+05	5.15E+05	NULL	AS	Q86SQ0	PHLDB2
1020.1	ATP-dependent DNA helicase Q	0.00E+00	5.20E+05	5.20E+05	5.20E+05	NULL	AS	P46063	RECQL
1871.1	Isoform B of Methyl-CpG-bindin	0.00E+00	5.21E+05	5.21E+05	5.21E+05	NULL	AS	P51608-2	MECP2
1029.1	Eukaryotic translation initiation	0.00E+00	5.22E+05	5.22E+05	5.22E+05	NULL	AS	B3KSH1	EIF3F
2976.1	Leucine-rich repeat-containing	0.00E+00	5.23E+05	5.23E+05	5.23E+05	NULL	AS	A6NM11	LRRC37A2
1884.1	Homeobox protein Nkx-6.1	0.00E+00	5.24E+05	5.24E+05	5.24E+05	NULL	AS	P78426	NKX6-1
2327.1	Tyrosine-protein phosphatase n	0.00E+00	5.24E+05	5.24E+05	5.24E+05	NULL	AS	Q9Y2R2	PTPN22
2319.1	Aspartate beta-hydroxylase don	0.00E+00	5.27E+05	5.27E+05	5.27E+05	NULL	AS	Q6ICH7	ASPHD2
830.1	40S ribosomal protein S29	0.00E+00	5.29E+05	5.29E+05	5.29E+05	NULL	AS	P62273	RPS29
1276.1	Probable peptidyl-tRNA hydrola	0.00E+00	5.29E+05	5.29E+05	5.29E+05	NULL	AS	Q86Y79	PTRH1
1921.1	26S proteasome non-ATPase re	0.00E+00	5.33E+05	5.33E+05	5.33E+05	NULL	AS	Q16401	PSMD5
2990.1	Periaxin	0.00E+00	5.38E+05	5.38E+05	5.38E+05	NULL	AS	Q9BXM0	PRX
617.2	Dynamin-2	0.00E+00	5.39E+05	5.39E+05	5.39E+05	NULL	AS	P50570	DNM2
700.1	Protein FAM114A2	0.00E+00	5.40E+05	5.40E+05	5.40E+05	NULL	AS	Q9NRY5	FAM114A2
1734.1	NLR family CARD domain-contai	0.00E+00	5.40E+05	5.40E+05	5.40E+05	NULL	AS	Q9NPP4	NLRC4
1160.1	Glutamate dehydrogenase 2, mi	0.00E+00	5.41E+05	5.41E+05	5.41E+05	NULL	AS	P49448	GLUD2
1961.1	Cytoskeleton-associated protei	0.00E+00	5.41E+05	5.41E+05	5.41E+05	NULL	AS	Q07065	CKAP4
198.2	Fragile X mental retardation syn	0.00E+00	5.43E+05	5.43E+05	5.43E+05	NULL	AS	P51116	FXR2
696.1	Succinyl-CoA ligase [ADP-formin	0.00E+00	5.44E+05	5.44E+05	5.44E+05	NULL	AS	Q9P2R7	SUCLA2
1000.1	Nuclear pore membrane glycop	0.00E+00	5.46E+05	5.46E+05	5.46E+05	NULL	AS	Q8TEM1	NUP210
856.1	Eukaryotic translation initiation	0.00E+00	5.48E+05	5.48E+05	5.48E+05	NULL	AS	O60841	EIF5B
1775.1	AT-rich interactive domain-cont	0.00E+00	5.48E+05	5.48E+05	5.48E+05	NULL	AS	Q68CP9	ARID2
2712.1	Isoform 3 of TPA-induced trans	0.00E+00	5.48E+05	5.48E+05	5.48E+05	NULL	AS	Q5BVD1-3	TTMP
615.1	Serine/threonine-protein phosp	0.00E+00	5.49E+05	5.49E+05	5.49E+05	NULL	AS	Q96QC0	PPP1R10
2046.1	Taperin	0.00E+00	5.53E+05	5.53E+05	5.53E+05	NULL	AS	Q4KMQ1	TPRN
1838.1	Actin-related protein 2/3 compl	0.00E+00	5.54E+05	5.54E+05	5.54E+05	NULL	AS	O15145	ARPC3
2508.1	C-Maf-inducing protein	0.00E+00	5.62E+05	5.62E+05	5.62E+05	NULL	AS	Q8IY22	CMIP
1145.1	Protocadherin gamma-A9	0.00E+00	5.63E+05	5.63E+05	5.63E+05	NULL	AS	Q9Y5G4	PCDHGA9
2364.1	Mitochondrial dynamic protein	0.00E+00	5.63E+05	5.63E+05	5.63E+05	NULL	AS	B0QY95	SMCR7L
1172.1	Density-regulated protein	0.00E+00	5.66E+05	5.66E+05	5.66E+05	NULL	AS	O43583	DENR
3173.1	Vacuolar protein sorting-associa	0.00E+00	5.66E+05	5.66E+05	5.66E+05	NULL	AS	Q86XT2	VPS37D
2743.1	Protein CREG2	0.00E+00	5.68E+05	5.68E+05	5.68E+05	NULL	AS	Q8IUH2	CREG2
1120.1	Protein FAM26E	0.00E+00	5.70E+05	5.70E+05	5.70E+05	NULL	AS	Q8N5C1	FAM26E
1219.1	Sterile alpha motif domain-cont	0.00E+00	5.70E+05	5.70E+05	5.70E+05	NULL	AS	Q5K651	SAMD9
3011.1	Isoform 3 of Peripheral-type be	0.00E+00	5.70E+05	5.70E+05	5.70E+05	NULL	AS	O95153-3	BZRAP1

1560.1	Isoform 2 of Dual specificity mit	0.00E+00	5.72E+05	5.72E+05	5.72E+05	NULL	AS	P45985-2	MAP2K4
2823.1	Inactive phospholipase D5	0.00E+00	5.75E+05	5.75E+05	5.75E+05	NULL	AS	Q8N7P1	PLD5
3223.1	ATP synthase mitochondrial F1 (	0.00E+00	5.75E+05	5.75E+05	5.75E+05	NULL	AS	J3KTB2	ATPAF2
2793.1	35 kDa inter-alpha-trypsin inhib	0.00E+00	5.78E+05	5.78E+05	5.78E+05	NULL	AS	B7ZKJ8	ITIH4
2703.1	Plasminogen receptor (KT)	0.00E+00	5.81E+05	5.81E+05	5.81E+05	NULL	AS	Q9HBL7	PLGRKT
3266.1	RNA exonuclease 1 homolog	0.00E+00	5.81E+05	5.81E+05	5.81E+05	NULL	AS	Q8N1G1	REXO1
962.1	AF4/FMR2 family member 4	0.00E+00	5.83E+05	5.83E+05	5.83E+05	NULL	AS	Q9UHB7	AFF4
1067.1	Enoyl-CoA hydratase, mitochon	0.00E+00	5.89E+05	5.89E+05	5.89E+05	NULL	AS	P30084	ECHS1
1903.1	Disco-interacting protein 2 hom	0.00E+00	5.90E+05	5.90E+05	5.90E+05	NULL	AS	Q9P265	DIP2B
2512.1	Sodium channel protein type 11	0.00E+00	5.90E+05	5.90E+05	5.90E+05	NULL	AS	Q9UI33	SCN11A
662.1	Lipoamide acyltransferase comp	0.00E+00	5.92E+05	5.92E+05	5.92E+05	NULL	AS	P11182	DBT
1904.1	von Willebrand factor A domain	0.00E+00	5.92E+05	5.92E+05	5.92E+05	NULL	AS	A3KMH1	VWA8
2272.1	Kinase D-interacting substrate o	0.00E+00	5.96E+05	5.96E+05	5.96E+05	NULL	AS	Q9ULH0	KIDINS220
1663.1	Isoform 2 of Rho GTPase-activat	0.00E+00	5.99E+05	5.99E+05	5.99E+05	NULL	AS	P42331-2	ARHGAP25
867.1	Isoform 5 of MAP7 domain-cont	0.00E+00	6.00E+05	6.00E+05	6.00E+05	NULL	AS	Q96T17-5	MAP7D2
502.1	Cordon-bleu protein-like 1	0.00E+00	6.01E+05	6.01E+05	6.01E+05	NULL	AS	G8JL86	COBLL1
873.1	Brain-specific angiogenesis inhil	0.00E+00	6.03E+05	6.03E+05	6.03E+05	NULL	AS	O14514	BAI1
526.1	Lon protease homolog, mitocho	0.00E+00	6.11E+05	6.11E+05	6.11E+05	NULL	AS	P36776	LONP1
628.1	ATP-binding cassette sub-family	0.00E+00	6.11E+05	6.11E+05	6.11E+05	NULL	AS	P61221	ABCE1
618.1	Carnitine O-acetyltransferase	0.00E+00	6.14E+05	6.14E+05	6.14E+05	NULL	AS	P43155	CRAT
1238.1	N-acetylaspartyl-glutamate synt	0.00E+00	6.14E+05	6.14E+05	6.14E+05	NULL	AS	Q8IXN7	RIMKLA
1770.1	Protein CEP170B	0.00E+00	6.20E+05	6.20E+05	6.20E+05	NULL	AS	J3KQR7	CEP170B
1943.1	Protein CASC5	0.00E+00	6.20E+05	6.20E+05	6.20E+05	NULL	AS	Q8NG31	CASC5
903.1	60S ribosomal protein L35a	0.00E+00	6.21E+05	6.21E+05	6.21E+05	NULL	AS	P18077	RPL35A
1583.1	Nucleolar GTP-binding protein 2	0.00E+00	6.21E+05	6.21E+05	6.21E+05	NULL	AS	Q13823	GNL2
1056.1	DKFZP586J0619 protein	0.00E+00	6.22E+05	6.22E+05	6.22E+05	NULL	AS	A4D212	DKFZP586J0619
425.1	26S proteasome non-ATPase re	0.00E+00	6.23E+05	6.23E+05	6.23E+05	NULL	AS	Q99460	PSMD1
853.1	Nuclear pore complex protein N	0.00E+00	6.23E+05	6.23E+05	6.23E+05	NULL	AS	F6QR24	NUP153
919.1	Isoform 2 of E3 ubiquitin-protei	0.00E+00	6.28E+05	6.28E+05	6.28E+05	NULL	AS	Q63HN8-4	RNF213
1534.1	Tetratricopeptide repeat protei	0.00E+00	6.28E+05	6.28E+05	6.28E+05	NULL	AS	Q5T0N1	TTC18
2546.1	RNA polymerase II elongation fa	0.00E+00	6.28E+05	6.28E+05	6.28E+05	NULL	AS	O00472	ELL2
1763.1	5'-AMP-activated protein kinase	0.00E+00	6.29E+05	6.29E+05	6.29E+05	NULL	AS	P54619	PRKAG1
2019.1	HCG30379, isoform CRA_d	0.00E+00	6.30E+05	6.30E+05	6.30E+05	NULL	AS	K4DI98	NULL
1272.1	Leucine-rich repeat-containing p	0.00E+00	6.31E+05	6.31E+05	6.31E+05	NULL	AS	Q7Z2Q7	LRRC70
1297.1	Acyl-Coenzyme A dehydrogenas	0.00E+00	6.39E+05	6.39E+05	6.39E+05	NULL	AS	Q5T4U5	ACADM

3046.1	Nesprin-1	0.00E+00	6.40E+05	6.40E+05	6.40E+05	NULL	AS	Q8NF91	SYNE1
2344.1	Anoctamin-3	0.00E+00	6.41E+05	6.41E+05	6.41E+05	NULL	AS	Q9BYT9	ANO3
1533.1	Isoform 2 of Megakaryocyte-ass	0.00E+00	6.42E+05	6.42E+05	6.42E+05	NULL	AS	P42679-2	MATK
2422.1	Poly(ADP-ribose) glycohydrolas	0.00E+00	6.42E+05	6.42E+05	6.42E+05	NULL	AS	Q86W56	PARG
1875.1	Matrix metalloproteinase-27	0.00E+00	6.43E+05	6.43E+05	6.43E+05	NULL	AS	Q9H306	MMP27
1132.1	Pre-mRNA-processing factor 40	0.00E+00	6.46E+05	6.46E+05	6.46E+05	NULL	AS	O75400	PRPF40A
2477.1	Krueppel-like factor 4	0.00E+00	6.46E+05	6.46E+05	6.46E+05	NULL	AS	O43474	KLF4
2557.1	Cadherin-12	0.00E+00	6.50E+05	6.50E+05	6.50E+05	NULL	AS	P55289	CDH12
1299.1	Junction-mediating and -regulat	0.00E+00	6.54E+05	6.54E+05	6.54E+05	NULL	AS	Q8N9B5	JMY
2414.1	Junctional sarcoplasmic reticulu	0.00E+00	6.59E+05	6.59E+05	6.59E+05	NULL	AS	Q96MG2	JSRP1
2190.1	Metastasis-associated protein	0.00E+00	6.69E+05	6.69E+05	6.69E+05	NULL	AS	E9PF88	MTA3
751.1	60S ribosomal protein L19	0.00E+00	6.70E+05	6.70E+05	6.70E+05	NULL	AS	P84098	RPL19
564.1	Purine nucleoside phosphorylas	0.00E+00	6.71E+05	6.71E+05	6.71E+05	NULL	AS	P00491	PNP
1411.1	Protein FAM186A	0.00E+00	6.72E+05	6.72E+05	6.72E+05	NULL	AS	A6NE01	FAM186A
2827.1	Glutathione S-transferase theta	0.00E+00	6.73E+05	6.73E+05	6.73E+05	NULL	AS	A8MPT4	GSTT4
784.1	Charged multivesicular body pr	0.00E+00	6.75E+05	6.75E+05	6.75E+05	NULL	AS	Q8WUX9	CHMP7
1479.1	Isoform 2 of Coiled-coil domain-	0.00E+00	6.81E+05	6.81E+05	6.81E+05	NULL	AS	Q8IXS2-2	CCDC65
1509.1	Epsin-2	0.00E+00	6.84E+05	6.84E+05	6.84E+05	NULL	AS	O95208	EPN2
2009.1	Isoform 2 of Mitochondrial inne	0.00E+00	6.84E+05	6.84E+05	6.84E+05	NULL	AS	Q8N8Q8-2	COX18
1666.1	Dipeptidyl aminopeptidase-like	0.00E+00	6.93E+05	6.93E+05	6.93E+05	NULL	AS	P42658	DPP6
2510.1	Rho guanine nucleotide exchan	0.00E+00	6.97E+05	6.97E+05	6.97E+05	NULL	AS	Q8TER5	ARHGEF40
3168.1	Isoform 3 of Centromere protei	0.00E+00	6.99E+05	6.99E+05	6.99E+05	NULL	AS	Q96H22-3	CENPN
3260.1	Cytosolic 10-formyltetrahydrof	0.00E+00	7.00E+05	7.00E+05	7.00E+05	NULL	AS	O75891	ALDH1L1
828.1	Down syndrome cell adhesion	0.00E+00	7.01E+05	7.01E+05	7.01E+05	NULL	AS	Q8TD84	DSCAML1
693.1	Transcription termination facto	0.00E+00	7.04E+05	7.04E+05	7.04E+05	NULL	AS	Q9UNY4	TTF2
60.2	Protein RBM14-RBM4	0.00E+00	7.04E+05	7.04E+05	7.04E+05	NULL	AS	Q96PK6	RBM14
1402.1	Periplakin	0.00E+00	7.05E+05	7.05E+05	7.05E+05	NULL	AS	O60437	PPL
2150.1	F-box only protein 43	0.00E+00	7.06E+05	7.06E+05	7.06E+05	NULL	AS	Q4G163	FBXO43
2073.1	Pleckstrin homology domain-co	0.00E+00	7.07E+05	7.07E+05	7.07E+05	NULL	AS	Q6ZR37	PLEKHG7
994.1	ATP-binding cassette sub-family	0.00E+00	7.08E+05	7.08E+05	7.08E+05	NULL	AS	Q86UQ4	ABCA13
1378.1	DNA polymerase delta subunit	0.00E+00	7.10E+05	7.10E+05	7.10E+05	NULL	AS	P49005	POLD2
1593.1	Chromodomain-helicase-DNA-b	0.00E+00	7.11E+05	7.11E+05	7.11E+05	NULL	AS	Q9HCK8	CHD8
2102.1	UPF0505 protein C16orf62	0.00E+00	7.11E+05	7.11E+05	7.11E+05	NULL	AS	E7EWW0	C16orf62
3000.1	Usher syndrome type-1G protei	0.00E+00	7.11E+05	7.11E+05	7.11E+05	NULL	AS	J3KSN5	USH1G
2900.1	Retinol dehydrogenase 12	0.00E+00	7.16E+05	7.16E+05	7.16E+05	NULL	AS	Q96NR8	RDH12

24.3	Tubulin alpha-3C/D chain	0.00E+00	7.23E+05	7.23E+05	7.23E+05	NULL	AS	Q13748	TUBA3C
2396.1	Lysine-specific demethylase 7	0.00E+00	7.26E+05	7.26E+05	7.26E+05	NULL	AS	Q6ZMT4	JHDM1D
1978.1	Bcl2 antagonist of cell death	0.00E+00	7.27E+05	7.27E+05	7.27E+05	NULL	AS	F5GYS3	BAD
3123.1	Isoform 2 of Sphingosine kinase	0.00E+00	7.27E+05	7.27E+05	7.27E+05	NULL	AS	Q9NYA1-2	SPHK1
1370.1	NADH dehydrogenase [ubiquin	0.00E+00	7.29E+05	7.29E+05	7.29E+05	NULL	AS	P51970	NDUFA8
991.1	CCR4-NOT transcription comple	0.00E+00	7.30E+05	7.30E+05	7.30E+05	NULL	AS	A5YKK6	CNOT1
1002.1	Glutamate receptor ionotropic,	0.00E+00	7.36E+05	7.36E+05	7.36E+05	NULL	AS	O60391	GRIN3B
2825.1	Immunoglobulin superfamily DC	0.00E+00	7.36E+05	7.36E+05	7.36E+05	NULL	AS	Q8TDY8	IGDCC4
1231.1	Ryanodine receptor 2	0.00E+00	7.39E+05	7.39E+05	7.39E+05	NULL	AS	H7BY35	RYR2
791.1	39S ribosomal protein L33, mito	0.00E+00	7.40E+05	7.40E+05	7.40E+05	NULL	AS	O75394	MRPL33
1513.1	Multiple epidermal growth fact	0.00E+00	7.47E+05	7.47E+05	7.47E+05	NULL	AS	Q7Z7M0	MEGF8
1416.1	Huntingtin-interacting protein 1	0.00E+00	7.51E+05	7.51E+05	7.51E+05	NULL	AS	O75146	HIP1R
600.1	Cathepsin B	0.00E+00	7.55E+05	7.55E+05	7.55E+05	NULL	AS	P07858	CTSB
1751.1	Isoform 3 of Neutrophil cytosol	0.00E+00	7.57E+05	7.57E+05	7.57E+05	NULL	AS	Q15080-3	NCF4
2430.1	Stabilin-2	0.00E+00	7.57E+05	7.57E+05	7.57E+05	NULL	AS	Q8WWQ8	STAB2
1043.1	Kelch domain-containing protei	0.00E+00	7.58E+05	7.58E+05	7.58E+05	NULL	AS	Q8IYD2	KLHDC8A
2792.1	TPR and ankyrin repeat-containi	0.00E+00	7.58E+05	7.58E+05	7.58E+05	NULL	AS	O15050	TRANK1
3022.1	Isoform 9 of DEP domain-contai	0.00E+00	7.78E+05	7.78E+05	7.78E+05	NULL	AS	O75140-9	DEPDC5
1016.1	Probable E3 ubiquitin-protein li	0.00E+00	7.82E+05	7.82E+05	7.82E+05	NULL	AS	Q8IVU3	HERC6
1249.1	Type 2 lactosamine alpha-2,3-si	0.00E+00	7.85E+05	7.85E+05	7.85E+05	NULL	AS	Q9Y274	ST3GAL6
1788.1	Galactose-3-O-sulfotransferase	0.00E+00	7.86E+05	7.86E+05	7.86E+05	NULL	AS	Q9H3Q3	GAL3ST2
712.1	Double-strand break repair prot	0.00E+00	7.87E+05	7.87E+05	7.87E+05	NULL	AS	B3KTC7	MRE11A
1648.1	PCNA-interacting partner	0.00E+00	7.87E+05	7.87E+05	7.87E+05	NULL	AS	B4DZ31	PARPBP
2000.1	E3 ubiquitin-protein ligase BRE1	0.00E+00	7.88E+05	7.88E+05	7.88E+05	NULL	AS	O75150	RNF40
2051.1	Arf-GAP with GTPase, ANK repe	0.00E+00	7.89E+05	7.89E+05	7.89E+05	NULL	AS	Q99490	AGAP2
536.1	Histone H1t	0.00E+00	7.91E+05	7.91E+05	7.91E+05	NULL	AS	P22492	HIST1H1T
1896.1	Protocadherin-15	0.00E+00	7.94E+05	7.94E+05	7.94E+05	NULL	AS	E7EMG8	PCDH15
869.1	ATP synthase subunit O, mitoch	0.00E+00	7.96E+05	7.96E+05	7.96E+05	NULL	AS	P48047	ATP5O
76.2	Heterogeneous nuclear ribonuc	0.00E+00	7.99E+05	7.99E+05	7.99E+05	NULL	AS	P55795	HNRNPH2
314.1	Isoform 2 of Hydroxyacyl-coenz	0.00E+00	8.01E+05	8.01E+05	8.01E+05	NULL	AS	Q16836-2	HADH
397.1	Nuclear pore complex protein N	0.00E+00	8.06E+05	8.06E+05	8.06E+05	NULL	AS	Q99567	NUP88
2140.1	Galactose-3-O-sulfotransferase	0.00E+00	8.06E+05	8.06E+05	8.06E+05	NULL	AS	Q96A11	GAL3ST3
1407.1	Isoform 3 of E3 ubiquitin-protei	0.00E+00	8.09E+05	8.09E+05	8.09E+05	NULL	AS	Q14669-3	TRIP12
375.1	Plasminogen activator inhibitor	0.00E+00	8.10E+05	8.10E+05	8.10E+05	NULL	AS	Q8NC51	SERBP1
2010.1	Tigger transposable element-de	0.00E+00	8.21E+05	8.21E+05	8.21E+05	NULL	AS	Q96MW7	TIGD1

912.1	Growth/differentiation factor 1	0.00E+00	8.23E+05	8.23E+05	8.23E+05	NULL	AS	Q99988	GDF15
2748.1	MAX gene-associated protein	0.00E+00	8.33E+05	8.33E+05	8.33E+05	NULL	AS	Q8IWI9	MGA
1799.1	Endonuclease III-like protein 1	0.00E+00	8.39E+05	8.39E+05	8.39E+05	NULL	AS	P78549	NTHL1
1952.1	Protein TBRG4	0.00E+00	8.39E+05	8.39E+05	8.39E+05	NULL	AS	Q969Z0	TBRG4
2326.1	Urocanate hydratase	0.00E+00	8.40E+05	8.40E+05	8.40E+05	NULL	AS	Q96N76	UROC1
1651.1	Peroxisomal biogenesis factor 1	0.00E+00	8.44E+05	8.44E+05	8.44E+05	NULL	AS	B7Z8B3	PEX19
2518.1	Transient receptor potential cat	0.00E+00	8.44E+05	8.44E+05	8.44E+05	NULL	AS	Q7Z2W7	TRPM8
308.1	Serine/arginine-rich splicing fact	0.00E+00	8.50E+05	8.50E+05	8.50E+05	NULL	AS	Q13247	SRSF6
437.1	Heterogeneous nuclear ribonuc	0.00E+00	8.50E+05	8.50E+05	8.50E+05	NULL	AS	Q13151	HNRNPA0
3126.1	Ral GTPase-activating protein su	0.00E+00	8.55E+05	8.55E+05	8.55E+05	NULL	AS	Q86X10	RALGAPB
429.1	40S ribosomal protein S8	0.00E+00	8.60E+05	8.60E+05	8.60E+05	NULL	AS	P62241	RPS8
3174.1	Isoform 2 of Ubiquitin carboxyl-	0.00E+00	8.60E+05	8.60E+05	8.60E+05	NULL	AS	Q9P275-2	USP36
1894.1	Chromosome 1 open reading fra	0.00E+00	8.61E+05	8.61E+05	8.61E+05	NULL	AS	J3KQM5	NULL
3002.1	Coiled-coil domain-containing p	0.00E+00	8.62E+05	8.62E+05	8.62E+05	NULL	AS	Q5T655	CCDC147
2877.1	Tetratricopeptide repeat protei	0.00E+00	8.66E+05	8.66E+05	8.66E+05	NULL	AS	Q7Z4L5	TTC21B
2139.1	Laminin subunit alpha-2	0.00E+00	8.67E+05	8.67E+05	8.67E+05	NULL	AS	P24043	LAMA2
2317.1	Protein NLRC5	0.00E+00	8.67E+05	8.67E+05	8.67E+05	NULL	AS	Q86WI3	NLRC5
1483.1	Enhancer of polycomb homolog	0.00E+00	8.70E+05	8.70E+05	8.70E+05	NULL	AS	Q9H2F5	EPC1
539.1	Chromosome transmission fidel	0.00E+00	8.73E+05	8.73E+05	8.73E+05	NULL	AS	P0CG12	CHTF8
69.2	ATP-dependent RNA helicase D	0.00E+00	8.78E+05	8.78E+05	8.78E+05	NULL	AS	O00148	DDX39A
1382.1	Immunoglobulin iota chain	0.00E+00	8.82E+05	8.82E+05	8.82E+05	NULL	AS	P12018	VPREB1
335.1	Citrate synthase, mitochondrial	0.00E+00	8.87E+05	8.87E+05	8.87E+05	NULL	AS	O75390	CS
2178.1	Thioredoxin-related transmemb	0.00E+00	8.89E+05	8.89E+05	8.89E+05	NULL	AS	Q9H3N1	TMX1
2378.1	Protein FAM22F	0.00E+00	8.92E+05	8.92E+05	8.92E+05	NULL	AS	A1L443	NUTM2F
988.1	Serine/threonine-protein kinase	0.00E+00	8.96E+05	8.96E+05	8.96E+05	NULL	AS	O14757	CHEK1
3070.1	BUD13 homolog	0.00E+00	8.96E+05	8.96E+05	8.96E+05	NULL	AS	Q9BRD0	BUD13
825.1	Sulfotransferase 1A2	0.00E+00	9.05E+05	9.05E+05	9.05E+05	NULL	AS	P50226	SULT1A2
2274.1	Ras-related protein Rab-27B	0.00E+00	9.17E+05	9.17E+05	9.17E+05	NULL	AS	O00194	RAB27B
3105.1	PiggyBac transposable element	0.00E+00	9.18E+05	9.18E+05	9.18E+05	NULL	AS	J3KNK5	PGBD5
654.1	Dynein heavy chain 7, axonemal	0.00E+00	9.25E+05	9.25E+05	9.25E+05	NULL	AS	Q8WXX0	DNAH7
1395.1	THUMP domain-containing prot	0.00E+00	9.27E+05	9.27E+05	9.27E+05	NULL	AS	Q9BTF0	THUMPD2
351.1	U5 small nuclear ribonucleoprot	0.00E+00	9.39E+05	9.39E+05	9.39E+05	NULL	AS	O75643	SNRNP200
393.1	60S ribosomal protein L34	0.00E+00	9.46E+05	9.46E+05	9.46E+05	NULL	AS	P49207	RPL34
798.1	FRAS1-related extracellular mat	0.00E+00	9.47E+05	9.47E+05	9.47E+05	NULL	AS	Q5SZK8	FREM2
953.1	Isoform 2 of Septin-2	0.00E+00	9.66E+05	9.66E+05	9.66E+05	NULL	AS	Q15019-2	SEPT2

419.1	Isoform 2 of Aminoacyl tRNA sy	0.00E+00	9.67E+05	9.67E+05	9.67E+05	NULL	AS	Q12904-2	AIMP1
1777.1	Serine/threonine-protein phosp	0.00E+00	9.75E+05	9.75E+05	9.75E+05	NULL	AS	Q06190	PPP2R3A
1773.1	Integrin alpha-4	0.00E+00	9.78E+05	9.78E+05	9.78E+05	NULL	AS	P13612	ITGA4
1574.1	WD repeat-containing protein 4	0.00E+00	9.80E+05	9.80E+05	9.80E+05	NULL	AS	Q8TAF3	WDR48
3208.1	Integrator complex subunit 3	0.00E+00	9.86E+05	9.86E+05	9.86E+05	NULL	AS	Q68E01	INTS3
1701.1	Zinc finger protein 468	0.00E+00	9.94E+05	9.94E+05	9.94E+05	NULL	AS	Q5VIY5	ZNF468
732.1	Enhancer of yellow 2 transcripti	0.00E+00	1.00E+06	1.00E+06	1.00E+06	NULL	AS	Q9NPA8	ENY2
590.1	Heterogeneous nuclear ribonuc	0.00E+00	1.01E+06	1.01E+06	1.01E+06	NULL	AS	P51991	HNRNPA3
665.1	Isoform 2 of Acid ceramidase	0.00E+00	1.01E+06	1.01E+06	1.01E+06	NULL	AS	Q13510-2	ASAH1
2506.1	Growth hormone-regulated TBC	0.00E+00	1.01E+06	1.01E+06	1.01E+06	NULL	AS	Q5TC63	GRTP1
909.1	Protein FAM207A	0.00E+00	1.02E+06	1.02E+06	1.02E+06	NULL	AS	Q9NSI2	FAM207A
976.1	Glycylpeptide N-tetradecanoylt	0.00E+00	1.03E+06	1.03E+06	1.03E+06	NULL	AS	P30419	NMT1
2755.1	Isoform 3 of Calmodulin-regulat	0.00E+00	1.03E+06	1.03E+06	1.03E+06	NULL	AS	Q5T5Y3-3	CAMSAP1
857.1	U6 snRNA-associated Sm-like pr	0.00E+00	1.04E+06	1.04E+06	1.04E+06	NULL	AS	P62310	LSM3
881.1	Discs, large homolog 3 (Neuroe	0.00E+00	1.05E+06	1.05E+06	1.05E+06	NULL	AS	Q5JUW8	DLG3
2693.1	Thioredoxin domain-containing	0.00E+00	1.05E+06	1.05E+06	1.05E+06	NULL	AS	Q8N427	NME8
796.1	ATP-dependent RNA helicase D	0.00E+00	1.06E+06	1.06E+06	1.06E+06	NULL	AS	Q7Z478	DHX29
2356.1	Isoform 2 of Alcohol dehydroge	0.00E+00	1.06E+06	1.06E+06	1.06E+06	NULL	AS	P40394-2	ADH7
2644.1	1-phosphatidylinositol 4,5-bisp	0.00E+00	1.06E+06	1.06E+06	1.06E+06	NULL	AS	Q9NQ66	PLCB1
1280.1	Isoform 2 of Bifunctional coenz	0.00E+00	1.07E+06	1.07E+06	1.07E+06	NULL	AS	Q13057-2	COASY
1478.1	Putative Polycomb group protei	0.00E+00	1.07E+06	1.07E+06	1.07E+06	NULL	AS	Q76L83	ASXL2
3016.1	Zinc finger protein 154	0.00E+00	1.07E+06	1.07E+06	1.07E+06	NULL	AS	Q13106	ZNF154
1645.1	Heat shock 70 kDa protein 4L	0.00E+00	1.08E+06	1.08E+06	1.08E+06	NULL	AS	E7ES43	HSPA4L
1973.1	Isoform 7 of CCR4-NOT transcri	0.00E+00	1.08E+06	1.08E+06	1.08E+06	NULL	AS	O95628-7	CNOT4
2608.1	Tubby-related protein 4	0.00E+00	1.10E+06	1.10E+06	1.10E+06	NULL	AS	Q9NRJ4	TULP4
2695.1	Serine/threonine-protein kinase	0.00E+00	1.10E+06	1.10E+06	1.10E+06	NULL	AS	O00444	PLK4
459.1	Ras GTPase-activating-like prote	0.00E+00	1.11E+06	1.11E+06	1.11E+06	NULL	AS	P46940	IQGAP1
1612.1	Matrix metalloproteinase-26	0.00E+00	1.11E+06	1.11E+06	1.11E+06	NULL	AS	Q9NRE1	MMP26
597.1	Putative 40S ribosomal protein	0.00E+00	1.12E+06	1.12E+06	1.12E+06	NULL	AS	Q5JNZ5	RPS26P11
834.1	Mitochondrial import inner me	0.00E+00	1.12E+06	1.12E+06	1.12E+06	NULL	AS	O60220	TIMM8A
1130.1	Alpha-fetoprotein	0.00E+00	1.12E+06	1.12E+06	1.12E+06	NULL	AS	J3KMX3	AFP
3191.1	Laminin subunit gamma-1	0.00E+00	1.12E+06	1.12E+06	1.12E+06	NULL	AS	P11047	LAMC1
730.1	V-type proton ATPase subunit D	0.00E+00	1.13E+06	1.13E+06	1.13E+06	NULL	AS	Q9Y5K8	ATP6V1D
918.1	Transformer-2 protein homolog	0.00E+00	1.13E+06	1.13E+06	1.13E+06	NULL	AS	P62995	TRA2B
386.1	Mitotic checkpoint protein BUB	0.00E+00	1.14E+06	1.14E+06	1.14E+06	NULL	AS	O43684	BUB3

882.1	Ran GTPase-activating protein 1	0.00E+00	1.14E+06	1.14E+06	1.14E+06	NULL	AS	P46060	RANGAP1
507.1	Transportin-1	0.00E+00	1.15E+06	1.15E+06	1.15E+06	NULL	AS	Q92973	TNPO1
423.1	Isoform Beta of Nucleolar and c	0.00E+00	1.16E+06	1.16E+06	1.16E+06	NULL	AS	Q14978-2	NOLC1
1095.1	Ubiquitin-like protein 5	0.00E+00	1.16E+06	1.16E+06	1.16E+06	NULL	AS	Q9BZL1	UBL5
1207.1	GATA zinc finger domain contai	0.00E+00	1.16E+06	1.16E+06	1.16E+06	NULL	AS	B5MC40	GATAD2A
859.1	Synaptic vesicle membrane prot	0.00E+00	1.17E+06	1.17E+06	1.17E+06	NULL	AS	Q99536	VAT1
934.1	Cyclic AMP-dependent transcrip	0.00E+00	1.17E+06	1.17E+06	1.17E+06	NULL	AS	P18850	ATF6
1338.1	E3 ubiquitin-protein ligase TRIM	0.00E+00	1.17E+06	1.17E+06	1.17E+06	NULL	AS	Q6AZZ1	TRIM68
1613.1	T-cell receptor delta chain C reg	0.00E+00	1.17E+06	1.17E+06	1.17E+06	NULL	AS	B7Z8K6	TRDC
2332.1	E3 ubiquitin-protein ligase CBL	0.00E+00	1.17E+06	1.17E+06	1.17E+06	NULL	AS	P22681	CBL
452.1	40S ribosomal protein S27	0.00E+00	1.18E+06	1.18E+06	1.18E+06	NULL	AS	H0YMV8	RPS27L
547.1	Isoform 2 of Cytochrome c oxida	0.00E+00	1.18E+06	1.18E+06	1.18E+06	NULL	AS	Q5JTJ3-2	COA6
594.1	Coronin-1B	0.00E+00	1.18E+06	1.18E+06	1.18E+06	NULL	AS	Q9BR76	CORO1B
1640.1	Protein FAM221A	0.00E+00	1.18E+06	1.18E+06	1.18E+06	NULL	AS	A4D161	FAM221A
1738.1	Sterol 26-hydroxylase, mitochor	0.00E+00	1.18E+06	1.18E+06	1.18E+06	NULL	AS	Q02318	CYP27A1
2494.1	Olfactory receptor 51B4	0.00E+00	1.18E+06	1.18E+06	1.18E+06	NULL	AS	Q9Y5P0	OR51B4
2591.1	Treslin	0.00E+00	1.18E+06	1.18E+06	1.18E+06	NULL	AS	Q7Z2Z1	TICRR
544.1	Nucleolar protein 56	0.00E+00	1.19E+06	1.19E+06	1.19E+06	NULL	AS	O00567	NOP56
1482.1	Utrophin	0.00E+00	1.19E+06	1.19E+06	1.19E+06	NULL	AS	P46939	UTRN
1459.1	Protein phosphatase 1 regulatoı	0.00E+00	1.20E+06	1.20E+06	1.20E+06	NULL	AS	Q86XI6	PPP1R3B
1540.1	Neuralized-like protein 4	0.00E+00	1.21E+06	1.21E+06	1.21E+06	NULL	AS	Q96JN8	NEURL4
411.1	Short/branched chain specific a	0.00E+00	1.23E+06	1.23E+06	1.23E+06	NULL	AS	P45954	ACADSB
1365.1	SUN domain-containing protein	0.00E+00	1.24E+06	1.24E+06	1.24E+06	NULL	AS	A4D2Q0	UNC84A
2155.1	Zinc finger MYM-type protein 6	0.00E+00	1.25E+06	1.25E+06	1.25E+06	NULL	AS	O95789	ZMYM6
1879.1	Tripartite motif-containing prot	0.00E+00	1.29E+06	1.29E+06	1.29E+06	NULL	AS	B5MCJ9	TRIM66
620.1	Eukaryotic translation initiation	0.00E+00	1.30E+06	1.30E+06	1.30E+06	NULL	AS	Q9BY44	EIF2A
2101.1	Hepatocyte nuclear factor 1-bet	0.00E+00	1.30E+06	1.30E+06	1.30E+06	NULL	AS	P35680	HNF1B
2840.1	Zinc finger protein 224	0.00E+00	1.32E+06	1.32E+06	1.32E+06	NULL	AS	Q9NZL3	ZNF224
1610.1	Catalase	0.00E+00	1.33E+06	1.33E+06	1.33E+06	NULL	AS	P04040	CAT
661.1	60S ribosomal protein L21	0.00E+00	1.34E+06	1.34E+06	1.34E+06	NULL	AS	P46778	RPL21
1541.1	Zinc finger CCCH domain-contai	0.00E+00	1.35E+06	1.35E+06	1.35E+06	NULL	AS	Q8IWR0	ZC3H7A
2786.1	Trinucleotide repeat-containing	0.00E+00	1.36E+06	1.36E+06	1.36E+06	NULL	AS	O15417	TNRC18
501.1	60S ribosomal protein L10	0.00E+00	1.41E+06	1.41E+06	1.41E+06	NULL	AS	P27635	RPL10
344.1	Eukaryotic translation initiation	0.00E+00	1.43E+06	1.43E+06	1.43E+06	NULL	AS	O15371	EIF3D
640.1	14 kDa phosphohistidine phospl	0.00E+00	1.46E+06	1.46E+06	1.46E+06	NULL	AS	Q9NRX4	PHPT1

977.1	Lysophospholipase-like protein	0.00E+00	1.48E+06	1.48E+06	1.48E+06	NULL	AS	Q5VWZ2	LYPLAL1
1443.1	Isoform 3 of Collagen type IV alp	0.00E+00	1.48E+06	1.48E+06	1.48E+06	NULL	AS	Q9Y5P4-3	COL4A3BP
1022.1	Putative SAGE1-like protein	0.00E+00	1.50E+06	1.50E+06	1.50E+06	NULL	AS	A6NJ88	SGE1L
2714.1	Zinc finger Ran-binding domain-	0.00E+00	1.51E+06	1.51E+06	1.51E+06	NULL	AS	O95218	ZRANB2
2224.1	Nck-associated protein 5	0.00E+00	1.53E+06	1.53E+06	1.53E+06	NULL	AS	O14513	NCKAP5
1877.1	Erlin-1	0.00E+00	1.56E+06	1.56E+06	1.56E+06	NULL	AS	O75477	ERLIN1
1294.1	Diphosphoinositol polyphospha	0.00E+00	1.57E+06	1.57E+06	1.57E+06	NULL	AS	O95989	NUDT3
440.1	Serine/arginine-rich-splicing fac	0.00E+00	1.59E+06	1.59E+06	1.59E+06	NULL	AS	J3KTL2	SRSF1
766.1	Hypermethylated in cancer 2 pr	0.00E+00	1.61E+06	1.61E+06	1.61E+06	NULL	AS	Q96JB3	HIC2
480.1	60S ribosomal protein L29	0.00E+00	1.62E+06	1.62E+06	1.62E+06	NULL	AS	P47914	RPL29
1712.1	Zinc finger and BTB domain-con	0.00E+00	1.63E+06	1.63E+06	1.63E+06	NULL	AS	Q86UZ6	ZBTB46
2236.1	Signal recognition particle recep	0.00E+00	1.68E+06	1.68E+06	1.68E+06	NULL	AS	Q9Y5M8	SRPRB
169.3	Keratin, type I cytoskeletal 27	0.00E+00	1.73E+06	1.73E+06	1.73E+06	NULL	AS	Q7Z3Y8	KRT27
1197.1	EF-hand calcium-binding domai	0.00E+00	1.74E+06	1.74E+06	1.74E+06	NULL	AS	Q5THR3	EFCAB6
2600.1	Coiled-coil domain-containing p	0.00E+00	1.74E+06	1.74E+06	1.74E+06	NULL	AS	Q96MC2	DRC1
342.1	Isoform 3 of Cleavage and polya	0.00E+00	1.75E+06	1.75E+06	1.75E+06	NULL	AS	Q8N684-3	CPSF7
407.1	RNA-binding protein 12B	0.00E+00	1.77E+06	1.77E+06	1.77E+06	NULL	AS	Q8IXT5	RBM12B
2940.1	Tryptophan 2,3-dioxygenase	0.00E+00	1.80E+06	1.80E+06	1.80E+06	NULL	AS	P48775	TDO2
746.1	40S ribosomal protein S23	0.00E+00	1.81E+06	1.81E+06	1.81E+06	NULL	AS	P62266	RPS23
341.1	Pyrroline-5-carboxylate reducta	0.00E+00	1.83E+06	1.83E+06	1.83E+06	NULL	AS	B4DMU0	PYCR1
422.1	60S ribosomal protein L27a	0.00E+00	1.83E+06	1.83E+06	1.83E+06	NULL	AS	P46776	RPL27A
373.1	Plakophilin-3	0.00E+00	1.84E+06	1.84E+06	1.84E+06	NULL	AS	Q9Y446	PKP3
506.1	Vigilin	0.00E+00	1.88E+06	1.88E+06	1.88E+06	NULL	AS	Q00341	HDLBP
3149.1	Liprin-alpha-2	0.00E+00	1.88E+06	1.88E+06	1.88E+06	NULL	AS	F8VWG6	PPFIA2
900.1	Protein syndesmos	0.00E+00	1.94E+06	1.94E+06	1.94E+06	NULL	AS	Q9BRJ7	NUDT16L1
1433.1	Isoform 4 of Vacuolar protein sc	0.00E+00	1.95E+06	1.95E+06	1.95E+06	NULL	AS	Q5VIR6-4	VPS53
475.1	Isoform 2 of Ferrochelatase, mit	0.00E+00	1.96E+06	1.96E+06	1.96E+06	NULL	AS	P22830-2	FECH
1936.1	Zinc finger and BTB domain-con	0.00E+00	1.96E+06	1.96E+06	1.96E+06	NULL	AS	O15062	ZBTB5
3113.1	Transmembrane protein 143	0.00E+00	1.96E+06	1.96E+06	1.96E+06	NULL	AS	B4DMT0	TMEM143
529.1	Isoform 2 of Chromodomain-hel	0.00E+00	1.97E+06	1.97E+06	1.97E+06	NULL	AS	Q14839-2	CHD4
891.1	WW domain-binding protein 11	0.00E+00	2.01E+06	2.01E+06	2.01E+06	NULL	AS	Q9Y2W2	WBP11
340.1	60S ribosomal protein L15	0.00E+00	2.03E+06	2.03E+06	2.03E+06	NULL	AS	P61313	RPL15
559.1	N-acetylglucosamine-6-sulfatase	0.00E+00	2.06E+06	2.06E+06	2.06E+06	NULL	AS	F6S8M0	GNS
447.1	60S ribosomal protein L23a	0.00E+00	2.07E+06	2.07E+06	2.07E+06	NULL	AS	A8MUS3	RPL23A
916.1	Isoform 2 of DNA (cytosine-5)-m	0.00E+00	2.09E+06	2.09E+06	2.09E+06	NULL	AS	P26358-2	DNMT1

817.1	Nuclear pore complex protein N	0.00E+00	2.10E+06	2.10E+06	2.10E+06	NULL	AS	P52948	NUP98
531.1	Septin-8	0.00E+00	2.12E+06	2.12E+06	2.12E+06	NULL	AS	Q92599	SEPT8
2008.1	Presenilin-1	0.00E+00	2.18E+06	2.18E+06	2.18E+06	NULL	AS	P49768	PSEN1
742.1	Activated RNA polymerase II tra	0.00E+00	2.21E+06	2.21E+06	2.21E+06	NULL	AS	P53999	SUB1
555.1	Glucosidase 2 subunit beta	0.00E+00	2.22E+06	2.22E+06	2.22E+06	NULL	AS	K7ELL7	PRKCSH
790.1	THO complex subunit 4	0.00E+00	2.22E+06	2.22E+06	2.22E+06	NULL	AS	E9PB61	ALYREF
333.1	Specifically androgen-regulated	0.00E+00	2.23E+06	2.23E+06	2.23E+06	NULL	AS	Q9BW04	SARG
2383.1	Serine/threonine-protein kinase	0.00E+00	2.24E+06	2.24E+06	2.24E+06	NULL	AS	P0C263	SBK2
850.1	CWF19-like protein 2	0.00E+00	2.28E+06	2.28E+06	2.28E+06	NULL	AS	Q2TBE0	CWF19L2
832.1	Importin subunit alpha	0.00E+00	2.31E+06	2.31E+06	2.31E+06	NULL	AS	F5GYL8	KPNA6
1621.1	Serine/threonine-protein kinase	0.00E+00	2.31E+06	2.31E+06	2.31E+06	NULL	AS	O00506	STK25
432.1	Eukaryotic translation initiation	0.00E+00	2.34E+06	2.34E+06	2.34E+06	NULL	AS	P20042	EIF2S2
278.1	60S ribosomal protein L3	0.00E+00	2.37E+06	2.37E+06	2.37E+06	NULL	AS	P39023	RPL3
410.1	DNA replication licensing factor	0.00E+00	2.37E+06	2.37E+06	2.37E+06	NULL	AS	P33992	MCM5
190.1	Kinectin	0.00E+00	2.39E+06	2.39E+06	2.39E+06	NULL	AS	Q86UP2	KTN1
707.1	Aldehyde dehydrogenase X, mit	0.00E+00	2.40E+06	2.40E+06	2.40E+06	NULL	AS	P30837	ALDH1B1
392.1	Selenoprotein H	0.00E+00	2.42E+06	2.42E+06	2.42E+06	NULL	AS	Q8IZQ5	SELH
599.1	Isoform 2 of Apoptosis inhibitor	0.00E+00	2.42E+06	2.42E+06	2.42E+06	NULL	AS	Q9BZZ5-2	API5
961.1	Huntingtin	0.00E+00	2.42E+06	2.42E+06	2.42E+06	NULL	AS	P42858	HTT
44.3	Peroxiredoxin-4	0.00E+00	2.45E+06	2.45E+06	2.45E+06	NULL	AS	Q13162	PRDX4
713.1	Isoform 3 of Protein scribble ho	0.00E+00	2.46E+06	2.46E+06	2.46E+06	NULL	AS	Q14160-3	SCRIB
434.1	Heterogeneous nuclear ribonuc	0.00E+00	2.48E+06	2.48E+06	2.48E+06	NULL	AS	P31942	HNRNPH3
359.1	E3 ubiquitin/ISG15 ligase TRIM2	0.00E+00	2.52E+06	2.52E+06	2.52E+06	NULL	AS	Q14258	TRIM25
1493.1	UPF0568 protein C14orf166	0.00E+00	2.53E+06	2.53E+06	2.53E+06	NULL	AS	Q9Y224	C14orf166
360.1	ATP-dependent RNA helicase A	0.00E+00	2.55E+06	2.55E+06	2.55E+06	NULL	AS	Q08211	DHX9
703.1	Protocadherin Fat 1	0.00E+00	2.56E+06	2.56E+06	2.56E+06	NULL	AS	Q14517	FAT1
842.1	Isoform Beta-4B of Integrin beta	0.00E+00	2.56E+06	2.56E+06	2.56E+06	NULL	AS	P16144-3	ITGB4
275.1	Regulator of microtubule dyna	0.00E+00	2.59E+06	2.59E+06	2.59E+06	NULL	AS	Q96DB5	RMDN1
2613.1	Cubilin	0.00E+00	2.68E+06	2.68E+06	2.68E+06	NULL	AS	O60494	CUBN
377.1	Ras GTPase-activating protein-b	0.00E+00	2.79E+06	2.79E+06	2.79E+06	NULL	AS	Q9UN86	G3BP2
837.1	Isoform SM-B1 of Small nuclear	0.00E+00	2.79E+06	2.79E+06	2.79E+06	NULL	AS	P14678-3	SNRPB
358.1	60S ribosomal protein L11	0.00E+00	2.85E+06	2.85E+06	2.85E+06	NULL	AS	P62913	RPL11
405.1	Interleukin enhancer binding fa	0.00E+00	2.90E+06	2.90E+06	2.90E+06	NULL	AS	Q12906	ILF3
472.1	Thioredoxin	0.00E+00	3.03E+06	3.03E+06	3.03E+06	NULL	AS	P10599	TXN
412.1	Isoform 2 of Succinyl-CoA ligase	0.00E+00	3.04E+06	3.04E+06	3.04E+06	NULL	AS	Q96I99-2	SUCLG2

385.1	U1 small nuclear ribonucleoprot	0.00E+00	3.08E+06	3.08E+06	3.08E+06	NULL	AS	P08621	SNRNP70
238.1	SAFB protein	0.00E+00	3.13E+06	3.13E+06	3.13E+06	NULL	AS	Q15424	SAFB
355.1	Serine/threonine-protein kinase	0.00E+00	3.33E+06	3.33E+06	3.33E+06	NULL	AS	O96013	PAK4
1470.1	Thioredoxin domain-containing	0.00E+00	3.37E+06	3.37E+06	3.37E+06	NULL	AS	Q6PKC3	TXNDC11
291.1	Isoform 3 of Cytoskeleton-assoc	0.00E+00	3.41E+06	3.41E+06	3.41E+06	NULL	AS	Q14008-3	CKAP5
259.1	60S ribosomal protein L7	0.00E+00	3.48E+06	3.48E+06	3.48E+06	NULL	AS	P18124	RPL7
327.1	Transcription elongation regulat	0.00E+00	3.53E+06	3.53E+06	3.53E+06	NULL	AS	O14776	TCERG1
415.1	Arginine--tRNA ligase, cytoplasn	0.00E+00	3.56E+06	3.56E+06	3.56E+06	NULL	AS	P54136	RARS
399.1	Alpha-L-iduronidase	0.00E+00	3.68E+06	3.68E+06	3.68E+06	NULL	AS	P35475	IDUA
292.1	ATP-binding cassette sub-family	0.00E+00	3.82E+06	3.82E+06	3.82E+06	NULL	AS	Q75MJ1	ABCF2
348.1	Heterogeneous nuclear ribonuc	0.00E+00	3.82E+06	3.82E+06	3.82E+06	NULL	AS	O14979	HNRPDL
279.1	Caprin-1	0.00E+00	3.92E+06	3.92E+06	3.92E+06	NULL	AS	Q14444	CAPRIN1
326.1	3-hydroxyacyl-CoA dehydrogena	0.00E+00	4.06E+06	4.06E+06	4.06E+06	NULL	AS	Q99714	HSD17B10
454.1	Elongation factor 1-beta	0.00E+00	4.08E+06	4.08E+06	4.08E+06	NULL	AS	P24534	EEF1B2
759.1	40S ribosomal protein S15	0.00E+00	4.09E+06	4.09E+06	4.09E+06	NULL	AS	K7ELC2	RPS15
490.1	Isoform 2 of Peptidyl-prolyl cis-t	0.00E+00	4.12E+06	4.12E+06	4.12E+06	NULL	AS	Q9Y237-2	PIN4
357.1	Septin-9	0.00E+00	4.16E+06	4.16E+06	4.16E+06	NULL	AS	Q9UHD8	SEPT9
404.1	40S ribosomal protein S4, X isof	0.00E+00	4.18E+06	4.18E+06	4.18E+06	NULL	AS	P62701	RPS4X
302.1	Mitochondrial import inner mer	0.00E+00	4.22E+06	4.22E+06	4.22E+06	NULL	AS	G3XAN8	TIMM8B
205.1	Heterogeneous nuclear ribonuc	0.00E+00	4.32E+06	4.32E+06	4.32E+06	NULL	AS	P14866	HNRNPL
309.1	60S ribosomal protein L7a	0.00E+00	4.43E+06	4.43E+06	4.43E+06	NULL	AS	P62424	RPL7A
538.1	Very long-chain-specific acyl-Co	0.00E+00	4.70E+06	4.70E+06	4.70E+06	NULL	AS	P49748	ACADVL
591.1	Dihydrolipoyl dehydrogenase, m	0.00E+00	4.77E+06	4.77E+06	4.77E+06	NULL	AS	P09622	DLD
281.1	High mobility group protein B1	0.00E+00	4.95E+06	4.95E+06	4.95E+06	NULL	AS	P09429	HMGB1
76.1	Heterogeneous nuclear ribonuc	0.00E+00	5.00E+06	5.00E+06	5.00E+06	NULL	AS	G8JLB6	HNRNPH1
406.1	Small nuclear ribonucleoprotein	0.00E+00	5.07E+06	5.07E+06	5.07E+06	NULL	AS	P62306	SNRPF
408.1	Small nuclear ribonucleoprotein	0.00E+00	5.11E+06	5.11E+06	5.11E+06	NULL	AS	P62316	SNRPD2
134.1	Poly [ADP-ribose] polymerase 1	0.00E+00	5.12E+06	5.12E+06	5.12E+06	NULL	AS	P09874	PARP1
578.1	Dedicator of cytokinesis protein	0.00E+00	5.37E+06	5.37E+06	5.37E+06	NULL	AS	Q14185	DOCK1
122.1	Serine hydroxymethyltransferas	0.00E+00	5.38E+06	5.38E+06	5.38E+06	NULL	AS	P34897	SHMT2
151.1	Electron transfer flavoprotein su	0.00E+00	5.45E+06	5.45E+06	5.45E+06	NULL	AS	P13804	ETFA
316.1	Protein RCC2	0.00E+00	5.46E+06	5.46E+06	5.46E+06	NULL	AS	Q9P258	RCC2
364.1	60S ribosomal protein L13a	0.00E+00	5.47E+06	5.47E+06	5.47E+06	NULL	AS	P40429	RPL13A
288.1	Isoform 4 of Double-stranded R	0.00E+00	5.48E+06	5.48E+06	5.48E+06	NULL	AS	P55265-4	ADAR
154.1	Phenylalanine--tRNA ligase beta	0.00E+00	5.53E+06	5.53E+06	5.53E+06	NULL	AS	Q9NSD9	FARSB

249.1	Coiled-coil domain-containing p	0.00E+00	5.60E+06	5.60E+06	5.60E+06	NULL	AS	Q96CT7	CCDC124
226.1	Isoform 2 of Cleavage and polya	0.00E+00	5.65E+06	5.65E+06	5.65E+06	NULL	AS	Q16630-2	CPSF6
588.1	Isoform 5 of RNA-binding protei	0.00E+00	5.75E+06	5.75E+06	5.75E+06	NULL	AS	Q01844-5	EWSR1
162.1	60S ribosomal protein L4	0.00E+00	6.22E+06	6.22E+06	6.22E+06	NULL	AS	P36578	RPL4
171.1	Bcl-2-associated transcription fa	0.00E+00	6.38E+06	6.38E+06	6.38E+06	NULL	AS	Q9NYF8	BCLAF1
159.1	Protein transport protein Sec24	0.00E+00	6.51E+06	6.51E+06	6.51E+06	NULL	AS	O95486	SEC24A
334.1	Glutathione reductase, mitocho	0.00E+00	6.55E+06	6.55E+06	6.55E+06	NULL	AS	P00390	GSR
320.1	40S ribosomal protein S16	0.00E+00	6.56E+06	6.56E+06	6.56E+06	NULL	AS	P62249	RPS16
213.1	Protein RPSAP58	0.00E+00	6.66E+06	6.66E+06	6.66E+06	NULL	AS	A6NE09	RPSAP58
936.1	Interleukin enhancer-binding fa	0.00E+00	6.70E+06	6.70E+06	6.70E+06	NULL	AS	Q12905	ILF2
285.1	Endothelial differentiation-relat	0.00E+00	7.09E+06	7.09E+06	7.09E+06	NULL	AS	O60869	EDF1
203.1	Isoform 7 of Fragile X mental re	0.00E+00	7.16E+06	7.16E+06	7.16E+06	NULL	AS	Q06787-7	FMR1
144.1	60S ribosomal protein L6	0.00E+00	7.28E+06	7.28E+06	7.28E+06	NULL	AS	Q02878	RPL6
282.1	40S ribosomal protein S21	0.00E+00	7.38E+06	7.38E+06	7.38E+06	NULL	AS	P63220	RPS21
499.1	Protein NipSnap homolog 1	0.00E+00	7.39E+06	7.39E+06	7.39E+06	NULL	AS	Q9BPW8	NIPSNAP1
240.1	60S ribosomal protein L27	0.00E+00	7.95E+06	7.95E+06	7.95E+06	NULL	AS	P61353	RPL27
86.1	ATP-dependent RNA helicase D	0.00E+00	8.39E+06	8.39E+06	8.39E+06	NULL	AS	Q92499	DDX1
256.1	Isoform 5 of Ubiquitin-associate	0.00E+00	8.67E+06	8.67E+06	8.67E+06	NULL	AS	Q14157-5	UBAP2L
301.1	Phenylalanine--tRNA ligase alph	0.00E+00	8.72E+06	8.72E+06	8.72E+06	NULL	AS	K7ER00	FARSA
207.1	60S ribosomal protein L8	0.00E+00	9.83E+06	9.83E+06	9.83E+06	NULL	AS	P62917	RPL8
180.1	60S ribosomal protein L24	0.00E+00	9.89E+06	9.89E+06	9.89E+06	NULL	AS	P83731	RPL24
156.1	Cold-inducible RNA-binding pro	0.00E+00	1.01E+07	1.01E+07	1.01E+07	NULL	AS	Q14011	CIRBP
387.1	60S ribosomal protein L32	0.00E+00	1.04E+07	1.04E+07	1.04E+07	NULL	AS	F8W727	RPL32
48.1	Serine/arginine repetitive matri	0.00E+00	1.07E+07	1.07E+07	1.07E+07	NULL	AS	Q9UQ35	SRRM2
619.1	Isoform 2 of Protein FAM98B	0.00E+00	1.08E+07	1.08E+07	1.08E+07	NULL	AS	Q52LJ0-2	FAM98B
165.1	60S ribosomal protein L5	0.00E+00	1.09E+07	1.09E+07	1.09E+07	NULL	AS	P46777	RPL5
102.1	Heterogeneous nuclear ribonuc	0.00E+00	1.10E+07	1.10E+07	1.10E+07	NULL	AS	P07910	HNRNPC
209.1	40S ribosomal protein S5	0.00E+00	1.15E+07	1.15E+07	1.15E+07	NULL	AS	P46782	RPS5
575.1	Protein FAM98A	0.00E+00	1.20E+07	1.20E+07	1.20E+07	NULL	AS	Q8NCA5	FAM98A
150.1	40S ribosomal protein S14	0.00E+00	1.30E+07	1.30E+07	1.30E+07	NULL	AS	P62263	RPS14
153.1	Thyroid hormone receptor-asso	0.00E+00	1.42E+07	1.42E+07	1.42E+07	NULL	AS	Q9Y2W1	THRAP3
246.1	Cleavage and polyadenylation s	0.00E+00	1.54E+07	1.54E+07	1.54E+07	NULL	AS	O43809	NUDT21
60.1	RNA-binding protein 14	0.00E+00	1.57E+07	1.57E+07	1.57E+07	NULL	AS	Q96PK6	RBM14
73.1	Paraspeckle component 1	0.00E+00	1.72E+07	1.72E+07	1.72E+07	NULL	AS	Q8WXF1	PSPC1
148.1	Ras GTPase-activating protein-b	0.00E+00	1.83E+07	1.83E+07	1.83E+07	NULL	AS	Q13283	G3BP1

198.1	Fragile X mental retardation syn	0.00E+00	2.12E+07	2.12E+07	2.12E+07	NULL	AS	P51114	FXR1
82.1	Protein transport protein Sec24	0.00E+00	2.53E+07	2.53E+07	2.53E+07	NULL	AS	B7ZKM8	SEC24B
268.1	KH domain-containing, RNA-bin	0.00E+00	2.59E+07	2.59E+07	2.59E+07	NULL	AS	Q07666	KHDRBS1
193.1	40S ribosomal protein S25	0.00E+00	2.70E+07	2.70E+07	2.70E+07	NULL	AS	P62851	RPS25
139.1	60S ribosomal protein L9	0.00E+00	3.13E+07	3.13E+07	3.13E+07	NULL	AS	P32969	RPL9
56.1	Prelamin-A/C	0.00E+00	3.28E+07	3.28E+07	3.28E+07	NULL	AS	P02545	LMNA
45.1	Isoform 4 of YLP motif-containi	0.00E+00	4.07E+07	4.07E+07	4.07E+07	NULL	AS	P49750-4	YLPM1
34.1	Nuclear receptor coactivator 5	0.00E+00	4.37E+07	4.37E+07	4.37E+07	NULL	AS	Q9HCD5	NCOA5
104.1	40S ribosomal protein S10	0.00E+00	6.52E+07	6.52E+07	6.52E+07	NULL	AS	P46783	RPS10
189.1	Isoform 2 of 40S ribosomal prot	0.00E+00	8.27E+07	8.27E+07	8.27E+07	NULL	AS	P60866-2	RPS20
57.1	40S ribosomal protein S19	0.00E+00	1.27E+08	1.27E+08	1.27E+08	NULL	AS	P39019	RPS19
66.1	TATA-binding protein-associate	0.00E+00	1.64E+08	1.64E+08	1.64E+08	NULL	AS	Q92804	TAF15
6.1	Splicing factor, proline- and glut	0.00E+00	2.51E+08	2.51E+08	2.51E+08	NULL	AS	P23246	SFPQ
2985.1	WD repeat domain phosphoino	4.27E+02	0.00E+00	-4.27E+02	-4.27E+02	NULL	AD	Q5MNZ6	WDR45B
1965.1	NACHT, LRR and PYD domains-c	9.93E+02	0.00E+00	-9.93E+02	-9.93E+02	NULL	AD	Q9NX02	NLRP2
2696.1	Isoform 2 of Small G protein sig	1.72E+03	0.00E+00	-1.72E+03	-1.72E+03	NULL	AD	O43147-2	SGSM2
1729.1	Probable helicase with zinc fing	1.74E+03	0.00E+00	-1.74E+03	-1.74E+03	NULL	AD	J3QS41	HELZ
1849.1	Methyl-CpG-binding domain pr	1.97E+03	0.00E+00	-1.97E+03	-1.97E+03	NULL	AD	O95983	MBD3
2993.1	Isoform 2 of Tumor suppressor	2.10E+03	0.00E+00	-2.10E+03	-2.10E+03	NULL	AD	Q12888-2	TP53BP1
2870.1	Aurora kinase A	2.14E+03	0.00E+00	-2.14E+03	-2.14E+03	NULL	AD	O14965	AURKA
2625.1	Immunoglobulin-like and fibron	2.16E+03	0.00E+00	-2.16E+03	-2.16E+03	NULL	AD	Q86VF2	IGFN1
2243.1	Protein very KIND	2.54E+03	0.00E+00	-2.54E+03	-2.54E+03	NULL	AD	E7ETM1	KNDC1
1447.1	Isoform 2 of Centromere protei	2.57E+03	0.00E+00	-2.57E+03	-2.57E+03	NULL	AD	Q8N0S6-2	CENPL
2467.1	Isoform 4 of Forkhead box prote	2.58E+03	0.00E+00	-2.58E+03	-2.58E+03	NULL	AD	Q08050-3	FOXM1
2184.1	X-linked retinitis pigmentosa GT	2.60E+03	0.00E+00	-2.60E+03	-2.60E+03	NULL	AD	Q96KN7	RPGRIP1
2863.1	Isoform 2A of N-glycosylase/DN	2.66E+03	0.00E+00	-2.66E+03	-2.66E+03	NULL	AD	O15527-4	OGG1
1881.1	RAP1, GTP-GDP dissociation sti	2.70E+03	0.00E+00	-2.70E+03	-2.70E+03	NULL	AD	P52306	RAP1GDS1
2306.1	SLIT-ROBO Rho GTPase-activati	3.01E+03	0.00E+00	-3.01E+03	-3.01E+03	NULL	AD	O75044	SRGAP2
2896.1	Polymerase I and transcript rele	3.30E+03	0.00E+00	-3.30E+03	-3.30E+03	NULL	AD	Q6NZI2	PTRF
1918.1	3-oxo-5-alpha-steroid 4-dehydr	3.84E+03	0.00E+00	-3.84E+03	-3.84E+03	NULL	AD	F5GXK9	SRD5A1
1859.1	1-phosphatidylinositol 4,5-bisph	4.22E+03	0.00E+00	-4.22E+03	-4.22E+03	NULL	AD	Q01970	PLCB3
2529.1	Protein SSUH2 homolog	4.73E+03	0.00E+00	-4.73E+03	-4.73E+03	NULL	AD	Q9Y2M2	SSUH2
959.1	Small subunit processome comp	4.78E+03	0.00E+00	-4.78E+03	-4.78E+03	NULL	AD	O75691	UTP20
1071.1	Leucine-rich repeat-containing	4.84E+03	0.00E+00	-4.84E+03	-4.84E+03	NULL	AD	Q9Y546	LRRC42
1836.1	Protein-arginine deiminase type	5.36E+03	0.00E+00	-5.36E+03	-5.36E+03	NULL	AD	Q9UM07	PADI4

2142.1	Cysteine-rich protein 2-binding	5.39E+03	0.00E+00	-5.39E+03	-5.39E+03	NULL	AD	Q9H8E8	CSRP2BP
1403.1	Leucine-rich repeat neuronal pr	5.42E+03	0.00E+00	-5.42E+03	-5.42E+03	NULL	AD	Q8WUT4	LRRN4
2800.1	One cut domain family member	5.42E+03	0.00E+00	-5.42E+03	-5.42E+03	NULL	AD	O60422	ONECUT3
1367.1	Bromodomain-containing prote	5.43E+03	0.00E+00	-5.43E+03	-5.43E+03	NULL	AD	Q9H0E9	BRD8
1636.1	Unconventional myosin-VIIa	5.50E+03	0.00E+00	-5.50E+03	-5.50E+03	NULL	AD	Q13402	MYO7A
2726.1	Mitogen-activated protein kinas	5.52E+03	0.00E+00	-5.52E+03	-5.52E+03	NULL	AD	Q9Y6R4	MAP3K4
2428.1	Replication factor C subunit 1	5.54E+03	0.00E+00	-5.54E+03	-5.54E+03	NULL	AD	P35251	RFC1
2914.1	Atrial natriuretic peptide recept	5.54E+03	0.00E+00	-5.54E+03	-5.54E+03	NULL	AD	B0ZBF1	NPR1
1830.1	Tenascin-X	5.78E+03	0.00E+00	-5.78E+03	-5.78E+03	NULL	AD	P22105	TNXB
2612.1	Death-associated protein kinase	5.87E+03	0.00E+00	-5.87E+03	-5.87E+03	NULL	AD	O43293	DAPK3
3098.1	Ubiquitin carboxyl-terminal hyd	5.89E+03	0.00E+00	-5.89E+03	-5.89E+03	NULL	AD	B5MEG5	USP19
2112.1	Coiled-coil domain-containing p	5.95E+03	0.00E+00	-5.95E+03	-5.95E+03	NULL	AD	Q6ZRK6	CCDC73
1825.1	Extracellular calcium-sensing re	5.97E+03	0.00E+00	-5.97E+03	-5.97E+03	NULL	AD	E7ENE0	CASR
2538.1	Isoform 2 of Protein FAM35A	6.16E+03	0.00E+00	-6.16E+03	-6.16E+03	NULL	AD	Q86V20-2	FAM35A
3169.1	Adenylate kinase 8	6.21E+03	0.00E+00	-6.21E+03	-6.21E+03	NULL	AD	Q96MA6	AK8
2573.1	ATPase family AAA domain-cont	6.23E+03	0.00E+00	-6.23E+03	-6.23E+03	NULL	AD	Q6PL18	ATAD2
1080.1	Isoform 3 of Zinc-activated ligan	6.31E+03	0.00E+00	-6.31E+03	-6.31E+03	NULL	AD	Q401N2-3	ZACN
1412.1	Isoform 4 of Protein CBFA2T2	6.40E+03	0.00E+00	-6.40E+03	-6.40E+03	NULL	AD	O43439-4	CBFA2T2
2098.1	Retinoic acid receptor alpha	6.40E+03	0.00E+00	-6.40E+03	-6.40E+03	NULL	AD	A8MUP8	RARA
2267.1	Nucleoporin GLE1	6.50E+03	0.00E+00	-6.50E+03	-6.50E+03	NULL	AD	Q53GS7	GLE1
2856.1	Thioredoxin domain-containing	6.58E+03	0.00E+00	-6.58E+03	-6.58E+03	NULL	AD	Q86VQ3	TXNDC2
1311.1	Calmodulin-binding transcriptio	6.58E+03	0.00E+00	-6.58E+03	-6.58E+03	NULL	AD	O94983	CAMTA2
2441.1	Heat shock protein beta-2	6.60E+03	0.00E+00	-6.60E+03	-6.60E+03	NULL	AD	Q16082	HSPB2
1624.1	Isoform 2 of Semaphorin-4B	6.68E+03	0.00E+00	-6.68E+03	-6.68E+03	NULL	AD	Q9NPR2-2	SEMA4B
2207.1	Isoamyl acetate-hydrolyzing est	6.89E+03	0.00E+00	-6.89E+03	-6.89E+03	NULL	AD	Q2TAA2	IAH1
1035.1	Isoform 2 of Dual specificity mit	6.92E+03	0.00E+00	-6.92E+03	-6.92E+03	NULL	AD	P46734-3	MAP2K3
1997.1	Protein TSSC4	6.92E+03	0.00E+00	-6.92E+03	-6.92E+03	NULL	AD	Q9Y5U2	TSSC4
1063.1	Solute carrier family 12 membe	6.97E+03	0.00E+00	-6.97E+03	-6.97E+03	NULL	AD	Q9Y666	SLC12A7
1057.1	Isoform 2 of Gamma-aminobuty	6.98E+03	0.00E+00	-6.98E+03	-6.98E+03	NULL	AD	P28472-2	GABRB3
2402.1	von Willebrand factor D and EG	7.12E+03	0.00E+00	-7.12E+03	-7.12E+03	NULL	AD	Q8N2E2	VWDE
2141.1	RNA polymerase II-associated p	7.35E+03	0.00E+00	-7.35E+03	-7.35E+03	NULL	AD	Q9H6T3	RPAP3
1271.1	NDRG family member 3	7.42E+03	0.00E+00	-7.42E+03	-7.42E+03	NULL	AD	Q5TH30	NDRG3
1865.1	V-set and immunoglobulin dom	7.52E+03	0.00E+00	-7.52E+03	-7.52E+03	NULL	AD	Q8N0Z9	VSIG10
2056.1	Ribosomal protein S6 kinase del	7.65E+03	0.00E+00	-7.65E+03	-7.65E+03	NULL	AD	Q96S38	RPS6KC1
3128.1	Isoform 3 of GRAM domain-con	7.73E+03	0.00E+00	-7.73E+03	-7.73E+03	NULL	AD	Q96HH9-3	GRAMD3

1333.1	Protein sidekick-1	8.15E+03	0.00E+00	-8.15E+03	-8.15E+03	NULL	AD	Q7Z5N4	SDK1
3246.1	Receptor-interacting serine/thre	8.22E+03	0.00E+00	-8.22E+03	-8.22E+03	NULL	AD	Q13546	RIPK1
1260.1	UDP-N-acetylglucosamine trans	8.40E+03	0.00E+00	-8.40E+03	-8.40E+03	NULL	AD	Q96F25	ALG14
2114.1	ELAV (Embryonic lethal, abnorm	8.48E+03	0.00E+00	-8.48E+03	-8.48E+03	NULL	AD	B1AM49	ELAVL2
1743.1	Isoform 3 of Trafficking protein	8.49E+03	0.00E+00	-8.49E+03	-8.49E+03	NULL	AD	P0DI81-3	TRAPPC2
2213.1	DNA-directed RNA polymerase I	8.57E+03	0.00E+00	-8.57E+03	-8.57E+03	NULL	AD	Q9NW08	POLR3B
1727.1	Brefeldin A-inhibited guanine nu	8.65E+03	0.00E+00	-8.65E+03	-8.65E+03	NULL	AD	Q5TH69	ARFGEF3
2677.1	Probable ATP-dependent DNA h	8.65E+03	0.00E+00	-8.65E+03	-8.65E+03	NULL	AD	A2PYH4	HFM1
2614.1	Non-receptor tyrosine-protein k	8.83E+03	0.00E+00	-8.83E+03	-8.83E+03	NULL	AD	Q13470	TNK1
1771.1	Protein TSSC1	8.89E+03	0.00E+00	-8.89E+03	-8.89E+03	NULL	AD	F8WB12	TSSC1
3232.1	DnaJ homolog subfamily C mem	9.32E+03	0.00E+00	-9.32E+03	-9.32E+03	NULL	AD	Q9Y5T4	DNAJC15
169.2	Keratin, type I cytoskeletal 13	9.41E+03	0.00E+00	-9.41E+03	-9.41E+03	NULL	AD	P13646	KRT13
1976.1	Zinc finger protein 331	9.49E+03	0.00E+00	-9.49E+03	-9.49E+03	NULL	AD	Q9NQX6	ZNF331
2480.1	Isoform 5 of Golgin subfamily A	9.51E+03	0.00E+00	-9.51E+03	-9.51E+03	NULL	AD	Q13439-5	GOLGA4
3095.1	Dual specificity protein kinase C	9.59E+03	0.00E+00	-9.59E+03	-9.59E+03	NULL	AD	P49760	CLK2
2745.1	HEAT repeat-containing protein	9.69E+03	0.00E+00	-9.69E+03	-9.69E+03	NULL	AD	A6NES4	MROH2A
2387.1	WD repeat-containing protein 8	9.84E+03	0.00E+00	-9.84E+03	-9.84E+03	NULL	AD	Q6ZMY6	WDR88
2716.1	Isoform 3 of Zinc transporter 10	1.01E+04	0.00E+00	-1.01E+04	-1.01E+04	NULL	AD	Q6XR72-3	SLC30A10
2659.1	Protein PRR5-ARHGAP8	1.02E+04	0.00E+00	-1.02E+04	-1.02E+04	NULL	AD	B1AHC4	ARHGAP8
2487.1	Group 3 secretory phospholipas	1.03E+04	0.00E+00	-1.03E+04	-1.03E+04	NULL	AD	Q9NZ20	PLA2G3
2507.1	Pikachurin	1.06E+04	0.00E+00	-1.06E+04	-1.06E+04	NULL	AD	Q63HQ2	EGFLAM
1423.1	Liprin alpha4	1.14E+04	0.00E+00	-1.14E+04	-1.14E+04	NULL	AD	B1N949	PPFIA4
2048.1	MRG/MORF4L-binding protein	1.15E+04	0.00E+00	-1.15E+04	-1.15E+04	NULL	AD	Q9NV56	MRGBP
1796.1	Leucine-rich repeat-containing	1.17E+04	0.00E+00	-1.17E+04	-1.17E+04	NULL	AD	Q96NW7	LRRC7
2016.1	Isoform 3 of Probable G-protein	1.21E+04	0.00E+00	-1.21E+04	-1.21E+04	NULL	AD	Q8IZF2-3	GPR116
3106.1	Transcription elongation factor	1.26E+04	0.00E+00	-1.26E+04	-1.26E+04	NULL	AD	P63272	SUPT4H1
943.2	Isoform 3 of Obscurin	1.27E+04	0.00E+00	-1.27E+04	-1.27E+04	NULL	AD	Q5VST9-3	OBSCN
1984.1	Zinc finger CCCH domain-contai	1.27E+04	0.00E+00	-1.27E+04	-1.27E+04	NULL	AD	Q9UPT8	ZC3H4
2261.1	Protein eyes shut homolog	1.29E+04	0.00E+00	-1.29E+04	-1.29E+04	NULL	AD	Q5T1H1	EYS
1794.1	Nucleosome-remodeling factor	1.30E+04	0.00E+00	-1.30E+04	-1.30E+04	NULL	AD	Q12830	BPTF
1876.1	E3 ubiquitin-protein ligase Praja	1.30E+04	0.00E+00	-1.30E+04	-1.30E+04	NULL	AD	Q8NG27	PJA1
2292.1	Protein FAM193A	1.30E+04	0.00E+00	-1.30E+04	-1.30E+04	NULL	AD	P78312	FAM193A
2956.1	Argininosuccinate synthase	1.30E+04	0.00E+00	-1.30E+04	-1.30E+04	NULL	AD	P00966	ASS1
1121.1	AH receptor-interacting protein	1.31E+04	0.00E+00	-1.31E+04	-1.31E+04	NULL	AD	O00170	AIP
2535.1	Neuronal migration protein dou	1.31E+04	0.00E+00	-1.31E+04	-1.31E+04	NULL	AD	O43602	DCX

1441.1	Free fatty acid receptor 4	1.35E+04	0.00E+00	-1.35E+04	-1.35E+04	NULL	AD	Q5NUL3	FFAR4
1795.1	Centrosomal protein C10orf90	1.35E+04	0.00E+00	-1.35E+04	-1.35E+04	NULL	AD	F5GZL2	C10orf90
2474.1	Zinc finger protein 408	1.35E+04	0.00E+00	-1.35E+04	-1.35E+04	NULL	AD	Q9H9D4	ZNF408
2732.1	Prokineticin-2	1.36E+04	0.00E+00	-1.36E+04	-1.36E+04	NULL	AD	Q9HC23	PROK2
1781.1	Frataxin, mitochondrial	1.36E+04	0.00E+00	-1.36E+04	-1.36E+04	NULL	AD	Q16595	FXN
2379.1	DNA mismatch repair protein M	1.37E+04	0.00E+00	-1.37E+04	-1.37E+04	NULL	AD	P52701	MSH6
2188.1	RRP15-like protein	1.40E+04	0.00E+00	-1.40E+04	-1.40E+04	NULL	AD	Q9Y3B9	RRP15
2468.1	Hypothetical gene supported by	1.42E+04	0.00E+00	-1.42E+04	-1.42E+04	NULL	AD	Q8N5S0	LOC389199
3064.1	NACHT, LRR and PYD domains-c	1.42E+04	0.00E+00	-1.42E+04	-1.42E+04	NULL	AD	Q7RTR0	NLRP9
3120.1	Isoform 2 of Single-strand select	1.44E+04	0.00E+00	-1.44E+04	-1.44E+04	NULL	AD	Q53HV7-2	SMUG1
1858.1	Ribosomal protein S6 kinase alp	1.46E+04	0.00E+00	-1.46E+04	-1.46E+04	NULL	AD	E9PKU3	RPS6KA4
1357.1	Probable tRNA threonylcarbam	1.48E+04	0.00E+00	-1.48E+04	-1.48E+04	NULL	AD	Q9H4B0	OSGEPL1
1439.1	Solute carrier organic anion tra	1.49E+04	0.00E+00	-1.49E+04	-1.49E+04	NULL	AD	F8W9W8	SLCO2A1
2132.1	PR domain zinc finger protein 2	1.51E+04	0.00E+00	-1.51E+04	-1.51E+04	NULL	AD	Q13029	PRDM2
2571.1	FERM and PDZ domain-containi	1.51E+04	0.00E+00	-1.51E+04	-1.51E+04	NULL	AD	Q5JV73	FRMPD3
3100.1	Serine/threonine-protein kinase	1.51E+04	0.00E+00	-1.51E+04	-1.51E+04	NULL	AD	F5H2J7	ULK1
1694.1	Isoform 2 of Chondroitin sulfate	1.54E+04	0.00E+00	-1.54E+04	-1.54E+04	NULL	AD	Q8N6G5-2	CSGALNACT2
3179.1	Diacylglycerol kinase kappa	1.54E+04	0.00E+00	-1.54E+04	-1.54E+04	NULL	AD	Q5KSL6	DGKK
1030.1	DNA-binding protein RFX7	1.57E+04	0.00E+00	-1.57E+04	-1.57E+04	NULL	AD	Q2KHR2	RFX7
1891.1	Poly [ADP-ribose] polymerase 2	1.58E+04	0.00E+00	-1.58E+04	-1.58E+04	NULL	AD	Q9UGN5	PARP2
1495.1	High affinity cAMP-specific and	1.60E+04	0.00E+00	-1.60E+04	-1.60E+04	NULL	AD	O60658	PDE8A
3224.1	60S ribosome subunit biogenesi	1.65E+04	0.00E+00	-1.65E+04	-1.65E+04	NULL	AD	Q9Y221	NIP7
1783.1	Tektin-2	1.66E+04	0.00E+00	-1.66E+04	-1.66E+04	NULL	AD	Q9UIF3	TEKT2
1438.1	Plastin-1	1.67E+04	0.00E+00	-1.67E+04	-1.67E+04	NULL	AD	Q14651	PLS1
2514.1	CUGBP Elav-like family member	1.68E+04	0.00E+00	-1.68E+04	-1.68E+04	NULL	AD	Q96J87	CELF6
2586.1	Hypoxia-inducible factor 1-alph	1.68E+04	0.00E+00	-1.68E+04	-1.68E+04	NULL	AD	Q9NWT6	HIF1AN
1068.1	Isoform 4 of Piezo-type mechan	1.69E+04	0.00E+00	-1.69E+04	-1.69E+04	NULL	AD	Q9H5I5-4	PIEZO2
2814.1	Isoform 2 of Adenosine recepto	1.70E+04	0.00E+00	-1.70E+04	-1.70E+04	NULL	AD	P33765-2	ADORA3
13.2	Pyruvate kinase isozymes R/L	1.71E+04	0.00E+00	-1.71E+04	-1.71E+04	NULL	AD	P30613	PKLR
1792.1	Putative olfactory receptor 52A	1.74E+04	0.00E+00	-1.74E+04	-1.74E+04	NULL	AD	A6NMU1	OR52A4
2765.1	Isoform 2 of Tyrosine-protein p	1.74E+04	0.00E+00	-1.74E+04	-1.74E+04	NULL	AD	P78324-2	SIRPA
3124.1	Zinc finger protein 560	1.74E+04	0.00E+00	-1.74E+04	-1.74E+04	NULL	AD	Q96MR9	ZNF560
2304.1	Phosphatase and actin regulato	1.77E+04	0.00E+00	-1.77E+04	-1.77E+04	NULL	AD	Q96KR7	PHACTR3
1543.1	DDB1- and CUL4-associated fact	1.78E+04	0.00E+00	-1.78E+04	-1.78E+04	NULL	AD	P61962	DCAF7
1982.1	Receptor-type tyrosine-protein	1.79E+04	0.00E+00	-1.79E+04	-1.79E+04	NULL	AD	Q16827	PTPRO

3130.1	Coiled-coil domain-containing p	1.79E+04	0.00E+00	-1.79E+04	-1.79E+04	NULL	AD	C9JV39	CCDC102B
1547.1	E3 ubiquitin-protein ligase HACE	1.82E+04	0.00E+00	-1.82E+04	-1.82E+04	NULL	AD	Q8IYU2	HACE1
1571.1	Isoform 7 of LETM1 domain-con	1.82E+04	0.00E+00	-1.82E+04	-1.82E+04	NULL	AD	Q6P1Q0-7	LETMD1
1649.1	Methylcytosine dioxygenase TE	1.82E+04	0.00E+00	-1.82E+04	-1.82E+04	NULL	AD	E7EQS8	TET2
2187.1	Neuropeptide W	1.82E+04	0.00E+00	-1.82E+04	-1.82E+04	NULL	AD	Q8N729	NPW
1007.1	Serine/threonine-protein kinase	1.83E+04	0.00E+00	-1.83E+04	-1.83E+04	NULL	AD	Q8TDX7	NEK7
3040.1	LIM domain-containing protein	1.84E+04	0.00E+00	-1.84E+04	-1.84E+04	NULL	AD	Q96IF1	AJUBA
2855.1	Zinc fingers and homeoboxes pr	1.85E+04	0.00E+00	-1.85E+04	-1.85E+04	NULL	AD	E5RGB8	ZHX1
2365.1	UDP-N-acetylglucosamine--pept	1.86E+04	0.00E+00	-1.86E+04	-1.86E+04	NULL	AD	O15294	OGT
2598.1	Kinesin-like protein KIF22	1.88E+04	0.00E+00	-1.88E+04	-1.88E+04	NULL	AD	Q14807	KIF22
769.1	BRO1 domain-containing protei	1.90E+04	0.00E+00	-1.90E+04	-1.90E+04	NULL	AD	Q5VW32	BROX
1390.1	Serine/threonine-protein kinase	1.92E+04	0.00E+00	-1.92E+04	-1.92E+04	NULL	AD	Q8TDR2	STK35
2014.1	Mediator of RNA polymerase II	1.94E+04	0.00E+00	-1.94E+04	-1.94E+04	NULL	AD	Q96HR3	MED30
2331.1	Isoform 2 of Peroxisome biogen	2.00E+04	0.00E+00	-2.00E+04	-2.00E+04	NULL	AD	O60683-2	PEX10
2005.1	Pumilio homolog 1	2.04E+04	0.00E+00	-2.04E+04	-2.04E+04	NULL	AD	Q5T1Z8	PUM1
1314.1	5'-3' exoribonuclease 2	2.05E+04	0.00E+00	-2.05E+04	-2.05E+04	NULL	AD	Q9H0D6	XRN2
2359.1	MAP3K12-binding inhibitory pr	2.06E+04	0.00E+00	-2.06E+04	-2.06E+04	NULL	AD	Q9NS73	MBIP
1923.1	Zinc finger protein 174	2.08E+04	0.00E+00	-2.08E+04	-2.08E+04	NULL	AD	Q15697	ZNF174
2045.1	Myelin-associated glycoprotein	2.09E+04	0.00E+00	-2.09E+04	-2.09E+04	NULL	AD	P20916	MAG
2065.1	cAMP-dependent protein kinase	2.11E+04	0.00E+00	-2.11E+04	-2.11E+04	NULL	AD	P17612	PRKACA
2463.1	Protein MMS22-like	2.11E+04	0.00E+00	-2.11E+04	-2.11E+04	NULL	AD	Q6ZRQ5	MMS22L
2249.1	Protein mago nashi homolog 2	2.13E+04	0.00E+00	-2.13E+04	-2.13E+04	NULL	AD	Q96A72	MAGOHB
1039.1	Isoform 2 of Transcription elong	2.18E+04	0.00E+00	-2.18E+04	-2.18E+04	NULL	AD	Q96EI5-2	TCEAL4
771.1	Target of rapamycin complex 2	2.19E+04	0.00E+00	-2.19E+04	-2.19E+04	NULL	AD	Q9BPZ7	MAPKAP1
1590.1	Mediator of RNA polymerase II	2.19E+04	0.00E+00	-2.19E+04	-2.19E+04	NULL	AD	Q15648	MED1
1156.1	Caprin-2	2.20E+04	0.00E+00	-2.20E+04	-2.20E+04	NULL	AD	Q6IMN6	CAPRIN2
772.1	7SK snRNA methylphosphate ca	2.21E+04	0.00E+00	-2.21E+04	-2.21E+04	NULL	AD	Q7L2J0	MEPCE
2404.1	Nuclear receptor coactivator 2	2.24E+04	0.00E+00	-2.24E+04	-2.24E+04	NULL	AD	Q15596	NCOA2
1523.1	Isoform 4 of Sperm flagellar pro	2.27E+04	0.00E+00	-2.27E+04	-2.27E+04	NULL	AD	Q9C093-4	SPEF2
3117.1	Partitioning defective 3 homolo	2.27E+04	0.00E+00	-2.27E+04	-2.27E+04	NULL	AD	Q8TEW8	PARD3B
1791.1	Rho guanine nucleotide exchan	2.32E+04	0.00E+00	-2.32E+04	-2.32E+04	NULL	AD	A1IGU5	ARHGEF37
1625.1	Spermatogenesis-associated pr	2.33E+04	0.00E+00	-2.33E+04	-2.33E+04	NULL	AD	Q7Z572	SPATA21
1516.1	Isoform 2 of Nuclear protein loc	2.34E+04	0.00E+00	-2.34E+04	-2.34E+04	NULL	AD	Q8TAT6-2	NPLOC4
3152.1	Probable G-protein coupled rec	2.36E+04	0.00E+00	-2.36E+04	-2.36E+04	NULL	AD	Q8IZ08	GPR135
876.1	Protein strawberry notch homol	2.37E+04	0.00E+00	-2.37E+04	-2.37E+04	NULL	AD	A3KN83	SBNO1

2025.1	Interferon regulatory factor 8	2.38E+04	0.00E+00	-2.38E+04	-2.38E+04	NULL	AD	Q02556	IRF8
2886.1	Isoform 5 of cAMP-specific 3',5'	2.40E+04	0.00E+00	-2.40E+04	-2.40E+04	NULL	AD	Q08499-6	PDE4D
1736.1	N-acyl-phosphatidylethanolami	2.41E+04	0.00E+00	-2.41E+04	-2.41E+04	NULL	AD	J3KR15	NAPEPLD
1785.1	Isoform 3 of Sodium channel pr	2.41E+04	0.00E+00	-2.41E+04	-2.41E+04	NULL	AD	Q9NY46-3	SCN3A
1981.1	Beta-adducin	2.41E+04	0.00E+00	-2.41E+04	-2.41E+04	NULL	AD	P35612	ADD2
1742.1	Beta-1,4-galactosyltransferase 3	2.43E+04	0.00E+00	-2.43E+04	-2.43E+04	NULL	AD	O60512	B4GALT3
168.2	Isoform 2 of Nucleoside diphos	2.44E+04	0.00E+00	-2.44E+04	-2.44E+04	NULL	AD	P15531-2	NME1
1550.1	Paired box protein Pax-1	2.44E+04	0.00E+00	-2.44E+04	-2.44E+04	NULL	AD	P15863	PAX1
2305.1	Vacuolar protein sorting-associa	2.47E+04	0.00E+00	-2.47E+04	-2.47E+04	NULL	AD	Q96RL7	VPS13A
2122.1	Tubulin polyglutamylase comple	2.51E+04	0.00E+00	-2.51E+04	-2.51E+04	NULL	AD	Q68CL5	TPGS2
1385.1	Cytoplasmic tRNA 2-thiolation p	2.54E+04	0.00E+00	-2.54E+04	-2.54E+04	NULL	AD	Q7Z7A3	CTU1
2925.1	Selenide, water dikinase 2	2.54E+04	0.00E+00	-2.54E+04	-2.54E+04	NULL	AD	J3KR58	SEPHS2
2665.1	Indoleamine 2,3-dioxygenase 1	2.57E+04	0.00E+00	-2.57E+04	-2.57E+04	NULL	AD	P14902	IDO1
1050.1	Protein unc-45 homolog A	2.59E+04	0.00E+00	-2.59E+04	-2.59E+04	NULL	AD	Q9H3U1	UNC45A
1496.1	Polymerase delta-interacting pr	2.62E+04	0.00E+00	-2.62E+04	-2.62E+04	NULL	AD	Q9BY77	POLDIP3
1703.1	Isoform 7 of Calcium/calmoduli	2.62E+04	0.00E+00	-2.62E+04	-2.62E+04	NULL	AD	Q13554-7	CAMK2B
1975.1	MOSC domain-containing prote	2.62E+04	0.00E+00	-2.62E+04	-2.62E+04	NULL	AD	Q969Z3	MARC2
2148.1	Glycerol kinase	2.62E+04	0.00E+00	-2.62E+04	-2.62E+04	NULL	AD	P32189	GK
2358.1	Neutral cholesterol ester hydrol	2.62E+04	0.00E+00	-2.62E+04	-2.62E+04	NULL	AD	F5H7K4	NCEH1
2648.1	Fukutin	2.62E+04	0.00E+00	-2.62E+04	-2.62E+04	NULL	AD	O75072	FKTN
2811.1	Next to BRCA1 gene 1 protein	2.62E+04	0.00E+00	-2.62E+04	-2.62E+04	NULL	AD	J3KPL5	NBR1
2058.1	EGF-like module-containing mu	2.64E+04	0.00E+00	-2.64E+04	-2.64E+04	NULL	AD	B4DWB8	EMR2
1384.1	Lysosomal protective protein	2.65E+04	0.00E+00	-2.65E+04	-2.65E+04	NULL	AD	P10619	CTSA
1044.1	Ras-related protein Rab-34, isof	2.75E+04	0.00E+00	-2.75E+04	-2.75E+04	NULL	AD	P0DI83	RAB34
1057.2	Isoform 3 of Gamma-aminobuty	2.77E+04	0.00E+00	-2.77E+04	-2.77E+04	NULL	AD	P47870-3	GABRB2
2163.1	TBC1 domain family member 19	2.77E+04	0.00E+00	-2.77E+04	-2.77E+04	NULL	AD	Q8N5T2	TBC1D19
923.1	Thioredoxin-like protein 1	2.82E+04	0.00E+00	-2.82E+04	-2.82E+04	NULL	AD	O43396	TXNL1
2042.1	Dynein heavy chain 6, axonemal	2.82E+04	0.00E+00	-2.82E+04	-2.82E+04	NULL	AD	Q9C0G6	DNAH6
1617.1	Protein arginine N-methyltransf	2.85E+04	0.00E+00	-2.85E+04	-2.85E+04	NULL	AD	O60678	PRMT3
1642.1	Isoform 4 of Fc receptor-like B	2.86E+04	0.00E+00	-2.86E+04	-2.86E+04	NULL	AD	Q6BAA4-4	FCRLB
1681.1	Poly(A) polymerase gamma	2.88E+04	0.00E+00	-2.88E+04	-2.88E+04	NULL	AD	Q9BWT3	PAPOLG
3109.1	Isoform 2 of Zinc finger protein	2.88E+04	0.00E+00	-2.88E+04	-2.88E+04	NULL	AD	Q6ZN55-2	ZNF574
2815.1	Zinc finger protein 821	2.95E+04	0.00E+00	-2.95E+04	-2.95E+04	NULL	AD	O75541	ZNF821
1672.1	Transmembrane emp24 domai	3.00E+04	0.00E+00	-3.00E+04	-3.00E+04	NULL	AD	Q13445	TMED1
2434.1	Ras-related protein R-Ras2	3.00E+04	0.00E+00	-3.00E+04	-3.00E+04	NULL	AD	B7Z5Z2	RRAS2

1128.1	CTTNBP2 N-terminal-like protei	3.02E+04	0.00E+00	-3.02E+04	-3.02E+04	NULL	AD	Q9P2B4	CTTNBP2NL
2034.1	Poly [ADP-ribose] polymerase 1	3.04E+04	0.00E+00	-3.04E+04	-3.04E+04	NULL	AD	Q460N5	PARP14
2580.1	Ataxin-7-like protein 2	3.08E+04	0.00E+00	-3.08E+04	-3.08E+04	NULL	AD	Q5T6C5	ATXN7L2
2831.1	Isoform 3 of Solute carrier famil	3.10E+04	0.00E+00	-3.10E+04	-3.10E+04	NULL	AD	O76082-3	SLC22A5
2616.1	Ras-related protein Rab-39B	3.25E+04	0.00E+00	-3.25E+04	-3.25E+04	NULL	AD	Q96DA2	RAB39B
2652.1	Zinc fingers and homeoboxes pr	3.25E+04	0.00E+00	-3.25E+04	-3.25E+04	NULL	AD	Q9UKY1	ZHX1
2986.1	Perilipin-1	3.29E+04	0.00E+00	-3.29E+04	-3.29E+04	NULL	AD	O60240	PLIN1
2417.1	Isoform 2 of Phosphatidylserine	3.31E+04	0.00E+00	-3.31E+04	-3.31E+04	NULL	AD	Q9UG56-2	PISD
956.1	Small glutamine-rich tetratricop	3.33E+04	0.00E+00	-3.33E+04	-3.33E+04	NULL	AD	O43765	SGTA
955.1	Cytoplasmic dynein 1 intermedi	3.46E+04	0.00E+00	-3.46E+04	-3.46E+04	NULL	AD	Q13409	DYNC1I2
1463.1	Insulin-like growth factor-bindin	3.54E+04	0.00E+00	-3.54E+04	-3.54E+04	NULL	AD	P18065	IGFBP2
2223.1	Krev interaction trapped protei	3.57E+04	0.00E+00	-3.57E+04	-3.57E+04	NULL	AD	O00522	KRIT1
2208.1	Probable ubiquitin carboxyl-terr	3.60E+04	0.00E+00	-3.60E+04	-3.60E+04	NULL	AD	O00507	USP9Y
2684.1	Isoform BMP1-7 of Bone morph	3.63E+04	0.00E+00	-3.63E+04	-3.63E+04	NULL	AD	P13497-6	BMP1
2237.1	WD repeat-containing protein 9	3.82E+04	0.00E+00	-3.82E+04	-3.82E+04	NULL	AD	F8VUX9	WDR90
1684.1	RB1-inducible coiled-coil protei	3.89E+04	0.00E+00	-3.89E+04	-3.89E+04	NULL	AD	Q8TDY2	RB1CC1
3194.1	NF-X1-type zinc finger protein N	3.96E+04	0.00E+00	-3.96E+04	-3.96E+04	NULL	AD	Q6ZNB6	NFXL1
3234.1	Isoform 4 of Transmembrane pr	3.96E+04	0.00E+00	-3.96E+04	-3.96E+04	NULL	AD	A2VDJ0-5	KIAA0922
2697.1	Steroidogenic factor 1	3.98E+04	0.00E+00	-3.98E+04	-3.98E+04	NULL	AD	Q13285	NR5A1
2895.1	Myosin light chain kinase, smoo	3.99E+04	0.00E+00	-3.99E+04	-3.99E+04	NULL	AD	Q15746	MYLK
3112.1	F-box only protein 40	3.99E+04	0.00E+00	-3.99E+04	-3.99E+04	NULL	AD	Q9UH90	FBXO40
2635.1	Vasoactive intestinal polypeptid	4.02E+04	0.00E+00	-4.02E+04	-4.02E+04	NULL	AD	P32241	VIPR1
2118.1	Isoform A of Pituitary-specific p	4.04E+04	0.00E+00	-4.04E+04	-4.04E+04	NULL	AD	P28069-2	POU1F1
2121.1	DnaJ homolog subfamily C mem	4.05E+04	0.00E+00	-4.05E+04	-4.05E+04	NULL	AD	Q99543	DNAJC2
1964.1	SLC5A2 protein	4.06E+04	0.00E+00	-4.06E+04	-4.06E+04	NULL	AD	A2RRD2	SLC5A2
2062.1	Spectrin alpha chain, erythrocyt	4.13E+04	0.00E+00	-4.13E+04	-4.13E+04	NULL	AD	P02549	SPTA1
2012.1	Complement C1r subcomponen	4.16E+04	0.00E+00	-4.16E+04	-4.16E+04	NULL	AD	F5H2Z5	C1RL
2050.1	Zinc finger protein 638	4.19E+04	0.00E+00	-4.19E+04	-4.19E+04	NULL	AD	Q14966	ZNF638
2227.1	Interferon alpha/beta receptor	4.23E+04	0.00E+00	-4.23E+04	-4.23E+04	NULL	AD	P17181	IFNAR1
2407.1	Synaptonemal complex protein	4.24E+04	0.00E+00	-4.24E+04	-4.24E+04	NULL	AD	Q9BX26	SYCP2
2527.1	Nitrogen permease regulator 2-	4.25E+04	0.00E+00	-4.25E+04	-4.25E+04	NULL	AD	Q8WTW4	NPRL2
2421.1	UV-stimulated scaffold protein	4.28E+04	0.00E+00	-4.28E+04	-4.28E+04	NULL	AD	Q2YD98	UVSSA
529.2	Chromodomain-helicase-DNA-b	4.34E+04	0.00E+00	-4.34E+04	-4.34E+04	NULL	AD	Q8TDI0	CHD5
2989.1	Ras-related protein Rab-3C	4.34E+04	0.00E+00	-4.34E+04	-4.34E+04	NULL	AD	Q96E17	RAB3C
2522.1	Isoform 2 of Scavenger recepto	4.39E+04	0.00E+00	-4.39E+04	-4.39E+04	NULL	AD	Q86VB7-2	CD163

1108.1	Pyridoxal kinase	4.45E+04	0.00E+00	-4.45E+04	-4.45E+04	NULL	AD	O00764	PDXK
1722.1	Dual oxidase maturation factor	4.45E+04	0.00E+00	-4.45E+04	-4.45E+04	NULL	AD	Q1HG44	DUOXA2
3185.1	EPS8L2 protein	4.45E+04	0.00E+00	-4.45E+04	-4.45E+04	NULL	AD	B7ZKL3	EPS8L2
2606.1	Nucleolar protein 8	4.46E+04	0.00E+00	-4.46E+04	-4.46E+04	NULL	AD	Q76FK4	NOL8
1733.1	Thioredoxin domain-containing	4.47E+04	0.00E+00	-4.47E+04	-4.47E+04	NULL	AD	O95881	TXNDC12
2789.1	Transient receptor potential cat	4.49E+04	0.00E+00	-4.49E+04	-4.49E+04	NULL	AD	Q9H1D0	TRPV6
1133.1	Nuclear factor of-activated T-ce	4.49E+04	0.00E+00	-4.49E+04	-4.49E+04	NULL	AD	O94916	NFAT5
2687.1	Isoform 3 of Solute carrier famil	4.50E+04	0.00E+00	-4.50E+04	-4.50E+04	NULL	AD	Q5BKX6-3	SLC45A4
3089.1	Isoform 2 of Protein FAM198B	4.52E+04	0.00E+00	-4.52E+04	-4.52E+04	NULL	AD	Q6UWH4-	FAM198B
2562.1	Isoform 2 of Zinc transporter ZI	4.53E+04	0.00E+00	-4.53E+04	-4.53E+04	NULL	AD	Q9BRY0-2	SLC39A3
1353.1	26S proteasome non-ATPase re	4.58E+04	0.00E+00	-4.58E+04	-4.58E+04	NULL	AD	P48556	PSMD8
2911.1	Conserved oligomeric Golgi co	4.64E+04	0.00E+00	-4.64E+04	-4.64E+04	NULL	AD	P83436	COG7
2397.1	Putative upstream-binding fact	4.73E+04	0.00E+00	-4.73E+04	-4.73E+04	NULL	AD	P0CB48	UBTFL6
2517.1	Leucine-rich repeat serine/thre	4.90E+04	0.00E+00	-4.90E+04	-4.90E+04	NULL	AD	Q38SD2	LRRK1
2788.1	Isoform 3 of Centrosomal prote	4.97E+04	0.00E+00	-4.97E+04	-4.97E+04	NULL	AD	Q9C0D2-3	KIAA1731
1152.1	Isoleucine--tRNA ligase, mitoch	4.99E+04	0.00E+00	-4.99E+04	-4.99E+04	NULL	AD	Q9NSE4	IARS2
2597.1	Oxysterol-binding protein-relat	5.00E+04	0.00E+00	-5.00E+04	-5.00E+04	NULL	AD	Q9H0X9	OSBPL5
2670.1	Zinc finger protein 385D	5.07E+04	0.00E+00	-5.07E+04	-5.07E+04	NULL	AD	Q9H6B1	ZNF385D
3176.1	Origin recognition complex sub	5.16E+04	0.00E+00	-5.16E+04	-5.16E+04	NULL	AD	Q9Y5N6	ORC6
870.1	BAG family molecular chaperon	5.17E+04	0.00E+00	-5.17E+04	-5.17E+04	NULL	AD	O95817	BAG3
1778.1	Coiled-coil domain-containing p	5.18E+04	0.00E+00	-5.18E+04	-5.18E+04	NULL	AD	Q9H6F5	CCDC86
2192.1	E3 ubiquitin-protein ligase HEC	5.20E+04	0.00E+00	-5.20E+04	-5.20E+04	NULL	AD	Q9ULT8	HECTD1
2739.1	Ectonucleoside triphosphate di	5.20E+04	0.00E+00	-5.20E+04	-5.20E+04	NULL	AD	O75356	ENTPD5
2771.1	E3 ubiquitin-protein ligase TRI	5.21E+04	0.00E+00	-5.21E+04	-5.21E+04	NULL	AD	Q9BRZ2	TRIM56
2676.1	Sodium-dependent multivitami	5.31E+04	0.00E+00	-5.31E+04	-5.31E+04	NULL	AD	Q9Y289	SLC5A6
1893.1	Isoform 2 of SKI family transcrip	5.37E+04	0.00E+00	-5.37E+04	-5.37E+04	NULL	AD	P84550-2	SKOR1
1962.1	Zinc finger protein ZFPM1	5.37E+04	0.00E+00	-5.37E+04	-5.37E+04	NULL	AD	Q8IX07	ZFPM1
1268.1	Armadillo repeat-containing pr	5.45E+04	0.00E+00	-5.45E+04	-5.45E+04	NULL	AD	Q6NXE6	ARMC6
3021.1	Bestrophin-1	5.47E+04	0.00E+00	-5.47E+04	-5.47E+04	NULL	AD	B7Z1N8	BEST1
3159.1	NACHT, LRR and PYD domains-c	5.48E+04	0.00E+00	-5.48E+04	-5.48E+04	NULL	AD	Q9C000	NLRP1
755.1	DCC-interacting protein 13-alph	5.50E+04	0.00E+00	-5.50E+04	-5.50E+04	NULL	AD	Q9UKG1	APPL1
3216.1	POM121-like protein 2	5.55E+04	0.00E+00	-5.55E+04	-5.55E+04	NULL	AD	C9J1I7	POM121L2
2946.1	Isoform 2 of Dolichol-phosphate	5.56E+04	0.00E+00	-5.56E+04	-5.56E+04	NULL	AD	Q9P2X0-2	DPM3
782.1	Interferon regulatory factor 6	5.60E+04	0.00E+00	-5.60E+04	-5.60E+04	NULL	AD	O14896	IRF6
1654.1	Vesicle-trafficking protein SEC2	5.61E+04	0.00E+00	-5.61E+04	-5.61E+04	NULL	AD	Q96IW7	SEC22A

1023.1	Isoform 7 of T-cell surface glyco	5.62E+04	0.00E+00	-5.62E+04	-5.62E+04	NULL	AD	P10966-8	CD8B
1643.1	Ras-related protein Rab-6B	5.68E+04	0.00E+00	-5.68E+04	-5.68E+04	NULL	AD	Q9NRW1	RAB6B
3164.1	Mitogen-activated protein kinas	5.68E+04	0.00E+00	-5.68E+04	-5.68E+04	NULL	AD	Q5TCX8	MLK4
1521.1	Serine--tRNA ligase, cytoplasmi	5.75E+04	0.00E+00	-5.75E+04	-5.75E+04	NULL	AD	Q5T5C7	SARS
1158.1	WD repeat-containing protein	5.77E+04	0.00E+00	-5.77E+04	-5.77E+04	NULL	AD	Q9NXC5	MIOS
2451.1	Bicaudal D-related protein 1	5.77E+04	0.00E+00	-5.77E+04	-5.77E+04	NULL	AD	Q6ZP65	CCDC64
2532.1	Isoform 4 of Phosphatidylinosit	5.77E+04	0.00E+00	-5.77E+04	-5.77E+04	NULL	AD	P27986-4	PIK3R1
2436.1	CUGBP Elav-like family member	5.81E+04	0.00E+00	-5.81E+04	-5.81E+04	NULL	AD	E9PC62	CELF2
1397.1	Neurofilament heavy polypepti	5.85E+04	0.00E+00	-5.85E+04	-5.85E+04	NULL	AD	P12036	NEFH
1202.1	Ubinuclein-1	5.86E+04	0.00E+00	-5.86E+04	-5.86E+04	NULL	AD	Q9NPG3	UBN1
2502.1	Interstitial collagenase	5.88E+04	0.00E+00	-5.88E+04	-5.88E+04	NULL	AD	P03956	MMP1
2475.1	TRAF3-interacting protein 1	5.90E+04	0.00E+00	-5.90E+04	-5.90E+04	NULL	AD	A8MTK4	TRAF3IP1
3180.1	Isoform 2 of Telomerase-bindin	5.94E+04	0.00E+00	-5.94E+04	-5.94E+04	NULL	AD	Q86US8-2	SMG6
1817.1	Protein FAM53C	6.01E+04	0.00E+00	-6.01E+04	-6.01E+04	NULL	AD	D6RE00	FAM53C
3119.1	Nuclear pore complex protein N	6.02E+04	0.00E+00	-6.02E+04	-6.02E+04	NULL	AD	F5H5C2	NUP133
3239.1	Hexokinase-2	6.03E+04	0.00E+00	-6.03E+04	-6.03E+04	NULL	AD	P52789	HK2
1969.1	Unconventional myosin-Ig	6.04E+04	0.00E+00	-6.04E+04	-6.04E+04	NULL	AD	B0I1T2	MYO1G
1900.1	Isoform 2 of Choriogonadotropi	6.06E+04	0.00E+00	-6.06E+04	-6.06E+04	NULL	AD	Q6NT52-2	CGB2
2460.1	Isoform 6 of DENN domain-cont	6.14E+04	0.00E+00	-6.14E+04	-6.14E+04	NULL	AD	Q8TEH3-6	DENND1A
1839.1	Fer-1-like protein 5	6.17E+04	0.00E+00	-6.17E+04	-6.17E+04	NULL	AD	A0AVI2	FER1L5
1090.1	Actin-binding protein anillin	6.21E+04	0.00E+00	-6.21E+04	-6.21E+04	NULL	AD	Q9NQW6	ANLN
1661.1	Leucine-rich repeat-containing	6.21E+04	0.00E+00	-6.21E+04	-6.21E+04	NULL	AD	Q6F5E8	RLTPR
2234.1	Prolyl 4-hydroxylase subunit alp	6.24E+04	0.00E+00	-6.24E+04	-6.24E+04	NULL	AD	O15460	P4HA2
1752.1	Cytochrome P450 4F11	6.25E+04	0.00E+00	-6.25E+04	-6.25E+04	NULL	AD	Q9HBI6	CYP4F11
2229.1	Tyrosine-protein phosphatase n	6.25E+04	0.00E+00	-6.25E+04	-6.25E+04	NULL	AD	Q06124	PTPN11
3182.1	Tubulin polyglutamylase TTLL13	6.29E+04	0.00E+00	-6.29E+04	-6.29E+04	NULL	AD	A6NNM8	TTLL13
1833.1	Macoilin	6.32E+04	0.00E+00	-6.32E+04	-6.32E+04	NULL	AD	Q8N5G2	TMEM57
1531.1	Prefoldin subunit 2	6.39E+04	0.00E+00	-6.39E+04	-6.39E+04	NULL	AD	Q9UHV9	PFDN2
1931.1	Isoform 2 of Synaptotagmin-like	6.43E+04	0.00E+00	-6.43E+04	-6.43E+04	NULL	AD	Q8TDW5-2	SYTL5
3195.1	Isoform 4 of Inter-alpha-trypsin	6.47E+04	0.00E+00	-6.47E+04	-6.47E+04	NULL	AD	Q86UX2-4	ITIH5
1741.1	5-hydroxytryptamine (Serotoni	6.50E+04	0.00E+00	-6.50E+04	-6.50E+04	NULL	AD	Q5VX04	HTR7
1567.1	von Willebrand factor A domain	6.55E+04	0.00E+00	-6.55E+04	-6.55E+04	NULL	AD	O00534	VWA5A
1691.1	Nuclear receptor subfamily 4 gr	6.67E+04	0.00E+00	-6.67E+04	-6.67E+04	NULL	AD	F5GXF0	NR4A1
2991.1	Translation initiation factor IF-3,	6.71E+04	0.00E+00	-6.71E+04	-6.71E+04	NULL	AD	Q9H2K0	MTIF3
774.1	B-cell CLL/lymphoma 9-like prot	6.75E+04	0.00E+00	-6.75E+04	-6.75E+04	NULL	AD	Q86UU0	BCL9L

1993.1	Potassium voltage-gated channe	6.78E+04	0.00E+00	-6.78E+04	-6.78E+04	NULL	AD	Q96PR1	KCNC2
2435.1	Hexokinase-1	6.78E+04	0.00E+00	-6.78E+04	-6.78E+04	NULL	AD	E7ENR4	HK1
2929.1	Putative homeodomain transcri	6.79E+04	0.00E+00	-6.79E+04	-6.79E+04	NULL	AD	Q9UMS5	PHTF1
2119.1	Phosphatidylinositol 3,4,5-trisph	6.80E+04	0.00E+00	-6.80E+04	-6.80E+04	NULL	AD	P60484	PTEN
2620.1	G-protein-coupled receptor fam	6.81E+04	0.00E+00	-6.81E+04	-6.81E+04	NULL	AD	B7Z831	GPRC5B
2209.1	Zinc finger protein 85	6.83E+04	0.00E+00	-6.83E+04	-6.83E+04	NULL	AD	Q03923	ZNF85
1480.1	PiggyBac transposable element-	6.94E+04	0.00E+00	-6.94E+04	-6.94E+04	NULL	AD	Q96DM1	PGBD4
3244.1	Isoform 2 of Choline transporte	6.94E+04	0.00E+00	-6.94E+04	-6.94E+04	NULL	AD	Q8WWI5-2	SLC44A1
2260.1	E3 ubiquitin-protein ligase RNF6	6.96E+04	0.00E+00	-6.96E+04	-6.96E+04	NULL	AD	Q9Y252	RNF6
1211.1	RING finger protein 150	7.02E+04	0.00E+00	-7.02E+04	-7.02E+04	NULL	AD	Q9ULK6	RNF150
2461.1	Isoform 2 of Signal transducing	7.02E+04	0.00E+00	-7.02E+04	-7.02E+04	NULL	AD	Q92783-2	STAM
2838.1	Xylosyltransferase 1	7.04E+04	0.00E+00	-7.04E+04	-7.04E+04	NULL	AD	Q86Y38	XYLT1
2978.1	Rab proteins geranylgeranyltra	7.08E+04	0.00E+00	-7.08E+04	-7.08E+04	NULL	AD	P26374	CHML
1288.1	Piwi-like protein 2	7.10E+04	0.00E+00	-7.10E+04	-7.10E+04	NULL	AD	Q8TC59	PIWIL2
1366.1	Zinc finger protein with KRAB a	7.10E+04	0.00E+00	-7.10E+04	-7.10E+04	NULL	AD	P17029	ZKSCAN1
2067.1	Dual oxidase 2	7.12E+04	0.00E+00	-7.12E+04	-7.12E+04	NULL	AD	Q9NRD8	DUOX2
1761.1	Prenylcysteine oxidase-like	7.13E+04	0.00E+00	-7.13E+04	-7.13E+04	NULL	AD	Q8NBM8	PCYOX1L
2628.1	Phosphatidylcholine-sterol acylt	7.21E+04	0.00E+00	-7.21E+04	-7.21E+04	NULL	AD	P04180	LCAT
808.1	Tumor protein D53	7.22E+04	0.00E+00	-7.22E+04	-7.22E+04	NULL	AD	J3KNE7	TPD52L1
1968.1	Putative TBC1 domain family m	7.24E+04	0.00E+00	-7.24E+04	-7.24E+04	NULL	AD	Q9UFV1	TBC1D29
2918.1	Acyl-coenzyme A synthetase AC	7.24E+04	0.00E+00	-7.24E+04	-7.24E+04	NULL	AD	Q53FZ2	ACSM3
2176.1	Isoform 12 of Sorbin and SH3 d	7.26E+04	0.00E+00	-7.26E+04	-7.26E+04	NULL	AD	Q9BX66-1	SORBS1
2603.1	Zinc finger protein 189	7.42E+04	0.00E+00	-7.42E+04	-7.42E+04	NULL	AD	O75820	ZNF189
2821.1	UDP-glucuronosyltransferase 2	7.46E+04	0.00E+00	-7.46E+04	-7.46E+04	NULL	AD	Q6UWM9	UGT2A3
2017.1	Synaptobrevin homolog YKT6	7.47E+04	0.00E+00	-7.47E+04	-7.47E+04	NULL	AD	O15498	YKT6
1599.1	Syntaxin-11	7.49E+04	0.00E+00	-7.49E+04	-7.49E+04	NULL	AD	O75558	STX11
2626.1	Isoform 2 of Alpha-1,6-mannosy	7.51E+04	0.00E+00	-7.51E+04	-7.51E+04	NULL	AD	Q3V5L5-2	MGAT5B
3209.1	YrdC domain-containing protein	7.51E+04	0.00E+00	-7.51E+04	-7.51E+04	NULL	AD	Q86U90	YRDC
2952.1	NmrA-like family domain-contai	7.52E+04	0.00E+00	-7.52E+04	-7.52E+04	NULL	AD	Q9HBL8	NMRAL1
1186.1	von Willebrand factor A domain	7.66E+04	0.00E+00	-7.66E+04	-7.66E+04	NULL	AD	Q9Y334	VWA7
1810.1	Serine/threonine-protein kinase	7.70E+04	0.00E+00	-7.70E+04	-7.70E+04	NULL	AD	Q9Y3S1	WNK2
3263.1	von Willebrand factor A domain	7.71E+04	0.00E+00	-7.71E+04	-7.71E+04	NULL	AD	Q6PCB0	VWA1
1227.1	Integrin-linked kinase-associate	7.78E+04	0.00E+00	-7.78E+04	-7.78E+04	NULL	AD	Q9H0C8	ILKAP
2865.1	PDZ domain-containing protein	7.84E+04	0.00E+00	-7.84E+04	-7.84E+04	NULL	AD	O15018	PDZD2
2760.1	Methyltransferase-like protein 8	7.88E+04	0.00E+00	-7.88E+04	-7.88E+04	NULL	AD	E7ETE0	METTL8

2449.1	AP-4 complex subunit epsilon-1	7.97E+04	0.00E+00	-7.97E+04	-7.97E+04	NULL	AD	Q9UPM8	AP4E1
3097.1	Roundabout homolog 4	8.05E+04	0.00E+00	-8.05E+04	-8.05E+04	NULL	AD	Q8WZ75	ROBO4
2554.1	Coiled-coil domain-containing p	8.11E+04	0.00E+00	-8.11E+04	-8.11E+04	NULL	AD	A2RUR9	CCDC144A
1417.1	Isoform 2 of Protein FAM76B	8.17E+04	0.00E+00	-8.17E+04	-8.17E+04	NULL	AD	Q5HYJ3-2	FAM76B
1637.1	Ran-binding protein 17	8.19E+04	0.00E+00	-8.19E+04	-8.19E+04	NULL	AD	Q9H2T7	RANBP17
2074.1	GTPase IMAP family member 7	8.23E+04	0.00E+00	-8.23E+04	-8.23E+04	NULL	AD	Q8NHV1	GIMAP7
2575.1	Cingulin	8.24E+04	0.00E+00	-8.24E+04	-8.24E+04	NULL	AD	Q9P2M7	CGN
2794.1	Potassium voltage-gated channe	8.24E+04	0.00E+00	-8.24E+04	-8.24E+04	NULL	AD	Q12809	KCNH2
1699.1	Phostensin	8.29E+04	0.00E+00	-8.29E+04	-8.29E+04	NULL	AD	Q6NYC8	PPP1R18
1955.1	UPF0764 protein C16orf89	8.30E+04	0.00E+00	-8.30E+04	-8.30E+04	NULL	AD	Q6UX73	C16orf89
673.1	Protein FAM168A	8.32E+04	0.00E+00	-8.32E+04	-8.32E+04	NULL	AD	Q92567	FAM168A
1300.1	Interferon-stimulated 20 kDa ex	8.36E+04	0.00E+00	-8.36E+04	-8.36E+04	NULL	AD	Q9H9L3	ISG20L2
2210.1	Gem-associated protein 7	8.40E+04	0.00E+00	-8.40E+04	-8.40E+04	NULL	AD	Q9H840	GEMIN7
3265.1	G protein-regulated inducer of r	8.41E+04	0.00E+00	-8.41E+04	-8.41E+04	NULL	AD	Q7Z2K8	GPRIN1
1424.1	Isoform 3 of LIM domain kinase	8.42E+04	0.00E+00	-8.42E+04	-8.42E+04	NULL	AD	P53671-3	LIMK2
2253.1	Immunoglobulin superfamily me	8.48E+04	0.00E+00	-8.48E+04	-8.48E+04	NULL	AD	Q6WRI0	IGSF10
2284.1	DNA excision repair protein ERC	8.57E+04	0.00E+00	-8.57E+04	-8.57E+04	NULL	AD	Q03468	ERCC6
3031.1	YTH domain-containing protein	8.62E+04	0.00E+00	-8.62E+04	-8.62E+04	NULL	AD	J3QR07	YTHDC1
1690.1	HCG2004619	8.63E+04	0.00E+00	-8.63E+04	-8.63E+04	NULL	AD	H0YNJ1	hCG_2004619
1766.1	TCF3 fusion partner	8.63E+04	0.00E+00	-8.63E+04	-8.63E+04	NULL	AD	A8MTQ3	TFPT
3087.1	Protein FAM219A	8.67E+04	0.00E+00	-8.67E+04	-8.67E+04	NULL	AD	Q8IW50	FAM219A
1633.1	Ubiquitin carboxyl-terminal hyd	8.68E+04	0.00E+00	-8.68E+04	-8.68E+04	NULL	AD	Q9P2H5	USP35
2951.1	HCG1987119, isoform CRA_a	8.68E+04	0.00E+00	-8.68E+04	-8.68E+04	NULL	AD	I3L077	MYO15B
1379.1	Ran-binding protein 3	8.72E+04	0.00E+00	-8.72E+04	-8.72E+04	NULL	AD	K7EJ17	RANBP3
1939.1	Heparan-sulfate 6-O-sulfotransf	8.79E+04	0.00E+00	-8.79E+04	-8.79E+04	NULL	AD	Q8IZP7	HS6ST3
2738.1	Mitochondrial-processing peptic	9.00E+04	0.00E+00	-9.00E+04	-9.00E+04	NULL	AD	O75439	PMPCB
2004.1	Chromodomain-helicase-DNA-b	9.06E+04	0.00E+00	-9.06E+04	-9.06E+04	NULL	AD	Q9P2D1	CHD7
1036.1	Nuclear speckle splicing regulato	9.07E+04	0.00E+00	-9.07E+04	-9.07E+04	NULL	AD	Q9H0G5	NSRP1
1551.1	Relaxin-3 receptor 1	9.13E+04	0.00E+00	-9.13E+04	-9.13E+04	NULL	AD	Q9NSD7	RXFP3
1935.1	Inactive phospholipase C-like pr	9.16E+04	0.00E+00	-9.16E+04	-9.16E+04	NULL	AD	Q15111	PLCL1
1476.1	GMP reductase	9.17E+04	0.00E+00	-9.17E+04	-9.17E+04	NULL	AD	H0YNJ6	GMPR2
3050.1	Plasma membrane calcium-tran	9.19E+04	0.00E+00	-9.19E+04	-9.19E+04	NULL	AD	P20020	ATP2B1
1967.1	RelA-associated inhibitor	9.20E+04	0.00E+00	-9.20E+04	-9.20E+04	NULL	AD	Q8WUF5	PPP1R13L
1275.1	Isoform 8 of C-type lectin domai	9.23E+04	0.00E+00	-9.23E+04	-9.23E+04	NULL	AD	Q9BXN2-8	CLEC7A
2819.1	Serine/threonine-protein kinase	9.24E+04	0.00E+00	-9.24E+04	-9.24E+04	NULL	AD	Q13535	ATR

3073.1	Isoform 3 of Phosphatidylinosit	9.25E+04	0.00E+00	-9.25E+04	-9.25E+04	NULL	AD	O60331-3	PIP5K1C
1293.1	RNA polymerase-associated pro	9.27E+04	0.00E+00	-9.27E+04	-9.27E+04	NULL	AD	Q92541	RTF1
2496.1	Kinesin-like protein KIFC3	9.28E+04	0.00E+00	-9.28E+04	-9.28E+04	NULL	AD	B7Z484	KIFC3
2645.1	Isoform 5 of Glutamate recepto	9.28E+04	0.00E+00	-9.28E+04	-9.28E+04	NULL	AD	Q05586-5	GRIN1
2579.1	Endothelin-2	9.33E+04	0.00E+00	-9.33E+04	-9.33E+04	NULL	AD	P20800	EDN2
2758.1	GAS2-like protein 1	9.35E+04	0.00E+00	-9.35E+04	-9.35E+04	NULL	AD	Q99501	GAS2L1
2615.1	Probable cation-transporting AT	9.37E+04	0.00E+00	-9.37E+04	-9.37E+04	NULL	AD	Q4VNC0	ATP13A5
1692.1	Isoform 5 of Regulator of G-pro	9.39E+04	0.00E+00	-9.39E+04	-9.39E+04	NULL	AD	P49802-5	RGS7
1164.1	Trifunctional enzyme subunit al	9.42E+04	0.00E+00	-9.42E+04	-9.42E+04	NULL	AD	P40939	HADHA
2708.1	Laminin subunit gamma-3	9.42E+04	0.00E+00	-9.42E+04	-9.42E+04	NULL	AD	Q5JTC4	LAMC3
809.1	Omega-amidase NIT2	9.55E+04	0.00E+00	-9.55E+04	-9.55E+04	NULL	AD	Q9NQR4	NIT2
1308.1	Putative GTP-binding protein 6	9.60E+04	0.00E+00	-9.60E+04	-9.60E+04	NULL	AD	O43824	GTPBP6
1046.1	Interferon-related IFRD2 (PC4-B	9.62E+04	0.00E+00	-9.62E+04	-9.62E+04	NULL	AD	Q9UJ88	IFRD2
1797.1	Isoform 3 of Forkhead box prot	9.76E+04	0.00E+00	-9.76E+04	-9.76E+04	NULL	AD	Q9BZS1-3	FOXP3
2380.1	Peroxisomal NADH pyrophosph	9.80E+04	0.00E+00	-9.80E+04	-9.80E+04	NULL	AD	Q9BQG2	NUDT12
1847.1	Glutathione S-transferase omeg	9.83E+04	0.00E+00	-9.83E+04	-9.83E+04	NULL	AD	P78417	GSTO1
1892.1	Mitochondrial uncoupling prote	9.87E+04	0.00E+00	-9.87E+04	-9.87E+04	NULL	AD	P55851	UCP2
2992.1	Protein dopey-2	9.91E+04	0.00E+00	-9.91E+04	-9.91E+04	NULL	AD	Q9Y3R5	DOPEY2
2790.1	Putative Polycomb group protei	9.92E+04	0.00E+00	-9.92E+04	-9.92E+04	NULL	AD	Q8IXJ9	ASXL1
2820.1	Protein RRP5 homolog	9.92E+04	0.00E+00	-9.92E+04	-9.92E+04	NULL	AD	Q14690	PDCD11
2382.1	Gamma-butyrobetaine dioxyge	9.95E+04	0.00E+00	-9.95E+04	-9.95E+04	NULL	AD	O75936	BBOX1
2587.1	Thrombospondin type-1 domai	9.96E+04	0.00E+00	-9.96E+04	-9.96E+04	NULL	AD	Q9NS62	THSD1
1907.1	Pre-mRNA-splicing factor 38A	9.99E+04	0.00E+00	-9.99E+04	-9.99E+04	NULL	AD	Q8NAV1	PRPF38A
569.1	Inositol monophosphatase 1	9.99E+04	0.00E+00	-9.99E+04	-9.99E+04	NULL	AD	P29218	IMPA1
2081.1	HCG2044781	1.01E+05	0.00E+00	-1.01E+05	-1.01E+05	NULL	AD	G3V2F7	TMEM189
1210.1	Isoform 1 of Transmembrane pr	1.02E+05	0.00E+00	-1.02E+05	-1.02E+05	NULL	AD	Q96A57-2	TMEM230
1888.1	Isoform 2 of Endophilin-B2	1.02E+05	0.00E+00	-1.02E+05	-1.02E+05	NULL	AD	Q9NR46-2	SH3GLB2
2770.1	EF-hand domain-containing fam	1.02E+05	0.00E+00	-1.02E+05	-1.02E+05	NULL	AD	Q8N7U6	EFHB
3254.1	PHD finger protein 21B	1.02E+05	0.00E+00	-1.02E+05	-1.02E+05	NULL	AD	B1AHC5	PHF21B
1816.1	Heat shock 27kDa protein famil	1.03E+05	0.00E+00	-1.03E+05	-1.03E+05	NULL	AD	Q8N241	HSPB7
2036.1	IgGFc-binding protein	1.03E+05	0.00E+00	-1.03E+05	-1.03E+05	NULL	AD	Q9Y6R7	FCGBP
2083.1	SWI/SNF complex subunit SMA	1.03E+05	0.00E+00	-1.03E+05	-1.03E+05	NULL	AD	F8VXC8	SMARCC2
2090.1	Ankyrin repeat domain-containi	1.03E+05	0.00E+00	-1.03E+05	-1.03E+05	NULL	AD	Q9BXX2	ANKRD30B
3038.1	Isoform 7 of Serpin A9	1.03E+05	0.00E+00	-1.03E+05	-1.03E+05	NULL	AD	Q86WD7-	SERPINA9
1028.1	Septin 10, isoform CRA_c	1.04E+05	0.00E+00	-1.04E+05	-1.04E+05	NULL	AD	B5ME97	SEPT10

2639.1	Ribosome production factor 2 h	1.04E+05	0.00E+00	-1.04E+05	-1.04E+05	NULL	AD	Q9H7B2	RPF2
2947.1	Isoform 6 of GTPase-activating p	1.04E+05	0.00E+00	-1.04E+05	-1.04E+05	NULL	AD	Q14C86-6	GAPVD1
3033.1	Ephrin type-A receptor 8	1.04E+05	0.00E+00	-1.04E+05	-1.04E+05	NULL	AD	P29322	EPHA8
1334.1	CTD small phosphatase-like prot	1.05E+05	0.00E+00	-1.05E+05	-1.05E+05	NULL	AD	F8WED2	CTDSPL
1380.1	E3 ubiquitin-protein ligase MAR	1.06E+05	0.00E+00	-1.06E+05	-1.06E+05	NULL	AD	F5H6W4	MARCH7
1683.1	Plasma membrane calcium-tran	1.06E+05	0.00E+00	-1.06E+05	-1.06E+05	NULL	AD	P23634	ATP2B4
3177.1	Probable G-protein coupled rec	1.06E+05	0.00E+00	-1.06E+05	-1.06E+05	NULL	AD	Q15760	GPR19
1934.1	Immunoglobulin-like domain-co	1.07E+05	0.00E+00	-1.07E+05	-1.07E+05	NULL	AD	Q71H61	ILDR2
2215.1	Ig lambda chain V-II region NIG-	1.07E+05	0.00E+00	-1.07E+05	-1.07E+05	NULL	AD	P04209	LV211
2553.1	Isoform 2 of L-amino-acid oxida	1.07E+05	0.00E+00	-1.07E+05	-1.07E+05	NULL	AD	Q96RQ9-2	IL4I1
2780.1	Ubiquitin-conjugating enzyme E	1.07E+05	0.00E+00	-1.07E+05	-1.07E+05	NULL	AD	F8W8F0	UBE2E2
2826.1	Potassium voltage-gated chann	1.07E+05	0.00E+00	-1.07E+05	-1.07E+05	NULL	AD	Q9NS40	KCNH7
970.1	Dipeptidyl peptidase 3	1.08E+05	0.00E+00	-1.08E+05	-1.08E+05	NULL	AD	G3V180	DPP3
1472.1	Supervillin	1.08E+05	0.00E+00	-1.08E+05	-1.08E+05	NULL	AD	O95425	SVIL
2890.1	Vitamin K-dependent protein C	1.08E+05	0.00E+00	-1.08E+05	-1.08E+05	NULL	AD	B4DPQ7	PROC
2104.1	Isoform 2 of Protein SSX2	1.10E+05	0.00E+00	-1.10E+05	-1.10E+05	NULL	AD	Q16385-2	SSX2
2455.1	Probable ribonuclease ZC3H12B	1.10E+05	0.00E+00	-1.10E+05	-1.10E+05	NULL	AD	E9PAJ6	ZC3H12B
2921.1	Isoform 2 of Microspherule prot	1.10E+05	0.00E+00	-1.10E+05	-1.10E+05	NULL	AD	Q96EZ8-2	MCRS1
1269.1	Interleukin-34	1.11E+05	0.00E+00	-1.11E+05	-1.11E+05	NULL	AD	Q6ZMJ4	IL34
1820.1	PAS domain-containing protein	1.11E+05	0.00E+00	-1.11E+05	-1.11E+05	NULL	AD	Q8IV76	PASD1
2250.1	Target of Nesh-SH3	1.11E+05	0.00E+00	-1.11E+05	-1.11E+05	NULL	AD	D3YTG3	ABI3BP
2537.1	NGFI-A-binding protein 1	1.11E+05	0.00E+00	-1.11E+05	-1.11E+05	NULL	AD	F8W8J7	NAB1
2933.1	Kinocilin	1.11E+05	0.00E+00	-1.11E+05	-1.11E+05	NULL	AD	A6PVL3	KNCN
3006.1	Solute carrier family 12 membe	1.11E+05	0.00E+00	-1.11E+05	-1.11E+05	NULL	AD	Q9UHW9	SLC12A6
3165.1	Metallo-beta-lactamase domain	1.11E+05	0.00E+00	-1.11E+05	-1.11E+05	NULL	AD	Q68D91	MBLAC2
1054.1	Protein-L-isoaspartate O-methy	1.12E+05	0.00E+00	-1.12E+05	-1.12E+05	NULL	AD	H7BY58	PCMT1
1603.1	Leucine zipper transcription fact	1.12E+05	0.00E+00	-1.12E+05	-1.12E+05	NULL	AD	F2Z2E6	LZTFL1
1910.1	Putative adenosylhomocysteina	1.12E+05	0.00E+00	-1.12E+05	-1.12E+05	NULL	AD	O43865	AHCYL1
864.1	Zinc finger protein 10	1.13E+05	0.00E+00	-1.13E+05	-1.13E+05	NULL	AD	P21506	ZNF10
1343.1	SCO-spondin	1.13E+05	0.00E+00	-1.13E+05	-1.13E+05	NULL	AD	A2VEC9	SSPO
1822.1	Keratin, type II cuticular Hb2	1.13E+05	0.00E+00	-1.13E+05	-1.13E+05	NULL	AD	Q9NSB4	KRT82
2097.1	Probable cation-transporting AT	1.13E+05	0.00E+00	-1.13E+05	-1.13E+05	NULL	AD	Q9HD20	ATP13A1
2736.1	Isoform 3 of Receptor expressio	1.13E+05	0.00E+00	-1.13E+05	-1.13E+05	NULL	AD	Q9H902-3	REEP1
2982.1	Monocarboxylate transporter 1	1.13E+05	0.00E+00	-1.13E+05	-1.13E+05	NULL	AD	Q8TF71	SLC16A10
2680.1	Zinc finger MIZ domain-containi	1.14E+05	0.00E+00	-1.14E+05	-1.14E+05	NULL	AD	Q9ULJ6	ZMIZ1

3188.1	Tubulin polyglutamylase TTLL7	1.14E+05	0.00E+00	-1.14E+05	-1.14E+05	NULL	AD	Q6ZT98	TTLL7
1700.1	Tripartite motif-containing prot	1.15E+05	0.00E+00	-1.15E+05	-1.15E+05	NULL	AD	O00635	TRIM38
3042.1	Orexin receptor type 1	1.15E+05	0.00E+00	-1.15E+05	-1.15E+05	NULL	AD	O43613	HCRTR1
1490.1	Arf-GAP domain and FG repeat-	1.15E+05	0.00E+00	-1.15E+05	-1.15E+05	NULL	AD	P52594	AGFG1
922.1	Proteasome activator complex s	1.16E+05	0.00E+00	-1.16E+05	-1.16E+05	NULL	AD	Q9UL46	PSME2
2185.1	Histamine H1 receptor	1.16E+05	0.00E+00	-1.16E+05	-1.16E+05	NULL	AD	P35367	HRH1
1728.1	Isoform 2 of Zinc finger protein	1.17E+05	0.00E+00	-1.17E+05	-1.17E+05	NULL	AD	Q8N988-2	ZNF557
1912.1	ETS-related transcription factor	1.17E+05	0.00E+00	-1.17E+05	-1.17E+05	NULL	AD	Q99607	ELF4
1945.1	DNA nucleotidylexotransferase	1.17E+05	0.00E+00	-1.17E+05	-1.17E+05	NULL	AD	P04053	DNTT
2254.1	Protein OSCP1	1.17E+05	0.00E+00	-1.17E+05	-1.17E+05	NULL	AD	Q8WVF1	OSCP1
1192.1	Isoform 3 of Rap guanine nucle	1.18E+05	0.00E+00	-1.18E+05	-1.18E+05	NULL	AD	Q13905-3	RAPGEF1
2961.1	F-box-like/WD repeat-containin	1.18E+05	0.00E+00	-1.18E+05	-1.18E+05	NULL	AD	Q9BZK7	TBL1XR1
3250.1	E3 ubiquitin-protein ligase TRIM	1.18E+05	0.00E+00	-1.18E+05	-1.18E+05	NULL	AD	Q86WT6	TRIM69
1001.1	Neurabin-2	1.19E+05	0.00E+00	-1.19E+05	-1.19E+05	NULL	AD	Q96SB3	PPP1R9B
1632.1	Isoform 2 of Presequence prote	1.19E+05	0.00E+00	-1.19E+05	-1.19E+05	NULL	AD	Q5JRX3-2	PITRM1
2409.1	Lysine-specific demethylase 2A	1.19E+05	0.00E+00	-1.19E+05	-1.19E+05	NULL	AD	Q9Y2K7	KDM2A
2776.1	Receptor-type tyrosine-protein	1.20E+05	0.00E+00	-1.20E+05	-1.20E+05	NULL	AD	Q9HD43	PTPRH
3133.1	Polyhomeotic-like protein 1	1.20E+05	0.00E+00	-1.20E+05	-1.20E+05	NULL	AD	P78364	PHC1
668.1	Isoform 2 of S-methyl-5'-thioad	1.21E+05	0.00E+00	-1.21E+05	-1.21E+05	NULL	AD	Q13126-2	MTAP
2617.1	Band 4.1-like protein 4A	1.21E+05	0.00E+00	-1.21E+05	-1.21E+05	NULL	AD	Q9HCS5	EPB41L4A
3055.1	Dual specificity protein phospha	1.21E+05	0.00E+00	-1.21E+05	-1.21E+05	NULL	AD	Q9H1R2	DUSP15
2787.1	Isoform 2 of F-box/WD repeat-c	1.22E+05	0.00E+00	-1.22E+05	-1.22E+05	NULL	AD	Q5XX13-2	FBXW10
1323.1	Endophilin-A2	1.23E+05	0.00E+00	-1.23E+05	-1.23E+05	NULL	AD	Q99961	SH3GL1
1312.1	PC4 and SFRS1-interacting prote	1.24E+05	0.00E+00	-1.24E+05	-1.24E+05	NULL	AD	O75475	PSIP1
1319.1	Sulfhydryl oxidase 1	1.24E+05	0.00E+00	-1.24E+05	-1.24E+05	NULL	AD	O00391	QSOX1
2484.1	Protein-associating with the car	1.24E+05	0.00E+00	-1.24E+05	-1.24E+05	NULL	AD	Q8IZE3	SCYL3
1929.1	Early endosome antigen 1	1.25E+05	0.00E+00	-1.25E+05	-1.25E+05	NULL	AD	Q15075	EEA1
1996.1	Anthrax toxin receptor 1	1.25E+05	0.00E+00	-1.25E+05	-1.25E+05	NULL	AD	Q9H6X2	ANTXR1
1575.1	C5a anaphylatoxin chemotactic	1.26E+05	0.00E+00	-1.26E+05	-1.26E+05	NULL	AD	P21730	C5AR1
2883.1	Homeobox protein Hox-B5	1.26E+05	0.00E+00	-1.26E+05	-1.26E+05	NULL	AD	P09067	HOXB5
3134.1	AF4/FMR2 family member 2	1.26E+05	0.00E+00	-1.26E+05	-1.26E+05	NULL	AD	P51816	AFF2
3202.1	Golgin subfamily A member 2	1.26E+05	0.00E+00	-1.26E+05	-1.26E+05	NULL	AD	Q08379	GOLGA2
812.1	Core histone macro-H2A.1	1.27E+05	0.00E+00	-1.27E+05	-1.27E+05	NULL	AD	O75367	H2AFY
905.1	Zinc finger protein 607	1.27E+05	0.00E+00	-1.27E+05	-1.27E+05	NULL	AD	Q96SK3	ZNF607
1987.1	Isoform 3 of Histone acetyltrans	1.27E+05	0.00E+00	-1.27E+05	-1.27E+05	NULL	AD	Q92993-3	KAT5

2179.1	Kallikrein-14	1.27E+05	0.00E+00	-1.27E+05	-1.27E+05	NULL	AD	Q9P0G3	KLK14
2248.1	Solute carrier family 25 membe	1.27E+05	0.00E+00	-1.27E+05	-1.27E+05	NULL	AD	Q6PIV7	SLC25A34
1501.1	AP-3 complex subunit beta-1	1.29E+05	0.00E+00	-1.29E+05	-1.29E+05	NULL	AD	O00203	AP3B1
2717.1	Probable UDP-sugar transporte	1.29E+05	0.00E+00	-1.29E+05	-1.29E+05	NULL	AD	Q9BS91	SLC35A5
2979.1	Isoform 2 of Bromodomain testi	1.29E+05	0.00E+00	-1.29E+05	-1.29E+05	NULL	AD	Q58F21-2	BRDT
3170.1	Protocadherin gamma-A11	1.29E+05	0.00E+00	-1.29E+05	-1.29E+05	NULL	AD	Q9Y5H2	PCDHGA11
2348.1	Cadherin-18	1.30E+05	0.00E+00	-1.30E+05	-1.30E+05	NULL	AD	Q13634	CDH18
1827.1	Cyclin-G-associated kinase	1.31E+05	0.00E+00	-1.31E+05	-1.31E+05	NULL	AD	O14976	GAK
872.1	Serine dehydratase-like	1.32E+05	0.00E+00	-1.32E+05	-1.32E+05	NULL	AD	Q96GA7	SDSL
1285.1	Isoform LCRMP-1 of Dihydropyr	1.32E+05	0.00E+00	-1.32E+05	-1.32E+05	NULL	AD	Q14194-2	CRMP1
1932.1	Olfactory receptor 2S2	1.32E+05	0.00E+00	-1.32E+05	-1.32E+05	NULL	AD	Q9NQN1	OR2S2
3155.1	NRF1 protein	1.32E+05	0.00E+00	-1.32E+05	-1.32E+05	NULL	AD	Q96AN2	NRF1
2592.1	Filamin-A-interacting protein 1	1.33E+05	0.00E+00	-1.33E+05	-1.33E+05	NULL	AD	Q7Z7B0	FILIP1
3253.1	Brain-specific angiogenesis inhib	1.33E+05	0.00E+00	-1.33E+05	-1.33E+05	NULL	AD	Q9UHR4	BAIAP2L1
1281.1	Isoform 3 of Kinesin light chain	1.34E+05	0.00E+00	-1.34E+05	-1.34E+05	NULL	AD	Q6P597-3	KLC3
1990.1	Nucleus accumbens-associated	1.35E+05	0.00E+00	-1.35E+05	-1.35E+05	NULL	AD	Q96RE7	NACC1
2405.1	ATP-dependent RNA helicase D	1.35E+05	0.00E+00	-1.35E+05	-1.35E+05	NULL	AD	Q9GZR7	DDX24
1602.1	Isoform 2 of Deleted in azoospe	1.36E+05	0.00E+00	-1.36E+05	-1.36E+05	NULL	AD	Q92904-2	DAZL
2152.1	Non-specific cytotoxic cell recep	1.36E+05	0.00E+00	-1.36E+05	-1.36E+05	NULL	AD	Q6ZVX7	NCCRP1
2279.1	Nipped-B-like protein	1.36E+05	0.00E+00	-1.36E+05	-1.36E+05	NULL	AD	Q6KC79	NIPBL
2844.1	General transcription factor IIH	1.36E+05	0.00E+00	-1.36E+05	-1.36E+05	NULL	AD	Q6P1K8	GTF2H2C
2924.1	Small membrane A-kinase anch	1.37E+05	0.00E+00	-1.37E+05	-1.37E+05	NULL	AD	Q9BSF0	C2orf88
807.1	Proteasome subunit beta type-1	1.39E+05	0.00E+00	-1.39E+05	-1.39E+05	NULL	AD	P20618	PSMB1
1200.1	Ankyrin repeat domain-containi	1.39E+05	0.00E+00	-1.39E+05	-1.39E+05	NULL	AD	O75179	ANKRD17
2341.1	Isoform 2 of Inversin	1.39E+05	0.00E+00	-1.39E+05	-1.39E+05	NULL	AD	Q9Y283-2	INVS
2729.1	Serine/threonine-protein kinase	1.39E+05	0.00E+00	-1.39E+05	-1.39E+05	NULL	AD	O94768	STK17B
1787.1	Isoform D of Nuclear RNA expor	1.41E+05	0.00E+00	-1.41E+05	-1.41E+05	NULL	AD	Q9H1B4-4	NXF5
2309.1	Contactin-associated protein 1	1.42E+05	0.00E+00	-1.42E+05	-1.42E+05	NULL	AD	K7EMM9	CNTNAP1
2847.1	Isoform 6 of Myocardial zonula	1.42E+05	0.00E+00	-1.42E+05	-1.42E+05	NULL	AD	P0CAP1-6	MYZAP
3060.1	Zinc finger protein 143	1.43E+05	0.00E+00	-1.43E+05	-1.43E+05	NULL	AD	P52747	ZNF143
1162.1	Netrin receptor DCC	1.44E+05	0.00E+00	-1.44E+05	-1.44E+05	NULL	AD	P43146	DCC
1252.1	Proline and serine-rich protein	1.44E+05	0.00E+00	-1.44E+05	-1.44E+05	NULL	AD	Q86WR7	PROSER2
2389.1	Isoform 3 of Phosphatidylinosit	1.44E+05	0.00E+00	-1.44E+05	-1.44E+05	NULL	AD	Q8TBX8-3	PIP4K2C
764.1	CD2-associated protein	1.45E+05	0.00E+00	-1.45E+05	-1.45E+05	NULL	AD	Q9Y5K6	CD2AP
1481.1	Fatty acid desaturase 6	1.45E+05	0.00E+00	-1.45E+05	-1.45E+05	NULL	AD	Q8N9I5	FADS6

1784.1	Ankyrin repeat domain 30A	1.45E+05	0.00E+00	-1.45E+05	-1.45E+05	NULL	AD	Q5W026	ANKRD30A
1867.1	Occludin/ELL domain-containing	1.46E+05	0.00E+00	-1.46E+05	-1.46E+05	NULL	AD	Q9H607	OCEL1
2308.1	Isoform 2 of Splicing factor, sup	1.46E+05	0.00E+00	-1.46E+05	-1.46E+05	NULL	AD	Q12872-2	SFSWAP
2351.1	Gastricsin	1.46E+05	0.00E+00	-1.46E+05	-1.46E+05	NULL	AD	P20142	PGC
1870.1	T-box transcription factor TBX3	1.47E+05	0.00E+00	-1.47E+05	-1.47E+05	NULL	AD	O15119	TBX3
2354.1	Transferrin receptor protein 2	1.47E+05	0.00E+00	-1.47E+05	-1.47E+05	NULL	AD	Q9UP52	TFR2
1232.1	5'-3' exoribonuclease 1	1.48E+05	0.00E+00	-1.48E+05	-1.48E+05	NULL	AD	Q8IZH2	XRN1
574.2	Isoform 2 of Zinc finger CCCH dc	1.49E+05	0.00E+00	-1.49E+05	-1.49E+05	NULL	AD	Q86VM9-2	ZC3H18
1855.1	Ras-GEF domain-containing fam	1.49E+05	0.00E+00	-1.49E+05	-1.49E+05	NULL	AD	Q0VAM2	RASGEF1B
1548.1	Ankyrin repeat domain-containi	1.50E+05	0.00E+00	-1.50E+05	-1.50E+05	NULL	AD	A2A2Z9	ANKRD18B
1572.1	Cullin-1	1.50E+05	0.00E+00	-1.50E+05	-1.50E+05	NULL	AD	Q13616	CUL1
2367.1	Laminin subunit beta-1	1.50E+05	0.00E+00	-1.50E+05	-1.50E+05	NULL	AD	G3XAI2	LAMB1
1327.1	Ankyrin repeat domain-containi	1.51E+05	0.00E+00	-1.51E+05	-1.51E+05	NULL	AD	Q9ULJ7	ANKRD50
2057.1	Protein FAM54A	1.51E+05	0.00E+00	-1.51E+05	-1.51E+05	NULL	AD	Q6P444	MTFR2
2174.1	Formin-1	1.51E+05	0.00E+00	-1.51E+05	-1.51E+05	NULL	AD	Q68DA7	FMN1
1607.1	Serine beta-lactamase-like prote	1.52E+05	0.00E+00	-1.52E+05	-1.52E+05	NULL	AD	P83111	LACTB
1942.1	SNW domain-containing protein	1.52E+05	0.00E+00	-1.52E+05	-1.52E+05	NULL	AD	G3V4X8	SNW1
2700.1	ARHGEF1 protein	1.52E+05	0.00E+00	-1.52E+05	-1.52E+05	NULL	AD	Q6NX52	ARHGEF1
3013.1	PH domain leucine-rich repeat-c	1.52E+05	0.00E+00	-1.52E+05	-1.52E+05	NULL	AD	H3BMS5	PHLPP2
1355.1	Tripartite motif-containing 2, isc	1.52E+05	0.00E+00	-1.52E+05	-1.52E+05	NULL	AD	Q9C040	TRIM2
1535.1	SH3 domain-containing kinase-b	1.54E+05	0.00E+00	-1.54E+05	-1.54E+05	NULL	AD	Q96B97	SH3KBP1
2240.1	39S ribosomal protein L28, mito	1.54E+05	0.00E+00	-1.54E+05	-1.54E+05	NULL	AD	Q13084	MRPL28
2391.1	Ras-related protein Rab-5A	1.54E+05	0.00E+00	-1.54E+05	-1.54E+05	NULL	AD	P20339	RAB5A
3143.1	Probable E3 ubiquitin-protein lig	1.54E+05	0.00E+00	-1.54E+05	-1.54E+05	NULL	AD	Q5TC82	RC3H1
1442.1	Protein S100-A13	1.55E+05	0.00E+00	-1.55E+05	-1.55E+05	NULL	AD	Q99584	S100A13
2275.1	Lebercilin-like protein	1.56E+05	0.00E+00	-1.56E+05	-1.56E+05	NULL	AD	O95447	LCA5L
2977.1	Isoform 2 of Kin of IRRE-like pro	1.56E+05	0.00E+00	-1.56E+05	-1.56E+05	NULL	AD	Q96J84-2	KIRREL
3217.1	Exophilin-5	1.56E+05	0.00E+00	-1.56E+05	-1.56E+05	NULL	AD	Q8NEV8	EXPH5
1863.1	Ras-related protein Rab-44	1.57E+05	0.00E+00	-1.57E+05	-1.57E+05	NULL	AD	Q7Z6P3	RAB44
2384.1	Phosphatidylinositol 4,5-bisphos	1.57E+05	0.00E+00	-1.57E+05	-1.57E+05	NULL	AD	P42338	PIK3CB
893.1	Serine/arginine repetitive matri	1.58E+05	0.00E+00	-1.58E+05	-1.58E+05	NULL	AD	A7MD48	SRRM4
3003.1	Butyrophilin-like protein 3	1.58E+05	0.00E+00	-1.58E+05	-1.58E+05	NULL	AD	Q6UXE8	BTNL3
2861.1	Spermatogenesis-associated prc	1.60E+05	0.00E+00	-1.60E+05	-1.60E+05	NULL	AD	Q9P0W8	SPATA7
1620.1	5'-AMP-activated protein kinase	1.61E+05	0.00E+00	-1.61E+05	-1.61E+05	NULL	AD	Q9UGJ0	PRKAG2
1634.1	CMP-sialic acid transporter	1.61E+05	0.00E+00	-1.61E+05	-1.61E+05	NULL	AD	P78382	SLC35A1

1730.1	VWFA and cache domain-contai	1.61E+05	0.00E+00	-1.61E+05	-1.61E+05	NULL	AD	Q5VU97	CACHD1
1469.1	Fanconi anemia group D2 protei	1.62E+05	0.00E+00	-1.62E+05	-1.62E+05	NULL	AD	Q9BXW9	FANCD2
2106.1	Brefeldin A-inhibited guanine nu	1.62E+05	0.00E+00	-1.62E+05	-1.62E+05	NULL	AD	Q9Y6D5	ARFGEF2
2761.1	Sushi, nidogen and EGF-like don	1.62E+05	0.00E+00	-1.62E+05	-1.62E+05	NULL	AD	Q8TER0	SNED1
2110.1	Down syndrome cell adhesion m	1.63E+05	0.00E+00	-1.63E+05	-1.63E+05	NULL	AD	O60469	DSCAM
2457.1	Syntaxin-binding protein 3	1.63E+05	0.00E+00	-1.63E+05	-1.63E+05	NULL	AD	O00186	STXBP3
3088.1	tRNA wybutosine-synthesizing p	1.63E+05	0.00E+00	-1.63E+05	-1.63E+05	NULL	AD	Q6NUM6	TYW1B
3220.1	ER membrane protein complex s	1.63E+05	0.00E+00	-1.63E+05	-1.63E+05	NULL	AD	Q8N766	EMC1
1569.1	Isoform 4 of Protein SMG7	1.64E+05	0.00E+00	-1.64E+05	-1.64E+05	NULL	AD	Q92540-4	SMG7
2032.1	Sodium channel protein type 5 s	1.64E+05	0.00E+00	-1.64E+05	-1.64E+05	NULL	AD	H9KVD2	SCN5A
2339.1	Isoform 3 of MBT domain-conta	1.64E+05	0.00E+00	-1.64E+05	-1.64E+05	NULL	AD	Q05BQ5-3	MBTD1
3074.1	Isoform 3 of Disks large-associat	1.64E+05	0.00E+00	-1.64E+05	-1.64E+05	NULL	AD	Q15398-3	DLGAP5
3.8	Desmin	1.66E+05	0.00E+00	-1.66E+05	-1.66E+05	NULL	AD	P17661	DES
2830.1	Ecotropic viral integration site 5	1.66E+05	0.00E+00	-1.66E+05	-1.66E+05	NULL	AD	F5H4R0	EVI5
1644.1	Phosphatidylinositol 3,4,5-trisph	1.67E+05	0.00E+00	-1.67E+05	-1.67E+05	NULL	AD	Q92835	INPP5D
1494.1	Charged multivesicular body pro	1.68E+05	0.00E+00	-1.68E+05	-1.68E+05	NULL	AD	Q14D22	CHMP4A
2015.1	Cyclin-dependent kinase 15	1.69E+05	0.00E+00	-1.69E+05	-1.69E+05	NULL	AD	Q96Q40	CDK15
2809.1	RCC1 and BTB domain-containin	1.69E+05	0.00E+00	-1.69E+05	-1.69E+05	NULL	AD	B4DWG0	RCBTB2
1723.1	Isoform 2 of E3 ubiquitin-protei	1.70E+05	0.00E+00	-1.70E+05	-1.70E+05	NULL	AD	Q5T4S7-2	UBR4
2265.1	Hamartin	1.70E+05	0.00E+00	-1.70E+05	-1.70E+05	NULL	AD	Q92574	TSC1
2269.1	Melanoma-associated antigen 8	1.70E+05	0.00E+00	-1.70E+05	-1.70E+05	NULL	AD	P43361	MAGEA8
2750.1	Tetratricopeptide repeat protei	1.70E+05	0.00E+00	-1.70E+05	-1.70E+05	NULL	AD	G3V3A5	TTC6
2988.1	KH domain-containing, RNA-bin	1.70E+05	0.00E+00	-1.70E+05	-1.70E+05	NULL	AD	Q5VWX1	KHDRBS2
2241.1	Alpha-2,8-sialyltransferase 8B	1.71E+05	0.00E+00	-1.71E+05	-1.71E+05	NULL	AD	Q92186	ST8SIA2
299.2	ATP-citrate synthase	1.72E+05	0.00E+00	-1.72E+05	-1.72E+05	NULL	AD	B4E3P0	ACLY
1048.1	LDLR chaperone MESD	1.72E+05	0.00E+00	-1.72E+05	-1.72E+05	NULL	AD	Q14696	MESDC2
2599.1	Mis18-binding protein 1	1.72E+05	0.00E+00	-1.72E+05	-1.72E+05	NULL	AD	Q6P0N0	MIS18BP1
2172.1	Copper-transporting ATPase 2	1.73E+05	0.00E+00	-1.73E+05	-1.73E+05	NULL	AD	P35670	ATP7B
2324.1	Membrane-associated guanylate	1.73E+05	0.00E+00	-1.73E+05	-1.73E+05	NULL	AD	Q96QZ7	MAGI1
7.2	Filamin-C	1.74E+05	0.00E+00	-1.74E+05	-1.74E+05	NULL	AD	Q14315	FLNC
2835.1	Protein cramped-like	1.74E+05	0.00E+00	-1.74E+05	-1.74E+05	NULL	AD	J3KR07	CRAMP1L
697.1	Protein arginine N-methyltransf	1.76E+05	0.00E+00	-1.76E+05	-1.76E+05	NULL	AD	O14744	PRMT5
2445.1	Period circadian protein homolo	1.77E+05	0.00E+00	-1.77E+05	-1.77E+05	NULL	AD	O15534	PER1
2733.1	Isoform 4 of DNA helicase MCM	1.77E+05	0.00E+00	-1.77E+05	-1.77E+05	NULL	AD	Q9UJA3-4	MCM8
2841.1	Transmembrane emp24 domair	1.77E+05	0.00E+00	-1.77E+05	-1.77E+05	NULL	AD	Q9Y3A6	TMED5

1803.1	Synaptotagmin-like protein 4	1.78E+05	0.00E+00	-1.78E+05	-1.78E+05	NULL	AD	F8W9B9	SYTL4
1329.1	Ubiquitin carboxyl-terminal hyd	1.79E+05	0.00E+00	-1.79E+05	-1.79E+05	NULL	AD	Q70EL2	USP45
3131.1	SURP and G-patch domain-cont	1.80E+05	0.00E+00	-1.80E+05	-1.80E+05	NULL	AD	Q8IX01	SUGP2
3086.1	Deoxynucleotidyltransferase ter	1.82E+05	0.00E+00	-1.82E+05	-1.82E+05	NULL	AD	Q5QJE6	DNTTIP2
1073.1	Pantothenate kinase 4	1.84E+05	0.00E+00	-1.84E+05	-1.84E+05	NULL	AD	Q9NVE7	PANK4
951.1	Testis-expressed sequence 10 p	1.85E+05	0.00E+00	-1.85E+05	-1.85E+05	NULL	AD	Q9NXF1	TEX10
2281.1	EMILIN-2	1.85E+05	0.00E+00	-1.85E+05	-1.85E+05	NULL	AD	Q9BXX0	EMILIN2
2705.1	Treacle protein	1.86E+05	0.00E+00	-1.86E+05	-1.86E+05	NULL	AD	E9PHK9	TCOF1
3125.1	Isoform 3 of Semaphorin-6C	1.86E+05	0.00E+00	-1.86E+05	-1.86E+05	NULL	AD	Q9H3T2-3	SEMA6C
1676.1	Zinc finger FYVE domain-contai	1.88E+05	0.00E+00	-1.88E+05	-1.88E+05	NULL	AD	Q68DK2	ZFYVE26
2349.1	DC-STAMP domain-containing p	1.90E+05	0.00E+00	-1.90E+05	-1.90E+05	NULL	AD	Q5T1A1	DCST2
2641.1	Probable ATP-dependent RNA h	1.90E+05	0.00E+00	-1.90E+05	-1.90E+05	NULL	AD	Q8IY37	DHX37
3192.1	Forkhead box protein O4	1.90E+05	0.00E+00	-1.90E+05	-1.90E+05	NULL	AD	P98177	FOXO4
2654.1	Alpha-2-macroglobulin	1.91E+05	0.00E+00	-1.91E+05	-1.91E+05	NULL	AD	P01023	A2M
2905.1	Probable tRNA threonylcarbam	1.91E+05	0.00E+00	-1.91E+05	-1.91E+05	NULL	AD	Q9NPF4	OSGEP
860.1	Annexin A6	1.92E+05	0.00E+00	-1.92E+05	-1.92E+05	NULL	AD	P08133	ANXA6
1872.1	Ferritin light chain	1.92E+05	0.00E+00	-1.92E+05	-1.92E+05	NULL	AD	P02792	FTL
2843.1	Vacuolar protein sorting-associa	1.92E+05	0.00E+00	-1.92E+05	-1.92E+05	NULL	AD	Q9H267	VPS33B
3037.1	Transcription factor HIVEP3	1.92E+05	0.00E+00	-1.92E+05	-1.92E+05	NULL	AD	Q5T1R4	HIVEP3
3077.1	Protein SOGA2	1.93E+05	0.00E+00	-1.93E+05	-1.93E+05	NULL	AD	Q9Y4B5	SOGA2
2002.1	Isoform 2 of M-phase phosphop	1.94E+05	0.00E+00	-1.94E+05	-1.94E+05	NULL	AD	Q99549-2	MPHOSPH8
1394.1	Phosphatidylinositol 3,4,5-trisph	1.96E+05	0.00E+00	-1.96E+05	-1.96E+05	NULL	AD	O15357	INPPL1
2159.1	Testis-expressed sequence 13A	1.96E+05	0.00E+00	-1.96E+05	-1.96E+05	NULL	AD	Q9BXU3	TEX13A
2531.1	Tumor necrosis factor receptor	1.96E+05	0.00E+00	-1.96E+05	-1.96E+05	NULL	AD	P19438	TNFRSF1A
827.1	G protein-regulated inducer of	1.97E+05	0.00E+00	-1.97E+05	-1.97E+05	NULL	AD	Q6ZVF9	GPRIN3
2773.1	Putative zinc finger protein 705	1.97E+05	0.00E+00	-1.97E+05	-1.97E+05	NULL	AD	A8MWA4	ZNF705E
2968.1	COMM domain-containing prot	1.97E+05	0.00E+00	-1.97E+05	-1.97E+05	NULL	AD	Q9Y6G5	COMMD10
2560.1	Taste receptor type 1 member 1	1.98E+05	0.00E+00	-1.98E+05	-1.98E+05	NULL	AD	Q7RTX1	TAS1R1
2749.1	Frizzled-10	1.98E+05	0.00E+00	-1.98E+05	-1.98E+05	NULL	AD	F5H450	FZD10
2851.1	Glutamate receptor-interacting	1.98E+05	0.00E+00	-1.98E+05	-1.98E+05	NULL	AD	Q9C0E4	GRIP2
2211.1	Dedicator of cytokinesis protein	1.99E+05	0.00E+00	-1.99E+05	-1.99E+05	NULL	AD	Q8NF50	DOCK8
2283.1	RUN domain-containing protein	1.99E+05	0.00E+00	-1.99E+05	-1.99E+05	NULL	AD	Q96NL0	RUNDC3B
2239.1	NudC domain-containing protei	2.01E+05	0.00E+00	-2.01E+05	-2.01E+05	NULL	AD	Q96RS6	NUDCD1
1919.1	Ephrin type-B receptor 6	2.02E+05	0.00E+00	-2.02E+05	-2.02E+05	NULL	AD	O15197	EPHB6
1446.1	TMF-regulated nuclear protein	2.03E+05	0.00E+00	-2.03E+05	-2.03E+05	NULL	AD	Q6NT89	TRNP1

2530.1	SH2 domain-containing protein	2.03E+05	0.00E+00	-2.03E+05	-2.03E+05	NULL	AD	Q8N5H7	SH2D3C
1667.1	Otolin-1	2.05E+05	0.00E+00	-2.05E+05	-2.05E+05	NULL	AD	A6NHN0	OTOL1
2437.1	Protein SOGA3	2.05E+05	0.00E+00	-2.05E+05	-2.05E+05	NULL	AD	Q5TF21	SOGA3
2416.1	Oncoprotein-induced transcript	2.06E+05	0.00E+00	-2.06E+05	-2.06E+05	NULL	AD	Q8WWZ8	OIT3
2876.1	Chloride channel protein 1	2.06E+05	0.00E+00	-2.06E+05	-2.06E+05	NULL	AD	P35523	CLCN1
638.2	YTH domain family protein 1	2.07E+05	0.00E+00	-2.07E+05	-2.07E+05	NULL	AD	Q9BYJ9	YTHDF1
1315.1	Myopalladin	2.07E+05	0.00E+00	-2.07E+05	-2.07E+05	NULL	AD	F5GWA6	MYPN
2399.1	Inositol 1,4,5-trisphosphate rece	2.07E+05	0.00E+00	-2.07E+05	-2.07E+05	NULL	AD	Q14571	ITPR2
2504.1	Lactoperoxidase	2.07E+05	0.00E+00	-2.07E+05	-2.07E+05	NULL	AD	P22079	LPO
2867.1	Growth hormone-inducible tran	2.07E+05	0.00E+00	-2.07E+05	-2.07E+05	NULL	AD	Q9H3K2	GHITM
1354.1	Wilms tumor protein 1-interacti	2.07E+05	0.00E+00	-2.07E+05	-2.07E+05	NULL	AD	A6NIX2	WTIP
1725.1	Steryl-sulfatase	2.08E+05	0.00E+00	-2.08E+05	-2.08E+05	NULL	AD	P08842	STS
2162.1	Fibulin-1	2.08E+05	0.00E+00	-2.08E+05	-2.08E+05	NULL	AD	F8W7M9	FBLN1
2386.1	Shugoshin-like 2	2.08E+05	0.00E+00	-2.08E+05	-2.08E+05	NULL	AD	Q562F6	SGOL2
1656.1	Pancreatic lipase-related protei	2.09E+05	0.00E+00	-2.09E+05	-2.09E+05	NULL	AD	Q17RR3	PNLIPRP3
3189.1	Transformation/transcription do	2.09E+05	0.00E+00	-2.09E+05	-2.09E+05	NULL	AD	Q9Y4A5	TRRAP
1674.1	Isoform 11 of Peroxisomal N(1)-	2.10E+05	0.00E+00	-2.10E+05	-2.10E+05	NULL	AD	Q6QHF9-9	PAOX
3084.1	PWWP domain-containing prote	2.10E+05	0.00E+00	-2.10E+05	-2.10E+05	NULL	AD	Q96N64	PWWP2A
3065.1	Histone-lysine N-methyltransfer	2.11E+05	0.00E+00	-2.11E+05	-2.11E+05	NULL	AD	Q96L73	NSD1
894.1	Plastin-3	2.12E+05	0.00E+00	-2.12E+05	-2.12E+05	NULL	AD	P13797	PLS3
1181.1	Zinc finger CCCH-type antiviral p	2.12E+05	0.00E+00	-2.12E+05	-2.12E+05	NULL	AD	C9J6P4	ZC3HAV1
1214.1	Meckelin	2.12E+05	0.00E+00	-2.12E+05	-2.12E+05	NULL	AD	Q5HYA8	TMEM67
1235.1	Nucleosome assembly protein 1	2.12E+05	0.00E+00	-2.12E+05	-2.12E+05	NULL	AD	Q9ULW6	NAP1L2
1576.1	SUMO-interacting motif-contair	2.12E+05	0.00E+00	-2.12E+05	-2.12E+05	NULL	AD	Q8NDZ2	SIMC1
2650.1	Maternal embryonic leucine zip	2.13E+05	0.00E+00	-2.13E+05	-2.13E+05	NULL	AD	Q14680	MELK
2563.1	Euchromatic histone-lysine N-m	2.14E+05	0.00E+00	-2.14E+05	-2.14E+05	NULL	AD	B0UZY1	EHMT2
2944.1	DIS3-like exonuclease 1	2.14E+05	0.00E+00	-2.14E+05	-2.14E+05	NULL	AD	Q8TF46	DIS3L
3009.1	Isoform 7 of Protein PRRC2C	2.14E+05	0.00E+00	-2.14E+05	-2.14E+05	NULL	AD	Q9Y520-7	PRRC2C
911.1	Ribonuclease H2 subunit A	2.16E+05	0.00E+00	-2.16E+05	-2.16E+05	NULL	AD	O75792	RNASEH2A
2196.1	Sodium channel and clathrin linl	2.17E+05	0.00E+00	-2.17E+05	-2.17E+05	NULL	AD	Q96NL6	SCLT1
2282.1	Dolichyl-diphosphooligosacchar	2.18E+05	0.00E+00	-2.18E+05	-2.18E+05	NULL	AD	P04843	RPN1
573.1	Isoform 2 of COP9 signalosome	2.19E+05	0.00E+00	-2.19E+05	-2.19E+05	NULL	AD	Q13098-7	GPS1
617.1	Dynamin-1	2.19E+05	0.00E+00	-2.19E+05	-2.19E+05	NULL	AD	Q05193	DNM1
1282.1	Protein Daple	2.19E+05	0.00E+00	-2.19E+05	-2.19E+05	NULL	AD	Q9P219	CCDC88C
1850.1	Death-inducer obliterator 1	2.19E+05	0.00E+00	-2.19E+05	-2.19E+05	NULL	AD	Q9BTC0	DIDO1

1096.1	Zinc finger protein 461	2.20E+05	0.00E+00	-2.20E+05	-2.20E+05	NULL	AD	Q8TAF7	ZNF461
3122.1	Protein PAT1 homolog 1	2.20E+05	0.00E+00	-2.20E+05	-2.20E+05	NULL	AD	Q86TB9	PATL1
1917.1	Erythrocyte band 7 integral mer	2.21E+05	0.00E+00	-2.21E+05	-2.21E+05	NULL	AD	P27105	STOM
2029.1	Zinc finger protein 500	2.21E+05	0.00E+00	-2.21E+05	-2.21E+05	NULL	AD	O60304	ZNF500
2935.1	Paired box protein Pax-5	2.21E+05	0.00E+00	-2.21E+05	-2.21E+05	NULL	AD	E7ERK2	PAX5
1532.1	Choline-phosphate cytidylyltran	2.22E+05	0.00E+00	-2.22E+05	-2.22E+05	NULL	AD	C9JEJ2	PCYT1A
1959.1	Myosin-8	2.22E+05	0.00E+00	-2.22E+05	-2.22E+05	NULL	AD	P13535	MYH8
2244.1	28S ribosomal protein S22, mitc	2.22E+05	0.00E+00	-2.22E+05	-2.22E+05	NULL	AD	P82650	MRPS22
2464.1	Acyl-coenzyme A thioesterase 8	2.22E+05	0.00E+00	-2.22E+05	-2.22E+05	NULL	AD	O14734	ACOT8
2941.1	Coiled-coil domain-containing p	2.23E+05	0.00E+00	-2.23E+05	-2.23E+05	NULL	AD	Q9UL16	CCDC19
1477.1	Cyclin-dependent kinase 3	2.25E+05	0.00E+00	-2.25E+05	-2.25E+05	NULL	AD	Q00526	CDK3
2566.1	Protocadherin Fat 3	2.27E+05	0.00E+00	-2.27E+05	-2.27E+05	NULL	AD	Q8TDW7	FAT3
2667.1	Secreted phosphoprotein 24	2.27E+05	0.00E+00	-2.27E+05	-2.27E+05	NULL	AD	Q13103	SPP2
2795.1	WD repeat-containing protein 2	2.27E+05	0.00E+00	-2.27E+05	-2.27E+05	NULL	AD	Q8TBZ3	WDR20
1203.1	Isoform 2 of BRCA2 and CDKN1/	2.28E+05	0.00E+00	-2.28E+05	-2.28E+05	NULL	AD	Q9P287-2	BCCIP
2901.1	CUB domain-containing protein	2.28E+05	0.00E+00	-2.28E+05	-2.28E+05	NULL	AD	Q9H5V8	CDCP1
2035.1	Insulinoma-associated protein 2	2.29E+05	0.00E+00	-2.29E+05	-2.29E+05	NULL	AD	Q96T92	INSM2
1706.1	Zinc finger protein 667	2.31E+05	0.00E+00	-2.31E+05	-2.31E+05	NULL	AD	E7EPS0	ZNF667
2369.1	Truncated apolipoprotein C-I	2.31E+05	0.00E+00	-2.31E+05	-2.31E+05	NULL	AD	K7EPF9	APOC1
1171.1	Isoform 2 of Nuclear factor relat	2.32E+05	0.00E+00	-2.32E+05	-2.32E+05	NULL	AD	Q6P4R8-2	NFRKB
2168.1	Integrin alpha-1	2.32E+05	0.00E+00	-2.32E+05	-2.32E+05	NULL	AD	P56199	ITGA1
2631.1	Isoform 3 of Fanconi anemia-as:	2.32E+05	0.00E+00	-2.32E+05	-2.32E+05	NULL	AD	Q6NZ36-3	FAAP20
2169.1	Zinc finger protein 280B	2.33E+05	0.00E+00	-2.33E+05	-2.33E+05	NULL	AD	Q86YH2	ZNF280B
1852.1	Sodium-dependent neutral amir	2.34E+05	0.00E+00	-2.34E+05	-2.34E+05	NULL	AD	Q9H1V8	SLC6A17
2285.1	Paired mesoderm homeobox pr	2.35E+05	0.00E+00	-2.35E+05	-2.35E+05	NULL	AD	Q99453	PHOX2B
3245.1	Lethal(2) giant larvae protein hc	2.35E+05	0.00E+00	-2.35E+05	-2.35E+05	NULL	AD	Q6P1M3	LLGL2
2813.1	H/ACA ribonucleoprotein compl	2.35E+05	0.00E+00	-2.35E+05	-2.35E+05	NULL	AD	Q96HR8	NAF1
2746.1	Isoform 2 of Ubiquitin conjugati	2.36E+05	0.00E+00	-2.36E+05	-2.36E+05	NULL	AD	Q14139-2	UBE4A
3.6	Keratin, type II cytoskeletal 2 or	2.37E+05	0.00E+00	-2.37E+05	-2.37E+05	NULL	AD	Q01546	KRT76
1914.1	Zinc finger protein 567	2.37E+05	0.00E+00	-2.37E+05	-2.37E+05	NULL	AD	Q8N184	ZNF567
21.3	Tropomyosin 2 (Beta)	2.38E+05	0.00E+00	-2.38E+05	-2.38E+05	NULL	AD	Q5TCU8	TPM2
1404.1	Zinc finger protein 64 homolog,	2.38E+05	0.00E+00	-2.38E+05	-2.38E+05	NULL	AD	Q9NTW7	ZFP64
993.1	Baculoviral IAP repeat-containin	2.39E+05	0.00E+00	-2.39E+05	-2.39E+05	NULL	AD	Q13490	BIRC2
1013.1	Ankyrin repeat and SOCS box pr	2.40E+05	0.00E+00	-2.40E+05	-2.40E+05	NULL	AD	J3KQJ5	ASB10
1460.1	Fibrous sheath-interacting prote	2.40E+05	0.00E+00	-2.40E+05	-2.40E+05	NULL	AD	J3QTJ6	FSIP2

1880.1	Transmembrane protein 176A	2.43E+05	0.00E+00	-2.43E+05	-2.43E+05	NULL	AD	Q96HP8	TMEM176A
2547.1	Tyrosine-protein kinase Fes/Fps	2.44E+05	0.00E+00	-2.44E+05	-2.44E+05	NULL	AD	P07332	FES
2721.1	Zinc finger protein 99	2.44E+05	0.00E+00	-2.44E+05	-2.44E+05	NULL	AD	A8MXY4	ZNF99
1641.1	Guanine nucleotide-binding pro	2.46E+05	0.00E+00	-2.46E+05	-2.46E+05	NULL	AD	P19086	GNAZ
1883.1	Protein FAM65C	2.47E+05	0.00E+00	-2.47E+05	-2.47E+05	NULL	AD	F5H0X2	FAM65C
2329.1	SUMO-activating enzyme subun	2.48E+05	0.00E+00	-2.48E+05	-2.48E+05	NULL	AD	Q9UBT2	UBA2
1905.1	Protein phosphatase 1 regulato	2.49E+05	0.00E+00	-2.49E+05	-2.49E+05	NULL	AD	Q13522	PPP1R1A
3062.1	Isoform 3 of SH3-containing GR	2.49E+05	0.00E+00	-2.49E+05	-2.49E+05	NULL	AD	Q9BQI5-3	SGIP1
941.1	Nucleolar pre-ribosomal-associa	2.50E+05	0.00E+00	-2.50E+05	-2.50E+05	NULL	AD	O60287	URB1
2719.1	Phosphorylated adapter RNA ex	2.50E+05	0.00E+00	-2.50E+05	-2.50E+05	NULL	AD	Q9H814	PHAX
629.1	tRNA-splicing endonuclease sub	2.51E+05	0.00E+00	-2.51E+05	-2.51E+05	NULL	AD	E7EQB3	TSEN34
2043.1	Zinc finger protein ubi-d4	2.53E+05	0.00E+00	-2.53E+05	-2.53E+05	NULL	AD	J3KMZ8	DPF2
3238.1	Lysine-specific demethylase 5A	2.53E+05	0.00E+00	-2.53E+05	-2.53E+05	NULL	AD	P29375	KDM5A
1137.1	T-lymphoma invasion and meta	2.59E+05	0.00E+00	-2.59E+05	-2.59E+05	NULL	AD	Q13009	TIAM1
1248.1	Isoform 2 of LIM and SH3 doma	2.59E+05	0.00E+00	-2.59E+05	-2.59E+05	NULL	AD	Q14847-2	LASP1
1342.1	Ankyrin repeat domain-contain	2.59E+05	0.00E+00	-2.59E+05	-2.59E+05	NULL	AD	Q6UB99	ANKRD11
1669.1	Isoform 2 of Diphosphoinositol	2.59E+05	0.00E+00	-2.59E+05	-2.59E+05	NULL	AD	Q9NZJ9-2	NUDT4
2316.1	Coiled-coil and C2 domain-cont	2.59E+05	0.00E+00	-2.59E+05	-2.59E+05	NULL	AD	Q6P1N0	CC2D1A
3156.1	Transcription factor Dp-1	2.60E+05	0.00E+00	-2.60E+05	-2.60E+05	NULL	AD	F5H452	TFDP1
2089.1	E3 ubiquitin-protein ligase RNF1	2.62E+05	0.00E+00	-2.62E+05	-2.62E+05	NULL	AD	Q96K19	RNF170
523.1	Cyclin-dependent kinase 1	2.63E+05	0.00E+00	-2.63E+05	-2.63E+05	NULL	AD	P06493	CDK1
1259.1	Rho-associated protein kinase 2	2.63E+05	0.00E+00	-2.63E+05	-2.63E+05	NULL	AD	O75116	ROCK2
1545.1	BTB/POZ domain-containing pr	2.64E+05	0.00E+00	-2.64E+05	-2.64E+05	NULL	AD	Q9BQ13	KCTD14
2642.1	Isoform 2 of MORN repeat-cont	2.64E+05	0.00E+00	-2.64E+05	-2.64E+05	NULL	AD	Q8NDC4-2	MORN4
1721.1	Vasoactive intestinal polypeptid	2.65E+05	0.00E+00	-2.65E+05	-2.65E+05	NULL	AD	E9PCR5	VIPR2
1462.1	A-kinase anchor protein 8	2.66E+05	0.00E+00	-2.66E+05	-2.66E+05	NULL	AD	O43823	AKAP8
1437.1	Phosphatidylinositol 4-phospha	2.68E+05	0.00E+00	-2.68E+05	-2.68E+05	NULL	AD	O00750	PIK3C2B
3081.1	Sodium/hydrogen exchanger 3	2.69E+05	0.00E+00	-2.69E+05	-2.69E+05	NULL	AD	P48764	SLC9A3
3206.1	Neurexin-1-beta	2.69E+05	0.00E+00	-2.69E+05	-2.69E+05	NULL	AD	P58400	NRXN1
9.3	Tubulin beta-2B chain	2.71E+05	0.00E+00	-2.71E+05	-2.71E+05	NULL	AD	Q9BVA1	TUBB2B
1594.1	EGF-like module-containing mu	2.71E+05	0.00E+00	-2.71E+05	-2.71E+05	NULL	AD	Q14246	EMR1
2656.1	Isoform 3 of Coiled-coil domain-	2.71E+05	0.00E+00	-2.71E+05	-2.71E+05	NULL	AD	Q6TFL3-4	CCDC171
937.1	Centrosomal protein of 128 kDa	2.72E+05	0.00E+00	-2.72E+05	-2.72E+05	NULL	AD	Q6ZU80	CEP128
1552.1	Rho GTPase-activating protein 3	2.72E+05	0.00E+00	-2.72E+05	-2.72E+05	NULL	AD	Q2M1Z3	ARHGAP31
2572.1	Zinc finger protein 549	2.72E+05	0.00E+00	-2.72E+05	-2.72E+05	NULL	AD	Q6P9A3	ZNF549

913.1	Ferritin heavy polypeptide-like 1	2.75E+05	0.00E+00	-2.75E+05	-2.75E+05	NULL	AD	Q9BXU8	FTHL17
1225.1	Lipoma-preferred partner	2.76E+05	0.00E+00	-2.76E+05	-2.76E+05	NULL	AD	Q93052	LPP
1596.1	Charged multivesicular body prc	2.76E+05	0.00E+00	-2.76E+05	-2.76E+05	NULL	AD	Q9H444	CHMP4B
1619.1	UPF0489 protein C5orf22	2.77E+05	0.00E+00	-2.77E+05	-2.77E+05	NULL	AD	B4DR92	C5orf22
2556.1	Nik-related protein kinase	2.77E+05	0.00E+00	-2.77E+05	-2.77E+05	NULL	AD	F5H049	NRK
3104.1	UHRF1-binding protein 1	2.77E+05	0.00E+00	-2.77E+05	-2.77E+05	NULL	AD	Q6BDS2	UHRF1BP1
1507.1	Disintegrin and metalloproteina	2.77E+05	0.00E+00	-2.77E+05	-2.77E+05	NULL	AD	P78325	ADAM8
3111.1	Polyadenylate-binding protein 5	2.78E+05	0.00E+00	-2.78E+05	-2.78E+05	NULL	AD	Q96DU9	PABPC5
2362.1	Isoform 2 of TNF receptor-assoc	2.80E+05	0.00E+00	-2.80E+05	-2.80E+05	NULL	AD	Q12933-2	TRAF2
1835.1	AP20 region protein 1	2.81E+05	0.00E+00	-2.81E+05	-2.81E+05	NULL	AD	Q8IVJ8	APRG1
2551.1	Coiled-coil domain-containing p	2.81E+05	0.00E+00	-2.81E+05	-2.81E+05	NULL	AD	Q8ND07	CCDC176
2373.1	ETS translocation variant 3	2.82E+05	0.00E+00	-2.82E+05	-2.82E+05	NULL	AD	P41162	ETV3
740.1	Chromosome 1 open reading fra	2.83E+05	0.00E+00	-2.83E+05	-2.83E+05	NULL	AD	Q5VSH5	C1orf122
2797.1	Uroporphyrinogen decarboxylas	2.83E+05	0.00E+00	-2.83E+05	-2.83E+05	NULL	AD	P06132	UROD
2846.1	Forkhead box protein D1	2.83E+05	0.00E+00	-2.83E+05	-2.83E+05	NULL	AD	J3KT45	FOXD1
2859.1	1,4-alpha-glucan-branching enzy	2.83E+05	0.00E+00	-2.83E+05	-2.83E+05	NULL	AD	Q04446	GBE1
2784.1	Putative U6 snRNA phosphodies	2.84E+05	0.00E+00	-2.84E+05	-2.84E+05	NULL	AD	Q9BQ65	USB1
1582.1	Polypeptide N-acetylgalactosam	2.86E+05	0.00E+00	-2.86E+05	-2.86E+05	NULL	AD	Q8IXK2	GALNT12
2311.1	Killer cell immunoglobulin-like r	2.88E+05	0.00E+00	-2.88E+05	-2.88E+05	NULL	AD	Q8NHK3	KIR2DL5B
2013.1	Envoplakin	2.90E+05	0.00E+00	-2.90E+05	-2.90E+05	NULL	AD	K7EKI0	EVPL
1536.1	Adapter molecule crk	2.91E+05	0.00E+00	-2.91E+05	-2.91E+05	NULL	AD	P46108	CRK
1175.1	Protein FAM217B	2.93E+05	0.00E+00	-2.93E+05	-2.93E+05	NULL	AD	Q9NTX9	FAM217B
2108.1	RRP12-like protein	2.93E+05	0.00E+00	-2.93E+05	-2.93E+05	NULL	AD	Q5JTH9	RRP12
2499.1	Quinone oxidoreductase PIG3	2.93E+05	0.00E+00	-2.93E+05	-2.93E+05	NULL	AD	Q53FA7	TP53I3
3178.1	Isoform 2 of Transcription facto	2.94E+05	0.00E+00	-2.94E+05	-2.94E+05	NULL	AD	Q33E94-2	RFX4
2995.1	O-acetyl-ADP-ribose deacetylase	2.96E+05	0.00E+00	-2.96E+05	-2.96E+05	NULL	AD	Q9Y530	OARD1
3141.1	Breast cancer anti-estrogen resi	2.98E+05	0.00E+00	-2.98E+05	-2.98E+05	NULL	AD	Q05GC8	BCAR2
1345.1	Cytokine inducible SH2-containi	3.00E+05	0.00E+00	-3.00E+05	-3.00E+05	NULL	AD	Q9NSE2	CISH
1834.1	DNA-binding protein RFX8	3.03E+05	0.00E+00	-3.03E+05	-3.03E+05	NULL	AD	Q6ZV50	RFX8
943.1	Obscurin	3.05E+05	0.00E+00	-3.05E+05	-3.05E+05	NULL	AD	H3BPX2	OBSCN
2578.1	Dynein heavy chain 1, axonemal	3.05E+05	0.00E+00	-3.05E+05	-3.05E+05	NULL	AD	Q9P2D7	DNAH1
2363.1	Multimerin-1	3.08E+05	0.00E+00	-3.08E+05	-3.08E+05	NULL	AD	Q13201	MMRN1
1693.1	Ankyrin repeat domain-containi	3.11E+05	0.00E+00	-3.11E+05	-3.11E+05	NULL	AD	Q69YU3	ANKRD34A
855.1	Golgin subfamily A member 3	3.12E+05	0.00E+00	-3.12E+05	-3.12E+05	NULL	AD	Q08378	GOLGA3
1008.1	UDP-GlcNAc:betaGal beta-1,3-N	3.12E+05	0.00E+00	-3.12E+05	-3.12E+05	NULL	AD	Q8NFL0	B3GNT7

1653.1	Vacuolar protein sorting-associa	3.12E+05	0.00E+00	-3.12E+05	-3.12E+05	NULL	AD	Q9P1Q0	VPS54
2691.1	DNA ligase 1	3.14E+05	0.00E+00	-3.14E+05	-3.14E+05	NULL	AD	P18858	LIG1
1862.1	Protein YIPF4	3.15E+05	0.00E+00	-3.15E+05	-3.15E+05	NULL	AD	Q9BSR8	YIPF4
10.2	Clathrin heavy chain 2	3.16E+05	0.00E+00	-3.16E+05	-3.16E+05	NULL	AD	P53675	CLTCL1
708.1	Na(+)/H(+) exchange regulatory	3.16E+05	0.00E+00	-3.16E+05	-3.16E+05	NULL	AD	O14745	SLC9A3R1
1504.1	UBX domain-containing protein	3.16E+05	0.00E+00	-3.16E+05	-3.16E+05	NULL	AD	Q14CS0	UBXN2B
2669.1	FtsJ methyltransferase domain-	3.18E+05	0.00E+00	-3.18E+05	-3.18E+05	NULL	AD	Q8IYT2	FTSJD1
3140.1	Homeobox protein MOX-2	3.18E+05	0.00E+00	-3.18E+05	-3.18E+05	NULL	AD	P50222	MEOX2
1974.1	Heat shock protein beta-3	3.20E+05	0.00E+00	-3.20E+05	-3.20E+05	NULL	AD	Q12988	HSPB3
943.3	Obscurin	3.21E+05	0.00E+00	-3.21E+05	-3.21E+05	NULL	AD	H7BY31	OBSCN
1250.1	HERV-K_3q12.3 provirus ancest	3.21E+05	0.00E+00	-3.21E+05	-3.21E+05	NULL	AD	Q9HDB9	ERVK-5
1930.1	Anoctamin-5	3.23E+05	0.00E+00	-3.23E+05	-3.23E+05	NULL	AD	Q75V66	ANO5
1506.1	Isoform 6 of Calcium/calmoduli	3.24E+05	0.00E+00	-3.24E+05	-3.24E+05	NULL	AD	Q13555-6	CAMK2G
1750.1	Sentrin-specific protease 1	3.25E+05	0.00E+00	-3.25E+05	-3.25E+05	NULL	AD	Q9P0U3	SENP1
2011.1	PHD and RING finger domain-co	3.25E+05	0.00E+00	-3.25E+05	-3.25E+05	NULL	AD	Q9P1Y6	PHRF1
2376.1	Isoform 4 of Tether containing U	3.27E+05	0.00E+00	-3.27E+05	-3.27E+05	NULL	AD	Q9BZE9-4	ASPSCR1
1731.1	Dendritic cell nuclear protein 1	3.28E+05	0.00E+00	-3.28E+05	-3.28E+05	NULL	AD	Q8TF63	DCNP1
2679.1	Isoform 5 of Bromodomain-cont	3.29E+05	0.00E+00	-3.29E+05	-3.29E+05	NULL	AD	Q9H8M2-1	BRD9
709.1	Isoform 3 of Clathrin interactor	3.30E+05	0.00E+00	-3.30E+05	-3.30E+05	NULL	AD	Q14677-3	CLINT1
1657.1	Frizzled-3	3.30E+05	0.00E+00	-3.30E+05	-3.30E+05	NULL	AD	Q9NPG1	FZD3
1239.1	Chromosome-associated kinesir	3.31E+05	0.00E+00	-3.31E+05	-3.31E+05	NULL	AD	Q2VIQ3	KIF4B
2136.1	CAAX prenyl protease 1 homolo	3.31E+05	0.00E+00	-3.31E+05	-3.31E+05	NULL	AD	O75844	ZMPSTE24
2618.1	ATP-binding cassette sub-family	3.31E+05	0.00E+00	-3.31E+05	-3.31E+05	NULL	AD	Q9UBJ2	ABCD2
1413.1	Olfactory receptor 52B6	3.32E+05	0.00E+00	-3.32E+05	-3.32E+05	NULL	AD	Q8NGF0	OR52B6
2565.1	Protein DBF4 homolog A	3.32E+05	0.00E+00	-3.32E+05	-3.32E+05	NULL	AD	Q9UBU7	DBF4
1138.1	Inner centromere protein	3.33E+05	0.00E+00	-3.33E+05	-3.33E+05	NULL	AD	Q9NQS7	INCENP
2325.1	Olfactory receptor 14J1	3.36E+05	0.00E+00	-3.36E+05	-3.36E+05	NULL	AD	Q9UGF5	OR14J1
2144.1	V-set and immunoglobulin doma	3.37E+05	0.00E+00	-3.37E+05	-3.37E+05	NULL	AD	Q9Y279	VSIG4
2266.1	Protein FAM184B	3.37E+05	0.00E+00	-3.37E+05	-3.37E+05	NULL	AD	Q9ULE4	FAM184B
1711.1	Macrophage metalloelastase	3.39E+05	0.00E+00	-3.39E+05	-3.39E+05	NULL	AD	P39900	MMP12
1765.1	Probable G-protein coupled rec	3.39E+05	0.00E+00	-3.39E+05	-3.39E+05	NULL	AD	Q6PRD1	GPR179
890.1	Isoform 2 of Allograft inflammat	3.40E+05	0.00E+00	-3.40E+05	-3.40E+05	NULL	AD	Q9BQI0-2	AIF1L
2027.1	F-box/LRR-repeat protein 5	3.40E+05	0.00E+00	-3.40E+05	-3.40E+05	NULL	AD	Q9UKA1	FBXL5
2605.1	Kinesin-like protein KIF19	3.40E+05	0.00E+00	-3.40E+05	-3.40E+05	NULL	AD	Q2TAC6	KIF19
1475.1	Collagen alpha-6(VI) chain	3.41E+05	0.00E+00	-3.41E+05	-3.41E+05	NULL	AD	F8W6Y7	COL6A6

2822.1	Radial spoke head protein 3 hor	3.41E+05	0.00E+00	-3.41E+05	-3.41E+05	NULL	AD	Q86UC2	RSPH3
2295.1	Probable tubulin polyglutamyla:	3.43E+05	0.00E+00	-3.43E+05	-3.43E+05	NULL	AD	O95922	TTLL1
2338.1	Cytoplasmic tyrosine-protein kir	3.43E+05	0.00E+00	-3.43E+05	-3.43E+05	NULL	AD	P51813	BMX
2742.1	PI-PLC X domain-containing prot	3.43E+05	0.00E+00	-3.43E+05	-3.43E+05	NULL	AD	Q0VAA5	PLCXD2
2864.1	Cyclin-dependent kinase 11B	3.44E+05	0.00E+00	-3.44E+05	-3.44E+05	NULL	AD	P21127	CDK11B
1453.1	Actin-related protein 10	3.47E+05	0.00E+00	-3.47E+05	-3.47E+05	NULL	AD	Q9NZ32	ACTR10
1398.1	Serine/threonine-protein kinase	3.51E+05	0.00E+00	-3.51E+05	-3.51E+05	NULL	AD	P51955	NEK2
2059.1	Sentrin-specific protease 6	3.51E+05	0.00E+00	-3.51E+05	-3.51E+05	NULL	AD	Q9GZR1	SENP6
1024.1	Protein misato homolog 1	3.52E+05	0.00E+00	-3.52E+05	-3.52E+05	NULL	AD	Q9BUK6	MSTO1
840.1	Ubiquitin carboxyl-terminal hyd	3.54E+05	0.00E+00	-3.54E+05	-3.54E+05	NULL	AD	P45974	USP5
1341.1	Glomulin	3.56E+05	0.00E+00	-3.56E+05	-3.56E+05	NULL	AD	Q92990	GLMN
2115.1	Zinc finger protein basonuclin-1	3.56E+05	0.00E+00	-3.56E+05	-3.56E+05	NULL	AD	Q01954	BNC1
1811.1	Flotillin-2	3.57E+05	0.00E+00	-3.57E+05	-3.57E+05	NULL	AD	E7EMK3	FLOT2
885.1	Kinesin-like protein KIF26A	3.59E+05	0.00E+00	-3.59E+05	-3.59E+05	NULL	AD	Q9ULI4	KIF26A
2509.1	C3 and PZP-like alpha-2-macrog	3.59E+05	0.00E+00	-3.59E+05	-3.59E+05	NULL	AD	Q8IZJ3	CPAMD8
2837.1	Desmoglein-3	3.59E+05	0.00E+00	-3.59E+05	-3.59E+05	NULL	AD	P32926	DSG3
3039.1	Ubiquitin-associated and SH3 dc	3.59E+05	0.00E+00	-3.59E+05	-3.59E+05	NULL	AD	Q8TF42	UBASH3B
1233.1	Histone-arginine methyltransfer	3.62E+05	0.00E+00	-3.62E+05	-3.62E+05	NULL	AD	Q86X55	CARM1
1206.1	Latent-transforming growth fact	3.63E+05	0.00E+00	-3.63E+05	-3.63E+05	NULL	AD	Q14767	LTBP2
2287.1	1-aminocyclopropane-1-carboxy	3.63E+05	0.00E+00	-3.63E+05	-3.63E+05	NULL	AD	Q96QU6	ACCS
2577.1	Prickle-like protein 1	3.63E+05	0.00E+00	-3.63E+05	-3.63E+05	NULL	AD	Q96MT3	PRICKLE1
2777.1	Nucleolar transcription factor 1	3.65E+05	0.00E+00	-3.65E+05	-3.65E+05	NULL	AD	E9PKP7	UBTF
3252.1	Ubiquitin carboxyl-terminal hyd	3.65E+05	0.00E+00	-3.65E+05	-3.65E+05	NULL	AD	Q92995	USP13
9.4	Tubulin beta-3 chain	3.69E+05	0.00E+00	-3.69E+05	-3.69E+05	NULL	AD	Q13509	TUBB3
958.1	Spindlin-2A	3.71E+05	0.00E+00	-3.71E+05	-3.71E+05	NULL	AD	Q99865	SPIN2A
2037.1	Procollagen-lysine,2-oxoglutara	3.74E+05	0.00E+00	-3.74E+05	-3.74E+05	NULL	AD	O60568	PLOD3
1129.1	Rap guanine nucleotide exchang	3.75E+05	0.00E+00	-3.75E+05	-3.75E+05	NULL	AD	O95398	RAPGEF3
2424.1	A-kinase anchor protein 11	3.76E+05	0.00E+00	-3.76E+05	-3.76E+05	NULL	AD	Q9UKA4	AKAP11
1339.1	Isoform SERCA3F of Sarcoplasm	3.81E+05	0.00E+00	-3.81E+05	-3.81E+05	NULL	AD	Q93084-7	ATP2A3
2779.1	Rho GTPase-activating protein 2	3.81E+05	0.00E+00	-3.81E+05	-3.81E+05	NULL	AD	Q52LW3	ARHGAP29
2955.1	Paired amphipathic helix proteir	3.81E+05	0.00E+00	-3.81E+05	-3.81E+05	NULL	AD	O75182	SIN3B
2232.1	Isoform 4 of Melanoma-associat	3.84E+05	0.00E+00	-3.84E+05	-3.84E+05	NULL	AD	Q96JG8-4	MAGED4
2318.1	TBC1 domain family member 8E	3.84E+05	0.00E+00	-3.84E+05	-3.84E+05	NULL	AD	Q0IIM8	TBC1D8B
1449.1	Isoform 7 of Tetratricopeptide r	3.87E+05	0.00E+00	-3.87E+05	-3.87E+05	NULL	AD	Q8NDW8-	TTC21A
2731.1	Anterior gradient protein 3 hom	3.88E+05	0.00E+00	-3.88E+05	-3.88E+05	NULL	AD	Q8TD06	AGR3

1060.1	MON1 homolog A (Yeast), isofo	3.90E+05	0.00E+00	-3.90E+05	-3.90E+05	NULL	AD	Q86VX9	MON1A
1584.1	Solute carrier family 15 membe	3.93E+05	0.00E+00	-3.93E+05	-3.93E+05	NULL	AD	P46059	SLC15A1
2737.1	Centrosomal protein of 192 kDa	3.94E+05	0.00E+00	-3.94E+05	-3.94E+05	NULL	AD	E9PF99	CEP192
2759.1	A disintegrin and metalloprotei	3.94E+05	0.00E+00	-3.94E+05	-3.94E+05	NULL	AD	Q9UP79	ADAMTS8
2881.1	Apolipoprotein B-100	3.98E+05	0.00E+00	-3.98E+05	-3.98E+05	NULL	AD	P04114	APOB
1520.1	Microtubule-associated tumor s	4.03E+05	0.00E+00	-4.03E+05	-4.03E+05	NULL	AD	J3KQA9	MTUS2
1148.1	Probable ribonuclease ZC3H12D	4.04E+05	0.00E+00	-4.04E+05	-4.04E+05	NULL	AD	J3QT81	ZC3H12D
645.1	Isoform 5 of Protein piccolo	4.05E+05	0.00E+00	-4.05E+05	-4.05E+05	NULL	AD	Q9Y6V0-5	PCLO
3068.1	Kinesin heavy chain isoform 5A	4.08E+05	0.00E+00	-4.08E+05	-4.08E+05	NULL	AD	Q12840	KIF5A
318.2	Vacuolar protein sorting-associa	4.09E+05	0.00E+00	-4.09E+05	-4.09E+05	NULL	AD	Q9UN37	VPS4A
2180.1	Intraflagellar transport protein	4.11E+05	0.00E+00	-4.11E+05	-4.11E+05	NULL	AD	Q9UG01	IFT172
3138.1	Ciliary neurotrophic factor rece	4.13E+05	0.00E+00	-4.13E+05	-4.13E+05	NULL	AD	P26992	CNTFR
2052.1	Translation initiation factor IF-2,	4.16E+05	0.00E+00	-4.16E+05	-4.16E+05	NULL	AD	P46199	MTIF2
3235.1	Zinc finger CW-type PWWP dom	4.17E+05	0.00E+00	-4.17E+05	-4.17E+05	NULL	AD	Q504Y3	ZCWPW2
1680.1	COBW domain-containing prote	4.20E+05	0.00E+00	-4.20E+05	-4.20E+05	NULL	AD	Q5RIA9	CBWD5
3242.1	DNA polymerase delta subunit 3	4.24E+05	0.00E+00	-4.24E+05	-4.24E+05	NULL	AD	Q15054	POLD3
1652.1	Transcriptional regulator ERG	4.26E+05	0.00E+00	-4.26E+05	-4.26E+05	NULL	AD	B4E3C5	ERG
1136.1	Isoform 3 of Charged multivesic	4.27E+05	0.00E+00	-4.27E+05	-4.27E+05	NULL	AD	Q9Y3E7-3	CHMP3
3210.1	Exosome complex component R	4.29E+05	0.00E+00	-4.29E+05	-4.29E+05	NULL	AD	Q96B26	EXOSC8
2135.1	Zinc finger protein 180	4.30E+05	0.00E+00	-4.30E+05	-4.30E+05	NULL	AD	Q9UJW8	ZNF180
1304.1	Nuclear receptor-interacting pr	4.35E+05	0.00E+00	-4.35E+05	-4.35E+05	NULL	AD	P48552	NRIP1
938.1	DNA polymerase theta	4.39E+05	0.00E+00	-4.39E+05	-4.39E+05	NULL	AD	O75417	POLQ
1409.1	Phospholipase D3	4.39E+05	0.00E+00	-4.39E+05	-4.39E+05	NULL	AD	Q8IV08	PLD3
2177.1	COMM domain-containing prote	4.39E+05	0.00E+00	-4.39E+05	-4.39E+05	NULL	AD	Q86X83	COMMD2
1580.1	Transcription elongation factor	4.40E+05	0.00E+00	-4.40E+05	-4.40E+05	NULL	AD	Q15370	TCEB2
1082.1	Protein QN1 homolog	4.41E+05	0.00E+00	-4.41E+05	-4.41E+05	NULL	AD	Q5TB80	KIAA1009
824.2	Isoform 4 of Lysine-specific dem	4.44E+05	0.00E+00	-4.44E+05	-4.44E+05	NULL	AD	Q8NHM5-	KDM2B
1273.1	PWWP domain-containing prote	4.46E+05	0.00E+00	-4.46E+05	-4.46E+05	NULL	AD	Q5H9M0	MUM1L1
2520.1	Kinesin-like protein KIF14	4.53E+05	0.00E+00	-4.53E+05	-4.53E+05	NULL	AD	Q15058	KIF14
2291.1	Msx2-interacting protein	4.57E+05	0.00E+00	-4.57E+05	-4.57E+05	NULL	AD	Q96T58	SPEN
2018.1	ATP-binding cassette sub-family	4.58E+05	0.00E+00	-4.58E+05	-4.58E+05	NULL	AD	Q9H222	ABCG5
363.1	Tubulin--tyrosine ligase-like pro	4.60E+05	0.00E+00	-4.60E+05	-4.60E+05	NULL	AD	Q14166	TTLL12
2533.1	Cyclic nucleotide-gated olfactor	4.60E+05	0.00E+00	-4.60E+05	-4.60E+05	NULL	AD	Q16280	CNGA2
1217.1	Alpha-centractin	4.69E+05	0.00E+00	-4.69E+05	-4.69E+05	NULL	AD	P61163	ACTR1A
1126.1	C11orf30 protein	4.73E+05	0.00E+00	-4.73E+05	-4.73E+05	NULL	AD	B7ZKU0	C11orf30

1159.1	Toll-interacting protein	4.74E+05	0.00E+00	-4.74E+05	-4.74E+05	NULL	AD	Q9H0E2	TOLLIP
3248.1	Putative lipocalin 1-like protein	4.75E+05	0.00E+00	-4.75E+05	-4.75E+05	NULL	AD	Q5VSP4	LCN1P1
2849.1	Fibroleukin	4.78E+05	0.00E+00	-4.78E+05	-4.78E+05	NULL	AD	Q14314	FGL2
803.1	Tight junction protein 1 (Zona o	4.79E+05	0.00E+00	-4.79E+05	-4.79E+05	NULL	AD	G3V1L9	TJP1
2226.1	NXPE family member 2	4.83E+05	0.00E+00	-4.83E+05	-4.83E+05	NULL	AD	Q96DL1	NXPE2
829.1	Isoform 3 of Dehydrogenase/re	4.84E+05	0.00E+00	-4.84E+05	-4.84E+05	NULL	AD	A0PJE2-3	DHRS12
1040.1	YEATS domain-containing prote	4.84E+05	0.00E+00	-4.84E+05	-4.84E+05	NULL	AD	Q9ULM3	YEATS2
1076.1	Centrin-2	4.88E+05	0.00E+00	-4.88E+05	-4.88E+05	NULL	AD	P41208	CETN2
2288.1	DNA replication factor Cdt1	4.89E+05	0.00E+00	-4.89E+05	-4.89E+05	NULL	AD	Q9H211	CDT1
3230.1	Isoform 4 of Transcription facto	4.90E+05	0.00E+00	-4.90E+05	-4.90E+05	NULL	AD	Q92994-4	BRF1
1696.1	Zinc finger protein 438	4.92E+05	0.00E+00	-4.92E+05	-4.92E+05	NULL	AD	Q7Z4V0	ZNF438
2785.1	Fractalkine	4.96E+05	0.00E+00	-4.96E+05	-4.96E+05	NULL	AD	H3BV86	CX3CL1
688.1	Cytoplasmic dynein 2 heavy cha	5.01E+05	0.00E+00	-5.01E+05	-5.01E+05	NULL	AD	Q8NCM8	DYNC2H1
1431.1	PH and SEC7 domain-containing	5.01E+05	0.00E+00	-5.01E+05	-5.01E+05	NULL	AD	Q9BQI7	PSD2
2039.1	Isoform 2 of Serine/threonine-p	5.08E+05	0.00E+00	-5.08E+05	-5.08E+05	NULL	AD	Q5VT25-2	CDC42BPA
2205.1	Helicase SKI2W	5.13E+05	0.00E+00	-5.13E+05	-5.13E+05	NULL	AD	Q15477	SKIV2L
1489.1	Collagen triple helix repeat-cont	5.14E+05	0.00E+00	-5.14E+05	-5.14E+05	NULL	AD	E7EVQ5	CTHRC1
1885.1	NF-kappa-B-repressing factor	5.14E+05	0.00E+00	-5.14E+05	-5.14E+05	NULL	AD	O15226	NKRF
920.1	Synaptotagmin-6	5.15E+05	0.00E+00	-5.15E+05	-5.15E+05	NULL	AD	Q5T7P8	SYT6
589.1	Isoform 3 of Ankyrin repeat dom	5.24E+05	0.00E+00	-5.24E+05	-5.24E+05	NULL	AD	Q6ZTN6-3	ANKRD13D
2099.1	Protein FAM134C	5.24E+05	0.00E+00	-5.24E+05	-5.24E+05	NULL	AD	Q86VR2	FAM134C
2366.1	Coiled-coil domain-containing p	5.25E+05	0.00E+00	-5.25E+05	-5.25E+05	NULL	AD	Q502W7	CCDC38
2216.1	Isoform 2 of PDZ domain-contai	5.28E+05	0.00E+00	-5.28E+05	-5.28E+05	NULL	AD	Q5EBL8-2	PDZD11
572.1	Adenine phosphoribosyltransfer	5.30E+05	0.00E+00	-5.30E+05	-5.30E+05	NULL	AD	P07741	APRT
3028.1	Glycosyltransferase 8 domain-co	5.31E+05	0.00E+00	-5.31E+05	-5.31E+05	NULL	AD	Q9H1C3	GLT8D2
2519.1	E3 ubiquitin-protein ligase RBBP	5.32E+05	0.00E+00	-5.32E+05	-5.32E+05	NULL	AD	Q7Z6E9	RBBP6
2280.1	Leucine-rich repeat-containing p	5.38E+05	0.00E+00	-5.38E+05	-5.38E+05	NULL	AD	Q8N456	LRRC18
1857.1	RNA-binding protein 47	5.41E+05	0.00E+00	-5.41E+05	-5.41E+05	NULL	AD	A0AV96	RBM47
3207.1	A disintegrin and metalloprotei	5.41E+05	0.00E+00	-5.41E+05	-5.41E+05	NULL	AD	Q8TE57	ADAMTS16
1606.1	Inositol hexakisphosphate and c	5.45E+05	0.00E+00	-5.45E+05	-5.45E+05	NULL	AD	Q6PFW1	PPIP5K1
1114.1	RNA-binding protein 43	5.52E+05	0.00E+00	-5.52E+05	-5.52E+05	NULL	AD	Q6ZSC3	RBM43
3015.1	Mesoderm posterior protein 2	5.53E+05	0.00E+00	-5.53E+05	-5.53E+05	NULL	AD	Q0VG99	MESP2
2100.1	Thyroid adenoma-associated pr	5.56E+05	0.00E+00	-5.56E+05	-5.56E+05	NULL	AD	Q6YHU6	THADA
1347.1	Lipase maturation factor 2	5.70E+05	0.00E+00	-5.70E+05	-5.70E+05	NULL	AD	Q9BU23	LMF2
3005.1	Dual specificity protein phospha	5.72E+05	0.00E+00	-5.72E+05	-5.72E+05	NULL	AD	Q8WTR2	DUSP19

675.1	Protocadherin gamma-C5	5.76E+05	0.00E+00	-5.76E+05	-5.76E+05	NULL	AD	Q9Y5F6	PCDHGC5
2916.1	Isoform 4 of Unconventional my	5.76E+05	0.00E+00	-5.76E+05	-5.76E+05	NULL	AD	B2RTY4-4	MYO9A
932.1	V-type proton ATPase 16 kDa pr	5.77E+05	0.00E+00	-5.77E+05	-5.77E+05	NULL	AD	P27449	ATP6V0C
3025.1	Atherin	5.79E+05	0.00E+00	-5.79E+05	-5.79E+05	NULL	AD	Q6SPF0	SAMD1
1901.1	Olfactory receptor 51Q1	5.89E+05	0.00E+00	-5.89E+05	-5.89E+05	NULL	AD	Q8NH59	OR51Q1
1241.1	Isoform 2 of Zinc finger protein	5.91E+05	0.00E+00	-5.91E+05	-5.91E+05	NULL	AD	Q6NUN9-2	ZNF746
624.1	Tubulin-folding cofactor B	5.95E+05	0.00E+00	-5.95E+05	-5.95E+05	NULL	AD	Q99426	TBCB
3091.1	UPF0461 protein C5orf24	5.96E+05	0.00E+00	-5.96E+05	-5.96E+05	NULL	AD	Q7Z6I8	C5orf24
1359.1	Isoform 2 of Protein ELYS	6.00E+05	0.00E+00	-6.00E+05	-6.00E+05	NULL	AD	Q8WYP5-2	AHCTF1
687.1	Niban-like protein 1	6.10E+05	0.00E+00	-6.10E+05	-6.10E+05	NULL	AD	Q96TA1	FAM129B
875.1	Cation-independent mannose-6	6.10E+05	0.00E+00	-6.10E+05	-6.10E+05	NULL	AD	P11717	IGF2R
3204.1	Charged multivesicular body pr	6.19E+05	0.00E+00	-6.19E+05	-6.19E+05	NULL	AD	Q9HD42	CHMP1A
858.1	Protein KTI12 homolog	6.44E+05	0.00E+00	-6.44E+05	-6.44E+05	NULL	AD	Q96EK9	WDR52
1332.1	Isoform 2 of WD repeat-contain	6.49E+05	0.00E+00	-6.49E+05	-6.49E+05	NULL	AD	Q96MT7-2	WDR52
2630.1	Hephaestin-like protein 1	6.50E+05	0.00E+00	-6.50E+05	-6.50E+05	NULL	AD	Q6MZM0	HEPHL1
1361.1	Negative elongation factor C/D	6.54E+05	0.00E+00	-6.54E+05	-6.54E+05	NULL	AD	Q8IXH7	NELFCD
904.1	E3 ubiquitin-protein ligase CHIP	6.56E+05	0.00E+00	-6.56E+05	-6.56E+05	NULL	AD	Q9UNE7	STUB1
546.1	Thioredoxin reductase 1, cytopl	6.59E+05	0.00E+00	-6.59E+05	-6.59E+05	NULL	AD	Q16881	TXNRD1
1325.1	Inactive pancreatic lipase-relate	6.60E+05	0.00E+00	-6.60E+05	-6.60E+05	NULL	AD	P54315	PNLIPRP1
3259.1	Cartilage intermediate layer pro	6.69E+05	0.00E+00	-6.69E+05	-6.69E+05	NULL	AD	K7EPJ4	CILP2
2465.1	SAM domain-containing protein	6.70E+05	0.00E+00	-6.70E+05	-6.70E+05	NULL	AD	F8WAA1	SAMSN1
1070.1	Coiled-coil domain-containing p	6.75E+05	0.00E+00	-6.75E+05	-6.75E+05	NULL	AD	Q8NCX0	CCDC150
1168.1	Deoxycytidine kinase	6.82E+05	0.00E+00	-6.82E+05	-6.82E+05	NULL	AD	D6RFG8	DCK
2681.1	Polycystic kidney disease 2-like	6.96E+05	0.00E+00	-6.96E+05	-6.96E+05	NULL	AD	Q9NZM6	PKD2L2
1662.1	E3 ubiquitin-protein ligase NEDI	6.99E+05	0.00E+00	-6.99E+05	-6.99E+05	NULL	AD	Q96PU5	NEDD4L
1004.1	Glutathione S-transferase Mu 3	7.01E+05	0.00E+00	-7.01E+05	-7.01E+05	NULL	AD	P21266	GSTM3
474.1	UDP-glucose 6-dehydrogenase	7.14E+05	0.00E+00	-7.14E+05	-7.14E+05	NULL	AD	O60701	UGDH
438.1	Serine/threonine-protein kinase	7.19E+05	0.00E+00	-7.19E+05	-7.19E+05	NULL	AD	Q9UHD2	TBK1
1511.1	Poly(ADP-ribose) glycohydrolase	7.21E+05	0.00E+00	-7.21E+05	-7.21E+05	NULL	AD	Q9NX46	ADPRHL2
537.1	Ataxin-10	7.24E+05	0.00E+00	-7.24E+05	-7.24E+05	NULL	AD	Q9UBB4	ATXN10
3186.1	DNA-directed RNA polymerase I	7.40E+05	0.00E+00	-7.40E+05	-7.40E+05	NULL	AD	O95602	POLR1A
883.1	Isoform 2 of Extended synaptot	7.42E+05	0.00E+00	-7.42E+05	-7.42E+05	NULL	AD	Q9BSJ8-2	ESYT1
2479.1	Major facilitator superfamily do	7.65E+05	0.00E+00	-7.65E+05	-7.65E+05	NULL	AD	Q8NBP5	MFSD9
1842.1	Kinesin-like protein KLP6	7.74E+05	0.00E+00	-7.74E+05	-7.74E+05	NULL	AD	B7ZC32	KLP6
2629.1	Zinc finger protein 660	7.92E+05	0.00E+00	-7.92E+05	-7.92E+05	NULL	AD	Q6AZW8	ZNF660

3044.1	Neogenin	8.02E+05	0.00E+00	-8.02E+05	-8.02E+05	NULL	AD	Q92859	NEO1
2456.1	Prefoldin subunit 5	8.04E+05	0.00E+00	-8.04E+05	-8.04E+05	NULL	AD	Q99471	PFDN5
1169.1	Acetoacetyl-CoA synthetase	8.07E+05	0.00E+00	-8.07E+05	-8.07E+05	NULL	AD	Q86V21	AACS
3019.1	Olfactory receptor 10A4	8.13E+05	0.00E+00	-8.13E+05	-8.13E+05	NULL	AD	Q9H209	OR10A4
2489.1	Pleckstrin homology domain-co	8.15E+05	0.00E+00	-8.15E+05	-8.15E+05	NULL	AD	E9PKC0	PLEKHA7
1660.1	Lysosomal acid phosphatase	8.17E+05	0.00E+00	-8.17E+05	-8.17E+05	NULL	AD	P11117	ACP2
514.1	Unconventional myosin-XVIIIa	8.32E+05	0.00E+00	-8.32E+05	-8.32E+05	NULL	AD	J3KNX9	MYO18A
2937.1	Isoform Flip of Glutamate recep	8.90E+05	0.00E+00	-8.90E+05	-8.90E+05	NULL	AD	P42263-2	GRIA3
1922.1	Olfactory receptor 51B6	9.09E+05	0.00E+00	-9.09E+05	-9.09E+05	NULL	AD	Q9H340	OR51B6
20.4	Putative heat shock protein HSP	9.10E+05	0.00E+00	-9.10E+05	-9.10E+05	NULL	AD	Q58FG1	HSP90AA4P
1522.1	Isoform 4 of Dynein heavy chain	9.17E+05	0.00E+00	-9.17E+05	-9.17E+05	NULL	AD	Q0VDD8-4	DNAH14
2690.1	Frizzled-8	9.33E+05	0.00E+00	-9.33E+05	-9.33E+05	NULL	AD	Q9H461	FZD8
427.1	EF-hand domain-containing pro	9.64E+05	0.00E+00	-9.64E+05	-9.64E+05	NULL	AD	Q96C19	EFHD2
1420.1	Probable tRNA(His) guanylyltrar	9.64E+05	0.00E+00	-9.64E+05	-9.64E+05	NULL	AD	Q9NWX6	THG1L
706.1	Glutathione synthetase	9.70E+05	0.00E+00	-9.70E+05	-9.70E+05	NULL	AD	P48637	GSS
1549.1	Chromodomain-helicase-DNA-b	9.76E+05	0.00E+00	-9.76E+05	-9.76E+05	NULL	AD	O14647	CHD2
3057.1	Caspase recruitment domain-co	9.81E+05	0.00E+00	-9.81E+05	-9.81E+05	NULL	AD	Q9BXL6	CARD14
318.3	Fidgetin-like protein 1	1.00E+06	0.00E+00	-1.00E+06	-1.00E+06	NULL	AD	Q6PIW4	FIGNL1
1994.1	Coiled-coil domain-containing p	1.01E+06	0.00E+00	-1.01E+06	-1.01E+06	NULL	AD	Q5T0U0	CCDC122
2766.1	Nexilin	1.01E+06	0.00E+00	-1.01E+06	-1.01E+06	NULL	AD	Q0ZGT2	NEXN
710.1	Tropomodulin-3	1.02E+06	0.00E+00	-1.02E+06	-1.02E+06	NULL	AD	Q9NYL9	TMOD3
1831.1	Piwi-like protein 1	1.03E+06	0.00E+00	-1.03E+06	-1.03E+06	NULL	AD	Q96J94	PIWIL1
3150.1	1-phosphatidylinositol 4,5-bisph	1.03E+06	0.00E+00	-1.03E+06	-1.03E+06	NULL	AD	Q4KWH8	PLCH1
488.1	Titin	1.03E+06	0.00E+00	-1.03E+06	-1.03E+06	NULL	AD	Q8WZ42	TTN
2534.1	Mitogen-activated protein kinas	1.05E+06	0.00E+00	-1.05E+06	-1.05E+06	NULL	AD	P53778	MAPK12
2701.1	Histone acetyltransferase KAT6I	1.06E+06	0.00E+00	-1.06E+06	-1.06E+06	NULL	AD	Q8WYB5	KAT6B
630.1	Annexin A11	1.07E+06	0.00E+00	-1.07E+06	-1.07E+06	NULL	AD	P50995	ANXA11
1072.1	Kit ligand	1.07E+06	0.00E+00	-1.07E+06	-1.07E+06	NULL	AD	P21583	KITLG
1055.1	NEU3 protein	1.09E+06	0.00E+00	-1.09E+06	-1.09E+06	NULL	AD	A8K327	NEU3
1062.1	Sister chromatid cohesion prote	1.09E+06	0.00E+00	-1.09E+06	-1.09E+06	NULL	AD	Q29RF7	PDS5A
1309.1	A disintegrin and metalloprotei	1.09E+06	0.00E+00	-1.09E+06	-1.09E+06	NULL	AD	Q8TE56	ADAMTS17
753.1	Isoform 6 of Calpastatin	1.12E+06	0.00E+00	-1.12E+06	-1.12E+06	NULL	AD	P20810-6	CAST
1125.1	ADP-ribosylation factor 3	1.13E+06	0.00E+00	-1.13E+06	-1.13E+06	NULL	AD	F5H423	ARF3
2862.1	Thiamine-triphosphatase	1.14E+06	0.00E+00	-1.14E+06	-1.14E+06	NULL	AD	Q9BU02	THTPA
1098.1	6-pyruvoyl tetrahydrobiopterin	1.15E+06	0.00E+00	-1.15E+06	-1.15E+06	NULL	AD	Q03393	PTS

1012.1	Isoform 3 of BEN domain-contai	1.27E+06	0.00E+00	-1.27E+06	-1.27E+06	NULL	AD	Q6ZU67-3	BEND4
585.1	IST1 homolog	1.31E+06	0.00E+00	-1.31E+06	-1.31E+06	NULL	AD	P53990	IST1
950.1	Nuclear transcription factor Y su	1.33E+06	0.00E+00	-1.33E+06	-1.33E+06	NULL	AD	Q13952	NFYC
1537.1	Receptor expression-enhancing	1.33E+06	0.00E+00	-1.33E+06	-1.33E+06	NULL	AD	Q6NUK4	REEP3
517.1	m7GpppX diphosphatase	1.34E+06	0.00E+00	-1.34E+06	-1.34E+06	NULL	AD	Q96C86	DCPS
580.1	UV excision repair protein RAD2	1.35E+06	0.00E+00	-1.35E+06	-1.35E+06	NULL	AD	P54727	RAD23B
2920.1	Coiled-coil domain-containing p	1.37E+06	0.00E+00	-1.37E+06	-1.37E+06	NULL	AD	Q8IWA6	CCDC60
14.3	Myosin-14	1.39E+06	0.00E+00	-1.39E+06	-1.39E+06	NULL	AD	G8JLL9	MYH14
565.1	Protein FAM83H	1.39E+06	0.00E+00	-1.39E+06	-1.39E+06	NULL	AD	Q6ZRV2	FAM83H
1841.1	SURP and G-patch domain-conta	1.44E+06	0.00E+00	-1.44E+06	-1.44E+06	NULL	AD	Q8IWZ8	SUGP1
975.1	DNA mismatch repair protein M	1.46E+06	0.00E+00	-1.46E+06	-1.46E+06	NULL	AD	P43246	MSH2
770.1	Reticulocalbin-1	1.52E+06	0.00E+00	-1.52E+06	-1.52E+06	NULL	AD	Q15293	RCN1
1081.1	Coronin	1.52E+06	0.00E+00	-1.52E+06	-1.52E+06	NULL	AD	P57737	CORO7
530.1	Annexin A7	1.53E+06	0.00E+00	-1.53E+06	-1.53E+06	NULL	AD	P20073	ANXA7
1970.1	Aldo-keto reductase family 1 me	1.55E+06	0.00E+00	-1.55E+06	-1.55E+06	NULL	AD	P17516	AKR1C4
731.1	Reticulocalbin-2	1.62E+06	0.00E+00	-1.62E+06	-1.62E+06	NULL	AD	F8WCY5	RCN2
558.1	Charged multivesicular body pro	1.70E+06	0.00E+00	-1.70E+06	-1.70E+06	NULL	AD	Q9UQN3	CHMP2B
931.1	V-set domain containing T cell a	1.75E+06	0.00E+00	-1.75E+06	-1.75E+06	NULL	AD	Q5T2L0	VTCN1
818.1	Diablo homolog, mitochondrial	1.76E+06	0.00E+00	-1.76E+06	-1.76E+06	NULL	AD	Q9NR28	DIABLO
1908.1	Zinc finger protein 350	1.89E+06	0.00E+00	-1.89E+06	-1.89E+06	NULL	AD	Q9GZX5	ZNF350
1064.1	Spondin-2	1.97E+06	0.00E+00	-1.97E+06	-1.97E+06	NULL	AD	Q9BUD6	SPON2
12.2	Isoform 3 of Alpha-actinin-1	2.23E+06	0.00E+00	-2.23E+06	-2.23E+06	NULL	AD	P12814-3	ACTN1
1801.1	Phospholipid scramblase 2	2.49E+06	0.00E+00	-2.49E+06	-2.49E+06	NULL	AD	Q9NRY7	PLSCR2
272.1	ATPase WRNIP1	2.68E+06	0.00E+00	-2.68E+06	-2.68E+06	NULL	AD	Q96S55	WRNIP1
1340.1	Protein DEK	2.69E+06	0.00E+00	-2.69E+06	-2.69E+06	NULL	AD	P35659	DEK
2020.1	Isoform 2 of Beta-parvin	2.76E+06	0.00E+00	-2.76E+06	-2.76E+06	NULL	AD	Q9HBI1-2	PARVB
680.1	Myoglobin	2.87E+06	0.00E+00	-2.87E+06	-2.87E+06	NULL	AD	P02144	MB
1087.1	Probable ATP-dependent RNA h	2.87E+06	0.00E+00	-2.87E+06	-2.87E+06	NULL	AD	F5GZS0	DHX36
336.1	Serine/threonine-protein kinase	2.90E+06	0.00E+00	-2.90E+06	-2.90E+06	NULL	AD	F8WBA3	PRKD1
1.3	Epiplakin	3.00E+06	0.00E+00	-3.00E+06	-3.00E+06	NULL	AD	E9PPU0	EPPK1
318.1	Vacuolar protein sorting-associa	3.03E+06	0.00E+00	-3.03E+06	-3.03E+06	NULL	AD	O75351	VPS4B
642.1	Sequestosome-1	3.07E+06	0.00E+00	-3.07E+06	-3.07E+06	NULL	AD	Q13501	SQSTM1
2420.1	Cell division cycle 7-related prot	3.43E+06	0.00E+00	-3.43E+06	-3.43E+06	NULL	AD	O00311	CDC7
2072.1	Tubulin epsilon chain	3.44E+06	0.00E+00	-3.44E+06	-3.44E+06	NULL	AD	Q9UJT0	TUBE1
416.1	Calpain small subunit 1	3.86E+06	0.00E+00	-3.86E+06	-3.86E+06	NULL	AD	K7ELJ7	CAPNS1

284.1	Vacuolar protein sorting-associa	4.42E+06	0.00E+00	-4.42E+06	-4.42E+06	NULL	AD	Q9NP79	VTA1
466.1	Programmed cell death protein	4.51E+06	0.00E+00	-4.51E+06	-4.51E+06	NULL	AD	O75340	PDCD6
321.1	Inorganic pyrophosphatase	4.65E+06	0.00E+00	-4.65E+06	-4.65E+06	NULL	AD	Q15181	PPA1
382.1	Tubulin-specific chaperone A	5.27E+06	0.00E+00	-5.27E+06	-5.27E+06	NULL	AD	E5RJD8	TBCA
126.1	Cytospin-A	6.73E+06	0.00E+00	-6.73E+06	-6.73E+06	NULL	AD	Q69YQ0	SPECC1L
163.1	Copine-3	7.68E+06	0.00E+00	-7.68E+06	-7.68E+06	NULL	AD	O75131	CPNE3
98.1	Drebrin	1.33E+07	0.00E+00	-1.33E+07	-1.33E+07	NULL	AD	A8MV58	DBN1
63.1	X-ray repair cross-complementi	1.37E+07	0.00E+00	-1.37E+07	-1.37E+07	NULL	AD	P13010	XRCC5
14.2	Myosin-10	1.37E+07	0.00E+00	-1.37E+07	-1.37E+07	NULL	AD	P35580	MYH10
61.1	X-ray repair cross-complementi	1.48E+07	0.00E+00	-1.48E+07	-1.48E+07	NULL	AD	P12956	XRCC6
7.1	Isoform 8 of Filamin-B	2.67E+07	0.00E+00	-2.67E+07	-2.67E+07	NULL	AD	O75369-8	FLNB
21.2	Tropomyosin alpha-1 chain	3.14E+07	0.00E+00	-3.14E+07	-3.14E+07	NULL	AD	B7Z596	TPM1
17.1	Probable ATP-dependent RNA h	1.23E+04	6.68E+07	5.42E+03	5.42E+03	10.00	8.60	H3BLZ8	DDX17
17.2	ATP-dependent RNA helicase DI	4.21E+04	5.59E+07	1.33E+03	1.33E+03	10.00	7.19	O00571	DDX3X
15.1	Non-POU domain-containing oc	4.68E+05	2.68E+08	5.73E+02	5.73E+02	10.00	6.35	Q15233	NONO
237.1	Catenin delta-1	1.56E+04	7.69E+06	4.94E+02	4.94E+02	10.00	6.20	O60716	CTNND1
1047.1	Protein furry homolog	2.96E+03	1.38E+06	4.66E+02	4.66E+02	10.00	6.14	Q5TBA9	FRY
113.1	40S ribosomal protein S3	3.27E+04	1.47E+07	4.50E+02	4.50E+02	10.00	6.11	P23396	RPS3
131.1	60S ribosomal protein L30	2.80E+04	1.17E+07	4.18E+02	4.18E+02	10.00	6.03	P62888	RPL30
184.1	Pyruvate carboxylase, mitochon	3.07E+04	7.65E+06	2.49E+02	2.49E+02	10.00	5.52	P11498	PC
451.1	Protein BUD31 homolog	1.32E+04	2.68E+06	2.02E+02	2.02E+02	10.00	5.31	P41223	BUD31
106.1	Delta(3,5)-Delta(2,4)-dienoyl-Co	3.89E+04	7.69E+06	1.98E+02	1.98E+02	10.00	5.29	Q13011	ECH1
946.1	Protein AHNAK2	4.77E+03	9.24E+05	1.94E+02	1.94E+02	10.00	5.27	Q8IVF2	AHNAK2
11.1	Heterogeneous nuclear ribonuc	7.09E+05	1.37E+08	1.93E+02	1.93E+02	10.00	5.26	P52272	HNRNPM
188.1	60S ribosomal protein L10a	3.86E+04	7.14E+06	1.85E+02	1.85E+02	10.00	5.22	P62906	RPL10A
778.1	Isoform 2 of Prostatic acid phos	1.85E+03	3.15E+05	1.70E+02	1.70E+02	10.00	5.14	P15309-2	ACPP
17.3	Probable ATP-dependent RNA h	1.41E+05	2.33E+07	1.66E+02	1.66E+02	10.00	5.11	P17844	DDX5
649.1	Polypeptide N-acetylgalactosam	5.52E+03	6.85E+05	1.24E+02	1.24E+02	10.00	4.82	Q7Z7M9	GALNT5
245.1	Mitochondrial import inner mer	1.98E+05	2.33E+07	1.18E+02	1.18E+02	10.00	4.77	Q9Y5L4	TIMM13
252.1	Methylcrotonoyl-CoA carboxyla	1.12E+04	1.22E+06	1.09E+02	1.09E+02	10.00	4.69	Q96RQ3	MCCC1
513.1	Small nuclear ribonucleoprotein	2.65E+04	2.80E+06	1.06E+02	1.06E+02	10.00	4.66	P62314	SNRPD1
260.1	Splicing factor 3A subunit 1	3.72E+04	3.88E+06	1.04E+02	1.04E+02	10.00	4.65	Q15459	SF3A1
90.1	Keratin, type I cytoskeletal 9	1.22E+05	1.19E+07	9.73E+01	9.73E+01	10.00	4.58	P35527	KRT9
450.1	Isoform 5 of Nuclear pore comp	5.90E+03	5.70E+05	9.65E+01	9.65E+01	10.00	4.57	P35658-5	NUP214
191.1	Putative RNA-binding protein 3	1.83E+05	1.73E+07	9.45E+01	9.45E+01	10.00	4.55	P98179	RBM3

1391.1	Remodeling and spacing factor	6.47E+03	5.74E+05	8.87E+01	8.87E+01	10.00	4.49	Q96T23	RSF1
129.1	Elongation factor Tu, mitochonc	1.02E+05	8.90E+06	8.72E+01	8.72E+01	10.00	4.47	P49411	TUFM
1261.1	Protein disulfide-isomerase-like	1.02E+04	8.64E+05	8.46E+01	8.46E+01	10.00	4.44	Q8N807	PDILT
83.1	Heterogeneous nuclear ribonuc	3.04E+05	2.44E+07	8.02E+01	8.02E+01	10.00	4.38	P22626	HNRNPA2B1
409.1	Eukaryotic translation initiation	2.51E+04	1.80E+06	7.18E+01	7.18E+01	10.00	4.27	B5ME19	EIF3CL
66.2	RNA-binding protein FUS	3.99E+05	2.50E+07	6.26E+01	6.26E+01	10.00	4.14	H3BPE7	FUS
371.1	Peptidyl-prolyl cis-trans isomera	4.99E+04	2.85E+06	5.71E+01	5.71E+01	10.00	4.04	Q00688	FKBP3
175.1	60S ribosomal protein L38	3.42E+05	1.93E+07	5.65E+01	5.65E+01	10.00	4.03	P63173	RPL38
77.1	Malate dehydrogenase, mitoch	3.92E+05	2.14E+07	5.46E+01	5.46E+01	10.00	4.00	P40926	MDH2
174.1	Cathepsin D	1.92E+05	1.04E+07	5.41E+01	5.41E+01	10.00	3.99	P07339	CTSD
1563.1	40S ribosomal protein S24	3.77E+04	1.94E+06	5.14E+01	5.14E+01	10.00	3.94	P62847	RPS24
570.1	Palmitoyl-protein thioesterase 1	4.24E+04	2.07E+06	4.89E+01	4.89E+01	10.00	3.89	P50897	PPT1
779.1	Proteasome subunit beta type-	1.19E+04	5.70E+05	4.78E+01	4.78E+01	10.00	3.87	P28070	PSMB4
1457.1	Myosin-6	4.65E+04	2.18E+06	4.69E+01	4.69E+01	10.00	3.85	P13533	MYH6
1085.1	E3 ubiquitin-protein ligase Topo	6.50E+03	3.02E+05	4.65E+01	4.65E+01	10.00	3.84	Q9NS56	TOPORS
838.1	Pre-mRNA-processing factor 19	9.21E+03	4.21E+05	4.57E+01	4.57E+01	10.00	3.82	Q9UMS4	PRPF19
576.1	Translation machinery-associate	6.22E+04	2.58E+06	4.15E+01	4.15E+01	10.00	3.73	Q9Y2S6	TMA7
96.2	Far upstream element-binding	1.10E+05	4.56E+06	4.14E+01	4.14E+01	10.00	3.72	B4DT31	FUBP1
267.1	40S ribosomal protein S2	2.48E+05	1.02E+07	4.12E+01	4.12E+01	10.00	3.72	P15880	RPS2
442.1	60S acidic ribosomal protein P2	1.07E+05	4.41E+06	4.12E+01	4.12E+01	10.00	3.72	P05387	RPLP2
939.1	Probable E3 ubiquitin-protein li	5.13E+03	2.00E+05	3.90E+01	3.90E+01	10.00	3.66	F8VWT9	HECTD4
112.1	ATP synthase subunit alpha, mit	3.35E+05	1.30E+07	3.88E+01	3.88E+01	10.00	3.66	P25705	ATP5A1
164.1	60S ribosomal protein L28	5.39E+05	2.03E+07	3.77E+01	3.77E+01	10.00	3.63	P46779	RPL28
582.1	26S proteasome non-ATPase re	2.98E+04	1.09E+06	3.65E+01	3.65E+01	10.00	3.60	O00487	PSMD14
2.1	Desmoplakin	1.66E+06	5.85E+07	3.53E+01	3.53E+01	10.00	3.56	P15924	DSP
274.1	V-type proton ATPase catalytic	3.63E+05	1.27E+07	3.50E+01	3.50E+01	10.00	3.56	P38606	ATP6V1A
47.1	Protein transport protein Sec23	6.01E+05	2.08E+07	3.46E+01	3.46E+01	10.00	3.54	Q15437	SEC23B
1027.1	Fer-1-like protein 4	5.87E+03	2.03E+05	3.46E+01	3.46E+01	10.00	3.54	A9Z1Z3	FER1L4
223.1	40S ribosomal protein S28	3.64E+05	1.20E+07	3.30E+01	3.30E+01	10.00	3.50	P62857	RPS28
1166.1	Nuclear valosin-containing prot	1.13E+05	3.72E+06	3.29E+01	3.29E+01	10.00	3.49	O15381	NVL
97.1	Nucleophosmin	9.64E+05	3.16E+07	3.28E+01	3.28E+01	10.00	3.49	P06748	NPM1
210.1	Stress-70 protein, mitochondria	1.97E+05	6.44E+06	3.27E+01	3.27E+01	10.00	3.49	P38646	HSPA9
611.1	Cytochrome c oxidase subunit 6	1.98E+04	6.47E+05	3.27E+01	3.27E+01	10.00	3.49	P14854	COX6B1
264.1	Chromobox protein homolog 3	2.55E+05	8.29E+06	3.25E+01	3.25E+01	10.00	3.48	Q13185	CBX3
417.1	Proteasome subunit alpha type-	8.47E+03	2.73E+05	3.22E+01	3.22E+01	10.00	3.47	P25788	PSMA3

586.1	Eukaryotic translation initiation	1.94E+04	6.23E+05	3.21E+01	3.21E+01	10.00	3.47	Q14152	EIF3A
211.1	40S ribosomal protein S12	1.10E+05	3.53E+06	3.20E+01	3.20E+01	10.00	3.47	P25398	RPS12
117.1	60S ribosomal protein L13	1.00E+06	3.16E+07	3.14E+01	3.14E+01	10.00	3.45	P26373	RPL13
225.1	40S ribosomal protein S6	8.37E+05	2.57E+07	3.07E+01	3.07E+01	10.00	3.42	P62753	RPS6
228.1	Beta-hexosaminidase subunit be	1.44E+05	4.38E+06	3.05E+01	3.05E+01	10.00	3.42	P07686	HEXB
108.1	Microtubule-associated protein	2.15E+05	6.42E+06	2.98E+01	2.98E+01	10.00	3.39	P46821	MAP1B
317.1	Pre-mRNA-processing factor 6	7.69E+04	2.25E+06	2.92E+01	2.92E+01	10.00	3.38	O94906	PRPF6
166.1	Heterogeneous nuclear ribonuc	3.17E+05	9.20E+06	2.90E+01	2.90E+01	10.00	3.37	Q14103	HNRNPD
100.1	tRNA-splicing ligase RtcB homol	4.29E+05	1.23E+07	2.87E+01	2.87E+01	10.00	3.36	Q9Y3I0	C22orf28
115.1	Isoform 2 of Regulator of chrom	8.59E+05	2.38E+07	2.77E+01	2.77E+01	10.00	3.32	P18754-2	RCC1
235.1	Puromycin-sensitive aminopept	9.18E+04	2.52E+06	2.75E+01	2.75E+01	10.00	3.31	P55786	NPEPPS
722.1	V-type proton ATPase subunit G	6.98E+04	1.85E+06	2.65E+01	2.65E+01	10.00	3.28	O75348	ATP6V1G1
283.1	Probable ATP-dependent RNA h	1.19E+05	3.14E+06	2.63E+01	2.63E+01	10.00	3.27	P26196	DDX6
47.2	Protein transport protein Sec23	7.20E+05	1.82E+07	2.53E+01	2.53E+01	10.00	3.23	Q15436	SEC23A
428.1	DNA replication licensing factor	5.20E+04	1.30E+06	2.50E+01	2.50E+01	10.00	3.22	P25205	MCM3
370.1	Splicing factor 3A subunit 3	1.26E+05	3.16E+06	2.50E+01	2.50E+01	10.00	3.22	Q12874	SF3A3
556.1	Eukaryotic translation initiation	6.22E+04	1.55E+06	2.49E+01	2.49E+01	10.00	3.22	P47813	EIF1AX
797.1	NEDD8-activating enzyme E1 re	1.08E+04	2.67E+05	2.47E+01	2.47E+01	10.00	3.21	A6NCK0	NAE1
2095.1	11-cis retinol dehydrogenase	1.01E+04	2.48E+05	2.47E+01	2.47E+01	10.00	3.20	Q92781	RDH5
347.1	Cysteine and glycine-rich protei	1.78E+04	4.38E+05	2.46E+01	2.46E+01	10.00	3.20	P21291	CSRP1
495.1	Protein FLJ22184	2.93E+04	7.21E+05	2.46E+01	2.46E+01	10.00	3.20	F5H1R7	FLJ22184
28.1	Isocitrate dehydrogenase [NAD	1.81E+06	4.42E+07	2.44E+01	2.44E+01	10.00	3.20	P48735	IDH2
261.1	Isoform Long of Proteasome su	3.86E+05	8.82E+06	2.28E+01	2.28E+01	10.00	3.13	P25786-2	PSMA1
783.1	Eukaryotic translation initiation	2.04E+04	4.46E+05	2.18E+01	2.18E+01	10.00	3.08	P78344	EIF4G2
343.1	Mesencephalic astrocyte-derive	2.28E+05	4.94E+06	2.16E+01	2.16E+01	10.00	3.07	P55145	MANF
669.1	Regulation of nuclear pre-mRN	7.31E+03	1.52E+05	2.08E+01	2.08E+01	10.00	3.03	Q96P16	RPRD1A
187.1	Isoform 2 of Protein disulfide-is	4.49E+05	9.06E+06	2.02E+01	2.02E+01	10.00	3.00	Q15084-2	PDIA6
71.1	Guanine nucleotide-binding pro	8.68E+05	1.75E+07	2.02E+01	2.02E+01	10.00	3.00	P63244	GNB2L1
263.1	28 kDa heat- and acid-stable ph	1.52E+05	3.05E+06	2.01E+01	2.01E+01	10.00	3.00	Q13442	PDAP1
232.1	Valine--tRNA ligase	2.64E+05	5.22E+06	1.98E+01	1.98E+01	10.00	2.98	P26640	VARS
394.1	Aspartate aminotransferase, cyt	2.48E+04	4.61E+05	1.86E+01	1.86E+01	10.00	2.92	P17174	GOT1
229.1	Staphylococcal nuclease domai	2.06E+05	3.81E+06	1.85E+01	1.85E+01	10.00	2.92	Q7KZF4	SND1
694.1	Cullin-4B	7.30E+04	1.34E+06	1.84E+01	1.84E+01	10.00	2.91	Q13620	CUL4B
843.1	Transcription initiation factor T	1.28E+05	2.31E+06	1.80E+01	1.80E+01	10.00	2.89	Q5VWG9	TAF3
179.1	Creatine kinase U-type, mitoch	7.41E+05	1.32E+07	1.78E+01	1.78E+01	10.00	2.88	P12532	CKMT1A

381.1	Microtubule-associated protein	1.82E+05	3.19E+06	1.75E+01	1.75E+01	10.00	2.86	Q15691	MAPRE1
201.1	ATP synthase subunit beta, mitc	5.64E+05	9.86E+06	1.75E+01	1.75E+01	10.00	2.86	P06576	ATP5B
216.1	40S ribosomal protein S18	4.70E+05	8.15E+06	1.73E+01	1.73E+01	10.00	2.85	P62269	RPS18
485.1	Serrate RNA effector molecule h	8.19E+04	1.40E+06	1.71E+01	1.71E+01	10.00	2.84	Q9BXP5	SRRT
1362.1	CDK5 regulatory subunit-associa	2.34E+05	3.85E+06	1.65E+01	1.65E+01	10.00	2.80	F8WBJ0	CDK5RAP2
637.1	UPF0556 protein C19orf10	1.22E+05	1.96E+06	1.60E+01	1.60E+01	10.00	2.77	Q969H8	C19orf10
1134.1	Protein pelota homolog	4.48E+04	7.00E+05	1.56E+01	1.56E+01	10.00	2.75	Q9BRX2	PELO
705.1	Protein phosphatase 1M	7.42E+06	1.15E+08	1.55E+01	1.55E+01	10.00	2.74	B7XGB9	ppm1m
670.1	Selenocysteine-specific elongati	1.61E+04	2.47E+05	1.54E+01	1.54E+01	10.00	2.73	P57772	EEFSEC
31.1	Microtubule-associated protein	1.62E+06	2.47E+07	1.53E+01	1.53E+01	10.00	2.73	E7EVA0	MAP4
172.1	Bifunctional glutamate/proline-	1.57E+05	2.37E+06	1.51E+01	1.51E+01	10.00	2.72	P07814	EPRS
560.1	AP-1 complex subunit gamma-1	1.26E+05	1.89E+06	1.50E+01	1.50E+01	10.00	2.71	B3KXW5	AP1G1
1485.1	Leukotriene A-4 hydrolase	7.95E+03	1.18E+05	1.48E+01	1.48E+01	10.00	2.70	P09960	LTA4H
158.1	Adenylate kinase 2, mitochondr	4.12E+05	6.12E+06	1.48E+01	1.48E+01	10.00	2.70	P54819	AK2
160.1	Leucine-rich repeat-containing p	4.86E+05	7.02E+06	1.44E+01	1.44E+01	10.00	2.67	Q8N1G4	LRRC47
176.1	40S ribosomal protein S9	6.58E+05	9.38E+06	1.43E+01	1.43E+01	10.00	2.66	P46781	RPS9
212.1	60S ribosomal protein L35	4.30E+06	6.08E+07	1.42E+01	1.42E+01	10.00	2.65	P42766	RPL35
518.1	Thioredoxin-dependent peroxid	6.00E+05	8.47E+06	1.41E+01	1.41E+01	10.00	2.65	P30048	PRDX3
542.1	Acylamino-acid-releasing enzym	1.83E+05	2.53E+06	1.38E+01	1.38E+01	10.00	2.63	C9JIF9	APEH
149.1	40S ribosomal protein S3a	7.76E+05	1.06E+07	1.37E+01	1.37E+01	10.00	2.61	P61247	RPS3A
388.1	Isoform 2 of Proteasome activat	2.53E+05	3.45E+06	1.37E+01	1.37E+01	10.00	2.61	P61289-2	PSME3
702.1	Non-histone chromosomal prot	1.66E+05	2.25E+06	1.36E+01	1.36E+01	10.00	2.61	P05114	HMGN1
418.1	Flap endonuclease 1	6.37E+05	8.58E+06	1.35E+01	1.35E+01	10.00	2.60	P39748	FEN1
266.1	60S ribosomal protein L23	5.83E+05	7.80E+06	1.34E+01	1.34E+01	10.00	2.59	P62829	RPL23
142.1	Isoform 3 of Elongation factor 1	8.05E+05	1.07E+07	1.33E+01	1.33E+01	10.00	2.59	P29692-3	EEF1D
243.1	Serine/threonine-protein phosp	4.23E+05	5.58E+06	1.32E+01	1.32E+01	10.00	2.58	P62140	PPP1CB
186.1	Heterogeneous nuclear ribonuc	1.13E+06	1.48E+07	1.31E+01	1.31E+01	10.00	2.57	P09651	HNRNPA1
598.1	ATP-dependent RNA helicase DI	8.38E+04	1.09E+06	1.30E+01	1.30E+01	10.00	2.57	Q86XP3	DDX42
516.1	U2 snRNP-associated SURP mot	1.08E+05	1.40E+06	1.29E+01	1.29E+01	10.00	2.56	E7ET15	U2SURP
464.1	Proteasome subunit beta type-(	5.40E+04	6.90E+05	1.28E+01	1.28E+01	10.00	2.55	P28072	PSMB6
639.1	Keratin, type I cuticular Ha1	1.43E+06	1.81E+07	1.27E+01	1.27E+01	10.00	2.54	Q15323	KRT31
65.1	DNA-dependent protein kinase	8.35E+05	1.05E+07	1.26E+01	1.26E+01	10.00	2.53	P78527	PRKDC
644.1	Vacuolar protein sorting-associa	1.23E+04	1.51E+05	1.22E+01	1.22E+01	10.00	2.50	Q709C8	VPS13C
439.1	40S ribosomal protein S30	3.71E+05	4.48E+06	1.21E+01	1.21E+01	10.00	2.49	E9PR30	FAU
497.1	Hematological and neurological	2.60E+04	3.05E+05	1.17E+01	1.17E+01	10.00	2.46	B4DLH4	HN1L

114.1	Proliferation-associated protein	7.66E+05	8.97E+06	1.17E+01	1.17E+01	10.00	2.46	Q9UQ80	PA2G4
178.1	NHP2 non-histone chromosome	1.41E+06	1.62E+07	1.15E+01	1.15E+01	10.00	2.44	B1AHD1	NHP2L1
18.1	Propionyl-CoA carboxylase alph	3.96E+06	4.34E+07	1.10E+01	1.10E+01	10.00	2.39	P05165	PCCA
3.4	Keratin, type II cytoskeletal 2 ep	2.45E+05	2.64E+06	1.08E+01	1.08E+01	10.00	2.38	P35908	KRT2
289.1	Tripeptidyl-peptidase 1	4.50E+05	4.81E+06	1.07E+01	1.07E+01	10.00	2.37	O14773	TPP1
22.1	Propionyl-CoA carboxylase beta	3.26E+06	3.40E+07	1.04E+01	1.04E+01	10.00	2.35	E7EX59	PCCB
622.1	Proteasome subunit alpha type-	5.87E+04	6.00E+05	1.02E+01	1.02E+01	10.00	2.32	O14818	PSMA7
552.1	Eukaryotic translation initiation	2.02E+06	2.04E+07	1.01E+01	1.01E+01	10.00	2.31	K7EM18	EIF1
659.1	Developmentally-regulated GTP	9.18E+04	9.14E+05	9.96E+00	9.96E+00	9.96	2.30	Q9Y295	DRG1
651.1	AP-1 complex subunit beta-1	2.10E+05	2.08E+06	9.89E+00	9.89E+00	9.89	2.29	Q10567	AP1B1
51.3	Ezrin	1.01E+05	9.88E+05	9.77E+00	9.77E+00	9.77	2.28	P15311	EZR
664.1	Selenide, water dikinase 1	2.72E+05	2.53E+06	9.30E+00	9.30E+00	9.30	2.23	P49903	SEPHS1
72.1	10 kDa heat shock protein, mito	3.16E+06	2.94E+07	9.29E+00	9.29E+00	9.29	2.23	P61604	HSPE1
568.1	60S ribosomal protein L3-like	4.87E+04	4.52E+05	9.28E+00	9.28E+00	9.28	2.23	Q92901	RPL3L
647.1	Ubiquilin-4	8.04E+04	7.39E+05	9.19E+00	9.19E+00	9.19	2.22	Q9NRR5	UBQLN4
254.1	6-phosphofructokinase	1.25E+06	1.15E+07	9.17E+00	9.17E+00	9.17	2.22	P08237	PFKM
436.1	Ribonuclease inhibitor	2.54E+05	2.30E+06	9.06E+00	9.06E+00	9.06	2.20	P13489	RNH1
848.1	WD repeat-containing protein W	6.80E+04	6.14E+05	9.02E+00	9.02E+00	9.02	2.20	Q9P2S5	WRAP73
204.1	Exportin-2	6.15E+05	5.37E+06	8.74E+00	8.74E+00	8.74	2.17	P55060	CSE1L
330.1	Aspartate aminotransferase, mi	1.36E+05	1.19E+06	8.72E+00	8.72E+00	8.72	2.17	P00505	GOT2
804.1	Histone-lysine N-methyltransfer	4.95E+04	4.17E+05	8.42E+00	8.42E+00	8.42	2.13	Q9NR48	ASH1L
593.1	Serine-threonine kinase recepto	4.52E+04	3.77E+05	8.34E+00	8.34E+00	8.34	2.12	B4DNJ6	STRAP
79.1	Keratin, type II cytoskeletal 1	2.02E+06	1.67E+07	8.26E+00	8.26E+00	8.26	2.11	P04264	KRT1
350.1	Pyrroline-5-carboxylate reducta	5.14E+05	4.24E+06	8.26E+00	8.26E+00	8.26	2.11	Q53H96	PYCRL
1154.1	Isoform 2 of Nesprin-2	8.40E+04	6.89E+05	8.20E+00	8.20E+00	8.20	2.10	Q8WXH0-	SYNE2
280.1	Eukaryotic translation initiation	2.46E+05	2.01E+06	8.18E+00	8.18E+00	8.18	2.10	P05198	EIF2S1
297.1	Prosaposin	1.01E+06	8.16E+06	8.07E+00	8.07E+00	8.07	2.09	B1AVU8	PSAP
239.1	Talin-1	6.50E+05	5.22E+06	8.03E+00	8.03E+00	8.03	2.08	Q9Y490	TLN1
445.1	Cancer-related nucleoside-triph	7.70E+04	6.01E+05	7.80E+00	7.80E+00	7.80	2.05	Q9BSD7	NTPCR
222.1	Inosine-5'-monophosphate dehy	8.66E+05	6.52E+06	7.53E+00	7.53E+00	7.53	2.02	P12268	IMPDH2
515.1	Programmed cell death protein	1.86E+05	1.39E+06	7.47E+00	7.47E+00	7.47	2.01	Q53EL6	PDCD4
353.1	Isoform 2 of C-terminal-binding	9.31E+04	6.95E+05	7.46E+00	7.46E+00	7.46	2.01	P56545-2	CTBP2
413.1	Eukaryotic peptide chain release	4.09E+05	3.05E+06	7.45E+00	7.45E+00	7.45	2.01	P62495	ETF1
43.2	116 kDa U5 small nuclear ribonu	1.21E+05	9.02E+05	7.43E+00	7.43E+00	7.43	2.01	Q15029	EFTUD2
231.1	Isoform 2 of Threonine--tRNA lig	3.31E+05	2.45E+06	7.41E+00	7.41E+00	7.41	2.00	P26639-2	TARS

478.1	Keratin, type I cuticular Ha7	2.42E+06	1.78E+07	7.37E+00	7.37E+00	7.37	2.00	O76014	KRT37
786.1	Mitogen-activated protein kinas	1.66E+05	1.22E+06	7.36E+00	7.36E+00	7.36	2.00	P27361	MAPK3
483.1	Nuclear mitotic apparatus prote	7.18E+04	5.26E+05	7.33E+00	7.33E+00	7.33	1.99	Q14980	NUMA1
602.1	SUMO-conjugating enzyme UBC	6.51E+05	4.72E+06	7.25E+00	7.25E+00	7.25	1.98	B0QYN7	UBE2I
479.1	HLA-B associated transcript 3, is	8.86E+04	6.40E+05	7.23E+00	7.23E+00	7.23	1.98	G3V1Z5	NULL
623.1	Epithelial splicing regulatory prc	7.85E+04	5.66E+05	7.21E+00	7.21E+00	7.21	1.98	Q6NXG1	ESRP1
965.1	Zinc finger protein 207	1.16E+05	8.28E+05	7.12E+00	7.12E+00	7.12	1.96	O43670	ZNF207
895.1	S-adenosylmethionine synthase	2.87E+05	2.03E+06	7.07E+00	7.07E+00	7.07	1.96	Q00266	MAT1A
367.1	E3 SUMO-protein ligase RanBP2	5.39E+05	3.76E+06	6.98E+00	6.98E+00	6.98	1.94	P49792	RANBP2
306.1	Isoform 5 of Splicing factor 1	1.50E+06	1.03E+07	6.88E+00	6.88E+00	6.88	1.93	Q15637-5	SF1
1348.1	Isoform 1 of Metabotropic gluta	1.33E+05	9.18E+05	6.88E+00	6.88E+00	6.88	1.93	P41594-2	GRM5
395.1	DNA damage-binding protein 1	3.81E+04	2.58E+05	6.77E+00	6.77E+00	6.77	1.91	Q16531	DDB1
484.1	Proteasome activator complex s	1.72E+05	1.14E+06	6.63E+00	6.63E+00	6.63	1.89	Q06323	PSME1
482.1	Isoform 2 of TAR DNA-binding p	2.39E+05	1.56E+06	6.54E+00	6.54E+00	6.54	1.88	Q13148-2	TARDBP
362.1	Importin subunit beta-1	2.24E+05	1.45E+06	6.46E+00	6.46E+00	6.46	1.87	Q14974	KPNB1
1316.1	Kallistatin	2.38E+04	1.53E+05	6.44E+00	6.44E+00	6.44	1.86	P29622	SERPINA4
400.1	Isoform 2 of Partner of Y14 and	3.81E+04	2.45E+05	6.43E+00	6.43E+00	6.43	1.86	Q9BRP8-2	WIBG
535.1	Isoform 2 of Serine/threonine-p	4.07E+05	2.60E+06	6.38E+00	6.38E+00	6.38	1.85	P63151-2	PPP2R2A
236.1	Hsc70-interacting protein	6.19E+05	3.89E+06	6.29E+00	6.29E+00	6.29	1.84	P50502	ST13
1139.1	Superoxide dismutase [Cu-Zn]	2.52E+05	1.58E+06	6.28E+00	6.28E+00	6.28	1.84	P00441	SOD1
299.1	ATP-citrate synthase	1.51E+05	9.44E+05	6.27E+00	6.27E+00	6.27	1.84	P53396	ACLY
902.1	Laminin subunit beta-3	7.52E+04	4.68E+05	6.22E+00	6.22E+00	6.22	1.83	Q13751	LAMB3
36.1	Transitional endoplasmic reticul	3.61E+06	2.20E+07	6.10E+00	6.10E+00	6.10	1.81	P55072	VCP
227.1	Aspartate--tRNA ligase, cytoplas	5.16E+05	3.14E+06	6.09E+00	6.09E+00	6.09	1.81	P14868	DARS
844.1	Dynein light chain roadblock-typ	9.89E+04	5.98E+05	6.05E+00	6.05E+00	6.05	1.80	B1AKR6	DYNLRB1
592.1	60 kDa SS-A/Ro ribonucleoprote	1.51E+05	8.95E+05	5.94E+00	5.94E+00	5.94	1.78	P10155	TROVE2
137.1	40S ribosomal protein S11	2.93E+06	1.74E+07	5.93E+00	5.93E+00	5.93	1.78	P62280	RPS11
54.1	Peptidyl-prolyl cis-trans isomera	5.66E+06	3.34E+07	5.90E+00	5.90E+00	5.90	1.77	P23284	PPIB
16.1	60 kDa heat shock protein, mito	1.70E+07	1.00E+08	5.89E+00	5.89E+00	5.89	1.77	P10809	HSPD1
369.1	Profilin-2	1.05E+05	6.13E+05	5.83E+00	5.83E+00	5.83	1.76	P35080	PFN2
356.1	Isoform 2 of Regulator of nonse	3.64E+05	2.11E+06	5.80E+00	5.80E+00	5.80	1.76	Q92900-2	UPF1
305.1	26S protease regulatory subunit	5.62E+05	3.23E+06	5.75E+00	5.75E+00	5.75	1.75	P35998	PSMC2
548.1	Isoform 2 of Histone-binding prc	2.09E+05	1.20E+06	5.73E+00	5.73E+00	5.73	1.75	Q16576-2	RBBP7
132.1	Poly(rC)-binding protein 1	6.25E+05	3.49E+06	5.59E+00	5.59E+00	5.59	1.72	Q15365	PCBP1
1176.1	Mucin-16	1.08E+05	6.00E+05	5.55E+00	5.55E+00	5.55	1.71	Q8WXI7	MUC16

295.1	Alcohol dehydrogenase [NADP(	8.46E+05	4.65E+06	5.50E+00	5.50E+00	5.50	1.70	P14550	AKR1A1
426.1	26S protease regulatory subunit	5.90E+05	3.23E+06	5.47E+00	5.47E+00	5.47	1.70	P43686	PSMC4
194.1	Isoform 2 of General vesicular t	1.18E+06	6.13E+06	5.18E+00	5.18E+00	5.18	1.65	O60763-2	USO1
603.1	Microtubule-actin cross-linking	3.44E+05	1.75E+06	5.09E+00	5.09E+00	5.09	1.63	H3BQK9	MACF1
699.1	Clathrin light chain B	9.43E+04	4.78E+05	5.07E+00	5.07E+00	5.07	1.62	P09497	CLTB
89.1	Cytochrome c	6.38E+06	3.23E+07	5.06E+00	5.06E+00	5.06	1.62	P99999	CYCS
130.1	Thymocyte nuclear protein 1	2.72E+06	1.37E+07	5.04E+00	5.04E+00	5.04	1.62	Q9P016	THYN1
214.1	Alpha-2-HS-glycoprotein	9.77E+05	4.85E+06	4.97E+00	4.97E+00	4.97	1.60	P02765	AHSG
871.1	ATPase inhibitor, mitochondrial	6.56E+05	3.19E+06	4.86E+00	4.86E+00	4.86	1.58	Q9UII2	ATPIF1
1279.1	GDP-fucose protein O-fucosyltra	5.90E+04	2.80E+05	4.74E+00	4.74E+00	4.74	1.56	Q9H488	POFUT1
718.1	Galactokinase	1.32E+05	6.27E+05	4.73E+00	4.73E+00	4.73	1.55	B4E1G6	GALK1
110.1	Isoform 2 of Coatomer subunit	2.69E+06	1.26E+07	4.69E+00	4.69E+00	4.69	1.54	P53621-2	COPA
254.3	Isoform 2 of 6-phosphofructoki	5.05E+05	2.36E+06	4.67E+00	4.67E+00	4.67	1.54	P17858-2	PFKL
1021.1	Sodium/potassium/calcium exc	4.80E+04	2.22E+05	4.62E+00	4.62E+00	4.62	1.53	Q71RS6	SLC24A5
1010.1	Cystatin-C	6.43E+04	2.96E+05	4.60E+00	4.60E+00	4.60	1.53	P01034	CST3
522.1	Cytoplasmic dynein 1 light inter	7.47E+04	3.42E+05	4.58E+00	4.58E+00	4.58	1.52	O43237	DYNC1LI2
551.1	Isoform 2 of Cytoplasmic FMR1-	3.21E+05	1.47E+06	4.57E+00	4.57E+00	4.57	1.52	Q7L576-2	CYFIP1
96.1	Far upstream element-binding	7.40E+05	3.34E+06	4.51E+00	4.51E+00	4.51	1.51	Q92945	KHSRP
1401.1	Serine/threonine-protein phosp	5.25E+04	2.36E+05	4.50E+00	4.50E+00	4.50	1.50	P67775	PPP2CA
349.1	Methionine--tRNA ligase, cytopl	1.10E+06	4.95E+06	4.49E+00	4.49E+00	4.49	1.50	P56192	MARS
476.1	Eukaryotic translation initiation	2.07E+05	9.14E+05	4.41E+00	4.41E+00	4.41	1.48	E7EX17	EIF4B
500.1	V(D)J recombination-activating	1.76E+05	7.62E+05	4.33E+00	4.33E+00	4.33	1.47	P15918	RAG1
121.1	Elongation factor 1-gamma	3.57E+06	1.54E+07	4.32E+00	4.32E+00	4.32	1.46	B4DTG2	EEF1G
967.1	Isoform 1 of Tudor domain-cont	2.22E+05	9.59E+05	4.31E+00	4.31E+00	4.31	1.46	Q8NAT2-1	TDRD5
1393.1	Folliculin-interacting protein 1	3.35E+03	1.44E+04	4.30E+00	4.30E+00	4.30	1.46	E9PCH4	FNIP1
124.1	Nucleolin	2.68E+06	1.14E+07	4.26E+00	4.26E+00	4.26	1.45	P19338	NCL
136.1	26S proteasome non-ATPase re	7.15E+05	3.03E+06	4.24E+00	4.24E+00	4.24	1.44	Q13200	PSMD2
169.1	Keratin, type I cytoskeletal 10	9.94E+05	4.13E+06	4.16E+00	4.16E+00	4.16	1.42	P13645	KRT10
352.1	26S protease regulatory subunit	1.28E+06	5.31E+06	4.14E+00	4.14E+00	4.14	1.42	P17980	PSMC3
487.1	Protein phosphatase 1G	1.09E+05	4.51E+05	4.13E+00	4.13E+00	4.13	1.42	O15355	PPM1G
132.2	Isoform 2 of Poly(rC)-binding pr	1.41E+06	5.66E+06	4.03E+00	4.03E+00	4.03	1.39	Q15366-2	PCBP2
1127.1	Isoform Alpha-2 of Glucocortico	1.55E+05	5.94E+05	3.84E+00	3.84E+00	3.84	1.35	P04150-3	NR3C1
1.1	Plectin	5.07E+07	1.94E+08	3.83E+00	3.83E+00	3.83	1.34	Q15149	PLEC
242.1	Calcyclin-binding protein	1.14E+06	4.37E+06	3.83E+00	3.83E+00	3.83	1.34	Q9HB71	CACYBP
999.1	Malate dehydrogenase	3.60E+05	1.37E+06	3.81E+00	3.81E+00	3.81	1.34	P40925	MDH1

614.1	ADP-ribosylation factor-like prot	7.47E+05	2.84E+06	3.80E+00	3.80E+00	3.80	1.34	F8VYN9	ARL1
265.1	Polyadenylate-binding protein 1	1.07E+06	4.07E+06	3.80E+00	3.80E+00	3.80	1.33	P11940	PABPC1
926.1	ATP-binding cassette sub-family	1.19E+04	4.51E+04	3.78E+00	3.78E+00	3.78	1.33	Q8NE71	ABCF1
69.1	Spliceosome RNA helicase DDX3	2.78E+06	1.05E+07	3.78E+00	3.78E+00	3.78	1.33	F8VQ10	DDX39B
1375.1	CD180 antigen	9.31E+04	3.49E+05	3.75E+00	3.75E+00	3.75	1.32	Q99467	CD180
105.1	Histone H4	7.46E+06	2.78E+07	3.73E+00	3.73E+00	3.73	1.32	P62805	HIST1H4A
510.1	Structural maintenance of chro	2.32E+05	8.61E+05	3.72E+00	3.72E+00	3.72	1.31	A6NHR9	SMCHD1
446.1	Dihydropyrimidinase-related pr	4.40E+05	1.63E+06	3.71E+00	3.71E+00	3.71	1.31	Q16555	DPYSL2
954.1	Cytoplasmic dynein 1 light inter	1.92E+04	7.07E+04	3.68E+00	3.68E+00	3.68	1.30	Q9Y6G9	DYNC1LI1
877.1	FYN-binding protein	1.75E+05	6.27E+05	3.58E+00	3.58E+00	3.58	1.28	O15117	FYB
1059.1	60S ribosomal protein L31	1.86E+05	6.63E+05	3.56E+00	3.56E+00	3.56	1.27	B7Z4C8	RPL31
1223.1	Probable phospholipid-transpor	1.20E+05	4.20E+05	3.49E+00	3.49E+00	3.49	1.25	Q9P241	ATP10D
10.1	Clathrin heavy chain 1	1.28E+07	4.45E+07	3.47E+00	3.47E+00	3.47	1.24	Q00610	CLTC
1014.1	DNA fragmentation factor subu	1.98E+05	6.84E+05	3.45E+00	3.45E+00	3.45	1.24	O00273	DFFA
863.1	Isoform 6 of Ankyrin repeat and	1.85E+05	6.32E+05	3.42E+00	3.42E+00	3.42	1.23	Q8IWZ3-6	ANKHD1
761.1	Transcription factor BTF3	9.29E+05	3.16E+06	3.40E+00	3.40E+00	3.40	1.22	P20290	BTF3
329.1	Isoleucine--tRNA ligase, cytopla	6.04E+05	2.04E+06	3.38E+00	3.38E+00	3.38	1.22	P41252	IARS
107.1	Archain 1, isoform CRA_a	4.48E+06	1.51E+07	3.37E+00	3.37E+00	3.37	1.22	B0YIW6	ARCN1
1467.1	SET and MYND domain-containi	8.94E+04	2.97E+05	3.32E+00	3.32E+00	3.32	1.20	Q9H7B4	SMYD3
93.1	Peptidyl-prolyl cis-trans isomer	7.29E+06	2.37E+07	3.25E+00	3.25E+00	3.25	1.18	Q02790	FKBP4
874.1	Centromere-associated protein	1.09E+05	3.54E+05	3.24E+00	3.24E+00	3.24	1.18	Q02224	CENPE
254.2	6-phosphofructokinase	1.52E+06	4.89E+06	3.22E+00	3.22E+00	3.22	1.17	Q01813	PFKP
1041.1	Myosin-2	8.46E+04	2.71E+05	3.20E+00	3.20E+00	3.20	1.16	Q9UKX2	MYH2
473.1	Splicing factor 3B subunit 3	3.10E+05	9.88E+05	3.18E+00	3.18E+00	3.18	1.16	Q15393	SF3B3
315.1	Chloride intracellular channel pr	9.26E+05	2.94E+06	3.17E+00	3.17E+00	3.17	1.16	O00299	CLIC1
39.1	Alpha-enolase	1.69E+07	5.27E+07	3.12E+00	3.12E+00	3.12	1.14	P06733	ENO1
87.1	40S ribosomal protein S13	1.06E+07	3.28E+07	3.09E+00	3.09E+00	3.09	1.13	P62277	RPS13
173.1	Phosphoenolpyruvate carboxyki	1.64E+06	5.05E+06	3.08E+00	3.08E+00	3.08	1.13	Q16822	PCK2
29.1	D-3-phosphoglycerate dehydro	1.42E+07	4.36E+07	3.08E+00	3.08E+00	3.08	1.13	O43175	PHGDH
294.1	Fructose-bisphosphate aldolase	2.15E+06	6.62E+06	3.07E+00	3.07E+00	3.07	1.12	P09972	ALDOC
311.1	Nucleoprotein TPR	9.67E+05	2.94E+06	3.04E+00	3.04E+00	3.04	1.11	P12270	TPR
660.1	Phosphoserine phosphatase	9.50E+04	2.88E+05	3.03E+00	3.03E+00	3.03	1.11	P78330	PSPH
1122.1	Isoform 5 of Nitric oxide synthas	7.65E+04	2.30E+05	3.01E+00	3.01E+00	3.01	1.10	P29475-5	NOS1
819.1	Multidrug resistance-associated	6.96E+04	2.09E+05	3.00E+00	3.00E+00	3.00	1.10	O15440	ABCC5
384.1	Oxysterol-binding protein 1	1.27E+05	3.75E+05	2.94E+00	2.94E+00	2.94	1.08	P22059	OSBP

94.1	Glyceraldehyde-3-phosphate de	2.85E+07	8.38E+07	2.94E+00	2.94E+00	2.94	1.08	P04406	GAPDH
821.1	Hsp90 co-chaperone Cdc37	2.67E+05	7.79E+05	2.92E+00	2.92E+00	2.92	1.07	Q16543	CDC37
51.2	Moesin	1.83E+06	5.33E+06	2.91E+00	2.91E+00	2.91	1.07	P26038	MSN
646.1	Hydroxyacylglutathione hydrola	2.65E+05	7.69E+05	2.90E+00	2.90E+00	2.90	1.07	Q16775	HAGH
1491.1	DNA polymerase	3.04E+05	8.77E+05	2.88E+00	2.88E+00	2.88	1.06	E7ETS8	POLE
44.2	Peroxiredoxin-2	2.25E+07	6.39E+07	2.83E+00	2.83E+00	2.83	1.04	P32119	PRDX2
307.1	Serine/threonine-protein kinase	1.55E+06	4.34E+06	2.81E+00	2.81E+00	2.81	1.03	Q13177	PAK2
800.1	Unconventional myosin-Va	9.09E+04	2.54E+05	2.79E+00	2.79E+00	2.79	1.03	F8W6H6	MYO5A
494.1	Putative RNA-binding protein Lu	4.68E+05	1.29E+06	2.76E+00	2.76E+00	2.76	1.01	Q9Y383	LUC7L2
140.1	Rab GDP dissociation inhibitor b	1.82E+06	5.01E+06	2.75E+00	2.75E+00	2.75	1.01	E7EU23	GDI2
20.5	Heat shock protein 75 kDa, mitc	3.36E+06	9.21E+06	2.74E+00	2.74E+00	2.74	1.01	Q12931	TRAP1
366.1	Eukaryotic translation initiation	4.00E+05	1.09E+06	2.72E+00	2.72E+00	2.72	1.00	Q15056	EIF4H
457.1	182 kDa tankyrase-1-binding pro	1.96E+05	5.32E+05	2.71E+00	2.71E+00	2.71	1.00	Q9C0C2	TNKS1BP1
947.1	V-type proton ATPase subunit E	9.49E+05	2.57E+06	2.71E+00	2.71E+00	2.71	1.00	P36543	ATP6V1E1
528.1	Enhancer of mRNA-decapping p	1.43E+06	3.84E+06	2.69E+00	2.69E+00	2.69	0.99	Q6P2E9	EDC4
550.1	Acetyl-CoA acetyltransferase, cy	3.48E+05	9.30E+05	2.67E+00	2.67E+00	2.67	0.98	B7Z233	ACAT2
241.1	V-type proton ATPase subunit B	3.94E+06	1.05E+07	2.66E+00	2.66E+00	2.66	0.98	P21281	ATP6V1B2
561.1	COP9 signalosome complex sub	2.19E+05	5.83E+05	2.66E+00	2.66E+00	2.66	0.98	D6RFN0	COPS4
300.1	Ribose-phosphate pyrophospho	1.84E+06	4.87E+06	2.65E+00	2.65E+00	2.65	0.97	P21108	PRPS1L1
1236.1	Ubiquitin carboxyl-terminal hyd	7.56E+04	2.00E+05	2.64E+00	2.64E+00	2.64	0.97	Q70CQ1	USP49
155.1	40S ribosomal protein S7	9.33E+06	2.45E+07	2.63E+00	2.63E+00	2.63	0.97	P62081	RPS7
725.1	Peptidyl-prolyl cis-trans isomera	3.40E+05	8.90E+05	2.62E+00	2.62E+00	2.62	0.96	K7EMU7	PIN1
219.1	Isoform 2 of Electron transfer fla	3.14E+06	8.23E+06	2.62E+00	2.62E+00	2.62	0.96	P38117-2	ETFB
1220.1	Zinc finger and BTB domain-con	1.99E+05	5.20E+05	2.61E+00	2.61E+00	2.61	0.96	P10074	ZBTB48
390.1	Eukaryotic translation initiation	9.74E+05	2.51E+06	2.58E+00	2.58E+00	2.58	0.95	Q04637	EIF4G1
739.1	Protein TFG	1.96E+05	4.92E+05	2.51E+00	2.51E+00	2.51	0.92	Q92734	TFG
652.1	CAD protein	1.60E+04	3.99E+04	2.50E+00	2.50E+00	2.50	0.92	P27708	CAD
125.1	Transcription elongation factor	6.40E+06	1.59E+07	2.48E+00	2.48E+00	2.48	0.91	P23193	TCEA1
103.1	Heat shock protein beta-1	1.51E+07	3.72E+07	2.47E+00	2.47E+00	2.47	0.90	P04792	HSPB1
1440.1	Actin-related protein 2/3 compl	1.37E+04	3.37E+04	2.45E+00	2.45E+00	2.45	0.90	O15143	ARPC1B
323.1	Peroxiredoxin-5, mitochondrial	1.93E+06	4.72E+06	2.44E+00	2.44E+00	2.44	0.89	P30044	PRDX5
2001.1	Ran-specific GTPase-activating p	2.08E+05	5.09E+05	2.44E+00	2.44E+00	2.44	0.89	F8WCY3	RANBP1
424.1	Leucine-rich repeat flightless-int	5.61E+04	1.37E+05	2.44E+00	2.44E+00	2.44	0.89	Q32MZ4	LRRFIP1
220.1	DNA replication licensing factor	2.01E+06	4.90E+06	2.44E+00	2.44E+00	2.44	0.89	P33993	MCM7
68.1	Fructose-bisphosphate aldolase	8.85E+06	2.15E+07	2.43E+00	2.43E+00	2.43	0.89	J3KPS3	ALDOA

324.1	26S protease regulatory subunit	7.14E+05	1.73E+06	2.42E+00	2.42E+00	2.42	0.89	P62195	PSMC5
42.1	Selenium-binding protein 1	5.18E+06	1.25E+07	2.41E+00	2.41E+00	2.41	0.88	Q13228	SELENBP1
511.1	Nicotinamide phosphoribosyltra	5.27E+05	1.27E+06	2.41E+00	2.41E+00	2.41	0.88	P43490	NAMPT
1324.1	Histone-lysine N-methyltransfer	9.53E+04	2.29E+05	2.40E+00	2.40E+00	2.40	0.88	Q8TEK3	DOT1L
2411.1	Isoform 3 of Oral-facial-digital s	1.79E+05	4.29E+05	2.40E+00	2.40E+00	2.40	0.87	O75665-3	OFD1
862.1	Ubiquitin-like modifier-activatin	1.80E+05	4.30E+05	2.39E+00	2.39E+00	2.39	0.87	Q9GZZ9	UBA5
750.1	Isoform 3 of Calcium-binding mi	1.25E+05	2.97E+05	2.37E+00	2.37E+00	2.37	0.86	Q6KCM7-3	SLC25A25
641.1	Isoform 2 of Hematological and	1.25E+06	2.97E+06	2.37E+00	2.37E+00	2.37	0.86	Q9UK76-2	HN1
74.1	Adenosylhomocysteinase	6.02E+06	1.40E+07	2.33E+00	2.33E+00	2.33	0.84	P23526	AHCY
27.1	T-complex protein 1 subunit del	1.81E+07	4.17E+07	2.30E+00	2.30E+00	2.30	0.83	P50991	CCT4
58.2	L-lactate dehydrogenase B chai	8.67E+06	1.98E+07	2.28E+00	2.28E+00	2.28	0.83	P07195	LDHB
13.1	Pyruvate kinase isozymes M1/	4.47E+07	1.02E+08	2.28E+00	2.28E+00	2.28	0.83	P14618	PKM
43.1	Elongation factor 2	7.10E+06	1.61E+07	2.27E+00	2.27E+00	2.27	0.82	P13639	EEF2
493.1	Macrophage migration inhibitor	2.40E+07	5.42E+07	2.26E+00	2.26E+00	2.26	0.82	P14174	MIF
532.1	dCTP pyrophosphatase 1	5.99E+05	1.35E+06	2.26E+00	2.26E+00	2.26	0.81	Q9H773	DCTPP1
1254.1	Tubby-related protein 1	1.85E+05	4.17E+05	2.25E+00	2.25E+00	2.25	0.81	O00294	TULP1
119.1	Ubiquitin-like modifier-activatin	5.20E+06	1.17E+07	2.25E+00	2.25E+00	2.25	0.81	P22314	UBA1
391.1	Thioredoxin domain-containing	9.35E+05	2.10E+06	2.25E+00	2.25E+00	2.25	0.81	Q9BRA2	TXNDC17
545.1	GMP synthase [glutamine-hydr	4.38E+05	9.82E+05	2.24E+00	2.24E+00	2.24	0.81	P49915	GMPS
610.1	Phosphoglucomutase-1	4.04E+05	9.07E+05	2.24E+00	2.24E+00	2.24	0.81	P36871	PGM1
58.1	Isoform 3 of L-lactate dehydrog	6.02E+06	1.33E+07	2.21E+00	2.21E+00	2.21	0.79	P00338-3	LDHA
924.1	Protein unc-119 homolog B	4.68E+04	1.03E+05	2.20E+00	2.20E+00	2.20	0.79	A6NIH7	UNC119B
147.1	Eukaryotic translation initiation	3.80E+06	8.33E+06	2.19E+00	2.19E+00	2.19	0.78	P41091	EIF2S3
1321.1	RNA-binding protein Raly	2.80E+05	6.05E+05	2.16E+00	2.16E+00	2.16	0.77	Q9UKM9	RALY
206.1	Coatomer subunit beta	2.22E+06	4.74E+06	2.13E+00	2.13E+00	2.13	0.76	P53618	COPB1
754.1	Splicing factor U2AF 65 kDa sub	7.63E+05	1.62E+06	2.12E+00	2.12E+00	2.12	0.75	P26368	U2AF2
1587.1	Protein KIAA0368	6.69E+04	1.42E+05	2.12E+00	2.12E+00	2.12	0.75	J3KN16	KIAA0368
933.1	TBC1 domain family member 8	7.40E+04	1.56E+05	2.11E+00	2.11E+00	2.11	0.75	J3KQ40	TBC1D8
1631.1	Melanoma-associated antigen	1.34E+06	2.83E+06	2.10E+00	2.10E+00	2.10	0.74	Q9UNF1	MAGED2
345.1	Proteasome subunit beta type-	4.27E+05	8.97E+05	2.10E+00	2.10E+00	2.10	0.74	P28074	PSMB5
978.1	ADP-ribosylation factor 5	1.39E+05	2.90E+05	2.09E+00	2.09E+00	2.09	0.74	P84085	ARF5
562.1	High mobility group nucleosom	7.95E+05	1.66E+06	2.09E+00	2.09E+00	2.09	0.74	P82970	HMGN5
671.1	Casein kinase II subunit alpha	2.58E+06	5.28E+06	2.05E+00	2.05E+00	2.05	0.72	E7EU96	CSNK2A1
2146.1	E3 ubiquitin-protein ligase CHF	5.72E+05	1.17E+06	2.04E+00	2.04E+00	2.04	0.72	Q96EP1	CHFR
609.1	Isoform 2 of COP9 signalosome	2.00E+05	4.08E+05	2.04E+00	2.04E+00	2.04	0.71	P61201-2	COPS2

127.1	Translational activator GCN1	1.70E+06	3.46E+06	2.04E+00	2.04E+00	2.04	0.71	Q92616	GCN1L1
46.1	Heterogeneous nuclear ribonuc	1.91E+07	3.88E+07	2.03E+00	2.03E+00	2.03	0.71	P61978	HNRNPK
273.1	Mitochondrial import receptor s	3.38E+06	6.81E+06	2.02E+00	2.02E+00	2.02	0.70	Q15785	TOMM34
820.1	Pro-cathepsin H	1.59E+05	3.19E+05	2.01E+00	2.01E+00	2.01	0.70	P09668	CTSH
331.1	Glutamate carboxypeptidase 2	1.37E+06	2.74E+06	1.99E+00	1.99E+00	1.99	0.69	Q04609	FOLH1
33.1	Protein disulfide-isomerase A3	1.52E+07	3.00E+07	1.98E+00	1.98E+00	1.98	0.68	P30101	PDIA3
884.1	Coatomer subunit epsilon	1.60E+06	3.15E+06	1.97E+00	1.97E+00	1.97	0.68	O14579	COPE
95.1	DNA-(apurinic or apyrimidinic si	1.68E+07	3.30E+07	1.97E+00	1.97E+00	1.97	0.68	P27695	APEX1
383.1	Histidine triad nucleotide-bindir	4.17E+06	8.15E+06	1.96E+00	1.96E+00	1.96	0.67	P49773	HINT1
971.1	Guanosine-3',5'-bis(diphosphate	4.79E+04	9.33E+04	1.95E+00	1.95E+00	1.95	0.67	Q8N4P3	HDDC3
868.1	Protein Shroom3	1.54E+05	2.99E+05	1.95E+00	1.95E+00	1.95	0.67	Q8TF72	SHROOM3
202.1	Coatomer subunit beta'	1.17E+06	2.26E+06	1.93E+00	1.93E+00	1.93	0.66	P35606	COPB2
5.1	Keratin, type I cytoskeletal 18	2.35E+08	4.52E+08	1.93E+00	1.93E+00	1.93	0.66	P05783	KRT18
972.1	Pescadillo homolog	1.07E+05	2.06E+05	1.92E+00	1.92E+00	1.92	0.65	B3KXD6	PES1
567.1	Protein NEDD8-MDP1	2.91E+05	5.59E+05	1.92E+00	1.92E+00	1.92	0.65	E9PS38	NEDD8-MDP1
26.1	Cytoplasmic dynein 1 heavy cha	7.19E+06	1.38E+07	1.92E+00	1.92E+00	1.92	0.65	Q14204	DYNC1H1
749.1	Midasin	1.37E+05	2.63E+05	1.91E+00	1.91E+00	1.91	0.65	Q9NU22	MDN1
51.1	Radixin	8.82E+05	1.68E+06	1.91E+00	1.91E+00	1.91	0.64	P35241	RDX
75.1	Cytosolic non-specific dipeptida	2.58E+06	4.91E+06	1.90E+00	1.90E+00	1.90	0.64	Q96KP4	CNDP2
217.1	Bifunctional purine biosynthesis	3.89E+06	7.38E+06	1.90E+00	1.90E+00	1.90	0.64	P31939	ATIC
325.1	Phosphatidylethanolamine-bind	2.27E+06	4.27E+06	1.88E+00	1.88E+00	1.88	0.63	P30086	PEBP1
9.2	Tubulin beta chain	1.10E+07	2.06E+07	1.87E+00	1.87E+00	1.87	0.63	P07437	TUBB
1461.1	Isoform 2 of Kinesin-like protein	1.09E+05	2.04E+05	1.87E+00	1.87E+00	1.87	0.63	Q12756-2	KIF1A
925.1	Isoform 2 of Melanoma-associat	1.00E+06	1.87E+06	1.86E+00	1.86E+00	1.86	0.62	Q8TD91-2	MAGEC3
177.1	Signal recognition particle 14 kD	1.23E+07	2.29E+07	1.86E+00	1.86E+00	1.86	0.62	P37108	SRP14
711.1	Adenosine kinase	1.66E+06	3.05E+06	1.84E+00	1.84E+00	1.84	0.61	P55263	ADK
248.1	Serine/threonine-protein phosp	8.70E+05	1.59E+06	1.83E+00	1.83E+00	1.83	0.60	P30153	PPP2R1A
402.1	26S proteasome non-ATPase re	1.03E+06	1.87E+06	1.81E+00	1.81E+00	1.81	0.60	O43242	PSMD3
990.1	Programmed cell death protein	2.89E+04	5.19E+04	1.79E+00	1.79E+00	1.79	0.58	Q9BRP1	PDCD2L
979.1	Talin-2	1.33E+04	2.38E+04	1.78E+00	1.78E+00	1.78	0.58	Q9Y4G6	TLN2
449.1	N-alpha-acetyltransferase 15, N	1.65E+05	2.90E+05	1.76E+00	1.76E+00	1.76	0.57	Q9BXJ9	NAA15
1038.1	Ras-like protein family member	3.44E+06	6.04E+06	1.76E+00	1.76E+00	1.76	0.56	Q6T310	RASL11A
748.1	Alpha-endosulfine	2.58E+05	4.51E+05	1.75E+00	1.75E+00	1.75	0.56	Q5T5H1	ENSA
566.1	Diacylglycerol kinase zeta	1.10E+06	1.92E+06	1.74E+00	1.74E+00	1.74	0.56	F5H033	DGKZ
914.1	Hepatoma-derived growth fact	9.64E+04	1.67E+05	1.73E+00	1.73E+00	1.73	0.55	Q7Z4V5	HDGFRP2

631.1	Prostaglandin E synthase 3	1.73E+05	2.99E+05	1.73E+00	1.73E+00	1.73	0.55	Q15185	PTGES3
604.1	Isoform 3 of Chitinase domain-c	2.94E+06	5.07E+06	1.72E+00	1.72E+00	1.72	0.54	Q9BWS9-3	CHID1
698.1	Isoform 2 of Glycogen synthase	8.70E+05	1.50E+06	1.72E+00	1.72E+00	1.72	0.54	P49841-2	GSK3B
805.1	Transcription factor BTF3 homo	3.56E+05	6.13E+05	1.72E+00	1.72E+00	1.72	0.54	Q96K17	BTF3L4
776.1	Vinculin	3.46E+05	5.93E+05	1.72E+00	1.72E+00	1.72	0.54	P18206	VCL
747.1	Proteasome subunit beta type-	4.50E+05	7.69E+05	1.71E+00	1.71E+00	1.71	0.54	Q99436	PSMB7
1143.1	Alpha-galactosidase A	1.13E+05	1.93E+05	1.70E+00	1.70E+00	1.70	0.53	P06280	GLA
1107.1	Integrator complex subunit 12	2.00E+05	3.41E+05	1.70E+00	1.70E+00	1.70	0.53	Q96CB8	INTS12
218.1	Serum albumin	2.09E+07	3.56E+07	1.70E+00	1.70E+00	1.70	0.53	P02768	ALB
471.1	Translationally-controlled tumo	8.36E+05	1.42E+06	1.70E+00	1.70E+00	1.70	0.53	Q5W0H4	TPT1
681.1	Trafficking protein particle comp	1.81E+05	3.00E+05	1.66E+00	1.66E+00	1.66	0.51	O43617	TRAPPC3
28.2	Isocitrate dehydrogenase [NAD	2.90E+06	4.75E+06	1.64E+00	1.64E+00	1.64	0.49	O75874	IDH1
1242.1	Protein cTAGE-2	4.75E+05	7.73E+05	1.63E+00	1.63E+00	1.63	0.49	Q96RT6	CTAGE1
92.1	Transaldolase	5.42E+06	8.80E+06	1.62E+00	1.62E+00	1.62	0.48	P37837	TALDO1
1284.1	Rho GTPase-activating protein 1	4.30E+05	6.78E+05	1.58E+00	1.58E+00	1.58	0.46	Q6P4F7	ARHGAP11A
253.1	Protein transport protein Sec24	3.89E+06	6.11E+06	1.57E+00	1.57E+00	1.57	0.45	P53992	SEC24C
88.4	14-3-3 protein theta	3.32E+05	5.20E+05	1.57E+00	1.57E+00	1.57	0.45	P27348	YWHAQ
716.1	S-formylglutathione hydrolase	2.96E+06	4.64E+06	1.57E+00	1.57E+00	1.57	0.45	P10768	ESD
533.1	Vesicle-fusing ATPase	1.51E+06	2.35E+06	1.56E+00	1.56E+00	1.56	0.44	P46459	NSF
888.1	Peptidyl-prolyl cis-trans isomera	3.92E+04	6.11E+04	1.56E+00	1.56E+00	1.56	0.44	Q9Y3C6	PPIL1
38.1	Putative elongation factor 1-alp	3.46E+06	5.38E+06	1.56E+00	1.56E+00	1.56	0.44	Q5VTE0	EEF1A1P5
40.1	T-complex protein 1 subunit gar	1.08E+07	1.68E+07	1.55E+00	1.55E+00	1.55	0.44	P49368	CCT3
608.1	Replication protein A 70 kDa DN	2.70E+05	4.16E+05	1.54E+00	1.54E+00	1.54	0.43	P27694	RPA1
286.1	Eukaryotic translation initiation	6.64E+06	1.02E+07	1.54E+00	1.54E+00	1.54	0.43	I3L504	EIF5A
303.1	WD repeat-containing protein 1	2.08E+06	3.16E+06	1.52E+00	1.52E+00	1.52	0.42	O75083	WDR1
20.2	Heat shock protein HSP 90-beta	1.64E+07	2.47E+07	1.51E+00	1.51E+00	1.51	0.41	P08238	HSP90AB1
477.1	Eukaryotic peptide chain releas	8.02E+05	1.20E+06	1.50E+00	1.50E+00	1.50	0.40	P15170	GSPT1
1554.1	Isoform 3 of PR domain zinc fing	9.27E+04	1.38E+05	1.49E+00	1.49E+00	1.49	0.40	Q9HAZ2-3	PRDM16
433.1	Coatomer subunit gamma-2	1.23E+06	1.83E+06	1.48E+00	1.48E+00	1.48	0.39	Q9UBF2	COPG2
1530.1	Zinc finger and BTB domain-con	1.56E+05	2.28E+05	1.46E+00	1.46E+00	1.46	0.38	O95625	ZBTB11
1155.1	Microtubule-associated protein	1.22E+05	1.79E+05	1.46E+00	1.46E+00	1.46	0.38	Q66K74	MAP1S
969.1	Protein transport protein Sec31	3.16E+05	4.63E+05	1.46E+00	1.46E+00	1.46	0.38	Q9NQW1	SEC31B
221.1	Calmodulin	8.89E+06	1.30E+07	1.46E+00	1.46E+00	1.46	0.38	E7EMB3	CALM2
157.1	Ankyrin-3	4.77E+06	6.95E+06	1.46E+00	1.46E+00	1.46	0.38	Q12955	ANK3
123.1	T-complex protein 1 subunit eta	6.95E+06	1.01E+07	1.45E+00	1.45E+00	1.45	0.37	Q99832	CCT7

520.1	Farnesyl pyrophosphate synthas	1.51E+05	2.18E+05	1.45E+00	1.45E+00	1.45	0.37	P14324	FDPS
8.1	Heat shock cognate 71 kDa prot	1.09E+08	1.58E+08	1.45E+00	1.45E+00	1.45	0.37	P11142	HSPA8
374.1	Coatomer subunit zeta-1	1.28E+06	1.85E+06	1.44E+00	1.44E+00	1.44	0.37	F8VVA7	COPZ1
1287.1	Zinc finger ZZ-type and EF-hand	2.10E+05	3.02E+05	1.44E+00	1.44E+00	1.44	0.36	O43149	ZZEF1
679.1	UMP-CMP kinase	1.25E+06	1.80E+06	1.44E+00	1.44E+00	1.44	0.36	P30085	CMPK1
3.1	Keratin, type II cytoskeletal 8	5.01E+08	7.18E+08	1.43E+00	1.43E+00	1.43	0.36	P05787	KRT8
677.1	Keratin, type II cuticular Hb1	3.31E+05	4.72E+05	1.43E+00	1.43E+00	1.43	0.36	Q14533	KRT81
88.2	14-3-3 protein beta/alpha	1.16E+06	1.65E+06	1.42E+00	1.42E+00	1.42	0.35	P31946	YWHAB
368.1	Lipopolysaccharide-responsive	1.04E+06	1.46E+06	1.40E+00	1.40E+00	1.40	0.34	F5H1X8	LRBA
116.1	Matrin-3	5.49E+06	7.57E+06	1.38E+00	1.38E+00	1.38	0.32	A8MXP9	MATR3
2722.1	Inhibitor of nuclear factor kapp	4.91E+05	6.77E+05	1.38E+00	1.38E+00	1.38	0.32	O14920	IKBKB
276.1	Protein SET	1.61E+07	2.20E+07	1.37E+00	1.37E+00	1.37	0.31	Q01105	SET
20.3	Endoplasmin	1.32E+07	1.81E+07	1.37E+00	1.37E+00	1.37	0.31	P14625	HSP90B1
25.1	Fatty acid synthase	1.14E+07	1.56E+07	1.37E+00	1.37E+00	1.37	0.31	P49327	FASN
30.1	Triosephosphate isomerase	3.32E+07	4.52E+07	1.36E+00	1.36E+00	1.36	0.31	P60174	TPI1
1445.1	FERM domain-containing protei	1.96E+05	2.67E+05	1.36E+00	1.36E+00	1.36	0.31	Q9Y2L6	FRMD4B
197.1	RuvB-like 2	1.58E+06	2.14E+06	1.36E+00	1.36E+00	1.36	0.31	Q9Y230	RUVBL2
24.2	Tubulin alpha-4A chain	2.07E+06	2.80E+06	1.35E+00	1.35E+00	1.35	0.30	P68366	TUBA4A
949.1	KIAA0423, isoform CRA_a	1.43E+06	1.92E+06	1.35E+00	1.35E+00	1.35	0.30	G3XAE9	FAM179B
505.1	26S protease regulatory subunit	6.24E+05	8.38E+05	1.34E+00	1.34E+00	1.34	0.30	P62333	PSMC6
53.1	T-complex protein 1 subunit zet	1.40E+07	1.84E+07	1.32E+00	1.32E+00	1.32	0.28	P40227	CCT6A
38.2	Elongation factor 1-alpha 2	2.86E+06	3.76E+06	1.31E+00	1.31E+00	1.31	0.27	Q05639	EEF1A2
701.1	Xin actin-binding repeat-contai	1.35E+05	1.78E+05	1.31E+00	1.31E+00	1.31	0.27	J3KNB1	XIRP2
62.1	Peptidyl-prolyl cis-trans isomer	9.59E+07	1.26E+08	1.31E+00	1.31E+00	1.31	0.27	P62937	PPIA
183.1	Phosphoserine aminotransferas	2.40E+06	3.14E+06	1.31E+00	1.31E+00	1.31	0.27	Q9Y617	PSAT1
80.1	Transcription intermediary fact	1.16E+07	1.52E+07	1.31E+00	1.31E+00	1.31	0.27	Q13263	TRIM28
255.1	Coatomer subunit gamma-1	2.29E+06	3.00E+06	1.31E+00	1.31E+00	1.31	0.27	Q9Y678	COPG1
571.1	Symplekin	3.80E+05	4.96E+05	1.30E+00	1.30E+00	1.30	0.27	Q92797	SYMPK
508.1	DnaJ homolog subfamily C mem	2.08E+06	2.68E+06	1.29E+00	1.29E+00	1.29	0.25	O75937	DNAJC8
823.1	Isoform Long of Ubiquitin fusio	4.00E+05	5.13E+05	1.28E+00	1.28E+00	1.28	0.25	Q92890-1	UFD1L
760.1	Protein FAM50A	1.39E+05	1.72E+05	1.24E+00	1.24E+00	1.24	0.22	Q14320	FAM50A
70.1	Alanine--tRNA ligase, cytoplasm	4.25E+06	5.25E+06	1.24E+00	1.24E+00	1.24	0.21	P49588	AARS
1045.1	Isoform 3 of LIM and calponin h	4.55E+04	5.61E+04	1.23E+00	1.23E+00	1.23	0.21	Q9UPQ0-3	LIMCH1
81.1	Isoform 2 of Glucose-6-phospha	1.45E+07	1.77E+07	1.22E+00	1.22E+00	1.22	0.20	P06744-2	GPI
181.1	Isoform 2 of Multifunctional pr	5.42E+06	6.56E+06	1.21E+00	1.21E+00	1.21	0.19	P22234-2	PAICS

612.1	Pterin-4-alpha-carbinolamine de	7.38E+05	8.88E+05	1.20E+00	1.20E+00	1.20	0.18	P61457	PCBD1
120.1	Profilin-1	1.77E+07	2.12E+07	1.20E+00	1.20E+00	1.20	0.18	P07737	PFN1
498.1	Activator of 90 kDa heat shock p	8.22E+05	9.76E+05	1.19E+00	1.19E+00	1.19	0.17	O95433	AHSA1
930.1	Glycine dehydrogenase [decarbo	1.59E+05	1.88E+05	1.18E+00	1.18E+00	1.18	0.17	P23378	GLDC
635.1	Myosin regulatory light chain 12	1.60E+06	1.89E+06	1.18E+00	1.18E+00	1.18	0.17	J3QRS3	MYL12A
49.1	T-complex protein 1 subunit eps	2.00E+07	2.36E+07	1.18E+00	1.18E+00	1.18	0.16	P48643	CCT5
815.1	E3 ubiquitin-protein ligase SMU	1.72E+05	2.02E+05	1.18E+00	1.18E+00	1.18	0.16	Q9HCE7	SMURF1
67.1	Protein disulfide-isomerase	9.76E+06	1.14E+07	1.17E+00	1.17E+00	1.17	0.16	P07237	P4HB
1301.1	Glycogen [starch] synthase, mus	7.04E+04	8.09E+04	1.15E+00	1.15E+00	1.15	0.14	P13807	GYS1
195.1	Hepatoma-derived growth facto	7.98E+06	9.16E+06	1.15E+00	1.15E+00	1.15	0.14	P51858	HDGF
85.1	14-3-3 protein epsilon	3.29E+07	3.77E+07	1.15E+00	1.15E+00	1.15	0.14	P62258	YWHAE
726.1	Signal transducer and activator	8.35E+05	9.58E+05	1.15E+00	1.15E+00	1.15	0.14	P40763	STAT3
489.1	Proteasome subunit alpha type-	1.42E+06	1.62E+06	1.14E+00	1.14E+00	1.14	0.14	P25789	PSMA4
199.1	Isoform 2 of DBIRD complex sub	3.53E+06	4.01E+06	1.14E+00	1.14E+00	1.14	0.13	Q8N163-2	KIAA1967
91.1	Asparagine--tRNA ligase, cytopla	9.24E+06	1.05E+07	1.14E+00	1.14E+00	1.14	0.13	O43776	NARS
230.1	Splicing factor 3B subunit 2	3.60E+06	4.07E+06	1.13E+00	1.13E+00	1.13	0.12	Q13435	SF3B2
626.1	Capping protein (Actin filament)	3.70E+05	4.15E+05	1.12E+00	1.12E+00	1.12	0.11	B1AK88	CAPZB
339.1	DNA replication licensing factor	1.05E+06	1.17E+06	1.11E+00	1.11E+00	1.11	0.11	P33991	MCM4
59.1	Isoform 2 of Neutral alpha-gluco	1.46E+07	1.60E+07	1.10E+00	1.10E+00	1.10	0.09	Q14697-2	GANAB
296.1	Programmed cell death protein	3.11E+06	3.42E+06	1.10E+00	1.10E+00	1.10	0.09	O14737	PDCD5
738.1	Transcription elongation factor	1.92E+05	2.10E+05	1.09E+00	1.09E+00	1.09	0.09	Q5H9L2	TCEAL5
270.1	Isoform 2 of AP-1 complex subu	7.26E+05	7.85E+05	1.08E+00	1.08E+00	1.08	0.08	Q9Y6Q5-2	AP1M2
1075.1	Serine/threonine-protein kinase	8.00E+04	8.63E+04	1.08E+00	1.08E+00	1.08	0.08	I3L0C1	SMG1
258.1	14-3-3 protein eta	9.22E+06	9.91E+06	1.07E+00	1.07E+00	1.07	0.07	Q04917	YWHAH
822.1	Kinesin-like protein KIF7	2.75E+05	2.93E+05	1.07E+00	1.07E+00	1.07	0.06	Q2M1P5	KIF7
519.1	26S proteasome non-ATPase reg	1.86E+06	1.98E+06	1.06E+00	1.06E+00	1.06	0.06	C9IZE4	PSMD6
312.1	14-3-3 protein sigma	9.00E+06	9.57E+06	1.06E+00	1.06E+00	1.06	0.06	P31947	SFN
78.1	Creatine kinase B-type	3.33E+07	3.52E+07	1.06E+00	1.06E+00	1.06	0.06	P12277	CKB
443.1	E3 ubiquitin-protein ligase HUW	8.39E+05	8.82E+05	1.05E+00	1.05E+00	1.05	0.05	Q7Z6Z7	HUWE1
1198.1	Isoform 7 of Granulocyte-macro	2.36E+05	2.47E+05	1.05E+00	1.05E+00	1.05	0.05	P15509-7	CSF2RA
322.1	Calreticulin	2.00E+06	2.09E+06	1.04E+00	1.04E+00	1.04	0.04	P27797	CALR
655.1	Selenocysteine lyase	3.72E+05	3.88E+05	1.04E+00	1.04E+00	1.04	0.04	Q96I15	SCLY
167.1	26S proteasome non-ATPase reg	5.42E+06	5.57E+06	1.03E+00	1.03E+00	1.03	0.03	Q5VWC4	PSMD4
4.1	Isoform 4 of Acetyl-CoA carboxy	4.50E+07	4.60E+07	1.02E+00	1.02E+00	1.02	0.02	Q13085-4	ACACA
616.1	Sister chromatid cohesion prote	4.29E+05	4.38E+05	1.02E+00	1.02E+00	1.02	0.02	Q9NTI5	PDS5B

37.1	Cullin-associated NEDD8-dissoci	8.80E+06	8.96E+06	1.02E+00	1.02E+00	1.02	0.02	Q86VP6	CAND1
109.1	Hypoxia up-regulated protein 1	8.33E+06	8.43E+06	1.01E+00	1.01E+00	1.01	0.01	Q9Y4L1	HYOU1
1812.1	Serine protease 23	1.24E+05	1.25E+05	1.01E+00	1.01E+00	1.01	0.01	O95084	PRSS23
852.1	SUMO-activating enzyme subun	2.38E+05	2.38E+05	1.00E+00	1.00E+00	1.00	0.00	Q9UBE0	SAE1
527.1	Isoform 2 of 26S proteasome nc	1.06E+06	1.06E+06	9.99E-01	-1.00E+00	-1.00	0.00	O00231-2	PSMD11
338.1	Protein S100-A11	3.21E+06	3.21E+06	9.98E-01	-1.00E+00	-1.00	0.00	P31949	S100A11
577.1	NAD(P)H-hydrate epimerase	3.58E+05	3.56E+05	9.95E-01	-1.01E+00	-1.01	-0.01	Q8NCW5	APOA1BP
431.1	NEDD8-conjugating enzyme Ub	6.74E+05	6.64E+05	9.85E-01	-1.02E+00	-1.02	-0.02	P61081	UBE2M
118.1	Neuroblast differentiation-asso	3.72E+06	3.66E+06	9.84E-01	-1.02E+00	-1.02	-0.02	Q09666	AHNAK
372.1	Nucleosome assembly protein 1	2.61E+06	2.52E+06	9.66E-01	-1.04E+00	-1.04	-0.03	P55209	NAP1L1
141.1	Cofilin-1	1.48E+07	1.41E+07	9.55E-01	-1.05E+00	-1.05	-0.05	E9PK25	CFL1
50.2	Isoform 2 of Eukaryotic initiatio	1.16E+06	1.11E+06	9.55E-01	-1.05E+00	-1.05	-0.05	Q14240-2	EIF4A2
247.1	4-trimethylaminobutyraldehyde	5.01E+06	4.78E+06	9.53E-01	-1.05E+00	-1.05	-0.05	P49189	ALDH9A1
728.1	Platelet-activating factor acetyl	3.87E+05	3.68E+05	9.50E-01	-1.05E+00	-1.05	-0.05	Q15102	PAFAH1B3
557.1	Proteasome subunit alpha type-	9.22E+05	8.74E+05	9.48E-01	-1.05E+00	-1.05	-0.05	P28066	PSMA5
182.1	Carbonyl reductase [NADPH] 1	5.38E+06	5.09E+06	9.46E-01	-1.06E+00	-1.06	-0.06	P16152	CBR1
435.1	Androgen receptor	1.11E+06	1.05E+06	9.44E-01	-1.06E+00	-1.06	-0.06	P10275	AR
1079.1	Leucine-rich repeat-containing	1.45E+05	1.35E+05	9.34E-01	-1.07E+00	-1.07	-0.07	Q9H9A6	LRRC40
269.1	Protein disulfide-isomerase A4	1.02E+06	9.51E+05	9.31E-01	-1.07E+00	-1.07	-0.07	P13667	PDIA4
584.1	Isoform 3 of NADPH:adrenodoxi	1.14E+05	1.06E+05	9.28E-01	-1.08E+00	-1.08	-0.07	P22570-3	FDXR
8.3	Heat shock 70 kDa protein 1A/1	6.59E+05	6.10E+05	9.25E-01	-1.08E+00	-1.08	-0.08	P08107	HSPA1A
607.1	Dynein light chain 1, cytoplasmi	1.58E+06	1.45E+06	9.19E-01	-1.09E+00	-1.09	-0.08	P63167	DYNLL1
1237.1	WASH complex subunit 7	3.93E+03	3.60E+03	9.15E-01	-1.09E+00	-1.09	-0.09	Q2M389	KIAA1033
1088.1	Drebrin-like protein	2.08E+04	1.90E+04	9.12E-01	-1.10E+00	-1.10	-0.09	Q9UJU6	DBNL
332.1	cAMP-dependent protein kinase	5.77E+05	5.26E+05	9.11E-01	-1.10E+00	-1.10	-0.09	P13861	PRKAR2A
76.3	Heterogeneous nuclear ribonuc	7.07E+06	6.42E+06	9.08E-01	-1.10E+00	-1.10	-0.10	P52597	HNRNPF
32.1	T-complex protein 1 subunit bet	3.08E+07	2.76E+07	8.95E-01	-1.12E+00	-1.12	-0.11	P78371	CCT2
8.2	78 kDa glucose-regulated protei	2.19E+07	1.96E+07	8.93E-01	-1.12E+00	-1.12	-0.11	P11021	HSPA5
1178.1	ATP synthase subunit b, mitoch	6.39E+05	5.70E+05	8.92E-01	-1.12E+00	-1.12	-0.11	P24539	ATP5F1
460.1	Tumor susceptibility gene 101 p	1.94E+06	1.72E+06	8.86E-01	-1.13E+00	-1.13	-0.12	Q99816	TSG101
365.1	Thioredoxin domain-containing	1.03E+06	9.13E+05	8.85E-01	-1.13E+00	-1.13	-0.12	Q8NBS9	TXNDC5
414.1	Phosphoribosyl pyrophosphate	9.55E+05	8.43E+05	8.82E-01	-1.13E+00	-1.13	-0.13	O60256	PRPSAP2
224.1	Protein DJ-1	7.34E+06	6.44E+06	8.77E-01	-1.14E+00	-1.14	-0.13	Q99497	PARK7
496.1	NSFL1 cofactor p47	3.70E+05	3.24E+05	8.76E-01	-1.14E+00	-1.14	-0.13	J3QK90	NSFL1C
262.1	Sialic acid synthase	8.98E+06	7.86E+06	8.76E-01	-1.14E+00	-1.14	-0.13	Q9NR45	NANS

35.1	Phosphoglycerate kinase 1	4.73E+07	4.14E+07	8.75E-01	-1.14E+00	-1.14	-0.13	P00558	PGK1
271.1	Parathymosin	1.61E+07	1.38E+07	8.58E-01	-1.16E+00	-1.16	-0.15	P20962	PTMS
1450.1	TBC1 domain family member 9	1.28E+05	1.09E+05	8.49E-01	-1.18E+00	-1.18	-0.16	Q6ZT07	TBC1D9
583.1	UPF0468 protein C16orf80	2.80E+04	2.35E+04	8.39E-01	-1.19E+00	-1.19	-0.18	Q9Y6A4	C16orf80
492.1	Dynactin subunit 1	1.49E+06	1.22E+06	8.21E-01	-1.22E+00	-1.22	-0.20	Q14203	DCTN1
907.1	DNA topoisomerase I, mitochon	6.39E+05	5.22E+05	8.17E-01	-1.22E+00	-1.22	-0.20	Q969P6	TOP1MT
2111.1	Flavin reductase (NADPH)	4.07E+04	3.29E+04	8.08E-01	-1.24E+00	-1.24	-0.21	P30043	BLVRB
20.1	Isoform 2 of Heat shock protein	3.47E+07	2.76E+07	7.96E-01	-1.26E+00	-1.26	-0.23	P07900-2	HSP90AA1
540.1	RNA-binding protein 12	3.39E+05	2.68E+05	7.91E-01	-1.26E+00	-1.26	-0.23	Q9NTZ6	RBM12
633.1	Isoform 2 of Histone H2A.J	1.07E+06	8.46E+05	7.89E-01	-1.27E+00	-1.27	-0.24	Q9BTM1-2	H2AFJ
401.1	Isoform 2 of Casein kinase I isof	1.25E+06	9.87E+05	7.87E-01	-1.27E+00	-1.27	-0.24	P48729-2	CSNK1A1
146.1	Isoform 2 of Programmed cell d	4.07E+06	3.20E+06	7.85E-01	-1.27E+00	-1.27	-0.24	Q8WUM4-	PDCD6IP
723.1	60S ribosomal protein L39	6.43E+06	5.05E+06	7.85E-01	-1.27E+00	-1.27	-0.24	P62891	RPL39
1015.1	Engulfment and cell motility pr	9.07E+05	7.10E+05	7.83E-01	-1.28E+00	-1.28	-0.24	Q92556	ELMO1
692.1	HEAT repeat-containing protein	2.45E+05	1.91E+05	7.81E-01	-1.28E+00	-1.28	-0.25	Q9P2D3	HEATR5B
811.1	Ran-binding protein 3	4.51E+05	3.50E+05	7.76E-01	-1.29E+00	-1.29	-0.25	Q9H6Z4	RANBP3
686.1	Charged multivesicular body pr	1.62E+06	1.24E+06	7.67E-01	-1.30E+00	-1.30	-0.27	Q7LBR1	CHMP1B
44.1	Peroxiredoxin-1	2.35E+07	1.79E+07	7.63E-01	-1.31E+00	-1.31	-0.27	Q06830	PRDX1
743.1	HBS1-like protein	4.85E+05	3.68E+05	7.58E-01	-1.32E+00	-1.32	-0.28	Q9Y450	HBS1L
133.1	Peroxiredoxin-6	2.83E+07	2.14E+07	7.56E-01	-1.32E+00	-1.32	-0.28	P30041	PRDX6
672.1	Protein NOXP20	3.06E+05	2.31E+05	7.54E-01	-1.33E+00	-1.33	-0.28	Q8IWE2	FAM114A1
298.1	Adenylate kinase 1	1.68E+06	1.26E+06	7.51E-01	-1.33E+00	-1.33	-0.29	Q5T9B7	AK1
50.1	Eukaryotic initiation factor 4A-I	1.30E+07	9.69E+06	7.43E-01	-1.35E+00	-1.35	-0.30	P60842	EIF4A1
52.1	T-complex protein 1 subunit alp	2.36E+07	1.75E+07	7.43E-01	-1.35E+00	-1.35	-0.30	P17987	TCP1
128.1	Transketolase	8.60E+06	6.31E+06	7.33E-01	-1.36E+00	-1.36	-0.31	P29401	TKT
973.1	Dynein heavy chain 17, axonem	9.42E+04	6.87E+04	7.29E-01	-1.37E+00	-1.37	-0.32	Q9UFH2	DNAH17
948.1	Nuclear export mediator factor	9.29E+04	6.77E+04	7.29E-01	-1.37E+00	-1.37	-0.32	O60524	NEMF
264.2	Chromobox protein homolog 1	1.13E+05	8.10E+04	7.15E-01	-1.40E+00	-1.40	-0.33	P83916	CBX1
208.1	Protein transport protein Sec31	3.72E+06	2.63E+06	7.07E-01	-1.41E+00	-1.41	-0.35	D6REX3	SEC31A
257.1	RuvB-like 1	1.02E+06	7.11E+05	6.96E-01	-1.44E+00	-1.44	-0.36	Q9Y265	RUVBL1
1190.1	NADP-dependent oxidoreductas	6.73E+05	4.67E+05	6.94E-01	-1.44E+00	-1.44	-0.37	Q6NXP6	NOXRED1
468.1	Endonuclease domain-containin	2.15E+05	1.49E+05	6.92E-01	-1.45E+00	-1.45	-0.37	O94919	ENDOD1
658.1	Isoform 2 of F-box only protein	3.90E+05	2.68E+05	6.87E-01	-1.46E+00	-1.46	-0.38	Q8NFZ0-2	FBXO18
9.1	Tubulin beta-4B chain	4.64E+07	3.15E+07	6.79E-01	-1.47E+00	-1.47	-0.39	P68371	TUBB4B
964.1	G-protein coupled receptor 98	2.45E+05	1.66E+05	6.78E-01	-1.47E+00	-1.47	-0.39	Q8WXG9	GPR98

1215.1	Nuclear RNA export factor 1	9.43E+04	6.39E+04	6.77E-01	-1.48E+00	-1.48	-0.39	Q9UBU9	NXF1
1270.1	Centriolar coiled-coil protein of	7.87E+05	5.30E+05	6.74E-01	-1.48E+00	-1.48	-0.39	O43303	CCP110
524.1	LanC-like protein 1	3.53E+05	2.37E+05	6.72E-01	-1.49E+00	-1.49	-0.40	O43813	LANCL1
250.1	Tumor protein D52	9.86E+05	6.62E+05	6.72E-01	-1.49E+00	-1.49	-0.40	F5H0B0	TPD52
581.1	Zinc finger homeobox protein 3	4.67E+05	3.10E+05	6.64E-01	-1.51E+00	-1.51	-0.41	Q15911	ZFHX3
574.1	Zinc finger CCCH domain-contai	1.04E+05	6.91E+04	6.64E-01	-1.51E+00	-1.51	-0.41	E7ERS3	ZC3H18
1097.1	Dynein assembly factor 1, axone	1.26E+05	8.32E+04	6.58E-01	-1.52E+00	-1.52	-0.42	Q8NEP3	DNAAF1
1292.1	Isoform 3 of AT-rich interactive	1.05E+05	6.81E+04	6.48E-01	-1.54E+00	-1.54	-0.43	Q8NFD5-3	ARID1B
1.2	Epiplakin	6.89E+07	4.45E+07	6.45E-01	-1.55E+00	-1.55	-0.44	P58107	EPPK1
596.1	Tyrosine--tRNA ligase, cytoplasn	7.27E+05	4.67E+05	6.42E-01	-1.56E+00	-1.56	-0.44	P54577	YARS
1146.1	Dynein heavy chain 8, axonemal	1.17E+05	7.46E+04	6.36E-01	-1.57E+00	-1.57	-0.45	H0Y7V4	DNAH8
851.1	Ubiquitin carboxyl-terminal hyd	5.07E+05	3.21E+05	6.34E-01	-1.58E+00	-1.58	-0.46	Q70CQ2	USP34
1065.1	Nuclear pore membrane glycop	5.90E+05	3.73E+05	6.32E-01	-1.58E+00	-1.58	-0.46	Q5VU65	NUP210L
469.1	Putative pre-mRNA-splicing fact	1.07E+06	6.69E+05	6.24E-01	-1.60E+00	-1.60	-0.47	O43143	DHX15
1078.1	Isoform KvB1.2 of Voltage-gate	3.59E+05	2.24E+05	6.24E-01	-1.60E+00	-1.60	-0.47	Q14722-3	KCNAB1
606.1	Haloacid dehalogenase-like hyd	3.55E+06	2.20E+06	6.20E-01	-1.61E+00	-1.61	-0.48	Q9H0R4	HDHD2
1025.1	Putative rhophilin-2-like protein	9.67E+04	5.88E+04	6.08E-01	-1.64E+00	-1.64	-0.50	A8MT19	RHPN2P1
101.1	Myosin light polypeptide 6	1.58E+07	9.59E+06	6.08E-01	-1.64E+00	-1.64	-0.50	B7Z6Z4	MYL6
1191.1	Synaptic vesicle glycoprotein 2B	3.78E+05	2.25E+05	5.95E-01	-1.68E+00	-1.68	-0.52	Q7L1I2	SV2B
462.1	N-alpha-acetyltransferase 50	1.04E+06	6.17E+05	5.93E-01	-1.69E+00	-1.69	-0.52	Q9GZZ1	NAA50
420.1	Long-chain-fatty-acid--CoA ligas	1.03E+05	6.06E+04	5.88E-01	-1.70E+00	-1.70	-0.53	P33121	ACSL1
1124.1	Adenomatous polyposis coli pro	4.91E+05	2.83E+05	5.76E-01	-1.74E+00	-1.74	-0.55	O95996	APC2
541.1	Protein HID1	8.54E+05	4.90E+05	5.74E-01	-1.74E+00	-1.74	-0.56	Q8IV36	HID1
88.3	14-3-3 protein gamma	6.54E+06	3.73E+06	5.70E-01	-1.75E+00	-1.75	-0.56	P61981	YWHAG
135.1	Sorbitol dehydrogenase	5.80E+06	3.28E+06	5.65E-01	-1.77E+00	-1.77	-0.57	Q00796	SORD
734.1	Vacuolar protein sorting-associa	1.01E+06	5.64E+05	5.58E-01	-1.79E+00	-1.79	-0.58	C9JJN9	VPS8
898.1	Interferon-induced very large G	1.27E+05	7.06E+04	5.54E-01	-1.80E+00	-1.80	-0.59	Q7Z2Y8	GVINP1
986.1	UPF0693 protein C10orf32	1.12E+04	6.14E+03	5.47E-01	-1.83E+00	-1.83	-0.60	Q96B45	C10orf32
794.1	Hyaluronan synthase 1	5.66E+05	3.08E+05	5.44E-01	-1.84E+00	-1.84	-0.61	Q92839	HAS1
328.1	DnaJ homolog subfamily A mem	1.13E+06	6.02E+05	5.32E-01	-1.88E+00	-1.88	-0.63	P31689	DNAJA1
685.1	Tektin-1	3.08E+04	1.63E+04	5.29E-01	-1.89E+00	-1.89	-0.64	Q969V4	TEKT1
304.1	Phosphoglycerate mutase 1	4.62E+06	2.43E+06	5.26E-01	-1.90E+00	-1.90	-0.64	P18669	PGAM1
234.1	C-1-tetrahydrofolate synthase,	3.70E+06	1.93E+06	5.22E-01	-1.92E+00	-1.92	-0.65	F5H2F4	MTHFD1
1455.1	Zinc finger CCCH domain-contai	2.59E+05	1.33E+05	5.14E-01	-1.95E+00	-1.95	-0.67	Q5T200	ZC3H13
380.1	Isoform 2 of Spectrin alpha chai	1.27E+06	6.45E+05	5.06E-01	-1.97E+00	-1.97	-0.68	Q13813-2	SPTAN1

145.1	Protein transport protein Sec16.	6.59E+06	3.32E+06	5.04E-01	-1.99E+00	-1.99	-0.69	J3KNL6	SEC16A
653.1	Acidic leucine-rich nuclear phos	1.15E+06	5.80E+05	5.03E-01	-1.99E+00	-1.99	-0.69	P39687	ANP32A
441.1	N(G),N(G)-dimethylarginine dim	1.86E+06	9.36E+05	5.03E-01	-1.99E+00	-1.99	-0.69	O94760	DDAH1
757.1	Protein LOC100653515	4.04E+05	1.98E+05	4.90E-01	-2.04E+00	-2.04	-0.71	Q96MC4	DDC8
1578.1	Nucleolar complex protein 3 hoı	5.51E+04	2.69E+04	4.88E-01	-2.05E+00	-2.05	-0.72	A6NJZ9	NOC3L
310.1	PEST proteolytic signal-containi	1.58E+06	7.67E+05	4.86E-01	-2.06E+00	-2.06	-0.72	Q8WW12	PCNP
704.1	Obg-like ATPase 1	2.44E+05	1.18E+05	4.84E-01	-2.06E+00	-2.06	-0.73	J3KQ32	OLA1
185.1	Paternally-expressed gene 3 prc	3.20E+06	1.55E+06	4.84E-01	-2.07E+00	-2.07	-0.73	Q9GZU2	PEG3
1368.1	Integrin alpha-2	1.78E+05	8.55E+04	4.81E-01	-2.08E+00	-2.08	-0.73	P17301	ITGA2
41.1	Unconventional myosin-VI	1.42E+07	6.71E+06	4.74E-01	-2.11E+00	-2.11	-0.75	Q9UM54	MYO6
444.1	Putative ubiquitin-conjugating e	3.54E+05	1.67E+05	4.72E-01	-2.12E+00	-2.12	-0.75	Q5JXB2	UBE2NL
899.1	Sorting nexin-6	1.56E+05	7.30E+04	4.69E-01	-2.13E+00	-2.13	-0.76	Q9UNH7	SNX6
929.1	C-Myc-binding protein	1.03E+05	4.68E+04	4.54E-01	-2.20E+00	-2.20	-0.79	Q99417	MYCBP
1414.1	Isoform 2 of Nck-associated pro	1.90E+05	8.59E+04	4.52E-01	-2.21E+00	-2.21	-0.79	Q9Y2A7-2	NCKAP1
24.1	Tubulin alpha-1B chain	3.59E+07	1.61E+07	4.49E-01	-2.23E+00	-2.23	-0.80	P68363	TUBA1B
491.1	Isoform 3 of Shootin-1	6.91E+05	3.09E+05	4.47E-01	-2.23E+00	-2.23	-0.80	A0MZ66-3	KIAA1598
780.1	Isoform 3 of DCC-interacting prc	6.14E+05	2.70E+05	4.40E-01	-2.27E+00	-2.27	-0.82	Q8NEU8-3	APPL2
983.1	26S proteasome non-ATPase reg	1.48E+05	6.49E+04	4.40E-01	-2.27E+00	-2.27	-0.82	O00233	PSMD9
170.1	Glycogen phosphorylase, brain f	6.16E+06	2.69E+06	4.37E-01	-2.29E+00	-2.29	-0.83	P11216	PYGB
398.1	Ran-specific GTPase-activating p	5.97E+05	2.61E+05	4.37E-01	-2.29E+00	-2.29	-0.83	P43487	RANBP1
1298.1	Interferon-induced guanylate-bi	9.12E+05	3.95E+05	4.33E-01	-2.31E+00	-2.31	-0.84	P32456	GBP2
534.1	Transcriptional activator proteir	2.40E+05	1.03E+05	4.30E-01	-2.33E+00	-2.33	-0.84	Q96QR8	PURB
1789.1	Sorting nexin-2	1.62E+04	6.94E+03	4.29E-01	-2.33E+00	-2.33	-0.85	O60749	SNX2
293.1	Charged multivesicular body prc	3.95E+06	1.69E+06	4.28E-01	-2.34E+00	-2.34	-0.85	O43633	CHMP2A
465.1	6-phosphogluconate dehydroge	9.78E+05	4.03E+05	4.12E-01	-2.43E+00	-2.43	-0.89	P52209	PGD
503.1	Trifunctional purine biosyntheti	1.92E+06	7.85E+05	4.09E-01	-2.45E+00	-2.45	-0.89	P22102	GART
621.1	Alpha/beta hydrolase domain-c	3.51E+06	1.42E+06	4.05E-01	-2.47E+00	-2.47	-0.90	Q96IU4	ABHD14B
1387.1	Protocadherin beta-16	4.55E+05	1.82E+05	4.00E-01	-2.50E+00	-2.50	-0.92	Q9NRJ7	PCDHB16
762.1	Calcium-regulated heat stable p	6.21E+05	2.43E+05	3.91E-01	-2.55E+00	-2.55	-0.94	Q9Y2V2	CARHSP1
816.1	Isoform 4 of Myotubularin-relat	6.83E+05	2.60E+05	3.80E-01	-2.63E+00	-2.63	-0.97	O95248-4	SBF1
1363.1	Centrosomal protein of 152 kDa	1.24E+05	4.70E+04	3.78E-01	-2.65E+00	-2.65	-0.97	O94986	CEP152
765.1	Isoform 2 of Eukaryotic translati	2.99E+05	1.13E+05	3.78E-01	-2.65E+00	-2.65	-0.97	P06730-2	EIF4E
695.1	Proteasome subunit alpha type-	1.05E+06	3.91E+05	3.72E-01	-2.69E+00	-2.69	-0.99	P25787	PSMA2
403.1	FLYWCH family member 2	1.40E+06	5.09E+05	3.65E-01	-2.74E+00	-2.74	-1.01	I3L1Y9	FLYWCH2
792.1	Amyotrophic lateral sclerosis 2 (	3.44E+04	1.23E+04	3.58E-01	-2.79E+00	-2.79	-1.03	Q53TS8	ALS2CR11

458.1	Cellular nucleic acid-binding pro	4.39E+06	1.57E+06	3.58E-01	-2.79E+00	-2.79	-1.03	P62633	CNBP
525.1	Tumor protein D52-like 2	1.95E+06	6.91E+05	3.54E-01	-2.82E+00	-2.82	-1.04	O43399	TPD52L2
168.1	Nucleoside diphosphate kinase	3.28E+05	1.16E+05	3.54E-01	-2.82E+00	-2.82	-1.04	Q32Q12	NME1-NME2
719.1	Acidic leucine-rich nuclear phos	1.10E+06	3.88E+05	3.52E-01	-2.84E+00	-2.84	-1.04	Q92688	ANP32B
1182.1	Neuroendocrine convertase 1	2.99E+05	1.04E+05	3.48E-01	-2.88E+00	-2.88	-1.06	P29120	PCSK1
1265.1	Serine/threonine-protein kinase	6.57E+04	2.28E+04	3.47E-01	-2.88E+00	-2.88	-1.06	Q96GX5	MASTL
1177.1	28S ribosomal protein S7, mitoc	1.12E+05	3.83E+04	3.41E-01	-2.93E+00	-2.93	-1.08	J3QLS3	MRPS7
998.1	Neurogenic locus notch homolo	3.44E+06	1.17E+06	3.40E-01	-2.94E+00	-2.94	-1.08	Q04721	NOTCH2
1295.1	Egl nine homolog 1	1.64E+05	5.51E+04	3.36E-01	-2.97E+00	-2.97	-1.09	Q9GZT9	EGLN1
801.1	Nuclear transport factor 2	1.27E+06	4.07E+05	3.20E-01	-3.13E+00	-3.13	-1.14	P61970	NUTF2
64.1	Calpain-1 catalytic subunit	1.48E+07	4.71E+06	3.19E-01	-3.13E+00	-3.13	-1.14	P07384	CAPN1
504.1	Small ubiquitin-related modifier	7.44E+06	2.34E+06	3.14E-01	-3.18E+00	-3.18	-1.16	B4DUW4	SUMO3
682.1	Son of sevenless homolog 2	1.03E+06	3.24E+05	3.14E-01	-3.18E+00	-3.18	-1.16	Q07890	SOS2
215.1	Lactoylglutathione lyase	8.38E+06	2.62E+06	3.13E-01	-3.20E+00	-3.20	-1.16	Q04760	GLO1
461.1	ADP-ribosylation factor GTPase-	3.43E+05	1.05E+05	3.06E-01	-3.26E+00	-3.26	-1.18	Q9NP61	ARFGAP3
55.1	T-complex protein 1 subunit the	1.27E+07	3.87E+06	3.04E-01	-3.29E+00	-3.29	-1.19	P50990	CCT8
1484.1	Adenylate cyclase type 8	5.04E+05	1.53E+05	3.03E-01	-3.30E+00	-3.30	-1.19	P40145	ADCY8
512.1	Tryptophan--tRNA ligase, cytopl	1.07E+07	3.24E+06	3.02E-01	-3.31E+00	-3.31	-1.20	P23381	WARS
773.1	Neuroblastoma-amplified seque	1.03E+06	3.09E+05	3.00E-01	-3.34E+00	-3.34	-1.21	A2RRP1	NBAS
835.1	G antigen 1	2.46E+06	7.29E+05	2.97E-01	-3.37E+00	-3.37	-1.21	Q13065	GAGE1
554.1	Endoplasmic reticulum resident	4.80E+05	1.39E+05	2.89E-01	-3.45E+00	-3.45	-1.24	P30040	ERP29
448.1	PDZ and LIM domain protein 5	5.38E+05	1.55E+05	2.88E-01	-3.47E+00	-3.47	-1.24	Q96HC4	PDLIM5
543.1	Ras-related protein Rab-10	4.85E+05	1.39E+05	2.86E-01	-3.49E+00	-3.49	-1.25	P61026	RAB10
896.1	Acidic leucine-rich nuclear phos	7.27E+05	2.02E+05	2.78E-01	-3.60E+00	-3.60	-1.28	Q9BTT0	ANP32E
161.1	Ubiquitin-40S ribosomal protein	5.14E+07	1.42E+07	2.76E-01	-3.62E+00	-3.62	-1.29	P62979	RPS27A
396.1	Proteasome subunit alpha type	3.04E+05	8.40E+04	2.76E-01	-3.62E+00	-3.62	-1.29	G3V5Z7	PSMA6
3.2	Vimentin	2.12E+07	5.80E+06	2.73E-01	-3.66E+00	-3.66	-1.30	P08670	VIM
952.1	Lysine-specific demethylase 3B	1.17E+05	3.20E+04	2.73E-01	-3.66E+00	-3.66	-1.30	Q7LBC6	KDM3B
337.1	Phosphoglucomutase-2	2.20E+06	5.94E+05	2.70E-01	-3.71E+00	-3.71	-1.31	Q96G03	PGM2
601.1	Isoform 3 of Serine/threonine-p	1.14E+06	3.04E+05	2.66E-01	-3.76E+00	-3.76	-1.32	O00743-3	PPP6C
763.1	Intercellular adhesion molecule	4.75E+04	1.24E+04	2.61E-01	-3.83E+00	-3.83	-1.34	Q9UMF0	ICAM5
1102.1	Na(+)/H(+) exchange regulatory	2.51E+05	6.48E+04	2.58E-01	-3.87E+00	-3.87	-1.35	Q15599	SLC9A3R2
1502.1	WAP, Kazal, immunoglobulin, Ku	3.81E+05	9.85E+04	2.58E-01	-3.87E+00	-3.87	-1.35	Q8TEU8	WFIKKN2
379.1	Protein SEC13 homolog	6.21E+06	1.60E+06	2.58E-01	-3.88E+00	-3.88	-1.36	B4DXJ1	SEC13
421.1	F-actin-capping protein subunit	1.49E+06	3.77E+05	2.54E-01	-3.94E+00	-3.94	-1.37	P47755	CAPZA2

430.1	Bifunctional ATP-dependent dih	1.62E+06	4.10E+05	2.53E-01	-3.95E+00	-3.95	-1.37	Q3LXA3	DAK
1444.1	EF-hand calcium-binding domai	2.72E+05	6.89E+04	2.53E-01	-3.95E+00	-3.95	-1.37	A4FU69	EFCAB5
1106.1	Cytochrome b-c1 complex subu	3.08E+05	7.77E+04	2.52E-01	-3.97E+00	-3.97	-1.38	P31930	UQCRC1
880.1	1-phosphatidylinositol 4,5-bisph	1.46E+06	3.64E+05	2.50E-01	-4.00E+00	-4.00	-1.39	E2QRH8	PLCB4
14.1	Myosin-9	2.88E+07	6.88E+06	2.39E-01	-4.19E+00	-4.19	-1.43	P35579	MYH9
346.1	Gamma-glutamylcyclotransfera	1.27E+06	2.97E+05	2.33E-01	-4.29E+00	-4.29	-1.46	O75223	GGCT
376.1	Nuclear autoantigenic sperm pr	6.41E+04	1.48E+04	2.31E-01	-4.33E+00	-4.33	-1.47	P49321	NASP
290.1	Glycine--tRNA ligase	1.73E+06	3.90E+05	2.26E-01	-4.43E+00	-4.43	-1.49	P41250	GARS
138.1	Proliferating cell nuclear antiger	9.11E+06	2.02E+06	2.22E-01	-4.51E+00	-4.51	-1.51	P12004	PCNA
233.1	tRNA (cytosine(34)-C(5))-methyl	1.94E+06	4.22E+05	2.17E-01	-4.60E+00	-4.60	-1.53	Q08J23	NSUN2
683.1	Sorting nexin-12	8.88E+05	1.92E+05	2.16E-01	-4.62E+00	-4.62	-1.53	Q9UMY4	SNX12
455.1	Exportin-1	3.90E+06	8.06E+05	2.07E-01	-4.84E+00	-4.84	-1.58	O14980	XPO1
587.1	Nebulin	1.02E+06	2.09E+05	2.05E-01	-4.89E+00	-4.89	-1.59	F8WCL5	NEB
724.1	Coiled-coil domain-containing p	5.30E+06	1.08E+06	2.04E-01	-4.91E+00	-4.91	-1.59	Q8NDH2	CCDC168
2158.1	SWI/SNF-related matrix-associa	3.23E+05	6.41E+04	1.99E-01	-5.03E+00	-5.03	-1.62	Q96GM5	SMARCD1
643.1	Multiple PDZ domain protein	8.79E+05	1.74E+05	1.98E-01	-5.05E+00	-5.05	-1.62	F5H1U9	MPDZ
353.2	C-terminal-binding protein 1	1.07E+06	2.08E+05	1.94E-01	-5.15E+00	-5.15	-1.64	Q13363	CTBP1
141.2	Destrin	3.55E+06	6.86E+05	1.93E-01	-5.17E+00	-5.17	-1.64	P60981	DSTN
486.1	Transgelin-2	8.40E+05	1.61E+05	1.92E-01	-5.22E+00	-5.22	-1.65	P37802	TAGLN2
1330.1	Signal transducer and activator	1.73E+05	3.24E+04	1.87E-01	-5.34E+00	-5.34	-1.67	P42224	STAT1
456.1	Ladinin-1	5.85E+05	1.08E+05	1.85E-01	-5.42E+00	-5.42	-1.69	E9PDI4	LAD1
1019.1	Clustered mitochondria protein	1.28E+05	2.34E+04	1.82E-01	-5.49E+00	-5.49	-1.70	O75153	CLUH
1033.1	Homeobox protein TGIF1	2.59E+05	4.62E+04	1.79E-01	-5.60E+00	-5.60	-1.72	Q15583	TGIF1
915.1	Spectrin beta chain, non-erythr	9.02E+05	1.57E+05	1.74E-01	-5.74E+00	-5.74	-1.75	Q9NRC6	SPTBN5
1187.1	1-phosphatidylinositol 4,5-bisph	7.87E+06	1.36E+06	1.73E-01	-5.78E+00	-5.78	-1.76	Q86YW0	PLCZ1
1053.1	Cell division cycle and apoptosis	1.73E+05	2.95E+04	1.71E-01	-5.86E+00	-5.86	-1.77	Q8IX12	CCAR1
378.1	Nascent polypeptide-associated	6.83E+06	1.16E+06	1.70E-01	-5.89E+00	-5.89	-1.77	E9PAV3	NACA
777.1	Mortality factor 4-like protein 2	1.63E+05	2.44E+04	1.50E-01	-6.67E+00	-6.67	-1.90	Q15014	MORF4L2
3.3	Keratin, type II cytoskeletal 6B	2.37E+05	3.51E+04	1.48E-01	-6.74E+00	-6.74	-1.91	P04259	KRT6B
1488.1	Protein-tyrosine sulfotransferas	2.02E+05	2.88E+04	1.42E-01	-7.02E+00	-7.02	-1.95	O60507	TPST1
111.1	Spectrin beta chain, non-erythr	5.18E+06	7.31E+05	1.41E-01	-7.08E+00	-7.08	-1.96	O15020	SPTBN2
251.1	Protein arginine N-methyltransf	5.16E+06	7.17E+05	1.39E-01	-7.19E+00	-7.19	-1.97	H7C2I1	PRMT1
200.1	Stress-induced-phosphoprotein	2.36E+06	3.17E+05	1.35E-01	-7.43E+00	-7.43	-2.01	P31948	STIP1
152.1	Src substrate cortactin	7.55E+06	1.01E+06	1.34E-01	-7.48E+00	-7.48	-2.01	Q14247	CTTN
19.1	Actin, cytoplasmic 2	2.20E+08	2.86E+07	1.30E-01	-7.71E+00	-7.71	-2.04	P63261	ACTG1

1255.1	Protein EFR3 homolog A	3.77E+05	4.80E+04	1.27E-01	-7.86E+00	-7.86	-2.06	H9KV44	EFR3A
980.1	Serine/threonine-protein phosp	9.06E+04	1.10E+04	1.21E-01	-8.23E+00	-8.23	-2.11	Q13362	PPP2R5C
845.1	Annexin A5	1.61E+05	1.94E+04	1.21E-01	-8.29E+00	-8.29	-2.11	P08758	ANXA5
277.1	Signal recognition particle 9 kDa	8.61E+06	1.02E+06	1.18E-01	-8.44E+00	-8.44	-2.13	P49458	SRP9
1009.1	Matrix metalloproteinase-28	1.01E+06	1.19E+05	1.18E-01	-8.45E+00	-8.45	-2.13	K7ENP0	MMP28
354.1	Transcription initiation factor IIE	1.29E+06	1.48E+05	1.14E-01	-8.74E+00	-8.74	-2.17	Q00403	GTF2B
625.1	UDP-glucose:glycoprotein gluco	2.45E+06	2.72E+05	1.11E-01	-8.99E+00	-8.99	-2.20	Q9NYU2	UGGT1
689.1	PHD finger protein 3	8.54E+05	9.44E+04	1.11E-01	-9.05E+00	-9.05	-2.20	Q92576	PHF3
361.1	Catechol O-methyltransferase	2.70E+06	2.55E+05	9.45E-02	-1.06E+01	-10.00	-2.36	P21964	COMT
244.1	LIM domain and actin-binding p	4.91E+06	4.56E+05	9.28E-02	-1.08E+01	-10.00	-2.38	Q9UHB6	LIMA1
714.1	Nuclear receptor corepressor 1	9.60E+04	8.70E+03	9.06E-02	-1.10E+01	-10.00	-2.40	O75376	NCOR1
1049.1	Protein NDRG1	1.17E+05	1.01E+04	8.61E-02	-1.16E+01	-10.00	-2.45	Q92597	NDRG1
928.1	Unconventional myosin-IXb	1.09E+06	8.69E+04	7.96E-02	-1.26E+01	-10.00	-2.53	Q13459	MYO9B
627.1	E3 ubiquitin-protein ligase RNF1	4.13E+06	3.03E+05	7.33E-02	-1.36E+01	-10.00	-2.61	C9J266	RNF123
775.1	Hydroxyacid-oxoacid transhydro	4.66E+05	3.33E+04	7.14E-02	-1.40E+01	-10.00	-2.64	Q8IWW8	ADHFE1
632.2	CLASP1 protein	1.59E+05	1.12E+04	7.06E-02	-1.42E+01	-10.00	-2.65	B7ZLX3	CLASP1
861.1	Splicing factor 3B subunit 1	1.37E+05	9.64E+03	7.01E-02	-1.43E+01	-10.00	-2.66	O75533	SF3B1
733.1	Beta-hexosaminidase subunit al	1.44E+05	9.31E+03	6.49E-02	-1.54E+01	-10.00	-2.74	H3BP20	HEXA
23.1	Isoform 3 of Caldesmon	2.89E+07	1.74E+06	6.02E-02	-1.66E+01	-10.00	-2.81	Q05682-3	CALD1
768.1	Isoform 2 of L-fucose kinase	2.82E+05	1.63E+04	5.78E-02	-1.73E+01	-10.00	-2.85	Q8N0W3-2	FUK
720.1	26S proteasome non-ATPase reg	3.08E+06	1.41E+05	4.57E-02	-2.19E+01	-10.00	-3.09	P51665	PSMD7
1318.1	Antigen KI-67	3.87E+05	1.54E+04	3.98E-02	-2.51E+01	-10.00	-3.22	P46013	MKI67
1032.1	Microtubule-associated protein	4.79E+05	1.40E+04	2.92E-02	-3.42E+01	-10.00	-3.53	P10636	MAPT
481.1	Serpin B6	5.73E+05	1.39E+04	2.42E-02	-4.12E+01	-10.00	-3.72	P35237	SERPINB6
470.1	Heterogeneous nuclear ribonuc	3.03E+06	7.32E+04	2.41E-02	-4.14E+01	-10.00	-3.72	Q00839	HNRNPU
831.1	Sacsin	1.22E+07	2.91E+05	2.38E-02	-4.20E+01	-10.00	-3.74	Q9NZJ4	SACS
1099.1	Receptor-type tyrosine-protein	5.29E+05	1.17E+04	2.21E-02	-4.52E+01	-10.00	-3.81	P10586	PTPRF
84.1	Filamin-A	6.94E+06	1.51E+05	2.18E-02	-4.59E+01	-10.00	-3.83	P21333	FLNA
1283.1	Isoform 2 of Nebulin-related-an	9.17E+05	1.83E+04	2.00E-02	-5.01E+01	-10.00	-3.91	Q86VF7-2	NRAP
1222.1	Retinoblastoma-associated prot	2.29E+05	4.49E+03	1.96E-02	-5.11E+01	-10.00	-3.93	P06400	RB1
21.1	Isoform 2 of Tropomyosin alpha	5.43E+07	6.98E+05	1.29E-02	-7.78E+01	-10.00	-4.35	P06753-2	TPM3
1180.1	Segment polarity protein dishev	5.70E+05	7.13E+03	1.25E-02	-8.00E+01	-10.00	-4.38	O14640	DVL1
12.1	Alpha-actinin-4	9.17E+07	1.03E+06	1.12E-02	-8.90E+01	-10.00	-4.49	O43707	ACTN4
992.1	Tetratricopeptide repeat protei	4.23E+06	3.88E+04	9.18E-03	-1.09E+02	-10.00	-4.69	Q8IYW2	TTC40
19.2	Actin, aortic smooth muscle	5.62E+07	5.00E+05	8.90E-03	-1.12E+02	-10.00	-4.72	P62736	ACTA2

389.1	Translin	3.71E+06	3.00E+04	8.09E-03	-1.24E+02	-10.00	-4.82	E9PGT1	TSN
196.1	Coiled-coil domain-containing p	4.60E+06	1.94E+04	4.22E-03	-2.37E+02	-10.00	-5.47	Q8IVM0	CCDC50
788.1	Nuclear migration protein nudC	6.35E+05	1.88E+03	2.96E-03	-3.38E+02	-10.00	-5.82	Q9Y266	NUDC
192.1	Protein phosphatase 1 regulatoı	4.25E+06	8.99E+03	2.12E-03	-4.72E+02	-10.00	-6.16	O14974	PPP1R12A

Supplemental Table 2. Known AR-interacting proteins identified in the proteomic screen

Data was collated through PUBMED, HPPRD, BIOGRID, BIND and McGill AR database and current publications

Note: Cells highlighted in green indicate proteins enriched in the *AD* sample, highlighted in red indicate proteins enriched in the *AS* sample, highlighted in yellow indicate 1:1 *AS*

Cells not highlighted were AR-interacting proteins not found in the proteomic screen.

Subgroup	Official Gene symbol	Other names	UniProt ID	Binding	Description	Author	Pubmed ID	Journal	MS Data (Fold Change)
16	ACTN4		O43707	Direct Binding	ACTN4_HUMAN Alpha-actinin-4	Jasavala R et al	17052974	Mol Cell Proteomics	-10.00
81	FLNA		P21333	direct binding	FLNA_HUMAN Filamin-A				-10.00
25	NCOR1		O75376	direct binding	NCOR1_HUMAN Nuclear receptor corepressor 1				-10.00
211	TGIF1		Q15583	direct, coR	TGIF1_HUMAN Homeobox protein TGIF1				-5.60
264	SMARCD1		Q96GM5	direct, coA	SMRD1_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1		19762545	van de Wijngaart DJ et al Mol Endocrinol 2009	-5.03
147	SUMO3		P55854	coA, coR	SUMO3_HUMAN Small ubiquitin-related modifier 3				-3.18
316	MYO6		Q9UM54	direct, coA	MYO6_HUMAN Myosin-VI		19787211		-2.11
112	ANP32A		P39687	direct binding	AN32A_HUMAN Acidic leucine-rich nuclear phosphoprotein 32 family member A				-1.99
313	APPL1		Q9UKG1	indirect, coR	DP13A_HUMAN DCC-interacting protein 13-alpha				Unique-AD
47	CDK1		P06493	shown to phosphoryla	CDK1_HUMAN Cyclin-dependent kinase 1				Unique-AD
219	HSPB2		Q16082	direct, coA	HSPB2_HUMAN Heat shock protein beta-2				Unique-AD
212	NCOA2		Q15596	direct, coA	NCOA2_HUMAN Nuclear receptor coactivator 2				Unique-AD
122	NRIP1		P48552	direct binding	NRIP1_HUMAN Nuclear receptor-interacting protein 1				Unique-AD
267	NSD1	STO	Q96L73	direct, coA	NSD1_HUMAN Histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific				Unique-AD

118	PIK3CB		P42338	p110b required for AR-	PK3CB_HUMAN Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit beta isoform			Unique-AD
92	PIK3R1		P27986	p85 required for AR-DI	P85A_HUMAN Phosphatidylinositol 3-kinase regulatory subunit alpha			Unique-AD
62	XRCC5		P13010	direct binding	XRCC5_HUMAN X-ray repair cross-complementing protein 5			Unique-AD
61	XRCC6		P12956	direct binding	XRCC6_HUMAN X-ray repair cross-complementing protein 6			Unique-AD
315	ZMIZ1		Q9ULJ6	direct, coA	ZMIZ1_HUMAN Zinc finger MIZ domain-containing protein 1			Unique-AD
237	TH1L		Q8IXH7	direct, affinity capture	NELFD_HUMAN Negative elongation factor C/D			Unique-AD
33	SVIL		O95425	direct binding	SVIL_HUMAN Supervillin			Unique-AD
213	MED1		Q15648	direct, coA	MED1_HUMAN Mediator of RNA polymerase II transcription subunit 1			Unique-AD
235	CARM1		Q86X55	indirect, coA	CARM1_HUMAN Histone-arginine methyltransferase CARM1			Unique-AD
208	PRKD1		Q15139	direct, coR	KPCD1_HUMAN Serine/threonine-protein kinase D1			Unique-AD
283	BRD8		Q9H0E9	direct, coA	BRD8_HUMAN Bromodomain-containing protein 8	18560202	Hosoya T et al Endocr J 55(4) 657-65 2008	Unique-AD
349	STUB1	CHIP	Q9UNE7	direct, target for degra	E3 ubiquitin-protein ligase CHIP	16725394	Rees I et al Bichim Biophys Acta. 2006 Jun; 1764(6): 1073-9. Epub 2006 Apr 4	Unique-AD
80	CDK11B		P21127	direct binding	CD11B_HUMAN Cell division protein kinase 11B			Unique-AD
12	DAPK3		O43293	Direct Binding	DAPK3_HUMAN Death-associated protein kinase 3			Unique-AD

266	EHMT2		Q96KQ7	indirect, coA	EHMT2_HUMAN Histone-lysine N-methyltransferase, H3 lysine-9 specific 3			Unique-AD
260	KAT5		Q92993	direct, coA	KAT5_HUMAN Histone acetyltransferase KAT5			Unique-AD
11	PER1		O15534	Direct Binding, coA	PER1_HUMAN Period circadian protein homolog 1			Unique-AD
149	PTEN		P60484	direct binidng	PTEN_HUMAN Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN			Unique-AD
321	RNF6		Q9Y252	direct, coA	RNF6_HUMAN RING finger protein 6			Unique-AD
17	SGTA		O43765	Direct Binding	SGTA_HUMAN Small glutamine-rich tetratricopeptide repeat-containing protein alpha			Unique-AD
342	CHD8		Q9HCK8	direct binding/coA	chromatin remodeling factor CHD8	20308527	Menon T et al Mol Endocrinol 24(6) 1165-74 2010	2.04
152	COPS2		P61201	direct bindinig	CSN2_HUMAN COP9 signalosome complex subunit 2			2.04
300	SENP1		Q9P0U3	indirect, coA	SENP1_HUMAN Sentrin-specific protease 1			2.41
257	KIFAP3		Q92845	direct, y-2-hybrid	KIFA3_HUMAN Kinesin-associated protein 3			2.44
103	MCM7		P33993	direct binding	MCM7_HUMAN DNA replication licensing factor MCM7			2.44
343	CBX1	HP1beta	P83916	direct binding/coA	Human heterochrmatin protein 1 isoform HP1beta	20308360	Shiota M et al Endocr Relat Cancer 17(2) 2010	2.92
221	CDC37		Q16543	direct, coA	CDC37_HUMAN Hsp90 co-chaperone Cdc37			2.92
7	GAK		O14976	Direct Binding	GAK_HUMAN Cyclin-G-associated kinase			2.94

41	GAPDH	P04406	direct binding	G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase			2.94
169	FKBP4	Q02790	indirect	FKBP4_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP4			3.25
58	ERG	P11308	direct binding	ERG_HUMAN Transcriptional regulator ERG			3.25
48	NPM1	P06748	direct	NPM_HUMAN Nucleophosmin			3.49
39	NR3C1	P04150	direct binding	GCR_HUMAN Glucocorticoid receptor			3.84
190	NR5A1	Q13285	direct	STF1_HUMAN Steroidogenic factor 1			3.84
249	PSPC1	Q8WXF1	direct, coA	PSPC1_HUMAN Paraspeckle component 1			4.14
46	RB1	P06400	direct	RB_HUMAN Retinoblastoma-associated protein			6.05
159	UBE2I	P63279	direct binding	UBC9_HUMAN SUMO-conjugating enzyme UBC9			7.25
209	NONO	Q15233	direct, coA/coR	NONO_HUMAN Non-POU domain-containing octamer-binding protein			10.00
319	PA2G4	Q9UQ80	direct, coR	PA2G4_HUMAN Proliferation-associated protein 2G4			10.00
162	PRKDC	P78527	indirect binding	PRKDC_HUMAN DNA-dependent protein kinase catalytic subunit			10.00
31	PRPF6	O94906	direct binding	PRP6_HUMAN Pre-mRNA-processing factor 6			10.00
71	DDX5	P17844	direct binding	DDX5_HUMAN Probable ATP-dependent RNA helicase DDX5	18829551	Clark EL et al Cancer Res 68(19) 7938-46 2008	10.00
158	GNB2L1	P63244	direct binding	GBLP_HUMAN Guanine nucleotide-binding protein subunit beta-2-like 1			10.00
351	CDK5	Q00535	direct binding/phosph	Cyclin-dependent kinase 5	21799006	Hsu FN et al J Biol Chem 2011 Sep 23;286(38):33141-9.	10.00

256	DDX17		Q92841	direct	DDX17_HUMAN Probable ATP-dependent RNA helicase DDX17			10.00
54	HNRNPA1		P09651	indirect	ROA1_HUMAN Heterogeneous nuclear ribonucleoprotein A1			10.00
231	ATAD2		Q6PL18	direct, coA	ATAD2_HUMAN ATPase family AAA domain-containing protein 2	20855524		Unique-AS
195	CUL4B		Q13620	indirect binding throug	CUL4B_HUMAN Cullin-4B			Unique-AS
226	EFCAB6		Q5THR3	direct, coA	EFCB6_HUMAN EF-hand calcium-binding domain-containing protein 6			Unique-AS
185	EP300		Q09472	direct	EP300_HUMAN Histone acetyltransferase p300			Unique-AS
51	HSPA1A		P08107	direct	HSP71_HUMAN Heat shock 70 kDa protein 1A/1B			Unique-AS
269	RBM14		Q96PK6	direct	RBM14_HUMAN RNA-binding protein 14			Unique-AS
233	SRCAP		Q6ZRS2	direct, affinity capture	SRCAP_HUMAN Helicase SRCAP			Unique-AS
334	ARD1	NAA10	P41227	direct binding	NAA10 N(alpha)-acetyltransferase 10, NatA catalytic subunit	PMID: 22315407		Unique-AS
8	HNRPDL		O14979	coA	HNRDL_HUMAN Heterogeneous nuclear ribonucleoprotein D-like			Unique-AS
265	PAWR		Q96IZ0	direct, coA	PAWR_HUMAN PRKC apoptosis WT1 regulator protein			Unique-AS
82	SFPQ		P23246	direct bindng	SFPQ_HUMAN Splicing factor, proline- and glutamine-rich			Unique-AS
181	KHDRBS1		Q07666	direct binding	KHDR1_HUMAN KH domain-containing, RNA-binding, signal transduction-associated protein 1			Unique-AS
165	CDK6		Q00534	direct binding	CDK6_HUMAN Cell division protein kinase 6			Unique-AS
129	CDK7		P50613	direct binding	CDK7_HUMAN Cell division protein kinase 7	21157430	Chymkowitch P et al EMBO J 2011	Unique-AS
104	CTNNB1		P35222	direct binding	CTNB1_HUMAN Catenin beta-1			Unique-AS
88	DNAJB1		P25685	direct binding	DNJB1_HUMAN DnaJ homolog subfamily B member 1			Unique-AS

196	DYRK1A	Q13627	indirect	DYR1A_HUMAN Dual specificity tyrosine-phosphorylation-regulated kinase 1A	Unique-AS
290	ENY2	Q9NPA8	coA	ENY2_HUMAN Enhancer of yellow 2 transcription factor homolog	Unique-AS
106	GTF2F1	P35269	direct binding	T2FA_HUMAN General transcription factor IIF subunit 1	Unique-AS
247	HDAC7	Q8WUI4	direct, coR	HDAC7_HUMAN Histone deacetylase 7	Unique-AS
53	HMGB1	P09429	direct binding	HMGB1_HUMAN High mobility group protein B1	Unique-AS
89	HMGB2	P26583	direct binding	HMGB2_HUMAN High mobility group protein B2	Unique-AS
20	KDM1A	O60341	direct binding	KDM1A_HUMAN Lysine-specific histone demethylase 1A (LSD1)	Unique-AS
229	KDM4D	Q6B0I6	direct, coA	KDM4D_HUMAN Lysine-specific demethylase 4D	Unique-AS
309	KDM5B	Q9UGL1	direct, coA	KDM5B_HUMAN Lysine-specific demethylase 5B	Unique-AS
307	RNF14	Q9UBS8	direct, coA	RNF14_HUMAN E3 ubiquitin-protein ligase RNF14	Unique-AS
110	SREBF1	P36956	direct binding	SRBP1_HUMAN Sterol regulatory element-binding protein 1	Unique-AS
182	TNK2	Q07912	direct	ACK1_HUMAN Activated CDC42 kinase 1	Unique-AS
228	TRIM68	Q6AZZ1	direct, coA	TRI68_HUMAN E3 ubiquitin-protein ligase TRIM68	Unique-AS
202	USP10	Q14694	direct	UBP10_HUMAN Ubiquitin carboxyl-terminal hydrolase 10	Unique-AS
278	WDR77	Q9BQA1	direct, coA	MEP50_HUMAN Methylosome protein 50	Unique-AS
34	WHSC1	O96028	direct binding	NSD2_HUMAN Probable histone-lysine N-methyltransferase NSD2	Unique-AS
275	PRMT1	Q99873	indirect, coA	ANM1_HUMAN Protein arginine N-methyltransferase 1	-1.91
99	DNAJA1	P31689	indirect binding	DNJA1_HUMAN DnaJ homolog subfamily A member 1	-1.88
243	ARID1B	Q8NFD5	coA	ARI1B_HUMAN AT-rich interactive domain-containing protein 1B	-1.54

145	TPD52	P55327	may upregulate AR an	TPD52_HUMAN Tumor protein D52				-1.49
179	RUVBL1	Q06455	direct biniding (wester	MTG8_HUMAN Protein CBFA2T1				-1.44
180	PRDX1	Q06830	direct binding	PRDX1_HUMAN Peroxiredoxin-1				-1.31
49	HSP90AA1	P07900	direct	HS90A_HUMAN Heat shock protein HSP 90-alpha				-1.26
272	PARK7	Q99497	direct, coA	PARK7_HUMAN Protein DJ-1				-1.14
274	TSG101	Q99816	indirect, coA/coR	TS101_HUMAN Tumor susceptibility gene 101 protein				-1.13
56	AR	P10275	direct binding	ANDR_HUMAN Androgen receptor				-1.06
189	SELENBP1	Q13228	direct (affinity caputur	SBP1_HUMAN Selenium-binding protein 1				0.88
91	CALR	P27797	direct	CALR_HUMAN Calreticulin				1.04
101	SFN	P31947	coA,	1433S_HUMAN 14-3-3 protein sigma				1.06
174	YWHAH	Q04917	direct	1433F_HUMAN 14-3-3 protein eta				1.07
239	KIAA1967	Q8N163	direct, coA	K1967_HUMAN Protein KIAA1967				1.14
114	STAT3	P40763	direct binding	STAT3_HUMAN Signal transducer and activator of transcription 3				1.15
72	PSMC3	P17980	direct binding	PRS6A_HUMAN 26S protease regulatory subunit 6A		19325002	Satoh T et al Endocrinology 150(7) 3283-90 2009	1.42
90	YWHAQ	P27348	direct binding	1433T_HUMAN 14-3-3 protein theta				1.57
127	GSK3B	P49841	direct binding	GSK3B_HUMAN Glycogen synthase kinase-3 beta				1.72
95	PPP2R1A	P30153	direct binding	2AAA_HUMAN Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform				1.83
186	KIF1A	Q12756	direct	KIF1A_HUMAN Kinesin-like protein KIF1A				1.87
296	MDN1	Q9NU22	direct, y-2-hybrid	MDN1_HUMAN Midasin				1.91
298	AATF	Q9NY61	direct, coA	AATF_HUMAN Protein AATF	Leister P et al, Burgdorf S et al	14761944	Signal Transduction and JBC	NA
150	ACTB	P60709	enhance supervillin-m	ACTB_HUMAN Actin, cytoplasmic 1	Ting HJ et al	15178419	BBRC	NA
108	ACTN2	P35609	indirect binding	ACTN2_HUMAN Alpha-actinin-2	Huang SM et al	15072553	J Mol Endocrinol	NA

6	ADAM10	O14672	Direct Binding	ADA10_HUMAN Disintegrin and metalloproteinase domain-containing protein 10	Arima T et al	17727679	Cancer Sci	NA
183	AES	Q08117	direct	AES_HUMAN Amino-terminal enhancer of split				NA
109	AHR	P35869	direct binding	AHR_HUMAN Aryl hydrocarbon receptor				NA
100	AKT1	P31749	direct binding	AKT1_HUMAN RAC-alpha serine/threonine-protein kinase				NA
250	APPBP2	Q92624	direct, coR	APBP2_HUMAN Amyloid protein-binding protein 2				NA
140	ARHGDIA	P52565	enhance AR transcripti	GDIR1_HUMAN Rho GDP-dissociation inhibitor 1				NA
3	ARID1A	O14497	coA	ARI1A_HUMAN AT-rich interactive domain-containing protein 1A				NA
171	ARID5A	Q03989	direct	ARI5A_HUMAN AT-rich interactive domain-containing protein 5A				NA
204	ARRB2	Q14865	direct	ARI5B_HUMAN AT-rich interactive domain-containing protein 5B				NA
68	ATF2	P15336	direct binding	ATF2_HUMAN Cyclic AMP-dependent transcription factor ATF-2				NA
346	ATF3	P18847	direct binding/corepres	Activating transcription factor (ATF3)		22665497	Wang H., et al Mol Cell Biol 2012 Jun 4 Epub ahead of print	NA
206	ATXN7L3	Q14CW9	direct, coA	AT7L3_HUMAN Ataxin-7-like protein 3				NA
276	BAG1	Q99933	direct, coA	BAG1_HUMAN BAG family molecular chaperone regulator 1				NA
111	BRCA1	P38398	direct binding	BRCA1_HUMAN Breast cancer type 1 susceptibility protein				NA
135	BRCA2	P51587	direct binding	BRCA2_HUMAN Breast cancer type 2 susceptibility protein				NA
291	BRD7	Q9NPI1	coR	BRD7_HUMAN Bromodomain-containing protein 7				NA
301	CALCOCO1	Q9P1Z2	indirect, coA	CACO1_HUMAN Calcium-binding and coiled-coil domain-containing protein 1				NA
155	CALM1	P62158	direct binding	CALM_HUMAN Calmodulin				NA
94	CASP1	P29466	direct binding	CASP1_HUMAN Caspase-1				NA
119	CASP3	P42574	direct binding	CASP3_HUMAN Caspase-3				NA
142	CASP7	P55210	direct binding	CASP7_HUMAN Caspase-7				NA

203	CASP8	Q14790	direct	CASP8_HUMAN Caspase-8		NA
170	CAV1	Q03135	direct	CAV1_HUMAN Caveolin-1		NA
85	CCND1	P24385	direct binding	CCND1_HUMAN G1/S-specific cyclin-D1		NA
96	CCND3	P30281	direct binding	CCND3_HUMAN G1/S-specific cyclin-D3		NA
86	CCNE1	P24864	direct binding	CCNE1_HUMAN G1/S-specific cyclin-E1		NA
139	CCNH	P51946	direct binding	CCNH_HUMAN Cyclin-H		NA
97	CDC25A	P30304	direct binding/corepres	MPIP1_HUMAN M-phase inducer phosphatase 1	19013180	NA
98	CDC25B	P30305	direct binding	MPIP2_HUMAN M-phase inducer phosphatase 2		NA
320	CDK11A	Q9UQ88	coA	CD11A_HUMAN Cell division protein kinase 11A		NA
4	CDK2AP1	O14519	coA	CDKA1_HUMAN Cyclin-dependent kinase 2-associated protein 1		NA
131	CDK9	P50750	direct binding	CDK9_HUMAN Cell division protein kinase 9		NA
125	CEBPA	P49715	direct binding	CEBPA_HUMAN CCAAT/enhancer-binding protein alpha		NA
70	CEBPB	P17676	direct binding	CEBPB_HUMAN CCAAT/enhancer-binding protein beta		NA
268	CMTM3	Q96MX0	coR	CKLF3_HUMAN CKLF-like MARVEL transmembrane domain-containing protein 3		NA
248	COBRA1	Q8WX92	direct, coR	NELFB_HUMAN Negative elongation factor B		NA
258	COPS5	Q92905	coA	CSN5_HUMAN COP9 signalosome complex subunit 5		NA
57	COX5B	P10606	direct binding	COX5B_HUMAN Cytochrome c oxidase subunit 5B, mitochondrial		NA
252	CREBBP	Q92793	direct, coA	CBP_HUMAN CREB-binding protein		NA
5	CTDSP2	O14595	Direct Binding	CTDS2_HUMAN Carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase 2		NA
312	DACH1	Q9UI36	coR	DACH1_HUMAN Dachshund homolog 1		NA
132	DAP3	P51398	direct binding	RT29_HUMAN 28S ribosomal protein S29, mitochondrial		NA
308	DAXX	Q9UER7	direct, coR	DAXX_HUMAN Death domain-associated protein 6	15572661	NA
224	DCAF6	Q58WW2	direct, coA	DCAF6_HUMAN DDB1- and CUL4-associated factor 6		NA

348	DDB2	Q92466	direct, target for degrac	DNA damage-binding protein 2	22846800	Chang SW et al Int J Biochem Cell Biolo 2012 July 28 Epub ahead of print	NA
78	DDC	P20711	direct binding	DDC_HUMAN Aromatic-L-amino-acid decarboxylase			NA
230	DENND5A	Q6IQ26	direct, y-2-hybrid	DEN5A_HUMAN DENN domain-containing protein 5A			NA
332	E2F3	O00716	direct/indirect	Cell cycle regulator, transcription factor E2F3	Mallik I et al. Biochim Biophys Acta 1783:1737-1744, 2008		NA
35	EGFR	P00533	direct binding	EGFR_HUMAN Epidermal growth factor receptor			NA
73	EGR1	P18146	direct binding	EGR1_HUMAN Early growth response protein 1			NA
42	ERBB2	P04626	indirect binding	ERBB2_HUMAN Receptor tyrosine-protein kinase erbB-2			NA
37	ESR1	P03372	direct binding	ESR1_HUMAN Estrogen receptor			NA
67	ETS1	P14921	direct binding	ETS1_HUMAN Protein C-ets-1			NA
128	ETV1	P50549	direct binding	ETV1_HUMAN ETS translocation variant 1			NA
115	ETV5	P41161	direct binding	ETV5_HUMAN ETS translocation variant 5			NA
200	FHL2	Q14192	direct	FHL2_HUMAN Four and a half LIM domains protein 2	17975004	Heemers HV, et al Cancer Res2007	NA
191	FKBP5	Q13451	indirect	FKBP5_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP5			NA
36	FOS	P01100	direct binding	FOS_HUMAN Proto-oncogene c-Fos			NA
144	FOXA1	P55317	direct binding	FOXA1_HUMAN Hepatocyte nuclear factor 3-alpha			NA
322	FOXA2	Q9Y261	direct, coA/coR	FOXA2_HUMAN Hepatocyte nuclear factor 3-beta			NA
143	FOXG1	P55316	direct binding	FOXG1_HUMAN Forkhead box protein G1			NA
28	FOXH1	O75593	direct binding	FOXH1_HUMAN Forkhead box protein H1			NA
187	FOXO1	Q12778	direct	FOXO1_HUMAN Forkhead box protein O1			NA

14	FOXO3	O43524	Direct Binding	FOXO3_HUMAN Forkhead box protein O3			NA
284	FOXP1	Q9H334	direct, coR	FOXP1_HUMAN Forkhead box protein P1			NA
244	GADD45GIP1	Q8TAE8	direct, coR	G45IP_HUMAN Growth arrest and DNA damage-inducible proteins-interacting protein 1			NA
83	GATA2	P23769	direct binding	GATA2_HUMAN Endothelial transcription factor GATA-2	25489091	He B et al Proc Natl Acad Sci U S A. 2014	NA
84	GATA3	P23771	coA	GATA3_HUMAN Trans-acting T-cell-specific transcription factor GATA-3			NA
324	GRIP1	Q9Y3R0	direct, coA	GRIP1_HUMAN Glutamate receptor-interacting protein 1			NA
126	GSK3A	P49840	direct binding	GSK3A_HUMAN Glycogen synthase kinase-3 alpha			NA
45	GSN	P06396	direct	GELS_HUMAN Gelsolin			NA
64	GTF2F2	P13984	direct binding	T2FB_HUMAN General transcription factor IIF subunit 2			NA
102	GTF2H1	P32780	direct binding	TF2H1_HUMAN General transcription factor IIH subunit 1			NA
141	HAP1	P54257	direct binding	HAP1_HUMAN Huntingtin-associated protein 1			NA
193	HDAC1	Q13547	direct	HDAC1_HUMAN Histone deacetylase 1			NA
10	HDAC3	O15379	Direct Binding	HDAC3_HUMAN Histone deacetylase 3			NA
148	HDAC4	P56524	direct binding	HDAC4_HUMAN Histone deacetylase 4			NA
305	HDAC6	Q9UBN7	indirect, coA	HDAC6_HUMAN Histone deacetylase 6			NA
328	HEY1	Q9Y5J3	direct, coR	HEY1_HUMAN Hairy/enhancer-of-split related with YRPW motif protein 1			NA
306	HEY2	Q9UBP5	coR	HEY2_HUMAN Hairy/enhancer-of-split related with YRPW motif protein 2			NA
222	HIF1A	Q16665	direct, coA	HIF1A_HUMAN Hypoxia-inducible factor 1-alpha			NA
2	HIP1	O00291	Direct Binding	HIP1_HUMAN Huntingtin-interacting protein 1			NA
286	HIPK3	Q9H422	direct, coA	HIPK3_HUMAN Homeodomain-interacting protein kinase 3			NA

116	HNF4A		P41235	colocalization	HNF4A_HUMAN Hepatocyte nuclear factor 4-alpha			NA
253	HOXB13		Q92826	direct, coR	HXB13_HUMAN Homeobox protein Hox-B13			NA
280	HTATIP2		Q9BUP3	coA	HTAI2_HUMAN Oxidoreductase HTATIP2			NA
65	IDE		P14735	direct binding	IDE_HUMAN Insulin-degrading enzyme			NA
223	IFI16		Q16666	direct, coR	IF16_HUMAN Gamma-interferon-inducible protein 16			NA
113	IL6ST		P40189	direct binding	IL6RB_HUMAN Interleukin-6 receptor subunit beta			NA
107	IRS1		P35568	direct binding	IRS1_HUMAN Insulin receptor substrate 1			NA
215	JMJD1C		Q15652	direct, coA	JHD2C_HUMAN Probable JmjC domain-containing histone demethylation protein 2C			NA
44	JUN		P05412	direct	JUN_HUMAN Transcription factor AP-1			NA
341	JunD		P17535	directbinding/coA	Transcription factor jun-D	20460526	Mehraein-Ghomi F et al Cancer Res 70(11) 4560-8	NA
254	KAT2A		Q92830	coA	KAT2A_HUMAN Histone acetyltransferase KAT2A			NA
255	KAT2B		Q92831	direct, coA	KAT2B_HUMAN Histone acetyltransferase KAT2B			NA
333	KAT7	MYST2	O95251	direct binding	KAT7_HUMAN Histone acetyltransferase			NA
326	KDM3A		Q9Y4C1	direct, coA	KDM3A_HUMAN Lysine-specific demethylase 3A			NA
24	KDM4A		O75164	direct binding	KDM4A_HUMAN Lysine-specific demethylase 4A (JMJD2A)			NA
285	KDM4C		Q9H3R0	direct, coA	KDM4C_HUMAN Lysine-specific demethylase 4C			NA
350	L1RE1	LINE-1 OR	Q9UN81	direct binding/coA	The pro-oncogene human Long Interspersed Nucleotide acid Element-1 (LINE-1) encodes LINE-1 ORF-1p	23153584	Lu Y et al Cell Signal. 2012 Nov; 25(2):479-489	NA
295	LATS2		Q9NRM7	direct, coR	LATS2_HUMAN Serine/threonine-protein kinase LATS2			NA
336	LCOR		Q96JN0	direct binding	Ligand-dependent corepressor	21856747		NA
22	LPXN		O60711	direct binding	LPXN_HUMAN Leupaxin			NA

277	MACROD1	Q9BQ69	direct, coA	MACD1_HUMAN MACRO domain-containing protein 1			NA
120	MAGEA11	P43364	direct binding	MAGAB_HUMAN Melanoma-associated antigen 11	18212060	Bai S, and Wilson EM Mol Cell Biol 2008	NA
79	MAK	P20794	direct binding	MAK_HUMAN Serine/threonine-protein kinase MAK			NA
93	MAPK1	P28482	direct binding	MK01_HUMAN Mitogen-activated protein kinase 1			NA
246	MAPK15	Q8TD08	indirect, coR	MK15_HUMAN Mitogen-activated protein kinase 15			NA
166	MDM2	Q00987	direct binding	MDM2_HUMAN E3 ubiquitin-protein ligase Mdm2			NA
236	MED12L	Q86YW9	direct, y-2-hybrid	MD12L_HUMAN Mediator of RNA polymerase II transcription subunit 12-like protein			NA
19	MED14	O60244	Direct Binding	MED14_HUMAN Mediator of RNA polymerase II transcription subunit 14			NA
297	MED17	Q9NVC6	coA	MED17_HUMAN Mediator of RNA polymerase II transcription subunit 17			NA
26	MED24	O75448	direct binding	MED24_HUMAN Mediator of RNA polymerase II transcription subunit 24			NA
311	MKRN1	Q9UHC7	coR	MKRN1_HUMAN E3 ubiquitin-protein ligase makorin-1			NA
310	MLH3	Q9UHC1	direct, y-2-hybrid	MLH3_HUMAN DNA mismatch repair protein Mlh3			NA
279	MYBBP1A	Q9BQG0	direct	MBB1A_HUMAN Myb-binding protein 1A			NA
216	NCOA1	Q15788	direct, coA	NCOA1_HUMAN Nuclear receptor coactivator 1			NA
330	NCOA3	Q9Y6Q9	direct, coA	NCOA3_HUMAN Nuclear receptor coactivator 3			NA
197	NCOA4	Q13772	direct	NCOA4_HUMAN Nuclear receptor coactivator 4			NA
201	NCOA6	Q14686	indirect	NCOA6_HUMAN Nuclear receptor coactivator 6			NA
329	NCOR2	Q9Y618	direct, coR	NCOR2_HUMAN Nuclear receptor corepressor 2			NA
205	NFIX	Q14938	direct, coA	NFIX_HUMAN Nuclear factor 1 X-type			NA
75	NFKB1	P19838	interact with p65, p52 r	NFKB1_HUMAN Nuclear factor NF-kappa-B p105 subunit			NA
303	NLK	Q9UBE8	direct, coR	NLK_HUMAN Serine/threonine-protein kinase NLK			NA

234	NLRP10	Q86W26	direct, y-2-hybrid	NAL10_HUMAN NACHT, LRR and PYD domains-containing protein 10			NA
138	NR0B1	P51843	direct binding	NR0B1_HUMAN Nuclear receptor subfamily 0 group B member 1			NA
210	NR0B2	Q15466	direct, coR	NR0B2_HUMAN Nuclear receptor subfamily 0 group B member 2			NA
63	NR2C1	P13056	direct binding	NR2C1_HUMAN Nuclear receptor subfamily 2 group C member 1			NA
124	NR2C2	P49116	direct binding	NR2C2_HUMAN Nuclear receptor subfamily 2 group C member 2			NA
294	PAK6	Q9NQU5	direct, coR	PAK6_HUMAN Serine/threonine-protein kinase PAK 6			NA
288	PATZ1	Q9HBE1	indirect, coR	PATZ1_HUMAN POZ-, AT hook-, and zinc finger-containing protein 1			NA
338	PAX6	P26367	directbinding/coR	paired box protein Pax6	21935435	Elvenes J et al PLoS One 6(9) 2011	NA
238	PELP1	Q8IZL8	direct, coA	PELP1_HUMAN Proline-, glutamic acid- and leucine-rich protein 1			NA
105	PHB	P35232	indirect binding	PHB_HUMAN Prohibitin			NA
29	PIAS1	O75925	direct binding	PIAS1_HUMAN E3 SUMO-protein ligase PIAS1			NA
30	PIAS2	O75928	direct binding	PIAS2_HUMAN E3 SUMO-protein ligase PIAS2			NA
331	PIAS3	Q9Y6X2	direct, coA/coR	PIAS3_HUMAN E3 SUMO-protein ligase PIAS3			NA
240	PIAS4	Q8N2W9	direct, coR	PIAS4_HUMAN E3 SUMO-protein ligase PIAS4			NA
335	PIM1	P11309	direct binding	Serine/threonine-protein kinase pim-1	PMID: 22584579		NA
220	PKN1	Q16512	direct, coA	PKN1_HUMAN Serine/threonine-protein kinase N1			NA
317	PLAGL1	Q9UM63	direct, coA	PLAL1_HUMAN Zinc finger protein PLAGL1			NA
262	PMEPA1	Q969W9	direct	PMEPA_HUMAN Transmembrane prostate androgen-induced protein			NA
188	PNRC1	Q12796	direct	PNRC1_HUMAN Proline-rich nuclear receptor coactivator 1			NA
292	PNRC2	Q9NPJ4	direct	PNRC2_HUMAN Proline-rich nuclear receptor coactivator 2			NA
66	POU2F1	P14859	direct binding	PO2F1_HUMAN POU domain, class 2, transcription factor 1 (Oct1)			NA
52	POU2F2	P09086	direct binding	PO2F2_HUMAN POU domain, class 2, transcription factor 2			NA

77	POU3F3		P20264	direct biniding	PO3F3_HUMAN POU domain, class 3, transcription factor 3			NA
184	PPID		Q08752	direct	PPID_HUMAN Peptidyl-prolyl cis-trans isomerase D			NA
154	PPP1CA		P62136	direct bindng	PP1A_HUMAN Serine/threonine-protein phosphatase PP1-alpha catalytic subunit			NA
23	PQBP1		O60828	Direct Binding	PQBP1_HUMAN Polyglutamine-binding protein 1			NA
345	PRGC1	PPARGC1	Q9UBK2	direct binding/coA	Peroxisome proliferator-activated receptor gamma coactivator 1-alpha	19884383	Shiota M., et al Mol Endocrinol 24(1):114-27	NA
282	PRIC285		Q9BYK8	coA	PR285_HUMAN Peroxisomal proliferator-activated receptor A-interacting complex 285 kDa protein			NA
146	PRMT2		P55345	direct binding	ANM2_HUMAN Protein arginine N-methyltransferase 2			NA
302	PSMC3IP		Q9P2W1	direct, coA	HOP2_HUMAN Homologous-pairing protein 2 homolog	19325002	Satoh T et al Endocrinology 150(7) 3283-90 2009	NA
123	PXN		P49023	direct binding	PAXI_HUMAN Paxillin			NA
151	RAC3		P60763	direct binding	RAC3_HUMAN Ras-related C3 botulinum toxin substrate 3			NA
325	RAD54L2		Q9Y4B4	direct, coA	ARIP4_HUMAN Helicase ARIP4	17003240	Domanskyi A et al Am J Physiol Metab 2007	NA
273	RAD9A		Q99638	direct, coR	RAD9A_HUMAN Cell cycle checkpoint control protein RAD9A			NA
38	RAF1		P04049	direct binding	RAF1_HUMAN RAF proto-oncogene serine/threonine-protein kinase			NA
156	RAN		P62826	direct binding	RAN_HUMAN GTP-binding nuclear protein Ran	18565325	Harada N et al 373(3) 373-7 2008	NA
232	RANBP10		Q6VN20	direct, coA	RBP10_HUMAN Ran-binding protein 10			NA
271	RANBP9		Q96S59	direct, coA	RANB9_HUMAN Ran-binding protein 9			NA
299	RBAK		Q9NYW8	direct, coA	RBAK_HUMAN RB-associated KRAB zinc finger protein			NA

270	RCHY1		Q96PM5	direct, coA	ZN363_HUMAN RING finger and CHY zinc finger domain-containing protein 1 (PIRH2)	16914734	Logan IR et al., Mol Cell Biol 2006	NA
173	REL		Q04864	direct	REL_HUMAN Proto-oncogene c-Rel			NA
172	RELA		Q04206	direct	TF65_HUMAN Transcription factor p65			NA
178	RNASEL		Q05823	direct	RN5A_HUMAN 2-5A-dependent ribonuclease			NA
161	RNF4		P78317	direct binding	RNF4_HUMAN RING finger protein 4			NA
137	RPS6KA3		P51812	modulate PSA express	KS6A3_HUMAN Ribosomal protein S6 kinase alpha-3			NA
251	RREB1		Q92766	direct, coR	RREB1_HUMAN Ras-responsive element-binding protein 1	17550981	Mukhopadhyay NK et al Mol Endocrinol 2007	NA
167	RUNX1		Q01196	direct binding	RUNX1_HUMAN Runt-related transcription factor 1			NA
198	RUNX2		Q13950	direct	RUNX2_HUMAN Runt-related transcription factor 2			NA
287	RWDD1		Q9H446	coA	RWDD1_HUMAN RWD domain-containing protein 1	22406838	Grotsch H et al Mol Cell Endocrinol 2012	NA
74	RXRA		P19793	direct binding	RXRA_HUMAN Retinoic acid receptor RXR-alpha			NA
207	SART3		Q15020	direct, coR	SART3_HUMAN Squamous cell carcinoma antigen recognized by T-cells 3			NA
340	SET9	SETD7	Q8WTS6	directbinding/coA	Histone-lysine N-methyltransferase SETD7 (SET9)	21273441	Ko S et al Mol Endorinol 25(3):433-44 2011	NA
241	SFRP1		Q8N474	coR	SFRP1_HUMAN Secreted frizzled-related protein 1			NA
1	SGK1		O00141	coR, no direct binding	SGK1_HUMAN Serine/threonine-protein kinase Sgk1			NA
263	SIRT1		Q96EB6	direct, coR	SIRT1_HUMAN NAD-dependent deacetylase sirtuin-1			NA
59	SLC25A4		P12235	direct binding (y-2-h)	ADT1_HUMAN ADP/ATP translocase 1			NA

347	SLUG	SNAI2	O43623	coactivator	Zinc finger protein SNAI2	22745193	Wu K., et al Mol Endocriol 2012 Jun 28 Epub ahead of print	NA
217	SMAD1		Q15797	direct, coR	SMAD1_HUMAN Mothers against decapentaplegic homolog 1			NA
164	SMAD3		P84022	direct binding	SMAD3_HUMAN Mothers against decapentaplegic homolog 3			NA
192	SMAD4		Q13485	direct	SMAD4_HUMAN Mothers against decapentaplegic homolog 4			NA
133	SMARCA2		P51531	imapct AR-mediated tra	SMCA2_HUMAN Probable global transcription activator SNF2L2			NA
134	SMARCA4		P51532	imapct AR-mediated tra	SMCA4_HUMAN Transcription activator BRG1			NA
259	SMARCC1		Q92922	direct, coA	SMRC1_HUMAN SWI/SNF complex subunit SMARCC1			NA
261	SMARCE1		Q969G3	direct, coA	SMCE1_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1			NA
40	SOD2		P04179	coR, no direct binding	SODM_HUMAN Superoxide dismutase [Mn], mitochondrial			NA
21	SORBS3		O60504	direct binding	VINEX_HUMAN Vinexin			NA
121	SOX9		P48436	direct binding	SOX9_HUMAN Transcription factor SOX-9			NA
50	SP1		P08047	direct	SP1_HUMAN Transcription factor Sp1			NA
339	SPBP	TCF20	Q9UGU0	directbinding/coA	transcription factor 20	21935435	Elvenes J et al PLoS One 6(9) 2011	NA
32	SPDEF		O95238	direct binding	SPDEF_HUMAN SAM pointed domain-containing Ets transcription factor			NA
18	SPOP		O43791	Direct Binding (y-2-h)	SPOP_HUMAN Speckle-type POZ protein			NA
289	SRA1		Q9HD15	direct, coA/coR	SRA1_HUMAN Steroid receptor RNA activator 1			NA
60	SRC		P12931	direct binding	SRC_HUMAN Proto-oncogene tyrosine-protein kinase Src			NA
175	SRY		Q05066	direct	SRY_HUMAN Sex-determining region Y protein			NA
117	STAT5A		P42229	direct binding	STA5A_HUMAN Signal transducer and activator of transcription 5A			NA

136	STAT5B	P51692	direct binding	STA5B_HUMAN Signal transducer and activator of transcription 5B			NA
157	SUMO1	P63165	coR	SUMO1_HUMAN Small ubiquitin-related modifier 1			NA
153	SUMO2	P61956	coA	SUMO2_HUMAN Small ubiquitin-related modifier 2			NA
27	TADA3	O75528	direct binding	TADA3_HUMAN Transcriptional adapter 3			NA
344	TAF1	P21675	direct binding/coA	TATA binding protein-associated factor 1	20181722	Tavassoli P et al Mol Endocrinol 24(4) 696-708	NA
168	TAGLN	Q01995	indirect	TAGL_HUMAN Transgelin			NA
76	TBP	P20226	direct binding	TBP_HUMAN TATA-box-binding protein			NA
15	TCF21	O43680	Direct Binding	TCF21_HUMAN Transcription factor 21			NA
69	TCF4	P15884	direct binding	ITF2_HUMAN Transcription factor 4			NA
293	TCF7L2	Q9NQB0	direct, coR	TF7L2_HUMAN Transcription factor 7-like 2			NA
194	TDG	Q13569	direct	TDG_HUMAN G/T mismatch-specific thymine DNA glycosylase			NA
13	TGFB1I1	O43294	Direct Binding	TGFI1_HUMAN Transforming growth factor beta-1-induced transcript 1 protein			NA
163	TMF1	P82094	direct binding	TMF1_HUMAN TATA element modulatory factor			NA
130	TOB1	P50616	direct binding	TOB1_HUMAN Protein Tob1			NA
199	TOB2	Q14106	indirect, coR, suppress	TOB2_HUMAN Protein Tob2			NA
43	TP53	P04637	indirect binding	P53_HUMAN Cellular tumor antigen p53			NA
9	TRIM24	O15164	Direct Binding	TIF1A_HUMAN Transcription intermediary factor 1-alpha			NA
214	TRIP4	Q15650	direct, coA	TRIP4_HUMAN Activating signal cointegrator 1			NA
245	UBA3	Q8TBC4	indirect, coR	UBA3_HUMAN NEDD8-activating enzyme E1 catalytic subunit			NA
55	UBC	P0CG48	ubiquitin	UBC_HUMAN Polyubiquitin-C			NA
160	UBE2L3	P68036	coA	UB2L3_HUMAN Ubiquitin-conjugating enzyme E2 L3			NA
176	UBE3A	Q05086	direct	UBE3A_HUMAN Ubiquitin-protein ligase E3A			NA

218	USF2		Q15853	direct/indirect, coA	USF2_HUMAN Upstream stimulatory factor 2			NA
318	USP22		Q9UPT9	direct, coA	UBP22_HUMAN Ubiquitin carboxyl-terminal hydrolase 22			NA
281	USP26		Q9BXU7	direct, affinity capture-	UBP26_HUMAN Ubiquitin carboxyl-terminal hydrolase 26			NA
304	UXT		Q9UBK9	direct, coA	UXT_HUMAN Protein UXT			NA
314	VAV3		Q9UKW4	indirect, coA	VAV3_HUMAN Guanine nucleotide exchange factor VAV3	21765461	Rao S et al Oncogene 2012	NA
225	WIPI1		Q5MNZ9	direct	WIPI1_HUMAN WD repeat domain phosphoinositide-interacting protein 1			NA
87	YY1		P25490	direct binding	TYY1_HUMAN Transcriptional repressor protein YY1			NA
323	ZBTB1		Q9Y2K1	direct, y-2-hybrid	ZBTB1_HUMAN Zinc finger and BTB domain-containing protein 1			NA
177	ZBTB16		Q05516	direct (y-2-hybrid)	ZBT16_HUMAN Zinc finger and BTB domain-containing protein 16			NA
242	ZMIZ2		Q8NF64	direct, coA	ZMIZ2_HUMAN Zinc finger MIZ domain-containing protein 2			NA
227	ZNF318		Q5VUA4	direct, coR	ZN318_HUMAN Zinc finger protein 318			NA
337	ZNF366	DC-SCRIP	Q8N895	co-IP	Zinc finger protein 366	22473304	Ansems M et al Prostate	NA
327	ZNF451		Q9Y4E5	direct/indirect, coA	ZN451_HUMAN Zinc finger protein 451	18656483	Karvonen et al J. Mol Biol 2008	NA

Supplemental Table 3. Summary of siRNA luciferase screen for modulators of AR-mediated transcription.

E3 ubiquitin protein ligases	**Description**	**Effect**	**% increase (+) or decrease (-)**		
NEDD4L	E3 ubiquitin-protein ligase which accepts ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a thioester and then directly transfers the ubiquitin to targeted substrates. Inhibits TGF-beta signaling by triggering SMAD2 and TGFBR1 ubiquitination and proteasome-dependent degradation. Promotes ubiquitination and internalization of various plasma membrane channels such as ENaC, Nav1.2, Nav1.3, Nav1.5, Nav1.7, Nav1.8, Kv1.3, EAAT1 or CLC5. Promotes ubiquitination and degradation of SGK1 and TNK2.	Potentiate	48%		
CHFR	E3 ubiquitin-protein ligase that functions in the antephase checkpoint by actively delaying passage into mitosis in response to microtubule poisons. Acts in early prophase before chromosome condensation, when the centrosome move apart from each other along the periphery of the nucleus. Probably involved in signaling the presence of mitotic stress caused by microtubule poisons by mediating the 'Lys-48'-linked ubiquitination of target proteins, leading to their degradation by the proteasome. Promotes the ubiquitination and subsequent degradation of AURKA and PLK1. Probably acts as a tumor suppressor, possibly by mediating the polyubiquitination of HDAC1, leading to its degradation. May also promote the formation of 'Lys-63'-linked polyubiquitin chains and functions with the specific ubiquitin-conjugating UBC13-MMS2 (UBE2N-UBE2V2) heterodimer. Substrates that are polyubiquitinated at 'Lys-63' are usually not targeted for degradation, but are rather involved in signaling cellular stress.	Potentiate	42%		
PELI1	E3 ubiquitin ligase catalyzing the covalent attachment of ubiquitin moieties onto substrate proteins. Involved in the TLR and IL-1 signaling pathways via interaction with the complex containing IRAK kinases and TRAF6. Mediates 'Lys-63'-linked polyubiquitination of IRAK1 allowin subsequent NF-kappa-B activation.	Potentiate	48%		
RNF6	E3 ubiquitin-protein ligase mediating 'Lys-48'-linked polyubiquitination of LIMK1 and its subsequent targeting to the proteasome for degradation. Negatively regulates axonal outgrowth through regulation of the LIMK1 turnover. Mediates 'Lys-6' and 'Lys-27'-linked polyubiquitination of AR/androgen receptor thereby modulating its transcriptional activity. May also bind DNA and function as a transcriptional regulator.	Potentiate	39%		
STUB1	E3 ubiquitin-protein ligase which targets misfolded chaperone substrates towards proteasomal degradation. Collaborates with ATXN3 in the degradation of misfolded chaperone substrates: ATXN3 restricting the length of ubiquitin chain attached to STUB1/CHIP substrates and preventing further chain extension. Ubiquitinates NOS1 in concert with Hsp70 and Hsp40. Modulates the activity of several chaperone complexes, including Hsp70, Hsc70 and Hsp90. Mediates transfer of non-canonical short ubiquitin chains to HSPA8 that have no effect on HSPA8 degradation. Mediates polyubiquitination of DNA polymerase beta (POLB) at 'Lys-41', 'Lys-61' and 'Lys-81', thereby playing a role in base-excision repair: catalyzes polyubiquitination by amplifying the HUWE1/ARF-BP1-dependent monoubiquitination and leading to POLB-degradation by the proteasome. Mediates polyubiquitination of CYP3A4. Ubiquitinates EPHA2 and may regulate the receptor stability and activity through proteasomal degradation.	Potentiate	34%		
MDM2	E3 ubiquitin-protein ligase that mediates ubiquitination of p53/TP53, leading to its degradation by the proteasome. Inhibits p53/TP53- and p73/TP73-mediated cell cycle arrest and apoptosis by binding its transcriptional activation domain. Also acts as a ubiquitin ligase E3 toward itself and ARRB1. Permits the nuclear export of p53/TP53. Promotes proteasome-dependent ubiquitin-independent degradation of retinoblastoma RB1 protein. Inhibits DAXX-mediated apoptosis by inducing its ubiquitination and degradation. Component of the TRIM28/KAP1-MDM2-p53/TP53 complex involved in stabilizing p53/TP53. Also component of the TRIM28/KAP1-ERBB4-MDM2 complex which links growth factor and DNA damage response pathways. Mediates ubiquitination and subsequent proteasome degradation of DYRK2 in nucleus. Ubiquitinates IGF1R and SNAI1 and promotes them to proteasomal degradation.	attenuate	-64%		
TRIM68	Functions as a ubiquitin E3 ligase. Acts as a coactivator of androgen receptor (AR) depending on its ubiquitin ligase activity.	attenuate	-74%		
HACE1	E3 ubiquitin-protein ligase involved in Golgi membrane fusion and regulation of small GTPases. Acts as a regulator of Golgi membrane dynamics during the cell cycle: recruited to Golgi membrane by Rab proteins and regulates postmitotic Golgi membrane fusion. Acts by mediating ubiquitination during mitotic Golgi disassembly, ubiquitination serving as a signal for Golgi reassembly later, after cell division. Specifically interacts with GTP-bound RAC1, mediating ubiquitination and subsequent degradation of active RAC1, thereby playing a role in host defense against pathogens. May also act as a transcription regulator via its interaction with RARB.	attenuate	-22%		
LRSAM1	E3 ubiquitin-protein ligase that mediates monoubiquitination of TSG101 at multiple sites, leading to inactivate the ability of TSG101 to sort endocytic (EGF receptors) and exocytic (HIV-1 viral proteins) cargos.	attenuate	-34%		
TRIM41	Functions as an E3 ligase that catalyzes the ubiquitin-mediated degradation of protein kinase C.	attenuate	-52%		

TOPORS	Functions as an E3 ubiquitin-protein ligase and as an E3 SUMO1-protein ligase. Probable tumor suppressor involved in cell growth, cell proliferation and apoptosis that regulates p53/TP53 stability through ubiquitin-dependent degradation. May regulate chromatin modification through sumoylation of several chromatin modification-associated proteins. May be involved in DNA damage-induced cell death through IKBKE sumoylation.	attenuate	-62%		
RNF123	Catalytic subunit of the KPC complex that acts as E3 ubiquitin-protein ligase. Required for poly-ubiquitination and proteasome-mediated degradation of CDKN1B during G1 phase of the cell cycle.	attenuate	-62%		
UBR4	E3 ubiquitin-protein ligase which is a component of the N-end rule pathway. Recognizes and binds to proteins bearing specific N-terminal residues that are destabilizing according to the N-end rule, leading to their ubiquitination and subsequent degradation. Together with clathrin, forms meshwork structures involved in membrane morphogenesis and cytoskeletal organization. Regulates integrin-mediated signaling. May play a role in activation of FAK in response to cell-matrix interactions. Mediates ubiquitination of ACLY, leading to its subsequent degradation.	attenuate	-16%		
HECTD3	E3 ubiquitin ligases accepts ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a thioester and then directly transfers the ubiquitin to targeted substrates. Mediates ubiquitination of TRIOBP and its subsequent proteasomal degradation, thus faciliting cell cycle progression by regulating the turn-over of TRIOBP. Mediates also ubiquitination of STX8	No effect	14%		
MARCH7	E3 ubiquitin-protein ligase which may specifically enhance the E2 activity of HIP2. E3 ubiquitin ligases accept ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a thioester and then directly transfer the ubiquitin to targeted substrates.	attenuate	-21%		
SMURF1	E3 ubiquitin-protein ligase that acts as a negative regulator of BMP signaling pathway. Mediates ubiquitination and degradation of SMAD1 and SMAD5, 2 receptor-regulated SMADs specific for the BMP pathway. Promotes ubiquitination and subsequent proteasomal degradation of TRAF family members and RHOA.	attenuate	-14%		
CBL	Adapter protein that functions as a negative regulator of many signaling pathways that are triggered by activation of cell surface receptors. Acts as an E3 ubiquitin-protein ligase, which accepts ubiquitin from specific E2 ubiquitin-conjugating enzymes, and then transfers it to substrates promoting their degradation by the proteasome. Recognizes activated receptor tyrosine kinases, including KIT, FLT1, FGFR1, FGFR2, PDGFRA, PDGFRB, EGFR, CSF1R, EPHA8 and KDR and terminates signaling. Recognizes membrane-bound HCK, SRC and other kinases of the SRC family and mediates their ubiquitination and degradation. Participates in signal transduction in hematopoietic cells. Plays an important role in the regulation of osteoblast differentiation and apoptosis. Essential for osteoclastic bone resorption. The 'Tyr-731' phosphorylated form induces the activation and recruitment of phosphatidylinositol 3-kinase to the cell membrane in a signaling pathway that is critical for osteoclast function. May be functionally coupled with the E2 ubiquitin-protein ligase UB2D3.	attenuate	-44%		
TRIP12	E3 ubiquitin-protein ligase involved in ubiquitin fusion degradation (UFD) pathway and regulation of DNA repair. Part of the ubiquitin fusion degradation (UFD) pathway, a process that mediates ubiquitination of protein at their N-terminus, regardeless of the presence of lysine residues in target proteins. In normal cells, mediates ubiquitination and degradation of isoform p19ARF/ARFof CDKN2A, a lysine-less tumor suppressor required for p53/TP53 activation under oncogenic stress. In cancer cells, however, isoform p19ARF/ARFand TRIP12 are located in different cell compartments, preventing isoform p19ARF/ARFubiquitination and degradation. Does not mediate ubiquitination of isoform p16-INK4aof CDKN2A. Also catalyzes ubiquitination of NAE1 and SMARCE1, leading to their degradation. Ubiquitination and degradation of target proteins is regulated by interaction with proteins such as MYC, TRADD or SMARCC1, which disrupt the interaction between TRIP12 and target proteins. Acts as a key regulator of DNA damage response by acting as a suppressor of RNF168, an E3 ubiquitin-protein ligase that promotes accumulation of 'Lys-63'-linked histone H2A and H2AX at DNA damage sites, thereby acting as a guard against excessive spreading of ubiquitinated chromatin at damaged chromosomes.	attenuate	-74%		
TRIM25	Functions as a ubiquitin E3 ligase and as an ISG15 E3 ligase. Involved in innate immune defense against viruses by mediating ubiquitination of DDX58. Mediates 'Lys-63'-linked polyubiquitination of the DDX58 N-terminal CARD-like region which is crucial for triggering the cytosolic signal transduction that leads to the production of interferons in response to viral infection. Promotes ISGylation of 14-3-3 sigma (SFN), an adapter protein implicated in the regulation of a large spectrum signaling pathway. Mediates estrogen action in various target organs.	attenuate	-80%		
HUWE1	E3 ubiquitin-protein ligase which mediates ubiquitination and subsequent proteasomal degradation of target proteins. Regulates apoptosis by catalyzing the polyubiquitination and degradation of MCL1. Mediates monoubiquitination of DNA polymerase beta (POLB) at 'Lys-41', 'Lys-61' and 'Lys-81', thereby playing a role in base-excision repair. Also ubiquitinates the p53/TP53 tumor suppressor and core histones including H1, H2A, H2B, H3 and H4. Binds to an upstream initiator-like sequence in the preprodynorphin gene. Regulates neural differentiation and proliferation by catalyzing the polyubiquitination and degradation of MYCN. May regulate abundance of CDC6 after DNA damage by polyubiquitinating and targeting CDC6 to degradation.	attenuate	-25%		

Sumoylation	**Description**	**Effect**	**% increase (+) or decrease (-)**		
CBX4	E3 SUMO-protein ligase CBX4	attenuate	-61%		
SUMO3	Small ubiquitin-related modifier 3	attenuate	-73%		
UBE2I	SUMO-conjugating enzyme UBC9	No effect	-14%		
RANBP2	E3 SUMO-protein ligase RanBP2	No effect	-9%		
De-ubiquitinases	**Description**	**Effect**	**% increase (+) or decrease (-)**		
USP10	Hydrolase that can remove conjugated ubiquitin from target proteins such as p53/TP53, BECN1, SNX3 and CFTR. Acts as an essential regulator of p53/TP53 stability: in unstressed cells, specifically deubiquitinates p53/TP53 in the cytoplasm, leading to counteract MDM2 action and stabilize p53/TP53. Following DNA damage, translocates to the nucleus and deubiquitinates p53/TP53, leading to regulate the p53/TP53-dependent DNA damage response. Component of a regulatory loop that controls autophagy and p53/TP53 levels: mediates deubiquitination of BECN1, a key regulator of autophagy, leading to stabilize the PIK3C3/VPS34-containing complexes. In turn, PIK3C3/VPS34-containing complexes regulate USP10 stability, suggesting the existence of a regulatory system by which PIK3C3/VPS34-containing complexes regulate p53/TP53 protein levels via USP10 and USP13. Does not deubiquitinate MDM2. Deubiquitinates CFTR in early endosomes, enhancing its endocytic recycling.	Potentiate	186%		
USP20	Deubiquitinating enzyme involved in beta-2 adrenergic receptor (ADRB2) recycling. Acts as a regulator of G-protein coupled receptor (GPCR) signaling by mediating the deubiquitination beta-2 adrenergic receptor (ADRB2). Plays a central role in ADRB2 recycling and resensitization after prolonged agonist stimulation by constitutively binding ADRB2, mediating deubiquitination of ADRB2 and inhibiting lysosomal trafficking of ADRB2. Upon dissociation, it is probably transferred to the translocated beta-arrestins, possibly leading to beta-arrestins deubiquitination and disengagement from ADRB2. This suggests the existence of a dynamic exchange between the ADRB2 and beta-arrestins. Deubiquitinates DIO2, thereby regulating thyroid hormone regulation. Deubiquitinates HIF1A, leading to stabilize HIF1A and enhance HIF1A-mediated activity. Mediates deubiquitination of both 'Lys-48'- and 'Lys-63'-linked polyubiquitin chains.	Potentiate	161%		
USP43	May recognize and hydrolyze the peptide bond at the C-terminal Gly of ubiquitin. Involved in the processing of poly-ubiquitin precursors as well as that of ubiquitinated proteins	Potentiate	218%		
USP45	Thiol-dependent hydrolysis of ester, thioester, amide, peptide and isopeptide bonds formed by the C-terminal Gly of ubiquitin (a 76-residue protein attached to proteins as an intracellular targeting signal).	Potentiate	80%		
USP38	Deubiquitinating enzyme exhibiting a preference towards 'Lys-63'-linked Ubiquitin chains.	Potentiate	73%		
USP49	Specifically deubiquitinates histone H2B at 'Lys-120' (H2BK120Ub). H2BK120Ub is a specific tag for epigenetic transcriptional activation and acts as a regulator of mRNA splicing. Deubiquitination is required for efficient cotranscriptional splicing of a large set of exons.	Potentiate	47%		
USP14	Proteasome-associated deubiquitinase which releases ubiquitin from the proteasome targeted ubiquitinated proteins. Ensures the regeneration of ubiquitin at the proteasome. Is a reversibly associated subunit of the proteasome and a large fraction of proteasome-free protein exists within the cell. Required for the degradation of the chemokine receptor CXCR4 which is critical for CXCL12-induced cell chemotaxis. Serves also as a physiological inhibitor of endoplasmic reticulum-associated degradation (ERAD) under the non-stressed condition by inhibiting the degradation of unfolded endoplasmic reticulum proteins via interaction with ERN1. Indispensable for synaptic development and function at neuromuscular junctions (NMJs).	no effect	5%		
USP13	Deubiquitinase that mediates deubiquitination of target proteins such as BECN1, MITF, SKP2 and USP10 and is involved in various processes such as autophagy and endoplasmic reticulum-associated degradation (ERAD). Component of a regulatory loop that controls autophagy and p53/TP53 levels: mediates deubiquitination of BECN1, a key regulator of autophagy, leading to stabilize the PIK3C3/VPS34-containing complexes. Also deubiquitinates USP10, an essential regulator of p53/TP53 stability. In turn, PIK3C3/VPS34-containing complexes regulate USP13 stability, suggesting the existence of a regulatory system by which PIK3C3/VPS34-containing complexes regulate p53/TP53 protein levels via USP10 and USP13. Recruited by nuclear UFD1 and mediates deubiquitination of SKP2, thereby regulating endoplasmic reticulum-associated degradation (ERAD). Mediates stabilization of SIAH2 independently of deubiquitinase activity: binds ubiquitinated SIAH2 and acts by impairing SIAH2 autoubiquitination. Has a weak deubiquitinase activity in vitro and preferentially cleaves 'Lys-63'-linked polyubiquitin chains. In contrast to USP5, it is not able to mediate unanchored polyubiquitin disassembly. Able to cleave ISG15 in vitro; however, additional experiments are required to confirm such data	No effect	-6%		

USP36	May be required for maintaining multiple types of adult stem cells. May function as a transcriptional repressor by continually deubiquiting histone H2B at the promoters of genes critical for cellular differentiation, thereby preventing histone H3 'Lys-4' trimethylation (H3K4)	potentiate	41%		
USP7	Hydrolase that deubiquitinates target proteins such as FOXO4, p53/TP53, MDM2, ERCC6, DNMT1, UHRF1, PTEN and DAXX. Together with DAXX, prevents MDM2 self-ubiquitination and enhances the E3 ligase activity of MDM2 towards p53/TP53, thereby promoting p53/TP53 ubiquitination and proteasomal degradation. Deubiquitinates p53/TP53 and MDM2 and strongly stabilizes p53/TP53 even in the presence of excess MDM2, and also induces p53/TP53-dependent cell growth repression and apoptosis. Deubiquitination of FOXO4 in presence of hydrogen peroxide is not dependent on p53/TP53 and inhibits FOXO4-induced transcriptional activity. In association with DAXX, is involved in the deubiquitination and translocation of PTEN from the nucleus to the cytoplasm, both processes that are counteracted by PML. Involved in cell proliferation during early embryonic development. Involved in transcription-coupled nucleotide excision repair (TC-NER) in response to UV damage: recruited to DNA damage sites following interaction with KIAA1530/UVSSA and promotes deubiquitination of ERCC6, preventing UV-induced degradation of ERCC6. Contributes to the overall stabilization and trans-activation capability of the herpesvirus 1 trans-acting transcriptional protein ICP0/VMW110 during HSV-1 infection. Involved in maintenance of DNA methylation via its interaction with UHRF1 and DNMT1: acts by mediating deubiquitination of UHRF1 and DNMT1, preventing their degradation and promoting DNA methylation by DNMT1. Exhibits a preference towards 'Lys-48'-linked Ubiquitin chains.	attenuate	-56%		
USP5	Cleaves linear and branched multiubiquitin polymers with a marked preference for branched polymers. Involved in unanchored 'Lys-48'-linked polyubiquitin disassembly. Binds linear and 'Lys-63'-linked polyubiquitin with a lower affinity. Knock-down of USP5 causes the accumulation o p53/TP53 and an increase in p53/TP53 transcriptional activity because the unanchored polyubiquitin that accumulates is able to compete with ubiquitinated p53/TP53 but not with MDM2 for proteasomal recognition.	attenuate	-41%		
USP35	Thiol-dependent hydrolysis of ester, thioester, amide, peptide and isopeptide bonds formed by the C-terminal Gly of ubiquitin (a 76-residue protein attached to proteins as an intracellular targeting signal).	attenuate	-51%		
COPI retrograde complex	**Description**	**Effect**	**% increase (+) or decrease (-)**		
ARF1	GTP-binding protein that functions as an allosteric activator of the cholera toxin catalytic subunit, an ADP-ribosyltransferase. Involved in protein trafficking among different compartments. Modulates vesicle budding and uncoating within the Golgi complex. Deactivation induces the redistribution of the entire Golgi complex to the endoplasmic reticulum, suggesting a crucial role in protein trafficking. In its GTP-bound form, its triggers the association with coat proteins with the Golgi membrane. The hydrolysis of ARF1-bound GTP, which is mediated by ARFGAPs proteins, is required for dissociation of coat proteins from Golgi membranes and vesicles. The GTP-bound form interacts with PICK1 to limit PICK1-mediated inhibition of Arp2/3 complex activity; the function is linked to AMPA receptor (AMPAR) trafficking, regulation of synaptic plasicity of excitatory synapses and spine shrinkage during long-term depression (LTD).	attenuate	-62%		
COPA	The coatomer is a cytosolic protein complex that binds to dilysine motifs and reversibly associates with Golgi non-clathrin-coated vesicles, which further mediate biosynthetic protein transport from the ER, via the Golgi up to the trans Golgi network. Coatomer complex is required for budding from Golgi membranes, and is essential for the retrograde Golgi-to-ER transport of dilysine-tagged proteins. In mammals, the coatomer can only be recruited by membranes associated to ADP-ribosylation factors (ARFs), which are small GTP-binding proteins; the complex also influences the Golgi structural integrity, as well as the processing, activity, and endocytic recycling of LDL receptors	attenuate	-61%		
COPD	The coatomer is a cytosolic protein complex that binds to dilysine motifs and reversibly associates with Golgi non-clathrin-coated vesicles, which further mediate biosynthetic protein transport from the ER, via the Golgi up to the trans Golgi network. Coatomer complex is required for budding from Golgi membranes, and is essential for the retrograde Golgi-to-ER transport of dilysine-tagged proteins. In mammals, the coatomer can only be recruited by membranes associated to ADP-ribosylation factors (ARFs), which are small GTP-binding proteins; the complex also influences the Golgi structural integrity, as well as the processing, activity, and endocytic recycling of LDL receptors	attenuate	-76%		
COPE	The coatomer is a cytosolic protein complex that binds to dilysine motifs and reversibly associates with Golgi non-clathrin-coated vesicles, which further mediate biosynthetic protein transport from the ER, via the Golgi up to the trans Golgi network. Coatomer complex is required for budding from Golgi membranes, and is essential for the retrograde Golgi-to-ER transport of dilysine-tagged proteins. In mammals, the coatomer can only be recruited by membranes associated to ADP-ribosylation factors (ARFs), which are small GTP-binding proteins; the complex also influences the Golgi structural integrity, as well as the processing, activity, and endocytic recycling of LDL receptors	attenuate	-43%		

COPG	The coatomer is a cytosolic protein complex that binds to dilysine motifs and reversibly associates with Golgi non-clathrin-coated vesicles, which further mediate biosynthetic protein transport from the ER, via the Golgi up to the trans Golgi network. Coatomer complex is required for budding from Golgi membranes, and is essential for the retrograde Golgi-to-ER transport of dilysine-tagged proteins. In mammals, the coatomer can only be recruited by membranes associated to ADP-ribosylation factors (ARFs), which are small GTP-binding proteins; the complex also influences the Golgi structural integrity, as well as the processing, activity, and endocytic recycling of LDL receptors	attenuate	-20%		
ER to Golgi					
Retromers and COPII complex	**Description**	**Effect**	**% increase (+) or decrease (-)**		
VPS26A	Essential component of the retromer complex, a complex required to retrieve lysosomal enzyme receptors (IGF2R and M6PR) from endosomes to the trans-Golgi network. Also required to regulate transcytosis of the polymeric immunoglobulin receptor (pIgR-pIgA). Component of the retromer complex composed of VPS26 (VPS26A or VPS26B), VPS29, VPS35, SNX1 and SNX2. Interacts directly with VPS35. Found in a complex with XPO7, EIF4A1, ARHGAP1, VPS26A, VPS29, VPS35 and SFN. Interacts with ECM29.	Attenuate	-36%		
VPS35	Essential component of the retromer complex, a complex required to retrieve lysosomal enzyme receptors (IGF2R and M6PR) from endosomes to the trans-Golgi network. Also required to regulate transcytosis of the polymeric immunoglobulin receptor (pIgR-pIgA).	Attenuate	-43%		
SEC24B	Component of the COPII coat, that covers ER-derived vesicles involved in transport from the endoplasmic reticulum to the Golgi apparatus. COPII acts in the cytoplasm to promote the transport of secretory, plasma membrane, and vacuolar proteins from the endoplasmic reticulum to the Golgi complex. COPII is composed of at least five proteins: the Sec23/24 complex, the Sec13/31 complex and SAR1. SEC24B is capable of forming heterodimers with SEC24A. Interacts with RNF139. Interacts with TMED2 and TMED10.	No effect	-45%		
SEC16A	Defines endoplasmic reticulum exit sites (ERES) and is required for secretory cargo traffic from the endoplasmic reticulum to the Golgi apparatus. SAR1A-GTP-dependent assembly of SEC16A on the ER membrane forms an organized scaffold defining an ERES. Required for normal transitional endoplasmic reticulum (tER) organization.	attenuate	-16%		
SEC24C	Component of the COPII coat, that covers ER-derived vesicles involved in transport from the endoplasmic reticulum to the Golgi apparatus. COPII acts in the cytoplasm to promote the transport of secretory, plasma membrane, and vacuolar proteins from the endoplasmic reticulum to the Golgi complex.	Attenuate	-65%		
Golgi and ER proteins	**Description**	**Effect**	**% increase (+) or decrease (-)**		
POMT1	Transfers mannosyl residues to the hydroxyl group of serine or threonine residues. Coexpression of both POMT1 and POMT2 is necessary for enzyme activity, expression of either POMT1 or POMT2 alone is insufficient.	attenuate	-87%		
ZDHHC17	Palmitoyltransferase specific for a subset of neuronal proteins, including SNAP25, DLG4/PSD95, GAD2, SYT1 and HD. Palmitoylates MPP1 in erythrocytes. May be involved in the sorting or targeting of critical proteins involved in the initiating events of endocytosis at the plasma membrane. Has transforming activity. Mediates Mg2+ transport.	attenuate	-57%		
UGT1A6	UDPGT is of major importance in the conjugation and subsequent elimination of potentially toxic xenobiotics and endogenous compounds. This isoform hasspecificity for phenols. Isoform 3 lacks transferase activity but acts as a negative regulator of isoform 1	potentiate	61%		
Others	**Description**	**Effect**	**% increase (+) or decrease (-)**		
UBA1	Activates ubiquitin by first adenylating its C-terminal glycine residue with ATP, and thereafter linking this residue to the side chain of a cysteine residue in E1, yielding a ubiquitin-E1 thioester and free AMP.	attenuate	-78%		
UBQLN2	Increases the half-life of proteins destined to be degraded by the proteasome; may modulate proteasome-mediated protein degradation.	attenuate	-84%		
NEDD8	Ubiquitin-like protein which plays an important role in cell cycle control and embryogenesis. Covalent attachment to its substrates requires prior activation by the E1 complex UBE1C-APPBP1 and linkage to the E2 enzyme UBE2M. Attachment of NEDD8 to cullins activates their associated E3 ubiquitin ligase activity, and thus promotes polyubiquitination and proteasomal degradation of cyclins and other regulatory proteins.	attenuate	-77%		
CAND1	Key assembly factor of SCF (SKP1-CUL1-F-box protein) E3 ubiquitin ligase complexes that promotes the exchange of the substrate-recognition F-box subunit in SCF complexes, thereby playing a key role in the cellular repertoire of SCF complexes.	attenuate	-78%		

SHBG	Functions as an androgen transport protein, but may also be involved in receptor mediated processes. Each dimer binds one molecule of steroid. Specific for 5-alpha-dihydrotestosterone, testosterone, and 17-beta-estradiol. Regulates the plasma metabolic clearance rate of steroid hormones by controlling their plasma concentration.	attenuate	-81%		
N4BP2	Has 5'-polynucleotide kinase and nicking endonuclease activity. May play a role in DNA repair or recombination.	attenuate	-77%		
SQSTM	Required both for the formation and autophagic degradation of polyubiquitin-containing bodies, called ALIS (aggresome-like induced structures). Links ALIS to the autophagic machinery via direct interaction with MAP1 LC3 family members. May regulate the activation of NFKB1 by TNF-alpha, nerve growth factor (NGF) and interleukin-1. May play a role in titin/TTN downstream signaling in muscle cells. May regulate signaling cascades through ubiquitination. Adapter that mediates the interaction between TRAF6 and CYLD By similarity. May be involved in cell differentiation, apoptosis, immune response and regulation of K+ channels	attenuate	-74%		
CDKAL1	Catalyzes the methylthiolation of N6-threonylcarbamoyladenosine (t6A), leading to the formation of 2-methylthio-N6-threonylcarbamoyladenosine (ms2t6A) at position 37 in tRNAs that read codons beginning with adenine	attenuate	-84%		
GANAB	Cleaves sequentially the 2 innermost alpha-1,3-linked glucose residues from the Glc2Man9GlcNAc2 oligosaccharide precursor of immature glycoproteins.	attenuate	-75%		
GBE1	Required for sufficient glycogen accumulation. The alpha 1-6 branches of glycogen play an important role in increasing the solubility of the molecule and, consequently, in reducing the osmotic pressure within cells.	attenuate	-60%		
TLR4	Cooperates with LY96 and CD14 to mediate the innate immune response to bacterial lipopolysaccharide (LPS). Acts via MYD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory response. Also involved in LPS-independent inflammatory responses triggered by Ni2+. These responses require non-conserved histidines and are, therefore, species-specific.	attenuate	-53%		
GGCT	Catalyzes the formation of 5-oxoproline from gamma-glutamyl dipeptides and may play a significant role in glutathione homeostasis. Induces release of cytochrome c from mitochondria with resultant induction of apoptosis	potentiate	800%		
TSG101	Component of the ESCRT-I complex, a regulator of vesicular trafficking process. Binds to ubiquitinated cargo proteins and is required for the sorting of endocytic ubiquitinated cargos into multivesicular bodies (MVBs). Mediates the association between the ESCRT-0 and ESCRT-I complex. Required for completion of cytokinesis; the function requires CEP55. May be involved in cell growth and differentiation. Acts as a negative growth regulator. Involved in the budding of many viruses through an interaction with viral proteins that contain a late-budding motif P-[ST]-A-P. This interaction is essential for viral particle budding of numerous retroviruses.	no effect	7%		
UBE2N	The UBE2V1-UBE2N and UBE2V2-UBE2N heterodimers catalyze the synthesis of non-canonical 'Lys-63'-linked polyubiquitin chains. This type of polyubiquitination does not lead to protein degradation by the proteasome. Mediates transcriptional activation of target genes. Plays a role in the control of progress through the cell cycle and differentiation. Plays a role in the error-free DNA repair pathway and contributes to the survival of cells after DNA damage. Acts together with the E3 ligases, HLTF and SHPRH, in the 'Lys-63'-linked poly-ubiquitination of PCNA upon genotoxic stress, which is required for DNA repair. Appears to act together with E3 ligase RNF5 in the 'Lys-63'-linked polyubiquitination of JKAMP thereby regulating JKAMP function by decreasing its association with components of the proteasome and ERAD. Promotes TRIM5 capsid-specific restriction activity and the UBE2V1-UBE2N heterodimer acts in concert with TRIM5 to generate 'Lys-63'-linked polyubiquitin chains which activate the MAP3K7/TAK1 complex which in turn results in the induction and expression of NF-kappa-B and MAPK-responsive inflammatory genes	no effect	12%		
NAGA	Removes terminal alpha-N-acetylgalactosamine residues from glycolipids and glycopeptides. Required for the breakdown of glycolipids.	attenuate	-47%		
USO1	Required for protein transport from the ER to the Golgi complex. Homodimer. Dimerizes by parallel association of the tails, resulting in an elongated structure with two globular head domains side by side, and a long rod-like tail structure.	attenuate	-46%		
SEC13	Functions as a component of the nuclear pore complex (NPC) and the COPII coat. At the endoplasmic reticulum, SEC13 is involved in the biogenesis of COPII-coated vesicles. As a component of the GATOR2 complex, inhibits GATOR1 complex, an inhibitor of the amino acid-sensing branch of the TORC1 pathway.	attenuate	-62%		
SEC22A	May be involved in vesicle transport between the ER and the Golgi complex	attenuate	-62%		

Supplemental Table 4. Detailed description of the peptides identified in the proteomic screen

Number	File Name	Charge State (z)	Score	# of Miss Cleavages	Total Intensity	Variable Modification Sites	Sequence	Sequence Map	Modifications	Retention Time (min)	m/z	Parent Mass	Delta Parent Mass	Delta Parent Mass (ppm)	Peptide PI	Protein Molecular Weight	Protein PI	Species	Accession Number	Entry Name
1	dirMS_041712_NAR_50mM_minus2.11374.11874.3	3	27.22	1	3.47E+06		(K)DVDEAY	(K)D V|D|E/A/Y/M/N/K/V/E/L/E/S R(L)		134.43	599.9481	1797.832	-0.0026	-1.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
2	dirMS_041712_NAR_20mM_minus.12370.12509.2	2	26.5	0	1.76E+06	M256m	(R)SLDmDS	(R)S/L|D|m|D|S/I/I|A/E/V/K(A)	m:Oxidized methionine	171.83	668.8364	1320.671	15.994	-0.7	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
3	dirMS_041712_NAR_30mM_plus2.11767.11828.2	2	26.5	0	5.40E+05		(K)VASGCLI	(K)V/A|S|G|C|L|D/I/N/S S V/K(G)	C:Carbamidomethylation	114.82	675.3393	1349.673	-0.0016	-1.2	5.81	56837	7.19	HUMAN	E7ETT1	Propionyl-CoA carboxylase beta chain, mitochondrial
4	dirMS_041712_NAR_120mM_minus.9646.9913.3	3	26.42	0	1.34E+07		(K)QEYDES	(K)Q E/Y/D E/S/G/P/S/I/V/H/R(K)		108.05	506.2424	1516.703	0.01	6.6	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
5	dirMS_041712_NAR_60mM_minus.9926.9945.3	3	26.39	1	5.20E+05		(K)GILAAD	(K)G I|L|A/A/D/E/S/T/G S I/A K/R(L)		115.15	496.9379	1488.802	-0.0025	-1.7	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
6	dirMS_041712_NAR_50mM_plus2.19239.19494.3	3	26.13	1	7.33E+05		(K)AIDLFTD	(K)A I|D|L/F/T/D/A/I/K/L/N/P R(L)		170.02	529.6346	1586.89	-0.0008	-0.5	6	18141.9	4.7	HUMAN	F6VDH7	Hsc70-interacting protein (Fragment)
7	dirMS_041712_NAR_50mM_minus2.17263.17557.3	3	25.96	1	9.35E+05		(K)IILDLISE	(K)I/I/L/D|L/I/S/E/S/P I/K/G R(A)		167.7	518.6444	1553.926	-0.0075	-4.8	6.07	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
8	dirMS_041712_NAR_50mM_plus2.20242.20602.3	3	25.85	1	1.67E+06		(R)TLAEIAK	(R)T/L|A|E/I/A/K/A/E/L/D/G T/I L/K(S)		175.92	562.6601	1685.968	-0.0026	-1.6	4.68	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
9	dirMS_041712_NAR_20mM_minus.12030.12362.2	2	25.51	0	2.70E+06	M256m	(R)SLDmDS	(R)S L|D|m/D|S/I|I|A|E|V/K(A)	m:Oxidized methionine	171.22	668.8364	1320.671	15.994	-0.7	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
10	dirMS_041712_NAR_30mM_plus2.6010.6010.2	2	25.48	0	1.72E+05		(R)GGSGGS	(R)G G/S G G S\Y|G/G G/G|S/G G G/Y/G/G/G S/G S/R(G)		85.83	896.3659	1791.728	-0.0032	-1.8	8.59	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
11	dirMS_041712_NAR_60mM_minus.13205.13246.3	3	25.37	1	9.10E+05		(K)DVDEAY	(K)D V|D|E/A/Y/M/N K/V/E/L/E/S R(L)		133.75	599.9463	1797.832	-0.008	-4.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
12	dirMS_041712_NAR_20mM_plus.18632.18838.2	2	25.32	0	2.48E+05		(K)IYVDDGI	(K)I/Y|V|D|D|G|L/I|S/L/Q/V/K(Q)		200.73	731.9068	1462.815	-0.0088	-6	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
13	dirMS_041712_NAR_60mM_plus.15198.15373.3	3	25.31	0	1.86E+06		(K)LGDVYV	(K)L/G|D|V|Y/V/N|D/A/F G T/A H/R(A)		136.52	545.6025	1634.792	0.0008	0.5	5.21	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
14	dirMS_041712_NAR_50mM_plus2.15826.15939.3	3	25.17	1	8.82E+06		(R)ALAEIAK	(R)A L|A|E|I/A/K/A/E|L/D/D/T|P M R(G)		151.43	581.9697	1743.895	0	0	4.32	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
15	dirMS_041712_NAR_60mM_plus.7116.7180.3	3	25.12	0	1.83E+06		(K)TIEAEAA	(K)T|I|E/A/E/A/A/H/G T V T/R(H)		95.58	452.5687	1355.691	0.0002	0.1	5.37	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
16	dirMS_041712_NAR_20mM_minus.12023.12355.2	2	25.07	0	2.70E+06	M256m	(R)SLDmDS	(R)S L|D|m/D|S/I|I|A/E|V/K(A)	m:Oxidized methionine	171.22	668.8364	1320.671	15.994	-0.7	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
17	dirMS_041712_NAR_60mM_plus.9174.9327.3	3	24.99	1	1.31E+06		(R)FNEVAA	(R)F/N|E|V/A/A/Q/Y/S E D K/A R(Q)		106.1	543.2616	1627.771	-0.0008	-0.5	4.68	14236.2	10.25	HUMAN	F5H1P5	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4
18	dirMS_041712_NAR_30mM_plus2.17905.18433.2	2	24.97	0	2.52E+07		(K)LLCGLLA	(K)L/L|C|G|L|L|A/E/R(L)	C:Carbamidomethylation	149.37	522.7969	1044.587	-0.0005	-0.5	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
19	dirMS_041712_NAR_60mM_plus.7190.7346.2	2	24.9	1	1.58E+06		(R)AAPGAE	(R)A/A/P/G|A/E/F|A/P N K/R(R)		96.2	614.8248	1228.643	-0.001	-0.8	8.79	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
20	dirMS_041712_NAR_30mM_plus2.19610.19610.2	2	24.73	0	1.56E+06		(R)ISEQFTA	(R)I/S|E/Q/F|T/A/M/F R(R)		157.08	615.3024	1229.598	-0.0008	-0.6	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
21	dirMS_041712_NAR_40mM_minus2.12093.12464.3	3	24.67	0	4.82E+05		(K)IAILTCPF	(K)I/A|I|L/T/C/P F/E/P/P K/P K(T)	C:Carbamidomethylation	155.75	537.6382	1610.898	0.0026	1.6	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
22	dirMS_041712_NAR_20mM_minus.12015.12351.2	2	24.66	0	2.70E+06	M256m	(R)SLDmDS	(R)S/L|D|m|D|S/I|I|A/E|V/K(A)	m:Oxidized methionine	171.22	668.8364	1320.671	15.994	-0.7	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
23	dirMS_041712_NAR_120mM_minus.10520.10874.3	3	24.61	1	1.14E+06		(R)YLAEFA	(R)Y/L|A|E/F/A/T/G N D/R K(E)		113.15	462.2338	1384.686	0.0013	0.9	6.07	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
24	dirMS_041712_NAR_50mM_plus2.18704.19214.3	3	24.56	1	6.37E+06		(R)GLFIIDD	(R)G L|F|I/I/D/D/K/G I L/R(Q)		167.33	453.9379	1359.8	-0.0003	-0.2	5.96	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
25	dirMS_041712_NAR_50mM_plus2.14519.14660.3	3	24.54	0	6.08E+05		(R)DLSYCLS	(R)D L|S|Y/C/L/S/G/M/Y D/H/R(Y)	C:Carbamidomethylation	144.83	539.5651	1616.683	-0.0024	-1.5	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
26	dirMS_041712_NAR_40mM_plus2.15542.15873.3	3	24.51	1	1.20E+06		(K)VLDSGA	(K)V/L|D|S/G/A|P I K I|P/V/G/P E/T L G R(I)		159.17	640.3668	1919.096	-0.0102	-5.3	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
27	dirMS_041712_NAR_60mM_minus.8692.8956.3	3	24.48	0	3.43E+07		(K)QEYDES	(K)Q E/Y/D E/S/G/P/S/I/V/H/R(K)		110.32	506.2391	1516.703	0.0001	0.1	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
28	dirMS_041712_NAR_50mM_plus2.18191.18666.3	3	24.39	1	6.46E+06		(K)IILDLISE	(K)I/I|L/D|L/I/S/E/S/P I K G R(A)		165.22	518.6453	1553.926	-0.0048	-3.1	6.07	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
29	dirMS_041712_NAR_20mM_plus.14147.14498.2	2	24.35	0	2.99E+06	M256m	(R)SLDmDS	(R)S/L|D|m|D|S/I/I|A/E/V/K(A)	m:Oxidized methionine	170.42	668.8371	1320.671	15.9954	0.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
30	dirMS_041712_NAR_50mM_plus2.18028.18329.3	3	24.35	1	1.46E+06		(K)VVLDDK	(K)V/V|L/D/D/K/D/Y/F/L/F/R(D)		164.12	510.6044	1529.8	-0.0012	-0.8	4.43	5189.9	4.56	HUMAN	B8ZZ54	10 kDa heat shock protein, mitochondrial
31	dirMS_041712_NAR_60mM_minus.8312.8435.3	3	24.3	0	8.83E+05		(K)VSYGIGI	(K)V/S|Y/G|I/G/D E E/H/D/Q/E/G R(V)		106.73	564.2471	1690.73	-0.0036	-2.1	4.17	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
32	dirMS_041712_NAR_60mM_plus.17341.17554.3	3	24.3	1	1.26E+06		(R)FLQDYFI	(R)F/L|Q/D/Y|F/D/G N L K/R(Y)		148.32	505.9247	1515.759	0.0005	0.3	5.96	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
33	dirMS_041712_NAR_60mM_minus.13943.14052.3	3	24.26	0	3.54E+05		(K)DCGATV	(K)D\C|G|A/T/W/V/V/L/G H S E R(R)	C:Carbamidomethylation	138.02	529.5838	1586.738	-0.0012	-0.7	5.32	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
34	dirMS_041712_NAR_60mM_plus.16586.16586.2	2	24.25	0	7.89E+05		(R)EHALLA	(R)E/H|A|L|L|A/Y/T L G V K(Q)		143.77	657.8735	1314.742	-0.0019	-1.4	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
35	dirMS_041712_NAR_30mM_minus2.7759.8008.2	2	24.16	0	1.38E+08		(K)AGFAGD	(K)A/G|F|A|G/D/D/A/P/R(A)		98.17	488.7304	976.448	0.0052	5.4	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
36	dirMS_041712_NAR_30mM_minus2.10293.10293.2	2	24.11	0	2.81E+05		(R)ETAEAD	(R)E T|A|E/A/D/V|A/S/L/N R(R)		110.08	638.3134	1275.618	0.002	1.6	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
37	dirMS_041712_NAR_50mM_plus2.18566.18715.3	3	24.08	1	5.28E+05		(K)TGISDVF	(K)T/G/I|S/D/V/F/A K N D|L/A/V|V/D/V R(I)		166.27	640.3449	1919.023	-0.0031	-1.6	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
38	dirMS_041712_NAR_50mM_plus2.20429.20706.3	3	24.05	1	1.51E+06		(K)SYLNMD	(K)S/Y|L/N/M/D/A/I/M/E/A I/K K(T)		177.6	542.9473	1626.823	0.0044	2.7	5.79	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
39	dirMS_041712_NAR_30mM_plus2.22541.22620.2	2	24.03	0	2.50E+06		(R)LEGLTDI	(R)L/E|G|L|T|D|E|I/N/F/L/R(Q)		175.42	710.3766	1419.748	-0.0019	-1.3	4.14	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
40	dirMS_041712_NAR_30mM_minus2.16515.16515.2	2	23.96	0	4.38E+05	M185m	(K)LAVNm	(K)L/A/V/N/m|V/P F/P R(L)	m:Oxidized methionine	142.67	580.3178	1143.634	15.994	-0.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
41	dirMS_041712_NAR_50mM_plus2.18057.18199.3	3	23.88	0	1.47E+06		(K)ALSAIAD	(K)A L|S|A/I/A/D/L/L/T/N/E H E R(V)		163.75	551.6254	1652.86	0.0014	0.9	4.65	105417.2	6.41	HUMAN	C9JZR2	Catenin delta-1
42	dirMS_041712_NAR_60mM_minus.15869.16146.3	3	23.86	1	5.23E+05		(R)IFDSEEIL	(R)I/F|D/S/E E/I/L/A/G/Y K R(E)		148.88	514.2713	1540.801	-0.0012	-0.8	4.68	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
43	dirMS_041712_NAR_20mM_plus.17653.17653.2	2	23.84	0	9.58E+04	M148m	(K)TFAPEEI	(K)T F/A/P E E I/S/A m|V L T K(M)	m:Oxidized methionine	193.53	776.8996	1536.798	15.9941	-0.5	4.53	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
44	dirMS_041712_NAR_30mM_minus2.10792.11262.2	2	23.79	0	6.68E+06		(R)ISVYYNE	(R)I/S|V|Y|Y/N/E|A/T/G G K(Y)		113.98	651.322	1301.637	-0.0005	-0.4	6	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
45	dirMS_041712_NAR_30mM_plus2.20410.20809.2	2	23.78	0	4.74E+05		(R)SLVPAAI	(R)S L|V|P/A/A/E/L|L/E/S/R(V)		162.17	642.8602	1284.716	-0.0027	-2.1	4.53	533778	5.74	HUMAN	Q15149	Plectin
46	dirMS_041712_NAR_40mM_minus2.11731.11772.3	3	23.77	1	2.86E+06		(R)IINEPTA	(R)I/I|N|E|P T/A/A/A/I/A/Y G L D/K K(V)		153.08	596.6671	1787.99	-0.0034	-1.9	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
47	dirMS_041712_NAR_50mM_minus2.13783.13937.3	3	23.77	1	3.91E+05		(K)ITDIIGKE	(K)I/T|D|I|I|G K/E E/G\I|G/P E N L\R(G)		146.9	618.665	1853.997	-0.0163	-8.8	4.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
48	dirMS_041712_NAR_120mM_plus.6082.6341.3	3	23.69	1	1.97E+06		(K)DSYVGD	(K)D S|Y|V/G/D/E/A/Q/S K R(G)		86.32	452.2133	1354.623	0.002	1.5	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
49	dirMS_041712_NAR_30mM_plus2.6085.6086.2	2	23.67	0	8.14E+05		(R)NQGGY	(R)N/Q|G/G|Y/G G/S/S/S/S/S/S/Y/G/S G R(R)		86.18	847.8524	1694.7	-0.0026	-1.5	8.59	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
50	dirMS_041712_NAR_50mM_minus2.12370.12391.3	3	23.66	0	1.08E+06		(K)LGDVYV	(K)L/G|D|V|Y|V/N/D/A/F G T A H R(A)		138.38	545.6023	1634.792	0.0002	0.1	5.21	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
51	dirMS_041712_NAR_30mM_plus2.15014.15522.2	2	23.66	0	1.03E+07		(K)LSELEAA	(K)L/S|E|L|E\A/A/L/Q/R(A)		132.32	565.3227	1129.621	0.017	15	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
52	dirMS_041712_NAR_20mM_plus.17576.17576.2	2	23.65	0	1.61E+05	M74m	(R)mIAGQ	(R)m I|A/G Q/V|L/D/I/N/L A\A E/P K(V)	m:Oxidized methionine	192.85	849.9568	1682.915	15.9918	-1.9	4.37	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
53	dirMS_041712_NAR_30mM_minus2.9185.9289.2	2	23.59	0	2.85E+06		(R)VIGSGCI	(R)V/I|G|S/G|C/N/L/D/S A/R(F)	C:Carbamidomethylation	104.52	624.8035	1248.6	-0.0004	-0.3	5.81	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
54	dirMS_041712_NAR_50mM_plus2.15833.15884.3	3	23.59	0	1.21E+06		(K)IAILTCPF	(K)I/A|I|L/T/C/P F/E/P P K/P K(T)	C:Carbamidomethylation	151.62	537.6393	1610.898	0.0059	3.7	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
55	dirMS_041712_NAR_60mM_plus.6358.6380.2	2	23.59	1	1.56E+06		(K)DSYVGD	(K)D/S|Y|V|G/D/E/A/Q/S K/R(G)		91.98	677.8149	1354.623	-0.0008	-0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
56	dirMS_041712_NAR_120mM_plus.17875.18084.3	3	23.58	0	7.30E+05		(R)HLLQAP	(R)H/L|L/Q|A|P V D D|A\Q/E|I/L/H S R(F)		146.82	648.0088	1942.014	-0.0023	-1.2	5.21	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
57	dirMS_041712_NAR_120mM_plus.22179.22245.4	4	23.56	1	5.80E+05		(R)SLHDAL	(R)S L H\D A\L|C|V|L|A/Q/T/V/K/D/S R(T)	C:Carbamidomethylation	170.13	479.0094	1912.991	0.0248	13	6.47	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
58	dirMS_041712_NAR_60mM_plus.11231.11231.2	2	23.51	0	2.12E+06		(K)GIVEFAS	(K)G I|V|E|F|A/S K/P A A/R(K)		116.18	623.3504	1245.695	-0.0015	-1.2	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
59	dirMS_041712_NAR_50mM_plus2.18646.18685.3	3	23.46	1	5.28E+05		(K)TGISDVF	(K)T/G|I|S/D/V|F/A K/N D|L/A|V/V D/V R(I)		166.27	640.3449	1919.023	-0.0031	-1.6	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
60	dirMS_041712_NAR_30mM_plus2.22038.22454.2	2	23.43	0	5.20E+06		(R)SLDMDS	(R)S L|D|M/D|S|I|I/A/E/V/K(A)		172.65	660.8437	1320.671	0.0086	6.5	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
61	dirMS_041712_NAR_60mM_plus.8483.8715.3	3	23.41	0	1.39E+06		(K)VDNDEN	(K)V/D|N/D/E/N/E/H/Q/L/S L/R(T)		102.82	523.5814	1568.73	-0.0003	-0.2	4.31	6862.5	4.32	HUMAN	E5RGW4	Nucleophosmin (Fragment)
62	dirMS_041712_NAR_50mM_minus2.9685.10118.3	3	23.34	0	4.86E+05		(R)EALLSSA	(R)E A|L|L/S/S/A/V|D|H G S D E/V/K(F)		124.27	552.9403	1656.807	-0.0012	-0.7	4.31	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
63	dirMS_041712_NAR_50mM_minus2.14827.15085.3	3	23.27	0	2.89E+05		(K)IAILTCPF	(K)I/A|I/L/T/C|P F/E/P P K/P K(T)	C:Carbamidomethylation	153.68	537.6375	1610.898	0.0005	0.3	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
64	dirMS_041712_NAR_50mM_plus2.14468.14468.3	3	23.27	0	1.06E+06		(R)ETHSAL	(R)E T H S A/L|G|P/A|L/Q|A/A F/K(L)		144.3	514.2745	1540.812	-0.0029	-1.9	6.85	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
65	dirMS_041712_NAR_60mM_minus.5545.5545.3	3	23.26	1	3.66E+07		(K)DSYVGD	(K)D S|Y|V/G D/E/A/Q/S K/R(G)		87.63	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
66	dirMS_041712_NAR_30mM_plus2.18721.18879.2	2	23.23	0	6.67E+05		(R)SYNDEL	(R)S/Y|N|D|E/L|Q/F/L/E/K(I)		152.13	693.335	1385.658	0.0044	3.2	4.14	19338.9	5.33	HUMAN	E7EQS9	tRNA-splicing ligase RtcB homolog
67	dirMS_041712_NAR_30mM_minus2.17505.18006.2	2	23.19	0	1.10E+07		(K)LLCGLLA	(K)L/L|C|G|L|L/A E/R(L)	C:Carbamidomethylation	151.02	522.7963	1044.587	-0.0017	-1.6	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
68	dirMS_041712_NAR_50mM_plus2.17516.17716.3	3	23.16	1	3.01E+06		(K)TVTAMD	(K)T V|T|A/M/D/V/V/Y A L K/R(Q)		161	489.6059	1466.804	-0.0004	-0.3	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
69	dirMS_041712_NAR_30mM_minus2.14938.15247.2	2	23.15	0	1.44E+07		(K)LSELEAA	(K)L/S|E|L|E\A/A|L/Q/R(A)		135.17	565.3142	1129.621	0	0	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
70	dirMS_041712_NAR_60mM_minus.16949.17072.3	3	23.15	0	1.02E+06		(K)ICDQWD	(K)I/C|D/Q/W D/A|L/G/S/L/T/H S R(R)	C:Carbamidomethylation	154.87	586.9446	1758.823	-0.0035	-2	5.21	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
71	dirMS_041712_NAR_50mM_plus2.12167.12387.3	3	23.11	1	1.69E+06		(K)ILIANTG	(K)I/L|I/A/N/T/G M/D/T D/K I K(I)		132.52	511.6172	1532.835	0.0018	1.2	5.96	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
72	dirMS_041712_NAR_40mM_plus2.14497.14828.3	3	23.09	0	5.43E+05		(K)IAILTCPF	(K)I/A|I/L/T/C/P F/E/P P K/P K(T)	C:Carbamidomethylation	153.55	537.6381	1610.898	0.0023	1.4	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
73	dirMS_041712_NAR_60mM_minus.16799.17030.3	3	23.07	0	1.02E+06		(K)ICDQWD	(K)I/C|D/Q/W/D A|L/G/S L/T/H S R(R)	C:Carbamidomethylation	154.87	586.9446	1758.823	-0.0035	-2	5.21	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
74	dirMS_041712_NAR_30mM_plus2.21279.21279.2	2	23.07	0	2.95E+05		(R)GVVQEL	(R)G V|V|Q/E|L|Q Q/A I/S/K(L)		165.93	650.3632	1299.727	-0.0076	-5.8	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
75	dirMS_041712_NAR_30mM_plus2.20024.20419.2	2	23.06	0	7.28E+05		(K)SYELPD	(K)S Y|E|L|P/D/G Q/V|I|T/I|G N E R(F)		159.77	895.9487	1790.892	-0.0018	-1	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
76	dirMS_041712_NAR_40mM_plus2.18063.18189.3	3	23.06	1	1.58E+06		(K)TFVNITP	(K)T F|V|N|I T/P A E V/G V/L|V/G K D/R(S)		173.02	639.0251	1915.065	-0.004	-2.1	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
77	dirMS_041712_NAR_120mM_plus.9769.9814.3	3	23.05	0	7.61E+05		(K)TVAIHSI	(K)T/V|A/I/H S D|V|D/A/S S V/H V K(M)		104.53	555.6244	1664.86	-0.0016	-0.9	5.91	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
78	dirMS_041712_NAR_30mM_minus2.16152.16559.2	2	23.03	0	4.42E+05	M185m	(K)LAVNm	(K)L/A|V|N/m|V|P/F/P/R(L)	m:Oxidized methionine	142.58	580.3178	1143.634	15.994	-0.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
79	dirMS_041712_NAR_60mM_plus.14548.14888.3	3	23.03	0	1.55E+06		(K)YYVTIID	(K)Y/Y|V/T/I/I/D/A/P/G H/R(D)		133.28	468.9136	1404.727	-0.0008	-0.6	6.74	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
80	dirMS_041712_NAR_30mM_minus2.11859.12019.2	2	23.02	0	2.09E+06		(K)GISQEQI	(K)G I|S|Q|E|Q|M/Q/E/F/R(A)		118.58	676.8161	1352.626	-0.0014	-1	4.53	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
81	dirMS_041712_NAR_50mM_plus2.10324.10326.3	3	23.02	0	3.78E+05		(R)MVQVH	(R)M/V|Q|V/H/E/L/S/C E/G/I S K(S)	C:Carbamidomethylation	121.6	539.5992	1616.777	0.006	3.7	5.38	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
82	dirMS_041712_NAR_60mM_plus.20191.20362.3	3	23.01	1	3.02E+05		(K)IILDLISE	(K)I/I|L/D/L/I/S/E/S/P I K/G R(A)		166.2	518.6452	1553.926	-0.0051	-3.3	6.07	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
83	dirMS_041712_NAR_30mM_plus2.18896.19212.2	2	23	0	3.29E+06		(R)QAQEYE	(R)Q A|Q|E|Y/E/A/L/L/N/I/K(V)		153.28	710.3766	1419.748	-0.0019	-1.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
84	dirMS_041712_NAR_30mM_plus2.8906.8906.2	2	22.99	0	7.37E+05		(R)GMGPG	(R)G M/G/P G/T/P/A G Y/G R(G)		100.28	560.7657	1120.52	0.0037	3.3	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
85	dirMS_041712_NAR_30mM_minus2.18844.18914.2	2	22.95	0	4.54E+05		(R)ISEQFTA	(R)I/S|E/Q|F/T/A/M/F/R(R)		157.42	615.3038	1229.598	0.002	1.6	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
86	dirMS_041712_NAR_60mM_plus.14889.14938.3	3	22.95	0	6.52E+05		(R)GIYAYGI	(R)G I|Y|A|Y|G/F/E/K/P S A I Q Q R(A)		134.65	609.9803	1827.939	-0.0125	-6.8	8.5	16071.1	4.8	HUMAN	B4E102	Eukaryotic initiation factor 4A-I
87	dirMS_041712_NAR_40mM_plus2.15894.16181.3	3	22.94	0	3.61E+05		(K)VAIVKP	(K)V/A|I|V/K/P G V|P|M/E I V L N/K(E)		161.22	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
88	dirMS_041712_NAR_60mM_plus.20165.20165.3	3	22.91	0	2.36E+05		(K)ALSAIAD	(K)A L/S/A/I A/D L/L/T/N E H E/R(V)		165.23	551.6246	1652.86	-0.001	-0.6	4.65	105417.2	6.41	HUMAN	C9JZR2	Catenin delta-1
89	dirMS_041712_NAR_120mM_minus.6663.6858.2	2	22.9	1	8.82E+06		(K)DSYVGD	(K)D/S|Y|V|G/D|E/A/Q/S K/R(G)		91.17	677.8145	1354.623	-0.0016	-1.2	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
90	dirMS_041712_NAR_120mM_plus.7561.7561.3	3	22.89	1	6.54E+05		(R)SGGYGG	(R)S/G|G/Y/G/G S R D Y Y/S S R(S)		93.37	504.5549	1511.651	-0.0008	-0.5	8.22	26585.7	11.25	HUMAN	B3KT17	Cold-inducible RNA-binding protein
91	dirMS_041712_NAR_30mM_plus2.18454.18633.2	2	22.89	0	2.28E+07		(K)LLCGLLA	(K)L/L|C|G|L|L|A E/R(L)	C:Carbamidomethylation	149.47	522.7969	1044.587	-0.0005	-0.5	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
92	dirMS_041712_NAR_30mM_plus2.11558.11826.2	2	22.87	0	1.28E+06		(R)GGGGN	(R)G G/G/G\N|F|G|P/G/P/G S/N F/R(G)		114.4	689.3175	1377.629	-0.0017	-1.2	9.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
93	dirMS_041712_NAR_30mM_plus2.6220.6338.2	2	22.87	0	5.37E+05		(K)DSYVGD	(K)D S|Y|V|G|D/E/A/Q/S/K(R)		87.18	599.7645	1198.522	-0.0005	-0.4	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
94	dirMS_041712_NAR_40mM_plus2.14663.14663.3	3	22.84	0	5.43E+05		(K)IAILTCPF	(K)I/A|I/L/T/C/P/F/E/P P K P K(T)	C:Carbamidomethylation	153.55	537.6381	1610.898	0.0023	1.4	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
95	dirMS_041712_NAR_30mM_plus2.16475.16761.2	2	22.83	0	7.62E+04		(K)LGEWV	(K)L/G|E|W|V|G/L/C|K(I)	C:Carbamidomethylation	139.5	531.2766	1061.545	0.0011	1	6	14914.1	6.84	HUMAN	P25398	40S ribosomal protein S12
96	dirMS_041712_NAR_50mM_plus2.15824.15965.3	3	22.8	1	1.33E+06		(R)VFIGNL	(R)V/F|I/G N L/N/T/L/V/V/K/K(S)		151.57	482.3007	1444.889	-0.0011	-0.7	10	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
97	dirMS_041712_NAR_60mM_plus.16048.16417.3	3	22.77	0	1.53E+06		(K)SLTNDW	(K)S L|T/N/D/W/E/D H/L/A V/K(H)		141.98	509.919	1527.744	-0.0014	-0.9	4.53	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
98	dirMS_041712_NAR_30mM_minus2.18014.18220.2	2	22.76	0	4.12E+05		(R)LLLNNDI	(R)L/L|L|N/N|D/N/L/L/R(E)		153.13	599.3487	1197.695	-0.0049	-4.1	5.84	19945.8	4.97	HUMAN	B4DG50	F-actin-capping protein subunit alpha-2
99	dirMS_041712_NAR_60mM_minus.7960.8074.3	3	22.75	1	4.84E+05		(R)YLAEVA	(R)Y/L|A/E/V/A/T/G E K/R(A)		104.27	412.8902	1236.658	-0.0022	-1.8	6.14	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
100	dirMS_041712_NAR_20mM_plus.16621.16621.2	2	22.74	0	5.45E+05		(K)LGGSAV	(K)L G G S A/V|I/S L|E/G\K|P L(-)		185.73	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
101	dirMS_041712_NAR_50mM_plus2.17513.17513.3	3	22.73	0	5.30E+05		(R)GGYVLH	(R)G G|Y/V|L/H/I/G T I/Y G D/L/K(V)		160.33	535.9588	1605.863	-0.0017	-1	6.74	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
102	dirMS_041712_NAR_30mM_minus2.16981.17142.2	2	22.72	0	1.97E+05		(R)SIQEELC	(R)S/I|Q|E|E|L/Q/Q/L/R(Q)		146.5	622.3359	1243.664	0.0004	0.3	4.53	533778	5.74	HUMAN	Q15149	Plectin
103	dirMS_041712_NAR_60mM_plus.9518.9518.2	2	22.72	0	1.98E+06		(R)FATHAA	(R)F/A|T/H/A|A|A\L S V R(N)		107.55	572.3143	1143.627	-0.0056	-4.9	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
104	dirMS_041712_NAR_40mM_plus2.17759.17893.3	3	22.69	0	2.92E+05		(K)LLYDLAD	(K)L/L|Y|D|L/A/D/Q L/H/A/A/V|G A S R(A)		171.35	604.9967	1812.96	0.0153	8.4	5.21	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial

105	dirMS_041712_NAR_120mM_minus.7109.7216.3	3	22.66	1	6.92E+05		(K)LEEAEK	(K)L/E|E/A/E/K/A/A/D/E/S E/R(G)		93.33	492.8986	1476.681	0	0	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
106	dirMS_041712_NAR_30mM_minus2.13352.13475.2	2	22.65	0	5.19E+05		(R)YALYDA	(R)Y/A|L|Y|D/A/T/Y/E/T/K(E)		126.48	669.3172	1337.626	0.0011	0.9	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
107	dirMS_041712_NAR_30mM_plus2.14084.14281.2	2	22.62	0	9.98E+05		(R)MGQM	(R)M/G/Q|M|A|M|G/G/A|M|G I/N/N/R(G)		127.32	769.8376	1538.67	-0.0015	-1	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
108	dirMS_041712_NAR_30mM_plus2.10864.10952.2	2	22.61	0	5.99E+05		(R)IIYGGSV	(R)I/I|Y|G|G|S/V/T/G A/T/C K(E)	C:Carbamidomethylation	110.2	663.839	1326.672	-0.0015	-1.1	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
109	dirMS_041712_NAR_40mM_plus2.16629.16682.3	3	22.61	1	5.08E+05		(K)FGEVVD	(K)F/G|E|V|V/D C T L/K/L/D|P I\T G R(S)	C:Carbamidomethylation	164.38	640.6667	1919.989	-0.004	-2.1	4.56	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
110	dirMS_041712_NAR_40mM_plus2.12260.12533.3	3	22.6	0	9.90E+05		(K)AGVVG	(K)A/G|V|V|G|P E L/H/E/Q L L/S A E K(A)		139.35	592.987	1776.949	-0.0026	-1.5	4.75	533778	5.74	HUMAN	Q15149	Plectin
111	dirMS_041712_NAR_50mM_minus2.14685.14751.3	3	22.59	0	6.40E+04		(K)VYTDVQ	(K)V/Y|T/D/V/Q/Q/V|A/S S L T/H/P R(F)		151.52	600.976	1800.924	-0.0104	-5.8	6.71	74230.8	5.34	HUMAN	B1AH89	Tubulin tyrosine ligase-like family, member 12
112	dirMS_041712_NAR_30mM_plus2.14728.14768.2	2	22.59	0	7.82E+05		(R)LDIDSPP	(R)L/D|I|D|S|P/P I/T A R(N)		130.72	599.3284	1197.647	0.0021	1.8	4.21	5755.5	5.75	HUMAN	H3BN34	Pyruvate kinase isozymes M1/M2 (Fragment)
113	dirMS_041712_NAR_60mM_minus.8984.9232.3	3	22.57	0	2.40E+06		(K)STAGDT	(K)S/T|A/G/D/T/H/L/G/G E/D F D/N R(M)		110.85	564.5795	1691.726	-0.0016	-1	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
114	dirMS_041712_NAR_40mM_plus2.13215.13547.3	3	22.55	1	2.56E+06		(K)VGEVIV	(K)V/G|E|V/I|V/T/K/D D A M L L/K(G)		145.32	544.307	1630.908	-0.002	-1.2	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
115	dirMS_041712_NAR_50mM_plus2.22248.22300.3	3	22.55	0	1.53E+06		(R)DALSDL	(R)D A|L/S|D/L/A/L/H/F L/N/K(M)		191.78	486.2644	1456.78	-0.0008	-0.6	5.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
116	dirMS_041712_NAR_20mM_plus.13986.14433.2	2	22.54	0	2.99E+06	M256m	(R)SLDmDS	(R)S L|D|m|D|S/I\I|A/E/V/K(A)	m:Oxidized methionine	170.42	668.8371	1320.671	15.9954	0.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
117	dirMS_041712_NAR_60mM_plus.4777.4943.3	3	22.51	1	1.78E+06		(R)AAEEED	(R)A/A|E/E/E/D/E/A/D/P K/R(Q)		80	453.872	1359.602	-0.0008	-0.6	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
118	dirMS_041712_NAR_40mM_plus2.18649.18908.3	3	22.46	1	4.43E+05		(R)TLAEIAK	(R)T/L|A/E/I/A/K/V/E L/D/N M/P L/R(G)		176.68	604.9967	1812.989	-0.0132	-7.3	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
119	dirMS_041712_NAR_60mM_minus.13983.14005.3	3	22.44	0	3.54E+05		(K)DCGATV	(K)D C|G A/T/W/V/V/L/G H/S E R(R)	C:Carbamidomethylation	138.02	529.5838	1586.738	-0.0012	-0.7	5.32	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
120	dirMS_041712_NAR_30mM_minus2.17319.17710.2	2	22.41	0	1.10E+07		(K)LLCGLLA	(K)L/L|C|G|L|L/A/E/R(L)	C:Carbamidomethylation	151.02	522.7963	1044.587	-0.0017	-1.6	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
121	dirMS_041712_NAR_50mM_minus2.18797.18842.3	3	22.41	1	2.24E+06		(R)LIALLEVI	(R)L/I|A|L|L/E/V/L/S Q K/R(M)		183.72	461.6289	1382.873	-0.0008	-0.6	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
122	dirMS_041712_NAR_40mM_plus2.14414.14743.3	3	22.41	1	7.60E+05		(K)IIVDELK	(K)I/I|V/D/E|L/K/Q|E/V/I/S T/S S K(A)		152.95	597.0023	1788.995	-0.003	-1.7	4.68	30149.5	5.96	HUMAN	D6RAC2	Guanine nucleotide-binding protein subunit beta-2-like 1
123	dirMS_041712_NAR_20mM_plus.16784.17048.2	2	22.4	0	3.93E+05		(K)VQIAVA	(K)V Q|I|A|V/A|N/A/Q|E L/L/Q R(M)		187.38	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
124	dirMS_041712_NAR_50mM_plus2.14478.14695.3	3	22.38	0	2.11E+06		(R)QVSASE	(R)Q/V|S/A/S E/L/H/T/S G I/L/G/P E T L R(D)		144.9	665.6855	1995.051	-0.0086	-4.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
125	dirMS_041712_NAR_30mM_plus2.13891.14114.2	2	22.36	0	2.02E+06		(K)YGEPGE	(K)Y/G|E|P/G E V|F/I/N/K(G)		126.27	626.8136	1252.621	-0.0009	-0.7	4.53	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
126	dirMS_041712_NAR_30mM_minus2.14968.15028.2	2	22.35	0	5.54E+05	M316m	(R)ISEQFTA	(R)I/S|E/Q/F/T/A/m/F/R(R)	m:Oxidized methionine	135.18	623.3014	1229.598	15.9972	1.8	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
127	dirMS_041712_NAR_40mM_minus2.12508.12525.3	3	22.35	1	5.98E+05		(R)VCENIPI	(R)V/C/E/N/I|P I V/L/C G N K V D|I/K(D)	C:Carbamidomethylation	157.7	657.6842	1971.04	-0.0021	-1.1	6.04	14844.8	5.89	HUMAN	B4DV51	GTP-binding nuclear protein Ran
128	dirMS_041712_NAR_50mM_plus2.19178.19505.3	3	22.35	1	4.80E+06		(K)TFVNITP	(K)T F|V|N|I/T/P A E V/G/V L/V/G K D R(S)		170.17	639.0247	1915.065	-0.0052	-2.7	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
129	dirMS_041712_NAR_60mM_plus.16636.16697.3	3	22.35	0	3.03E+05		(R)DLSYCLS	(R)D L|S/Y/C/L/S/G/M/Y/D/H/R(Y)	C:Carbamidomethylation	143.93	539.5662	1616.683	0.0009	0.5	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
130	dirMS_041712_NAR_50mM_minus2.13513.13971.3	3	22.34	0	1.98E+06		(K)MLDAED	(K)M/L|D|A|E/D/I/V/N T A R|P D/E K(A)		147.25	606.2965	1816.875	0.0004	0.2	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
131	dirMS_041712_NAR_120mM_minus.13490.13534.3	3	22.33	2	9.83E+05		(R)AQKDEE	(R)A Q|K/D E/E/K/M E|I|Q/E|I/Q\L/K(E)		128.13	654.0058	1960.006	-0.0027	-1.4	4.58	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
132	dirMS_041712_NAR_50mM_plus2.9971.10230.3	3	22.32	1	1.70E+06		(K)TLQEVT	(K)T L|Q/E/V/T/E/M/D/S V K/R(Y)		120.07	512.5958	1535.773	-0.0005	-0.3	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
133	dirMS_041712_NAR_20mM_plus.9586.9891.2	2	22.31	0	6.61E+05		(R)ISVYYNE	(R)I/S|V|Y|Y/N/E\A/T/G G K(Y)		138.4	651.3211	1301.637	-0.0023	-1.8	6	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
134	dirMS_041712_NAR_30mM_plus2.11097.11141.2	2	22.31	0	2.79E+05		(R)TLIQNC	(R)T L|I|Q|N|C/G A/S/T/I/R(L)	C:Carbamidomethylation	111.48	667.3485	1333.689	0.0005	0.3	9.41	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
135	dirMS_041712_NAR_60mM_minus.5567.5879.2	2	22.3	1	4.42E+06		(K)DSYVGD	(K)D/S|Y|V|G/D/E/A Q/S/K/R(G)		87.58	677.8144	1354.623	-0.0018	-1.3	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
136	dirMS_041712_NAR_60mM_plus.11688.11819.3	3	22.3	1	2.17E+06		(K)TLQEVT	(K)T/L|Q/E/V/T/E/M/D/S V K/R(Y)		118.97	512.5957	1535.773	-0.0008	-0.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
137	dirMS_041712_NAR_50mM_minus2.14184.14477.3	3	22.29	1	6.62E+05		(R)VEKIPG	(R)V E|K I|P G G\I|I|E|D/S/C/V|L/R(G)	C:Carbamidomethylation	149.1	595.6534	1784.958	-0.0118	-6.6	4.68	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
138	dirMS_041712_NAR_50mM_plus2.17791.17974.3	3	22.27	1	1.07E+05		(K)TVDNFV	(K)T/V|D/N|F/V/A/L|A T/G E K G F G Y K(N)		161.83	639.6639	1916.975	0.0019	1	5.73	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
139	dirMS_041712_NAR_60mM_plus.7014.7056.3	3	22.26	1	2.99E+06		(K)IVSGKD	(K)I/V|S/G/K/D/Y/N|V/T/A N/S K(L)		95.17	499.2612	1495.775	-0.0061	-4	8.5	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
140	dirMS_041712_NAR_60mM_plus.11619.11800.3	3	22.25	0	2.82E+06		(K)INEKPQ	(K)I/N|E/K/P\Q\V|I|A|D|Y/E/S G R(A)		118.52	573.6312	1718.871	0.0083	4.8	4.68	16368.4	9.95	HUMAN	O60869	Endothelial differentiation-related factor 1
141	dirMS_041712_NAR_30mM_plus2.18410.18507.2	2	22.24	0	2.03E+05		(R)AVLNPL	(R)A V|L|N|P/L/C Q/V/D/Y R(A)	C:Carbamidomethylation	150.18	724.3703	1447.736	-0.0029	-2	5.88	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
142	dirMS_041712_NAR_50mM_plus2.10999.11247.3	3	22.23	0	1.32E+06		(K)VGSLDN	(K)V/G|S|L/D/N V/G/H/L|P/A G G A V/K(I)		126.15	530.9567	1590.86	-0.0043	-2.7	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
143	dirMS_041712_NAR_30mM_minus2.10796.11283.2	2	22.22	0	5.46E+06		(R)INVYYN	(R)I/N|V|Y|Y|N/E/A/T/G G K(Y)		113.98	664.8273	1328.648	-0.0008	-0.6	6	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
144	dirMS_041712_NAR_30mM_plus2.6165.6171.2	2	22.22	0	1.84E+05		(K)CDSSPD	(K)C/D|S|S|P/D/S/A/E|D|V/R(K)	C:Carbamidomethylation	86.6	669.2671	1337.527	-0.0005	-0.4	3.84	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
145	dirMS_041712_NAR_60mM_plus.14265.14266.3	3	22.22	0	1.28E+06		(R)VRPCVV	(R)V R\P C\V\V|Y|G G\A/D|I|G\Q/Q I/R(D)	C:Carbamidomethylation	131.43	629.9993	1887.986	-0.0024	-1.3	8.71	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
146	dirMS_041712_NAR_50mM_plus2.22481.22496.3	3	22.21	1	1.26E+06		(R)GVMLA	(R)G V|M/L/A/V/D/A V I/A E L K/K(Q)		195.7	519.6393	1556.908	-0.0047	-3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
147	dirMS_041712_NAR_60mM_plus.6333.6424.3	3	22.21	1	7.26E+06		(K)DSYVGD	(K)D S|Y|V/G/D/E/A/Q/S K R(G)		91.98	452.213	1354.623	0.0011	0.8	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
148	dirMS_041712_NAR_50mM_plus2.15840.16066.3	3	22.19	0	8.00E+06		(R)LLIHQSL	(R)L/L|I/H Q|S\L|A/G/G I/I/G V/K(G)		151.85	506.9836	1518.937	-0.0004	-0.2	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
149	dirMS_041712_NAR_120mM_plus.8745.9153.3	3	22.18	0	8.60E+06		(R)FACHSA	(R)F/A|C/H/S/A/S|L/T\V/R(N)	C:Carbamidomethylation	101.02	416.8772	1248.615	0.0017	1.3	9.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
150	dirMS_041712_NAR_30mM_minus2.15723.16244.2	2	22.17	0	4.79E+06		(K)YMACCL	(K)Y/M|A|C|C/L/L|Y/R(G)	C:Carbamidomethylation	140.28	625.2802	1249.553	0.0005	0.4	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
151	dirMS_041712_NAR_120mM_minus.6639.7209.3	3	22.15	1	3.27E+07		(K)DSYVGD	(K)D S|Y|V/G/D/E/A/Q/S K R(G)		91.23	452.2134	1354.623	0.0023	1.7	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
152	dirMS_041712_NAR_40mM_plus2.13574.13991.3	3	22.15	1	1.93E+06		(K)TVGVEP	(K)T/V|G|V/E/P A A D/G K G V V V/V/I/K(R)		147.37	580.0077	1738.011	-0.0024	-1.4	5.73	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
153	dirMS_041712_NAR_40mM_minus2.14676.14676.3	3	22.13	1	1.37E+06		(K)TFVNITP	(K)T F|V/N|I|T/P A E V/G V L V G K D R(S)		171.75	639.0252	1915.065	-0.0037	-1.9	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
154	dirMS_041712_NAR_50mM_minus2.18150.18359.3	3	22.12	0	4.52E+06		(K)ALESPE	(K)A/L|E|S|P E/R P/F L|A/I/L|G G A K(V)		174.72	590.3356	1768.996	-0.0033	-1.9	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
155	dirMS_041712_NAR_30mM_plus2.19575.19903.2	2	22.1	0	1.62E+06		(R)ISEQFTA	(R)I/S|E/Q|F/T/A/M/F/R(R)		157.12	615.3024	1229.598	-0.0008	-0.6	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
156	dirMS_041712_NAR_30mM_plus2.6115.6115.2	2	22.09	0	8.14E+05		(R)NQGGY	(R)N/Q|G/G|Y/G G S S/S S/S S Y|G S G R(R)		86.18	847.8524	1694.7	-0.0026	-1.5	8.59	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
157	dirMS_041712_NAR_50mM_plus2.10344.10364.3	3	22.08	1	8.18E+05		(K)LLEDKN	(K)L/L|E|D/K/N|G\E|V/Q N L A/V/K(C)		121.98	557.3066	1669.912	-0.0067	-4	4.68	6116.1	5.2	HUMAN	F5H6I6	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
158	dirMS_041712_NAR_40mM_plus2.13885.14237.2	2	22.07	0	5.22E+05		(K)LLCGLLA	(K)L/L|C|G|L|L/A E/R(L)	C:Carbamidomethylation	148.95	522.7962	1044.587	-0.0019	-1.8	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
159	dirMS_041712_NAR_60mM_minus.18877.19124.3	3	22.06	1	3.75E+06		(R)GLFIIDD	(R)G L|F|I/I/D/D/K/G I/L/R(Q)		168.1	453.9368	1359.8	-0.0036	-2.7	5.96	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
160	dirMS_041712_NAR_30mM_plus2.15962.16172.2	2	22.06	0	6.55E+05		(R)ICCDLD	(R)I/C|C|D|L/D/V/L|A/S/K(K)	C:Carbamidomethylation	137.37	647.3131	1293.618	0.0012	0.9	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
161	dirMS_041712_NAR_20mM_minus.8898.9091.2	2	22.05	0	1.86E+06		(K)LVSESSD	(K)L/V|S|E/S/S D|V/L|P K(-)		139.67	587.321	1173.636	-0.0014	-1.2	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
162	dirMS_041712_NAR_30mM_minus2.10066.10660.2	2	22.05	0	7.01E+07		(R)GYSFTT	(R)G/Y|S|F/T/T/T/A/E/R(E)		109.67	566.7699	1132.527	0.0056	4.9	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
163	dirMS_041712_NAR_60mM_plus.14323.14446.3	3	22.05	1	1.92E+06		(K)DVDEAY	(K)D V|D|E|A/Y/M/N K/V/E/L E/S R(L)		131.82	599.9485	1797.832	-0.0014	-0.8	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
164	dirMS_041712_NAR_40mM_minus2.12206.12206.3	3	22.03	0	4.57E+05		(K)IAILTCP	(K)I/A/I/L/T C|P F E/P P K/P K(T)	C:Carbamidomethylation	155.68	537.6382	1610.898	0.0026	1.6	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
165	dirMS_041712_NAR_20mM_plus.17508.17640.2	2	22.01	0	3.08E+05		(K)SYELPD	(K)S Y|E|L|P D/G Q/V|I|T|I|G N E R(F)		193.17	895.9492	1790.892	-0.0008	-0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
166	dirMS_041712_NAR_120mM_plus.5522.5607.3	3	21.96	1	2.74E+06		(R)SGGGY	(R)S/G|G|G|Y/G/G D/R|G G G/Y/G G D/R(G)		82.1	515.5539	1544.647	-0.0001	-0.1	5.68	21563.9	10.01	HUMAN	K7EKB2	TATA-binding protein-associated factor 2N (Fragment)
167	dirMS_041712_NAR_120mM_minus.7110.7112.3	3	21.93	1	6.92E+05		(K)LEEAEK	(K)L/E|E\A/E/K/A/A/D/E S E/R(G)		93.33	492.8986	1476.681	0	0	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
168	dirMS_041712_NAR_60mM_minus.8691.9230.3	3	21.93	0	3.43E+07		(K)QEYDES	(K)Q E/Y/D E/S/G/P/S/I/V/H/R(K)		110.32	506.2391	1516.703	0.0001	0.1	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
169	dirMS_041712_NAR_20mM_plus.9658.9658.2	2	21.88	0	3.06E+05		(K)LVLVGD	(K)L V|L|V/G D/G G T G/K(T)		137.43	508.292	1015.578	-0.0015	-1.5	5.84	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
170	dirMS_041712_NAR_20mM_minus.6164.6206.2	2	21.85	0	3.80E+06		(K)DSYVGD	(K)D S|Y|V|G/D/E/A/Q/S K(R)		103.87	599.7642	1198.522	-0.0011	-0.9	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
171	dirMS_041712_NAR_30mM_minus2.10375.10539.2	2	21.83	0	3.64E+05		(R)IIYGGSV	(R)I/I|Y|G/G/S/V|T/G/A T C K(E)	C:Carbamidomethylation	110.8	663.8388	1326.672	-0.0019	-1.4	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
172	dirMS_041712_NAR_30mM_minus2.13401.13511.2	2	21.82	0	6.43E+05		(K)YLGQDY	(K)Y/L|G|Q|D|Y/E/Q L/R(V)		126.6	642.814	1284.622	-0.0012	-0.9	4.37	7312.2	6.55	HUMAN	E9PIA9	Calpain-1 catalytic subunit (Fragment)
173	dirMS_041712_NAR_40mM_plus2.11905.12188.3	3	21.82	1	1.25E+06	M356m	(K)VGEVIV	(K)V/G|E|V|I|V/T/K D D A m L L/K(G)	m:Oxidized methionine	137	549.6385	1630.908	15.9925	-1.5	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
174	dirMS_041712_NAR_30mM_plus2.8204.8287.2	2	21.8	0	2.10E+05		(R)DSYDSY	(R)D S|Y/D|S|Y/A/T/H/N/E(-)		97.03	651.2492	1301.492	-0.0005	-0.4	4.31	18647.7	9.51	HUMAN	Q14011	Cold-inducible RNA-binding protein
175	dirMS_041712_NAR_60mM_plus.18103.18432.3	3	21.78	1	1.39E+06		(K)SIYGEKF	(K)S I|Y/G/E/K/F/E/D/E N F/I/L/K(H)		152.97	611.3091	1831.911	0.0015	0.8	4.41	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
176	dirMS_041712_NAR_30mM_plus2.16301.16715.2	2	21.77	0	1.64E+06		(R)FGLNVS	(R)F/G|L|N|V/S/S/I/S/R(K)		139.38	540.3016	1079.584	0.0115	10.7	9.75	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
177	dirMS_041712_NAR_40mM_plus2.18667.18667.3	3	21.75	1	4.00E+05		(R)TLAEIAK	(R)T L|A/E/I/A/K V E/L D/N M/P L/R(G)		176.57	604.9967	1812.989	-0.0132	-7.3	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
178	dirMS_041712_NAR_50mM_plus2.12284.12550.3	3	21.75	1	6.98E+06		(K)DVDEAY	(K)D V|D|E/A|Y/M/N/K V/E L E/S R(L)		133.37	599.9499	1797.832	0.0028	1.6	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
179	dirMS_041712_NAR_30mM_minus2.15500.15543.2	2	21.73	0	3.51E+05		(K)LLYNNV	(K)L/L|Y|N|N|V|S/N/F/G R(L)		137.97	648.8355	1296.67	-0.0058	-4.5	8.75	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
180	dirMS_041712_NAR_60mM_minus.9133.9274.3	3	21.73	0	2.84E+05		(K)ATAGDT	(K)A/T|A/G/D/T/H/L/G G E D F D/N R(L)		111.4	559.2488	1675.731	0.0012	0.7	4.22	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
181	dirMS_041712_NAR_20mM_plus.18769.18769.2	2	21.73	0	2.87E+05		(K)LAVEAL	(K)L A|V/E\A/L|S/S L/D/G D L A/G R(Y)		200.48	793.9214	1586.838	-0.0029	-1.8	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
182	dirMS_041712_NAR_60mM_plus.15550.15591.3	3	21.73	0	3.56E+05		(K)GVGISVI	(K)G V|G/I/S/V/L/E/M/S H/R(S)		137.95	428.8957	1284.673	-0.0003	-0.3	6.75	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
183	dirMS_041712_NAR_20mM_minus.10715.10715.2	2	21.72	0	1.92E+05		(R)TTPSYV	(R)T T|P/S/Y\V/A/F T D/T E/R(L)		154.67	744.3547	1487.701	0.0009	0.6	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
184	dirMS_041712_NAR_50mM_plus2.20823.21133.3	3	21.72	0	4.90E+06		(R)AGKPVI	(R)A G K\P V\I\C\A|T|Q|M/L/E/S M I/K(K)	C:Carbamidomethylation	179.65	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
185	dirMS_041712_NAR_60mM_plus.11793.11822.3	3	21.72	1	3.83E+05		(R)LAEVEA	(R)L/A|E/V/E/A/A/L/E K Q/R(Q)		118.88	452.9164	1356.748	-0.0135	-10	4.79	533778	5.74	HUMAN	Q15149	Plectin
186	dirMS_041712_NAR_50mM_plus2.16401.16470.3	3	21.71	0	5.57E+05		(R)QVVQGI	(R)Q V|V/Q|G|L\L/S/E/T/Y/L|E A H R(I)		154.53	614.9984	1842.971	0.0098	5.3	5.4	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
187	dirMS_041712_NAR_30mM_plus2.17013.17033.2	2	21.7	0	5.59E+05	M256m	(R)SLDmDS	(R)S L|D/m|D/S/I/I|A/E/V/K(A)	m:Oxidized methionine	142.3	668.8384	1320.671	15.998	2.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
188	dirMS_041712_NAR_50mM_plus2.15772.15850.3	3	21.69	0	1.47E+06		(R)SLESLHS	(R)S L|E/S/L/H/S/F V/A A/A/T/K(E)		151.33	487.5964	1460.774	0.0003	0.2	6.47	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
189	dirMS_041712_NAR_30mM_minus2.10630.10712.2	2	21.67	0	4.29E+05		(R)TLIQNC	(R)T L|I|Q|N/C|G A/S/T I/R(L)	C:Carbamidomethylation	111.82	667.348	1333.689	-0.0005	-0.4	9.41	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
190	dirMS_041712_NAR_40mM_minus2.14585.14585.3	3	21.67	1	1.39E+06	M116m	(R)ELAILLG	(R)E L|A\I/L/L/G m/L D/P A E K D E K(G)	m:Oxidized methionine	171.13	634.338	1884.999	16.0008	3.1	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
191	dirMS_041712_NAR_60mM_minus.12175.12219.3	3	21.67	0	7.53E+05		(K)QADLYIS	(K)Q A/D\L/Y/I/S/E/G L/H/P R(I)		128.07	500.2603	1498.765	0.0015	1	5.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
192	dirMS_041712_NAR_20mM_minus.6161.6256.2	2	21.66	0	3.80E+06		(K)DSYVGD	(K)D S|Y|V|G/D/E/A/Q|S K(R)		103.87	599.7642	1198.522	-0.0011	-0.9	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
193	dirMS_041712_NAR_30mM_plus2.20464.20854.2	2	21.65	0	8.74E+05		(R)TVQSLEI	(R)T/V|Q|S|L|E|I\D/L/D/S M R(N)		162.18	753.8768	1506.747	-0.0005	-0.3	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
194	dirMS_041712_NAR_50mM_plus2.11559.11841.3	3	21.65	1	1.68E+06		(R)ISVYYNE	(R)I/S|V/Y/Y/N/E\A/T/G G\K/Y V/P R(A)		128.42	606.3123	1816.923	-0.0005	-0.3	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
195	dirMS_041712_NAR_60mM_minus.5537.5919.3	3	21.64	1	4.91E+07		(K)DSYVGD	(K)D S|Y|V/G/D/E/A/Q/S K R(G)		87.95	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
196	dirMS_041712_NAR_40mM_plus2.12274.12516.3	3	21.64	0	3.98E+05		(K)AASDIA	(K)A A|S D/I/A/M/T E/L/P/P T H/P I R(L)		139.83	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
197	dirMS_041712_NAR_30mM_minus2.14981.14981.2	2	21.61	0	5.54E+05	M316m	(R)ISEQFTA	(R)I/S/E/Q/F/T/A m/F R(R)	m:Oxidized methionine	135.18	623.3014	1229.598	15.9972	1.8	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
198	dirMS_041712_NAR_50mM_minus2.13028.13255.3	3	21.61	1	7.72E+05		(K)VLAGDK	(K)V/L|A/G D K/N/F|I|T/A E/E/L R(R)		142.88	559.3044	1675.901	-0.0027	-1.6	4.68	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
199	dirMS_041712_NAR_20mM_minus.8912.8965.2	2	21.6	0	1.86E+06		(K)LVSESSD	(K)L/V|S|E/S/S D V/L/P/K(-)		139.67	587.321	1173.636	-0.0014	-1.2	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
200	dirMS_041712_NAR_30mM_plus2.16201.16467.2	2	21.59	0	8.03E+05		(R)GLCAIA	(R)G L/C|A|I|A|Q|A/E|S L|R(Y)	C:Carbamidomethylation	138.63	644.8372	1288.668	-0.0007	-0.5	6	18529.2	9.98	HUMAN	E9PL45	40S ribosomal protein S3
201	dirMS_041712_NAR_30mM_minus2.18473.18796.2	2	21.54	0	8.57E+05		(K)LLQDFF	(K)L/L|Q|D/F|F/N/G/K(E)		156.12	541.2823	1081.568	-0.0103	-9.6	5.84	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
202	dirMS_041712_NAR_30mM_plus2.11417.11811.2	2	21.54	0	3.02E+06		(R)INVYYN	(R)I/N|V|Y|Y|N/E/A/T/G G K(Y)		114.07	664.8272	1328.648	-0.001	-0.7	6	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
203	dirMS_041712_NAR_50mM_plus2.13286.13286.3	3	21.52	0	2.96E+06		(K)LGDVYV	(K)L/G|D\V/Y V/N/D A/F G/T A H/R(A)		138.15	545.6029	1634.792	0.002	1.2	5.21	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
204	dirMS_041712_NAR_60mM_plus.9934.10245.3	3	21.51	0	1.00E+07		(R)LESGMC	(R)L/E|S G/M|Q/N/M/S/I/H/T K(T)		110.2	492.5712	1475.698	0.0009	0.6	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
205	dirMS_041712_NAR_60mM_minus.15664.15891.3	3	21.49	1	4.07E+05		(R)AEGAIA	(R)A/E|G|A|I/A/G F\R D/P F/S/G/K(Q)		147.98	508.2601	1522.765	0.0009	0.6	6.12	266161	5.68	HUMAN	E9PPU0	Epiplakin
206	dirMS_041712_NAR_60mM_minus.6037.6305.3	3	21.46	1	2.51E+06		(K)LEEAEK	(K)L/E|E|A/E/K/A/A/D/E/S E R(G)		93.27	492.8981	1476.681	-0.0015	-1	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
207	dirMS_041712_NAR_50mM_plus2.10120.10258.3	3	21.45	0	6.15E+05		(K)VGQEIE	(K)V/G|Q|E/I E/V/R P G/I V/S K(D)		121.05	504.2907	1510.859	-0.0012	-0.8	6.11	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
208	dirMS_041712_NAR_50mM_minus2.14690.14916.3	3	21.44	1	9.62E+05		(R)IINEPTA	(R)I/I|N|E/P T A/A/A I/A/Y/G L D/K/R(E)		152.6	606.0022	1815.996	-0.0043	-2.4	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
209	dirMS_041712_NAR_60mM_plus.11253.11253.3	3	21.44	0	1.93E+06		(R)EIVHIQA	(R)E/I/V H I Q A G/Q/C/G N Q I/G A/K(F)	C:Carbamidomethylation	116.42	608.311	1822.923	-0.0044	-2.4	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
210	dirMS_041712_NAR_30mM_plus2.16217.16712.2	2	21.43	0	5.57E+06		(K)YMACCL	(K)Y/M|A|C/C/L|L|Y/R(G)	C:Carbamidomethylation	139.3	625.2798	1249.553	-0.0003	-0.2	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
211	dirMS_041712_NAR_30mM_plus2.6742.6801.2	2	21.4	0	2.92E+05		(R)EAGEQG	(R)E A|G\E/Q|G/D/I/E/P R(R)		89.77	600.7772	1200.549	-0.002	-1.7	4	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
212	dirMS_041712_NAR_30mM_plus2.6145.6152.2	2	21.39	0	1.41E+05		(R)CSQAVY	(R)C/S|Q|A|V/Y/A/A E/K(V)	C:Carbamidomethylation	86.47	563.7624	1126.52	-0.0022	-2	6	16685.6	9.7	HUMAN	E9PND2	Cysteine and glycine-rich protein 1 (Fragment)
213	dirMS_041712_NAR_50mM_plus2.16479.16479.3	3	21.37	1	2.02E+06		(K)QGGLGF	(K)Q G/G/L/G P M N I/P/L/V S/D/P K R(T)		154.68	593.6536	1778.958	-0.0119	-6.7	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1

214	dirMS_041712_NAR_50mM_plus2.19552.19846.3	3	21.36	1	5.91E+05		(R)VLEALLP	(R)V/L|E/A/L L/P L/K/G L E/E/R(V)		172.03	527.318	1579.942	-0.0023	-1.5	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
215	dirMS_041712_NAR_60mM_plus.6783.6783.3	3	21.36	0	1.82E+06		(K)CIGKPG	(K)C I|G/K/P G G\S L/D N/S E Q K(C)	C:Carbamidomethylation	94.07	530.5904	1589.759	-0.0021	-1.4	6.07	9122.2	9.22	HUMAN	K7EIT2	Mitochondrial import inner membrane translocase subunit Tim13
216	dirMS_041712_NAR_30mM_minus2.16618.16618.2	2	21.33	0	2.83E+05		(R)ASLEAAI	(R)A S|L/E|A/A|I/A/D A E Q R(G)		143.92	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
217	dirMS_041712_NAR_50mM_minus2.5658.5671.3	3	21.33	1	3.66E+05		(K)DSYVGD	(K)D S|Y|V/G/D/E/A/Q/S K R(G)		92.95	452.2119	1354.623	-0.0022	-1.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
218	dirMS_041712_NAR_40mM_plus2.13719.14138.3	3	21.33	1	3.53E+06		(R)IINEPTA	(R)I/I|N|E/P T A/A/A/I/A/Y G L D/K K(V)		148.57	596.6671	1787.99	-0.0034	-1.9	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
219	dirMS_041712_NAR_30mM_plus2.6644.6644.2	2	21.32	0	2.92E+05		(R)EAGEQG	(R)E A G E/Q/G/D I/E/P/R(R)		89.77	600.7772	1200.549	-0.002	-1.7	4	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
220	dirMS_041712_NAR_20mM_minus.13467.13467.2	2	21.31	0	6.67E+05		(K)DAGTIA	(K)D/A\G|T/I|A/G/L N/V/L R(I)		184.97	600.3403	1199.674	-0.0009	-0.8	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
221	dirMS_041712_NAR_30mM_minus2.7087.7087.2	2	21.31	0	2.76E+05		(R)CGCLDE	(R)C/G\C|L|D/E/D T Q R(Q)	C:Carbamidomethylation	93.07	627.2485	1253.488	0.0012	1	4.03	266161	5.68	HUMAN	E9PPU0	Epiplakin
222	dirMS_041712_NAR_40mM_minus2.13969.14030.3	3	21.31	0	3.46E+05		(R)LLEVLSG	(R)L/L\E|V/L/S/G E|I L/P K/P T K(G)		166.62	546.333	1636.988	-0.0039	-2.4	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
223	dirMS_041712_NAR_30mM_plus2.6064.6064.2	2	21.31	0	8.14E+05		(R)NQGGY	(R)N|Q|G G Y|G/G/S/S/S S S/S Y/G S G R(R)		86.18	847.8524	1694.7	-0.0026	-1.5	8.59	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
224	dirMS_041712_NAR_50mM_plus2.16023.16294.3	3	21.31	1	1.20E+06		(K)CEFQDA	(K)C/E|F/Q D\A|Y|V|L/L/S E/K K(I)	C:Carbamidomethylation	152.32	577.2866	1729.847	-0.0013	-0.8	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
225	dirMS_041712_NAR_30mM_plus2.6045.6045.2	2	21.3	0	1.50E+05		(R)VGSTSEI	(R)V/G/S|T/S/E/N I/T Q/K(V)		85.97	582.2983	1163.59	-0.0009	-0.8	5.97	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
226	dirMS_041712_NAR_30mM_minus2.8734.8997.2	2	21.29	0	1.42E+06		(K)SNVSDA	(K)S/N|V|S|D/A|V|A|Q/S T R(I)		102.9	617.8045	1234.602	-0.0005	-0.4	5.55	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
227	dirMS_041712_NAR_60mM_minus.10546.10745.3	3	21.29	1	1.64E+06		(K)TLQEVTI	(K)T L|Q/E/V/T/E/M/D/S V K/R(Y)		119.37	512.5957	1535.773	-0.0008	-0.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
228	dirMS_041712_NAR_30mM_plus2.18229.18506.2	2	21.29	0	5.45E+05		(R)GYISPYF	(R)G Y|I|S|P/Y/F/I/N T S K(G)		149.72	695.3554	1389.705	-0.0014	-1	8.5	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
229	dirMS_041712_NAR_50mM_plus2.9823.9863.3	3	21.29	1	2.67E+03		(R)TAGVKV	(R)T|A|G/V/K/V/E T/T/E/D L V/A K(L)		120.5	520.9473	1560.848	-0.0206	-13.2	4.68	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
230	dirMS_041712_NAR_50mM_plus2.17668.17805.3	3	21.27	1	9.79E+05		(R)SELELTL	(R)S/E|L/E/L/T/L/G/K L/E Q V/R(S)		161.43	538.9727	1614.906	-0.0026	-1.6	4.78	533778	5.74	HUMAN	Q15149	Plectin
231	dirMS_041712_NAR_50mM_minus2.15638.15905.3	3	21.25	1	6.66E+05		(K)SIYGEKF	(K)S I|Y/G E/K/F/E/D/E/N F/I/L/K(H)		158	611.3086	1831.911	0	0	4.41	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
232	dirMS_041712_NAR_30mM_plus2.17547.17801.2	2	21.25	0	5.16E+05		(K)LLGELLQ	(K)L/L|G|E|L|L|Q/D/N A K(L)		145.75	607.3423	1213.679	-0.0014	-1.1	4.37	35556.4	9.3	HUMAN	F2Z393	Transaldolase
233	dirMS_041712_NAR_40mM_plus2.12376.12376.3	3	21.25	0	3.04E+05		(K)AASDIAI	(K)A A S D|I/A/M/T/E L/P/P T H P I R(L)		139.47	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
234	dirMS_041712_NAR_50mM_plus2.6416.6650.3	3	21.25	1	6.47E+05		(R)IVDGKV	(R)I/V|D/G K/V/V/S/E/T N D/T/K(V)		98.57	502.2651	1504.785	-0.0046	-3	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
235	dirMS_041712_NAR_40mM_plus2.17359.17812.3	3	21.24	1	3.01E+06		(R)LFVGNLI	(R)L/F|V/G/N/L/P A D/I/T E/D E F K R(L)		170.08	655.3421	1964.012	-0.0006	-0.3	4.32	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
236	dirMS_041712_NAR_60mM_plus.8502.8943.3	3	21.24	1	4.46E+06		(R)VVASDK	(R)V/V|A/S/D/K/E/T/Y/E/L/R(Y)		103.67	470.5798	1409.727	-0.0022	-1.6	4.68	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
237	dirMS_041712_NAR_40mM_plus2.19252.19362.3	3	21.22	0	1.61E+06		(R)AGKPVI	(R)A G K\P V\I\C\A|T|Q|M/L/E/S M I/K(K)	C:Carbamidomethylation	180.63	626.3273	1876.969	-0.002	-1.1	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
238	dirMS_041712_NAR_20mM_plus.12569.12768.2	2	21.21	0	9.33E+05	M92m	(R)ImNTFS	(R)I/m|N|T|F/S/V/V|P/S/P K(V)	m:Oxidized methionine	160.22	668.3516	1319.703	15.9931	-1.3	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
239	dirMS_041712_NAR_20mM_plus.18580.18580.2	2	21.18	0	1.75E+05	M332m	(R)IVSQLLT	(R)I V|S Q\L/L/T L/m D G L K(Q)	m:Oxidized methionine	199.38	723.9145	1430.829	15.993	-1.3	5.84	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
240	dirMS_041712_NAR_50mM_minus2.14497.14497.3	3	21.16	1	7.89E+05		(K)EAFSLFD	(K)E A/F/S/L/F/D K/D G D/G T I T T K(E)		150.35	615.6336	1844.891	-0.005	-2.7	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
241	dirMS_041712_NAR_30mM_plus2.18668.18824.2	2	21.16	0	3.77E+05		(R)LLLNNDI	(R)L/L|L|N|N/D/N L/L/R(E)		151.37	599.3506	1197.695	-0.0011	-0.9	5.84	19945.8	4.97	HUMAN	B4DG50	F-actin-capping protein subunit alpha-2
242	dirMS_041712_NAR_60mM_plus.10321.10826.3	3	21.16	1	3.53E+07		(R)LQAEIEG	(R)L/Q|A/E/I/E/G L/K/G Q/R(A)		112.38	447.9186	1341.748	-0.0072	-5.4	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
243	dirMS_041712_NAR_50mM_minus2.15087.15397.3	3	21.15	0	9.01E+05		(R)LLIHQSL	(R)L L|I/H/Q\S\L|A|G G I/I/G V/K(G)		154.83	506.9833	1518.937	-0.0013	-0.8	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
244	dirMS_041712_NAR_60mM_plus.11699.11883.3	3	21.15	0	4.34E+06		(K)TGNLGN	(K)T/G|N|L/G N V/V/H/I/E/R(F)		119.1	436.9042	1308.702	-0.0038	-2.9	6.41	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
245	dirMS_041712_NAR_30mM_plus2.15362.15362.2	2	21.11	0	3.86E+05		(R)MAGAIA	(R)M/A/G\A/I/A/Q G L/I/R(A)		133.18	550.816	1100.624	0.0002	0.2	9.5	4449.1	11.42	HUMAN	F8WEI0	Pyrroline-5-carboxylate reductase 3
246	dirMS_041712_NAR_60mM_plus.5551.5673.3	3	21.1	0	1.11E+06		(K)TATPQQ	(K)T A|T/P Q/Q/A/Q/E/V/H E K(L)		87.6	489.5727	1466.723	-0.0198	-13.5	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
247	dirMS_041712_NAR_120mM_minus.11767.11847.3	3	21.08	0	6.27E+05		(K)FYEEVHI	(K)F/Y/E/E/V/H/D/L E R(K)		118.58	446.2102	1336.617	-0.0008	-0.6	4.4	18209.2	5.03	HUMAN	A8MXH2	Nucleosome assembly protein 1-like 4 (Fragment)
248	dirMS_041712_NAR_120mM_minus.7402.7935.3	3	21.08	1	8.15E+05		(K)IQDKEGI	(K)I Q|D K E G|I|P/P/D/Q Q/R(L)		94.9	508.5981	1523.781	-0.0015	-1	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
249	dirMS_041712_NAR_50mM_minus2.7228.7330.3	3	21.08	0	1.02E+06		(K)QEYDES	(K)Q E/Y/D E/S/G/P/S/I/V/H/R(K)		108.38	506.2404	1516.703	0.004	2.6	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
250	dirMS_041712_NAR_50mM_minus2.7702.7745.3	3	21.08	0	2.46E+05		(R)AALAHS	(R)A/A\L A H S/E\E\V|T|A/S/Q/V/A|A\T K(T)		110.93	595.3104	1783.919	-0.0018	-1	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
251	dirMS_041712_NAR_50mM_minus2.10265.10432.3	3	21.07	1	5.22E+05		(K)IAQLEEC	(K)I/A|Q|L/E/E/Q/L/D/N E/T K E R(Q)		127.12	605.9737	1815.908	-0.0018	-1	4.25	227783.5	5.5	HUMAN	P35579	Myosin-9
252	dirMS_041712_NAR_60mM_plus.20478.20766.3	3	21.07	1	3.50E+06		(R)GLFIIDD	(R)G L|F|I/I/D/D/K/G I L/R(Q)		168.3	453.9368	1359.8	-0.0036	-2.7	5.96	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
253	dirMS_041712_NAR_40mM_minus2.8174.8349.3	3	21.06	1	5.29E+05		(R)DVVICPI	(R)D V|V|I/C/P D/A S L E D/A K K(E)	C:Carbamidomethylation	129.32	553.9467	1659.826	-0.0003	-0.2	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
254	dirMS_041712_NAR_30mM_plus2.12277.12277.2	2	21.06	0	2.21E+05		(K)VLQATV	(K)V L|Q/A|T/V|V/A/V/G S G S K(G)		117.57	658.3806	1315.758	-0.0041	-3.1	8.72	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
255	dirMS_041712_NAR_40mM_plus2.11300.11372.3	3	21.06	0	1.67E+05		(R)SVIDPVF	(R)S V|I|D|P/V/P A/P V G D S H V D G A A K(S)		132.95	644.3327	1930.987	-0.0033	-1.7	4.41	58326.8	5.7	HUMAN	Q13177	Serine/threonine-protein kinase PAK 2
256	dirMS_041712_NAR_20mM_plus.12303.12303.2	2	21.05	0	1.17E+05		(K)VNQIGS	(K)V N/Q|I|G/S/V/T E/S I/Q A C K(L)	C:Carbamidomethylation	157.67	817.4114	1633.821	-0.0059	-3.6	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
257	dirMS_041712_NAR_30mM_plus2.18461.18461.2	2	21.05	0	2.03E+05		(R)AVLNPL	(R)A V|L|N/P\L/C/Q V D/Y R(A)	C:Carbamidomethylation	150.18	724.3703	1447.736	-0.0029	-2	5.88	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
258	dirMS_041712_NAR_50mM_plus2.18585.19063.3	3	21.03	1	6.37E+06		(R)GLFIIDD	(R)G L|F|I/I/D/D/K/G I L/R(Q)		167.33	453.9379	1359.8	-0.0003	-0.2	5.96	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
259	dirMS_041712_NAR_120mM_plus.13426.13492.3	3	21.02	0	1.03E+06		(K)THINIVV	(K)T H|I|N\I\V|V|I/G/H V/D|S G K(S)		123.78	530.2975	1588.881	-0.0026	-1.6	6.61	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
260	dirMS_041712_NAR_20mM_plus.16540.16540.2	2	21.02	0	1.75E+05		(R)LLEAQIA	(R)L L|E|A\Q/I|A/T/G G I I/D|P K(E)		185.47	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
261	dirMS_041712_NAR_60mM_minus.14195.14255.3	3	21.01	1	8.82E+05		(R)SILKIDD	(R)S I|L/K/I/D/D|V|V/N T R(-)		139.22	458.2637	1372.78	-0.0029	-2.1	5.68	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
262	dirMS_041712_NAR_40mM_plus2.13909.14086.3	3	21.01	0	3.53E+05		(K)LVEALC	(K)L/V|E/A/L/C/A/E/H Q I N L/I/K(V)	C:Carbamidomethylation	148.62	584.3205	1750.952	-0.0051	-2.9	5.4	14914.1	6.84	HUMAN	P25398	40S ribosomal protein S12
263	dirMS_041712_NAR_120mM_plus.19984.20517.4	4	21	1	3.55E+07		(K)AAIDWF	(K)A A|I/D/W/F/D/G K E/F H/G N I I/K(V)		159.08	491.0027	1960.992	-0.0026	-1.3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
264	dirMS_041712_NAR_20mM_plus.10018.10215.2	2	21	0	1.43E+06		(K)LVSESSD	(K)L/V|S|E|S/S/D\V/L/P/K(-)		143.17	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
265	dirMS_041712_NAR_20mM_plus.15583.15583.2	2	20.99	0	2.37E+05		(K)TITLEVEI	(K)T I/T|L E|V/E|P S D T I E N V K(A)		179.03	894.4658	1787.927	-0.003	-1.7	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
266	dirMS_041712_NAR_30mM_plus2.18710.18886.2	2	20.99	0	5.47E+05		(R)NFWVS	(R)N F|W|V|S|G/L/S/S/T T R(A)		151.8	677.8411	1354.675	-0.0001	0	9.75	103309.5	5.34	HUMAN	A0AV56	SAFB protein
267	dirMS_041712_NAR_50mM_plus2.9415.9796.3	3	20.99	1	2.21E+06		(K)ALIEMEI	(K)A L|I|E/M/E/K/Q/Q/Q/D/Q V D/R(N)		117.33	610.9732	1830.901	0.0036	2	4.32	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)
268	dirMS_041712_NAR_50mM_plus2.14479.14757.3	3	20.96	1	3.88E+06		(K)VGEVIV	(K)V/G|E|V/I/V|T K/D D A M L/L/K(G)		145.3	544.3052	1630.908	-0.0074	-4.5	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
269	dirMS_041712_NAR_50mM_minus2.15141.15549.3	3	20.95	1	8.73E+05		(K)ILLAELE	(K)I/L|L/A/E/L/E Q/L/K/G Q/G K(S)		155.78	513.9739	1539.911	-0.0033	-2.2	6.14	49709.6	5.19	HUMAN	B0YJC4	Vimentin
270	dirMS_041712_NAR_60mM_minus.8538.8538.3	3	20.95	0	9.13E+04		(R)ISVYYNE	(R)I/S V/Y/Y N E A/S S/H K(Y)		107.72	466.5604	1397.67	-0.0029	-2.1	6.75	18402.2	5.06	HUMAN	G3V2N6	HCG1983504, isoform CRA_d
271	dirMS_041712_NAR_20mM_minus.12096.12461.2	2	20.94	0	9.01E+05	M185m	(K)LAVNm	(K)L/A|V|N/m|V|P/F/P R(L)	m:Oxidized methionine	171.88	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
272	dirMS_041712_NAR_30mM_minus2.16134.16406.2	2	20.94	0	4.42E+05	M185m	(K)LAVNm	(K)L/A|V/N|m|V|P F/P R(L)	m:Oxidized methionine	142.58	580.3178	1143.634	15.994	-0.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
273	dirMS_041712_NAR_20mM_plus.9211.9211.2	2	20.94	0	4.54E+04		(R)IIYGGSV	(R)I/I|Y/G/G S\V T G A T/C K(E)	C:Carbamidomethylation	135.4	663.8412	1326.672	0.0029	2.2	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
274	dirMS_041712_NAR_50mM_plus2.17433.17690.3	3	20.94	0	9.60E+05		(R)VLDPFTI	(R)V/L|D|P/F/T/I/K/P L D/R(K)		160.52	471.9408	1413.81	-0.0022	-1.5	5.93	63448.4	7.29	HUMAN	B4E022	Transketolase
275	dirMS_041712_NAR_50mM_plus2.17808.18100.3	3	20.94	1	1.43E+06		(K)AILILDNI	(K)A I|L|I|L/D/N D G D/R L F/A/K(Y)		162.65	558.6425	1673.922	-0.0091	-5.5	4.43	18430.9	4.79	HUMAN	F8VS17	Coatomer subunit zeta-1
276	dirMS_041712_NAR_20mM_minus.9246.9283.2	2	20.93	0	2.79E+05		(R)AQIFAN	(R)A Q|I|F|A|N/T/V/D/N A/R(I)		142.32	660.3388	1319.67	0.0001	0.1	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
277	dirMS_041712_NAR_50mM_minus2.14104.14336.3	3	20.93	1	1.24E+06		(R)LLDAQL	(R)L/L|D|A/Q|L|A/T/G G L V C P A R/R(L)	C:Carbamidomethylation	149.03	604.3359	1810.996	-0.0025	-1.4	9.6	266161	5.68	HUMAN	E9PPU0	Epiplakin
278	dirMS_041712_NAR_30mM_minus2.13279.13279.2	2	20.92	0	3.00E+05		(K)STYGWT	(K)S T|Y/G|W/T/A N/M E R(I)		125.7	658.2918	1315.574	0.0028	2.1	5.72	47825.1	5.07	HUMAN	Q58FG1	Putative heat shock protein HSP 90-alpha A4
279	dirMS_041712_NAR_60mM_minus.6938.7029.3	3	20.92	1	2.74E+05		(R)IVDGKV	(R)I/V|D/G K/V/V/S/E/T N D/T/K(V)		97.95	502.2642	1504.785	-0.0073	-4.8	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
280	dirMS_041712_NAR_60mM_minus.5948.6095.3	3	20.91	1	3.30E+06		(K)DSYVGD	(K)D S|Y|V/G/D/E/A/Q/S K R(G)		90.38	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
281	dirMS_041712_NAR_20mM_plus.12043.12043.2	2	20.9	0	1.20E+05		(R)IYVVDV	(R)I Y|V|V|D|V/G S E P R(A)		156.17	617.3237	1233.647	-0.0073	-5.9	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
282	dirMS_041712_NAR_50mM_plus2.14862.15203.3	3	20.9	1	1.13E+06		(R)VEKIPG	(R)V E|K I|P G G\I|I|E|D/S/C V|L/R(G)	C:Carbamidomethylation	146.32	595.6548	1784.958	-0.0076	-4.3	4.68	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
283	dirMS_041712_NAR_20mM_minus.10850.10850.2	2	20.89	0	1.35E+06	M92m	(R)ImNTFS	(R)I/m|N/T|F S/V/V|P S/P K(V)	m:Oxidized methionine	157.03	668.3513	1319.703	15.9925	-1.8	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
284	dirMS_041712_NAR_30mM_minus2.6914.7024.2	2	20.89	0	5.37E+05		(K)ISSPTETI	(K)I/S|S/P/T/E/T E/R(C)		92.23	510.2598	1019.5	0.0119	11.7	4.53	11854.4	6.57	HUMAN	P31949	Protein S100-A11
285	dirMS_041712_NAR_50mM_minus2.12203.12272.3	3	20.89	0	4.54E+05		(R)GIYAYGI	(R)G I|Y|A|Y|G/F E K/P S A/I Q Q R(A)		137.8	609.9832	1827.939	-0.0038	-2.1	8.5	16071.1	4.8	HUMAN	B4E102	Eukaryotic initiation factor 4A-I
286	dirMS_041712_NAR_30mM_plus2.7058.7058.2	2	20.89	0	1.83E+04		(R)SGGGG	(R)S G/G G G/G/G|G/L/G S/G G S I|R(S)		92.03	616.8023	1232.598	-0.0005	-0.4	9.47	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
287	dirMS_041712_NAR_40mM_plus2.18211.18211.3	3	20.89	1	3.46E+04		(K)TFVNITP	(K)T F|V/N/I/T/P A E V/G V L V G K/D/R(S)		173.53	639.0251	1915.065	-0.004	-2.1	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
288	dirMS_041712_NAR_60mM_plus.13252.13291.3	3	20.87	1	8.50E+05		(R)INVYYNI	(R)I/N|V|Y/Y|N E/A/T/G G K/Y/V P R(A)		126.17	615.3146	1843.934	-0.0045	-2.4	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
289	dirMS_041712_NAR_60mM_plus.6821.6823.3	3	20.87	0	4.10E+06		(R)SGSMDI	(R)S/G|S|M/D/P/S G A/H P/S V/R(Q)		94.32	462.2129	1384.627	-0.0032	-2.3	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
290	dirMS_041712_NAR_30mM_plus2.11892.11924.2	2	20.86	0	1.89E+06		(K)LVSESSD	(K)L/V|S|E/S/S D|V/L|P/K(-)		115.87	587.3208	1173.636	-0.0018	-1.6	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
291	dirMS_041712_NAR_30mM_plus2.17255.17784.2	2	20.86	0	2.26E+06		(K)FLDGIYV	(K)F/L|D|G|I|Y|V/S E/K(G)		145.7	585.8057	1170.604	0	0	4.37	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
292	dirMS_041712_NAR_30mM_plus2.22101.22497.2	2	20.86	0	1.20E+06		(K)IGFPWSI	(K)I/G|F|P/W/S/E/I/R(N)		173.2	552.8032	1104.584	0.0155	14	6	71218.8	6.3	HUMAN	A7YIJ8	Radixin
293	dirMS_041712_NAR_20mM_plus.17686.18043.2	2	20.85	0	4.39E+05		(R)ILVATNL	(R)I/L|V|A|T|N/L/F G R(G)		194.57	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
294	dirMS_041712_NAR_30mM_plus2.12054.12298.2	2	20.85	0	3.34E+06		(R)AQIFAN	(R)A Q|I|F|A|N|T/V/D/N A R(I)		116.82	660.338	1319.67	-0.0015	-1.1	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
295	dirMS_041712_NAR_60mM_minus.7573.7819.3	3	20.84	1	6.66E+05		(K)IVADKD	(K)I/V|A D/K/D/Y/S/V/T/A N/S/K(I)		102.58	504.2624	1510.775	-0.0021	-1.4	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
296	dirMS_041712_NAR_40mM_plus2.13318.13318.3	3	20.84	0	6.01E+05		(R)QVSASE	(R)Q V/S A/S E/L/H T S G I/L/G/P/E T L R(D)		145.08	665.6807	1995.051	-0.023	-11.5	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
297	dirMS_041712_NAR_40mM_plus2.13962.14006.3	3	20.84	0	2.92E+05		(R)LASTLVI	(R)L/A|S T L/V/H L|G E\Y\Q A|A/V/D/G A R(K)		148.43	657.6841	1971.029	0.0083	4.2	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
298	dirMS_041712_NAR_60mM_minus.18717.18768.3	3	20.83	0	2.88E+05		(K)TFLVWV	(K)T F|L|V/W/V/N/E E D/H L R(V)		165.82	553.2818	1657.833	-0.0024	-1.5	4.65	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
299	dirMS_041712_NAR_50mM_plus2.5960.5978.3	3	20.83	0	2.45E+05		(R)VEAKPE	(R)V/E|A/K/P E|V|Q/S/Q/P P R(V)		95.53	488.9312	1464.781	-0.0015	-1	6.11	54177.2	5.41	HUMAN	Q9UN86	Ras GTPase-activating protein-binding protein 2
300	dirMS_041712_NAR_120mM_plus.9981.10506.3	3	20.82	1	4.08E+06		(R)LQAEIEG	(R)L/Q|A/E/I/E/G L/K/G Q R(A)		106.57	447.9207	1341.748	-0.0009	-0.7	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
301	dirMS_041712_NAR_30mM_plus2.12402.12924.2	2	20.82	0	1.13E+06		(R)YSGSYNI	(R)Y/S|G/S/Y/N/D/Y/L/R(A)		119.33	619.2776	1237.548	-0.0005	-0.4	5.83	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
302	dirMS_041712_NAR_30mM_plus2.14248.14706.2	2	20.82	0	4.31E+06		(K)LLQLVEI	(K)L/L|Q|L|V/E/D/R(G)		129.2	493.2867	985.568	-0.0015	-1.6	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
303	dirMS_041712_NAR_50mM_plus2.11379.11434.3	3	20.82	1	9.91E+05		(K)VIQEIVD	(K)V/I|Q/E/I/V/D/K/S/G V V/R(V)		127.82	481.2834	1441.837	-0.0017	-1.1	6.04	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
304	dirMS_041712_NAR_50mM_minus2.11070.11090.3	3	20.81	1	4.01E+05		(R)INVYYNI	(R)I/N|V|Y/Y|N/E/A/T/G G K/Y/V/P R(A)		131.28	615.3184	1843.934	0.0069	3.8	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
305	dirMS_041712_NAR_20mM_plus.10886.10886.2	2	20.81	0	2.19E+05	M33m	(K)VAGmD	(K)V/A|G/m\D V|E L/T/V|E E/R(N)	m:Oxidized methionine	147.28	732.3555	1447.71	15.994	-0.6	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
306	dirMS_041712_NAR_20mM_plus.15139.15520.2	2	20.81	0	8.10E+05		(K)LLCGLLA	(K)L/L|C|G|L|L/A E/R(L)	C:Carbamidomethylation	177.65	522.7971	1044.587	-0.0001	-0.1	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
307	dirMS_041712_NAR_60mM_plus.11855.11884.3	3	20.81	0	8.64E+05		(R)NSNLVG	(R)N/S|N|L|V/G A/A/H/E/E/L Q Q S R(I)		119.28	584.9576	1752.862	-0.0041	-2.3	5.4	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
308	dirMS_041712_NAR_120mM_minus.10076.10591.3	3	20.8	0	1.94E+06		(R)GFCLPPI	(R)G F|C|L/P/P/H/C S R(G)	C:Carbamidomethylation	110.38	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
309	dirMS_041712_NAR_20mM_plus.13156.13562.2	2	20.8	0	8.91E+05		(R)VLQALE	(R)V/L|Q|A/L/E/G L/K(M)		164.68	485.8004	970.593	0.0004	0.4	5.97	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
310	dirMS_041712_NAR_50mM_minus2.8998.9175.3	3	20.79	1	9.01E+05		(K)TLQEVTI	(K)T L|Q|E/V/T/E/M/D/S V K/R(Y)		119.9	512.5962	1535.773	0.0007	0.4	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
311	dirMS_041712_NAR_40mM_plus2.13447.13447.3	3	20.79	0	2.62E+05		(R)LSAMLV	(R)L/S/A M\L|V/P V T/P E V K/P K(R)		145.78	536.9848	1608.939	0.0005	0.3	8.59	31524.1	4.5	HUMAN	P82970	High mobility group nucleosome-binding domain-containing protein 5
312	dirMS_041712_NAR_40mM_plus2.6587.6782.2	2	20.79	0	4.08E+05		(K)AGFAGD	(K)A/G/F|A|G/D D/A/P R(A)		99.45	488.728	976.448	0.0004	0.4	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
313	dirMS_041712_NAR_40mM_minus2.9134.9256.3	3	20.78	1	6.96E+05	M356m	(K)VGEVIV	(K)V G|E|V/I/V/T/K/D/D A m L L/K(G)	m:Oxidized methionine	136.93	549.6354	1630.908	15.9832	-7.1	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
314	dirMS_041712_NAR_60mM_minus.9314.9316.3	3	20.77	0	1.02E+06		(K)QEYDES	(K)Q E/Y/D E/S/G/P/S/I/V/H/R(K)		111.27	506.2391	1516.703	0.0001	0.1	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
315	dirMS_041712_NAR_30mM_minus2.16659.16659.2	2	20.76	0	2.71E+05	M2243m	(K)mSIYQA	(K)m\S|I|Y/Q/A/M/W/K(G)	m:Oxidized methionine	144.3	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
316	dirMS_041712_NAR_60mM_minus.7978.7978.3	3	20.73	1	4.69E+05		(R)YLAEVA	(R)Y/L|A E/V/A T/G E/K/R(A)		104.32	412.8902	1236.658	-0.0022	-1.8	6.14	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
317	dirMS_041712_NAR_60mM_minus.17116.17158.3	3	20.72	1	6.23E+05		(K)EVNKFQ	(K)E V/N K F Q|M/A|Y/S/N/L L/R(A)		155.47	571.6279	1712.879	-0.0097	-5.7	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
318	dirMS_041712_NAR_20mM_plus.13932.14162.2	2	20.7	0	2.45E+05		(R)AALQELI	(R)A/A|L|Q/E/L/L/S K(G)		168.75	486.789	972.572	-0.0017	-1.7	6.05	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
319	dirMS_041712_NAR_20mM_plus.9939.10187.2	2	20.7	0	1.43E+06		(K)LVSESSD	(K)L/V|S/E/S|S D|V/L/P K(-)		143.17	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
320	dirMS_041712_NAR_50mM_plus2.15701.15770.3	3	20.7	1	2.33E+05		(R)IFDSEEIL	(R)I/F|D/S E/E/I/L/A/G Y K/R(E)		151.1	514.2745	1540.801	0.0084	5.4	4.68	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
321	dirMS_041712_NAR_50mM_plus2.15480.15703.3	3	20.69	0	1.14E+06		(R)LVLEVA	(R)L/V|L/E/V A Q/H/L/G E/S T V/R(T)		150.15	550.9763	1650.917	-0.003	-1.8	5.4	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
322	dirMS_041712_NAR_20mM_plus.14686.14686.2	2	20.68	0	1.30E+05		(K)LVILANN	(K)L V|I|L|A|N/N C|P A L/R(K)	C:Carbamidomethylation	172.67	677.3851	1353.767	-0.0042	-3.1	9.75	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)

323	dirMS_041712_NAR_30mM_minus2.14870.14870.2	2	20.67	0	1.09E+07		(R)FPGQLN	(R)F/P/G/Q|L/N A D|L R(K)		134.72	565.7971	1130.595	-0.0084	-7.4	5.84	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
324	dirMS_041712_NAR_50mM_plus2.16028.16028.3	3	20.67	0	1.05E+06		(R)LSFQHD	(R)L/S/F Q H D\P\E/T/S/V/L/V/L R(K)		152.42	580.9801	1740.928	-0.0022	-1.2	5.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
325	dirMS_041712_NAR_50mM_plus2.19209.19271.3	3	20.67	0	5.40E+05		(K)HLLQAP	(K)H L L Q\A\P\L|D\D\A|Q/E|I/L/Q/A/R(F)		169.5	644.3484	1931.035	-0.0039	-2	4.54	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
326	dirMS_041712_NAR_60mM_minus.13375.13606.3	3	20.66	1	1.16E+06		(R)LATALQI	(R)L/A|T/A/L Q/K/L/E E/A E/K(A)		135.37	481.9376	1443.805	-0.0071	-4.9	4.79	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
327	dirMS_041712_NAR_60mM_minus.4659.4719.3	3	20.66	1	1.35E+06		(R)AAEEED	(R)A/A|E/E/E/D/E/A D/P K/R(Q)		78.07	453.872	1359.602	-0.0008	-0.6	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
328	dirMS_041712_NAR_60mM_plus.9285.9322.3	3	20.66	0	4.31E+06		(K)QEYDES	(K)Q E/Y/D E/S/G/P/S/I/V/H/R(K)		107.12	506.2392	1516.703	0.0004	0.3	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
329	dirMS_041712_NAR_20mM_minus.10124.10124.2	2	20.65	0	1.24E+05		(R)YALYDA	(R)Y A|L|Y/D/A T Y/E T K(E)		150.82	669.3156	1337.626	-0.0021	-1.5	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
330	dirMS_041712_NAR_30mM_plus2.21438.21438.2	2	20.65	0	1.58E+05		(R)VFIGNL	(R)V F|I/G/N L|N T L V/V K(K)		167.38	658.8983	1316.794	-0.0043	-3.3	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
331	dirMS_041712_NAR_20mM_plus.17561.17641.3	3	20.64	0	1.96E+05		(K)SYELPD	(K)S/Y\E\L/P D/G Q|V|I/T/I/G/N E R(F)		193.17	597.6357	1790.892	0.0006	0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
332	dirMS_041712_NAR_50mM_minus2.12498.12622.3	3	20.63	0	1.09E+06	M114m M:	(R)AGKPVI	(R)A G K|P V/I|C A\T|Q|m|L E/S m I/K(K)	C:Carbamidomethylation m:Oxid	139.87	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
333	dirMS_041712_NAR_30mM_plus2.21784.21784.2	2	20.63	0	3.77E+05		(R)FSWNV	(R)F S/W/N|V W/P\S S R(L)		169.4	633.3085	1265.606	0.0035	2.8	9.75	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
334	dirMS_041712_NAR_30mM_minus2.8675.9044.2	2	20.62	0	2.22E+07		(K)AQYEDI	(K)A/Q|Y|E|D/I|A/N/R(S)		103	540.2601	1079.512	0.0013	1.2	4.37	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
335	dirMS_041712_NAR_20mM_plus.17067.17110.3	3	20.62	0	2.36E+05		(R)AIVAIEN	(R)A I\V|A\I\E/N|P A/D|V/S/V/I/S S R(N)		188.88	580.9864	1740.949	-0.0044	-2.5	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
336	dirMS_041712_NAR_30mM_plus2.15151.15729.2	2	20.62	0	7.20E+06		(R)VLQALE	(R)V/L|Q|A|L/E/G L/K(M)		133.6	485.7997	970.593	-0.001	-1.1	5.97	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
337	dirMS_041712_NAR_30mM_plus2.7678.7679.2	2	20.62	0	6.45E+05		(K)TGQAPG	(K)T G\Q|A|P|G Y/S/Y T A/A/N/K(N)		94.28	714.841	1428.675	-0.0007	-0.5	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
338	dirMS_041712_NAR_50mM_plus2.15871.15895.3	3	20.6	1	2.05E+06		(K)VVEEAP	(K)V/V|E|E|A/P/S I/F L D/A E T R/R(A)		151.53	611.3256	1831.955	0.0074	4	4.41	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
339	dirMS_041712_NAR_60mM_plus.9965.9995.2	2	20.6	0	9.64E+05		(R)LESGMC	(R)L/E|S\G/M/Q/N M/S I/H/T K(T)		110.1	738.3522	1475.698	-0.001	-0.7	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
340	dirMS_041712_NAR_50mM_minus2.18443.18502.3	3	20.58	1	1.47E+06		(R)VISGVLC	(R)V/I|S/G V/L/Q/L/G N I V/F/K/K(E)		177	539.0018	1614.994	-0.0033	-2	10	227783.5	5.5	HUMAN	P35579	Myosin-9
341	dirMS_041712_NAR_30mM_plus2.7765.8299.2	2	20.58	0	1.86E+07		(K)AQYEDI	(K)A/Q|Y|E/D/I|A/N/R(S)		95.88	540.2594	1079.512	-0.0001	-0.1	4.37	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
342	dirMS_041712_NAR_50mM_minus2.14140.14161.3	3	20.57	1	4.43E+05		(R)LYSILGT	(R)L/Y|S/I/L/G T T L/K D/E/G K(L)		148.45	513.2863	1537.847	-0.0029	-1.9	6.07	66876.9	6.17	HUMAN	O75083	WD repeat-containing protein 1
343	dirMS_041712_NAR_20mM_plus.18311.18393.3	3	20.57	0	3.15E+05		(R)AAVEEG	(R)A A V E E G I\V|L/G/G/G/C A L/L/R(C)	C:Carbamidomethylation	198.02	562.3058	1684.905	-0.0022	-1.3	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
344	dirMS_041712_NAR_60mM_plus.15562.15563.3	3	20.57	0	4.04E+05		(K)YGYTHL	(K)Y/G|Y/T/H/L/S/T G/D/L/L/R(S)		138.05	499.2612	1495.754	0.0151	10.1	6.74	21748.6	8.92	HUMAN	P00568	Adenylate kinase isoenzyme 1
345	dirMS_041712_NAR_30mM_minus2.7389.7390.2	2	20.55	0	3.68E+05		(K)VAVTEG	(K)V/A|V|T|E/G/C/Q|P S R(V)	C:Carbamidomethylation	94.73	602.2935	1203.579	0.0011	0.9	5.97	258215.9	5.48	HUMAN	E7EN95	Filamin-B
346	dirMS_041712_NAR_50mM_plus2.15574.15721.3	3	20.55	0	5.05E+06		(R)MGPLGI	(R)M/G|P/L/G/L D/H/M/A/S S I E/R(M)		150.08	538.6007	1613.777	0.0101	6.3	5.3	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
347	dirMS_041712_NAR_50mM_minus2.17627.17920.3	3	20.54	1	2.12E+06		(R)GLFIIDD	(R)G L|F|I/I/D/D/K/G I L R(Q)		170.03	453.9381	1359.8	0.0003	0.2	5.96	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
348	dirMS_041712_NAR_60mM_minus.9592.9718.3	3	20.54	0	3.48E+05		(R)QLSQAG	(R)Q L|S|Q/A/G/S/F/S/D/G T H/G G L R(Y)		113.6	573.2781	1717.825	-0.0055	-3.2	6.74	266161	5.68	HUMAN	E9PPU0	Epiplakin
349	dirMS_041712_NAR_50mM_plus2.12928.13230.3	3	20.54	0	1.86E+06		(R)GIYAYG	(R)G I|Y|A|Y/G/F E/K/P/S A I Q Q R(A)		136.68	609.9821	1827.939	-0.0071	-3.9	8.5	16071.1	4.8	HUMAN	B4E102	Eukaryotic initiation factor 4A-I
350	dirMS_041712_NAR_20mM_minus.13250.13250.2	2	20.53	0	2.34E+05		(R)GVVDSE	(R)G V|V|D/S/E/D I|P/L N/L S R(E)		183.02	757.3944	1513.786	-0.0041	-2.7	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
351	dirMS_041712_NAR_60mM_minus.6371.6435.3	3	20.53	0	3.61E+05		(K)AVTEQG	(K)A V|T/E/Q/G/H/E/L/S N E/E R(N)		94.27	533.585	1598.741	-0.0001	0	4.48	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
352	dirMS_041712_NAR_30mM_plus2.7761.8213.2	2	20.53	0	1.59E+06		(K)SNVSDA	(K)S/N|V|S|D/A|V|A/Q/S T R(I)		95.68	617.8044	1234.602	-0.0007	-0.6	5.55	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
353	dirMS_041712_NAR_50mM_plus2.15440.15708.3	3	20.53	1	1.57E+06		(R)ISGLIYEE	(R)I/S|G|L|I/Y/E E T R G V/L/K(V)		149.97	526.6345	1577.89	-0.0008	-0.5	6.14	11367.1	11.36	HUMAN	P62805	Histone H4
354	dirMS_041712_NAR_50mM_plus2.22130.22130.3	3	20.53	1	2.51E+05		(R)KEGGLG	(R)K E G G L G P L N|I|P/L/L|A/D V T R(R)		189.68	621.6925	1863.07	-0.0069	-3.7	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
355	dirMS_041712_NAR_60mM_plus.6542.6660.3	3	20.53	0	1.19E+06		(K)AVTEQG	(K)A/V|T/E/Q/G/H/E/L/S/N E/E/R(N)		93.05	533.5844	1598.741	-0.0019	-1.2	4.48	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
356	dirMS_041712_NAR_50mM_minus2.13486.13853.3	3	20.52	0	5.60E+05		(K)LQMEAI	(K)L/Q|M/E/A/P/H/I/I/V/G T P G R(V)		145.63	540.2947	1618.873	-0.0038	-2.4	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
357	dirMS_041712_NAR_30mM_plus2.12922.12922.2	2	20.51	0	3.14E+05		(K)QQIQSI	(K)Q Q/I|Q/S/I/Q Q/S/I E R(L)		120.75	729.3893	1457.771	0.0006	0.4	6	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
358	dirMS_041712_NAR_40mM_plus2.14899.14953.3	3	20.51	1	3.92E+05		(K)VTADVI	(K)V/T|A/D|V|I/N A/A E K/L/Q V V G R(A)		154.68	595.0062	1783.007	-0.0032	-1.8	6.04	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
359	dirMS_041712_NAR_40mM_plus2.7966.8020.3	3	20.51	1	1.36E+05		(K)GAVAED	(K)G A|V|A|E/D/G D/E/L R T E/P E/A/K(K)		107.38	596.2867	1786.845	0.0002	0.1	4.08	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
360	dirMS_041712_NAR_50mM_plus2.17934.18302.3	3	20.49	1	1.06E+06		(R)LFVGNLI	(R)L/F|V/G/N/L/P T D/I/T E E D F K R(L)		163.23	665.3443	1994.023	-0.0046	-2.3	4.32	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
361	dirMS_041712_NAR_60mM_minus.13593.13714.3	3	20.47	1	1.05E+06		(R)VFDKDG	(R)V/F|D K D G N/G\Y|I/S/A/A/E/L R(H)		136.05	585.6277	1754.871	-0.0022	-1.3	4.56	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
362	dirMS_041712_NAR_60mM_plus.7009.7035.3	3	20.47	1	1.65E+06		(R)IVDGKV	(R)I/V|D/G K/V/V/S/E/T N D/T K(V)		95.08	502.2639	1504.785	-0.0082	-5.4	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
363	dirMS_041712_NAR_50mM_minus2.12652.12861.3	3	20.45	1	6.87E+05		(R)TFNTST	(R)T F|N/T/S/T/G G L|L/L/P S D/T K R(S)		140.78	603.3247	1807.955	0.0047	2.6	8.41	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
364	dirMS_041712_NAR_30mM_plus2.8236.8273.2	2	20.45	0	8.54E+05		(R)ALANSL	(R)A L|A|N/S/L\A/C/Q/G K(Y)	C:Carbamidomethylation	97.53	566.7922	1132.578	-0.0008	-0.7	8.8	13951.6	9.48	HUMAN	H3BR68	Fructose-bisphosphate aldolase A (Fragment)
365	dirMS_041712_NAR_30mM_minus2.15403.15696.2	2	20.44	0	4.05E+05		(K)EIIDPVL	(K)E I|I/D|P/V/L/D/R(I)		138.15	535.299	1069.589	0.0019	1.8	4.03	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
366	dirMS_041712_NAR_20mM_plus.16903.16903.2	2	20.44	0	3.11E+05		(K)VQIAVA	(K)V Q|I\A/V/A/N/A/Q E/L/L Q R(M)		187.77	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
367	dirMS_041712_NAR_40mM_plus2.18538.18799.3	3	20.44	0	4.34E+05		(K)ALIEVLQ	(K)A L|I|E\V|L/Q/P L/I/A\E H Q A R(R)		176.12	601.0146	1801.033	-0.0038	-2.1	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
368	dirMS_041712_NAR_60mM_minus.18153.18419.3	3	20.43	1	1.56E+06		(K)SLLGKD	(K)S/L|L/G/K/D\V|L F/L/K(D)		163.42	411.5912	1232.761	-0.0022	-1.8	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
369	dirMS_041712_NAR_30mM_plus2.13411.13423.2	2	20.42	0	3.82E+05		(R)GATQQI	(R)G A/T|Q|Q|I|L/D|E|A E/R(S)		123.63	665.834	1330.66	0.001	0.7	4.14	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
370	dirMS_041712_NAR_20mM_plus.18418.18418.2	2	20.41	0	1.95E+05		(R)AAVEEG	(R)A A/V/E E|G I|V|L/G/G/G/C A L L R(C)	C:Carbamidomethylation	197.9	842.9549	1684.905	-0.0025	-1.5	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
371	dirMS_041712_NAR_30mM_plus2.13855.13977.2	2	20.41	0	1.26E+06		(R)NTGIICT	(R)N/T|G|I|I|C/T/I|G|P A S R(S)	C:Carbamidomethylation	125.83	680.3557	1359.705	-0.0008	-0.6	9.75	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
372	dirMS_041712_NAR_50mM_plus2.18844.19195.3	3	20.41	0	9.37E+05		(K)LLYDLA	(K)L/L|Y|D|L/A/D/Q L/H/A A/V|G A S R(A)		168.2	604.9965	1812.96	0.0147	8.1	5.21	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
373	dirMS_041712_NAR_50mM_plus2.22290.22290.3	3	20.41	0	1.53E+06		(R)DALSDL	(R)D/A|L|S D L/A L/H/F L/N/K(M)		191.78	486.2644	1456.78	-0.0008	-0.6	5.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
374	dirMS_041712_NAR_20mM_minus.13198.13258.2	2	20.4	0	4.63E+05		(K)TITLEVE	(K)T I|T|L/E|V|E|P S D T I/E/N V K(A)		183.05	894.4654	1787.927	-0.0038	-2.1	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
375	dirMS_041712_NAR_120mM_minus.19359.19501.3	3	20.39	1	3.72E+05		(K)NLRDID	(K)N L/R D I\D|E|V|S|S/L/L/R(T)		161.42	510.614	1529.828	-0.0007	-0.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
376	dirMS_041712_NAR_40mM_minus2.10853.11006.3	3	20.39	1	1.95E+06		(K)TITLEVE	(K)T I|T|L/E|V/E/P S D T I E N V K A K(I)		146.88	663.0226	1987.059	-0.0061	-3.1	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
377	dirMS_041712_NAR_50mM_plus2.15861.16082.3	3	20.39	1	6.63E+06		(R)VVVDAL	(R)V/V|V/D/A/L/S/G/L/K/G D L A G R(Y)		151.98	523.9715	1569.896	0.0041	2.6	5.93	26949.2	7.99	HUMAN	C9JSQ1	Creatine kinase U-type, mitochondrial (Fragment)
378	dirMS_041712_NAR_60mM_plus.20100.20163.3	3	20.39	1	2.57E+05		(K)VVLDDK	(K)V/V|L/D/D/K/D/Y/F/L/F/R(D)		165.47	510.6056	1529.8	0.0024	1.6	4.43	5189.9	4.56	HUMAN	B8ZZ54	10 kDa heat shock protein, mitochondrial
379	dirMS_041712_NAR_60mM_plus.9284.9451.3	3	20.39	0	4.31E+06		(K)QEYDES	(K)Q E/Y/D E/S/G/P/S/I/V/H/R(K)		107.12	506.2392	1516.703	0.0004	0.3	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
380	dirMS_041712_NAR_120mM_plus.6094.6118.3	3	20.38	1	1.75E+06		(K)DSYVGD	(K)D S|Y|V/G D/E/A/Q/S K R(G)		86.23	452.2133	1354.623	0.002	1.5	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
381	dirMS_041712_NAR_40mM_plus2.18043.18251.3	3	20.38	0	2.92E+06		(K)ISSIQSIV	(K)I/S|S I/Q/S/I/V/P A L E I/A/N/A H R(K)		173.12	640.3668	1919.071	0.015	7.8	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
382	dirMS_041712_NAR_50mM_plus2.14402.14657.3	3	20.38	0	2.70E+06		(R)LSQYQE	(R)L/S|Q/Y/Q/E/P L/H L/P G V R(V)		144.57	546.2968	1636.881	-0.0047	-2.9	6.75	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
383	dirMS_041712_NAR_50mM_plus2.19996.20200.3	3	20.38	0	4.85E+05		(K)ALIEVLQ	(K)A L|I|E|V\L/Q/P/L/I/A E H Q A R(R)		174.2	601.0191	1801.033	0.0097	5.4	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
384	dirMS_041712_NAR_40mM_minus2.8183.8251.3	3	20.37	1	5.29E+05		(R)DVVICP	(R)D V|V|I/C/P D A/S L/E D/A K K(E)	C:Carbamidomethylation	129.32	553.9467	1659.826	-0.0003	-0.2	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
385	dirMS_041712_NAR_50mM_plus2.16989.17013.3	3	20.37	0	7.61E+05		(R)QYYTLL	(R)Q Y/Y/T|L/L N Q/A/P/D|M L H/R(K)		156.97	621.6447	1862.922	-0.0022	-1.2	6.74	4335.1	9.82	HUMAN	E5RH00	Ras GTPase-activating protein-binding protein 1
386	dirMS_041712_NAR_120mM_minus.11654.11740.4	4	20.36	2	9.96E+05		(R)SGKYDLI	(R)S\G K Y D\L|D|F K/S/P D/D/P/S/R(Y)		117.92	457.4692	1826.855	-0.0006	-0.3	4.58	47510.4	7.04	HUMAN	P06733	Alpha-enolase
387	dirMS_041712_NAR_20mM_plus.10086.10327.2	2	20.36	0	1.43E+06		(K)LVSESSD	(K)L/V|S|E/S/S D|V/L/P K(-)		143.17	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
388	dirMS_041712_NAR_50mM_plus2.15034.15460.3	3	20.36	1	1.02E+06		(R)GDVVPK	(R)G D/V|V|P/K/D V N/A/A/I/A T I/K(T)		147.9	537.6393	1610.911	-0.0079	-4.9	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
389	dirMS_041712_NAR_30mM_minus2.15454.15733.2	2	20.35	0	3.22E+05		(R)AAPFSLE	(R)A/A|P/F/S/L/E/Y/R(V)		138.3	527.2782	1053.536	0.0128	12.1	6.04	33115.9	5.54	HUMAN	Q15181	Inorganic pyrophosphatase
390	dirMS_041712_NAR_50mM_minus2.9026.9027.3	3	20.35	1	9.01E+05		(K)TLQEVT	(K)T/L|Q E/V/T/E/M/D S V K/R(Y)		119.9	512.5962	1535.773	0.0007	0.4	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
391	dirMS_041712_NAR_60mM_plus.15572.15573.3	3	20.34	1	2.74E+05		(K)YYKVEPL	(K)Y Y/K V E|P|L|D|F/G G T Q K(Q)		138	548.9468	1644.827	-0.001	-0.6	6.07	23480.1	5.04	HUMAN	H0Y9B6	Beta-hexosaminidase subunit beta (Fragment)
392	dirMS_041712_NAR_40mM_plus2.11715.11715.3	3	20.33	1	2.82E+05		(R)IVAPGK	(R)I/V|A|P G K G I L/A A/D/E S T G S/I/A K(R)		135.38	633.3568	1898.059	-0.0035	-1.8	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
393	dirMS_041712_NAR_50mM_minus2.16427.16699.3	3	20.32	1	1.07E+06		(R)VTFSGLF	(R)V/T|F/S/G/L R D T\V|T|P G E L L K(A)		162.5	611.672	1833.012	-0.0102	-5.6	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
394	dirMS_041712_NAR_30mM_plus2.12906.13152.2	2	20.31	0	6.06E+05		(R)LIVENLS	(R)L/I|V|E/N/L/S S/R(V)		121.58	515.7979	1030.589	-0.0006	-0.6	6	14608.1	10.7	HUMAN	B4DJK0	Serine/arginine-rich-splicing factor 5
395	dirMS_041712_NAR_120mM_minus.12329.12647.3	3	20.3	0	1.12E+06		(K)TFTAWC	(K)T F|T/A/W/C/N S/H L/R(K)	C:Carbamidomethylation	121.85	464.8871	1392.648	-0.001	-0.7	9.44	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
396	dirMS_041712_NAR_50mM_minus2.12223.12223.3	3	20.3	0	2.59E+06	M240m	(K)mLDAED	(K)m L|D|A/E/D I/V N T A/R/P D|E K(A)	m:Oxidized methionine	137.85	611.6283	1816.875	15.9958	0.5	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
397	dirMS_041712_NAR_30mM_plus2.21017.21316.2	2	20.3	0	6.89E+05		(K)IPDWFLI	(K)I/P|D|W/F/L/N/R(Q)		165.78	530.785	1060.557	0.0053	5	5.84	9767.1	11.41	HUMAN	J3JS69	40S ribosomal protein S18
398	dirMS_041712_NAR_60mM_plus.12913.13042.3	3	20.3	1	8.37E+05		(R)EFEVYGI	(R)E F/E/V/Y/G/P I/K/R(I)		124.55	413.2246	1237.658	0.0017	1.4	6.24	51612.9	9.98	HUMAN	P08621	U1 small nuclear ribonucleoprotein 70 kDa
399	dirMS_041712_NAR_60mM_plus.8419.8738.3	3	20.3	0	1.91E+06		(K)VSYGIGD	(K)V/S|Y/G/I/G D E E/H/D/Q E/G R(V)		102.5	564.2485	1690.73	0.0006	0.4	4.17	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
400	dirMS_041712_NAR_40mM_minus2.9611.9951.3	3	20.29	0	4.90E+05		(R)VVIIGAC	(R)V/V|I|I|G/A G K/P A A\V/V|L Q T K(G)		139.28	555.3529	1664.047	-0.0028	-1.7	10	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
401	dirMS_041712_NAR_60mM_plus.18721.18870.3	3	20.28	0	5.48E+05		(K)GISDLAC	(K)G I|S/D/L/A/Q/H/Y/L M/R(A)		155.78	468.5804	1403.71	0.0167	11.9	6.74	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
402	dirMS_041712_NAR_60mM_plus.8439.8440.3	3	20.28	0	6.06E+06		(R)FACHSA	(R)F/A/C/H/S/A/S/L/T\V/R(N)	C:Carbamidomethylation	102.83	416.8777	1248.615	0.0032	2.5	9.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
403	dirMS_041712_NAR_50mM_plus2.16288.16540.3	3	20.27	1	4.20E+06		(K)LLQDFF	(K)L/L|Q/D/F/F/N/G K E L N K(S)		154.6	522.6137	1565.832	-0.0057	-3.6	6.07	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
404	dirMS_041712_NAR_20mM_minus.13493.13603.3	3	20.26	0	8.96E+05	M221m	(R)ALTVPEL	(R)A L\T\V/P E/L/T/Q/Q/m F/D/A/K(N)	m:Oxidized methionine	186.35	569.9577	1691.867	15.9913	-2.1	4.37	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
405	dirMS_041712_NAR_40mM_minus2.12726.13015.3	3	20.26	0	3.18E+06		(R)VSLDVN	(R)V/S|L/D/V/N H/F/A/P D/E L T V K(T)		159.18	595.3178	1783.922	0.0164	9.2	4.54	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
406	dirMS_041712_NAR_30mM_plus2.13295.13624.2	2	20.26	0	1.80E+07		(R)IVLQIDN	(R)I/V|L|Q|I|D/N A/R(L)		123.83	521.3067	1041.605	0.001	1	5.84	20842.9	5.32	HUMAN	C9JM50	Keratin, type I cytoskeletal 19 (Fragment)
407	dirMS_041712_NAR_30mM_plus2.6091.6130.2	2	20.26	0	4.04E+05		(R)FSSSSGY	(R)F/S|S/S/S|G/Y/G/G G/S S R(V)		86.35	618.2674	1235.529	-0.0012	-1	8.75	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
408	dirMS_041712_NAR_30mM_minus2.18932.19162.2	2	20.25	0	6.26E+05		(K)LALFQAI	(K)L/A|L|F/Q/A/I|G/K(E)		158.72	480.7964	960.588	-0.0022	-2.2	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
409	dirMS_041712_NAR_50mM_minus2.17568.17568.3	3	20.25	0	4.20E+05		(K)VAHALA	(K)V A H A L A E G L|G\V|I/A/C I/G E/K(L)	C:Carbamidomethylation	168.75	603.3247	1807.974	-0.0139	-7.7	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
410	dirMS_041712_NAR_120mM_plus.8294.8316.4	4	20.24	2	3.75E+06		(K)KGAVAE	(K)K\G A\V\A|E|D|G/D/E L R T E/P E/A/K(K)		97.05	479.4909	1914.94	0.0014	0.8	4.36	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
411	dirMS_041712_NAR_20mM_plus.9933.10184.2	2	20.24	0	1.43E+06		(K)LVSESSD	(K)L V|S|E/S/S D|V/L/P/K(-)		143.17	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
412	dirMS_041712_NAR_50mM_plus2.14640.14702.3	3	20.24	0	5.16E+05		(K)MLDAED	(K)M/L|D/A|E/D/I/V/N T A R/P D/E K(A)		144.95	606.2972	1816.875	0.0025	1.4	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
413	dirMS_041712_NAR_20mM_plus.14136.14136.2	2	20.23	0	1.57E+06	M313m	(R)TVQSLEI	(R)T V/Q|S/L|E|I D/L/D S m R(N)	m:Oxidized methionine	170.15	761.8738	1506.747	15.9935	-0.9	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
414	dirMS_041712_NAR_30mM_plus2.17456.17857.2	2	20.23	0	1.26E+06		(K)FANPFP	(K)F/A|N|P|F/P A A V/R(G)		145.62	545.2953	1089.584	-0.0007	-0.6	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
415	dirMS_041712_NAR_60mM_minus.15624.15828.3	3	20.22	1	6.80E+05		(R)FLQDYFI	(R)F L|Q|D/Y/F/D/G N/L K/R(Y)		147.7	505.924	1515.759	-0.0016	-1.1	5.96	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
416	dirMS_041712_NAR_120mM_plus.9819.9832.3	3	20.22	1	2.43E+05		(K)DTGKTP	(K)D T/G K/T P V\E|P/E/V/A/I/H R(I)		104.82	550.2928	1648.865	-0.0015	-0.9	5.45	5429.1	9.6	HUMAN	E5RIP1	40S ribosomal protein S20
417	dirMS_041712_NAR_40mM_plus2.18067.18152.3	3	20.22	0	1.19E+05		(K)LVLIGSN	(K)L/V|L/I/G S/N/H/S/L/P F L/K(F)		172.83	513.3081	1537.91	-0.0003	-0.2	8.76	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
418	dirMS_041712_NAR_120mM_minus.13808.13808.2	2	20.21	1	4.32E+06		(K)FASFIDK	(K)F/A|S/F/I/D/K/V R(F)		130.17	541.7968	1082.599	-0.013	-12	8.75	19569.8	9.88	HUMAN	F8VRG4	Keratin, type II cytoskeletal 8 (Fragment)
419	dirMS_041712_NAR_30mM_minus2.19439.19659.2	2	20.21	0	1.46E+06		(R)LFDQAF	(R)L/F|D|Q|A/F/G L|P R(L)		162.58	582.315	1163.621	0.002	1.7	5.84	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
420	dirMS_041712_NAR_20mM_plus.15505.15505.2	2	20.21	0	4.20E+05		(R)GVVDSE	(R)G V/V/D/S|E\D|I|P L N/L/S/R(E)		179.18	757.3956	1513.786	-0.0017	-1.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
421	dirMS_041712_NAR_50mM_plus2.5643.5736.3	3	20.21	1	1.06E+06		(K)TAGPIAS	(K)T/A|G/P/I/A/S/A Q K Q/P A/G K(V)		91.9	475.5987	1424.786	-0.0041	-2.8	10	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
422	dirMS_041712_NAR_50mM_minus2.13422.13423.3	3	20.19	0	5.13E+05		(K)SLTNDW	(K)S/L|T/N/D W/E/D H/L/A V/K(H)		144.2	509.9192	1527.744	-0.0008	-0.5	4.53	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
423	dirMS_041712_NAR_20mM_minus.10829.11097.2	2	20.17	0	1.62E+06	M92m	(R)ImNTFS	(R)I/m|N|T|F|S/V/V|P S/P K(V)	m:Oxidized methionine	157.15	668.3513	1319.703	15.9925	-1.8	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
424	dirMS_041712_NAR_40mM_minus2.14623.14851.3	3	20.16	1	1.45E+06		(K)TFVNITP	(K)T F|V|N|I/T/P A E/V/G V L/V/G K D R(S)		171.8	639.0252	1915.065	-0.0037	-1.9	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
425	dirMS_041712_NAR_20mM_plus.17495.17667.2	2	20.16	0	2.22E+05		(K)LLYAFAE	(K)L L|Y|A|F|A E/A/T|V/P K(V)		192.97	661.8712	1322.736	-0.0003	-0.3	6	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
426	dirMS_041712_NAR_40mM_minus2.15009.15151.3	3	20.15	0	2.68E+06		(K)ALESPEF	(K)A/L|E|S/P/E/R P/F L/A I/L/G G/A K(V)		174.77	590.3353	1768.996	-0.0042	-2.4	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
427	dirMS_041712_NAR_50mM_plus2.8925.9007.3	3	20.15	0	2.21E+06		(K)GIVEFSG	(K)G I|V/E/F/S|G K/P A A/R(K)		114.52	411.2309	1231.679	-0.0012	-1	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
428	dirMS_041712_NAR_30mM_plus2.18568.18568.2	2	20.14	0	1.90E+05		(-)SDVLELT	(-)S D V|L|E|L/T/D D N F E S R(I)		150.83	820.3752	1639.745	-0.0015	-0.9	3.77	13747.3	6.8	HUMAN	H7BZJ3	Thioredoxin (Fragment)
429	dirMS_041712_NAR_50mM_plus2.18953.19379.3	3	20.13	1	1.72E+06		(K)LIQLMEI	(K)L/I|Q|L/M/E/E I/M/A E K E/N K(T)		169.7	606.9845	1818.934	0.005	2.7	4.49	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
430	dirMS_041712_NAR_30mM_minus2.12397.12397.2	2	20.12	0	2.17E+05		(R)TLSGME	(R)T L/S/G/M/E/S/Y/C V R(A)	C:Carbamidomethylation	121.88	651.795	1302.582	0.001	0.8	5.66	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
431	dirMS_041712_NAR_30mM_minus2.14061.14421.2	2	20.12	0	1.16E+06		(R)GLLEDV	(R)G L|L|E|D|V|Q/E/G R(T)		130.88	558.2882	1115.569	0	0	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin

432	dirMS_041712_NAR_50mM_minus2.12140.12289.3	3	20.12	0	2.59E+06	M240m	(K)mLDAED	(K)m/L|D|A/E/D/I/V/N T A R P D/E K(A)	m:Oxidized methionine	137.85	611.6283	1816.875	15.9958	0.5	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
433	dirMS_041712_NAR_60mM_plus.12325.12325.3	3	20.1	1	9.36E+05		(R)LSFDKD	(R)L/S|F/D K/D/A M/V/A/R(A)		121.18	418.2158	1252.635	-0.0026	-2.1	5.96	35556.4	9.3	HUMAN	F2Z393	Transaldolase
434	dirMS_041712_NAR_60mM_minus.17094.17178.3	3	20.09	1	9.85E+05		(K)SIYGEKF	(K)S I|Y|G/E/K/F E/D/E/N F/I L/K(H)		155.53	611.3103	1831.911	0.0051	2.8	4.41	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
435	dirMS_041712_NAR_30mM_plus2.23481.23641.2	2	20.09	0	4.18E+06		(R)IAIYELLF	(R)I/A|I|Y/E\L\L/F/K(E)		191.57	555.3331	1109.661	-0.0016	-1.4	6	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
436	dirMS_041712_NAR_50mM_plus2.18208.18443.3	3	20.09	1	6.23E+05		(K)LLEPVLL	(K)L/L|E|P/V/L/L/L/G K E R(F)		164.48	460.6256	1379.862	0.0002	0.1	6.14	16559.1	10.36	HUMAN	P62249	40S ribosomal protein S16
437	dirMS_041712_NAR_60mM_plus.17879.17930.3	3	20.09	1	3.01E+05		(R)KGFSEG	(R)K G F S\E G\L\W|E|I/E|N/N|P\T V K(A)		150.67	650.0017	1947.981	0.0095	4.9	4.79	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
438	dirMS_041712_NAR_60mM_plus.10432.10898.3	3	20.08	1	1.15E+07		(R)VKYETEL	(R)V/K\Y E T|E|L/A/M/R(Q)		113.28	413.8859	1239.64	0.003	2.4	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
439	dirMS_041712_NAR_30mM_minus2.11313.11583.2	2	20.05	0	9.49E+05		(K)LVSESSD	(K)L/V|S/E/S/S D|V|L/P/K(-)		115.78	587.3211	1173.636	-0.0012	-1	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
440	dirMS_041712_NAR_60mM_minus.15810.15810.3	3	20.05	1	3.06E+05		(R)IDTRNEL	(R)I/D/T/R\N E L|E|S|Y/A Y/S/L/K(N)		148.1	601.3049	1801.897	0.0035	1.9	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
441	dirMS_041712_NAR_20mM_plus.10541.10541.2	2	20.05	0	3.12E+05		(K)VLQATV	(K)V L|Q/A|T/V/V/A/V/G/S G S K(G)		145.67	658.3823	1315.758	-0.0007	-0.5	8.72	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
442	dirMS_041712_NAR_50mM_plus2.19783.20199.3	3	20.05	0	4.80E+06		(K)ALESPEF	(K)A/L|E|S|P E R P/F L|A/I/L/G/G A K(V)		173.65	590.3344	1768.996	-0.0069	-3.9	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
443	dirMS_041712_NAR_50mM_plus2.18223.18545.3	3	20.04	0	5.14E+05	M195m	(R)LHFFmP	(R)L H\F\F m|P G|F|A|P/L/T S R(G)	m:Oxidized methionine	164.23	546.2803	1620.835	15.9908	-2.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
444	dirMS_041712_NAR_120mM_plus.9369.9407.4	4	20.03	2	1.18E+06		(K)LTDCVVI	(K)L/T/D/C/V/V/M R D|P A/S K/R(S)	C:Carbamidomethylation	102.65	412.7134	1647.831	0.0012	0.8	8.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
445	dirMS_041712_NAR_40mM_plus2.18294.18294.3	3	20.01	0	3.29E+05		(R)EAVELPL	(R)E A/V/E/L/P L T/H F E/L Y K(Q)		173.87	563.6336	1688.889	-0.0032	-1.9	4.75	47479.5	5.09	HUMAN	P43686	26S protease regulatory subunit 6B
446	dirMS_041712_NAR_50mM_plus2.17271.17453.3	3	20	0	6.18E+05		(K)VLISSLQ	(K)V/L|I|S/S/L/Q/D C L/H/G I E/S/K(S)	C:Carbamidomethylation	159.32	600.3189	1798.937	0.0054	3	5.32	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
447	dirMS_041712_NAR_60mM_minus.10360.10502.3	3	19.99	1	6.05E+05	M88m	(K)DVDEAY	(K)D V|D|E/A/Y/m/N/K/V/E L E/S R(L)	m:Oxidized methionine	118.37	605.2791	1797.832	15.9904	-2.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
448	dirMS_041712_NAR_20mM_plus.8329.8362.2	2	19.99	0	8.56E+04		(R)LAPEYE	(R)L/A|P/E/Y/E/A/A/A T/R(L)		127.75	596.3035	1191.6	-0.0007	-0.6	4.53	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
449	dirMS_041712_NAR_50mM_plus2.12012.12160.3	3	19.99	0	2.97E+05		(R)VVVLM	(R)V/V|V|L|M/G S T/S/D L/G H/C E K(I)	C:Carbamidomethylation	131.5	577.9512	1731.84	-0.0014	-0.8	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
450	dirMS_041712_NAR_30mM_minus2.16081.16323.2	2	19.98	0	3.06E+05		(R)GEVTAA	(R)G E|V|T|A|A|D\L/F/N\S R(V)		141.75	640.3185	1279.628	0.002	1.6	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
451	dirMS_041712_NAR_30mM_plus2.18829.19255.2	2	19.98	0	3.29E+06		(R)QAQEYE	(R)Q A|Q|E/Y/E/A/L/L/N/I/K(V)		153.28	710.3766	1419.748	-0.0019	-1.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
452	dirMS_041712_NAR_120mM_minus.13798.14077.2	2	19.97	1	4.39E+06		(K)FASFIDK	(K)F/A|S|F/I/D/K V/R(F)		130.18	541.7968	1082.599	-0.013	-12	8.75	19569.8	9.88	HUMAN	F8VRG4	Keratin, type II cytoskeletal 8 (Fragment)
453	dirMS_041712_NAR_50mM_minus2.15782.15782.3	3	19.97	0	1.29E+05		(K)FTISDHP	(K)F/T|I/S/D/H P Q P I D|P L L K(N)		157.77	574.3122	1720.927	-0.0048	-2.8	5.21	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
454	dirMS_041712_NAR_60mM_minus.16663.17032.3	3	19.97	0	2.45E+06		(R)DGLAFN	(R)D G|L|A/F/N/A/L/I/H/R(H)		154.08	409.5576	1226.664	-0.0058	-4.7	6.74	146974	5.55	HUMAN	C9JRP8	Spectrin beta chain, non-erythrocytic 4
455	dirMS_041712_NAR_20mM_plus.10864.10864.2	2	19.97	0	2.19E+05	M33m	(K)VAGmD	(K)V A|G/m/D|V|E L/T V/E/E/R(N)	m:Oxidized methionine	147.28	732.3555	1447.71	15.994	-0.6	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
456	dirMS_041712_NAR_30mM_plus2.7466.7467.2	2	19.97	0	4.86E+05		(K)SLAAEEE	(K)S L|A|A/E|E/E/A A/R(Q)		93.58	523.7605	1046.511	0.0024	2.3	4.25	533778	5.74	HUMAN	Q15149	Plectin
457	dirMS_041712_NAR_60mM_plus.9986.9987.2	2	19.97	0	2.35E+05		(R)GCHLLV	(R)G C/H|L|L/V|A|T|P G R(L)	C:Carbamidomethylation	110.13	590.8148	1180.626	-0.0032	-2.7	9.75	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
458	dirMS_041712_NAR_20mM_plus.11939.12109.2	2	19.96	0	2.63E+05		(K)YGEPGE	(K)Y/G|E|P/G/E\V/F I/N K(G)		156.1	626.8223	1252.621	0.0165	13.2	4.53	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
459	dirMS_041712_NAR_30mM_plus2.15749.16120.2	2	19.96	0	2.79E+06		(R)VLQALE	(R)V/L|Q|A/L/E/G L/K(M)		134.72	485.7997	970.593	-0.001	-1.1	5.97	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
460	dirMS_041712_NAR_40mM_plus2.18216.18216.3	3	19.96	0	1.04E+05		(K)VLSLPKP	(K)V/L|S L|P K P T I|I/L/S/A/Y Q R(K)		173.45	600.3613	1799.079	-0.0096	-5.3	9.99	80080.5	5.54	HUMAN	J3KMX1	Nuclear pore complex protein Nup88 (Fragment)
461	dirMS_041712_NAR_50mM_plus2.15980.16317.3	3	19.96	1	1.50E+06		(K)ILLAELE	(K)I/L|L/A/E/L/E/Q L/K/G Q/G K(S)		152.23	513.9741	1539.911	-0.0027	-1.8	6.14	49709.6	5.19	HUMAN	B0YJC4	Vimentin
462	dirMS_041712_NAR_50mM_plus2.16192.16396.3	3	19.96	0	2.89E+05		(K)ACQSIYF	(K)A C|Q/S|I/Y/P/L/H D/V F V R(K)	C:Carbamidomethylation	154.4	568.9562	1704.853	0.0014	0.8	6.79	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
463	dirMS_041712_NAR_30mM_plus2.14237.14259.2	2	19.95	0	9.98E+05		(R)MGQM	(R)M/G Q|M|A|M|G/G/A M|G/I N N R(G)		127.32	769.8376	1538.67	-0.0015	-1	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
464	dirMS_041712_NAR_50mM_plus2.20887.21236.3	3	19.95	0	8.86E+06		(R)LHFFMP	(R)L H\F\F\M|P/G|F|A|P|L/T S R(G)		181.52	540.9498	1620.835	-0.0007	-0.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
465	dirMS_041712_NAR_20mM_minus.8498.8498.2	2	19.94	0	7.57E+04		(R)IIYGGSV	(R)I I|Y/G G S/V/T/G A T C K(E)	C:Carbamidomethylation	134.28	663.8403	1326.672	0.0011	0.8	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
466	dirMS_041712_NAR_30mM_minus2.9625.10182.2	2	19.94	0	7.15E+06		(K)TAVCDI	(K)T A|V|C/D|I|P|P/R(G)	C:Carbamidomethylation	107.48	514.7641	1028.519	0.0016	1.5	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
467	dirMS_041712_NAR_20mM_plus.18012.18012.2	2	19.94	0	1.91E+05		(K)GADFLV	(K)G A D|F|L|V|T E V\E/N G G S L/G S K(K)		195.25	890.4414	1779.876	-0.0004	-0.2	4.14	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
468	dirMS_041712_NAR_30mM_plus2.7333.7333.2	2	19.94	1	2.13E+05		(R)YSGGNY	(R)Y S|G/G/N/Y R D N\Y|D|N(-)		93.03	719.2864	1437.567	-0.001	-0.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
469	dirMS_041712_NAR_60mM_plus.9269.9452.3	3	19.93	0	4.31E+06		(K)QEYDES	(K)Q E/Y/D E/S/G/P/S/I/V H/R(K)		107.12	506.2392	1516.703	0.0004	0.3	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
470	dirMS_041712_NAR_30mM_minus2.10678.10781.2	2	19.92	0	7.70E+05		(K)TVSPALI	(K)T V|S|P/A/L/I/S/R(F)		111.87	472.2815	943.557	-0.0014	-1.5	9.41	50425	5.53	HUMAN	H0YH27	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
471	dirMS_041712_NAR_30mM_minus2.13154.13194.2	2	19.92	0	2.97E+05		(R)GATQQI	(R)G A/T|Q|Q|I|L|D|E/A/E R(S)		125.18	665.833	1330.66	-0.001	-0.8	4.14	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
472	dirMS_041712_NAR_120mM_plus.16995.16995.3	3	19.92	1	5.91E+05		(K)YYVTIID	(K)Y/Y|V/T/I I/D/A/P G H R D F I K(N)		142.13	636.6716	1908.001	-0.0012	-0.6	6.75	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
473	dirMS_041712_NAR_20mM_minus.12230.12536.2	2	19.91	0	9.01E+05	M185m	(K)LAVNm	(K)L/A|V|N/m|V/P F/P/R(L)	m:Oxidized methionine	171.88	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
474	dirMS_041712_NAR_50mM_minus2.7088.7104.3	3	19.91	0	1.74E+05		(R)SAEEEA	(R)S A|E|E E/A/A/D/L/P T K/P T K(I)		106.92	529.6012	1586.791	-0.0018	-1.1	4.41	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
475	dirMS_041712_NAR_20mM_plus.10781.10971.2	2	19.9	0	7.16E+05		(K)IGGIGTV	(K)I/G|G\I|G|T/V|P V/G/R(V)		147.43	513.3057	1025.61	-0.0061	-5.9	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
476	dirMS_041712_NAR_50mM_plus2.14834.14954.3	3	19.9	0	5.02E+05		(K)TTISVAH	(K)T/T|I/S/V/A H/L/L/A A/R(Q)		146.45	418.2499	1252.737	-0.002	-1.6	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
477	dirMS_041712_NAR_30mM_minus2.7395.7395.2	2	19.88	0	1.14E+05		(K)EAEGAP	(K)E/A/E/G A|P Q/V/E/A/G\K(R)		94.65	593.2913	1185.575	0.0007	0.6	4.25	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
478	dirMS_041712_NAR_60mM_plus.11647.11781.3	3	19.88	1	1.45E+06		(R)VLTVIN	(R)V/L|T|V/I/N Q/T/Q/K/E N L R(K)		118.62	552.6521	1655.944	-0.0021	-1.3	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
479	dirMS_041712_NAR_120mM_minus.10163.10163.3	3	19.87	1	1.07E+06		(K)IFRDGEE	(K)I F R D G E E|A|G|A/Y/D/G P R(T)		110.25	551.5928	1652.766	-0.0025	-1.5	4.32	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
480	dirMS_041712_NAR_20mM_plus.15630.15630.2	2	19.87	0	3.47E+05		(K)VGINYQ	(K)V G I N Y|Q|P/P T V/V|P G G/D L/A/K(V)		179.05	912.9952	1824.985	-0.0023	-1.3	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
481	dirMS_041712_NAR_30mM_plus2.19925.19925.2	2	19.87	0	7.84E+05		(K)MSIYQA	(K)M/S|I|Y/Q A M W/K(G)		158.77	579.2783	1157.548	0.0011	1	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
482	dirMS_041712_NAR_20mM_plus.10529.10603.2	2	19.86	0	3.12E+05		(K)VLQATV	(K)V L|Q|A|T|V/V/A/V|G S\G S K(G)		145.67	658.3823	1315.758	-0.0007	-0.5	8.72	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
483	dirMS_041712_NAR_50mM_plus2.9373.9476.3	3	19.86	1	5.41E+05		(K)GILAAD	(K)G I|L|A|A/D/E/S/T/G S I A K/R(L)		116.73	496.9389	1488.802	0.0005	0.3	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
484	dirMS_041712_NAR_20mM_plus.8889.8890.2	2	19.85	0	1.30E+05		(K)VLEEAN	(K)V L|E|E|A|N/Q|A|I|N|P K(L)		131.6	663.353	1325.706	-0.0072	-5.5	4.53	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
485	dirMS_041712_NAR_30mM_plus2.9056.9056.2	2	19.84	0	3.94E+05		(K)IYIDSNN	(K)I/Y|I/D/S/N N/N|P E R(F)		101.15	667.8205	1334.633	0.0002	0.2	4.37	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
486	dirMS_041712_NAR_120mM_plus.10634.10783.3	3	19.83	1	7.19E+05		(R)FYKNEG	(R)F/Y/K N E/G/G|T/W/S/V E/K(V)		109.07	515.5841	1544.738	-0.0002	-0.2	6.14	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
487	dirMS_041712_NAR_60mM_minus.15091.15226.3	3	19.82	1	1.31E+06		(R)ELISNAS	(R)E L|I/S/N/A/S|D|A L/D/K I R(L)		144.2	515.6165	1544.828	0.0071	4.6	4.56	5582.4	4.81	HUMAN	F8W026	Endoplasmin (Fragment)
488	dirMS_041712_NAR_30mM_plus2.13709.13784.2	2	19.82	0	7.16E+05		(R)YALYDA	(R)Y/A|L|Y/D|A T/Y/E/T K(E)		125	669.317	1337.626	0.0007	0.6	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
489	dirMS_041712_NAR_30mM_plus2.19579.19828.2	2	19.82	0	2.31E+05		(K)LLQDFF	(K)L/L|Q/D/F|F/N/G R(D)		156.9	555.2902	1109.574	-0.0007	-0.6	5.84	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
490	dirMS_041712_NAR_40mM_plus2.7744.7744.2	2	19.82	0	8.63E+04		(R)FGQGG	(R)F G/Q/G/G/A|G|P V/G G Q G P R(G)		105.47	671.3368	1341.666	0.0005	0.4	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
491	dirMS_041712_NAR_60mM_plus.6446.6468.3	3	19.82	1	2.23E+05		(K)LEEAEK	(K)L/E|E|A E/K/A/A/D/E|S E/R(G)		92.37	492.8967	1476.681	-0.0057	-3.9	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
492	dirMS_041712_NAR_30mM_plus2.22641.22743.2	2	19.81	0	8.66E+05		(R)IDLAVLL	(R)I/D|L|A|V|L|L/G/K(T)		176.32	471.3029	941.603	-0.0045	-4.7	5.84	113668.7	6.2	HUMAN	F8W726	Ubiquitin-associated protein 2-like
493	dirMS_041712_NAR_20mM_plus.10586.10586.2	2	19.8	0	5.11E+04		(R)ELAEDG	(R)E L|A|E/D/G Y/S/G V/E V R(V)		145.7	712.3373	1423.67	-0.0026	-1.9	4	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
494	dirMS_041712_NAR_40mM_plus2.18486.18486.3	3	19.79	1	3.08E+04		(K)LLLEGVE	(K)L/L|L/E/G V E N K L I/P G L/K(I)		175.08	546.0066	1636.004	0.0009	0.5	6.14	59384	7.79	HUMAN	B7Z3Z9	Long-chain-fatty-acid--CoA ligase 1
495	dirMS_041712_NAR_60mM_plus.14451.14491.3	3	19.79	1	4.71E+05		(K)ISNYGW	(K)I/S|N/Y/G W/D/Q/S D/K F V/K(I)		132.32	562.9416	1686.812	-0.002	-1.2	5.96	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
496	dirMS_041712_NAR_120mM_minus.8814.8997.3	3	19.78	0	9.66E+05		(K)HTGPNS	(K)H T G\P N\S/P/D|T|A/N/D/G F V/R(L)		103.18	562.2599	1684.767	-0.0022	-1.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
497	dirMS_041712_NAR_30mM_plus2.21465.21465.2	2	19.78	0	1.58E+05		(R)VFIGNL	(R)V F|I/G N/L N T/L/V V/K(K)		167.38	658.8983	1316.794	-0.0043	-3.3	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
498	dirMS_041712_NAR_30mM_plus2.8028.8028.2	2	19.78	0	2.20E+05		(K)IAVAAQ	(K)I/A|V|A|A Q N C Y/K(V)	C:Carbamidomethylation	96.05	569.2905	1137.572	0.0016	1.4	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
499	dirMS_041712_NAR_50mM_plus2.15744.15766.3	3	19.78	1	3.70E+06		(K)ISDSEGF	(K)I/S|D/S|E/G F/K/A/N L/S/L L R(R)		151.2	550.6331	1649.886	-0.001	-0.6	6.07	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
500	dirMS_041712_NAR_50mM_plus2.9807.9881.3	3	19.78	1	2.67E+03		(R)TAGVKV	(R)T/A|G V/K V/E T/T E/D|L/V/A/K(L)		120.5	520.9473	1560.848	-0.0206	-13.2	4.68	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
501	dirMS_041712_NAR_60mM_plus.13655.13655.3	3	19.78	1	5.75E+05		(R)ISVYYNE	(R)I/S|V/Y/Y N E A T G/G K Y V P R(A)		128.33	606.3113	1816.923	-0.0035	-1.9	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
502	dirMS_041712_NAR_30mM_minus2.16093.16093.2	2	19.77	0	1.16E+05		(K)EQFLDG	(K)E/Q|F/L/D/G D G W/T S R(W)		141.08	705.8174	1410.628	-0.0009	-0.6	4.03	28545.1	4.5	HUMAN	K7EJB9	Calreticulin (Fragment)
503	dirMS_041712_NAR_50mM_minus2.8667.8971.3	3	19.77	1	3.08E+06	M88m	(K)DVDEAY	(K)D V|D|E|A/Y/m N K/V/E/L/E/S R(L)	m:Oxidized methionine	118	605.2717	1797.832	15.9682	-14.7	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
504	dirMS_041712_NAR_40mM_plus2.12859.13027.3	3	19.77	0	3.08E+05		(K)VVEIAP	(K)V/V|E|I/A/P/A A/H/L D/P Q L R(T)		142.65	543.6417	1628.912	-0.0013	-0.8	5.32	58266.4	9.46	HUMAN	B4DN00	Pyruvate carboxylase, mitochondrial
505	dirMS_041712_NAR_40mM_plus2.17146.17314.3	3	19.76	1	3.36E+05		(K)VIAATN	(K)V/I|A|A/T/N R V/D\I|L/D/P A L L R(S)		168.1	617.3636	1850.086	-0.0096	-5.2	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
506	dirMS_041712_NAR_20mM_plus.15481.15855.2	2	19.75	0	5.10E+05		(R)GVVDSE	(R)G V|V|D|S|E/D|I|P L N/L/S R(E)		179.4	757.3956	1513.786	-0.0017	-1.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
507	dirMS_041712_NAR_20mM_plus.9334.9334.2	2	19.75	0	1.86E+05		(K)SVTNED	(K)S V/T\N E/D\V/T Q/E E/L/G G A/K(T)		136	838.9014	1676.797	-0.0018	-1.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
508	dirMS_041712_NAR_40mM_plus2.12886.13195.3	3	19.75	0	9.15E+05		(R)VVIIGAG	(R)V/V|I|I/G/A G K/P A A\V/V|L Q/T K(G)		143.22	555.3527	1664.047	-0.0034	-2	10	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
509	dirMS_041712_NAR_50mM_plus2.16024.16024.3	3	19.75	1	1.20E+06		(K)CEFQDA	(K)C E/F Q D A\Y/V/L/L/S E K K(I)	C:Carbamidomethylation	152.32	577.2866	1729.847	-0.0013	-0.8	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
510	dirMS_041712_NAR_30mM_plus2.6028.6044.2	2	19.74	0	4.93E+05		(R)QEMQE	(R)Q E|M|Q|E|V/Q/S/S R(S)		85.92	611.2799	1221.553	-0.0003	-0.2	4.53	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
511	dirMS_041712_NAR_40mM_minus2.14295.14295.3	3	19.73	1	1.61E+05		(K)TGISDVF	(K)T G|I/S D V F A K/N D|L/A/V/V D/V R(I)		168.48	640.3454	1919.023	-0.0016	-0.8	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
512	dirMS_041712_NAR_50mM_plus2.20243.20243.3	3	19.73	1	1.43E+06		(R)TLAEIAK	(R)T L|A/E/I/A K/A/E L D G T/I/L/K(S)		175.75	562.6601	1685.968	-0.0026	-1.6	4.68	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
513	dirMS_041712_NAR_50mM_plus2.9854.9854.3	3	19.73	1	2.58E+05		(K)ALDLDS	(K)A L/D L/D/S S/C K E|A|A D/G/Y Q/R(C)	C:Carbamidomethylation	119.3	633.6225	1898.855	-0.0019	-1	4.23	60404.6	6.4	HUMAN	F5H0T1	Stress-induced-phosphoprotein 1
514	dirMS_041712_NAR_60mM_plus.16202.16383.3	3	19.73	0	5.95E+05		(K)WIGLDL	(K)W|I|G L/D/L/S/N/G K/P R(D)		142.1	452.5864	1355.743	0.0016	1.2	8.75	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
515	dirMS_041712_NAR_50mM_minus2.9551.9864.3	3	19.72	1	2.86E+06		(R)MQKEIT	(R)M Q\K\E I T/A|L|A|P S/T M/K(I)		123.52	516.9426	1548.812	0.0008	0.5	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
516	dirMS_041712_NAR_50mM_plus2.12452.12452.3	3	19.72	0	3.93E+05		(R)LDDTVH	(R)L/D/D T/V H V/V/I/A/T/P G/R(I)		133.35	498.2741	1492.812	-0.0041	-2.7	5.21	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
517	dirMS_041712_NAR_60mM_plus.9165.9204.3	3	19.71	1	2.99E+05		(R)FVKQDC	(R)F V/K Q D|Q|V/C/I|A/R(L)	C:Carbamidomethylation	106	455.2428	1363.715	-0.0012	-0.9	8.75	53458.1	5.47	HUMAN	H3BR35	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A (Fragment)
518	dirMS_041712_NAR_30mM_plus2.10701.10909.2	2	19.7	0	8.88E+05		(R)AEAESM	(R)A E|A|E|S|M/Y/Q/I/K(Y)		109.97	585.2792	1169.551	0.0004	0.4	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
519	dirMS_041712_NAR_30mM_plus2.5469.5469.2	2	19.7	0	3.75E+04		(K)SAAQAA	(K)S A/A/Q/A/A/A|Q|T/N S N A A|G K(Q)		82.75	730.8568	1460.709	-0.0025	-1.7	8.47	45021.6	8.74	HUMAN	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein
520	dirMS_041712_NAR_30mM_minus2.16236.16236.2	2	19.69	0	3.06E+05		(R)GEVTAA	(R)G E/V/T/A/A/D L|F N S R(V)		141.75	640.3185	1279.628	0.002	1.6	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
521	dirMS_041712_NAR_40mM_minus2.14609.14863.3	3	19.68	1	1.45E+06		(K)TFVNITP	(K)T F|V|N|I/T/P A E V G V L/V/G\K D/R(S)		171.8	639.0252	1915.065	-0.0037	-1.9	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
522	dirMS_041712_NAR_50mM_minus2.5839.5843.3	3	19.68	0	1.31E+05		(R)AGAAG	(R)A/G|A|A|G|G/P E/E|E A E K/P V K(T)		95.32	513.9233	1539.765	-0.0096	-6.2	4.49	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
523	dirMS_041712_NAR_120mM_plus.20439.20673.3	3	19.68	1	9.13E+05		(R)RFDEILE	(R)R F D E\I\L|E|A|S/D/G|I/M/V/A R(G)		160.97	607.9762	1821.916	-0.0023	-1.3	4.32	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
524	dirMS_041712_NAR_120mM_plus.7483.7760.3	3	19.67	1	6.54E+05		(R)SGGYGG	(R)S/G|G|Y/G/G S R/D/Y/Y/S S/R(S)		93.37	504.5549	1511.651	-0.0008	-0.5	8.22	26585.7	11.25	HUMAN	B3KT17	Cold-inducible RNA-binding protein
525	dirMS_041712_NAR_50mM_plus2.8635.8970.3	3	19.67	0	1.55E+06		(R)LESGMC	(R)L/E|S G M/Q|N/M/S/I/H/T K(T)		113.23	492.5704	1475.698	-0.0015	-1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
526	dirMS_041712_NAR_30mM_minus2.12505.12908.2	2	19.66	0	7.93E+05		(R)GVVGPE	(R)G V|V|G|P/E/L/Y/G/R(L)		122.53	523.7834	1046.563	-0.0034	-3.2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
527	dirMS_041712_NAR_60mM_plus.7709.7728.3	3	19.66	1	6.81E+05		(K)AVPKED	(K)A V|P K E D I|Y|S/G/G/G/G G G\S R(S)		98.43	536.2643	1606.782	-0.0036	-2.3	6.11	31011.2	9.5	HUMAN	Q13151	Heterogeneous nuclear ribonucleoprotein A0
528	dirMS_041712_NAR_30mM_minus2.11608.11895.2	2	19.65	0	8.43E+06		(R)AQIFAN	(R)A Q|I|F|A|N/T/V/D/N A R(I)		117.53	660.3384	1319.67	-0.0007	-0.5	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
529	dirMS_041712_NAR_20mM_plus.18029.18029.2	2	19.64	0	1.86E+05		(K)GADFLV	(K)G A D F L|V|T E/V/E/N/G G S L/G S\K(K)		195.27	890.4414	1779.876	-0.0004	-0.2	4.14	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
530	dirMS_041712_NAR_50mM_plus2.17679.17679.3	3	19.64	1	8.31E+05		(R)DSEQVA	(R)D S|E/Q/V/A E L/K Q E L A T L K(S)		161.07	601.322	1801.954	-0.0027	-1.5	4.41	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
531	dirMS_041712_NAR_60mM_plus.11701.11810.3	3	19.64	1	5.36E+05		(K)GVAINM	(K)G V|A|I/N|M/V/T E E D/K/R(T)		118.67	487.9162	1461.737	-0.0026	-1.7	4.68	46381.4	5.32	HUMAN	P60842	Eukaryotic initiation factor 4A-I
532	dirMS_041712_NAR_60mM_plus.18540.18540.3	3	19.64	1	2.60E+05		(R)RGDINLI	(R)R G D I\N/L|L|M/L/G D/P G T A/K(S)		154.52	557.6331	1670.889	-0.0047	-2.8	5.96	78390.7	9.27	HUMAN	B1AHB1	DNA replication licensing factor MCM5
533	dirMS_041712_NAR_50mM_minus2.17642.17712.3	3	19.63	1	2.12E+06		(R)GLFIIDD	(R)G L|F|I/I/D/D/K/G I L/R(Q)		170.03	453.9381	1359.8	0.0003	0.2	5.96	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
534	dirMS_041712_NAR_120mM_plus.11362.11563.3	3	19.63	0	3.86E+06		(R)FAQHGT	(R)F A Q H G T\F\E|Y|E|Y/S Q R(W)		113.27	588.2657	1762.782	0.0006	0.3	5.4	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
535	dirMS_041712_NAR_50mM_plus2.17825.18326.3	3	19.63	0	3.82E+07		(R)IHFPLAT	(R)I H\F\P L A\T|Y|A|P/V/I/S A E K(A)		164.67	586.3252	1756.963	-0.0022	-1.2	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
536	dirMS_041712_NAR_20mM_minus.9802.10034.2	2	19.62	0	8.73E+05		(R)IVLQIDN	(R)I/V|L|Q|I/D/N A/R(L)		149.7	521.3059	1041.605	-0.0006	-0.6	5.84	20842.9	5.32	HUMAN	C9JM50	Keratin, type I cytoskeletal 19 (Fragment)
537	dirMS_041712_NAR_40mM_minus2.5861.6011.2	2	19.62	0	1.35E+06		(K)AGFAGD	(K)A/G/F|A|G/D/D/A/P/R(A)		98.18	488.7279	976.448	0.0002	0.2	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
538	dirMS_041712_NAR_60mM_minus.7198.7631.3	3	19.62	1	2.09E+06		(K)IQDKEGI	(K)I/Q|D K E G|I|P/P/D/Q Q R(L)		99.35	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
539	dirMS_041712_NAR_20mM_plus.12651.12651.2	2	19.62	0	1.21E+05		(K)GTIQVIT	(K)G T/I/Q|V|I T Q G T/S L K(N)		160.13	673.3872	1345.769	-0.0014	-1.1	8.75	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
540	dirMS_041712_NAR_60mM_plus.11012.11192.3	3	19.62	1	1.31E+06		(K)GILAAD	(K)G I|L|A/A/D/E/S/T/G/S I A K/R(L)		115.78	496.9383	1488.802	-0.0013	-0.9	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)

541	dirMS_041712_NAR_30mM_minus2.10438.10644.2	2	19.61	0	9.33E+05		(K)GSDFDC	(K)G/S|D|F|D/C/E/L/R(L)	C:Carbamidomethylation	111.28	549.7307	1098.452	0.0021	1.9	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
542	dirMS_041712_NAR_60mM_plus.6726.6757.3	3	19.61	1	1.28E+06		(K)SESPKEP	(K)S E|S/P/K/E/P E/Q L/R(K)		93.87	433.8892	1299.654	-0.0009	-0.7	4.78	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
543	dirMS_041712_NAR_30mM_minus2.14312.14849.2	2	19.6	0	1.12E+07		(R)FPGQLN	(R)F/P|G\Q|L/N/A D|L/R(K)		134.67	565.7971	1130.595	-0.0084	-7.4	5.84	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
544	dirMS_041712_NAR_40mM_minus2.15621.15666.3	3	19.6	1	4.96E+05		(K)ALFEEVF	(K)A L|F/E/E/V/P E/L/L/T E/A E K K(E)		181.8	615.9988	1845.984	-0.0026	-1.4	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
545	dirMS_041712_NAR_30mM_plus2.20506.20914.2	2	19.6	0	2.26E+06		(R)LFDQAF	(R)L/F|D|Q/A/F/G L|P R(L)		162.9	582.3164	1163.621	0.0048	4.1	5.84	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
546	dirMS_041712_NAR_50mM_plus2.14953.14953.3	3	19.6	0	5.02E+05		(K)TTISVAH	(K)T T/I/S/V/A/H/L|L/A/A/R(Q)		146.45	418.2499	1252.737	-0.002	-1.6	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
547	dirMS_041712_NAR_60mM_plus.11232.11232.2	2	19.6	0	2.12E+06		(K)GIVEFAS	(K)G I|V/E/F/A/S K/P A A R(K)		116.18	623.3504	1245.695	-0.0015	-1.2	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
548	dirMS_041712_NAR_30mM_plus2.7980.8001.2	2	19.59	0	1.46E+06		(K)SNVSDA	(K)S N|V|S|D/A/V|A/Q|S\T/R(I)		95.83	617.8044	1234.602	-0.0007	-0.6	5.55	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
549	dirMS_041712_NAR_50mM_plus2.18695.18929.3	3	19.59	1	2.23E+05		(K)IGEEFLT	(K)I/G/E/E/F/L/T/D L S Q/L K K(L)		167.02	540.965	1620.884	-0.0039	-2.4	4.68	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
550	dirMS_041712_NAR_20mM_plus.15278.15563.2	2	19.55	0	8.10E+05		(K)LLCGLLA	(K)L L|C|G/L|L/A/E/R(L)	C:Carbamidomethylation	177.65	522.7971	1044.587	-0.0001	-0.1	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
551	dirMS_041712_NAR_40mM_plus2.10934.11032.3	3	19.54	1	3.24E+05		(R)DVVICPI	(R)D V|V|I/C/P D A S L E D/A K K(E)	C:Carbamidomethylation	130.9	553.9465	1659.826	-0.0009	-0.5	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
552	dirMS_041712_NAR_40mM_plus2.17402.17402.3	3	19.54	0	2.47E+04		(R)GTEDITS	(R)G T|E/D/I/T/S P/H G I/P L D\L\L D R(V)		169.42	650.3372	1948.997	-0.0004	-0.2	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
553	dirMS_041712_NAR_50mM_plus2.9894.9902.3	3	19.54	1	1.55E+06	M88m	(K)DVDEAY	(K)D V|D|E/A/Y/m/N K/V/E L/E/S R(L)	m:Oxidized methionine	119.62	605.2794	1797.832	15.9913	-2	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
554	dirMS_041712_NAR_120mM_minus.10434.10876.3	3	19.53	1	3.61E+06		(R)LQAEIEG	(R)L/Q|A/E/I/E/G L/K/G Q R(A)		111.42	447.9206	1341.748	-0.0012	-0.9	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
555	dirMS_041712_NAR_50mM_plus2.15976.16046.3	3	19.53	1	1.11E+06		(R)GQFSTD	(R)G Q|F/S/T/D/E/L/V/A/E V/E/K R(N)		152.07	569.959	1707.855	0.0076	4.5	4.41	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
556	dirMS_041712_NAR_30mM_plus2.7498.7515.2	2	19.52	0	1.00E+06		(R)IQEAGTI	(R)I/Q|E|A/G/T/E/V/V/K(A)		93.7	537.2931	1073.584	-0.0048	-4.5	4.53	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
557	dirMS_041712_NAR_40mM_plus2.17015.17080.3	3	19.52	1	3.08E+05		(R)LFVGNLI	(R)L/F|V/G/N|L/P T D I/T/E E D F K R(L)		166.38	665.3502	1994.023	0.0131	6.6	4.32	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
558	dirMS_041712_NAR_30mM_plus2.12800.12800.2	2	19.51	0	3.70E+05		(R)ELAEDG	(R)E L/A/E/D G\Y/S|G/V/E V/R(V)		120.6	712.3382	1423.67	-0.0008	-0.6	4	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
559	dirMS_041712_NAR_120mM_plus.11532.11569.4	4	19.5	2	1.47E+06		(R)SGKYDLI	(R)S\G K Y D\L/D|F K/S/P D/D|P/S R(Y)		113.65	457.4697	1826.855	0.0014	0.8	4.58	47510.4	7.04	HUMAN	P06733	Alpha-enolase
560	dirMS_041712_NAR_20mM_plus.16103.16330.2	2	19.5	0	4.91E+05		(K)DAGTIA	(K)D A|G|T|I|A|G/L/N V L/R(I)		183.63	600.3422	1199.674	0.0029	2.4	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
561	dirMS_041712_NAR_20mM_minus.12178.12542.2	2	19.49	0	9.01E+05	M185m	(K)LAVNm\	(K)L/A|V|N/m/V/P F/P R(L)	m:Oxidized methionine	171.88	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
562	dirMS_041712_NAR_30mM_minus2.13508.14029.2	2	19.49	0	3.96E+06		(K)ALDFIAS	(K)A/L|D|F|I/A/S/K(G)		128.55	432.7445	864.482	-0.0008	-1	5.88	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
563	dirMS_041712_NAR_50mM_minus2.10991.11138.3	3	19.49	1	4.01E+05		(R)INVYYNI	(R)I/N|V|Y/Y|N E/A/T/G G K/Y/V P R(A)		131.28	615.3184	1843.934	0.0069	3.8	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
564	dirMS_041712_NAR_50mM_minus2.15418.15484.3	3	19.49	0	3.28E+05		(R)LSFQHD	(R)L/S|F Q H D|P E/T|S/V/L/V L R(K)		156.07	580.9793	1740.928	-0.0046	-2.6	5.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
565	dirMS_041712_NAR_50mM_plus2.18488.18652.3	3	19.49	0	4.12E+05		(R)VYAILTH	(R)V Y|A|I/L/T H/G I/F/S G/P A I S R(I)		165.83	601.3347	1801.996	-0.0064	-3.5	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
566	dirMS_041712_NAR_60mM_minus.6105.6190.3	3	19.48	1	2.51E+06		(K)LEEAEKA	(K)L/E|E/A/E/K/A/A/D/E/S E R(G)		93.27	492.8981	1476.681	-0.0015	-1	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
567	dirMS_041712_NAR_30mM_plus2.20539.20730.2	2	19.48	0	8.74E+05		(R)TVQSLEI	(R)T V|Q|S|L|E|I\D/L/D/S M R(N)		162.18	753.8768	1506.747	-0.0005	-0.3	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
568	dirMS_041712_NAR_60mM_minus.18480.18887.3	3	19.47	0	9.16E+06	M195m	(R)LHFFmP	(R)L H\F\F m|P G|F|A|P/L/T S R(G)	m:Oxidized methionine	165.65	546.2843	1620.835	16.0028	4.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
569	dirMS_041712_NAR_30mM_plus2.13173.13333.2	2	19.47	0	7.47E+05		(R)GYFDEEI	(R)G/Y|F|D/E/E/M/N/R(V)		122.82	580.7378	1160.468	0.0006	0.5	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
570	dirMS_041712_NAR_30mM_plus2.8720.8894.2	2	19.47	0	1.01E+06		(K)VEIIAND	(K)V/E|I|I|A|N/D|Q/G N R(T)		99.7	614.8154	1228.628	-0.0045	-3.7	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
571	dirMS_041712_NAR_30mM_plus2.14186.14543.2	2	19.46	0	7.98E+05		(R)GLLEDV	(R)G L|L|E|D/V|Q/E/G\R(T)		128.15	558.2879	1115.569	-0.0006	-0.5	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
572	dirMS_041712_NAR_60mM_plus.20120.20402.3	3	19.46	0	1.45E+06		(R)IHFPLAT	(R)I H F\P L A\T|Y|A|P/V/I/S A E K(A)		165.98	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
573	dirMS_041712_NAR_50mM_minus2.14352.14558.3	3	19.45	1	1.10E+06		(K)EAFSLFD	(K)E A|F/S/L/F/D/K D G D/G T/I/T T K(E)		149.92	615.6336	1844.891	-0.005	-2.7	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
574	dirMS_041712_NAR_40mM_plus2.18496.18735.3	3	19.45	0	1.98E+06		(K)ALESPEF	(K)A/L|E|S|P E R/P/F L|A/I/L/G/G A K(V)		175.55	590.3359	1768.996	-0.0024	-1.4	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
575	dirMS_041712_NAR_30mM_plus2.18230.18230.2	2	19.44	0	4.74E+05		(R)GYISPYF	(R)G Y\I|S|P Y/F/I\N T/S K(G)		149.62	695.3554	1389.705	-0.0014	-1	8.5	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
576	dirMS_041712_NAR_50mM_plus2.9579.9832.3	3	19.44	1	1.99E+05		(R)AGTGVD	(R)A/G|T|G/V/D/N V/D L/E/A/A T R K(G)		118.75	539.6108	1616.824	-0.006	-3.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
577	dirMS_041712_NAR_60mM_plus.11201.11230.3	3	19.44	1	1.81E+06		(K)ALIEMEI	(K)A L|I|E/M/E/K/Q Q Q/D/Q/V D/R(N)		116.28	610.971	1830.901	-0.003	-1.6	4.32	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)
578	dirMS_041712_NAR_40mM_plus2.7019.7160.2	2	19.43	0	7.71E+05		(K)AQYEDI	(K)A/Q|Y|E|D/I/A/N/R(S)		101.75	540.2589	1079.512	-0.0011	-1	4.37	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
579	dirMS_041712_NAR_60mM_plus.11213.11213.2	2	19.43	0	2.12E+06		(K)GIVEFAS	(K)G I/V|E/F/A S K/P A A/R(K)		116.18	623.3504	1245.695	-0.0015	-1.2	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
580	dirMS_041712_NAR_20mM_plus.18595.18595.2	2	19.42	0	1.70E+05	M332m	(R)IVSQLLT	(R)I V|S/Q\L|L|T/L/m D G L K(Q)	m:Oxidized methionine	199.42	723.9145	1430.829	15.993	-1.3	5.84	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
581	dirMS_041712_NAR_40mM_plus2.15526.15813.3	3	19.42	1	1.20E+06		(K)VLDSGA	(K)V/L\D|S G/A|P I\K I|P/V/G/P E T L G R(I)		159.17	640.3668	1919.096	-0.0102	-5.3	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
582	dirMS_041712_NAR_50mM_minus2.15234.15377.3	3	19.41	1	8.73E+05		(K)ILLAELE	(K)I/L|L/A/E L/E Q L/K/G Q/G K(S)		155.78	513.9739	1539.911	-0.0033	-2.2	6.14	49709.6	5.19	HUMAN	B0YJC4	Vimentin
583	dirMS_041712_NAR_120mM_plus.20210.20427.3	3	19.41	0	2.78E+05		(R)INLWHL	(R)I/N|L/W/H/L/E I/T D/R(S)		159.48	470.5889	1409.754	-0.0014	-1	5.32	52204.6	5.82	HUMAN	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
584	dirMS_041712_NAR_30mM_plus2.17011.17056.2	2	19.41	0	1.58E+05		(R)IALTDN	(R)I/A|L|T|D/N/A L/I/A/R(S)		142.3	585.8454	1170.684	-0.0006	-0.5	5.84	24489.6	10.74	HUMAN	A8MUD9	60S ribosomal protein L7
585	dirMS_041712_NAR_40mM_plus2.18249.18455.3	3	19.41	1	1.59E+06		(R)GDLGIEI	(R)G D/L/G|I|E/I/P A E K V F L A Q K(M)		173.97	610.0115	1828.022	-0.0015	-0.8	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
586	dirMS_041712_NAR_50mM_plus2.19302.19591.3	3	19.41	1	9.05E+05		(R)ASLEAAI	(R)A S|L|E|A/A|I A/D/A E Q R G E L A I K(D)		170.58	652.6835	1956.04	-0.0037	-1.9	4.41	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
587	dirMS_041712_NAR_60mM_minus.13278.13414.3	3	19.4	1	9.72E+05		(R)ELISNSSI	(R)E L|I/S/N/S/S/D/A\L D/K/I/R(Y)		134.78	520.9443	1560.823	-0.0044	-2.8	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
588	dirMS_041712_NAR_60mM_minus.9525.9719.3	3	19.4	0	3.48E+05		(R)QLSQAG	(R)Q L|S Q/A/G/S/F/S/D|G T/H G G L R(Y)		113.6	573.2781	1717.825	-0.0055	-3.2	6.74	266161	5.68	HUMAN	E9PPU0	Epiplakin
589	dirMS_041712_NAR_30mM_plus2.21335.21498.2	2	19.39	0	3.90E+05		(R)VNQAIW	(R)V N\Q|A|I|W|L|L|C/T/G/A R(E)	C:Carbamidomethylation	166.88	751.3976	1501.794	-0.0065	-4.3	9.72	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
590	dirMS_041712_NAR_40mM_plus2.16092.16092.3	3	19.39	0	8.57E+03		(K)TAMLLA	(K)T A|M|L/L|A L|Q R P E L V|E R(L)		161.05	580.663	1739.984	-0.0092	-5.3	5.81	34746.4	9.67	HUMAN	Q8NFV4	Alpha/beta hydrolase domain-containing protein 11
591	dirMS_041712_NAR_30mM_minus2.10439.10492.2	2	19.38	0	9.33E+05		(K)GSDFDC	(K)G S|D|F/D|C/E/L/R(L)	C:Carbamidomethylation	111.28	549.7307	1098.452	0.0021	1.9	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
592	dirMS_041712_NAR_60mM_plus.6760.6804.3	3	19.38	1	1.08E+06		(K)TGQAPG	(K)T/G|Q|A|P G Y S Y/T/A/A N K/N K(G)		93.97	557.6087	1670.813	-0.0017	-1	9.52	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
593	dirMS_041712_NAR_30mM_plus2.13209.13290.2	2	19.37	0	1.08E+06		(R)IGLAEEII	(R)I/G|L|A|E/E/I/R(H)		122.77	450.7605	900.515	-0.0012	-1.3	4.53	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
594	dirMS_041712_NAR_40mM_plus2.14789.14897.3	3	19.37	0	3.03E+05		(R)IEGDMI	(R)I/E|G/D/M/I V/C/A/A Y|A H E L/P K(Y)	C:Carbamidomethylation	153.93	639.6498	1916.925	0.0104	5.4	4.65	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
595	dirMS_041712_NAR_50mM_plus2.16416.16575.3	3	19.37	1	2.02E+06		(K)QGGLGF	(K)Q G/G L/G/P M/N\I|P/L/V/S D/P K R(T)		154.68	593.6536	1778.958	-0.0119	-6.7	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
596	dirMS_041712_NAR_60mM_plus.18165.18437.3	3	19.37	1	9.69E+05		(K)EVNKFQ	(K)E V/N K F Q/M/A|Y/S/N/L L/R(A)		152.75	571.6293	1712.879	-0.0055	-3.2	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
597	dirMS_041712_NAR_120mM_minus.10471.10471.3	3	19.36	0	2.20E+05		(R)SSGPYG	(R)S/S/G/P/Y/G G G G Q Y F/A K P\R(N)		111.27	543.5972	1628.782	-0.0045	-2.8	9.7	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
598	dirMS_041712_NAR_50mM_plus2.16710.17196.3	3	19.36	1	1.65E+07		(R)VSFELFA	(R)V/S|F/E/L/F/A D K V/P K(T)		156.82	460.5906	1379.757	0.0003	0.2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
599	dirMS_041712_NAR_120mM_plus.19556.19595.3	3	19.35	1	7.12E+05		(R)DFNHIN	(R)D F/N H I\N\V|E|L/S/L L/G K K(K)		155.85	576.3192	1726.949	-0.0056	-3.2	6.75	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
600	dirMS_041712_NAR_120mM_plus.19996.19996.4	4	19.35	1	6.21E+05		(K)AAIDWF	(K)A A/I/D/W/F/D G K E F H G N I I K(V)		158.17	491.0027	1960.992	-0.0026	-1.3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
601	dirMS_041712_NAR_60mM_minus.11644.11743.3	3	19.34	1	3.63E+05		(K)IAQLEEC	(K)I/A|Q|L/E/E Q/L/D/N E T K E R(Q)		125.08	605.9739	1815.908	-0.0012	-0.6	4.25	227783.5	5.5	HUMAN	P35579	Myosin-9
602	dirMS_041712_NAR_60mM_plus.11248.11249.3	3	19.34	1	1.87E+06		(K)LKGEAT	(K)L K G E A|T\V|S|F/D/D|P P S A K(A)		116.45	554.615	1661.838	-0.0076	-4.6	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
603	dirMS_041712_NAR_40mM_minus2.14855.15005.3	3	19.33	1	5.46E+05		(R)GDLGIEI	(R)G D/L/G|I|E/I/P A E K V F L/A Q K(M)		173.02	610.0109	1828.022	-0.0033	-1.8	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
604	dirMS_041712_NAR_30mM_plus2.12098.12159.2	2	19.33	0	4.46E+05		(R)GGAEGE	(R)G G A|E|G/E|L|Q/A/L/R(A)		116.58	550.7883	1100.57	-0.0001	-0.1	4.53	533778	5.74	HUMAN	Q15149	Plectin
605	dirMS_041712_NAR_50mM_plus2.9927.9929.3	3	19.33	0	1.61E+06		(R)VMLGET	(R)V/M|L|G|E/T/N/P A D/S K/P G T I R(G)		119.75	595.9774	1785.916	0.0013	0.7	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
606	dirMS_041712_NAR_60mM_plus.11016.11322.3	3	19.33	0	1.46E+07		(K)GIVEFAS	(K)G I|V/E/F/A/S/K P A A/R(K)		116.15	415.9031	1245.695	-0.0003	-0.2	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
607	dirMS_041712_NAR_20mM_plus.18373.18373.2	2	19.32	0	1.95E+05		(R)AAVEEG	(R)A A V/E\E G|I|V/L|G|G/G C A L L/R(C)	C:Carbamidomethylation	197.9	842.9549	1684.905	-0.0025	-1.5	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
608	dirMS_041712_NAR_40mM_plus2.17406.17644.3	3	19.32	0	4.48E+05		(R)DVCTELI	(R)D V|C|T|E L/L/P L I/K/P Q/G R(V)	C:Carbamidomethylation	169.65	580.3213	1738.952	-0.0027	-1.5	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
609	dirMS_041712_NAR_60mM_plus.8469.8487.3	3	19.32	1	4.16E+05		(K)QGIETPE	(K)Q/G I/E/T/P E/D/Q N D/L R/K(M)		102.63	548.2719	1642.803	-0.002	-1.2	4.32	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
610	dirMS_041712_NAR_30mM_minus2.10650.10713.2	2	19.31	0	2.85E+05		(K)IINNTEN	(K)I/I|N|N|T/E/N L/V/R(E)		111.92	593.3316	1185.659	-0.0027	-2.3	6	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
611	dirMS_041712_NAR_60mM_minus.14506.14925.3	3	19.31	0	1.67E+06		(K)SLTNDW	(K)S L|T/N/D/W/E D H L/A V/K(H)		142.15	509.9191	1527.744	-0.0011	-0.7	4.53	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
612	dirMS_041712_NAR_30mM_plus2.19909.20377.2	2	19.31	0	3.32E+06		(K)LAVNM	(K)L/A|V|N|M|V|P F/P R(L)		159.35	572.32	1143.634	-0.0016	-1.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
613	dirMS_041712_NAR_30mM_plus2.7494.7513.2	2	19.31	0	8.65E+05		(K)TPGPGA	(K)T/P|G|P/G/A/Q/S/A L/R(A)		93.72	527.785	1054.564	-0.0013	-1.2	9.41	14466.4	9.92	HUMAN	E5RH77	40S ribosomal protein S14
614	dirMS_041712_NAR_30mM_plus2.8215.8269.2	2	19.31	0	1.36E+06		(K)QGGGG	(K)Q G/G/G|G/G/G/G S|V|P/G I E/R(M)		97.17	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
615	dirMS_041712_NAR_60mM_plus.11479.11596.3	3	19.31	0	1.11E+06		(R)SIFQHIQ	(R)S I|F/Q/H/I/Q/S A Q/S Q/R(S)		117.93	510.6056	1529.782	0.0203	13.3	9.49	108720.9	10.17	HUMAN	Q9Y2W1	Thyroid hormone receptor-associated protein 3
616	dirMS_041712_NAR_30mM_plus2.16972.17014.2	2	19.3	0	2.53E+05	M313m	(R)TVQSLEI	(R)T V|Q|S/L|E|I\D/L D/S m/R(N)	m:Oxidized methionine	142.07	761.8741	1506.747	15.9941	-0.5	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
617	dirMS_041712_NAR_50mM_plus2.17497.17551.3	3	19.3	0	5.30E+05		(R)GGYVLH	(R)G G|Y|V/L/H/I/G T I/Y/G D/L K(V)		160.33	535.9588	1605.863	-0.0017	-1	6.74	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
618	dirMS_041712_NAR_30mM_plus2.6741.6802.2	2	19.29	0	2.92E+05		(R)EAGEQG	(R)E A/G E|Q/G/D|I/E/P R(R)		89.77	600.7772	1200.549	-0.002	-1.7	4	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
619	dirMS_041712_NAR_50mM_plus2.19906.19906.3	3	19.29	1	1.01E+06		(K)LKEAELL	(K)L K E A E L\L|E|P/L|M/P A I R(A)		172.58	574.9989	1722.982	-0.0001	-0.1	4.79	56164.6	6.01	HUMAN	E9PP73	Coatomer subunit beta (Fragment)
620	dirMS_041712_NAR_30mM_plus2.7349.7410.2	2	19.28	0	6.39E+05		(R)AMNGE	(R)A/M|N|G/E/S/L/D/G/R(Q)		93.25	525.238	1049.468	0.0007	0.7	4.37	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
621	dirMS_041712_NAR_50mM_plus2.15464.15625.3	3	19.28	1	1.01E+06		(R)KVPGVT	(R)K\V/P G V T A\I|E|L|D/E/D|T/G/T F R(I)		149.87	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
622	dirMS_041712_NAR_60mM_plus.18127.18143.3	3	19.28	1	1.18E+06		(K)SIYGEKF	(K)S I|Y/G/E/K/F/E/D E/N F I L/K(H)		152.82	611.3091	1831.911	0.0015	0.8	4.41	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
623	dirMS_041712_NAR_20mM_plus.14000.14378.2	2	19.27	0	1.57E+06	M313m	(R)TVQSLEI	(R)T V|Q|S|L|E|I\D|L/D/S m R(N)	m:Oxidized methionine	170.15	761.8738	1506.747	15.9935	-0.9	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
624	dirMS_041712_NAR_50mM_plus2.18735.18838.3	3	19.27	1	4.32E+05		(K)ITQDIFQ	(K)I/T|Q/D/I/F/Q Q/L L K R(G)		167.02	501.627	1502.869	-0.0025	-1.7	8.75	72796.9	6.75	HUMAN	A6NC17	Methionine--tRNA ligase, cytoplasmic
625	dirMS_041712_NAR_60mM_plus.17498.17655.3	3	19.27	1	6.27E+05		(R)IFDSEEIL	(R)I/F|D/S E/E/I/L/A/G Y K/R(E)		148.98	514.2744	1540.801	0.0081	5.2	4.68	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
626	dirMS_041712_NAR_60mM_minus.15583.15807.3	3	19.26	1	1.58E+06		(R)KDDPVT	(R)K D D\P V\T N\L|N|N|A|F/E/V/A E/K(Y)		147.43	635.317	1903.94	-0.0032	-1.7	4.32	21601.4	6.27	HUMAN	K7EJH8	Alpha-actinin-4 (Fragment)
627	dirMS_041712_NAR_20mM_plus.12924.13145.2	2	19.26	0	4.19E+05		(K)LSELEAA	(K)L/S|E|L|E\A/A L/Q/R(A)		161.97	565.3132	1129.621	-0.002	-1.8	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
628	dirMS_041712_NAR_20mM_plus.16627.16627.2	2	19.26	0	1.99E+05		(K)VQIAVA	(K)V Q|I/A|V/A\N/A/Q\E/L/L/Q R(M)		186.25	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
629	dirMS_041712_NAR_20mM_plus.7632.7632.2	2	19.26	0	1.57E+05		(K)IAVAAQ	(K)I/A|V/A/A Q N/C Y K(V)	C:Carbamidomethylation	122.43	569.2902	1137.572	0.001	0.9	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
630	dirMS_041712_NAR_50mM_plus2.7689.7689.3	3	19.26	1	1.64E+05		(K)VDDSSEI	(K)V/D/D/S/S E D K T/E F T/V K(N)		106.45	533.9169	1599.738	-0.0023	-1.4	4.11	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
631	dirMS_041712_NAR_60mM_plus.5345.5392.3	3	19.26	1	1.02E+06		(K)CDSSPD	(K)C/D|S/S|P D|S/A/E/D V R K(V)	C:Carbamidomethylation	85.72	489.2128	1465.622	0.0015	1	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
632	dirMS_041712_NAR_30mM_minus2.14149.14400.2	2	19.25	0	4.17E+05		(K)MFLYAD	(K)M/F|L|Y|A/D/N E D/R(A)		131.08	637.2806	1273.552	0.0022	1.7	4.03	24724.1	5.17	HUMAN	E7ETQ7	Vacuolar protein sorting-associated protein VTA1 homolog
633	dirMS_041712_NAR_40mM_minus2.14042.14256.3	3	19.25	0	6.88E+05		(R)IHFPLAT	(R)I H F P L\A\T|Y|A|P/V/I/S A E K(A)		167.82	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
634	dirMS_041712_NAR_30mM_plus2.17600.17804.2	2	19.25	0	8.61E+05		(R)SIQEELC	(R)S I|Q|E|E|L/Q/Q/L/R(Q)		146.02	622.336	1243.664	0.0006	0.5	4.53	533778	5.74	HUMAN	Q15149	Plectin
635	dirMS_041712_NAR_30mM_plus2.18866.18926.2	2	19.25	0	4.85E+05		(K)ALQFLEE	(K)A L|Q|F|L/E/E/V/K(V)		152.2	538.8034	1076.599	0.0009	0.8	4.53	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
636	dirMS_041712_NAR_50mM_plus2.11015.11076.3	3	19.25	0	1.32E+06		(K)VGSLDN	(K)V/G|S/L/D|N/V/G/H L/P A G G A V/K(I)		126.15	530.9567	1590.86	-0.0043	-2.7	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
637	dirMS_041712_NAR_50mM_plus2.19118.19420.3	3	19.25	0	1.09E+06		(K)LVLIGSN	(K)L/V|L/I/G/S N H S L/P F/L/K(F)		169.83	513.3073	1537.91	-0.0027	-1.8	8.76	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
638	dirMS_041712_NAR_50mM_plus2.20152.20152.3	3	19.25	1	3.53E+06		(R)TLAEIAK	(R)T\L|A|E/I/A/K V E L D/N M P L R(G)		174.82	604.9965	1812.989	-0.0138	-7.6	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
639	dirMS_041712_NAR_40mM_plus2.13150.13259.3	3	19.24	0	3.31E+05		(K)LQMEAF	(K)L/Q|M/E/A/P H I|I/V/G T/P G R(V)		144.07	540.2954	1618.873	-0.0017	-1.1	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
640	dirMS_041712_NAR_50mM_plus2.11170.11273.3	3	19.24	1	3.14E+05		(R)DLDRIA	(R)D L/D R\I\A|G\Q|V/A/A/A/N K(K)		126.77	481.2661	1441.776	0.008	5.5	5.96	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
641	dirMS_041712_NAR_60mM_minus.17881.17998.3	3	19.23	1	3.70E+05		(K)NLRDIDE	(K)N/L R D I\D|E|V/S|S/L/L/R(T)		160.93	510.6099	1529.828	-0.013	-8.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
642	dirMS_041712_NAR_120mM_plus.11649.11780.3	3	19.23	1	8.12E+05		(R)ARQEEL	(R)A R Q E E\L|Y|S|E|L/Q/A/R(E)		114.23	531.6047	1592.803	-0.0032	-2	4.79	533778	5.74	HUMAN	Q15149	Plectin
643	dirMS_041712_NAR_60mM_plus.21519.21663.3	3	19.23	0	9.30E+06		(R)LHFFMP	(R)L H\F\F\M|P/G\F|A|P\L/T S R(G)		180.4	540.9492	1620.835	-0.0025	-1.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
644	dirMS_041712_NAR_30mM_minus2.14816.15006.2	2	19.22	0	9.32E+05		(R)LSLYQA	(R)L/S|L/Y|Q/A/M/R(Q)		134.88	491.2611	981.519	-0.0037	-3.8	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
645	dirMS_041712_NAR_20mM_plus.19016.19016.2	2	19.22	0	1.05E+05		(K)DTSYLFI	(K)D T S/Y/L/F I/T|G P D/V/V/K(S)		201.92	777.9049	1554.805	-0.0025	-1.6	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
646	dirMS_041712_NAR_30mM_plus2.16226.16717.2	2	19.22	0	1.88E+06		(R)GGIVDE	(R)G G/I|V|D|E\G/A/L/L/R(A)		139.2	550.3082	1099.611	-0.0015	-1.3	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
647	dirMS_041712_NAR_30mM_plus2.17316.17482.2	2	19.22	0	9.94E+05		(R)IMNTFS	(R)I/M|N|T/F|S/V/V/P S/P K(V)		145.17	660.3537	1319.703	-0.0027	-2	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
648	dirMS_041712_NAR_20mM_plus.13957.13957.2	2	19.21	0	1.97E+05		(R)AALQELI	(R)A A|L|Q/E L L/S K(G)		168.48	486.789	972.572	-0.0017	-1.7	6.05	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
649	dirMS_041712_NAR_30mM_plus2.13241.13438.2	2	19.21	0	1.26E+06		(R)MVPAGI	(R)M V|P/A|G/M/G/A/G L E R(M)		123.2	594.797	1188.586	0.0003	0.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M

650	dirMS_041712_NAR_30mM_plus2.20290.20779.2	2	19.21	0	1.40E+06		(R)ILVATNL	(R)I/L|V|A/T/N/L/F/G R(G)		162.17	552.331	1103.657	-0.0024	-2.2	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
651	dirMS_041712_NAR_50mM_plus2.22205.22205.3	3	19.21	1	1.35E+06		(K)EGGLGP	(K)E G|G L/G/P/L/N/I/P L L A D/V T R R(L)		191	631.029	1891.076	-0.0035	-1.9	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
652	dirMS_041712_NAR_60mM_minus.13966.14069.3	3	19.2	0	2.71E+05		(K)YGGELV	(K)Y/G|G E L/V/P H/F/P A R(V)		138.02	448.2371	1342.69	0.0065	4.8	6.75	258215.9	5.48	HUMAN	E7EN95	Filamin-B
653	dirMS_041712_NAR_50mM_plus2.15749.15880.3	3	19.2	1	3.47E+06		(K)IIVDELK	(K)I/I|V/D/E L/K/Q E|V/I/S T S S K(A)		151.23	597.0024	1788.995	-0.0027	-1.5	4.68	30149.5	5.96	HUMAN	D6RAC2	Guanine nucleotide-binding protein subunit beta-2-like 1
654	dirMS_041712_NAR_50mM_plus2.18698.19170.3	3	19.2	0	1.48E+06		(R)LGFHLPL	(R)L G\F H L\P L|E|V|A/Y/Q/R(G)		167.67	514.9522	1542.843	-0.0007	-0.4	6.75	533778	5.74	HUMAN	Q15149	Plectin
655	dirMS_041712_NAR_30mM_plus2.16786.16786.2	2	19.19	0	2.84E+05		(R)SIQADG	(R)S I/Q|A/D/G L V|W/G S S K(L)		140.7	674.3475	1347.69	-0.0026	-1.9	5.55	24934.4	4.5	HUMAN	P24534	Elongation factor 1-beta
656	dirMS_041712_NAR_50mM_plus2.18481.18481.2	2	19.19	0	5.79E+05		(R)IHFPLAT	(R)I H|F|P\L/A\T/Y A P V I S A E K(A)		164.92	878.9842	1756.963	-0.0021	-1.2	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
657	dirMS_041712_NAR_50mM_plus2.5972.6087.3	3	19.19	1	2.51E+06		(R)AQLGGF	(R)A Q|L|G/G/P E A/A K/S D/E T A/A/K(-)		95.82	548.6114	1643.824	-0.0039	-2.3	4.68	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
658	dirMS_041712_NAR_60mM_minus.9546.9893.3	3	19.18	1	1.92E+07		(R)LQAEIEC	(R)L/Q|A/E/I/E/G L/K/G Q R(A)		114.12	447.9164	1341.748	-0.0138	-10.3	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
659	dirMS_041712_NAR_120mM_plus.13419.13590.4	4	19.18	2	1.02E+06	M100m	(K)KQGGLG	(K)K\Q G G L G\P m/N\I/P/L/V/S D/P K R(T)	m:Oxidized methionine	123.85	481.5167	1907.053	15.9918	-1.6	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
660	dirMS_041712_NAR_30mM_plus2.12856.13261.2	2	19.18	0	2.83E+06		(R)EYQELM	(R)E Y|Q/E/L/M/N/V/K(L)		121.65	577.2809	1153.556	-0.0013	-1.1	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
661	dirMS_041712_NAR_40mM_minus2.12773.13018.3	3	19.17	0	4.66E+05		(K)FTISDHP	(K)F/T|I/S/D/H|P Q/P I D/P L/L/K(N)		159.58	574.3124	1720.927	-0.0042	-2.4	5.21	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
662	dirMS_041712_NAR_50mM_plus2.15966.16063.3	3	19.17	1	1.50E+06		(K)VTADVII	(K)V/T|A/D|V/I/N A/A E K L/Q/V V G R(A)		152.23	595.0057	1783.007	-0.0047	-2.6	6.04	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
663	dirMS_041712_NAR_60mM_minus.12002.12158.3	3	19.16	1	5.65E+05		(R)ISVYYNE	(R)I/S|V/Y/Y/N E/A/T/G G K Y/V/P R(A)		127.47	606.3103	1816.923	-0.0065	-3.6	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
664	dirMS_041712_NAR_60mM_minus.6761.7216.3	3	19.16	1	1.58E+06		(K)IQDKEGI	(K)I/Q|D K E G|I|P/P/D/Q Q R(L)		95.47	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
665	dirMS_041712_NAR_20mM_plus.13976.13976.2	2	19.16	0	1.85E+05	M98m	(R)TLTIVDT	(R)T L|T I/V|D/T G/I/G/m T/K(A)	m:Oxidized methionine	167.67	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
666	dirMS_041712_NAR_20mM_minus.14682.14682.2	2	19.15	0	2.10E+05		(K)LAVEALS	(K)L A/V E|A|L/S|S/L D|G D\L A/G R(Y)		201.28	793.922	1586.838	-0.0017	-1.1	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
667	dirMS_041712_NAR_50mM_plus2.9514.9734.3	3	19.15	1	3.83E+05		(K)LTSDDVI	(K)L/T|S/D/D/V/K/E Q I/Y/K(L)		118.77	480.2521	1438.742	-0.0007	-0.5	4.56	12573.5	10.39	HUMAN	E9PS50	40S ribosomal protein S13 (Fragment)
668	dirMS_041712_NAR_30mM_minus2.10220.10242.2	2	19.14	0	3.59E+05		(R)EQAEAE	(R)E/Q|A|E/A/E V/A|S/L/N R(R)		109.7	658.8239	1316.644	-0.0036	-2.7	4.25	11017	4.8	HUMAN	D6R904	Tropomyosin alpha-3 chain
669	dirMS_041712_NAR_50mM_minus2.14673.14957.3	3	19.13	1	9.62E+05		(R)IINEPTA	(R)I/I|N|E/P T A/A/A/I/A/Y/G L D/K R(E)		152.6	606.0022	1815.996	-0.0043	-2.4	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
670	dirMS_041712_NAR_30mM_plus2.14536.14905.2	2	19.13	0	7.19E+06		(R)FPGQLN	(R)F/P/G|Q|L/N A D|L/R(K)		131.27	565.801	1130.595	-0.0006	-0.5	5.84	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
671	dirMS_041712_NAR_60mM_plus.19768.19915.3	3	19.13	1	1.10E+06		(K)SLLGKD	(K)S L|L/G/K/D/V|L F L/K(D)		163.93	411.5915	1232.761	-0.0013	-1.1	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
672	dirMS_041712_NAR_30mM_minus2.18091.18091.2	2	19.12	0	2.57E+05		(K)EGMNIV	(K)E G\M|N/I|V|E/A/M/E/R(F)		152.28	639.7955	1278.582	0.002	1.6	4.25	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
673	dirMS_041712_NAR_40mM_minus2.15115.15247.3	3	19.12	0	7.51E+05		(K)ALIEVLQ	(K)A L|I|E|V|L Q/P L/I/A E H Q A R(R)		175.3	601.0146	1801.033	-0.0038	-2.1	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
674	dirMS_041712_NAR_50mM_plus2.16569.16781.3	3	19.12	1	1.87E+05	M132m	(R)TLAEIAK	(R)T/L|A|E/I/A/K/V/E L/D/N m/P L R(G)	m:Oxidized methionine	155.92	610.3302	1812.989	15.9873	-4.2	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
675	dirMS_041712_NAR_30mM_minus2.9300.9335.2	2	19.11	0	4.41E+05		(K)VTEDTS	(K)V/T|E|D|T/S/S/V/L/R(S)		104.87	553.7841	1106.569	-0.0079	-7.1	4.37	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
676	dirMS_041712_NAR_40mM_minus2.15017.15086.3	3	19.11	0	2.68E+06		(K)ALESPEF	(K)A/L|E/S/P E/R P F\L/A I L/G G/A/K(V)		174.77	590.3353	1768.996	-0.0042	-2.4	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
677	dirMS_041712_NAR_60mM_minus.9385.9502.3	3	19.11	0	2.44E+06		(R)LESGMC	(R)L/E|S/G M/Q/N/M/S I/H/T K(T)		112.38	492.571	1475.698	0.0003	0.2	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
678	dirMS_041712_NAR_120mM_plus.11606.11632.3	3	19.1	2	7.09E+05		(R)TIEKFEK	(R)T/I|E/K/F E/K/E/A A E/M/G K(G)		113.92	537.6079	1610.809	-0.0003	-0.2	4.94	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
679	dirMS_041712_NAR_50mM_plus2.15420.15670.3	3	19.1	0	1.21E+06		(K)LVEALC	(K)L/V|E/A/L/C/A E/H Q I/N L I/K(V)	C:Carbamidomethylation	149.78	584.3209	1750.952	-0.0039	-2.2	5.4	14914.1	6.84	HUMAN	P25398	40S ribosomal protein S12
680	dirMS_041712_NAR_60mM_plus.13658.13801.3	3	19.1	0	1.07E+06		(K)QADLYIS	(K)Q A D L/Y/I/S/E/G L/H/P/R(I)		128.62	500.2592	1498.765	-0.0018	-1.2	5.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
681	dirMS_041712_NAR_120mM_minus.17365.17567.3	3	19.09	1	5.23E+05		(R)KVNNAD	(R)K V N N\A\D\D|F|P/N|L/F/R(Q)		150.12	517.2634	1549.776	-0.0001	-0.1	5.96	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
682	dirMS_041712_NAR_30mM_minus2.15171.15171.2	2	19.09	0	1.56E+06		(R)QITVND	(R)Q/I/T/V|N D/L/P V/G R(S)		135.22	606.3404	1211.674	-0.0007	-0.6	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
683	dirMS_041712_NAR_30mM_minus2.6899.6899.2	2	19.09	0	2.07E+05		(K)VTEGGE	(K)V/T|E/G G/E/P Y/R(L)		91.93	504.238	1007.479	-0.0105	-10.4	4.53	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
684	dirMS_041712_NAR_30mM_plus2.17289.17577.2	2	19.09	0	1.12E+06		(R)IMNTFS	(R)I/M|N|T|F|S V/V/P S/P K(V)		145.32	660.3537	1319.703	-0.0027	-2	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
685	dirMS_041712_NAR_60mM_plus.8471.8529.3	3	19.09	1	4.56E+05		(K)ALAAAG	(K)A L|A|A/A/G Y|D/V/E|K N N S/R(I)		102.5	526.9346	1578.787	0.0022	1.4	6.11	21864.9	11.03	HUMAN	P10412	Histone H1.4
686	dirMS_041712_NAR_50mM_minus2.8817.8945.3	3	19.08	1	2.50E+06	M227m	(R)mQKEIT	(R)m Q K E\I/T|A|L|A|P/S T M K(I)	m:Oxidized methionine	118.07	522.2727	1548.812	15.9911	-2.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
687	dirMS_041712_NAR_50mM_minus2.10663.11053.3	3	19.07	1	6.57E+05		(R)IAEFTTN	(R)I/A|E|F/T/T/N/L/T/E/E E E K/S K(S)		130.48	623.6418	1868.912	-0.0015	-0.8	4.32	227783.5	5.5	HUMAN	P35579	Myosin-9
688	dirMS_041712_NAR_50mM_minus2.9509.9958.3	3	19.06	1	2.86E+06		(R)MQKEIT	(R)M Q K E I T/A|L|A/P S/T M K(I)		123.52	516.9426	1548.812	0.0008	0.5	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
689	dirMS_041712_NAR_30mM_plus2.18738.18738.2	2	19.06	0	6.67E+05		(R)SYNDEL	(R)S/Y/N/D\E/L|Q/F/L E/K(I)		152.13	693.335	1385.658	0.0044	3.2	4.14	19338.9	5.33	HUMAN	E7EQS9	tRNA-splicing ligase RtcB homolog
690	dirMS_041712_NAR_50mM_plus2.19513.19756.3	3	19.06	0	6.79E+05		(R)EAVELPL	(R)E A|V/E/L/P L/T/H F E L/Y/K(Q)		171.62	563.6357	1688.889	0.0031	1.9	4.75	47479.5	5.09	HUMAN	P43686	26S protease regulatory subunit 6B
691	dirMS_041712_NAR_20mM_plus.14211.14480.2	2	19.05	0	6.74E+05	M185m	(K)LAVNm\	(K)L A|V/N/m|V|P F/P R(L)	m:Oxidized methionine	170.62	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
692	dirMS_041712_NAR_30mM_plus2.22133.22133.2	2	19.05	0	2.08E+05		(K)NSSYFVE	(K)N S\S Y F V/E/W|I|P N N V K(V)		171.85	848.9189	1696.833	-0.0024	-1.4	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
693	dirMS_041712_NAR_50mM_plus2.10047.10047.3	3	19.05	1	1.70E+06		(K)TLQEVTE	(K)T L|Q/E/V/T/E M D/S/V/K R(Y)		120.07	512.5958	1535.773	-0.0005	-0.3	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
694	dirMS_041712_NAR_60mM_plus.11308.11642.2	2	19.05	1	1.49E+06		(R)ALAAFLK	(R)A/L|A|A/F/L/K/K(S)		117.2	431.2814	861.556	-0.0001	-0.1	10	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
695	dirMS_041712_NAR_120mM_plus.24592.24592.3	3	19.04	1	5.86E+05		(R)GHYTIGI	(R)G H|Y/T I/G\K\E\I/I|D L/V L D/R(I)		184.32	614.6745	1842.012	-0.003	-1.6	5.38	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
696	dirMS_041712_NAR_60mM_plus.13823.13956.3	3	19.04	0	1.56E+06		(K)LAQANG	(K)L/A|Q/A N/G W/G V/M\V/S/H R(S)		129.07	509.2606	1525.769	-0.002	-1.3	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
697	dirMS_041712_NAR_50mM_minus2.6639.6669.3	3	19.03	1	2.15E+05		(K)IVADKDY	(K)I/V|A/D/K/D/Y/S|V/T/A/N S K(I)		104.22	504.2623	1510.775	-0.0024	-1.6	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
698	dirMS_041712_NAR_60mM_minus.8539.8569.3	3	19.03	0	9.13E+04		(R)ISVYYNE	(R)I|S|V/Y/Y/N/E/A S/S H K(Y)		107.72	466.5604	1397.67	-0.0029	-2.1	6.75	18402.2	5.06	HUMAN	G3V2N6	HCG1983504, isoform CRA_d
699	dirMS_041712_NAR_50mM_plus2.9051.9301.3	3	19.03	1	1.70E+06		(R)LQAEIEC	(R)L/Q|A/E/I/E/G L/K/G Q R(A)		115.58	447.921	1341.748	0	0	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
700	dirMS_041712_NAR_60mM_minus.5544.5546.3	3	19.02	1	3.66E+07		(K)DSYVGD	(K)D S|Y/V/G/D/E/A/Q S K R(G)		87.63	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
701	dirMS_041712_NAR_40mM_plus2.17020.17521.3	3	19.02	0	7.79E+05		(R)IHFPLAT	(R)I H F\P L A\T|Y|A|P/V/I/S A E K(A)		168.35	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
702	dirMS_041712_NAR_30mM_minus2.9007.9605.2	2	19.01	0	7.60E+06		(K)TAVCDIF	(K)T A|V|C/D|I|P|P/R(G)	C:Carbamidomethylation	105.43	514.7641	1028.519	0.0016	1.5	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
703	dirMS_041712_NAR_40mM_plus2.13550.13550.3	3	19.01	0	6.25E+05		(R)TIQVENS	(R)T I|Q|V/E N\S H L I L/T|G A G A L/N K(V)		146.55	660.3654	1979.092	-0.0104	-5.2	6.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
704	dirMS_041712_NAR_60mM_plus.14404.14467.3	3	19.01	1	1.01E+06		(K)YGKIETI	(K)Y G K\I E T\I|E|V|M/E/D/R(Q)		132.13	528.2635	1582.778	-0.0022	-1.4	4.41	34329.8	8.74	HUMAN	E7EWI9	Heterogeneous nuclear ribonucleoprotein A3
705	dirMS_041712_NAR_30mM_plus2.21359.21564.2	2	19	0	3.50E+05		(K)FDGILGN	(K)F D|G\I|L|G/M/A/Y/P R(I)		167.42	620.3199	1239.619	0.0135	10.9	5.83	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
706	dirMS_041712_NAR_50mM_minus2.16956.17380.3	3	18.99	0	2.11E+07		(R)IHFPLAT	(R)I H\F\P L A\T|Y|A|P/V/I/S A E K(A)		167.2	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
707	dirMS_041712_NAR_20mM_plus.18770.18770.2	2	18.99	0	2.33E+05		(K)TAVETA	(K)T A\V|E|T/A/V L|L L R(I)		200.18	593.3625	1185.72	-0.0024	-2	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
708	dirMS_041712_NAR_60mM_plus.16348.16577.3	3	18.99	0	4.91E+05		(R)EAYPGD	(R)E A|Y/P/G D V/F/Y/L/H S R(L)		142.67	518.5855	1553.738	0.0036	2.3	5.32	48851.3	9.2	HUMAN	K7EK63	ATP synthase subunit alpha, mitochondrial
709	dirMS_041712_NAR_30mM_plus2.13187.13187.2	2	18.98	0	2.83E+05		(R)TNEGVIE	(R)T/N|E|G/V/I/E/F R(S)		122.2	532.7727	1064.537	0.001	1	4.53	39700.2	11.49	HUMAN	Q13247	Serine/arginine-rich splicing factor 6
710	dirMS_041712_NAR_30mM_plus2.20720.20853.2	2	18.98	0	2.60E+05		(R)ASLSLW	(R)A/S/L/S/L|W/Q/A/M/E/K(G)		162.9	632.3231	1263.64	-0.0013	-1	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
711	dirMS_041712_NAR_50mM_plus2.15368.15649.3	3	18.98	0	1.46E+06		(R)LASTLVH	(R)L/A|S/T L/V/H L|G E\Y Q A|A/V/D/G A R(K)		149.63	657.6802	1971.029	-0.0034	-1.7	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
712	dirMS_041712_NAR_50mM_minus2.10016.10200.3	3	18.97	0	5.86E+05	M147m	(K)LQmEAF	(K)L/Q|m/E A/P H|I|I/V/G T P G R(V)	m:Oxidized methionine	125.53	545.6267	1618.873	15.9922	-1.7	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
713	dirMS_041712_NAR_30mM_plus2.17012.17115.2	2	18.97	0	3.76E+04	M185m	(K)LAVNm\	(K)L A|V|N/m/V|P F/P/R(L)	m:Oxidized methionine	142.12	580.3176	1143.634	15.9936	-1.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
714	dirMS_041712_NAR_50mM_plus2.12976.13247.3	3	18.97	1	1.45E+06		(R)VVDALG	(R)V/V|D|A/L/G N A/I/D/G K G P I/G S/K(T)		137.43	570.9829	1710.939	-0.0043	-2.5	5.93	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
715	dirMS_041712_NAR_60mM_minus.11186.11719.3	3	18.95	1	9.28E+05	M232m	(R)MSmKE	(R)M/S m K E V\D E\Q|M|L|N/V|Q/N K(N)	m:Oxidized methionine	122.78	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
716	dirMS_041712_NAR_60mM_minus.17319.17358.3	3	18.94	0	3.22E+05		(K)GSDHSA	(K)G S D H S A\S L E|P|G|E|L|A/E/L V R(S)		156.83	622.9764	1866.919	-0.0045	-2.4	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
717	dirMS_041712_NAR_30mM_plus2.19850.19850.2	2	18.94	0	2.33E+05		(K)GFAFVQ	(K)G F A|F|V/Q/Y/V/N E/R(N)		157.58	665.3326	1329.659	-0.0007	-0.5	6	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
718	dirMS_041712_NAR_60mM_minus.6326.6366.3	3	18.93	0	2.63E+05		(K)TVEAEA	(K)T\V|E/A/E/A/A/H/G T V T/R(H)		94.07	447.8959	1341.676	-0.0026	-1.9	5.37	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
719	dirMS_041712_NAR_60mM_minus.9420.9890.3	3	18.93	1	1.79E+06		(K)TAVCDIF	(K)T/A|V/C/D/I/P/P R G L K(M)	C:Carbamidomethylation	114.42	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
720	dirMS_041712_NAR_50mM_plus2.19955.20323.3	3	18.93	1	3.53E+06		(R)TLAEIAK	(R)T L|A|E/I/A/K/V/E L/D/N M/P L R(G)		174.82	604.9965	1812.989	-0.0138	-7.6	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
721	dirMS_041712_NAR_30mM_minus2.12952.13095.2	2	18.92	0	2.92E+05		(K)LSELEPG	(K)L S|E|L|E|P/G T G D/L R(F)		124.57	643.8325	1286.659	-0.0009	-0.7	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
722	dirMS_041712_NAR_120mM_plus.21127.21479.4	4	18.92	1	1.53E+06		(R)DYLHLPI	(R)D Y/L H L|P|P/E\I/V/P A T L R/R(S)		163.77	473.2689	1890.06	-0.0058	-3.1	6.75	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
723	dirMS_041712_NAR_30mM_plus2.21853.22069.2	2	18.92	0	3.14E+05		(R)DLLFQAI	(R)D L|L|F/Q/A|L/G/R(T)		170.52	516.7959	1032.584	0.0009	0.8	5.84	66742	6.4	HUMAN	Q9NSD9	Phenylalanine--tRNA ligase beta subunit
724	dirMS_041712_NAR_30mM_minus2.13575.14062.2	2	18.91	0	2.59E+06		(K)AVLSLYA	(K)A V|L|S/L|Y|A/S/G R(T)		128.68	518.7898	1036.579	-0.0062	-6	8.79	14579.3	5.13	HUMAN	K7EM38	Actin, cytoplasmic 2, N-terminally processed (Fragment)
725	dirMS_041712_NAR_50mM_minus2.17934.17949.3	3	18.91	1	8.25E+05		(K)TFVNITP	(K)T F|V/N|I|T/P A/E V G V L/V G K D/R(S)		171.32	639.0247	1915.065	-0.0052	-2.7	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
726	dirMS_041712_NAR_60mM_minus.11272.11272.3	3	18.91	1	7.95E+05		(K)MKEIAE	(K)M/K/E I A|E|A/Y/L/G K(T)		122.48	418.226	1252.661	0.0029	2.3	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
727	dirMS_041712_NAR_30mM_plus2.18528.18605.2	2	18.91	0	5.62E+05		(R)GVVDSE	(R)G V|V/D|S|E/D|I|P L N/L|S\R(E)		150.85	757.3957	1513.786	-0.0015	-1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
728	dirMS_041712_NAR_60mM_minus.17151.17363.3	3	18.9	1	3.81E+05		(R)KAPSDL	(R)K\A P S D\L|Y|Q/I/I|L/K(A)		156.22	463.6095	1388.815	-0.0008	-0.6	8.5	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
729	dirMS_041712_NAR_30mM_plus2.8693.8927.2	2	18.9	0	5.33E+06		(R)FGQGG	(R)F/G|Q|G|G/A|G|P V|G G Q/G/P R(G)		99.67	671.3359	1341.666	-0.0013	-1	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
730	dirMS_041712_NAR_60mM_plus.15561.15602.3	3	18.9	0	7.49E+05		(K)DLAGCI	(K)D L|A/G/C I/H/G/L S N V/K(L)	C:Carbamidomethylation	138.1	461.9069	1383.705	0.0012	0.9	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
731	dirMS_041712_NAR_30mM_minus2.16097.16097.2	2	18.89	0	2.90E+05		(R)GEVTAA	(R)G E|V/T|A/A|D L/F N S R(V)		141.68	640.3185	1279.628	0.002	1.6	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
732	dirMS_041712_NAR_20mM_plus.18992.18992.2	2	18.89	0	1.91E+05		(R)STGEAF	(R)S T G E/A/F/V|Q/F/A|S Q E I/A E K(A)		202.2	921.4477	1841.892	-0.0035	-1.9	4.25	24249.1	6.99	HUMAN	D6RBM0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
733	dirMS_041712_NAR_30mM_plus2.6933.6933.2	2	18.89	0	1.33E+05		(R)TAPAAN	(R)T/A|P/A/A/N L/A S R(I)		90.78	486.2674	971.527	0.0007	0.7	9.41	300351.7	12.1	HUMAN	Q9UQ35	Serine/arginine repetitive matrix protein 2
734	dirMS_041712_NAR_50mM_plus2.12470.12470.3	3	18.89	0	3.93E+05		(R)LDDTVH	(R)L/D/D\T V/H/V|V|I/A T/P G/R(I)		133.35	498.2741	1492.812	-0.0041	-2.7	5.21	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
735	dirMS_041712_NAR_30mM_plus2.22649.22750.2	2	18.88	0	5.16E+05		(K)LAAFWL	(K)L/A|A|F/W|L/M/K(A)		176.55	490.2728	979.543	-0.005	-5.2	8.75	32535.6	9.19	HUMAN	B4DZW6	Regulator of microtubule dynamics protein 1
736	dirMS_041712_NAR_50mM_plus2.18508.18631.3	3	18.88	0	4.12E+05		(R)VYAILTH	(R)V/Y|A\I/L T/H/G I/F/S G/P A I S R(I)		165.83	601.3347	1801.996	-0.0064	-3.5	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
737	dirMS_041712_NAR_50mM_plus2.7409.7480.3	3	18.88	0	3.13E+05		(K)VSYGIGI	(K)V/S|Y/G/I/G/D E/E/H/D/Q E G R(V)		105.08	564.2484	1690.73	0.0003	0.2	4.17	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
738	dirMS_041712_NAR_60mM_minus.14235.14306.3	3	18.86	0	4.62E+05		(R)SDSFENI	(R)S D|S|F/E N/P V/L/Q/Q/H/F R(N)		139.27	568.6086	1703.814	-0.0024	-1.4	5.3	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
739	dirMS_041712_NAR_20mM_plus.16889.17299.2	2	18.86	0	6.93E+05		(K)VLTPELY	(K)V L|T|P/E/L Y/A E/L/R(A)		189.62	652.3664	1303.726	-0.0001	-0.1	4.53	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
740	dirMS_041712_NAR_30mM_plus2.10821.11021.2	2	18.86	0	1.39E+06		(K)GSDFDC	(K)G/S|D|F/D/C/E/L/R(L)	C:Carbamidomethylation	110.72	549.7297	1098.452	0.0001	0.1	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
741	dirMS_041712_NAR_30mM_minus2.10811.10811.2	2	18.85	0	6.40E+05		(K)TVSPALI	(K)T V/S|P/A L/I S R(F)		112.1	472.2815	943.557	-0.0014	-1.5	9.41	50425	5.53	HUMAN	H0YH27	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
742	dirMS_041712_NAR_30mM_minus2.13407.13481.2	2	18.85	0	5.61E+05		(K)VANVEL	(K)V/A|N|V|E|L/Y/Y/R(A)		125.93	563.7964	1126.589	-0.0036	-3.2	5.97	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
743	dirMS_041712_NAR_40mM_minus2.14316.14316.3	3	18.85	1	1.61E+05		(K)TGISDVF	(K)T G I|S/D/V F A K N D L|A/V V/D/V/R(I)		168.48	640.3454	1919.023	-0.0016	-0.8	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
744	dirMS_041712_NAR_60mM_minus.10856.11043.3	3	18.85	1	4.59E+05		(K)GSITISAI	(K)G S|I/T|I/S/A E E/I/K/D/N R(V)		121.13	511.6045	1532.792	0.0075	4.9	4.68	27142.4	5.34	HUMAN	E5RG68	Copine-3 (Fragment)
745	dirMS_041712_NAR_50mM_plus2.19450.19586.3	3	18.85	1	1.20E+06		(R)GDLGIEI	(R)G D/L/G|I|E/I/P A E K V F L/A Q K(M)		171.73	610.0104	1828.022	-0.0048	-2.6	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
746	dirMS_041712_NAR_60mM_plus.11214.11214.2	2	18.85	0	2.12E+06		(K)GIVEFAS	(K)G I/V|E/F/A/S\K/P A A/R(K)		116.18	623.3504	1245.695	-0.0015	-1.2	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
747	dirMS_041712_NAR_120mM_plus.18780.18947.3	3	18.84	2	5.39E+05		(R)KIEEIKDI	(R)K|I/E\E/I|K|D|F/L/L/T A R(R)		152.18	525.9746	1575.911	-0.0012	-0.8	6.18	2559	9.99	HUMAN	J3KSP2	60S ribosomal protein L38 (Fragment)
748	dirMS_041712_NAR_20mM_plus.16456.16781.2	2	18.84	0	5.45E+05		(K)LGGSAV	(K)L G\G S|A|V|I|S L/E|G/K|P L(-)		185.73	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
749	dirMS_041712_NAR_30mM_plus2.13376.13545.2	2	18.84	0	1.36E+06		(K)ALMDEV	(K)A/L|M/D/E V/V/K(A)		123.52	452.7448	904.481	0.0015	1.7	4.37	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
750	dirMS_041712_NAR_50mM_plus2.13337.13654.3	3	18.82	1	2.13E+06	M357m	(R)ALAEIAK	(R)A L|A|E|I/A/K/A E L/D D/T/P m R(G)	m:Oxidized methionine	139.13	587.3005	1743.895	15.9924	-1.4	4.32	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
751	dirMS_041712_NAR_50mM_plus2.10242.10322.3	3	18.81	0	4.49E+05		(R)TIVITSHI	(R)T I|V/I/T/S H/P/G Q I/V/K(H)		121.67	464.946	1392.821	0.0025	1.8	8.44	27999.4	5.61	HUMAN	B7Z5C0	DnaJ homolog subfamily A member 1
752	dirMS_041712_NAR_50mM_plus2.10335.10366.3	3	18.81	0	2.80E+05		(R)TPVIDAI	(R)T/P|V|I/D/A D|K/P/V/S S Q L R(V)		121.88	542.6394	1625.886	0.0179	11	5.62	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
753	dirMS_041712_NAR_50mM_plus2.8894.9154.3	3	18.81	0	2.21E+06		(K)GIVEFSG	(K)G I|V/E/F/S/G K/P A A R(K)		114.52	411.2309	1231.679	-0.0012	-1	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
754	dirMS_041712_NAR_40mM_minus2.11082.11253.3	3	18.8	0	7.92E+05		(R)QVSASE	(R)Q V|S/A/S E L/H/T S G I/L/G/P E T L R(D)		148.75	665.6822	1995.051	-0.0185	-9.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
755	dirMS_041712_NAR_50mM_minus2.8723.8723.3	3	18.8	1	1.13E+05		(K)TAVCDIF	(K)T A/V/C/D/I/P P R G L K(M)	C:Carbamidomethylation	117.28	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
756	dirMS_041712_NAR_30mM_plus2.8283.8511.2	2	18.8	0	4.04E+05		(K)IANPVE	(K)I/A|N|P/V/E/G/S T D/R(Q)		97.95	579.7908	1158.575	-0.0006	-0.5	4.37	34267.8	9.05	HUMAN	B4DXP5	Poly(rC)-binding protein 2
757	dirMS_041712_NAR_120mM_minus.10142.10404.3	3	18.79	1	1.07E+06		(K)IFRDGEE	(K)I/F/R D G E\E\A|G|A|Y/D/G P R(T)		110.25	551.5928	1652.766	-0.0025	-1.5	4.32	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
758	dirMS_041712_NAR_20mM_minus.12079.12079.2	2	18.79	0	8.51E+05	M313m	(R)TVQSLEI	(R)T V|Q|S|L/E/I D|L\D S m/R(N)	m:Oxidized methionine	170.4	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18

759	dirMS_041712_NAR_30mM_plus2.12019.12040.2	2	18.79	0	1.99E+05		(R)VFNETPI	(R)V/F|N|E|T/P I/N/P R(K)		116.15	593.8147	1186.622	0.0006	0.5	5.97	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
760	dirMS_041712_NAR_30mM_minus2.11822.12204.2	2	18.78	0	1.06E+06		(K)VLQLYP	(K)V/L|Q|L|Y|P/N/N K(A)		118.48	544.8076	1088.61	-0.0019	-1.8	8.56	9740.1	10.08	HUMAN	H0YFG2	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed (Fragment)
761	dirMS_041712_NAR_30mM_minus2.12685.12926.2	2	18.78	0	4.46E+06		(R)EYQELM	(R)E Y|Q/E/L/M/N/V/K(L)		122.25	577.2825	1153.556	0.0019	1.7	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
762	dirMS_041712_NAR_60mM_minus.10837.11063.3	3	18.78	1	6.02E+05		(K)IQVLQQ	(K)I/Q|V|L/Q/Q/Q/A D/D A E E R A E R(L)		121.07	666.9983	1998.984	-0.0036	-1.8	4.18	26611.3	4.47	HUMAN	A6NL28	Putative tropomyosin alpha-3 chain-like protein
763	dirMS_041712_NAR_60mM_minus.15462.15462.3	3	18.78	1	4.49E+05		(R)LLDAQL	(R)L L/D|A/Q/L/A/T G G L V C P A R R(L)	C:Carbamidomethylation	146.02	604.3344	1810.996	-0.007	-3.8	9.6	266161	5.68	HUMAN	E9PPU0	Epiplakin
764	dirMS_041712_NAR_50mM_plus2.8654.8967.3	3	18.78	0	7.69E+05		(R)AALAHS	(R)A A L A H S/E E\V|T|A/S/Q/V A/A|T/K(T)		113.47	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
765	dirMS_041712_NAR_50mM_minus2.17504.17927.3	3	18.77	0	1.53E+07		(R)IHFPLAT	(R)I H\F\P L A\T|Y|A|P/V/I/S A E K(A)		167.6	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
766	dirMS_041712_NAR_30mM_plus2.18764.19319.2	2	18.77	0	3.07E+06		(R)ADLIAYL	(R)A/D|L|I|A/Y/L/K(K)		153.18	453.7673	906.529	-0.0022	-2.4	5.88	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
767	dirMS_041712_NAR_30mM_plus2.8302.8302.2	2	18.77	0	2.13E+05		(R)VAIEPG	(R)V A|I/E/P/G A/P/R(E)		97.67	455.2602	909.515	-0.0021	-2.3	5.97	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
768	dirMS_041712_NAR_50mM_minus2.6763.6763.3	3	18.76	1	2.52E+05		(R)ASVDTK	(R)A S|V/D/T K E/A E G\A/P/Q V/E A G K(R)		104.8	596.2904	1786.882	-0.0251	-14	4.41	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
769	dirMS_041712_NAR_30mM_plus2.12907.12907.2	2	18.76	0	3.70E+05		(R)ELAEDG	(R)E L/A|E/D/G Y/S/G/V E/V R(V)		120.6	712.3382	1423.67	-0.0008	-0.6	4	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
770	dirMS_041712_NAR_30mM_plus2.6103.6103.2	2	18.76	0	1.32E+05	M697m	(K)EGALCE	(K)E/G A|L/C|E/E/N m/R(G)	C:Carbamidomethylation m:Oxid	86.15	612.7525	1208.503	15.9943	-0.5	4.25	96306.4	6.41	HUMAN	P13639	Elongation factor 2
771	dirMS_041712_NAR_30mM_plus2.8114.8280.2	2	18.76	0	3.43E+05		(K)EGALCE	(K)E G|A|L/C|E|E/N M/R(G)	C:Carbamidomethylation	96.82	604.7561	1208.503	0.0015	1.2	4.25	96306.4	6.41	HUMAN	P13639	Elongation factor 2
772	dirMS_041712_NAR_50mM_plus2.15638.15660.3	3	18.76	1	9.32E+06		(R)IINEPTA	(R)I/I|N|E|P T A A/A/I A/Y G L D/K K(V)		149.67	596.6673	1787.99	-0.0028	-1.6	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
773	dirMS_041712_NAR_60mM_plus.20400.20400.3	3	18.76	1	4.21E+05		(K)NAAGAL	(K)N/A/A/G A L/D/L L/K E L/K(N)		166.93	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
774	dirMS_041712_NAR_40mM_plus2.19790.19790.3	3	18.75	0	3.68E+05		(R)DLLDTV	(R)D L|L|D T\V L/P H L Y N E T K(V)		185.23	590.9774	1770.927	-0.0096	-5.4	4.54	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
775	dirMS_041712_NAR_50mM_plus2.9837.9837.3	3	18.75	0	1.92E+06		(R)EIVHIQA	(R)E/I V H\I Q A|G/Q|C/G N Q I/G A/K(F)	C:Carbamidomethylation	119.02	608.3107	1822.923	-0.0053	-2.9	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
776	dirMS_041712_NAR_30mM_plus2.16796.16859.2	2	18.74	0	2.03E+06		(K)YMACCL	(K)Y/M|A|C/C/L L/Y/R(G)	C:Carbamidomethylation	140.15	625.2798	1249.553	-0.0003	-0.2	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
777	dirMS_041712_NAR_50mM_plus2.14475.14708.3	3	18.74	0	1.61E+05		(K)TGEEIFG	(K)T|G|E|E|I|F/G T/I/G M R P N A K(N)		144.42	574.2925	1720.869	-0.0057	-3.3	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
778	dirMS_041712_NAR_120mM_minus.15257.15446.3	3	18.73	2	9.57E+05		(R)ALKDEE	(R)A L/K|D E\E|K/M/E/L/Q/E|I\Q|L/K(E)		137.72	649.0139	1945.031	-0.0039	-2	4.58	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
779	dirMS_041712_NAR_120mM_minus.8075.8075.3	3	18.73	0	1.23E+06		(K)HSGPNS	(K)H S\G P N\S\A|D|S A/N/D/G/F V/R(L)		98.42	544.2477	1630.72	0.0081	5	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
780	dirMS_041712_NAR_30mM_minus2.12047.12225.2	2	18.73	0	3.38E+05		(K)ILYSQCG	(K)I/L|Y|S|Q/C/G D/V M R(A)	C:Carbamidomethylation	119.22	671.3183	1341.629	0.0004	0.3	5.83	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
781	dirMS_041712_NAR_30mM_minus2.15738.15941.2	2	18.73	0	8.39E+05		(R)GGIVDE	(R)G G/I|V|D|E\G A/L/L/R(A)		139.92	550.3083	1099.611	-0.0013	-1.2	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
782	dirMS_041712_NAR_30mM_plus2.10917.11153.2	2	18.73	0	2.64E+06		(R)APIIAVT	(R)A/P|I|I|A/V/T/R(N)		111.08	420.7688	840.53	0.0002	0.2	9.79	53557.7	6.39	HUMAN	H3BTN5	Pyruvate kinase (Fragment)
783	dirMS_041712_NAR_30mM_plus2.6019.6033.2	2	18.73	0	1.18E+05		(R)YEVTSG	(R)Y/E|V|T|S/G/G/G G T S R(M)		85.87	585.7729	1170.539	0	0	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
784	dirMS_041712_NAR_120mM_minus.11522.11537.3	3	18.72	1	2.55E+05		(R)VDWQE	(R)V/D|W/Q/E/N D F/S K/R(I)		117	475.225	1423.66	0.0004	0.3	4.56	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
785	dirMS_041712_NAR_20mM_plus.11322.11410.2	2	18.72	0	3.86E+05		(K)LITPAVV	(K)L I|T|P/A/V/V/S\E/R(L)		150.87	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
786	dirMS_041712_NAR_30mM_plus2.13972.14040.2	2	18.72	0	6.56E+05		(R)IYVVDV	(R)I/Y|V|V|D|V/G|S E/P R(A)		126.27	617.3263	1233.647	-0.0021	-1.7	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
787	dirMS_041712_NAR_30mM_plus2.21207.21437.2	2	18.72	0	7.11E+05		(R)IINDLLQ	(R)I/I|N|D|L|L/Q/S L/R(S)		166.7	592.8453	1184.7	-0.0164	-13.9	5.84	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
788	dirMS_041712_NAR_50mM_plus2.12429.12762.3	3	18.72	1	1.68E+07		(K)KVPQVS	(K)K\V\P\Q V S\T|P/T|L|V/E/V S R(N)		134.13	547.3169	1639.938	-0.0016	-1	8.75	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
789	dirMS_041712_NAR_30mM_minus2.12547.12939.2	2	18.71	0	2.40E+06		(R)GYFDEE	(R)G/Y|F|D|E/E M/N/R(V)		123.02	580.7374	1160.468	-0.0002	-0.2	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
790	dirMS_041712_NAR_20mM_plus.17539.17915.2	2	18.71	0	1.37E+06		(R)YLTVAA	(R)Y/L|T|V/A/A/V/F/R(G)		193.83	520.3009	1039.593	0.001	1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
791	dirMS_041712_NAR_30mM_plus2.8963.9443.2	2	18.71	0	1.80E+06		(K)TAVCDI	(K)T A|V|C/D/I|P|P/R(G)	C:Carbamidomethylation	100.42	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
792	dirMS_041712_NAR_20mM_plus.15733.15733.2	2	18.7	0	5.04E+05		(R)GVVDSE	(R)G/V|V|D/S\E/D/I|P L\N L\S R(E)		179.42	757.3956	1513.786	-0.0017	-1.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
793	dirMS_041712_NAR_50mM_minus2.14662.14810.3	3	18.69	1	1.72E+06		(K)AGTQIE	(K)A/G|T|Q/I/E/N I D/E D/F R D G L K(L)		152.02	640.9832	1920.93	0.0053	2.8	4.11	59872.5	4.85	HUMAN	F5GXS2	Alpha-actinin-4
794	dirMS_041712_NAR_60mM_minus.14244.14541.3	3	18.69	1	1.30E+06		(R)MSMKE	(R)M/S M K E V D\E\Q|M|L/N/V/Q/N/K(N)		140.47	641.9701	1923.897	-0.0015	-0.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
795	dirMS_041712_NAR_120mM_plus.24541.24575.3	3	18.69	1	5.86E+05		(R)GHYTIG	(R)G H|Y|T|I G K E|I|I|D L/V|L D/R(I)		184.32	614.6745	1842.012	-0.003	-1.6	5.38	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
796	dirMS_041712_NAR_120mM_plus.6478.6637.2	2	18.69	1	3.71E+06		(R)TKTEISE	(R)T/K|T|E|I/S/E/M N/R(N)		88.15	604.8002	1208.594	-0.0008	-0.7	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
797	dirMS_041712_NAR_30mM_plus2.11494.11519.2	2	18.69	0	3.82E+05		(K)VAGQD	(K)V/A|G/Q|D/G S V V/Q|F/K(I)		113.82	617.8214	1234.643	-0.0071	-5.8	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
798	dirMS_041712_NAR_40mM_plus2.17122.17333.3	3	18.69	1	3.36E+05		(K)VIAATN	(K)V I|A|A/T/N R V D\I/L|D/P A L L/R(S)		168.1	617.3636	1850.086	-0.0096	-5.2	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
799	dirMS_041712_NAR_20mM_plus.18760.18911.2	2	18.68	0	2.32E+05		(R)IITLAGP	(R)I I|T|L|A|G/P T N\A I F K(A)		200.97	679.9039	1358.804	-0.0037	-2.7	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
800	dirMS_041712_NAR_30mM_minus2.15045.15045.2	2	18.67	0	7.03E+05		(K)SADTLW	(K)S/A|D|T|L|W/G I Q K(E)		135.23	559.8008	1118.584	0.0103	9.2	5.55	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
801	dirMS_041712_NAR_50mM_minus2.11366.11388.3	3	18.67	1	9.59E+04		(R)LLIVSTT	(R)L/L|I|V|S T T/P/Y/S E K D/T/K(Q)		133.12	565.6428	1694.921	-0.0072	-4.3	6.07	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
802	dirMS_041712_NAR_60mM_minus.14232.14360.3	3	18.67	1	2.23E+06		(R)TEMENE	(R)T|E|M/E/N E|F/V/L/I/K K(D)		139.38	494.2594	1480.772	-0.0079	-5.4	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
803	dirMS_041712_NAR_30mM_plus2.20197.20262.3	3	18.67	0	5.11E+05		(K)SYELPD	(K)S Y\E|L|P D G Q|V|I/T/I/G N E R(F)		159.87	597.6334	1790.892	-0.0063	-3.5	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
804	dirMS_041712_NAR_60mM_plus.11766.11791.3	3	18.67	0	9.46E+05	M271m	(R)DLNYCF	(R)D L|N/Y/C/F/S/G m S D/H R(Y)	C:Carbamidomethylation m:Oxid	118.98	539.886	1601.647	15.9963	0.9	5.21	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
805	dirMS_041712_NAR_40mM_minus2.5847.5974.2	2	18.66	0	1.35E+06		(K)AGFAGD	(K)A/G|F|A|G/D/D A/P R(A)		98.18	488.7279	976.448	0.0002	0.2	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
806	dirMS_041712_NAR_120mM_plus.10178.10566.3	3	18.66	1	1.42E+06		(R)YLAEFA	(R)Y/L|A/E/F/A/T/G N D/R K(E)		107.77	462.2337	1384.686	0.001	0.7	6.07	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
807	dirMS_041712_NAR_50mM_plus2.12405.12405.3	3	18.66	1	7.86E+05		(K)IEVEKPF	(K)I/E|V E/K/P F A I A K E(-)		133.12	458.5944	1373.767	0.0012	0.8	5.01	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
808	dirMS_041712_NAR_60mM_plus.9359.9487.3	3	18.66	0	7.99E+06		(K)STAGDT	(K)S T|A/G/D/T/H/L/G/G E/D F D/N R(M)		107.4	564.5799	1691.726	-0.0004	-0.3	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
809	dirMS_041712_NAR_50mM_minus2.6142.6144.3	3	18.65	1	1.78E+05		(R)IVDGKV	(R)I/V|D/G K/V/V/S\E/T N D/T/K(V)		97.65	502.2662	1504.785	-0.0013	-0.9	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
810	dirMS_041712_NAR_120mM_plus.19581.19620.3	3	18.65	0	8.75E+05		(R)NSVSNF	(R)N|S|V/S/N/F/L/H S/L E/R(G)		156.15	468.2345	1402.707	-0.0184	-13.1	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
811	dirMS_041712_NAR_30mM_plus2.8265.8279.2	2	18.65	0	1.96E+05		(R)TENCLS	(R)T/E|N|C|L/S/S/C V/D/R(F)	C:Carbamidomethylation	97.15	670.7815	1340.557	-0.0012	-0.9	4.37	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
812	dirMS_041712_NAR_40mM_plus2.14289.14289.3	3	18.65	1	9.15E+05		(R)IINEPTA	(R)I/I|N|E/P T A A/A I A Y G L D K K(V)		150.23	596.6671	1787.99	-0.0034	-1.9	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
813	dirMS_041712_NAR_50mM_plus2.18757.18757.3	3	18.65	1	4.36E+05		(K)AAIDWF	(K)A/A/I/D|W/F D G K\E F/S G N P I/K(V)		167.18	632.3186	1894.933	0.0079	4.1	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
814	dirMS_041712_NAR_30mM_plus2.21133.21133.2	2	18.64	0	6.89E+05		(K)IPDWFL	(K)I/P/D/W/F L N R(Q)		165.78	530.785	1060.557	0.0053	5	5.84	9767.1	11.41	HUMAN	J3JS69	40S ribosomal protein S18
815	dirMS_041712_NAR_50mM_plus2.14589.14589.3	3	18.64	1	2.01E+06		(R)VAGGP	(R)V/A|G G/P Q/M/I Q L S L D/G K R(L)		144.47	557.3066	1669.905	-0.0002	-0.1	8.72	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
816	dirMS_041712_NAR_50mM_plus2.18228.18228.3	3	18.64	1	6.23E+05		(K)LLEPVLL	(K)L/L|E/P/V/L/L/L G K E/R(F)		164.48	460.6256	1379.862	0.0002	0.1	6.14	16559.1	10.36	HUMAN	P62249	40S ribosomal protein S16
817	dirMS_041712_NAR_50mM_plus2.9892.9892.3	3	18.64	1	1.74E+05		(R)LLDEEE	(R)L/L|D/E E/E/A/T/D N D L R/A K(F)		119.38	577.9512	1731.84	-0.0005	-0.3	4.02	96649	6.13	HUMAN	Q8WUM4	Programmed cell death 6-interacting protein
818	dirMS_041712_NAR_20mM_minus.14447.14447.2	2	18.63	0	9.57E+04		(R)LTGQLF	(R)L T/G/Q|L/F/L\G G S/I/V/K(G)		198.62	666.8967	1332.789	-0.0024	-1.8	8.75	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
819	dirMS_041712_NAR_120mM_plus.17058.17540.4	4	18.63	2	2.50E+06		(R)NLKASL	(R)N/L K/A S\L|E/N/S L/R E V/E/A/R(Y)		143.6	458.0016	1828.988	-0.003	-1.6	6.23	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
820	dirMS_041712_NAR_120mM_plus.8397.8400.3	3	18.63	1	3.91E+05		(K)NGRVEI	(K)N G R V\E\I\I|A|N/D/Q/G N/R(I)		97.38	519.2706	1555.794	0.0037	2.4	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
821	dirMS_041712_NAR_20mM_plus.14788.14788.2	2	18.63	0	1.98E+05	M179m M	(K)mFVLDE	(K)m F|V|L|D E|A/D E m L/S R(G)	m:Oxidized methionine	173.6	794.3555	1555.713	31.9906	0.5	3.91	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
822	dirMS_041712_NAR_50mM_plus2.13243.13243.3	3	18.63	1	9.66E+05		(R)ELNITA	(R)E L/N/I/T A/A K/E I/E/V/G G G R(K)		137.7	552.9671	1656.892	-0.0048	-2.9	4.79	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
823	dirMS_041712_NAR_50mM_minus2.8793.8903.3	3	18.62	0	2.36E+05		(R)VMLGET	(R)V/M|L\G/E/T N/P A/D/S K/P G T I R(G)		118.3	595.9744	1785.916	-0.0077	-4.3	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
824	dirMS_041712_NAR_50mM_minus2.9374.9409.3	3	18.62	0	6.84E+04		(R)AASIFG	(R)A/A|S/I/F/G/G A K/P V D/T A A R(E)		121.62	511.2773	1531.823	-0.0054	-3.5	8.79	64861.3	5.86	HUMAN	B4DS13	Eukaryotic translation initiation factor 4B
825	dirMS_041712_NAR_60mM_minus.13834.13965.3	3	18.62	0	1.38E+06		(K)LGDVYV	(K)L/G|D|V/Y V/N\D/A/F G T/A\H/R(A)		136.73	545.603	1634.792	0.0023	1.4	5.21	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
826	dirMS_041712_NAR_20mM_plus.10885.10885.2	2	18.62	0	2.19E+05	M33m	(K)VAGmD	(K)V/A/G/m/D V|E/L/T V E E R(N)	m:Oxidized methionine	147.28	732.3555	1447.71	15.994	-0.6	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
827	dirMS_041712_NAR_20mM_plus.9639.9640.2	2	18.62	0	6.24E+05		(R)ISVYYNE	(R)I/S|V/Y|Y/N|E\A/T G G K(Y)		138.33	651.3211	1301.637	-0.0023	-1.8	6	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
828	dirMS_041712_NAR_30mM_plus2.18267.18267.2	2	18.62	0	5.29E+05		(R)GYISPYF	(R)G Y\I/S|P Y F I N T/S K(G)		149.7	695.3554	1389.705	-0.0014	-1	8.5	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
829	dirMS_041712_NAR_30mM_plus2.8198.8198.2	2	18.62	0	3.43E+05		(K)EGALCE	(K)E/G/A|L/C/E/E/N/M R(G)	C:Carbamidomethylation	96.82	604.7561	1208.503	0.0015	1.2	4.25	96306.4	6.41	HUMAN	P13639	Elongation factor 2
830	dirMS_041712_NAR_30mM_plus2.8767.8810.2	2	18.62	0	6.99E+05		(R)AAPGAE	(R)A/A|P/G/A E/F/A|P N/K(R)		100.33	536.7755	1072.542	0.0015	1.4	6.05	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
831	dirMS_041712_NAR_50mM_plus2.21347.21427.3	3	18.62	1	5.13E+05	M145m	(R)GVmLA	(R)G V|m/L/A V/D/A V/I/A E/L K K(Q)	m:Oxidized methionine	182.28	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
832	dirMS_041712_NAR_50mM_minus2.8715.8715.3	3	18.61	1	4.19E+04	M88m	(K)DVDEAY	(K)D V/D|E/A/Y m N K/V/E L E S R(L)	m:Oxidized methionine	117.5	605.2817	1797.832	15.9982	1.8	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
833	dirMS_041712_NAR_20mM_plus.8087.8087.2	2	18.61	0	2.12E+05		(R)FGQGG	(R)F G/Q/G|G/A|G/P V/G G Q G P R(G)		125.2	671.3361	1341.666	-0.0009	-0.7	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
834	dirMS_041712_NAR_60mM_plus.12038.12171.3	3	18.61	0	1.36E+06		(K)VYNYNH	(K)V/Y|N/Y/N/H/L/M/P T|R(Y)		120.25	469.8993	1407.684	-0.0004	-0.3	8.57	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
835	dirMS_041712_NAR_60mM_plus.12052.12052.2	2	18.61	1	1.52E+06		(R)DGKLVS	(R)D G K|L|V|S/E/S S D/V/L|P K(-)		120.25	737.3869	1473.78	-0.013	-8.8	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
836	dirMS_041712_NAR_30mM_minus2.8053.8053.2	2	18.6	0	2.96E+05		(R)FLNAEN	(R)F/L|N|A/E/N A\Q/K(F)		98.62	517.7675	1034.526	0.0012	1.1	6	20592.3	9.75	HUMAN	B3KUP2	RAN binding protein 1, isoform CRA_f
837	dirMS_041712_NAR_60mM_minus.13647.13695.3	3	18.6	1	2.69E+05		(K)SLLSNLD	(K)S/L|L/S/N/L/D E V K K(E)		136	415.9055	1245.705	-0.0029	-2.4	5.79	96649	6.13	HUMAN	Q8WUM4	Programmed cell death 6-interacting protein
838	dirMS_041712_NAR_20mM_plus.14038.14253.2	2	18.6	0	1.57E+06	M313m	(R)TVQSLE	(R)T V|Q|S|L|E|I\D/L/D/S m R(N)	m:Oxidized methionine	170.15	761.8738	1506.747	15.9935	-0.9	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
839	dirMS_041712_NAR_30mM_plus2.12433.12433.2	2	18.6	0	7.27E+05		(K)NAGVEG	(K)N A|G|V|E/G/S L I/V/E K(I)		118.2	608.3313	1215.658	-0.0026	-2.2	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
840	dirMS_041712_NAR_30mM_plus2.19911.20112.2	2	18.6	0	8.41E+05		(K)MSIYQA	(K)M/S|I|Y/Q/A/M W/K(G)		158.83	579.2783	1157.548	0.0011	1	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
841	dirMS_041712_NAR_40mM_plus2.9008.9008.3	3	18.6	0	5.80E+04		(R)AALAHS	(R)A A L A H S/E E\V|T|A/S|Q/V/A/A T K(T)		115.18	595.3161	1783.919	0.0153	8.6	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
842	dirMS_041712_NAR_60mM_minus.19724.19900.3	3	18.59	0	6.61E+06		(R)LHFFMP	(R)L H F\F\M|P/G\F|A|P\L/T S R(G)		179.58	540.9491	1620.835	-0.0028	-1.7	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
843	dirMS_041712_NAR_40mM_plus2.11314.11314.3	3	18.59	0	1.67E+05		(R)SVIDPV	(R)S V\I/D|P/V/P/A/P V G D S H V D G A A K(S)		132.95	644.3327	1930.987	-0.0033	-1.7	4.41	58326.8	5.7	HUMAN	Q13177	Serine/threonine-protein kinase PAK 2
844	dirMS_041712_NAR_40mM_plus2.15106.15404.3	3	18.59	0	3.27E+05		(K)GVTIIGP	(K)G V|T|I/I|G/P A T V/G G I/K/P G C F K(I)	C:Carbamidomethylation	156.22	624.683	1872.041	-0.0067	-3.6	10	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
845	dirMS_041712_NAR_120mM_minus.17941.18438.3	3	18.58	1	3.33E+06		(R)ARFEEL	(R)A R\F E\E\L|N|A|D/L/F/R(G)		154.37	494.2561	1480.754	-0.0006	-0.4	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
846	dirMS_041712_NAR_20mM_plus.16093.16353.2	2	18.58	0	4.91E+05		(K)DAGTIA	(K)D A|G T|I|A|G L/N/V L/R(I)		183.63	600.3422	1199.674	0.0029	2.4	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
847	dirMS_041712_NAR_30mM_plus2.6375.6391.2	2	18.58	0	1.01E+05		(R)SVSPCS	(R)S V|S|P/C|S N/V E/S R(L)	C:Carbamidomethylation	87.83	611.2799	1221.553	-0.0003	-0.2	5.72	99885.2	12.36	HUMAN	I3L182	Serine/arginine repetitive matrix protein 2 (Fragment)
848	dirMS_041712_NAR_50mM_plus2.14344.14344.3	3	18.58	1	1.80E+05		(K)TITLEVE	(K)T I|T|L/E/V E/P S D T/I/E N V K A K(I)		143.57	663.0232	1987.059	-0.0043	-2.2	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
849	dirMS_041712_NAR_50mM_plus2.7499.7584.3	3	18.58	0	3.69E+05		(R)VGQAVD	(R)V/G|Q/A/V D\V/V/G Q/A/G K/P K(T)		105.72	484.9438	1452.817	-0.0001	0	8.56	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
850	dirMS_041712_NAR_60mM_minus.6112.6112.3	3	18.57	1	2.64E+05		(K)LEEAEK	(K)L/E/E/A/E/K/A A D/E\S E R(G)		92.57	492.8981	1476.681	-0.0015	-1	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
851	dirMS_041712_NAR_20mM_plus.14459.14499.2	2	18.57	0	6.32E+05	M185m	(K)LAVNm	(K)L/A|V/N/m|V|P/F P R(L)	m:Oxidized methionine	170.68	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
852	dirMS_041712_NAR_30mM_plus2.13044.13426.2	2	18.56	0	6.09E+06		(K)IGGIGTV	(K)I/G|G|I|G/T/V|P V G R(V)		122.85	513.3084	1025.61	-0.0007	-0.7	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
853	dirMS_041712_NAR_60mM_plus.11843.11882.3	3	18.56	1	2.80E+06		(K)YGEPGE	(K)Y/G|E|P/G E V|F/I/N K G K(G)		119.42	479.9219	1437.737	0.0139	9.7	6.14	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
854	dirMS_041712_NAR_30mM_minus2.10250.10294.2	2	18.55	0	2.90E+05		(K)DQVAN	(K)D Q|V|A|N/S/A/F/V/E/R(L)		109.8	618.303	1235.602	-0.0028	-2.2	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
855	dirMS_041712_NAR_40mM_minus2.12486.12708.3	3	18.55	1	5.98E+05		(R)VCENIPI	(R)V/C|E|N/I|P I\V/L C G N K V D\I/K(D)	C:Carbamidomethylation	157.7	657.6842	1971.04	-0.0021	-1.1	6.04	14844.8	5.89	HUMAN	B4DV51	GTP-binding nuclear protein Ran
856	dirMS_041712_NAR_60mM_minus.6831.7286.3	3	18.55	1	2.64E+06		(K)IQDKEG	(K)I/Q/D\K E G|I|P|P/D/Q Q R(L)		97.3	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
857	dirMS_041712_NAR_50mM_plus2.9942.9989.3	3	18.55	0	1.16E+06		(K)INEKPQ	(K)I/N/E K/P\Q\V|I|A/D/Y/E/S G R(A)		119.77	573.6314	1718.871	0.0089	5.2	4.68	16368.4	9.95	HUMAN	O60869	Endothelial differentiation-related factor 1
858	dirMS_041712_NAR_60mM_plus.11259.11452.3	3	18.55	0	4.00E+06		(K)NFYVEH	(K)N F/Y/V/E/H/P E V A/R(L)		116.57	454.2286	1360.664	0.0068	5	5.4	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
859	dirMS_041712_NAR_60mM_plus.16220.16357.3	3	18.55	0	5.85E+05		(K)WIGLDL	(K)W/I|G/L/D/L/S/N/G K/P R(D)		142.08	452.5864	1355.743	0.0016	1.2	8.75	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
860	dirMS_041712_NAR_60mM_plus.8494.8718.3	3	18.55	0	6.18E+05		(K)GQVCV	(K)G Q|V/C/V/M/I/H S G S R(G)	C:Carbamidomethylation	103.1	444.2219	1330.636	0.0157	11.8	9.75	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
861	dirMS_041712_NAR_50mM_minus2.13786.14034.3	3	18.54	0	1.67E+06		(R)QVSASE	(R)Q V|S/A/S E/L/H T S G I/L/G/P E T L R(D)		147.53	665.688	1995.051	-0.0011	-0.6	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
862	dirMS_041712_NAR_60mM_minus.9217.9217.3	3	18.54	0	2.84E+05		(K)ATAGDT	(K)A/T|A/G D T H/L|G G E D F/D/N R(L)		111.4	559.2488	1675.731	0.0012	0.7	4.22	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
863	dirMS_041712_NAR_20mM_plus.8287.8287.2	2	18.54	0	9.05E+04		(K)GGEIQP	(K)G G\E/I|Q/P V/S/V/K(V)		127.42	507.2841	1013.563	-0.0017	-1.6	6	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
864	dirMS_041712_NAR_120mM_minus.13295.13295.4	4	18.53	1	8.85E+05		(K)SVHSSV	(K)S V H S\S\V|P L/L/N S/K D/P I D\R(I)		127.12	466.7525	1863.992	-0.0041	-2.2	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
865	dirMS_041712_NAR_120mM_minus.14480.14500.4	4	18.53	1	5.55E+05		(R)ETNLDS	(R)E T N L D S\L P/L/V/D/T/H S K/R(T)		133.47	456.992	1824.945	0.0012	0.6	5.38	53707.8	5.06	HUMAN	P08670	Vimentin
866	dirMS_041712_NAR_30mM_minus2.16876.17163.2	2	18.53	0	5.12E+05		(K)NSLESY	(K)N S|L|E|S/Y/A/F/N/M K(A)		146.62	652.3031	1303.599	0.0002	0.2	6	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
867	dirMS_041712_NAR_40mM_minus2.12312.12312.3	3	18.53	0	4.42E+05		(K)IAILTCP	(K)I A|I/L/T C/P F/E/P P K P K(T)	C:Carbamidomethylation	155.88	537.6382	1610.898	0.0026	1.6	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon

868	dirMS_041712_NAR_30mM_plus2.8400.8400.2	2	18.53	0	1.29E+06		(K)QGGGG	(K)Q G/G\G G/G G/G/S V/P G I/E R(M)		97.22	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
869	dirMS_041712_NAR_40mM_plus2.17055.17336.3	3	18.53	1	3.36E+05		(K)VIAATN	(K)V/I|A|A/T/N R V/D\I/L/D/P A L L R(S)		168.1	617.3636	1850.086	-0.0096	-5.2	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
870	dirMS_041712_NAR_50mM_plus2.15456.15458.3	3	18.53	1	8.05E+05		(K)EAFSLFD	(K)E A|F|S/L/F/D/K D G D G T I T/T/K(E)		149.45	615.6348	1844.891	-0.0014	-0.8	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
871	dirMS_041712_NAR_30mM_minus2.15030.15420.2	2	18.51	0	1.29E+06		(K)FDLMYA	(K)F/D/L|M/Y/A/K(R)		136.1	444.2205	887.433	0.0006	0.6	5.83	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
872	dirMS_041712_NAR_30mM_minus2.18176.18176.2	2	18.51	0	1.96E+05		(K)VADIGL	(K)V/A|D|I/G/L\A/A W G R(K)		152.82	564.8076	1128.616	-0.0081	-7.2	5.81	48285.8	5.93	HUMAN	P23526	Adenosylhomocysteinase
873	dirMS_041712_NAR_20mM_minus.14122.14122.3	3	18.5	0	1.04E+06		(K)SYELPD	(K)S Y E\L/P D|G Q|V\I/T/I/G N E R(F)		194.2	597.6345	1790.892	-0.003	-1.7	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
874	dirMS_041712_NAR_50mM_minus2.7806.7806.3	3	18.5	1	5.68E+04		(R)LGAAPE	(R)L/G/A/A/P E E E S A Y V/A/G E K R(Q)		111.32	592.9614	1776.876	-0.0066	-3.7	4.5	30276.7	5	HUMAN	F2Z2K0	NSFL1 cofactor p47
875	dirMS_041712_NAR_60mM_minus.10174.10174.3	3	18.49	0	4.78E+06		(R)GSAVH	(R)G S/A/V/H/Q/L|S/E/E L/R(C)		117.2	442.5648	1325.681	-0.001	-0.7	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
876	dirMS_041712_NAR_30mM_plus2.10927.11069.2	2	18.49	0	6.88E+05		(K)TGQEIP	(K)T/G|Q|E|I|P V/N V/R(F)		111	556.8073	1112.606	0.0015	1.3	5.66	28051.5	4.98	HUMAN	J3QKT2	Cytosolic non-specific dipeptidase (Fragment)
877	dirMS_041712_NAR_30mM_plus2.12226.12422.2	2	18.49	0	6.57E+05		(R)LAAEQE	(R)L/A|A|E|Q/E/L/I/R(L)		117.67	521.7961	1042.589	-0.0042	-4	4.53	533778	5.74	HUMAN	Q15149	Plectin
878	dirMS_041712_NAR_40mM_plus2.11399.11519.3	3	18.49	0	3.79E+05		(R)MPLPAP	(R)M/P/L|P/A/P S L S H\Q|P/P/P A P R(V)		133.63	598.3202	1792.953	-0.0066	-3.7	9.52	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
879	dirMS_041712_NAR_50mM_plus2.16549.16758.3	3	18.49	0	1.39E+06		(R)GFGHIG	(R)G F G H I\G I\A\V|P/D/V/Y/S A/C K(R)	C:Carbamidomethylation	155.57	597.634	1790.889	-0.002	-1.1	6.74	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
880	dirMS_041712_NAR_50mM_minus2.12753.13155.3	3	18.48	1	3.42E+06		(R)TEMENE	(R)T|E|M/E/N E F/V/L/I/K/K(D)		141.77	494.2621	1480.772	0.0002	0.1	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
881	dirMS_041712_NAR_50mM_minus2.15166.15420.3	3	18.47	0	9.01E+05		(R)LLIHQSL	(R)L L/I/H/Q\S\L|A/G/G I/I/G V/K(G)		154.83	506.9833	1518.937	-0.0013	-0.8	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
882	dirMS_041712_NAR_120mM_plus.10758.10856.3	3	18.47	0	1.18E+06		(K)NFYQEH	(K)N/F/Y/Q E/H/P D/L A/R(R)		109.72	463.8906	1389.655	0.0027	1.9	5.32	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
883	dirMS_041712_NAR_20mM_plus.15456.15810.2	2	18.47	0	1.28E+06	M73m	(R)AILVDLE	(R)A I|L|V|D|L|E|P G T/m D S V R(S)	m:Oxidized methionine	179.22	816.4181	1615.836	15.9929	-1.2	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
884	dirMS_041712_NAR_30mM_plus2.8747.8928.2	2	18.47	0	8.74E+05		(R)VLNTNI	(R)V/L|N|T|N/I/D/G R(R)		100.02	501.2717	1001.537	-0.0013	-1.3	5.81	17718.4	10.99	HUMAN	P62269	40S ribosomal protein S18
885	dirMS_041712_NAR_30mM_plus2.9012.9012.2	2	18.47	0	6.30E+05		(R)SSQSSS	(R)S S/Q/S S/S Q/Q F|S|G/I/G\R(S)		101.03	728.345	1455.682	0.0005	0.3	9.47	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
886	dirMS_041712_NAR_50mM_plus2.14408.14590.3	3	18.47	1	2.01E+06		(R)VAGGP	(R)V/A/G/G/P Q M/I/Q/L/S L D/G K/R(L)		144.47	557.3066	1669.905	-0.0002	-0.1	8.72	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
887	dirMS_041712_NAR_50mM_plus2.8160.8206.3	3	18.47	0	2.70E+05		(K)STAGDT	(K)S|T|A/G D/T/H/L/G/G E D F D/N R(M)		109.7	564.5793	1691.726	-0.0022	-1.3	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
888	dirMS_041712_NAR_30mM_minus2.15044.15108.2	2	18.46	0	7.03E+05		(K)SADTLW	(K)S A|D|T|L|W/G/I/Q/K(E)		135.23	559.8008	1118.584	0.0103	9.2	5.55	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
889	dirMS_041712_NAR_60mM_plus.12901.12901.3	3	18.46	1	5.95E+05		(R)MAAPID	(R)M/A|A/P/I D R V G Q T I E/R(M)		124.35	519.6122	1556.821	0.0007	0.5	5.82	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
890	dirMS_041712_NAR_60mM_plus.9218.9268.3	3	18.46	1	9.89E+05		(K)YAGKDG	(K)Y/A|G/K/D/G\Y N/Y T/L/S/K(T)		106.37	493.9098	1479.711	0.0034	2.3	8.38	11854.4	6.57	HUMAN	P31949	Protein S100-A11
891	dirMS_041712_NAR_60mM_plus.9975.10370.3	3	18.46	0	2.65E+07		(K)GIVEFS	(K)G I|V/E/F/S/G K/P A A/R(K)		111.28	411.2315	1231.679	0.0006	0.5	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
892	dirMS_041712_NAR_20mM_minus.13114.13259.2	2	18.45	0	1.21E+06	M73m	(R)AILVDLE	(R)A I|L|V|D|L|E|P G T/m D S V R(S)	m:Oxidized methionine	182.73	816.4184	1615.836	15.9935	-0.8	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
893	dirMS_041712_NAR_30mM_minus2.10305.10559.2	2	18.45	0	1.45E+06		(R)AEAESM	(R)A E|A|E|S/M|Y/Q/I/K(Y)		110.47	585.2783	1169.551	-0.0014	-1.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
894	dirMS_041712_NAR_60mM_minus.6338.6844.3	3	18.45	1	3.02E+06		(K)IQDKEG	(K)I Q|D K E G|I|P/P/D/Q Q R(L)		94.92	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
895	dirMS_041712_NAR_120mM_minus.13498.13623.4	4	18.44	2	8.32E+05	M100m	(K)KQGGL	(K)K\Q G G L\G|P m|N\I/P/L/V/S D/P K R(T)	m:Oxidized methionine	128.55	481.5173	1907.053	15.9942	-0.3	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
896	dirMS_041712_NAR_120mM_minus.14864.14921.3	3	18.44	0	3.67E+05		(K)HLEINP	(K)H/L|E|I\N\P D|H|P/I V/E T\L R(Q)		135.25	594.9872	1782.95	-0.0027	-1.5	5.27	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
897	dirMS_041712_NAR_40mM_minus2.6432.6432.3	3	18.44	1	1.94E+05		(K)GAVAED	(K)G A|V/A|E/D/G D E L R T E P E A/K(K)		104.53	596.2893	1786.845	0.008	4.5	4.08	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
898	dirMS_041712_NAR_40mM_plus2.14601.14684.3	3	18.44	0	5.43E+05		(K)IAILTCP	(K)I/A|I|L/T/C/P F E/P P K P K(T)	C:Carbamidomethylation	153.55	537.6381	1610.898	0.0023	1.4	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
899	dirMS_041712_NAR_60mM_plus.6792.6801.3	3	18.44	1	1.28E+06		(K)SLDEME	(K)S/L|D/E/M/E/K/Q/Q/R(E)		94.13	421.8717	1263.6	0.0008	0.6	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
900	dirMS_041712_NAR_50mM_minus2.10413.10880.3	3	18.43	1	7.18E+06	M72m	(R)TEmENE	(R)T|E|m/E N E|F/V L/I/K/K(D)	m:Oxidized methionine	129.07	499.5937	1480.772	15.995	0	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
901	dirMS_041712_NAR_50mM_minus2.13801.13801.3	3	18.43	0	2.28E+06		(R)VAPDEH	(R)V A|P D E H P I L/L/T/E A/P L N P K(I)		146.07	652.0252	1954.064	-0.0034	-1.7	4.65	42344.8	5.39	HUMAN	Q562R1	Beta-actin-like protein 2
902	dirMS_041712_NAR_50mM_minus2.13951.14163.3	3	18.43	1	1.67E+06		(R)ELISNAS	(R)E L\I/S/N/A/S|D|A L/D/K I/R(L)		148.03	515.6179	1544.828	0.0113	7.3	4.56	5582.4	4.81	HUMAN	F8W026	Endoplasmin (Fragment)
903	dirMS_041712_NAR_20mM_plus.8127.8127.2	2	18.43	0	2.02E+05		(R)FGQGG	(R)F G/Q|G/G/A/G/P V/G G/Q/G P R(G)		125.25	671.3361	1341.666	-0.0009	-0.7	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
904	dirMS_041712_NAR_40mM_plus2.9869.9890.3	3	18.43	0	1.23E+05		(R)VMLGET	(R)V/M|L|G E T/N|P/A D/S K/P G T I R(G)		122.05	595.9778	1785.916	0.0025	1.4	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
905	dirMS_041712_NAR_30mM_plus2.12199.12199.2	2	18.42	0	9.10E+05		(K)EVDEQ	(K)E V|D E/Q/M L/N/V/Q/N K(N)		117.03	723.8478	1446.689	-0.001	-0.7	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
906	dirMS_041712_NAR_30mM_plus2.15986.16336.2	2	18.42	0	1.74E+06		(R)MGAG	(R)M/G|A|G|M|G/F/G L/E/R(M)		137.58	563.2636	1125.518	0.002	1.7	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
907	dirMS_041712_NAR_50mM_plus2.9972.10073.3	3	18.42	1	7.62E+05		(K)ITIKNDP	(K)I/T|I/K N D|P/S|L/P E/P K(C)		119.92	484.6079	1451.81	-0.0013	-0.9	6.07	20203.8	9.79	HUMAN	B4DG16	Asparagine--tRNA ligase, cytoplasmic
908	dirMS_041712_NAR_50mM_minus2.14854.14854.3	3	18.41	1	2.91E+05		(R)EAVTEIL	(R)E A V/T/E/I/L/G I/E/P D R E K(G)		152.33	566.9683	1698.891	-0.0005	-0.3	4.25	25685.9	6.4	HUMAN	E9PGT1	Translin
909	dirMS_041712_NAR_60mM_minus.16116.16361.3	3	18.41	1	5.82E+05		(K)LKLSILY	(K)L K\L S I\L|Y|P/A/T T G R(N)		150.5	478.2883	1432.852	-0.0019	-1.3	9.99	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
910	dirMS_041712_NAR_60mM_minus.18333.18333.3	3	18.41	1	4.80E+05		(K)TQLNLL	(K)T/Q|L/N/L L/L/D/K L R(S)		163.37	442.9403	1326.81	-0.004	-3	8.41	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
911	dirMS_041712_NAR_30mM_plus2.8964.8964.2	2	18.41	0	1.80E+06		(K)TAVCDI	(K)T A|V/C/D/I|P\P/R(G)	C:Carbamidomethylation	100.42	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
912	dirMS_041712_NAR_60mM_plus.6787.6787.3	3	18.41	1	7.29E+05		(R)AQLGG	(R)A Q|L/G G/P E A/A K S D E T A\A K(-)		93.87	548.6115	1643.824	-0.0036	-2.2	4.68	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
913	dirMS_041712_NAR_50mM_plus2.15986.16170.3	3	18.4	1	1.29E+06		(K)GADFLV	(K)G A|D|F|L|V/T/E|V/E/N G G S L G S K K(G)		152.28	636.6618	1907.971	-0.0001	0	4.68	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
914	dirMS_041712_NAR_60mM_plus.7460.7684.3	3	18.4	1	7.87E+06		(R)VITEEEK	(R)V/I|T/E/E/E/K N F/K(A)		97.9	412.8904	1236.647	0.0096	7.8	4.79	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
915	dirMS_041712_NAR_50mM_minus2.11769.11950.3	3	18.39	1	6.11E+05		(R)ELISNSS	(R)E L|I/S/N/S/S/D/A\L D/K I R(Y)		135.85	520.9445	1560.823	-0.0038	-2.5	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
916	dirMS_041712_NAR_50mM_minus2.12818.12818.3	3	18.39	1	3.63E+05		(R)LSEDYG	(R)L/S/E/D Y/G V/L/K T/D E G I A Y R(G)		141.42	643.6561	1928.96	-0.0063	-3.2	4.32	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
917	dirMS_041712_NAR_120mM_plus.8155.8171.3	3	18.39	0	1.78E+06		(K)HSGPNS	(K)H S G P N\S\A|D|S|A/N/D/G F/V/R(L)		96.53	544.2457	1630.72	0.0021	1.3	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
918	dirMS_041712_NAR_30mM_plus2.17842.17889.2	2	18.39	0	3.47E+05		(R)MADAL	(R)M/A|D|A|L|D/N/Y\V/I/R(G)		147.02	640.8182	1280.63	-0.0012	-1	4.21	15838.9	7.03	HUMAN	H0Y5U0	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
919	dirMS_041712_NAR_30mM_plus2.18982.18982.2	2	18.39	0	3.18E+06		(R)QAQEYE	(R)Q A Q|E/Y/E/A L/L/N\I/K(V)		153.23	710.3766	1419.748	-0.0019	-1.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
920	dirMS_041712_NAR_50mM_plus2.10378.10406.3	3	18.39	0	5.32E+05		(R)LQAQQ	(R)L/Q|A\Q/Q D A\V/N/I/V/C H/S K(T)	C:Carbamidomethylation	122.2	570.9571	1710.859	-0.0024	-1.4	6.74	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
921	dirMS_041712_NAR_50mM_plus2.11206.11350.3	3	18.39	0	1.71E+06		(R)GITINAA	(R)G I|T|I/N/A/A/H/V/E Y S T A A R(H)		127.07	558.6237	1673.861	-0.004	-2.4	6.75	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
922	dirMS_041712_NAR_50mM_plus2.20952.21302.3	3	18.39	0	8.90E+06		(R)LHFFMP	(R)L H\F\F\M\P G|F|A|P|L/T S/R(G)		181.53	540.9498	1620.835	-0.0007	-0.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
923	dirMS_041712_NAR_60mM_plus.11217.11235.3	3	18.39	1	1.69E+06		(K)VIADNV	(K)V/I|A/D/N/V/K/D W S/K(V)		116.35	425.563	1274.674	0.0005	0.4	5.93	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
924	dirMS_041712_NAR_30mM_minus2.10201.10788.2	2	18.38	0	3.78E+06		(K)TAVCDI	(K)T A|V|C/D|I|P|P/R(G)	C:Carbamidomethylation	109.92	514.7641	1028.519	0.0016	1.5	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
925	dirMS_041712_NAR_40mM_minus2.11962.11962.3	3	18.38	0	2.64E+05		(K)DAGEGL	(K)D A|G|E/G L/L A/V/Q I/T D/P E G K\P K(K)		153.95	646.6785	1938.018	0.0031	1.6	4.32	283472.4	5.71	HUMAN	P21333	Filamin-A
926	dirMS_041712_NAR_50mM_minus2.15712.15712.3	3	18.38	0	2.54E+05	M460m	(R)ISIEmN	(R)I/S|I/E/m N G T L E/D Q L/S H L/K(Q)	m:Oxidized methionine	157.28	648.6635	1927.979	15.9966	0.9	4.65	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
927	dirMS_041712_NAR_50mM_minus2.9254.9387.3	3	18.38	1	6.52E+05		(K)VTVAGL	(K)V/T|V|A|G/L/A|G K/D/P V Q/C S R(D)	C:Carbamidomethylation	121.4	553.2936	1657.869	-0.0028	-1.7	8.72	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
928	dirMS_041712_NAR_30mM_plus2.11976.11976.2	2	18.38	0	4.31E+05		(K)AYGGAY	(K)A/Y|G/G|A|Y D/V M S S K(H)		115.77	624.7816	1248.556	-0.0006	-0.5	5.88	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
929	dirMS_041712_NAR_40mM_plus2.18490.18945.3	3	18.38	0	8.75E+05		(R)DYLHLP	(R)D Y L H\L\P\P E\I|V|P/A/T L R(R)		176.45	578.6565	1733.959	-0.0035	-2	5.32	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
930	dirMS_041712_NAR_50mM_plus2.17429.17555.3	3	18.37	0	4.75E+05		(R)DLISHDE	(R)D L|I/S/H D E\M/F/S D I/Y K(I)		160.08	571.5992	1712.784	-0.0006	-0.3	4.22	19709.1	4.83	HUMAN	P13693	Translationally-controlled tumor protein
931	dirMS_041712_NAR_50mM_plus2.6002.6002.3	3	18.37	0	1.14E+05		(R)AGAAG	(R)A/G|A|A/G/G/P E E/E/A E K P V K(T)		95.73	513.9259	1539.765	-0.0018	-1.2	4.49	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
932	dirMS_041712_NAR_60mM_plus.7542.7542.2	2	18.37	1	7.47E+05		(R)VITEEEK	(R)V/I|T/E/E E K N F K(A)		97.92	618.8282	1236.647	0.0021	1.7	4.79	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
933	dirMS_041712_NAR_20mM_plus.18694.18694.2	2	18.36	0	2.87E+05		(K)LAVEAL	(K)L A V|E\A|L|S/S/L/D/G D L A G R(Y)		200.48	793.9214	1586.838	-0.0029	-1.8	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
934	dirMS_041712_NAR_30mM_plus2.21270.21393.2	2	18.36	0	3.90E+05		(R)VNQAI	(R)V N|Q|A|I|W/L|L|C/T G A R(E)	C:Carbamidomethylation	166.88	751.3976	1501.794	-0.0065	-4.3	9.72	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
935	dirMS_041712_NAR_120mM_minus.7948.8178.2	2	18.35	0	1.65E+07		(R)HQGVM	(R)H|Q|G\V|M|V|G\M|G Q|K(D)		98.12	586.2907	1171.571	0.0031	2.6	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
936	dirMS_041712_NAR_40mM_plus2.7485.7910.2	2	18.35	0	6.83E+05		(K)ASLENS	(K)A/S|L/E/N/S/L/R(E)		105.45	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
937	dirMS_041712_NAR_50mM_minus2.8902.8902.3	3	18.34	0	2.36E+05		(R)VMLGET	(R)V M/L/G/E T N/P A D S K/P G T I R(G)		118.3	595.9744	1785.916	-0.0077	-4.3	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
938	dirMS_041712_NAR_30mM_plus2.17985.18018.2	2	18.34	0	3.00E+05		(R)VNPALA	(R)V/N|P/A|L|A/E L/N L/R(S)		147.82	605.3509	1209.695	-0.0005	-0.4	5.97	20026.6	4.67	HUMAN	E9PIK5	Ribonuclease inhibitor (Fragment)
939	dirMS_041712_NAR_40mM_minus2.12094.12094.3	3	18.33	0	2.65E+05		(K)IAILTCP	(K)I A|I\L T/C/P F/E/P P K/P K(T)	C:Carbamidomethylation	155.12	537.6382	1610.898	0.0026	1.6	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
940	dirMS_041712_NAR_60mM_minus.14304.14549.3	3	18.33	0	3.65E+05		(R)VWYVS	(R)V/W|Y/V/S/N I/D/G T H I/A/K(T)		140.38	534.9461	1602.828	-0.0037	-2.3	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
941	dirMS_041712_NAR_20mM_plus.16614.16972.2	2	18.33	0	4.12E+05		(K)VQIAVA	(K)V Q|I|A|V|A/N/A Q E L/L Q/R(M)		187.28	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
942	dirMS_041712_NAR_30mM_plus2.22545.22643.3	3	18.33	0	1.19E+06		(R)LEGLTD	(R)L E\G\L\T D\E|I/N/F/L/R(Q)		175.42	473.9205	1419.748	-0.0009	-0.6	4.14	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
943	dirMS_041712_NAR_30mM_plus2.9547.10051.2	2	18.33	0	4.96E+05		(K)TAVCDI	(K)T A|V|C|D|I|P|P/R(G)	C:Carbamidomethylation	105.07	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
944	dirMS_041712_NAR_30mM_minus2.10957.10957.2	2	18.32	0	5.68E+05		(K)VAGQD	(K)V/A|G Q D/G S/V V/Q/F K(I)		113.77	617.824	1234.643	-0.0019	-1.5	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
945	dirMS_041712_NAR_120mM_plus.15314.15459.3	3	18.32	0	9.71E+05		(K)FYVHND	(K)F/Y/V/H/N D/I/F/R(Y)		133.88	404.2038	1210.6	-0.0035	-2.9	6.74	17042.2	9.19	HUMAN	E5RIZ6	Ras GTPase-activating protein-binding protein 1 (Fragment)
946	dirMS_041712_NAR_20mM_minus.14662.14662.2	2	18.3	0	2.10E+05		(K)LAVEAL	(K)L A\V E/A|L|S/S L/D|G D L A G R(Y)		201.28	793.922	1586.838	-0.0017	-1.1	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
947	dirMS_041712_NAR_30mM_minus2.9418.9499.2	2	18.3	0	1.28E+06		(K)SVEAAA	(K)S V|E|A|A|A/E|L/S A/K(D)		105.75	538.2838	1075.563	-0.0027	-2.5	4.53	12131.5	11.14	HUMAN	F5GXR3	Parathymosin
948	dirMS_041712_NAR_40mM_minus2.13737.13737.3	3	18.3	1	3.98E+05		(R)VTFSGL	(R)V/T|F/S|G L R\D T V/T P G E L L K(A)		164.73	611.6742	1833.012	-0.0036	-2	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
949	dirMS_041712_NAR_50mM_minus2.16863.16869.3	3	18.3	1	2.96E+05		(R)SELELTL	(R)S E|L/E/L/T/L/G/K L/E/Q V R(S)		163.73	538.9725	1614.906	-0.0032	-2	4.78	533778	5.74	HUMAN	Q15149	Plectin
950	dirMS_041712_NAR_60mM_minus.6708.7196.3	3	18.3	0	1.27E+06	M434m	(R)LESGm	(R)L/E|S/G m Q/N/M/S I|H/T K(T)	m:Oxidized methionine	97.23	497.9023	1475.698	15.9942	-0.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
951	dirMS_041712_NAR_120mM_plus.20098.20417.3	3	18.3	1	3.71E+06		(K)AAIDWF	(K)A A|I/D|W/F/D/G K E F/H/G N I I|K(V)		158.78	654.3334	1960.992	-0.0059	-3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
952	dirMS_041712_NAR_120mM_plus.6714.6765.3	3	18.3	0	4.95E+05		(K)NNRPSE	(K)N/N/R\P S E|G|P/L/Q/T R(L)		88.55	456.902	1368.698	-0.0064	-4.7	9.6	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
953	dirMS_041712_NAR_60mM_plus.5734.5734.3	3	18.3	1	1.91E+05		(R)SSGGGY	(R)S/S/G/G G/Y/S G D R S G G G/Y G G D\R(S)		88.07	583.5777	1748.722	-0.0033	-1.9	5.68	21563.9	10.01	HUMAN	K7EKB2	TATA-binding protein-associated factor 2N (Fragment)
954	dirMS_041712_NAR_30mM_plus2.16969.16969.2	2	18.29	0	5.39E+05	M256m	(R)SLDmDS	(R)S L/D\m/D S/I I|A E/V/K(A)	m:Oxidized methionine	142.17	668.8384	1320.671	15.998	2.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
955	dirMS_041712_NAR_30mM_plus2.8630.8753.2	2	18.29	0	7.03E+06		(K)ASLENS	(K)A/S|L/E|N/S/L/R(E)		99.25	445.2405	889.474	0	-0.1	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
956	dirMS_041712_NAR_50mM_minus2.16446.16446.3	3	18.28	0	4.54E+05		(R)VLDPFT	(R)V/L/D/P F/T/I K/P L D/R(K)		161.98	471.9411	1413.81	-0.0013	-0.9	5.93	63448.4	7.29	HUMAN	B4E022	Transketolase
957	dirMS_041712_NAR_60mM_minus.10683.10683.3	3	18.28	1	5.44E+05	M239m	(R)MSMKE	(R)M/S/M K E V D E Q m|L/N|V|Q N K(N)	m:Oxidized methionine	119.9	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
958	dirMS_041712_NAR_20mM_plus.10629.10629.3	3	18.28	0	8.07E+04		(K)TTTLSGT	(K)T T T L S G T A|P A/A/G V/V|P S R(V)		145.97	529.2872	1585.854	-0.0074	-4.6	9.41	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
959	dirMS_041712_NAR_50mM_plus2.12363.12551.3	3	18.28	1	1.70E+06		(R)SGKAPIL	(R)S G K A P I\L|I|A|T/D/V|A/S/R(G)		133.47	500.2911	1498.859	0	0	8.46	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
960	dirMS_041712_NAR_60mM_plus.12653.12866.3	3	18.28	1	1.08E+06		(R)DLDRIA	(R)D L/D R\I\A|G\Q|V/A/A/A/N K(K)		123.85	481.263	1441.776	-0.0013	-0.9	5.96	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
961	dirMS_041712_NAR_120mM_plus.5255.5378.3	3	18.27	0	4.05E+05		(R)YIDTEH	(R)Y/I|D/T/E/H/G/G/S Q A R(F)		80.98	445.2109	1333.613	0.005	3.8	5.32	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
962	dirMS_041712_NAR_20mM_plus.9866.9866.2	2	18.27	0	2.24E+05		(K)IVVVTA	(K)I/V|V|V/T A G V R(Q)		139.22	457.2945	913.583	-0.0012	-1.3	9.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
963	dirMS_041712_NAR_20mM_minus.13222.13222.2	2	18.26	0	2.34E+05		(R)GVVDSE	(R)G V|V/D|S/E D|I|P\L N/L/S\R(E)		183.02	757.3944	1513.786	-0.0041	-2.7	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
964	dirMS_041712_NAR_50mM_minus2.5832.5860.3	3	18.26	1	1.62E+06		(R)AQLGG	(R)A Q|L|G/G/P E A/A/K/S D/E T A A/K(-)		95.6	548.6119	1643.824	-0.0024	-1.4	4.68	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
965	dirMS_041712_NAR_120mM_plus.13369.13557.3	3	18.26	0	1.45E+06		(K)YNPTW	(K)Y/N|P/T/W/H/C I/V G/R(N)	C:Carbamidomethylation	123.37	468.2345	1402.669	0.0205	14.6	8.75	10536.9	6.9	HUMAN	P63167	Dynein light chain 1, cytoplasmic
966	dirMS_041712_NAR_30mM_plus2.15319.15464.2	2	18.26	0	4.57E+05		(R)MAGAI	(R)M/A|G|A|I/A/Q/G L/I/R(A)		133.38	550.816	1100.624	0.0002	0.2	9.5	4449.1	11.42	HUMAN	F8WEI0	Pyrroline-5-carboxylate reductase 3
967	dirMS_041712_NAR_30mM_plus2.17062.17558.2	2	18.26	0	1.21E+06		(R)MNVLA	(R)M/N|V|L/A/D/A/L/K(S)		143.63	487.7743	974.534	0.0074	7.6	5.59	27396	9.9	HUMAN	H3BN98	Uncharacterized protein (Fragment)
968	dirMS_041712_NAR_30mM_plus2.20053.20053.2	2	18.26	0	2.32E+05		(K)LALFQA	(K)L/A|L/F/Q A/I/G K(E)		158.63	480.795	960.588	-0.005	-5.2	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
969	dirMS_041712_NAR_30mM_plus2.22861.22959.2	2	18.26	0	1.84E+06		(R)GFGFVL	(R)G/F|G|F/V/L|F/K(E)		179.85	457.76	914.514	-0.0007	-0.8	8.75	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
970	dirMS_041712_NAR_50mM_plus2.18653.18653.3	3	18.26	0	3.54E+05		(R)LLLDGA	(R)L L|L/D G A/P/L/I A I H K(A)		165.82	458.622	1373.852	-0.0001	0	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
971	dirMS_041712_NAR_30mM_plus2.9565.9565.2	2	18.25	0	3.57E+05		(R)LLTYNA	(R)L/L/T/Y/N/A A/R(L)		104.33	461.2586	921.515	-0.0053	-5.8	8.75	36309.7	5.86	HUMAN	B4DQ51	Short/branched chain-specific acyl-CoA dehydrogenase, mitochondrial
972	dirMS_041712_NAR_50mM_plus2.9483.9862.3	3	18.25	0	2.45E+06		(K)GIVEFAS	(K)G I|V|E/F/A S/K P A A/R(K)		118.82	415.9028	1245.695	-0.0012	-0.9	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
973	dirMS_041712_NAR_20mM_minus.8911.9148.2	2	18.24	0	1.86E+06		(K)LVSESSD	(K)L/V|S|E/S/S D\V/L/P K(-)		139.67	587.321	1173.636	-0.0014	-1.2	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
974	dirMS_041712_NAR_30mM_minus2.19883.20040.2	2	18.24	0	2.49E+06		(K)EIIDLVL	(K)E I|I|D|L|V/L/D/R(I)		167.68	543.3132	1085.62	-0.001	-0.9	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
975	dirMS_041712_NAR_50mM_minus2.13163.13214.3	3	18.24	0	3.97E+05		(K)VTHAVV	(K)V T H\A V\V\T\V|P/A/Y/F/N D/A Q/R(Q)		143.42	629.9954	1887.971	0.0005	0.3	6.71	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
976	dirMS_041712_NAR_50mM_minus2.16807.16807.3	3	18.24	1	2.99E+05		(R)SELELTL	(R)S E|L/E/L/T/L/G K L E/Q V R(S)		163.72	538.9725	1614.906	-0.0032	-2	4.78	533778	5.74	HUMAN	Q15149	Plectin

977	dirMS_041712_NAR_20mM_plus.14128.14128.2	2	18.24	0	7.05E+04	M313m	(R)TVQSLEI	(R)T V|Q|S L/E|I D L/D S m R(N)	m:Oxidized methionine	169.18	761.8738	1506.747	15.9935	-0.9	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
978	dirMS_041712_NAR_30mM_plus2.16361.16530.2	2	18.24	0	7.76E+04		(K)AELNEFL	(K)A E|L|N/E|F/L/T/R(E)		137.2	546.7844	1092.568	-0.0069	-6.3	4.53	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
979	dirMS_041712_NAR_30mM_plus2.7671.7718.2	2	18.24	0	9.82E+05		(R)VLEEGS	(R)V/L|E|E/G S/V/E/A/R(T)		94.18	544.7829	1088.558	0.0003	0.3	4.25	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
980	dirMS_041712_NAR_50mM_plus2.13226.13226.3	3	18.24	1	9.66E+05		(R)ELNITAA	(R)E L/N|I/T/A/A\K/E I E/V/G G G R(K)		137.7	552.9671	1656.892	-0.0048	-2.9	4.79	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
981	dirMS_041712_NAR_60mM_plus.20144.20144.3	3	18.24	0	2.36E+05		(K)ALSAIAD	(K)A L|S A/I A D/L/L/T/N E H E/R(V)		165.23	551.6246	1652.86	-0.001	-0.6	4.65	105417.2	6.41	HUMAN	C9JZR2	Catenin delta-1
982	dirMS_041712_NAR_20mM_plus.16162.16180.2	2	18.23	0	4.91E+05		(K)DAGTIA	(K)D A|G\T|I/A|G/L/N/V/L/R(I)		183.63	600.3422	1199.674	0.0029	2.4	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
983	dirMS_041712_NAR_30mM_plus2.11385.11537.2	2	18.23	0	4.41E+05		(R)FASGGC	(R)F/A|S|G/G/C/D N L|I/K(L)	C:Carbamidomethylation	113.55	591.286	1181.562	0.0028	2.4	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
984	dirMS_041712_NAR_30mM_plus2.7454.7455.2	2	18.23	0	1.02E+07		(K)AGFAGD	(K)A/G|F|A|G/D/D/A/P/R(A)		93.67	488.7269	976.448	-0.0018	-1.8	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
985	dirMS_041712_NAR_50mM_minus2.7106.7106.3	3	18.22	0	1.07E+05		(R)VGQAVD	(R)V/G|Q/A/V D V/V/G Q/A G K P K(T)		107.38	484.9436	1452.817	-0.0007	-0.5	8.56	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
986	dirMS_041712_NAR_30mM_plus2.22026.22026.2	2	18.22	0	1.56E+05		(R)QSSFALL	(R)Q S/S F/A/L/L/G/D L T K(A)		170.63	640.3472	1279.689	-0.0021	-1.7	5.84	46579.3	4.96	HUMAN	E5RI07	Transportin-1
987	dirMS_041712_NAR_30mM_plus2.7504.7520.2	2	18.22	0	4.91E+05		(K)YQAECS	(K)Y/Q|A|E|C/S/Q/F K(A)	C:Carbamidomethylation	93.72	580.7556	1160.504	-0.0002	-0.1	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
988	dirMS_041712_NAR_50mM_minus2.9057.9057.3	3	18.21	0	7.04E+04		(R)EANALA	(R)E A N/A/L/A/A G H/P A Q A V/A I N A R(L)		119.77	615.6611	1844.973	-0.0038	-2.1	6.85	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
989	dirMS_041712_NAR_20mM_minus.10099.10099.2	2	18.2	0	1.24E+05		(R)YALYDA	(R)Y/A|L|Y|D/A T/Y E\T K(E)		150.82	669.3156	1337.626	-0.0021	-1.5	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
990	dirMS_041712_NAR_60mM_minus.9496.9496.3	3	18.2	0	3.19E+05		(R)QLSQAG	(R)Q L/S/Q/A/G S/F/S|D/G T H G G L R(Y)		113.52	573.2781	1717.825	-0.0055	-3.2	6.74	266161	5.68	HUMAN	E9PPU0	Epiplakin
991	dirMS_041712_NAR_50mM_plus2.17748.18021.3	3	18.2	0	2.13E+06		(K)LILPHVD	(K)L/I|L/P/H/V/D/I Q/L K(Y)		162.02	430.2706	1288.799	-0.0015	-1.2	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
992	dirMS_041712_NAR_30mM_minus2.18425.18425.2	2	18.19	0	4.47E+05		(R)QAQEYE	(R)Q/A/Q E|Y/E/A L L/N I/K(V)		154.67	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
993	dirMS_041712_NAR_60mM_minus.15367.15367.3	3	18.19	0	1.09E+06		(R)LSDQFH	(R)L/S|D Q F/H/D/I/L/I R(K)		145.58	452.9148	1356.727	0.0028	2.1	5.21	12284.6	4.89	HUMAN	H0Y9X3	Programmed cell death protein 6 (Fragment)
994	dirMS_041712_NAR_60mM_minus.9279.9335.3	3	18.19	1	6.00E+05		(K)LEAEIAT	(K)L/E|A/E/I/A T Y R/R(L)		111.95	407.8897	1221.659	-0.0041	-3.3	6.14	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
995	dirMS_041712_NAR_30mM_plus2.16008.16541.2	2	18.19	0	2.44E+06		(K)ICSWNV	(K)I/C|S|W/N/V/D/G L/R(A)	C:Carbamidomethylation	138.07	610.3003	1219.589	0.0045	3.7	5.84	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
996	dirMS_041712_NAR_30mM_plus2.21421.21421.2	2	18.19	0	3.50E+05		(K)FDGILGM	(K)F D|G\I|L/G/M A Y P R(I)		167.42	620.3199	1239.619	0.0135	10.9	5.83	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
997	dirMS_041712_NAR_60mM_plus.19593.19593.3	3	18.19	1	6.22E+05		(K)TVTAMD	(K)T/V|T/A/M D V/V/Y A/L K\R(Q)		161.05	489.6071	1466.804	0.0032	2.2	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
998	dirMS_041712_NAR_60mM_plus.9488.9488.3	3	18.19	0	1.08E+06		(R)IQFKPDD	(R)I/Q/F K/P D D/G T T/P/E/R(I)		107.58	501.923	1503.744	0.0106	7.1	4.56	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
999	dirMS_041712_NAR_30mM_minus2.13876.14023.2	2	18.18	0	2.89E+05		(R)IYVVDV	(R)I/Y|V|V/D|V|G\S E/P R(A)		129.45	617.3267	1233.647	-0.0013	-1	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
1000	dirMS_041712_NAR_30mM_minus2.19026.19044.2	2	18.18	0	9.29E+05		(K)MSIYQA	(K)M/S|I|Y/Q/A/M W/K(G)		158.9	579.2789	1157.548	0.0023	2	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
1001	dirMS_041712_NAR_30mM_plus2.9019.9019.3	3	18.18	0	4.28E+05		(R)SSQSSS	(R)S S\Q S S/S Q/Q|F/S/G/I G/R(S)		101.03	485.8992	1455.682	0.0008	0.5	9.47	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
1002	dirMS_041712_NAR_50mM_plus2.18409.18752.3	3	18.18	0	3.64E+07		(R)IHFPLAT	(R)I H F\P L A\T|Y|A|P/V/I/S A E K(A)		164.83	586.3252	1756.963	-0.0022	-1.2	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
1003	dirMS_041712_NAR_60mM_plus.6540.6570.3	3	18.18	0	3.97E+05		(R)VEAKPE	(R)V/E|A/K/P E V/Q/S/Q/P P R(V)		92.83	488.9311	1464.781	-0.0018	-1.2	6.11	54177.2	5.41	HUMAN	Q9UN86	Ras GTPase-activating protein-binding protein 2
1004	dirMS_041712_NAR_20mM_minus.12229.12535.2	2	18.17	0	9.01E+05	M185m	(K)LAVNm	(K)L/A|V|N/m/V|P F/P R(L)	m:Oxidized methionine	171.88	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1005	dirMS_041712_NAR_30mM_minus2.11371.11371.2	2	18.17	0	1.19E+06		(K)FSASGEL	(K)F S|A/S/G E/L/G/N G N I K(L)		114.97	647.3253	1293.643	0	0	6	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
1006	dirMS_041712_NAR_50mM_minus2.8453.8453.3	3	18.17	1	2.40E+05		(R)AGTGVD	(R)A G T/G/V/D N V D/L E/A/A/T R K(G)		116.53	539.6119	1616.824	-0.0027	-1.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
1007	dirMS_041712_NAR_60mM_plus.19594.19594.3	3	18.17	0	1.33E+05		(R)NSVSNF	(R)N S|V|S N/F/L/H/S L E R(G)		161.23	468.2401	1402.707	-0.0016	-1.1	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
1008	dirMS_041712_NAR_50mM_minus2.5320.5320.3	3	18.16	0	8.24E+05		(K)TATPQQ	(K)T A/T/P Q Q/A Q/E/V/H E K(L)		88.02	489.5768	1466.723	-0.0075	-5.1	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
1009	dirMS_041712_NAR_30mM_plus2.18681.18681.2	2	18.15	0	1.67E+05		(K)TVLSNV	(K)T/V|L|S|N V/Q\E E L D/R(M)		151	701.8633	1402.717	0.0021	1.5	4.14	45232	5.78	HUMAN	B4DZP4	Cytoplasmic dynein 1 light intermediate chain 2
1010	dirMS_041712_NAR_50mM_plus2.14390.14463.3	3	18.15	1	9.68E+05		(R)LAIKLPD	(R)L/A|I/K|L|P D D Q I/P K(T)		144.23	450.9373	1350.799	-0.0018	-1.3	5.96	26413	9.18	HUMAN	B1APP6	6-phosphofructokinase type C (Fragment)
1011	dirMS_041712_NAR_50mM_plus2.16471.16506.3	3	18.14	0	2.19E+05		(K)FTISDHP	(K)F/T|I/S D/H/P Q/P I D/P L L/K(N)		154.8	574.3119	1720.927	-0.0057	-3.3	5.21	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
1012	dirMS_041712_NAR_60mM_plus.14957.15120.3	3	18.14	0	7.90E+05		(R)SCTVNIM	(R)S C|T|V/N I|M/F/G/T/P Q E/H R(N)	C:Carbamidomethylation	135.17	592.9433	1776.816	-0.0003	-0.1	6.47	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
1013	dirMS_041712_NAR_30mM_minus2.15858.15963.2	2	18.13	0	3.84E+05		(R)FGLNVS	(R)F/G|L|N|V/S/S/I/S/R(K)		139.93	540.2895	1079.584	-0.0127	-11.7	9.75	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
1014	dirMS_041712_NAR_60mM_minus.16753.16951.3	3	18.13	1	3.66E+05		(K)ILLAELE	(K)I/L|L/A/E L E/Q L/K/G Q/G K(S)		154.27	513.9734	1539.911	-0.0048	-3.1	6.14	49709.6	5.19	HUMAN	B0YJC4	Vimentin
1015	dirMS_041712_NAR_60mM_minus.16880.17038.3	3	18.13	1	2.55E+05		(R)YRVPDV	(R)Y R V P D\V\L\V|A/D/P/P I A/R(L)		154.5	560.9843	1680.943	-0.0048	-2.9	5.96	96499.9	5.43	HUMAN	F5H6X6	Neutral alpha-glucosidase AB
1016	dirMS_041712_NAR_60mM_minus.17122.17337.3	3	18.13	1	7.39E+05		(K)QLDDLK	(K)Q/L|D/D/L K/V/E/L/S/Q/L/R(V)		156.18	519.6267	1556.864	0.0013	0.8	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
1017	dirMS_041712_NAR_20mM_plus.15795.15795.2	2	18.13	0	4.27E+05		(R)GVVDSE	(R)G V|V|D S/E|D|I/P L N/L/S/R(E)		179.57	757.3956	1513.786	-0.0017	-1.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
1018	dirMS_041712_NAR_30mM_plus2.18611.18611.2	2	18.13	0	1.90E+05		(-)SDVLELT	(-)S D V/L/E|L|T|D D N F E/S R(I)		150.83	820.3752	1639.745	-0.0015	-0.9	3.77	13747.3	6.8	HUMAN	H7BZJ3	Thioredoxin (Fragment)
1019	dirMS_041712_NAR_40mM_plus2.14909.14909.3	3	18.13	1	7.65E+05		(R)VCENIPI	(R)V/C|E/N\I|P I V L C G N K V D|I K(D)	C:Carbamidomethylation	154.7	657.6841	1971.04	-0.0024	-1.2	6.04	14844.8	5.89	HUMAN	B4DV51	GTP-binding nuclear protein Ran
1020	dirMS_041712_NAR_50mM_plus2.21745.21761.3	3	18.13	1	2.38E+05		(K)LGFAGL	(K)L/G|F/A/G/L/V Q/E I/S F G T T K D K(M)		184.83	637.6781	1911.022	-0.0025	-1.3	6.07	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
1021	dirMS_041712_NAR_60mM_plus.16659.16865.3	3	18.13	1	1.13E+06		(R)ELISNAS	(R)E L|I/S/N/A/S/D|A L D/K I R(L)		144.67	515.6144	1544.828	0.0008	0.5	4.56	5582.4	4.81	HUMAN	F8W026	Endoplasmin (Fragment)
1022	dirMS_041712_NAR_30mM_minus2.7454.7510.2	2	18.12	0	4.30E+05		(R)VLADPSI	(R)V/L|A|D|P S D/D/T K(G)		95.23	530.7694	1060.516	0.0158	14.9	3.93	266161	5.68	HUMAN	E9PPU0	Epiplakin
1023	dirMS_041712_NAR_30mM_minus2.9745.9745.2	2	18.12	0	1.91E+05	M129m	(K)ILYSQCG	(K)I L|Y/S/Q/C G D/V/m R(A)	C:Carbamidomethylation m:Oxid	107.67	679.3145	1341.629	15.9928	-1.6	5.83	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
1024	dirMS_041712_NAR_20mM_plus.10453.10527.2	2	18.12	0	2.32E+05		(R)AQIFAN	(R)A Q|I|F|A|N/T V/D/N A R(I)		145.25	660.3343	1319.67	-0.0089	-6.8	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1025	dirMS_041712_NAR_20mM_plus.13661.13850.2	2	18.12	0	2.77E+05		(R)GDLGIEI	(R)G D/L|G/I|E|I|P/A E/K(V)		166.72	571.3075	1141.61	-0.0022	-1.9	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
1026	dirMS_041712_NAR_30mM_plus2.13439.13584.2	2	18.12	0	1.53E+06		(R)LSESQLS	(R)L/S|E/S/Q/L/S F R(R)		124.13	533.777	1066.553	-0.006	-5.7	6	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
1027	dirMS_041712_NAR_30mM_plus2.17628.17852.2	2	18.12	0	6.11E+05		(K)NSLESYA	(K)N S|L|E|S|Y/A/F/N M K(A)		146.15	652.303	1303.599	0	0	6	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
1028	dirMS_041712_NAR_50mM_plus2.16208.16208.3	3	18.12	0	2.89E+05		(K)ACQSIYF	(K)A C|Q/S I/Y/P L/H/D V F V R(K)	C:Carbamidomethylation	154.4	568.9562	1704.853	0.0014	0.8	6.79	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
1029	dirMS_041712_NAR_50mM_plus2.7423.7604.3	3	18.12	1	2.39E+06		(K)GAVAED	(K)G A/V|A|E/D/G D E/L R T E/P E/A K(K)		105.58	596.2908	1786.845	0.0125	7	4.08	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
1030	dirMS_041712_NAR_60mM_plus.11513.11746.3	3	18.12	1	1.90E+06		(R)LMEEIM	(R)L/M|E/E/I/M/S E K/E/N K(T)		118.2	494.2424	1480.702	0.0105	7.1	4.49	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
1031	dirMS_041712_NAR_60mM_plus.6514.7111.3	3	18.12	1	3.15E+06		(K)IQDKEGI	(K)I Q|D K E G|I|P/P/D/Q Q R(L)		94	508.5982	1523.781	-0.0012	-0.8	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
1032	dirMS_041712_NAR_20mM_minus.10702.10888.2	2	18.11	0	4.20E+05		(K)DVNAAI	(K)D V|N|A/A/I/A A/I/K(T)		155.98	493.287	985.568	-0.0009	-1	5.84	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
1033	dirMS_041712_NAR_50mM_minus2.9302.9407.3	3	18.11	1	3.41E+05		(K)LLEDKN	(K)L/L|E/D/K/N/G E|V/Q N L A V K(C)		121.45	557.3071	1669.912	-0.0052	-3.1	4.68	6116.1	5.2	HUMAN	F5H6I6	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
1034	dirMS_041712_NAR_120mM_plus.12294.12719.4	4	18.11	2	9.28E+05		(K)KGTVEG	(K)K\G T V\E|G\F\E|P/A/D/N K/C L L/R(A)	C:Carbamidomethylation	118.9	484.2468	1933.98	-0.0147	-7.6	6.18	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
1035	dirMS_041712_NAR_60mM_plus.13078.13419.3	3	18.11	1	8.86E+05		(R)VIDRELY	(R)V/I|D/R E\L\Y|Q/Q|L/Q/R(G)		125.78	520.952	1560.849	-0.0078	-5	6.04	533778	5.74	HUMAN	Q15149	Plectin
1036	dirMS_041712_NAR_120mM_minus.14026.14527.4	4	18.1	2	5.90E+06		(K)VLAGDK	(K)V L|A/G/D/K/N/F/I/T A E E L R/R(E)		131.72	458.7498	1832.003	-0.0251	-13.7	6.15	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
1037	dirMS_041712_NAR_50mM_minus2.12421.12940.3	3	18.1	1	7.56E+06		(R)IQLVEEE	(R)I/Q|L|V/E E/E/L D/R A Q E/R(L)		140.42	576.6348	1727.892	-0.0024	-1.4	4.25	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
1038	dirMS_041712_NAR_40mM_plus2.7770.7770.2	2	18.1	0	5.58E+04		(R)VIGSGCI	(R)V/I|G S/G/C N L/D/S/A R(F)	C:Carbamidomethylation	105.37	624.8021	1248.6	-0.0032	-2.6	5.81	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
1039	dirMS_041712_NAR_60mM_plus.21515.21674.3	3	18.1	0	9.30E+06		(R)LHFFMP	(R)L H\F\F M|P G|F|A|P|L/T S R(G)		180.4	540.9492	1620.835	-0.0025	-1.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1040	dirMS_041712_NAR_30mM_minus2.19454.19730.2	2	18.09	0	2.68E+06		(K)EGLLLW	(K)E G\L|L|L|W/C/Q/R(K)	C:Carbamidomethylation	162.88	587.8058	1174.604	0.0006	0.5	6.1	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
1041	dirMS_041712_NAR_40mM_plus2.12292.12292.2	2	18.09	0	1.06E+05		(R)VLQALE	(R)V/L|Q/A/L\E\G L/K(M)		138.8	485.8002	970.593	0	0	5.97	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
1042	dirMS_041712_NAR_60mM_minus.11193.11333.3	3	18.08	1	3.02E+06		(R)MQKEIT	(R)M Q/K E I T/A|L|A/P/S T M K(I)		123.32	516.9421	1548.812	-0.0007	-0.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
1043	dirMS_041712_NAR_30mM_plus2.9689.9854.2	2	18.08	0	7.94E+05		(K)EAESSPF	(K)E\A|E|S/S/P/F/V/E/R(L)		105.18	575.7726	1150.537	0.0004	0.4	4.25	92752.5	4.76	HUMAN	P14625	Endoplasmin
1044	dirMS_041712_NAR_50mM_plus2.18467.18808.3	3	18.08	1	9.58E+06		(R)LFVGNLI	(R)L/F|V\G/N/L/P A D/I/T E D E F K R(L)		166.67	655.3417	1964.012	-0.0018	-0.9	4.32	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
1045	dirMS_041712_NAR_60mM_plus.6762.6788.3	3	18.08	1	7.29E+05		(R)AQLGGF	(R)A Q|L|G/G/P E A|A/K S D E/T A\A/K(-)		93.87	548.6115	1643.824	-0.0036	-2.2	4.68	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
1046	dirMS_041712_NAR_30mM_minus2.14066.14231.2	2	18.07	0	3.27E+05		(K)FGVYDID	(K)F/G|V|Y/D/I/D|N K(T)		130.5	535.762	1070.515	0.0014	1.3	4.21	27142.4	5.34	HUMAN	E5RG68	Copine-3 (Fragment)
1047	dirMS_041712_NAR_60mM_minus.14940.15054.3	3	18.07	1	3.27E+05	M557m	(K)mFGIDR	(K)m/F|G/I/D/R D A\I/A/Q/A V/R(G)	m:Oxidized methionine	143.58	526.9353	1562.811	15.9806	-9.1	5.71	63448.4	7.29	HUMAN	B4E022	Transketolase
1048	dirMS_041712_NAR_30mM_plus2.11053.11176.2	2	18.07	0	7.00E+05		(K)TVSPALI	(K)T V|S|P/A/L/I/S/R(F)		111.05	472.2823	943.557	0.0002	0.2	9.41	50425	5.53	HUMAN	H0YH27	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
1049	dirMS_041712_NAR_40mM_plus2.17423.17423.3	3	18.07	1	3.09E+05		(K)TGISDVF	(K)T/G\I/S/D\V/F/A K N/D L/A V V D|V R(I)		169.3	640.3451	1919.023	-0.0025	-1.3	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
1050	dirMS_041712_NAR_50mM_plus2.16121.16162.3	3	18.07	0	1.05E+06		(R)LSFQHD	(R)L/S/F Q H D\P E/T|S/V/L/V/L/R(K)		152.42	580.9801	1740.928	-0.0022	-1.2	5.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
1051	dirMS_041712_NAR_60mM_plus.12979.12979.3	3	18.07	1	1.36E+06		(K)NQVAM	(K)N Q|V|A\M|N/P T N T V/F D A K/R(L)		124.48	602.6367	1805.896	-0.0007	-0.4	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
1052	dirMS_041712_NAR_20mM_minus.12264.12387.2	2	18.06	0	9.88E+05	M313m	(R)TVQSLEI	(R)T V|Q|S/L|E|I D/L/D/S m R(N)	m:Oxidized methionine	171.08	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1053	dirMS_041712_NAR_60mM_minus.17179.17179.3	3	18.06	1	3.11E+05		(K)DANAKL	(K)D A/N/A\K L S E|L/E/A|A/L/Q R(A)		156.03	543.6239	1628.86	-0.0031	-1.9	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1054	dirMS_041712_NAR_120mM_plus.12737.13213.3	3	18.06	1	2.42E+06		(R)GYVKEQ	(R)G Y|V/K/E/Q|F/A/W/R(H)		121.9	428.5561	1283.653	0.0006	0.5	8.59	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
1055	dirMS_041712_NAR_20mM_plus.8083.8083.2	2	18.06	0	4.16E+05	M239m	(K)EVDEQm	(K)E V/D E/Q m L/N|V/Q/N/K(N)	m:Oxidized methionine	125.1	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
1056	dirMS_041712_NAR_30mM_plus2.11137.11563.2	2	18.06	0	1.70E+06		(K)LVLVGD	(K)L/V|L|V|G/D/G G/T/G K(T)		112.93	508.2931	1015.578	0.0007	0.7	5.84	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
1057	dirMS_041712_NAR_30mM_plus2.16940.17116.2	2	18.06	0	5.93E+05	M256m	(R)SLDmDS	(R)S L|D\m/D|S/I/I\A E/V/K(A)	m:Oxidized methionine	142.28	668.8384	1320.671	15.998	2.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
1058	dirMS_041712_NAR_30mM_plus2.9840.9879.2	2	18.06	1	1.01E+05		(K)AIYKGP	(K)A I|Y/K/G\P G S E|A|G|P(-)		105.18	573.7938	1146.579	0.0014	1.2	6.04	30492.9	5.26	HUMAN	P21964	Catechol O-methyltransferase
1059	dirMS_041712_NAR_50mM_minus2.7332.7393.3	3	18.05	1	1.43E+05		(R)VLVNDA	(R)V/L|V|N/D A Q/K|V/T/E/G Q Q E/R(L)		108.8	605.3171	1813.94	-0.0035	-1.9	4.68	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
1060	dirMS_041712_NAR_30mM_minus2.12049.12329.2	2	18.04	0	2.33E+05		(R)EYQELM	(R)E/Y/Q/E/L/M/N/V/K(L)		117.8	577.2825	1153.556	0.0019	1.7	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1061	dirMS_041712_NAR_20mM_plus.18093.18093.3	3	18.04	0	1.36E+05		(R)AILVDLE	(R)A I L V D L/E/P/G/T M/D S V R(S)		196.55	539.2833	1615.836	-0.0006	-0.4	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
1062	dirMS_041712_NAR_30mM_plus2.18420.18420.2	2	18.04	0	1.65E+05		(K)QFLSQFI	(K)Q F\L|S/Q/F/E/M Q S R(K)		150.25	700.8358	1400.663	0.0016	1.2	6	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
1063	dirMS_041712_NAR_30mM_plus2.7430.7457.2	2	18.04	0	7.06E+05		(K)GPSSVEI	(K)G/P|S|S/V/E/D|I|K(A)		93.43	466.2425	931.473	0.0046	5	4.37	32745.6	4.64	HUMAN	P06748	Nucleophosmin
1064	dirMS_041712_NAR_50mM_plus2.16047.16047.3	3	18.04	1	7.23E+05		(R)EGLTSIE	(R)E G/L/T/S/I|E E/V T K N L Q/K(F)		152.15	563.6357	1688.907	-0.014	-8.3	4.79	533778	5.74	HUMAN	Q15149	Plectin
1065	dirMS_041712_NAR_50mM_plus2.9540.9540.3	3	18.04	1	1.58E+05		(R)LGGSPF	(R)L/G/G S|P/F G|P A G/T G K T E S V K(A)		117.22	563.9657	1689.881	0.0019	1.1	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
1066	dirMS_041712_NAR_30mM_minus2.11101.11152.2	2	18.03	0	6.60E+05		(K)VAGQD	(K)V/A|G|Q|D|G S V V/Q|F/K(I)		114.03	617.824	1234.643	-0.0019	-1.5	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
1067	dirMS_041712_NAR_30mM_plus2.10629.10630.2	2	18.03	0	2.32E+05		(K)VLEEAN	(K)V/L|E/E|A|N Q|A|I|N|P K(L)		109.18	663.3575	1325.706	0.0018	1.3	4.53	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
1068	dirMS_041712_NAR_50mM_plus2.14284.14401.3	3	18.03	0	1.56E+06		(K)SLTNDW	(K)S L|T/N/D/W/E/D H L A V/K(H)		143.63	509.9193	1527.744	-0.0005	-0.3	4.53	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
1069	dirMS_041712_NAR_50mM_plus2.20512.20532.3	3	18.03	1	1.87E+05		(K)SYLNMD	(K)S Y|L/N/M/D/A I/M/E/A/I/K K(T)		176.7	542.9473	1626.823	0.0044	2.7	5.79	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
1070	dirMS_041712_NAR_20mM_minus.9640.9793.2	2	18.02	0	3.36E+05		(K)IGGIGTV	(K)I/G|G|I|G/T/V/P V G R(V)		147.47	513.3075	1025.61	-0.0025	-2.4	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
1071	dirMS_041712_NAR_30mM_minus2.9205.9205.2	2	18.02	0	2.85E+06		(R)VIGSGCI	(R)V/I|G\S/G/C/N L/D/S/A/R(F)	C:Carbamidomethylation	104.52	624.8035	1248.6	-0.0004	-0.3	5.81	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
1072	dirMS_041712_NAR_120mM_plus.20101.20528.3	3	18.02	1	3.71E+06		(K)AAIDWF	(K)A/A|I|D\W/F/D/G K E/F H G N\I I/K(V)		158.78	654.3334	1960.992	-0.0059	-3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
1073	dirMS_041712_NAR_60mM_plus.7790.7915.3	3	18.02	1	1.79E+06		(R)YLAEVA	(R)Y/L|A/E/V/A/T/G E/K R(A)		99.27	412.8904	1236.658	-0.0016	-1.3	6.14	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
1074	dirMS_041712_NAR_30mM_minus2.10934.11153.2	2	18.01	0	6.66E+05		(K)VAGQD	(K)V A|G Q|D/G/S/V/V/Q/F/K(I)		114.02	617.824	1234.643	-0.0019	-1.5	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
1075	dirMS_041712_NAR_40mM_plus2.9046.9046.2	2	18.01	0	8.93E+04		(K)GSDFDC	(K)G S/D/F/D|C E/L/R(L)	C:Carbamidomethylation	115.47	549.7296	1098.452	-0.0001	-0.1	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
1076	dirMS_041712_NAR_60mM_plus.16822.16822.3	3	18.01	0	1.02E+06		(K)TTISVAH	(K)T T/I/S/V/A H/L/L A A/R(Q)		144.5	418.2478	1252.737	-0.0083	-6.7	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
1077	dirMS_041712_NAR_120mM_plus.7136.7265.3	3	18	1	2.69E+06		(K)SLDEME	(K)S/L|D/E/M/E/K/Q Q/R(E)		91.23	421.8744	1263.6	0.0089	7	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
1078	dirMS_041712_NAR_120mM_minus.14499.14545.4	4	17.99	1	5.55E+05		(R)ETNLDSI	(R)E T N L D S\L/P/L/V/D/T/H S K/R(T)		133.47	456.992	1824.945	0.0012	0.6	5.38	53707.8	5.06	HUMAN	P08670	Vimentin
1079	dirMS_041712_NAR_120mM_minus.6640.6647.3	3	17.99	1	2.91E+05		(K)DSYVGD	(K)D S|Y/V/G/D/E A Q/S K R(G)		90.67	452.2134	1354.623	0.0023	1.7	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
1080	dirMS_041712_NAR_30mM_minus2.18231.18553.2	2	17.99	0	4.47E+05		(R)QAQEYE	(R)Q/A/Q/E|Y/E/A/L/L N/I/K(V)		154.67	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1081	dirMS_041712_NAR_20mM_plus.17980.17980.2	2	17.99	0	1.81E+05		(R)SLVPAAI	(R)S L|V|P A A/E/L/L E/S/R(V)		195.08	642.8613	1284.716	-0.0005	-0.4	4.53	533778	5.74	HUMAN	Q15149	Plectin
1082	dirMS_041712_NAR_30mM_plus2.8663.8728.2	2	17.99	0	3.15E+05		(K)TAEFQV	(K)T|A|E|F/Q/V/A/R(T)		99.3	461.2413	921.479	-0.0035	-3.8	5.66	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
1083	dirMS_041712_NAR_50mM_plus2.20960.21310.3	3	17.99	0	8.90E+06		(R)LHFFMP	(R)L H F\F\M|P/G\F|A|P|L/T S/R(G)		181.53	540.9498	1620.835	-0.0007	-0.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1084	dirMS_041712_NAR_30mM_minus2.6484.6730.2	2	17.98	0	4.22E+05		(K)VLEEEE	(K)V/L|E|E/E/E/Q/R(R)		90.3	516.2552	1031.5	0.0027	2.7	4.09	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
1085	dirMS_041712_NAR_20mM_plus.19047.19047.2	2	17.98	0	1.91E+05		(R)STGEAF	(R)S T G E A F/V/Q|F/A|S Q/E I/A/E K(A)		202.2	921.4477	1841.892	-0.0035	-1.9	4.25	24249.1	6.99	HUMAN	D6RBM0	Heterogeneous nuclear ribonucleoprotein H (Fragment)

1086	dirMS_041712_NAR_20mM_plus.8729.8729.2	2	17.98	0	2.45E+05		(R)VPPPPPI	(R)V/P|P/P/P P I A R(A)		130.62	472.2851	943.572	-0.0094	-10	9.72	32085.2	8.93	HUMAN	B4DY08	Heterogeneous nuclear ribonucleoproteins C1/C2
1087	dirMS_041712_NAR_60mM_plus.11254.11407.3	3	17.98	0	4.60E+06		(R)GSAVHC	(R)G S|A/V/H/Q/L/S/E/E/L R(C)		116.45	442.5666	1325.681	0.0044	3.4	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
1088	dirMS_041712_NAR_30mM_plus2.8424.8424.2	2	17.97	0	5.88E+05		(R)LGLGEG	(R)L/G|L|G/E/G A E E K(S)		98.35	501.7639	1002.51	0.0103	10.3	4.25	40096.8	9.24	HUMAN	C9JW69	Regulator of chromosome condensation (Fragment)
1089	dirMS_041712_NAR_60mM_plus.10456.10456.2	2	17.97	1	4.41E+06		(R)LQAEIEG	(R)L/Q|A E/I/E/G L K G Q/R(A)		112.33	671.3774	1341.748	-0.001	-0.7	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1090	dirMS_041712_NAR_30mM_minus2.14650.14650.2	2	17.96	0	1.01E+05		(R)LDIDSPP	(R)L/D|I/D/S/P/P/I T A R(N)		133.55	599.3249	1197.647	-0.0049	-4.1	4.21	5755.5	5.75	HUMAN	H3BN34	Pyruvate kinase isozymes M1/M2 (Fragment)
1091	dirMS_041712_NAR_50mM_minus2.10567.10567.3	3	17.96	0	1.60E+05		(R)LLELGPK	(R)L L|E|L/G P/K/P E V|A\Q Q T R(K)		128.52	560.3182	1678.949	-0.0086	-5.1	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
1092	dirMS_041712_NAR_50mM_minus2.5833.5833.3	3	17.96	0	1.31E+05		(R)AGAAGC	(R)A/G/A|A/G/G/P E/E E A E K P/V K(T)		95.32	513.9233	1539.765	-0.0096	-6.2	4.49	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
1093	dirMS_041712_NAR_50mM_plus2.13295.13558.3	3	17.95	0	1.58E+07		(R)LIDLHSP	(R)L/I|D/L H/S/P S E I/V/K(Q)		138.68	450.9258	1350.763	0.0001	0.1	5.32	7304.3	9.39	HUMAN	G3XAN0	40S ribosomal protein S20
1094	dirMS_041712_NAR_50mM_plus2.16567.16567.3	3	17.95	1	6.78E+06		(K)QLDDLK	(K)Q\L/D\D/L/K|V/E L/S\Q/L R(V)		155.75	519.6261	1556.864	-0.0005	-0.3	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
1095	dirMS_041712_NAR_50mM_plus2.19242.19419.3	3	17.95	0	8.48E+05		(R)DFNHIN	(R)D F/N H\I\N|V|E|L/S L/L/G K(K)		170.1	533.6223	1598.854	-0.0013	-0.8	5.32	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
1096	dirMS_041712_NAR_60mM_plus.14912.15009.3	3	17.95	1	1.52E+06		(R)VFDKDG	(R)V/F/D K D G N G\Y|I/S/A/A/E/L R(H)		134.8	585.6281	1754.871	-0.001	-0.6	4.56	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
1097	dirMS_041712_NAR_60mM_plus.15519.15537.3	3	17.95	1	8.88E+05		(R)LSAEERD	(R)L/S|A/E/E R D Q|L|L|P N L R(A)		137.98	551.9672	1653.892	-0.0048	-2.9	4.68	12056.4	6.28	HUMAN	P61457	Pterin-4-alpha-carbinolamine dehydratase
1098	dirMS_041712_NAR_50mM_minus2.11744.12118.3	3	17.94	1	6.40E+06		(K)KVPQVS	(K)K\V\P\Q\V S T|P/T|L|V/E V S R(N)		136.33	547.3172	1639.938	-0.0007	-0.4	8.75	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
1099	dirMS_041712_NAR_50mM_minus2.14571.14571.3	3	17.94	1	1.93E+05		(R)AEGAIA	(R)A/E|G/A/I/A G F R/D/P F/S/G/K(Q)		151.2	508.2599	1522.765	0.0003	0.2	6.12	266161	5.68	HUMAN	E9PPU0	Epiplakin
1100	dirMS_041712_NAR_30mM_plus2.19013.19013.2	2	17.94	0	3.45E+05		(R)LTAEDLF	(R)L/T|A/E\D L/F/E/A R(I)		153.22	582.796	1164.59	-0.0048	-4.1	4.14	533778	5.74	HUMAN	Q15149	Plectin
1101	dirMS_041712_NAR_50mM_plus2.13658.13837.3	3	17.94	0	1.76E+06		(K)DLAGCIH	(K)D L|A/G C I/H/G L S N V/K(L)	C:Carbamidomethylation	140.22	461.9061	1383.705	-0.0012	-0.8	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
1102	dirMS_041712_NAR_50mM_plus2.16408.16548.3	3	17.94	1	7.41E+05		(R)TIAQDY	(R)T I|A|Q/D/Y G V/L K/A/D/E G I S F R(G)		154.53	661.6783	1983.018	0.0022	1.1	4.56	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
1103	dirMS_041712_NAR_50mM_plus2.9952.10153.3	3	17.94	1	3.10E+06		(R)VLTVINC	(R)V/L|T|V/I/N Q/T Q K/E N L R(K)		119.9	552.6527	1655.944	-0.0003	-0.2	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
1104	dirMS_041712_NAR_60mM_plus.13236.13719.3	3	17.94	1	9.94E+05		(R)INVYYNI	(R)I/N|V|Y/Y|N E A/T G G K/Y V/P R(A)		128.25	615.3146	1843.934	-0.0045	-2.4	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
1105	dirMS_041712_NAR_30mM_minus2.12076.12602.2	2	17.93	0	4.46E+06		(R)EYQELM	(R)E Y/Q/E/L/M/N/V/K(L)		122.25	577.2825	1153.556	0.0019	1.7	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1106	dirMS_041712_NAR_30mM_plus2.13931.14014.2	2	17.93	0	3.99E+05		(K)IGPLGLS	(K)I/G|P|L/G/L/S/P K(K)		126.17	441.2762	881.545	-0.0004	-0.4	8.75	17989.4	9.77	HUMAN	P30050	60S ribosomal protein L12
1107	dirMS_041712_NAR_30mM_plus2.8641.8641.2	2	17.93	1	2.10E+05		(R)GVEEEEI	(R)G V|E/E|E/E|E/D/G E/M/R\E(-)		98.92	769.301	1537.596	-0.0011	-0.7	3.88	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F
1108	dirMS_041712_NAR_40mM_plus2.19232.19375.3	3	17.93	1	4.28E+05		(K)LLPLVSD	(K)L L|P/L/V/S/D/E V F I R D/V/A/K(V)		180.72	605.3503	1814.042	-0.0059	-3.2	4.56	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
1109	dirMS_041712_NAR_50mM_plus2.5727.5727.3	3	17.93	0	1.00E+05		(K)ATCAPQ	(K)A T/C|A/P Q/H G A/P G/P G/P\A D A S K(V)	C:Carbamidomethylation	92.7	597.2829	1789.829	0.0055	3.1	6.79	83264.1	6.04	HUMAN	E9PHF0	Filamin-A
1110	dirMS_041712_NAR_50mM_plus2.9828.9865.3	3	17.93	1	2.54E+05		(K)TTDMAF	(K)T/T|D|M/A/P S K/E/T E/M A L A K(D)		119.22	575.2802	1723.824	0.0019	1.1	4.68	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
1111	dirMS_041712_NAR_50mM_plus2.9896.9896.3	3	17.93	1	1.41E+05		(K)TCVFEKE	(K)T C|V/F E K E/N D|P/S V M R(S)	C:Carbamidomethylation	119.48	571.2629	1711.778	-0.0037	-2.1	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
1112	dirMS_041712_NAR_60mM_plus.9474.9495.3	3	17.93	0	4.79E+05		(K)ATAGDT	(K)A/T|A/G D/T/H/L/G/G E D F D/N R(L)		107.57	559.2488	1675.731	0.0012	0.7	4.22	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
1113	dirMS_041712_NAR_50mM_minus2.12759.12759.3	3	17.92	1	3.86E+05		(K)NTVELLV	(K)N T|V/E/L/L/V/E D K G N Q V Y R(C)		140.47	626.3309	1876.976	0.0018	1	4.68	258215.9	5.48	HUMAN	E7EN95	Filamin-B
1114	dirMS_041712_NAR_20mM_plus.16786.16786.2	2	17.92	0	3.08E+05		(K)VQIAVA	(K)V Q|I A|V/A/N/A Q E L/L/Q R(M)		187.02	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
1115	dirMS_041712_NAR_30mM_plus2.13387.13389.2	2	17.92	0	2.65E+05		(K)LSELEPG	(K)L/S\E|L|E|P G T\G D/L R(F)		123.58	643.8321	1286.659	-0.0017	-1.4	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
1116	dirMS_041712_NAR_60mM_plus.10085.10360.3	3	17.92	1	1.48E+06		(K)IFRDGEE	(K)I/F R D G E\E\A|G|A|Y/D/G P R(T)		111.47	551.593	1652.766	-0.0019	-1.1	4.32	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
1117	dirMS_041712_NAR_40mM_minus2.15008.15222.3	3	17.91	0	2.68E+06		(K)ALESPEF	(K)A/L|E|S|P/E/R P/F L/A I/L/G G A/K(V)		174.77	590.3353	1768.996	-0.0042	-2.4	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
1118	dirMS_041712_NAR_60mM_plus.15545.15545.3	3	17.91	1	4.40E+05		(R)IQLVEEE	(R)I/Q|L/V/E E E/L D/R A Q E/R(L)		137.98	576.6345	1727.892	-0.0033	-1.9	4.25	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
1119	dirMS_041712_NAR_120mM_plus.18196.18196.4	4	17.9	1	6.50E+05		(R)ILEFFGLI	(R)I/L/E/F/F/G L K/K E E C/P A V R(L)	C:Carbamidomethylation	148.63	484.7638	1936.036	-0.0027	-1.4	6.23	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
1120	dirMS_041712_NAR_30mM_plus2.12180.12240.2	2	17.9	0	9.10E+05		(K)EVDEQM	(K)E V|D/E/Q\M\L|N/V|Q/N/K(N)		117.03	723.8478	1446.689	-0.001	-0.7	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
1121	dirMS_041712_NAR_40mM_plus2.19956.19979.3	3	17.9	1	1.55E+06		(R)ELAILLG	(R)E L/A|I/L/L/G/M L/D/P A E/K D/E K(G)		189.1	629.003	1884.999	-0.0042	-2.3	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
1122	dirMS_041712_NAR_60mM_plus.18267.18392.3	3	17.9	1	9.23E+05		(K)EVNKFQ	(K)E V/N K F Q|M/A|Y/S N/L/L R(A)		152.83	571.6293	1712.879	-0.0055	-3.2	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
1123	dirMS_041712_NAR_120mM_minus.6262.6459.3	3	17.89	1	1.05E+06		(R)TEERAEI	(R)T/E|E/R A E|L|A/E/S/R(C)		89	430.8806	1290.628	-0.0012	-0.9	4.49	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
1124	dirMS_041712_NAR_30mM_plus2.20391.20546.2	2	17.89	0	3.12E+05		(R)FEELNAI	(R)F/E|E|L|N A/D/L/F/R(G)		161.05	627.3106	1253.616	-0.0022	-1.7	4.14	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
1125	dirMS_041712_NAR_50mM_plus2.17344.17536.3	3	17.89	1	7.36E+05		(K)SELVAM	(K)S E|L|V/A/M/L/E/E E E L R K(A)		159.72	559.2899	1675.857	-0.002	-1.2	4.32	18679.2	5.61	HUMAN	B4DWW1	ADP-ribosylation factor-like protein 1
1126	dirMS_041712_NAR_60mM_plus.10416.10691.3	3	17.89	1	1.83E+06		(R)YLAEFAT	(R)Y/L|A/E/F/A/T/G N D R K(E)		112.82	462.2281	1384.686	-0.0158	-11.4	6.07	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
1127	dirMS_041712_NAR_40mM_minus2.11403.11497.3	3	17.88	0	8.05E+05		(R)TIQVENS	(R)T I|Q|V/E N\S H L|I|L/T/G A G A L N K(V)		151	660.3663	1979.092	-0.0077	-3.9	6.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
1128	dirMS_041712_NAR_50mM_minus2.13809.13885.3	3	17.88	0	1.67E+06		(R)QVSASE	(R)Q V|S A/S E L H/T/S/G I/L/G/P E/T L R(D)		147.53	665.688	1995.051	-0.0011	-0.6	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
1129	dirMS_041712_NAR_120mM_plus.8746.8858.3	3	17.88	0	5.55E+05		(R)FACHSA	(R)F/A/C/H/S A/S/L/T\V/R(N)	C:Carbamidomethylation	99.62	416.8772	1248.615	0.0017	1.3	9.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
1130	dirMS_041712_NAR_50mM_plus2.14467.14570.3	3	17.88	0	1.06E+06		(R)ETHSALC	(R)E T/H S A L|G|P/A|L/Q/A/A/F K(L)		144.3	514.2745	1540.812	-0.0029	-1.9	6.85	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
1131	dirMS_041712_NAR_60mM_plus.17342.17361.3	3	17.88	1	1.26E+06		(R)FLQDYFI	(R)F/L|Q|D/Y/F/D/G N L K/R(Y)		148.32	505.9247	1515.759	0.0005	0.3	5.96	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
1132	dirMS_041712_NAR_60mM_plus.17392.17559.3	3	17.88	1	4.10E+05		(R)ISGLIYEE	(R)I/S|G|L|I/Y/E E T R G V/L/K(V)		148.38	526.634	1577.89	-0.0023	-1.4	6.14	11367.1	11.36	HUMAN	P62805	Histone H4
1133	dirMS_041712_NAR_30mM_minus2.19560.19560.2	2	17.87	0	4.67E+05		(R)ASLSLW	(R)A S/L/S/L|W Q/A/M/E K(G)		162.73	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
1134	dirMS_041712_NAR_50mM_minus2.15109.15109.3	3	17.87	1	2.85E+05		(K)VVEEAPS	(K)V V|E/E/A/P S I F L D/A/E T R R(A)		153.48	611.3243	1831.955	0.0035	1.9	4.41	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
1135	dirMS_041712_NAR_30mM_minus2.7367.7367.2	2	17.86	0	1.25E+05		(K)VQYPQS	(K)V Q|Y|P/Q S Q A/C K(M)	C:Carbamidomethylation	94.43	604.7902	1208.573	0.0003	0.2	8.56	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
1136	dirMS_041712_NAR_50mM_minus2.16990.17053.3	3	17.86	1	3.18E+05		(K)AILILDNI	(K)A I|L|I/L/D N D/G D/R L F/A K(Y)		165.27	558.6442	1673.922	-0.004	-2.4	4.43	18430.9	4.79	HUMAN	F8VS17	Coatomer subunit zeta-1
1137	dirMS_041712_NAR_20mM_plus.10967.11358.2	2	17.86	0	1.43E+06		(R)IVLQIDN	(R)I/V|L|Q|I|D/N A R(L)		149.23	521.3056	1041.605	-0.0012	-1.1	5.84	20842.9	5.32	HUMAN	C9JM50	Keratin, type I cytoskeletal 19 (Fragment)
1138	dirMS_041712_NAR_40mM_plus2.19948.19948.3	3	17.86	0	4.60E+05	M166m	(K)VLDFEHI	(K)V/L|D/F E H F\L|P m L Q T V A/K(N)	m:Oxidized methionine	187.63	635.3379	1888.004	15.9954	0.3	5.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
1139	dirMS_041712_NAR_50mM_plus2.18797.18839.3	3	17.86	0	4.20E+05		(R)AGLGSG	(R)A G/L|G|S/G/L/S\L/S/G L V/H P/E\L S R(S)		167.15	617.3412	1850.013	-0.004	-2.2	6.79	73325.2	9.19	HUMAN	F5H2A9	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial
1140	dirMS_041712_NAR_120mM_minus.10480.10950.3	3	17.85	1	1.50E+07		(R)VKYETEI	(R)V/K Y E/T|E|L/A/M/R(Q)		113.32	413.885	1239.64	0.0003	0.2	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1141	dirMS_041712_NAR_60mM_minus.11900.12067.3	3	17.85	1	3.03E+06	M72m	(R)TEmENE	(R)T/E|m/E N\E|F/V L I/K K(D)	m:Oxidized methionine	126.87	499.5941	1480.772	15.9962	0.8	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
1142	dirMS_041712_NAR_50mM_plus2.18274.18312.3	3	17.85	1	5.52E+05		(K)VIAATNI	(K)V/I|A/A/T N R\V D|I|L/D/P A L L R(S)		164.48	617.3645	1850.086	-0.0069	-3.7	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
1143	dirMS_041712_NAR_120mM_minus.7696.7842.3	3	17.84	1	2.74E+06	M281m	(R)SRAEAES	(R)S R\A E\A\E|S/m/Y/Q/I/K(Y)	m:Oxidized methionine	96.75	476.8951	1412.684	15.9869	-5.6	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
1144	dirMS_041712_NAR_30mM_minus2.11695.11753.2	2	17.84	0	9.21E+05		(K)EVDEQM	(K)E V|D/E|Q|M\L/N/V|Q/N K(N)		117.53	723.8476	1446.689	-0.0014	-1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
1145	dirMS_041712_NAR_40mM_minus2.9627.9627.2	2	17.84	0	1.24E+06		(R)VAPEEH	(R)V A/P E/E/H/P V\L L/T E A/P L N|P K(A)		139.8	977.5343	1954.064	-0.0031	-1.6	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
1146	dirMS_041712_NAR_50mM_minus2.16320.16342.3	3	17.84	1	1.47E+05		(R)LGLSTLG	(R)L/G|L|S|T/L/G E/L/K/Q N L S R(S)		160.87	543.6477	1628.933	-0.0044	-2.7	8.75	22294.4	5.26	HUMAN	O43399	Tumor protein D54
1147	dirMS_041712_NAR_30mM_plus2.6065.6065.2	2	17.84	0	8.14E+05		(R)NQGGY(	(R)N/Q|G G\Y|G/G|S S/S S/S S/Y/G S G R(R)		86.18	847.8524	1694.7	-0.0026	-1.5	8.59	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
1148	dirMS_041712_NAR_20mM_plus.17556.17556.2	2	17.83	0	1.61E+05	M74m	(R)mIAGQV	(R)m I|A\G/Q/V/L D/I|N L/A/A E P K(V)	m:Oxidized methionine	192.85	849.9568	1682.915	15.9918	-1.9	4.37	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
1149	dirMS_041712_NAR_30mM_plus2.14063.14239.2	2	17.83	0	9.48E+05	M320m	(K)YmACCL	(K)Y/m|A|C/C/L/L|Y/R(G)	C:Carbamidomethylation m:Oxid	127.2	633.2777	1249.553	15.9955	0.5	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
1150	dirMS_041712_NAR_40mM_plus2.9028.9047.2	2	17.83	0	8.93E+04		(K)GSDFDC	(K)G/S|D|F/D/C/E/L/R(L)	C:Carbamidomethylation	115.47	549.7296	1098.452	-0.0001	-0.1	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
1151	dirMS_041712_NAR_50mM_plus2.6707.6707.3	3	17.83	0	4.53E+04		(K)ITPAHD(	(K)I/T|P/A/H D/Q N/D Y/E V/G Q R(H)		100.07	581.6074	1742.809	-0.0016	-0.9	4.54	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
1152	dirMS_041712_NAR_30mM_minus2.8502.8585.2	2	17.82	0	4.89E+05	M281m	(R)AEAESm	(R)A/E|A|E/S/m/Y Q/I/K(Y)	m:Oxidized methionine	101.12	593.2765	1169.551	15.995	0.1	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
1153	dirMS_041712_NAR_50mM_minus2.12670.12670.3	3	17.82	1	3.98E+05		(K)NTVELLV	(K)N T/V/E/L L|V/E D K G N Q V Y R(C)		140.43	626.3309	1876.976	0.0018	1	4.68	258215.9	5.48	HUMAN	E7EN95	Filamin-B
1154	dirMS_041712_NAR_50mM_minus2.7045.7045.3	3	17.82	1	2.04E+05		(K)GAVAED	(K)G A|V/A|E/D G D E L R T E P E/A K(K)		106.92	596.2904	1786.845	0.0113	6.3	4.08	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
1155	dirMS_041712_NAR_40mM_plus2.16109.16109.3	3	17.82	0	4.11E+04		(K)VLISSLQ	(K)V L|I/S/S/L/Q D C L/H G I E/S/K(S)	C:Carbamidomethylation	161.47	600.3172	1798.937	0.0003	0.2	5.32	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
1156	dirMS_041712_NAR_40mM_plus2.8978.8978.2	2	17.82	0	1.19E+05		(R)GYSFTTT	(R)G/Y|S\F/T/T/T A E/R(E)		114.9	566.7672	1132.527	0.0002	0.2	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
1157	dirMS_041712_NAR_50mM_plus2.13705.14147.3	3	17.82	1	1.07E+07		(R)TEMENE	(R)T|E|M/E/N E|F/V/L I/K K(D)		141.2	494.262	1480.772	-0.0001	-0.1	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
1158	dirMS_041712_NAR_120mM_minus.10683.11147.3	3	17.81	0	9.56E+05		(R)GFCLPPI	(R)G F|C/L/P/P/H/C S/R(G)	C:Carbamidomethylation	113.55	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
1159	dirMS_041712_NAR_120mM_minus.8138.8283.4	4	17.81	2	2.31E+06		(K)KGAVAE	(K)K\G A\V\A\E/D/G/D/E L R T/E/P E/A/K(K)		99.28	479.4901	1914.94	-0.0018	-0.9	4.36	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
1160	dirMS_041712_NAR_30mM_plus2.7392.7419.2	2	17.81	0	1.53E+06		(R)FSTPEQ/	(R)F/S|T/P/E/Q A A/K(N)		93.63	489.7474	978.489	-0.0016	-1.6	6	64759.2	8.88	HUMAN	P14866	Heterogeneous nuclear ribonucleoprotein L
1161	dirMS_041712_NAR_50mM_plus2.8653.8655.3	3	17.81	0	4.30E+05		(R)AALAHS	(R)A A/L A H S E E\V|T|A/S Q V|A A|T K(T)		112.93	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
1162	dirMS_041712_NAR_30mM_minus2.9027.9088.2	2	17.8	0	3.74E+05		(K)IANPVE(	(K)I/A|N|P/V/E|G S T D/R(Q)		103.72	579.7876	1158.575	-0.007	-6.1	4.37	34267.8	9.05	HUMAN	B4DXP5	Poly(rC)-binding protein 2
1163	dirMS_041712_NAR_40mM_minus2.12871.13017.3	3	17.8	0	3.35E+05		(R)DVQIGD	(R)D V|Q|I|G/D/I/V/T/V/G E C R P L S K(T)	C:Carbamidomethylation	159.67	662.684	1986.033	0.005	2.5	4.56	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
1164	dirMS_041712_NAR_20mM_plus.16338.16462.2	2	17.8	0	1.09E+05		(K)FIIPNVV	(K)F/I|I|P/N V/V K(Y)		184.45	465.2935	929.582	-0.0021	-2.3	8.75	17529.3	9.3	HUMAN	F5GXY2	L-lactate dehydrogenase A chain (Fragment)
1165	dirMS_041712_NAR_30mM_minus2.19034.19034.2	2	17.79	0	9.18E+05		(K)MSIYQA	(K)M/S/I/Y/Q A M|W/K(G)		158.88	579.2789	1157.548	0.0023	2	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
1166	dirMS_041712_NAR_50mM_minus2.7123.7144.3	3	17.79	0	1.07E+05		(R)VGQAVI	(R)V/G/Q|A/V/D|V/V/G Q/A G K P K(T)		107.38	484.9436	1452.817	-0.0007	-0.5	8.56	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
1167	dirMS_041712_NAR_30mM_plus2.8673.8740.2	2	17.79	0	1.26E+06		(R)INISEGN	(R)I/N|I|S|E/G N|C/P E/R(I)	C:Carbamidomethylation	99.47	644.8007	1288.595	-0.0009	-0.7	4.53	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
1168	dirMS_041712_NAR_50mM_plus2.9944.9995.3	3	17.79	1	5.47E+05		(R)LMEEIM	(R)L/M|E/E/I/M/S E K/E/N K(T)		119.72	494.241	1480.702	0.0063	4.2	4.49	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
1169	dirMS_041712_NAR_60mM_plus.15502.15524.3	3	17.79	0	3.36E+05		(K)SKPGAA	(K)S K|P G A A\M\V|E|M/A/D/G Y/A/V D R(A)		137.83	623.2943	1867.868	0.0007	0.3	4.56	64759.2	8.88	HUMAN	P14866	Heterogeneous nuclear ribonucleoprotein L
1170	dirMS_041712_NAR_20mM_minus.13375.13483.2	2	17.77	0	6.91E+05		(K)DAGTIA(	(K)D A\G/T|I|A|G/L/N V L/R(I)		184.93	600.3403	1199.674	-0.0009	-0.8	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
1171	dirMS_041712_NAR_40mM_minus2.11083.11127.3	3	17.77	0	7.92E+05		(R)QVSASE	(R)Q V|S/A/S E/L H T S G I/L/G/P E T L R(D)		148.75	665.6822	1995.051	-0.0185	-9.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
1172	dirMS_041712_NAR_30mM_plus2.13306.13409.2	2	17.77	0	4.02E+05		(K)AFCGFEI	(K)A F|C|G\F|E D|P/R(T)	C:Carbamidomethylation	123.03	549.7374	1098.467	0.0002	0.2	4.37	533778	5.74	HUMAN	Q15149	Plectin
1173	dirMS_041712_NAR_30mM_plus2.18610.18610.2	2	17.77	0	2.24E+05		(R)GNPTVE	(R)G N|P T/V/E/V D L F T S K(G)		150.92	703.8613	1406.716	-0.0009	-0.6	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
1174	dirMS_041712_NAR_30mM_plus2.8139.8139.2	2	17.77	0	3.24E+05		(K)IAVAAQ	(K)I A|V/A/A Q/N C Y K(V)	C:Carbamidomethylation	96	569.2905	1137.572	0.0016	1.4	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
1175	dirMS_041712_NAR_40mM_minus2.15966.16010.3	3	17.76	0	1.60E+06	M166m	(K)VLDFEHI	(K)V L|D/F E H F\L|P m L Q/T V/A/K(N)	m:Oxidized methionine	187.72	635.3376	1888.004	15.9945	-0.2	5.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
1176	dirMS_041712_NAR_60mM_plus.12884.13004.3	3	17.76	0	1.05E+06		(K)GFVEFA/	(K)G F|V/E/F/A/A/K/P P A|R(K)		124.37	430.5686	1289.7	-0.0088	-6.9	8.75	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
1177	dirMS_041712_NAR_60mM_plus.15038.15244.3	3	17.76	0	5.71E+05		(K)LSMKPE	(K)L/S|M/K/P E/P/L/F/R(S)		135.85	406.5616	1217.671	-0.0008	-0.7	8.75	75482.2	6.34	HUMAN	D6RA32	Microtubule-associated protein 1B (Fragment)
1178	dirMS_041712_NAR_30mM_minus2.10575.10661.2	2	17.75	0	8.47E+05		(K)TGQEIP\	(K)T G|Q|E|I|P V/N V R(F)		111.63	556.8062	1112.606	-0.0007	-0.7	5.66	28051.5	4.98	HUMAN	J3QKT2	Cytosolic non-specific dipeptidase (Fragment)
1179	dirMS_041712_NAR_30mM_minus2.11862.11862.2	2	17.75	0	9.21E+05		(K)EVDEQM	(K)E V/D/E/Q M L|N/V/Q N/K(N)		117.53	723.8476	1446.689	-0.0014	-1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
1180	dirMS_041712_NAR_50mM_minus2.14688.14859.3	3	17.75	1	4.18E+05		(K)GCLELIK	(K)G C|L|E|L I\K E T/G\V|P/I/A/G R(H)	C:Carbamidomethylation	151.82	571.6494	1712.936	-0.0027	-1.6	6.14	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
1181	dirMS_041712_NAR_40mM_plus2.11002.11038.3	3	17.75	1	6.32E+04		(K)VAVVAG	(K)V/A|V|V|A/G|Y G D/V G K G C A Q A L/R(G)	C:Carbamidomethylation	131.05	630.9981	1890.985	-0.0057	-3	8.56	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
1182	dirMS_041712_NAR_50mM_plus2.9774.9880.3	3	17.75	0	1.92E+06		(R)EIVHIQA	(R)E/I V H I Q\A\G/Q/C|G/N Q I|G A/K(F)	C:Carbamidomethylation	119.02	608.3107	1822.923	-0.0053	-2.9	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
1183	dirMS_041712_NAR_50mM_minus2.5827.5939.3	3	17.74	1	1.62E+06		(R)AQLGGF	(R)A Q|L|G/G/P E/A/A/K S D E T A A/K(-)		95.6	548.6119	1643.824	-0.0024	-1.4	4.68	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
1184	dirMS_041712_NAR_20mM_plus.7655.7773.2	2	17.74	0	6.94E+05		(K)VIDDTNI	(K)V/I|D|D|T/N/I/T/R(L)		123.18	523.7766	1046.548	-0.0017	-1.7	4.21	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1185	dirMS_041712_NAR_30mM_plus2.16154.16154.2	2	17.74	0	2.79E+05		(K)MDQAII	(K)M/D/Q|A|I/I/F C R(T)	C:Carbamidomethylation	137.37	577.2809	1153.549	0.0053	4.6	5.59	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
1186	dirMS_041712_NAR_30mM_plus2.18712.18963.2	2	17.74	0	5.37E+05		(R)LIDFLES(	(R)L/I|D|F/L/E/S/G K(T)		152.02	511.2819	1021.556	0.0001	0.1	4.37	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
1187	dirMS_041712_NAR_60mM_plus.9705.9887.3	3	17.74	1	1.31E+06		(K)LAELKQE	(K)L/A|E/L/K/Q/E/C L A/R(G)	C:Carbamidomethylation	109.57	444.2368	1330.715	-0.0189	-14.2	6.14	6106	9.22	HUMAN	F8VS12	SAP domain-containing ribonucleoprotein
1188	dirMS_041712_NAR_120mM_minus.10925.11027.3	3	17.73	1	6.07E+05		(R)FYKNEG	(R)F/Y|K N E G/G/T|W S/V/E K(V)		113.78	515.5834	1544.738	-0.0023	-1.5	6.14	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
1189	dirMS_041712_NAR_20mM_plus.18660.18660.2	2	17.73	0	2.87E+05		(K)LAVEALS	(K)L A V\E/A/L|S S L/D G D L/A/G R(Y)		200.48	793.9214	1586.838	-0.0029	-1.8	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
1190	dirMS_041712_NAR_40mM_plus2.18357.18357.3	3	17.73	1	6.16E+04		(R)VLEALLP	(R)V/L|E/A L L/P L K/G L E E R(V)		174.47	527.3177	1579.942	-0.0032	-2	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
1191	dirMS_041712_NAR_50mM_plus2.10309.10384.3	3	17.73	1	1.53E+06		(K)VTVAGL	(K)V/T|V|A/G/L/A/G K/D/P V Q/C S R(D)	C:Carbamidomethylation	121.92	553.2933	1657.869	-0.0037	-2.2	8.72	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
1192	dirMS_041712_NAR_60mM_plus.10836.11129.3	3	17.73	1	6.41E+06		(R)QQEGFK	(R)Q Q/E/G F/K/G T/F/P/D/A R(E)		115.52	494.2424	1480.718	-0.0053	-3.6	6.07	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
1193	dirMS_041712_NAR_20mM_minus.12161.12161.2	2	17.72	0	1.06E+06	M313m	(R)TVQSLEI	(R)T V|Q S/L/E|I D L/D S m R(N)	m:Oxidized methionine	170.63	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1194	dirMS_041712_NAR_50mM_minus2.14931.15297.3	3	17.72	1	1.13E+06		(R)DVDFELI	(R)D V|D/F/E/L I/K V/E/G K(V)		154.02	464.5852	1391.742	-0.0006	-0.4	4.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon

1195	dirMS_041712_NAR_50mM_minus2.15612.15888.3	3	17.72	1	4.93E+05		(K)QGGLGF	(K)Q G G L/G/P\M N\I/P L/V/S/D/P K R(T)		157.5	593.6566	1778.958	-0.0029	-1.6	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
1196	dirMS_041712_NAR_50mM_minus2.16970.17157.3	3	17.72	0	1.33E+07		(R)IHFPLAT	(R)I H F\P L\A\T|Y|A|P/V/I/S A E K(A)		166.73	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
1197	dirMS_041712_NAR_120mM_plus.10712.10817.3	3	17.72	0	4.24E+05		(K)GSYVSIH	(K)G S|Y/V/S I/H/S/S G\F/R(D)		109.6	432.8823	1296.633	-0.0008	-0.6	8.75	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
1198	dirMS_041712_NAR_50mM_plus2.17471.17576.3	3	17.72	1	7.15E+05		(R)CITDPQ	(R)C|I|T/D/P Q T/G/L/C L/L/P L K E K(K)	C:Carbamidomethylation	160.15	662.6825	1986.04	-0.0069	-3.5	6.07	533778	5.74	HUMAN	Q15149	Plectin
1199	dirMS_041712_NAR_120mM_minus.12286.12808.3	3	17.71	1	3.70E+06		(K)VKLEAEI	(K)V K L E\A\E|I|A/T/Y/R(R)		123.3	431.5783	1292.721	-0.0005	-0.4	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1200	dirMS_041712_NAR_120mM_minus.19581.19642.3	3	17.71	0	7.14E+05		(R)NSVSNF	(R)N/S|V/S N/F/L/H/S L E/R(G)		162.22	468.2346	1402.707	-0.0181	-12.9	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
1201	dirMS_041712_NAR_30mM_minus2.12675.13014.2	2	17.71	0	7.94E+05		(K)LVIITAG	(K)L/V|I|I/T/A|G A/R(Q)		123.4	457.2948	913.583	-0.0006	-0.7	9.75	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
1202	dirMS_041712_NAR_40mM_minus2.11638.11940.3	3	17.71	1	2.86E+06		(R)IINEPTA	(R)I I\N|E/P T/A/A/A/I/A/Y G L D/K K(V)		153.08	596.6671	1787.99	-0.0034	-1.9	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
1203	dirMS_041712_NAR_50mM_minus2.17277.17289.3	3	17.71	1	8.80E+05		(K)IILDLISE	(K)I/I|L/D/L/I/S/E S P I K G/R(A)		167.65	518.6444	1553.926	-0.0075	-4.8	6.07	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
1204	dirMS_041712_NAR_60mM_plus.17408.17595.3	3	17.71	0	1.38E+06		(R)MGPLGL	(R)M/G|P|L/G/L D/H/M/A/S S I E/R(M)		148.47	538.5969	1613.777	-0.0013	-0.8	5.3	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
1205	dirMS_041712_NAR_30mM_minus2.18465.18465.2	2	17.7	0	1.20E+06		(R)DLTDYL	(R)D L|T/D|Y/L M/K(I)		155.48	499.7499	998.486	0.0062	6.2	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
1206	dirMS_041712_NAR_60mM_minus.15271.15542.3	3	17.7	1	4.74E+05		(R)LLDAQL	(R)L/L|D|A/Q|L|A T/G G L V C/P A R R(L)	C:Carbamidomethylation	146.02	604.3344	1810.996	-0.007	-3.8	9.6	266161	5.68	HUMAN	E9PPU0	Epiplakin
1207	dirMS_041712_NAR_30mM_plus2.22595.22612.2	2	17.7	0	1.01E+06		(R)FLTWILN	(R)F/L|T|W\I/L/N/R(Y)		175.88	531.8078	1062.61	-0.0012	-1.1	9.75	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
1208	dirMS_041712_NAR_40mM_plus2.15142.15142.3	3	17.7	0	3.07E+05		(K)GVTIIGP	(K)G V|T|I/I/G/P A T V/G G I K P G C F K(I)	C:Carbamidomethylation	156.13	624.683	1872.041	-0.0067	-3.6	10	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
1209	dirMS_041712_NAR_60mM_plus.13241.13241.3	3	17.7	1	2.80E+04		(K)AAAGKA	(K)A A/A/G/K A E L|E/L E\L/G R(I)		126.13	476.5985	1427.785	-0.0043	-3	4.79	533778	5.74	HUMAN	Q15149	Plectin
1210	dirMS_041712_NAR_20mM_plus.8342.8342.2	2	17.69	0	8.56E+04		(R)LAPEYE	(R)L A|P/E/Y E/A A/A T/R(L)		127.75	596.3035	1191.6	-0.0007	-0.6	4.53	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
1211	dirMS_041712_NAR_40mM_plus2.18217.18412.3	3	17.69	0	3.43E+05		(R)EAVELPL	(R)E A|V/E/L/P L/T/H F E L/Y K(Q)		173.8	563.6336	1688.889	-0.0032	-1.9	4.75	47479.5	5.09	HUMAN	P43686	26S protease regulatory subunit 6B
1212	dirMS_041712_NAR_50mM_minus2.11307.11475.3	3	17.68	0	1.47E+05		(K)IVLEDGT	(K)I/V|L|E/D G T L/H/V/T E/G S G R(Y)		133.15	561.6271	1682.871	-0.004	-2.4	4.65	62748.9	5.95	HUMAN	Q16555	Dihydropyrimidinase-related protein 2
1213	dirMS_041712_NAR_50mM_minus2.12464.12464.3	3	17.68	0	2.90E+05		(K)AASDIAI	(K)A/A/S D\I/A|M T E L/P P T H/P I R(L)		139.23	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
1214	dirMS_041712_NAR_50mM_minus2.12681.12736.3	3	17.68	0	2.42E+05		(K)FLSDPQ	(K)F/L|S/D/P Q/V/H/T V/L V E R(S)		140.57	547.2977	1639.88	-0.0017	-1	5.32	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
1215	dirMS_041712_NAR_50mM_minus2.8944.8944.3	3	17.68	1	1.16E+05	M88m	(K)DVDEAY	(K)D V|D E/A/Y m N K/V/E L E/S R(L)	m:Oxidized methionine	118.62	605.2817	1797.832	15.9982	1.8	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
1216	dirMS_041712_NAR_120mM_plus.21148.21365.4	4	17.68	1	1.33E+06		(R)DYLHLPI	(R)D Y L H/L|P|P/E I/V/P A T L R/R(S)		163.95	473.2689	1890.06	-0.0058	-3.1	6.75	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
1217	dirMS_041712_NAR_30mM_plus2.15648.15648.2	2	17.68	0	1.34E+06		(R)QITVND	(R)Q I|T V/N/D/L|P V G/R(S)		133.82	606.3403	1211.674	-0.0009	-0.8	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
1218	dirMS_041712_NAR_30mM_plus2.16488.16511.2	2	17.68	0	3.06E+05		(K)LLDLVQ	(K)L L|D\L|V|Q|Q|S/C N/Y K(Q)	C:Carbamidomethylation	139.12	740.8751	1480.746	-0.0035	-2.4	5.83	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
1219	dirMS_041712_NAR_50mM_plus2.18175.18446.3	3	17.68	1	5.52E+05		(K)VIAATNI	(K)V/I|A|A/T N R V D\I|L/D/P A L L/R(S)		164.48	617.3645	1850.086	-0.0069	-3.7	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
1220	dirMS_041712_NAR_120mM_minus.13297.13297.3	3	17.67	2	2.61E+05		(R)AQKDEE	(R)A Q/K/D/E E/K/M E|I/Q/E/I\Q L K(E)		126.68	654.0058	1960.006	-0.0027	-1.4	4.58	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
1221	dirMS_041712_NAR_30mM_minus2.12641.13113.2	2	17.67	0	2.03E+06		(K)IGGIGTV	(K)I/G|G|I|G/T/V|P V G R(V)		123.42	513.3086	1025.61	-0.0003	-0.3	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
1222	dirMS_041712_NAR_30mM_plus2.18129.18129.2	2	17.67	0	2.94E+05		(R)VNPALA	(R)V N/P A/L/A/E L/N L/R(S)		147.85	605.3509	1209.695	-0.0005	-0.4	5.97	20026.6	4.67	HUMAN	E9PIK5	Ribonuclease inhibitor (Fragment)
1223	dirMS_041712_NAR_30mM_plus2.23507.23551.2	2	17.67	0	4.18E+06		(R)IAIYELLF	(R)I/A|I|Y/E|L/L/F K(E)		191.57	555.3331	1109.661	-0.0016	-1.4	6	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
1224	dirMS_041712_NAR_40mM_plus2.12982.12982.3	3	17.67	1	9.95E+05		(K)TITLEVEI	(K)T I|T|L/E V/E/P S D T I E N V K A K(I)		143.45	663.0201	1987.059	-0.0136	-6.9	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
1225	dirMS_041712_NAR_60mM_minus.10726.11191.3	3	17.66	1	2.04E+06		(R)FPGQLN	(R)F/P/G/Q|L/N/A/D/L R\K(L)		121.02	420.2346	1258.69	-0.001	-0.8	8.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1226	dirMS_041712_NAR_20mM_plus.14630.14843.2	2	17.66	0	9.93E+04		(K)FLDGIYV	(K)F/L|D|G/I|Y/V/S E/K(G)		173.5	585.8066	1170.604	0.0018	1.5	4.37	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
1227	dirMS_041712_NAR_60mM_minus.13279.13481.3	3	17.65	1	5.13E+05	M313m	(R)RTVQSLI	(R)R T V\Q\S\L|E|I/D|L/D/S m R(N)	m:Oxidized methionine	134.52	560.2852	1662.848	15.9931	-1.1	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1228	dirMS_041712_NAR_20mM_plus.17111.17111.3	3	17.65	0	2.26E+05		(R)AIVAIEN	(R)A I\V/A I E/N/P A/D V/S/V/I/S S R(N)		188.93	580.9864	1740.949	-0.0044	-2.5	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
1229	dirMS_041712_NAR_30mM_minus2.9362.9458.2	2	17.64	0	1.72E+06	M406m	(R)EYQELm	(R)E Y/Q|E/L/m/N V/K(L)	m:Oxidized methionine	105.6	585.2783	1153.556	15.9935	-1.2	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1230	dirMS_041712_NAR_50mM_minus2.15493.15547.3	3	17.64	1	1.73E+05		(K)DVLFLK	(K)D V|L|F|L K/D C V/G/P/E/V E K(A)	C:Carbamidomethylation	156.42	583.3014	1747.893	-0.0039	-2.2	4.32	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
1231	dirMS_041712_NAR_20mM_plus.18652.18744.2	2	17.64	0	2.37E+05		(K)IYVDDGI	(K)I Y|V/D/D|G|L/I S/L/Q V K(Q)		200.67	731.9068	1462.815	-0.0088	-6	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
1232	dirMS_041712_NAR_50mM_plus2.12510.12510.3	3	17.64	1	3.06E+05		(R)SGVGLS	(R)S G V|G L/S/S Y/L/S T E K D A S|P K(T)		133.63	609.3102	1825.918	-0.0018	-1	5.79	64248.4	9.08	HUMAN	Q9BW04	Specifically androgen-regulated gene protein
1233	dirMS_041712_NAR_60mM_plus.15811.15877.3	3	17.64	0	4.58E+05		(R)VWYVSN	(R)V/W|Y V/S/N I/D/G T H I A/K(T)		139.78	534.9464	1602.828	-0.0028	-1.8	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
1234	dirMS_041712_NAR_60mM_plus.16200.16318.3	3	17.64	0	6.45E+05		(R)ETHSAL	(R)E T H S A|L|G/P|A|L|Q/A A/F K(L)		141.95	514.2744	1540.812	-0.0032	-2.1	6.85	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
1235	dirMS_041712_NAR_60mM_plus.20223.20223.3	3	17.64	1	3.02E+05		(K)IILDLISE	(K)I I/L/D/L I|S E S P/I K G\R(A)		166.2	518.6452	1553.926	-0.0051	-3.3	6.07	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
1236	dirMS_041712_NAR_20mM_plus.17117.17452.2	2	17.63	0	1.44E+06		(R)VLITTDL	(R)V/L|I|T|T/D/L/L/A R(G)		191	557.8442	1114.683	-0.0019	-1.7	5.81	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
1237	dirMS_041712_NAR_40mM_plus2.12334.12334.2	2	17.63	0	1.06E+05		(R)VLQALE	(R)V/L|Q|A L E/G/L K(M)		138.8	485.8002	970.593	0	0	5.97	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
1238	dirMS_041712_NAR_40mM_plus2.13516.13717.3	3	17.63	0	6.25E+05		(R)TIQVENS	(R)T/I|Q|V/E N\S H L/I|L/T/G A/G A L N K(V)		146.55	660.3654	1979.092	-0.0104	-5.2	6.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
1239	dirMS_041712_NAR_120mM_plus.11631.11631.2	2	17.62	1	8.55E+05		(R)NLKASLE	(R)N/L/K/A/S|L E/N S L R(E)		114.02	622.8511	1244.696	-0.0008	-0.6	8.75	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1240	dirMS_041712_NAR_30mM_plus2.15835.15835.2	2	17.62	0	5.00E+05		(K)LLYNNV	(K)L/L|Y|N/N V/S/N/F G R(L)		136.15	648.8354	1296.67	-0.006	-4.6	8.75	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
1241	dirMS_041712_NAR_50mM_plus2.14007.14007.3	3	17.62	1	7.05E+05		(R)VLELVSI	(R)V L|E\L|V/S/I/T A/N K N/T C P G D R(S)	C:Carbamidomethylation	141.97	663.0129	1987.028	-0.0036	-1.8	6.04	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
1242	dirMS_041712_NAR_50mM_plus2.18245.18245.3	3	17.62	1	6.23E+05		(K)LLEPVLL	(K)L/L/E/P/V/L/L/L G K E R(F)		164.48	460.6256	1379.862	0.0002	0.1	6.14	16559.1	10.36	HUMAN	P62249	40S ribosomal protein S16
1243	dirMS_041712_NAR_60mM_minus.18772.18772.3	3	17.61	1	1.31E+05		(K)IILDLISE	(K)I/I/L/D\L/I/S E S P I K G R(A)		166.22	518.6442	1553.926	-0.0081	-5.2	6.07	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
1244	dirMS_041712_NAR_120mM_plus.20802.21062.3	3	17.61	2	1.39E+06		(R)TLAEIAK	(R)T L|A|E|I|A K V E L D/N M/P L R G K(Q)		162.92	666.7047	1998.105	-0.0057	-2.8	5.85	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
1245	dirMS_041712_NAR_30mM_plus2.13530.13637.2	2	17.61	0	5.55E+05		(K)VGLQVV	(K)V/G|L|Q|V/V/A|V/K(A)		124.08	456.7974	912.588	-0.0002	-0.2	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
1246	dirMS_041712_NAR_120mM_minus.9669.9789.3	3	17.6	1	6.41E+05		(R)AREQAE	(R)A R E Q A\E\A|E|V|A|S/L/N\R(R)		107.8	515.2649	1543.782	-0.0022	-1.4	4.79	11017	4.8	HUMAN	D6R904	Tropomyosin alpha-3 chain
1247	dirMS_041712_NAR_30mM_minus2.14972.14986.2	2	17.6	0	1.45E+05		(K)GFFEGTI	(K)G/F|F|E/G T I/A/S/K(G)		134.95	528.7721	1056.536	0.0009	0.8	6	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
1248	dirMS_041712_NAR_50mM_minus2.6762.6762.3	3	17.6	1	2.52E+05		(R)ASVDTK	(R)A S|V/D T K E A E|G\A|P Q V E/A G K(R)		104.8	596.2904	1786.882	-0.0251	-14	4.41	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
1249	dirMS_041712_NAR_120mM_plus.9633.9705.3	3	17.6	1	4.59E+05		(R)KAYGGA	(R)K\A Y G\G\A|Y|D|V/M/S/S/K(H)		104.08	459.5555	1376.651	0.0005	0.3	8.43	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
1250	dirMS_041712_NAR_30mM_minus2.19133.19133.2	2	17.59	0	2.61E+05		(K)SYELPDC	(K)S Y E/L|P D G Q/V I\T I G N E/R(F)		158.88	895.9492	1790.892	-0.0008	-0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
1251	dirMS_041712_NAR_50mM_minus2.13298.13470.3	3	17.59	1	5.24E+05		(K)ATLPSPI	(K)A/T|L/P/S/P D/K L/P G F K(M)		144.18	457.5912	1370.768	-0.0088	-6.4	8.64	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
1252	dirMS_041712_NAR_20mM_plus.14109.14109.2	2	17.59	0	2.29E+05		(R)AALQELI	(R)A/A/L/Q/E|L L/S K(G)		168.83	486.789	972.572	-0.0017	-1.7	6.05	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
1253	dirMS_041712_NAR_20mM_plus.9356.9356.2	2	17.59	0	1.86E+05		(K)SVTNED	(K)S V\T N E/D/V/T Q/E/E/L/G G/A K(T)		136	838.9014	1676.797	-0.0018	-1.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
1254	dirMS_041712_NAR_30mM_plus2.21350.21481.3	3	17.59	0	5.51E+05		(R)VNQAIW	(R)V N Q\A\I\W|L|L/C/T/G A R(E)	C:Carbamidomethylation	166.88	501.2717	1501.794	0.0062	4.1	9.72	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
1255	dirMS_041712_NAR_40mM_plus2.12377.12710.3	3	17.59	0	4.54E+05		(K)AASDIAI	(K)A A|S/D|I/A/M/T E/L/P P T H/P I R(L)		140.07	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
1256	dirMS_041712_NAR_30mM_minus2.7281.7281.2	2	17.58	0	2.62E+05		(K)DAQGQI	(K)D A|Q/G/Q|P/G L/E R(A)		93.63	535.762	1070.523	-0.0058	-5.4	4.37	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
1257	dirMS_041712_NAR_30mM_minus2.7580.7616.2	2	17.58	0	2.78E+05		(K)ITITNDQ	(K)I/T|I/T|N D/Q/N R(L)		95.85	537.7798	1074.554	-0.0015	-1.4	5.84	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
1258	dirMS_041712_NAR_50mM_minus2.17906.17977.3	3	17.58	1	8.25E+05		(K)TFVNITP	(K)T F|V|N/I|T/P A/E V G V/L V G K D R(S)		171.32	639.0247	1915.065	-0.0052	-2.7	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
1259	dirMS_041712_NAR_30mM_plus2.15895.15895.2	2	17.58	0	3.21E+05		(R)YSVDIPL	(R)Y/S|V/D/I/P L/D/K(T)		136.13	525.2819	1049.551	0.0052	4.9	4.21	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
1260	dirMS_041712_NAR_60mM_plus.7874.7918.3	3	17.58	0	7.33E+05		(K)YKPESEE	(K)Y K|P E S E/E|L|T/A/E/R(I)		99.3	484.5717	1451.701	-0.0007	-0.5	4.5	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
1261	dirMS_041712_NAR_50mM_minus2.16333.16333.3	3	17.57	1	1.91E+05		(R)EGDVLT	(R)E G\D V/L/T/L L/E/S E R E/A R(R)		160.42	572.9609	1716.876	-0.0081	-4.7	4.25	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
1262	dirMS_041712_NAR_50mM_minus2.9034.9112.3	3	17.57	1	1.91E+05		(R)VLTVINC	(R)V/L|T|V/I/N Q/T Q K/E N L R(K)		119.83	552.6528	1655.944	0	0	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
1263	dirMS_041712_NAR_120mM_plus.13203.13412.4	4	17.57	0	1.76E+06		(R)VLSAPPI	(R)V L|S A/P/P/H/F/H/F/G Q T N R(T)		123.07	427.7235	1707.871	0.0008	0.5	9.74	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
1264	dirMS_041712_NAR_20mM_plus.15856.15856.2	2	17.57	0	2.93E+05		(R)GVVDSE	(R)G V/V/D/S E/D\I|P L/N L S R(E)		179.8	757.3956	1513.786	-0.0017	-1.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
1265	dirMS_041712_NAR_20mM_plus.16480.16480.3	3	17.57	0	2.24E+05		(K)TVTNAV	(K)T V\T N A V V T V|P/A Y/F/N D S Q R(Q)		184.53	661.3368	1981.998	-0.0019	-1	5.5	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
1266	dirMS_041712_NAR_40mM_plus2.10703.10703.3	3	17.57	0	1.85E+05		(K)VGSLDN	(K)V/G/S L/D N V/G H/L/P A/G G A V K(I)		128.15	530.9567	1590.86	-0.0043	-2.7	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
1267	dirMS_041712_NAR_40mM_plus2.6202.6202.3	3	17.57	1	3.14E+04		(R)AQLGGF	(R)A Q|L/G G/P E/A A K\S D E T A/A/K(-)		95.22	548.6136	1643.824	0.0027	1.7	4.68	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
1268	dirMS_041712_NAR_60mM_plus.14353.14486.3	3	17.57	0	3.25E+06		(R)DLNYCF	(R)D L|N|Y/C/F/S/G M/S D/H R(Y)	C:Carbamidomethylation	132.4	534.5555	1601.647	0.0048	3	5.21	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
1269	dirMS_041712_NAR_60mM_minus.5118.5328.3	3	17.56	0	2.04E+06		(K)TATPQQ	(K)T/A|T|P Q/Q/A/Q E/V/H E K(L)		84.4	489.5763	1466.723	-0.009	-6.2	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
1270	dirMS_041712_NAR_120mM_plus.10620.10763.4	4	17.56	2	5.03E+05		(K)SKGCGV	(K)S K G C G\V V\K F E\S|P/E|V/A/E/R(A)	C:Carbamidomethylation	109.53	470.4895	1878.938	-0.0017	-0.9	5.95	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
1271	dirMS_041712_NAR_120mM_plus.8742.8945.2	2	17.56	0	6.12E+05		(R)NGVMP	(R)N/G|V|M|P/S H|F|S R(G)		99.97	566.274	1131.536	0.0043	3.8	9.75	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
1272	dirMS_041712_NAR_30mM_plus2.8967.9004.2	2	17.56	0	5.36E+05		(K)QADVNL	(K)Q/A|D|V/N/L|V/N/A/K(L)		100.82	536.2922	1071.579	-0.0022	-2	5.84	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
1273	dirMS_041712_NAR_50mM_plus2.15340.15500.3	3	17.56	1	8.72E+05		(K)EAFSLFD	(K)E/A|F/S/L/F/D/K D/G D/G T I/T T K(E)		149.53	615.6348	1844.891	-0.0014	-0.8	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
1274	dirMS_041712_NAR_50mM_plus2.17772.17876.3	3	17.56	1	3.77E+05		(K)IEEIKDFL	(K)I/E|E|I K/D\F L/L/T A/R(R)		161.72	483.2728	1447.815	-0.0117	-8.1	4.68	2559	9.99	HUMAN	J3KSP2	60S ribosomal protein L38 (Fragment)
1275	dirMS_041712_NAR_50mM_plus2.17833.17976.3	3	17.56	0	2.47E+05		(R)ILVTLLH	(R)I/L|V/T/L/L/H/T L E/R(M)		162.4	436.6064	1307.805	0.0001	0.1	6.75	45212.4	9.41	HUMAN	B7Z233	Acetyl-CoA acetyltransferase, cytosolic
1276	dirMS_041712_NAR_50mM_plus2.18740.19159.3	3	17.56	0	9.39E+05		(R)CRPDQL	(R)C R P D\Q\L|T|G\L|S|L/L/P L/S E K(A)	C:Carbamidomethylation	167.58	643.0148	1927.032	-0.0019	-1	6.07	533778	5.74	HUMAN	Q15149	Plectin
1277	dirMS_041712_NAR_50mM_plus2.21391.21420.3	3	17.56	1	1.64E+05		(K)ALFEEVF	(K)A L/F/E|E/V/P E L L/T E A E K K(E)		182.58	615.9987	1845.984	-0.0029	-1.6	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
1278	dirMS_041712_NAR_30mM_minus2.11058.11058.2	2	17.55	0	9.13E+05		(K)SSFLVD	(K)S S|F/L/V/D C/S K(A)	C:Carbamidomethylation	113.6	521.7502	1042.487	0.0058	5.5	5.55	258215.9	5.48	HUMAN	E7EN95	Filamin-B
1279	dirMS_041712_NAR_50mM_minus2.14815.14815.3	3	17.55	1	3.01E+05		(R)EAVTEIL	(R)E A|V/T E/I/L/G\I/E/P D R E K(G)		152.28	566.9683	1698.891	-0.0005	-0.3	4.25	25685.9	6.4	HUMAN	E9PGT1	Translin
1280	dirMS_041712_NAR_20mM_plus.15172.15172.2	2	17.55	0	3.01E+05		(K)LLCGLLA	(K)L/L|C G|L/L/A E/R(L)	C:Carbamidomethylation	176.75	522.7971	1044.587	-0.0001	-0.1	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
1281	dirMS_041712_NAR_30mM_plus2.9880.9904.2	2	17.55	0	4.03E+05		(K)ILGPQGI	(K)I/L|G|P/Q/G N T I/K(R)		105.27	520.808	1040.61	-0.0011	-1.1	8.75	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
1282	dirMS_041712_NAR_50mM_plus2.14373.14404.3	3	17.55	0	5.99E+05		(R)AVAIDLF	(R)A V|A/I/D/L/P G L G H S K(E)		143.8	426.5786	1277.721	0	0	6.79	19983.6	8.14	HUMAN	B4DQI4	Alpha/beta hydrolase domain-containing protein 14B
1283	dirMS_041712_NAR_50mM_plus2.20548.20549.3	3	17.55	1	1.87E+05		(K)SYLNMD	(K)S/Y|L/N/M D A/I/M E A I/K/K(T)		176.7	542.9473	1626.823	0.0044	2.7	5.79	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
1284	dirMS_041712_NAR_60mM_plus.12750.12750.3	3	17.55	1	1.03E+06		(R)DLDRIA	(R)D/L/D R I\A/G|Q|V/A/A A N/K(K)		123.8	481.263	1441.776	-0.0013	-0.9	5.96	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
1285	dirMS_041712_NAR_50mM_plus2.16578.16704.3	3	17.54	1	5.82E+05		(K)DANAKL	(K)D A/N/A\K L\S E\L|E|A|A/L/Q R(A)		155.78	543.6256	1628.86	0.002	1.2	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1286	dirMS_041712_NAR_50mM_minus2.5627.5676.3	3	17.53	1	3.66E+05		(K)DSYVGD	(K)D S|Y|V/G D/E/A Q\S K R(G)		92.95	452.2119	1354.623	-0.0022	-1.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
1287	dirMS_041712_NAR_120mM_plus.8270.8283.3	3	17.53	1	3.10E+05		(K)KYEEIDN	(K)K\Y/E E\I D|N|A/P/E/E/R(A)		96.95	498.2388	1492.691	0.0104	7	4.25	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
1288	dirMS_041712_NAR_30mM_plus2.6013.6034.2	2	17.53	0	1.16E+05		(K)VLENAE	(K)V/L|E/N/A/E/G A R(T)		85.83	479.7542	958.495	0.0059	6.1	4.53	6809.6	9.69	HUMAN	D6RA73	Stress-70 protein, mitochondrial (Fragment)
1289	dirMS_041712_NAR_60mM_plus.14954.15128.3	3	17.53	0	5.61E+05		(R)YLDLHD	(R)Y/L/D/L/H/D/C Y L/K(Y)	C:Carbamidomethylation	135	447.2169	1339.635	0.001	0.8	5.21	52796.2	5.19	HUMAN	E7EUT8	Splicing factor 3A subunit 3
1290	dirMS_041712_NAR_20mM_plus.14500.14500.2	2	17.52	0	5.73E+05	M185m	(K)LAVNm\	(K)L A|V/N/m V/P F P R(L)	m:Oxidized methionine	170.77	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1291	dirMS_041712_NAR_20mM_plus.15313.15716.2	2	17.52	0	1.28E+06	M73m	(R)AILVDLE	(R)A I|L|V|D|L|E|P/G T/m D S V R(S)	m:Oxidized methionine	179.22	816.4181	1615.836	15.9929	-1.2	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
1292	dirMS_041712_NAR_30mM_plus2.7226.7226.2	2	17.52	0	1.83E+04		(R)SGGGG	(R)S/G G G/G G/G|G/L/G/S\G/G S I R(S)		92.03	616.8023	1232.598	-0.0005	-0.4	9.47	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
1293	dirMS_041712_NAR_30mM_minus2.14015.14413.2	2	17.51	0	3.71E+06	M320m	(K)YmACCL	(K)Y/m|A|C/C/L/L|Y/R(G)	C:Carbamidomethylation m:Oxid	130.8	633.2775	1249.553	15.9951	0.1	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
1294	dirMS_041712_NAR_50mM_minus2.10095.10179.3	3	17.51	0	5.46E+05	M147m	(K)LQmEAI	(K)L Q|m/E/A/P H|I|I/V/G T P G R(V)	m:Oxidized methionine	125.63	545.6267	1618.873	15.9922	-1.7	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
1295	dirMS_041712_NAR_50mM_minus2.12869.13235.3	3	17.51	1	1.62E+06		(K)ALQQGL	(K)A/L|Q/Q/G L/V/G L/E/L K E K(L)		142.47	509.3022	1525.895	-0.0028	-1.8	6.18	266161	5.68	HUMAN	E9PPU0	Epiplakin
1296	dirMS_041712_NAR_50mM_minus2.14918.14999.3	3	17.51	0	4.48E+05		(R)LQQELD	(R)L Q|Q|E/L/D D L/T/V/D/L/D H Q\R(Q)		153.03	646.6559	1937.956	-0.0032	-1.6	4.03	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
1297	dirMS_041712_NAR_50mM_minus2.15545.15566.3	3	17.51	0	1.90E+06		(R)VSLDVN	(R)V/S|L/D V/N H/F|A/P D E L T V K(T)		157.4	595.3104	1783.922	-0.0058	-3.3	4.54	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
1298	dirMS_041712_NAR_120mM_plus.14690.15128.3	3	17.51	0	1.55E+06		(-)MVNHFI	(-)M/V/N/H/F/I/A E/F/K(R)		131.67	412.5446	1235.624	-0.0049	-4	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
1299	dirMS_041712_NAR_20mM_plus.8427.8427.2	2	17.51	0	9.13E+04		(K)VVTDTD	(K)V/V|T/D|T|D E T/E L A R(Q)		128.17	674.8318	1348.659	-0.0027	-2	3.91	36396.8	5.02	HUMAN	P05198	Eukaryotic translation initiation factor 2 subunit 1
1300	dirMS_041712_NAR_50mM_plus2.15903.15923.3	3	17.51	0	6.05E+05		(R)MVILLC	(R)M/V|I/L/L/C N L/K/P A/K(M)	C:Carbamidomethylation	151.52	467.2775	1399.816	0.0016	1.1	10	34637.3	8.91	HUMAN	Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1
1301	dirMS_041712_NAR_50mM_plus2.19425.19821.3	3	17.51	1	1.20E+06		(R)GDLGIEI	(R)G D/L|G|I|E/I/P A E K V F L A Q K(M)		171.73	610.0104	1828.022	-0.0048	-2.6	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
1302	dirMS_041712_NAR_20mM_minus.12442.12442.2	2	17.5	0	6.00E+05	M185m	(K)LAVNm\	(K)L A/V/N/m/V/P F/P R(L)	m:Oxidized methionine	172.52	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1303	dirMS_041712_NAR_30mM_plus2.17134.17134.2	2	17.5	0	7.63E+05		(R)MNVLAI	(R)M/N|V/L/A\D A L/K(S)		143.1	487.7743	974.534	0.0074	7.6	5.59	27396	9.9	HUMAN	H3BN98	Uncharacterized protein (Fragment)

1304	dirMS_041712_NAR_30mM_plus2.19614.19614.2	2	17.5	0	2.87E+04		(K)NQALFP	(K)N/Q|A|L/F/P A C V L K(N)	C:Carbamidomethylation	157.75	630.8399	1260.677	-0.0044	-3.5	8.75	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
1305	dirMS_041712_NAR_30mM_plus2.7526.7541.2	2	17.5	0	6.31E+05		(K)SFQQSSI	(K)S F|Q|Q|S/S/L/S/R(D)		93.8	520.2659	1039.517	0.0078	7.5	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
1306	dirMS_041712_NAR_50mM_plus2.14819.14819.3	3	17.5	0	6.51E+05		(K)SPAPPLL	(K)S/P|A/P/P L L H V A A L/G Q K(Q)		145.78	500.2911	1498.874	-0.0153	-10.2	8.49	17549.1	10.39	HUMAN	E5RFJ3	DBIRD complex subunit KIAA1967 (Fragment)
1307	dirMS_041712_NAR_60mM_plus.17727.17899.3	3	17.5	1	4.14E+05		(R)RDDGTG	(R)R D D G T G Q\L|L|L|P L/S D/A R(K)		150.38	576.3069	1726.908	-0.0021	-1.2	4.43	533778	5.74	HUMAN	Q15149	Plectin
1308	dirMS_041712_NAR_20mM_minus.14653.14653.2	2	17.49	0	2.10E+05		(K)LAVEALS	(K)L A V/E|A|L|S|S/L D G D L A/G R(Y)		201.28	793.922	1586.838	-0.0017	-1.1	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
1309	dirMS_041712_NAR_20mM_minus.7656.7656.2	2	17.49	0	6.65E+05	M239m	(K)EVDEQm	(K)E V|D E Q/m L/N|V/Q|N|K(N)	m:Oxidized methionine	125.12	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
1310	dirMS_041712_NAR_50mM_plus2.22224.22224.3	3	17.49	1	1.35E+06		(K)EGGLGP	(K)E G G/L/G/P L/N I/P L L A D V T R R(L)		191	631.029	1891.076	-0.0035	-1.9	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
1311	dirMS_041712_NAR_60mM_plus.18891.19267.3	3	17.49	1	1.21E+06		(R)EGDVLT	(R)E/G|D|V/L/T/L/L/E/S E R E/A R(R)		157.1	572.9638	1716.876	0.0006	0.3	4.25	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
1312	dirMS_041712_NAR_20mM_plus.10867.11339.2	2	17.48	0	2.99E+06		(K)DVNAAI	(K)D V|N|A|A/I/A/T/I/K(T)		150.08	508.292	1015.578	-0.0015	-1.5	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
1313	dirMS_041712_NAR_30mM_plus2.7254.7350.2	2	17.48	0	4.29E+05		(R)IYVSANS	(R)I/Y|V|S/A/N/S/G A/R(I)		92.9	519.2668	1037.537	-0.0111	-10.7	8.75	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
1314	dirMS_041712_NAR_50mM_plus2.9840.9840.3	3	17.48	1	1.04E+06		(K)LKGEAT	(K)L K G E\A|T\V|S/F/D/D|P/P S A K(A)		119.12	554.6155	1661.838	-0.0061	-3.7	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
1315	dirMS_041712_NAR_20mM_minus.13136.13136.3	3	17.47	0	4.00E+05		(K)TITLEVEI	(K)T I T L E V/E|P/S/D T/I E/N V K(A)		183.03	596.6453	1787.927	-0.006	-3.3	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
1316	dirMS_041712_NAR_120mM_plus.5512.5550.3	3	17.47	0	7.03E+05		(R)STFETEH	(R)S/T|F/E/T/E/H/A G Q R(D)		82.03	421.5315	1262.576	0.0039	3.1	5.38	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
1317	dirMS_041712_NAR_20mM_plus.14768.14768.2	2	17.47	0	1.10E+05		(K)LLGELLQ	(K)L/L|G/E\L/L/Q D N/A K(L)		173.65	607.3421	1213.679	-0.0018	-1.4	4.37	35556.4	9.3	HUMAN	F2Z393	Transaldolase
1318	dirMS_041712_NAR_30mM_plus2.18871.18912.2	2	17.47	0	2.41E+05		(R)LLFNDV	(R)L/L|F/N/D V/Q/T L K(D)		152.38	595.8347	1190.678	-0.0158	-13.3	5.84	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
1319	dirMS_041712_NAR_30mM_plus2.5977.5990.2	2	17.47	0	5.16E+04		(K)SYSVGA	(K)S Y|S|V/G/A/S/G|S/S S/R(K)		85.65	572.7644	1144.523	-0.0014	-1.2	8.46	26261.9	9.78	HUMAN	F5GWE6	Cleavage and polyadenylation-specificity factor subunit 7
1320	dirMS_041712_NAR_30mM_plus2.7684.7752.2	2	17.47	0	8.54E+05		(K)GANPVE	(K)G A|N|P/V/E/I/R(R)		94.42	428.241	855.468	0.0064	7.5	6	17213.7	10.05	HUMAN	B7Z712	60 kDa heat shock protein, mitochondrial
1321	dirMS_041712_NAR_30mM_plus2.8708.8926.2	2	17.47	0	2.54E+06		(K)YIDQEEL	(K)Y/I|D|Q/E E L|N/K(T)		99.85	576.2833	1151.558	0.0014	1.2	4.14	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
1322	dirMS_041712_NAR_40mM_plus2.12275.12275.3	3	17.47	0	2.19E+05		(K)AASDIAI	(K)A A/S/D/I/A/M T E L/P P T H/P I R(L)		139.18	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
1323	dirMS_041712_NAR_40mM_plus2.19946.20032.3	3	17.47	1	1.56E+06		(R)ELAILLG	(R)E L|A|I/L/L/G M L/D/P A E K D/E K(G)		189.1	629.003	1884.999	-0.0042	-2.3	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
1324	dirMS_041712_NAR_50mM_plus2.11371.11477.3	3	17.47	1	1.25E+06		(K)NQVAM	(K)N Q|V|A/M/N|P T/N/T V/F D A K/R(L)		127.8	602.6354	1805.896	-0.0046	-2.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
1325	dirMS_041712_NAR_50mM_minus2.18793.18879.3	3	17.46	1	2.24E+06		(R)LIALLEVI	(R)L/I|A|L/L/E/V L/S Q K/R(M)		183.72	461.6289	1382.873	-0.0008	-0.6	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
1326	dirMS_041712_NAR_20mM_plus.12262.12262.2	2	17.46	0	4.61E+04		(K)VALSSET	(K)V A|L/S/S/E/T E/V/A/L/A/R(D)		157.62	673.3693	1345.732	-0.0008	-0.6	4.53	246695.2	5.91	HUMAN	E7EVA0	Microtubule-associated protein
1327	dirMS_041712_NAR_30mM_plus2.12946.12946.2	2	17.46	0	3.14E+05		(K)QQIQSIC	(K)Q Q|I|Q/S I Q/Q S/I E/R(L)		120.75	729.3893	1457.771	0.0006	0.4	6	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
1328	dirMS_041712_NAR_50mM_plus2.8198.8198.3	3	17.46	0	7.80E+04		(K)QEYDES	(K)Q E/Y/D E/S/G/P/S/I V H/R(K)		109.4	506.2382	1516.703	-0.0026	-1.7	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
1329	dirMS_041712_NAR_30mM_minus2.19123.19123.2	2	17.45	0	2.61E+05		(K)SYELPDC	(K)S Y E\L|P/D G Q V I/T I/G N E R(F)		158.88	895.9492	1790.892	-0.0008	-0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
1330	dirMS_041712_NAR_60mM_minus.18441.18594.3	3	17.45	0	2.26E+06		(R)IHFPLAT	(R)I H F\P L A\T|Y|A|P/V/I/S A E K(A)		165.67	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
1331	dirMS_041712_NAR_60mM_minus.5071.5276.3	3	17.45	0	3.20E+06		(R)AEAEAG	(R)A E|A|E|A/G/S P R P D|P/R(E)		83.35	451.5562	1352.655	-0.0013	-0.9	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
1332	dirMS_041712_NAR_30mM_plus2.15103.15448.2	2	17.45	0	9.39E+05		(R)VWQVTI	(R)V/W|Q|V/T/I/G T/R(-)		132.57	530.3002	1059.595	-0.0014	-1.4	9.72	30149.5	5.96	HUMAN	D6RAC2	Guanine nucleotide-binding protein subunit beta-2-like 1
1333	dirMS_041712_NAR_30mM_plus2.18383.18417.2	2	17.45	0	2.22E+05		(K)GVEGLII	(K)G V|E/G|L|I/D/I/E/N/P\N R(V)		149.45	713.3669	1425.733	-0.0067	-4.7	4.14	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
1334	dirMS_041712_NAR_30mM_plus2.9098.9629.2	2	17.45	0	1.04E+06		(R)ILSGVVT	(R)I/L|S/G V/V/T/K(M)		102.98	408.7614	816.519	-0.0034	-4.2	8.75	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
1335	dirMS_041712_NAR_50mM_plus2.16336.16568.3	3	17.45	0	7.81E+06		(R)VSLDVN	(R)V/S|L/D/V N/H/F/A/P D E L T V K(T)		154.68	595.312	1783.922	-0.001	-0.6	4.54	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
1336	dirMS_041712_NAR_60mM_minus.14053.14216.3	3	17.44	1	6.76E+05		(R)LSAEERI	(R)L/S|A/E/E R D Q|L|L|P N L R(A)		138.75	551.9683	1653.892	-0.0015	-0.9	4.68	12056.4	6.28	HUMAN	P61457	Pterin-4-alpha-carbinolamine dehydratase
1337	dirMS_041712_NAR_60mM_minus.19901.19901.3	3	17.44	1	1.39E+06		(K)EIIDLVLI	(K)E I/I/D/L/V/L D R I/R(K)		180.2	452.2739	1354.805	0.0019	1.4	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
1338	dirMS_041712_NAR_40mM_plus2.19253.19253.3	3	17.44	1	1.93E+05		(K)TSAQVV	(K)T S/A/Q/V/V/L D G L/V D K I G D/V K(C)		180.37	619.6811	1857.033	-0.004	-2.2	4.43	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
1339	dirMS_041712_NAR_50mM_plus2.13659.13660.3	3	17.44	0	1.68E+06		(K)DLAGCIH	(K)D L|A/G/C/I/H/G L S N V/K(L)	C:Carbamidomethylation	140.15	461.9061	1383.705	-0.0012	-0.8	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
1340	dirMS_041712_NAR_60mM_plus.11692.11840.3	3	17.44	0	9.22E+06		(R)FAQHGT	(R)F A Q H G T\F\E|Y|E|Y/S Q R(W)		118.63	588.265	1762.782	-0.0015	-0.9	5.4	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
1341	dirMS_041712_NAR_30mM_plus2.18308.18308.2	2	17.43	0	3.70E+05		(R)SQVEEEI	(R)S Q|V/E/E E/L/F S/V R(V)		149.38	661.8302	1322.659	-0.0055	-4.2	4.25	533778	5.74	HUMAN	Q15149	Plectin
1342	dirMS_041712_NAR_30mM_plus2.22006.22006.2	2	17.43	0	2.06E+05		(K)QSLGELI	(K)Q S\L|G/E|L/I|G T L N A A/K(V)		170.27	707.8889	1414.79	-0.0195	-13.8	6	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
1343	dirMS_041712_NAR_30mM_plus2.22226.22226.2	2	17.43	0	9.21E+05		(K)IGFPWSI	(K)I G/F/P/W/S E I/R(N)		173	552.8032	1104.584	0.0155	14	6	71218.8	6.3	HUMAN	A7YIJ8	Radixin
1344	dirMS_041712_NAR_30mM_minus2.13195.13346.2	2	17.42	0	7.20E+05		(K)YGVSGY	(K)Y/G|V|S|G/Y/P T\L/K(I)		125.7	542.7876	1084.567	0.0006	0.5	8.5	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
1345	dirMS_041712_NAR_40mM_minus2.12104.12438.3	3	17.42	1	7.28E+05		(R)IIAFVGS	(R)I/I|A\F/V|G/S/P V E D N E K D L V/K(L)		156.48	658.3553	1973.059	-0.0076	-3.9	4.32	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
1346	dirMS_041712_NAR_40mM_minus2.14275.14275.3	3	17.42	0	1.23E+05		(R)GTEDITS	(R)G T|E/D I/T/S/P H G I/P L D\L L D/R(V)		168.55	650.3366	1948.997	-0.0022	-1.1	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
1347	dirMS_041712_NAR_50mM_minus2.10711.10711.3	3	17.42	0	1.79E+05		(R)LLELGPK	(R)L/L|E/L/G P K P E/V/A Q Q\T R(K)		128.88	560.3182	1678.949	-0.0086	-5.1	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
1348	dirMS_041712_NAR_60mM_minus.9552.9589.3	3	17.42	0	2.61E+05		(K)GIVEFSG	(K)G I|V/E/F/S/G K/P/A A R(K)		113.3	411.2274	1231.679	-0.0117	-9.5	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
1349	dirMS_041712_NAR_120mM_plus.20482.21019.4	4	17.42	1	3.77E+06		(R)DYLHLPI	(R)D Y\L H/L|P|P|E I/V/P A T L R R(S)		162.23	473.2689	1890.06	-0.0058	-3.1	6.75	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
1350	dirMS_041712_NAR_30mM_plus2.13763.13885.2	2	17.42	0	6.06E+05		(R)ISGLIYEE	(R)I/S|G|L|I|Y/E E/T/R(G)		125.55	590.8136	1180.621	-0.0009	-0.8	4.53	11367.1	11.36	HUMAN	P62805	Histone H4
1351	dirMS_041712_NAR_50mM_plus2.17754.17764.3	3	17.42	0	2.72E+05		(R)LGIEGLS	(R)L/G|I|E/G L/S L/H N V L K(L)		161.6	464.946	1392.821	0.0025	1.8	6.75	177928	5.42	HUMAN	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1
1352	dirMS_041712_NAR_50mM_minus2.8808.8808.3	3	17.41	0	2.36E+05		(R)VMLGET	(R)V/M/L/G/E|T N P A D S K P G T I R(G)		118.3	595.9744	1785.916	-0.0077	-4.3	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
1353	dirMS_041712_NAR_120mM_plus.19557.19573.3	3	17.41	1	7.12E+05		(R)DFNHIN	(R)D F/N H I N\V|E|L/S|L/L/G K/K(K)		155.85	576.3192	1726.949	-0.0056	-3.2	6.75	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
1354	dirMS_041712_NAR_20mM_plus.11117.11458.2	2	17.41	0	2.99E+06		(K)DVNAAI	(K)D V|N|A|A/I/A/T I/K(T)		150.08	508.292	1015.578	-0.0015	-1.5	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
1355	dirMS_041712_NAR_30mM_plus2.14029.14164.2	2	17.41	0	5.04E+05		(R)VLSIGDC	(R)V/L|S|I/G/D/G/I A R(V)		126.68	500.7889	1000.579	-0.008	-8	5.81	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
1356	dirMS_041712_NAR_30mM_plus2.18586.18607.2	2	17.41	0	3.64E+05		(R)SSFYVN	(R)S S|F|Y|V|N/G L/T\L/G G Q K(C)		150.97	735.8825	1470.759	-0.001	-0.7	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
1357	dirMS_041712_NAR_20mM_minus.11251.11251.2	2	17.4	0	2.79E+05		(K)LSELEAA	(K)L/S|E|L/E A/A/L/Q R(A)		159.5	565.3134	1129.621	-0.0016	-1.5	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1358	dirMS_041712_NAR_50mM_minus2.12364.12396.3	3	17.4	0	6.53E+05		(K)AGVVGF	(K)A/G/V|V|G/P/E/L/H E Q L/L S A E K(A)		139.25	592.9866	1776.949	-0.0038	-2.1	4.75	533778	5.74	HUMAN	Q15149	Plectin
1359	dirMS_041712_NAR_50mM_minus2.14553.14624.3	3	17.4	1	1.93E+05		(R)AEGAIA	(R)A/E|G A|I/A/G F R D/P F S/G K(Q)		151.2	508.2599	1522.765	0.0003	0.2	6.12	266161	5.68	HUMAN	E9PPU0	Epiplakin
1360	dirMS_041712_NAR_30mM_plus2.20195.20703.2	2	17.4	0	7.48E+06		(R)YLTVAA	(R)Y/L|T|V/A/A/V/F/R(G)		160.82	520.2996	1039.593	-0.0016	-1.5	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
1361	dirMS_041712_NAR_30mM_plus2.20465.20465.2	2	17.4	0	6.53E+04		(K)SYELPDC	(K)S Y\E|L|P D G Q V|I/T\I/G N E R(F)		160.92	895.9487	1790.892	-0.0018	-1	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
1362	dirMS_041712_NAR_40mM_plus2.15087.15525.3	3	17.4	0	9.12E+05		(R)DVQIGD	(R)D V|Q|I|G/D/I/V/T V/G E C R P L S K(T)	C:Carbamidomethylation	157.25	662.6815	1986.033	-0.0025	-1.3	4.56	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
1363	dirMS_041712_NAR_50mM_minus2.16106.16106.3	3	17.39	0	1.46E+05		(K)LDPHLVI	(K)L D/P H L/V|L/D/Q L/R(C)		160.2	440.2533	1318.748	-0.0024	-1.8	5.21	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
1364	dirMS_041712_NAR_120mM_plus.13671.14030.2	2	17.39	1	5.06E+06		(K)FASFIDK	(K)F/A|S|F/I/D/K V/R(F)		125.95	541.7966	1082.599	-0.0134	-12.4	8.75	19569.8	9.88	HUMAN	F8VRG4	Keratin, type II cytoskeletal 8 (Fragment)
1365	dirMS_041712_NAR_20mM_plus.17540.17540.2	2	17.39	0	3.36E+04		(R)YLTVAA	(R)Y L|T/V/A/A/V F|R(G)		192.65	520.3009	1039.593	0.001	1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
1366	dirMS_041712_NAR_30mM_plus2.10188.10573.2	2	17.39	0	8.70E+05		(R)SPSTLLP	(R)S/P|S/T/L/L|P/K(K)		107.97	421.7559	842.498	0.0063	7.5	8.47	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
1367	dirMS_041712_NAR_30mM_plus2.10801.10860.2	2	17.39	0	6.16E+05		(K)EAAENS	(K)E A|A/E/N/S L/V/A/Y/K(A)		110.12	597.8036	1194.6	-0.0002	-0.1	4.53	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
1368	dirMS_041712_NAR_30mM_plus2.19109.19109.2	2	17.39	0	3.47E+05		(R)LTAEDLF	(R)L/T/A/E/D L/F E/A R(I)		153.45	582.796	1164.59	-0.0048	-4.1	4.14	533778	5.74	HUMAN	Q15149	Plectin
1369	dirMS_041712_NAR_50mM_plus2.14766.15033.3	3	17.39	1	1.14E+05		(R)LLDAQL	(R)L/L|D|A/Q/L/A/T/G G L V C P A R/R(L)	C:Carbamidomethylation	147.2	604.3351	1810.996	-0.0049	-2.7	9.6	266161	5.68	HUMAN	E9PPU0	Epiplakin
1370	dirMS_041712_NAR_50mM_plus2.18107.18552.3	3	17.39	1	1.01E+06		(K)GYPPED	(K)G Y|P/P E D I/F/N L/V/G K/K(V)		164.65	526.2834	1576.837	-0.0013	-0.8	6.07	40763.2	6.29	HUMAN	Q9NR45	Sialic acid synthase
1371	dirMS_041712_NAR_120mM_minus.10681.11169.3	3	17.38	0	9.56E+05		(R)GFCLPPI	(R)G F|C/L/P/P/H C S/R(G)	C:Carbamidomethylation	113.55	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
1372	dirMS_041712_NAR_120mM_minus.14965.15189.3	3	17.38	1	1.12E+06		(K)VKEGMI	(K)V K E G M\N\I|V|E/A/M/E/R(F)		136.7	502.5853	1505.745	-0.0037	-2.5	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
1373	dirMS_041712_NAR_120mM_plus.11134.11339.2	2	17.38	1	8.18E+05		(R)ALAAFLI	(R)A/L|A|A/F/L/K/K(S)		112.15	431.2797	861.556	-0.0035	-4.1	10	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
1374	dirMS_041712_NAR_40mM_plus2.16140.16140.3	3	17.38	0	4.91E+05		(R)FGVPVI	(R)F/G V|P/V/I/A D G G I Q N V/G H I A/K(A)		162.27	631.3436	1892.039	-0.0226	-12	6.74	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
1375	dirMS_041712_NAR_20mM_minus.10885.10885.2	2	17.37	0	1.53E+06	M92m	(R)ImNTFS	(R)I m|N\T/F/S/V V/P S P K(V)	m:Oxidized methionine	157.12	668.3513	1319.703	15.9925	-1.8	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
1376	dirMS_041712_NAR_50mM_minus2.7873.7873.3	3	17.37	0	4.58E+04		(R)QLSQAG	(R)Q/L/S/Q/A G/S F/S D G T H/G G L R(Y)		111.92	573.2875	1717.825	0.0227	13.2	6.74	266161	5.68	HUMAN	E9PPU0	Epiplakin
1377	dirMS_041712_NAR_30mM_plus2.15301.15301.2	2	17.37	0	2.82E+05		(R)LLCNFM	(R)L/L|C/N F M/R(Q)	C:Carbamidomethylation	132.92	477.2409	953.47	0.005	5.2	9.75	18685.5	9.45	HUMAN	B4DEV8	Proteasome subunit alpha type
1378	dirMS_041712_NAR_60mM_plus.18308.18783.3	3	17.37	1	2.81E+06		(K)QLDDLK	(K)Q L|D/D/L/K/V/E/L/S/Q L R(V)		154.67	519.6254	1556.864	-0.0026	-1.7	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
1379	dirMS_041712_NAR_30mM_minus2.10292.10373.2	2	17.36	0	2.81E+05		(R)ETAEAD	(R)E T/A/E/A/D/V|A|S/L/N|R(R)		110.08	638.3134	1275.618	0.002	1.6	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
1380	dirMS_041712_NAR_50mM_minus2.14836.14836.3	3	17.36	1	2.96E+05		(R)EAVTEIL	(R)E/A/V/T/E/I/L/G I/E P D R E K(G)		152.32	566.9683	1698.891	-0.0005	-0.3	4.25	25685.9	6.4	HUMAN	E9PGT1	Translin
1381	dirMS_041712_NAR_30mM_plus2.12579.12579.2	2	17.36	0	7.73E+05		(R)YSGSYNI	(R)Y/S|G S/Y N/D/Y L/R(A)		119.15	619.2776	1237.548	-0.0005	-0.4	5.83	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
1382	dirMS_041712_NAR_30mM_plus2.17087.17087.2	2	17.36	0	1.82E+05		(K)GVVDSD	(K)G V\V/D S D/D/L/P L/N V/S R(E)		142.53	743.3807	1485.754	-0.0002	-0.2	3.93	92752.5	4.76	HUMAN	P14625	Endoplasmin
1383	dirMS_041712_NAR_30mM_plus2.6360.6387.2	2	17.36	0	2.52E+05		(K)GEGQLG	(K)G E|G\Q/L|G/P/A/E/R(A)		87.53	507.2537	1013.501	-0.0009	-0.9	4.53	96306.4	6.41	HUMAN	P13639	Elongation factor 2
1384	dirMS_041712_NAR_40mM_plus2.13442.13442.3	3	17.36	0	6.01E+05		(R)QVSASE	(R)Q\V/S/A S E L H T S G I/L/G/P E T L R(D)		145.08	665.6807	1995.051	-0.023	-11.5	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
1385	dirMS_041712_NAR_50mM_plus2.11416.11436.3	3	17.36	1	6.51E+05		(R)DVVICPI	(R)D V|V|I/C/P D A/S L E D A K K(E)	C:Carbamidomethylation	127.98	553.9467	1659.826	-0.0003	-0.2	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
1386	dirMS_041712_NAR_30mM_minus2.11561.11685.2	2	17.35	0	8.84E+05		(K)CGDLVF	(K)C/G/D|L/V|F|A/K(M)	C:Carbamidomethylation	117	455.2306	909.45	0.0041	4.5	5.84	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
1387	dirMS_041712_NAR_120mM_plus.9999.9999.2	2	17.35	0	4.61E+05		(R)VHIEIGP	(R)V/H|I|E\I|G|P D G R(V)		105.95	546.7931	1092.58	-0.0007	-0.6	5.32	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
1388	dirMS_041712_NAR_50mM_minus2.11749.12017.3	3	17.34	1	6.11E+05		(R)ELISNSSI	(R)E L/I/S/N/S/S/D/A\L/D/K I R(Y)		135.85	520.9445	1560.823	-0.0038	-2.5	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
1389	dirMS_041712_NAR_20mM_plus.13700.13805.2	2	17.34	0	6.17E+05		(R)GALQNI	(R)G A/L|Q|N|I|I\P A/S T G A/A/K(A)		167.23	706.3975	1411.79	-0.0026	-1.9	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
1390	dirMS_041712_NAR_30mM_plus2.10567.10805.2	2	17.34	0	3.23E+06		(R)GYSFTTT	(R)G Y|S/F/T/T/T/A E/R(E)		109.3	566.7674	1132.527	0.0006	0.5	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
1391	dirMS_041712_NAR_30mM_plus2.17717.17776.2	2	17.34	0	3.19E+05		(K)SLEDQV	(K)S L|E|D|Q/V/E/M/L/R(T)		145.85	610.3003	1219.599	-0.0054	-4.4	4.14	61161.1	4.34	HUMAN	K7ELL7	Glucosidase 2 subunit beta
1392	dirMS_041712_NAR_40mM_plus2.13862.13862.3	3	17.34	0	2.23E+05		(K)VALLLLD	(K)V A|L/L/L L/D Q/G A/S/P H A/A A K(N)		148.13	558.9886	1674.954	-0.0025	-1.5	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
1393	dirMS_041712_NAR_40mM_plus2.15014.15435.3	3	17.34	0	4.51E+06		(R)VSLDVN	(R)V/S|L/D/V/N H/F/A/P D E L T V/K(T)		156.22	595.3161	1783.922	0.0113	6.3	4.54	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
1394	dirMS_041712_NAR_30mM_minus2.18226.18226.2	2	17.33	0	7.01E+04		(R)SYNDEL	(R)S Y/N/D E/L/Q F L/E\K(I)		153.58	693.3327	1385.658	-0.0002	-0.2	4.14	19338.9	5.33	HUMAN	E7EQS9	tRNA-splicing ligase RtcB homolog
1395	dirMS_041712_NAR_120mM_plus.21211.21211.4	4	17.33	1	9.54E+05		(R)DYLHLPI	(R)D Y L H L/P|P E\I/V/P A T L R R(S)		164.53	473.2689	1890.06	-0.0058	-3.1	6.75	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
1396	dirMS_041712_NAR_30mM_plus2.12181.12201.2	2	17.33	0	3.82E+05		(R)QYFEEIC	(R)Q/Y|F/E/E/I/Q/R(R)		117.02	556.7725	1112.537	0.0006	0.6	4.53	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
1397	dirMS_041712_NAR_30mM_plus2.16885.16914.2	2	17.33	0	1.67E+05		(K)EQFLDG	(K)E Q|F|L/D/G/D/G W/T/S R(W)		141.32	705.8178	1410.628	-0.0001	-0.1	4.03	28545.1	4.5	HUMAN	K7EJB9	Calreticulin (Fragment)
1398	dirMS_041712_NAR_50mM_plus2.8630.8630.3	3	17.33	1	1.17E+05		(K)TENSGE	(K)T/E|N/S/G E A L A K V E D/S N/P Q K(T)		112.38	639.6441	1916.92	-0.0018	-1	4.41	13579.2	9.99	HUMAN	E9PPQ6	Thymocyte nuclear protein 1 (Fragment)
1399	dirMS_041712_NAR_120mM_minus.13497.13795.4	4	17.32	2	8.32E+05	M100m	(K)KQGGLG	(K)K\Q G G L\G\P m\N I|P L/V/S D/P K/R(T)	m:Oxidized methionine	128.55	481.5173	1907.053	15.9942	-0.3	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
1400	dirMS_041712_NAR_30mM_minus2.19188.19188.2	2	17.32	0	1.31E+06		(K)LAVNM	(K)L A/V/N/M/V|P/F/P/R(L)		159.15	572.3143	1143.634	-0.013	-11.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1401	dirMS_041712_NAR_50mM_minus2.9216.9217.3	3	17.32	0	1.99E+05		(K)VGQEIE	(K)V/G|Q/E/I/E V R P G/I V/S/K(D)		120.43	504.2902	1510.859	-0.0027	-1.8	6.11	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
1402	dirMS_041712_NAR_60mM_minus.9960.9960.3	3	17.32	1	1.21E+05		(K)IFQKGES	(K)I/F/Q\K G E S/P|V/D/Y/D G G R(T)		115.3	556.6051	1667.802	-0.0016	-1	4.56	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
1403	dirMS_041712_NAR_20mM_plus.10585.10585.3	3	17.32	0	8.25E+04		(K)VLQATV	(K)V L\Q A T V/V/A/V G S/G/S/K(G)		145.63	439.2573	1315.758	-0.0006	-0.5	8.72	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
1404	dirMS_041712_NAR_20mM_plus.8294.8307.2	2	17.32	0	9.35E+04		(R)LATNTS	(R)L A|T|N/T/S A/P D/L K(N)		127.33	565.806	1130.605	-0.0005	-0.4	5.84	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
1405	dirMS_041712_NAR_30mM_plus2.17870.17870.2	2	17.32	0	1.40E+05		(R)NELSGA	(R)N/E|L|S/G/A/L T/G/L T R(V)		146.73	616.3341	1231.664	-0.0032	-2.6	6	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
1406	dirMS_041712_NAR_30mM_minus2.14904.14904.2	2	17.31	0	1.75E+05		(K)SLAEGYI	(K)S L|A|E/G Y/F D A A/G R(L)		134.77	628.7988	1256.591	-0.0003	-0.2	4.37	22270.1	8.67	HUMAN	E9PHS0	LanC-like protein 1 (Fragment)
1407	dirMS_041712_NAR_30mM_minus2.18864.18864.2	2	17.31	0	1.06E+05		(K)NLIDAG	(K)N L|I|D/A G V D/A L/R(V)		157.17	578.811	1156.632	-0.0173	-15	4.21	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
1408	dirMS_041712_NAR_120mM_plus.13642.13935.3	3	17.31	1	7.43E+05		(R)IAWDDE	(R)I/A|W/D/D/E E/T R D/G F/R(L)		125.52	537.248	1609.724	0.0053	3.3	4.11	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
1409	dirMS_041712_NAR_30mM_plus2.16759.16759.2	2	17.31	0	2.91E+05		(R)SIQADG	(R)S/I/Q|A|D G L/V/W/G S S K(L)		140.63	674.3475	1347.69	-0.0026	-1.9	5.55	24934.4	4.5	HUMAN	P24534	Elongation factor 1-beta
1410	dirMS_041712_NAR_50mM_plus2.13207.13207.3	3	17.31	0	1.63E+06		(R)GIYAYGI	(R)G I/Y|A/Y/G F E K/P S A/I Q\Q R(A)		136.78	609.9821	1827.939	-0.0071	-3.9	8.5	16071.1	4.8	HUMAN	B4E102	Eukaryotic initiation factor 4A-I
1411	dirMS_041712_NAR_60mM_minus.12230.12230.3	3	17.3	1	4.75E+05		(R)INVYYNI	(R)I/N/V/Y/Y N E/A/T/G/G K/Y V P R(A)		127.67	615.3145	1843.934	-0.0048	-2.6	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
1412	dirMS_041712_NAR_60mM_minus.7326.7758.3	3	17.3	1	1.38E+06		(K)IQDKEGI	(K)I Q|D K E G|I|P/P/D Q Q R(L)		100.07	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin

1413	dirMS_041712_NAR_30mM_plus2.18533.18948.2	2	17.3	0	2.82E+06		(R)GLFIIDG	(R)G/L|F|I I D/G/K(G)		151.62	431.7495	862.503	-0.0116	-13.4	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
1414	dirMS_041712_NAR_30mM_plus2.8237.8669.2	2	17.3	0	1.48E+07		(R)AQYDEL	(R)A/Q|Y|D/E/L/A/R(K)		99.1	483.2388	965.469	0.0016	1.7	4.37	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1415	dirMS_041712_NAR_40mM_plus2.13984.13984.3	3	17.3	0	2.92E+05		(R)LASTLVH	(R)L A|S T L/V H L G E/Y Q/A/A/V D/G A R(K)		148.43	657.6841	1971.029	0.0083	4.2	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
1416	dirMS_041712_NAR_50mM_plus2.19128.19236.3	3	17.3	0	5.12E+05		(R)GFGFITF	(R)G F|G|F|I|T/F/T/N/P E H A S V A M R(A)		168.95	661.3258	1981.959	0.004	2	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
1417	dirMS_041712_NAR_60mM_plus.18328.18659.3	3	17.3	1	8.26E+05		(R)IRIDSLS/	(R)I R I D S\L\S\A|Q|L|S/Q L Q/K(Q)		154.22	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
1418	dirMS_041712_NAR_60mM_plus.7954.7954.3	3	17.3	0	1.02E+06		(K)EAYPDH	(K)E A/Y/P D/H/T/Q/F/E K(N)		99.42	455.5423	1364.612	0.0006	0.5	4.65	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1
1419	dirMS_041712_NAR_30mM_minus2.15751.15902.2	2	17.29	0	8.09E+05		(K)ICSWNV	(K)I/C|S|W/N/V|D/G L/R(A)	C:Carbamidomethylation	139.38	610.2986	1219.589	0.0011	0.9	5.84	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
1420	dirMS_041712_NAR_50mM_minus2.14943.15317.3	3	17.29	1	1.13E+06		(R)DVDFELI	(R)D V|D/F/E/L/I/K V E/G K(V)		154.02	464.5852	1391.742	-0.0006	-0.4	4.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
1421	dirMS_041712_NAR_50mM_minus2.7913.7950.3	3	17.29	1	3.13E+05		(R)LQAEIEC	(R)L/Q|A/E/I/E/G L/K/G Q R(A)		112.3	447.921	1341.748	0	0	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1422	dirMS_041712_NAR_60mM_minus.12057.12275.3	3	17.29	1	4.75E+05		(R)INVYYNI	(R)I/N|V/Y/Y/N E/A|T/G G K Y/V P R(A)		127.67	615.3145	1843.934	-0.0048	-2.6	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
1423	dirMS_041712_NAR_120mM_plus.16800.16841.3	3	17.29	0	2.20E+06		(R)EHALLA	(R)E\H\A\L\L|A|Y/T/L/G V/K(Q)		141.53	438.9167	1314.742	-0.0061	-4.6	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
1424	dirMS_041712_NAR_30mM_plus2.21678.21678.2	2	17.29	0	4.75E+04		(K)EIIDLVLI	(K)E I|I|D/L/V/L D/R(I)		168.75	543.3133	1085.62	-0.0008	-0.7	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
1425	dirMS_041712_NAR_50mM_plus2.10927.10927.3	3	17.29	0	6.36E+04		(K)MVMIQI	(K)M V|M/I/Q/D|G P Q N T G/A D K P L/R(I)		125.3	657.663	1970.979	-0.0042	-2.1	5.71	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
1426	dirMS_041712_NAR_50mM_plus2.18436.18436.3	3	17.29	0	5.12E+05		(K)VHLVGII	(K)V H L V G\I/D|I/F/T/G/K(K)		165.02	433.5865	1298.747	-0.0018	-1.3	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
1427	dirMS_041712_NAR_60mM_plus.12364.12632.3	3	17.29	1	3.75E+06		(R)LTPYEVI	(R)L/T|P/Y E/V D/E/L R/R(K)		121.9	464.2489	1390.733	-0.0004	-0.3	4.68	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
1428	dirMS_041712_NAR_30mM_minus2.15860.16068.2	2	17.28	0	3.66E+05		(R)STLNEIY	(R)S T|L/N|E|I|Y/F/G K(T)		140.15	586.3085	1171.599	0.0104	8.8	5.72	29580	6.46	HUMAN	B1AK87	Capping protein (Actin filament) muscle Z-line, beta
1429	dirMS_041712_NAR_30mM_minus2.18966.19150.2	2	17.28	0	9.54E+05		(K)MSIYQA	(K)M/S|I/Y/Q/A/M/W/K(G)		158.93	579.2789	1157.548	0.0023	2	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
1430	dirMS_041712_NAR_50mM_minus2.11008.11008.3	3	17.28	1	5.59E+05		(K)QQEAAL	(K)Q\Q/E/A/A L/E/L/E E L|K/K(K)		131.1	510.2775	1528.822	-0.0038	-2.5	4.49	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
1431	dirMS_041712_NAR_50mM_minus2.13614.13614.3	3	17.28	1	5.22E+05		(K)LTEDKAI	(K)L T|E D K A/D V Q|S/I|I/G/L Q/R(F)		144.82	595.9939	1785.97	-0.0034	-1.9	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
1432	dirMS_041712_NAR_60mM_minus.15621.15621.3	3	17.28	1	5.92E+05	M81m	(K)EVNKFQ	(K)E V/N K F/Q m/A/Y/S/N/L L/R(A)	m:Oxidized methionine	146.73	576.9619	1712.879	15.9923	-1.5	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
1433	dirMS_041712_NAR_30mM_plus2.14122.14283.2	2	17.28	0	1.13E+04		(R)QLLEEEL	(R)Q/L/L|E/E/E/L/A/R(L)		128.93	550.8009	1100.595	-0.0001	-0.1	4.25	533778	5.74	HUMAN	Q15149	Plectin
1434	dirMS_041712_NAR_20mM_minus.13035.13270.3	3	17.27	0	1.85E+06	M73m	(R)AILVDLE	(R)A I\L\V D\L E/P/G T/m/D/S V R(S)	m:Oxidized methionine	182.72	544.6138	1615.836	15.9909	-2.5	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
1435	dirMS_041712_NAR_30mM_minus2.11287.11611.2	2	17.27	0	1.61E+06		(K)FYEAFSK	(K)F/Y|E/A/F/S/K(N)		115.67	446.2172	891.425	0.0024	2.7	6	20127.1	9.4	HUMAN	H0Y598	Heat shock protein HSP 90-beta (Fragment)
1436	dirMS_041712_NAR_30mM_minus2.7027.7109.2	2	17.27	0	2.76E+05		(R)CGCLDE	(R)C/G|C|L/D/E/D/T Q/R(Q)	C:Carbamidomethylation	93.07	627.2485	1253.488	0.0012	1	4.03	266161	5.68	HUMAN	E9PPU0	Epiplakin
1437	dirMS_041712_NAR_60mM_minus.15430.15638.3	3	17.27	0	2.06E+06		(R)QIFHPEC	(R)Q I/F H/P E/Q/L/I/T/G/K(E)		146.53	470.9285	1410.774	-0.003	-2.1	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
1438	dirMS_041712_NAR_20mM_plus.11282.11282.2	2	17.27	0	1.40E+05		(K)STGGAP	(K)S T/G/G/A|P/T F N V T V T K(T)		150.18	690.3592	1379.717	-0.0054	-3.9	8.47	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
1439	dirMS_041712_NAR_50mM_plus2.10003.10030.3	3	17.27	1	2.08E+05		(K)GVAINM	(K)G V/A|I/N\M/V/T E E D/K R(T)		119.98	487.9171	1461.737	0.0001	0.1	4.68	46381.4	5.32	HUMAN	P60842	Eukaryotic initiation factor 4A-I
1440	dirMS_041712_NAR_50mM_plus2.6083.6083.3	3	17.27	0	1.85E+05		(R)ATAPQT	(R)A T/A/P Q/T/Q H/V S/P M\R(Q)		96.3	475.2418	1423.711	-0.0002	-0.1	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
1441	dirMS_041712_NAR_30mM_plus2.16095.16587.2	2	17.26	0	2.35E+06		(R)AALQELI	(R)A A|L|Q/E/L/L|S/K(G)		138.78	486.7894	972.572	-0.0009	-0.9	6.05	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
1442	dirMS_041712_NAR_30mM_plus2.16980.17520.2	2	17.26	0	1.59E+06		(R)LFEGNA	(R)L/F|E|G/N/A/L/L/R(R)		143.53	516.7959	1032.584	0.0009	0.8	6	16684.5	11.19	HUMAN	B5MCT8	40S ribosomal protein S9
1443	dirMS_041712_NAR_30mM_plus2.22646.22646.2	2	17.26	0	8.66E+05		(R)IDLAVLL	(R)I/D|L/A/V L/L G K(T)		176.32	471.3029	941.603	-0.0045	-4.7	5.84	113668.7	6.2	HUMAN	F8W726	Ubiquitin-associated protein 2-like
1444	dirMS_041712_NAR_30mM_plus2.6200.6237.2	2	17.26	0	3.45E+05		(R)GAGSIA(	(R)G A|G\S|I|A/G/A/S A S/P K(E)		86.83	537.2812	1073.559	-0.0034	-3.2	8.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
1445	dirMS_041712_NAR_50mM_plus2.17779.17845.3	3	17.26	1	6.96E+05		(K)SLLGKD\	(K)S/L|L/G K/D\V/L F/L/K(D)		161.7	411.5915	1232.761	-0.0013	-1.1	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
1446	dirMS_041712_NAR_50mM_plus2.18318.18553.3	3	17.26	0	5.12E+05		(K)VHLVGII	(K)V H\L\V\G\I|D|I/F/T/G K(K)		165.02	433.5865	1298.747	-0.0018	-1.3	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
1447	dirMS_041712_NAR_60mM_plus.14437.14579.3	3	17.26	1	7.09E+05		(R)ELISNSSI	(R)E L|I/S/N/S/S D/A\L D/K I/R(Y)		132.23	520.952	1560.823	0.0187	12	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
1448	dirMS_041712_NAR_50mM_minus2.15187.15187.3	3	17.25	0	8.93E+05		(R)LLIHQSL	(R)L/L|I H Q\S\L/A/G/G I/I/G V K(G)		154.82	506.9833	1518.937	-0.0013	-0.8	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
1449	dirMS_041712_NAR_50mM_minus2.16425.16593.3	3	17.25	0	4.54E+05		(R)VLDPFTI	(R)V/L|D|P/F/T I K/P L D/R(K)		161.98	471.9411	1413.81	-0.0013	-0.9	5.93	63448.4	7.29	HUMAN	B4E022	Transketolase
1450	dirMS_041712_NAR_60mM_minus.13653.13718.3	3	17.25	0	4.50E+05		(R)ANPQV(	(R)A N|P Q/V/G V/A/F/P H I K(H)		135.95	459.9265	1377.764	0.0012	0.9	8.8	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
1451	dirMS_041712_NAR_60mM_minus.9362.9405.3	3	17.25	1	2.35E+05		(R)ILKEEQE	(R)I/L|K/E E Q/E|L/Y Q/K(E)		112.08	474.2636	1420.768	0.008	5.6	4.79	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
1452	dirMS_041712_NAR_30mM_plus2.7595.7612.2	2	17.25	0	2.89E+05	M35m	(R)VEFmDI	(R)V/E|F/m/D/D/T/S R(S)	m:Oxidized methionine	94.03	558.2383	1099.473	15.9969	1.8	4.03	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
1453	dirMS_041712_NAR_50mM_plus2.14700.14818.3	3	17.25	0	1.17E+06		(R)EHALLA	(R)E H\A\L\L|A|Y/T/L/G/V/K(Q)		145.75	438.9176	1314.742	-0.0034	-2.6	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
1454	dirMS_041712_NAR_50mM_plus2.15502.15578.3	3	17.25	1	8.65E+05		(R)AITGASL	(R)A I|T/G A/S/L/A/D I/M A K/R(N)		150.37	473.2658	1417.783	-0.0003	-0.2	8.79	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
1455	dirMS_041712_NAR_30mM_minus2.12077.12580.2	2	17.24	0	4.46E+06		(R)EYQELM	(R)E Y|Q/E/L/M/N/V/K(L)		122.25	577.2825	1153.556	0.0019	1.7	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1456	dirMS_041712_NAR_50mM_minus2.16777.16777.3	3	17.24	0	2.38E+05		(R)LGIEGLS	(R)L/G/I/E/G L/S L/H N V L K(L)		164.13	464.9452	1392.821	0.0001	0.1	6.75	177928	5.42	HUMAN	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1
1457	dirMS_041712_NAR_120mM_plus.5716.5716.4	4	17.24	2	4.78E+05		(R)KTGQAP	(R)K\T G Q\A/P/G/Y/S Y/T/A A N K N K(G)		83.5	450.4826	1798.908	0.0003	0.2	9.83	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
1458	dirMS_041712_NAR_30mM_plus2.8721.8791.2	2	17.24	0	3.36E+05		(R)SLETEN/	(R)S L|E|T/E/N/A/G L/R(L)		99.57	545.28	1089.554	-0.0008	-0.7	4.53	74423.5	6.57	HUMAN	P02545	Prelamin-A/C
1459	dirMS_041712_NAR_50mM_plus2.17774.17875.3	3	17.24	1	4.80E+05		(R)LSCLPAF	(R)L/S|C/L/P A F/K D/L I/A/K(V)	C:Carbamidomethylation	162.05	492.6138	1475.829	-0.0022	-1.5	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
1460	dirMS_041712_NAR_20mM_minus.9898.10122.2	2	17.23	0	3.42E+06		(K)DVNAAI	(K)D V|N|A|A|I/A/T I/K(T)		150.18	508.2919	1015.578	-0.0017	-1.7	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
1461	dirMS_041712_NAR_30mM_minus2.16814.17102.2	2	17.23	0	3.39E+05		(K)FANPFP/	(K)F A|N|P|F|P A A V R(G)		146.38	545.2937	1089.584	-0.0039	-3.5	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
1462	dirMS_041712_NAR_30mM_minus2.17164.17626.2	2	17.23	0	1.82E+06		(K)AILFVPR	(K)A I|L|F|V/P/R(R)		149.63	408.2606	815.514	0.0001	0.2	9.79	57660.2	6.38	HUMAN	Q9NQH7	Probable Xaa-Pro aminopeptidase 3
1463	dirMS_041712_NAR_60mM_minus.18426.18828.3	3	17.23	0	2.38E+06		(R)IHFPLAT	(R)I H F\P L A\T|Y|A|P/V/I/S A E K(A)		165.73	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
1464	dirMS_041712_NAR_60mM_minus.8473.8473.3	3	17.23	0	1.38E+04		(R)SAEEEA/	(R)S/A/E/E\E/A A/D L/P T K/P T K(I)		107.37	529.6002	1586.791	-0.0048	-3	4.41	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
1465	dirMS_041712_NAR_20mM_plus.16418.16418.2	2	17.23	0	4.06E+05		(K)LGGSAV	(K)L G\G S A|V/I/S L/E/G K/P L(-)		185.42	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
1466	dirMS_041712_NAR_30mM_plus2.11898.11898.2	2	17.23	0	4.07E+05		(K)GEATVSI	(K)G E|A T\V/S/F/D D|P P S/A K(A)		115.65	710.8312	1420.659	-0.0039	-2.8	4.03	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
1467	dirMS_041712_NAR_30mM_plus2.6702.6820.2	2	17.23	0	5.39E+05		(K)LMSPTG	(K)L/M|S|P/T/G G/R(V)		90.03	409.7135	818.419	0.0008	1	9.75	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
1468	dirMS_041712_NAR_30mM_plus2.8471.8471.2	2	17.23	0	4.04E+05		(K)IANPVE(	(K)I/A|N/P|V/E/G S\T D R(Q)		97.95	579.7908	1158.575	-0.0006	-0.5	4.37	34267.8	9.05	HUMAN	B4DXP5	Poly(rC)-binding protein 2
1469	dirMS_041712_NAR_40mM_plus2.12812.12812.3	3	17.23	1	3.87E+05		(R)VLELVSI	(R)V L|E|L/V/S I T A N K N T\C P G D/R(S)	C:Carbamidomethylation	142.58	663.0201	1987.028	0.018	9.1	6.04	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
1470	dirMS_041712_NAR_50mM_plus2.12512.12677.3	3	17.23	1	8.84E+05		(R)ELISNSSI	(R)E L|I/S/N/S|S/D A|L/D K I/R(Y)		134.15	520.9473	1560.823	0.0046	2.9	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
1471	dirMS_041712_NAR_20mM_plus.18935.18935.2	2	17.22	0	1.05E+05		(K)DTSYLFI	(K)D T S/Y/L/F/I/T/G|P D V/V K(S)		201.92	777.9049	1554.805	-0.0025	-1.6	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
1472	dirMS_041712_NAR_50mM_plus2.16946.16946.3	3	17.22	0	7.80E+05		(R)QYYTLLI	(R)Q Y/Y/T/L L/N\Q A/P D\M L H/R(K)		156.93	621.6447	1862.922	-0.0022	-1.2	6.74	4335.1	9.82	HUMAN	E5RH00	Ras GTPase-activating protein-binding protein 1
1473	dirMS_041712_NAR_30mM_minus2.7745.7767.2	2	17.21	0	1.61E+05		(K)IFAQDGI	(K)I/F|A/Q/D|G E/G Q R(I)		96.53	560.7727	1120.538	0	0	4.37	258215.9	5.48	HUMAN	E7EN95	Filamin-B
1474	dirMS_041712_NAR_120mM_plus.17422.17422.3	3	17.21	2	7.46E+05		(R)NLKASLI	(R)N/L|K/A/S/L E N S L/R E V E|A R(Y)		143.9	610.332	1828.988	-0.0061	-3.3	6.23	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1475	dirMS_041712_NAR_50mM_plus2.21077.21077.3	3	17.21	0	3.77E+06		(R)AGKPVI(	(R)A G K\P V I\C\A/T/Q/M/L/E S M I K(K)	C:Carbamidomethylation	180.08	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
1476	dirMS_041712_NAR_120mM_minus.4747.4747.3	3	17.2	1	3.96E+05		(K)AGADEE	(K)A/G/A/D/E E R A E T A/R(L)		76.8	425.8687	1275.592	-0.0008	-0.7	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
1477	dirMS_041712_NAR_120mM_minus.7382.7401.3	3	17.2	1	3.19E+05		(K)IYEDGDI	(K)I/Y/E/D/G D/D D M/K/R(T)		94.63	452.8645	1356.574	0.0053	3.9	4.03	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
1478	dirMS_041712_NAR_50mM_minus2.10263.10325.3	3	17.2	0	2.72E+05		(R)TFIAIKPI	(R)T/F|I/A I/K/P/D/G V Q/R(G)		126.83	448.923	1344.763	-0.009	-6.7	8.41	6640.6	8.25	HUMAN	C9K028	Nucleoside diphosphate kinase A (Fragment)
1479	dirMS_041712_NAR_120mM_plus.9773.10358.3	3	17.2	0	9.16E+05		(R)GFCLPPI	(R)G F|C/L/P/P/H/C S/R(G)	C:Carbamidomethylation	104.65	410.8593	1230.551	0.0127	10.3	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
1480	dirMS_041712_NAR_20mM_minus.12201.12201.2	2	17.19	0	1.07E+06	M313m	(R)TVQSLEI	(R)T V/Q/S L/E|I\D/L D/S/m R(N)	m:Oxidized methionine	170.83	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1481	dirMS_041712_NAR_60mM_minus.13292.13292.3	3	17.19	1	2.81E+05	M194m	(R)KLQEEEI	(R)K\L Q E E E\L\L\A/T|Q/V|D/m R(A)	m:Oxidized methionine	133.93	606.9793	1802.932	15.9917	-1.8	4.41	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
1482	dirMS_041712_NAR_20mM_plus.12068.12068.2	2	17.19	0	1.20E+05		(R)IYVVDV(	(R)I/Y/V|V/D|V/G S E/P R(A)		156.17	617.3237	1233.647	-0.0073	-5.9	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
1483	dirMS_041712_NAR_30mM_plus2.13816.13816.2	2	17.19	0	7.43E+05		(R)GDFCIQ	(R)G D/F/C/I/Q V|G/R(-)	C:Carbamidomethylation	125.57	526.2542	1051.499	0.0022	2.1	5.84	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
1484	dirMS_041712_NAR_30mM_plus2.14833.14833.2	2	17.19	0	3.81E+05		(K)VELDNM	(K)V/E|L|D/N|M/P L/R(G)		130.8	543.7824	1086.561	-0.0037	-3.4	4.37	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
1485	dirMS_041712_NAR_50mM_plus2.16541.16922.3	3	17.19	1	6.78E+06		(K)QLDDLK	(K)Q/L/D/D/L/K/V/E/L/S/Q L R(V)		155.75	519.6261	1556.864	-0.0005	-0.3	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
1486	dirMS_041712_NAR_120mM_minus.8157.8241.4	4	17.18	2	2.31E+06		(K)KGAVAE	(K)K\G A\V\A|E|D/G/D/E L R T E/P E/A/K(K)		99.28	479.4901	1914.94	-0.0018	-0.9	4.36	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
1487	dirMS_041712_NAR_50mM_minus2.9278.9450.3	3	17.18	1	1.55E+06		(K)IQVLQQ	(K)I/Q|V|L|Q/Q/Q/A D D/A E E R A E R(L)		121.5	666.9985	1998.984	-0.003	-1.5	4.18	26611.3	4.47	HUMAN	A6NL28	Putative tropomyosin alpha-3 chain-like protein
1488	dirMS_041712_NAR_60mM_minus.7884.8120.3	3	17.18	1	8.24E+05		(R)LREDEN/	(R)L R E D\E\N\A\E|P|V/G T/T/Y Q K(T)		104.68	617.3015	1849.893	-0.0027	-1.5	4.41	76925.9	4.46	HUMAN	A8MV58	Drebrin
1489	dirMS_041712_NAR_120mM_plus.18704.18836.3	3	17.18	1	2.43E+05		(K)SIYGEKF	(K)S I|Y|G/E K/F/E D/E/N F I L/K(H)		151.63	611.3079	1831.911	-0.0021	-1.2	4.41	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
1490	dirMS_041712_NAR_20mM_plus.12650.12671.2	2	17.18	0	1.21E+05		(K)GTIQVIT	(K)G T/I/Q|V|I|T/Q/G T/S L K(N)		160.13	673.3872	1345.769	-0.0014	-1.1	8.75	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
1491	dirMS_041712_NAR_30mM_plus2.22865.22902.2	2	17.18	0	1.84E+06		(R)GFGFVLI	(R)G/F|G|F/V/L/F/K(E)		179.85	457.76	914.514	-0.0007	-0.8	8.75	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
1492	dirMS_041712_NAR_40mM_plus2.6824.6824.2	2	17.18	0	4.44E+04		(K)SFQQSSI	(K)S F|Q/Q/S/S/L\S/R(D)		100.17	520.2619	1039.517	-0.0002	-0.2	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
1493	dirMS_041712_NAR_60mM_plus.12956.13016.3	3	17.18	1	1.55E+06	M72m	(R)TEmENE	(R)T|E|m/E N E|F/V L/I/K/K(D)	m:Oxidized methionine	124.62	499.594	1480.772	15.9959	0.6	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
1494	dirMS_041712_NAR_60mM_minus.15787.15787.3	3	17.17	1	2.97E+05		(R)IDTRNEL	(R)I/D T R N E\L/E|S/Y/A Y S L K(N)		148.05	601.3049	1801.897	0.0035	1.9	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
1495	dirMS_041712_NAR_60mM_minus.8964.8964.2	2	17.17	0	9.67E+05		(K)QEYDES(	(K)Q|E\Y\D/E S/G\P/S/I/V/H/R(K)		110.35	758.8539	1516.703	-0.0021	-1.4	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
1496	dirMS_041712_NAR_50mM_plus2.10846.10846.3	3	17.17	1	2.46E+06		(R)MQKEIT	(R)M/Q/K E I T A|L/A|P S T M K(I)		124.03	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
1497	dirMS_041712_NAR_120mM_minus.9268.9390.3	3	17.16	1	7.92E+05		(K)EFFNGKI	(K)E F/F N/G K/E/P/S/R(G)		105.4	404.2008	1210.585	0.0027	2.3	6.24	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
1498	dirMS_041712_NAR_20mM_minus.13142.13271.2	2	17.16	0	4.63E+05		(K)TITLEVEI	(K)T I|T|L/E/V|E|P S D T I E N V/K(A)		183.05	894.4654	1787.927	-0.0038	-2.1	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
1499	dirMS_041712_NAR_30mM_minus2.20094.20246.2	2	17.16	0	1.53E+06		(R)VIFGLFG	(R)V/I|F/G/L/F/G/K(T)		170.93	440.768	880.529	-0.0004	-0.4	8.72	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
1500	dirMS_041712_NAR_40mM_minus2.12208.12396.3	3	17.16	1	6.50E+05		(R)IIAFVGS	(R)I/I|A|F/V/G/S/P V E D N E K D L V K(L)		156.3	658.3553	1973.059	-0.0076	-3.9	4.32	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
1501	dirMS_041712_NAR_50mM_minus2.18083.18083.3	3	17.16	1	1.52E+05		(R)GDLGIEI	(R)G D L/G/I|E\I/P A E K V F/L A Q K(M)		172.1	610.0112	1828.022	-0.0024	-1.3	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
1502	dirMS_041712_NAR_60mM_minus.14270.14528.3	3	17.16	1	5.52E+05		(K)VLAGDK	(K)V/L|A/G D K/N/F|I/T/A E E/L R(R)		140.2	559.3035	1675.901	-0.0054	-3.2	4.68	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
1503	dirMS_041712_NAR_20mM_plus.14237.14237.2	2	17.16	0	3.41E+04		(R)IALTDN/	(R)I/A|L/T/D/N/A/L/I A R(S)		170.65	585.8432	1170.684	-0.005	-4.2	5.84	24489.6	10.74	HUMAN	A8MUD9	60S ribosomal protein L7
1504	dirMS_041712_NAR_40mM_plus2.17549.17711.3	3	17.16	1	5.62E+05		(R)GLLPGLI	(R)G L|L|P\G L/L/P\A/P A D K L T/P K(G)		170.58	567.6811	1701.031	-0.0022	-1.3	8.59	153084.9	5.55	HUMAN	Q6P2E9	Enhancer of mRNA-decapping protein 4
1505	dirMS_041712_NAR_50mM_minus2.12728.13107.3	3	17.15	0	4.17E+06	M84m	(K)YPIEHGI	(K)Y/P/I E H G I I|T|N|W D D m E K(I)	m:Oxidized methionine	141.65	659.6398	1960.911	15.9939	-0.5	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
1506	dirMS_041712_NAR_120mM_plus.13261.13261.3	3	17.15	2	6.46E+05		(R)ELNITAA	(R)E L|N/I/T A/A K E I E/V/G G G R K(A)		123.02	595.6661	1784.987	-0.0027	-1.5	6.33	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
1507	dirMS_041712_NAR_20mM_plus.16440.16440.2	2	17.15	0	1.40E+05		(R)QAQEYE	(R)Q A/Q/E/Y/E/A L|L/N|I\K(V)		184.52	710.3754	1419.748	-0.0043	-3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1508	dirMS_041712_NAR_50mM_plus2.11538.11997.3	3	17.15	1	1.27E+06		(R)INVYYNI	(R)I/N|V|Y/Y|N E/A/T/G G K Y V/P R(A)		128.47	615.3151	1843.934	-0.003	-1.6	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
1509	dirMS_041712_NAR_60mM_plus.11875.11888.3	3	17.15	0	4.38E+05		(R)MVQVH	(R)M/V|Q|V/H/E|L/S C E/G I/S K(S)	C:Carbamidomethylation	119.42	539.5969	1616.777	-0.0009	-0.6	5.38	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
1510	dirMS_041712_NAR_30mM_minus2.14901.15325.2	2	17.14	0	1.56E+06		(R)QITVND	(R)Q I|T|V|N/D/L/P V/G R(S)		135.22	606.3404	1211.674	-0.0007	-0.6	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
1511	dirMS_041712_NAR_50mM_minus2.16685.16870.3	3	17.13	1	2.99E+05		(R)SELELTL(	(R)S E|L|E/L/T/L/G K L/E Q V R(S)		163.72	538.9725	1614.906	-0.0032	-2	4.78	533778	5.74	HUMAN	Q15149	Plectin
1512	dirMS_041712_NAR_50mM_minus2.17260.17598.3	3	17.13	0	1.05E+06	M195m	(R)LHFFmP	(R)L H F\F m|P G|F|A|P/L/T S R(G)	m:Oxidized methionine	167.33	546.2872	1620.835	16.0115	10.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1513	dirMS_041712_NAR_20mM_plus.17481.17925.2	2	17.13	0	1.37E+06		(R)YLTVAA\	(R)Y/L|T|V/A/A/V/F/R(G)		193.83	520.3009	1039.593	0.001	1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
1514	dirMS_041712_NAR_20mM_plus.18779.18779.2	2	17.13	0	2.87E+05		(K)LAVEALS	(K)L A V E\A|L|S/S L/D G D\L A/G R(Y)		200.48	793.9214	1586.838	-0.0029	-1.8	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
1515	dirMS_041712_NAR_30mM_plus2.16868.16868.2	2	17.13	0	1.67E+05		(K)EQFLDG	(K)E Q/F|L/D/G D/G/W T S/R(W)		141.32	705.8178	1410.628	-0.0001	-0.1	4.03	28545.1	4.5	HUMAN	K7EJB9	Calreticulin (Fragment)
1516	dirMS_041712_NAR_50mM_plus2.12861.13214.3	3	17.13	1	1.61E+06		(K)LIADVAF	(K)L/I|A/D/V/A/P S A I R E N D/I/K(S)		136.73	575.6533	1724.954	-0.0088	-5.1	4.56	18388.8	6.85	HUMAN	F5H1Y3	Flap endonuclease 1 (Fragment)
1517	dirMS_041712_NAR_50mM_minus2.15278.15278.3	3	17.12	1	8.56E+05		(K)ILLAELE(	(K)I/L|L/A/E L/E Q L K/G Q G K(S)		155.77	513.9739	1539.911	-0.0033	-2.2	6.14	49709.6	5.19	HUMAN	B0YJC4	Vimentin
1518	dirMS_041712_NAR_120mM_minus.10518.10827.3	3	17.11	1	6.68E+05		(R)RGVVGF	(R)R G V\V\G|P/E|L/Y/G/R(L)		113.2	401.559	1202.664	-0.0016	-1.3	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
1519	dirMS_041712_NAR_30mM_minus2.10368.10514.2	2	17.11	0	6.05E+05		(K)EAAENS	(K)E A|A|E/N/S L/V/A/Y/K(A)		110.8	597.8033	1194.6	-0.0008	-0.6	4.53	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
1520	dirMS_041712_NAR_30mM_minus2.14927.15110.2	2	17.11	0	9.43E+05		(K)LYLADPI	(K)L/Y|L|A|D|P/M/K(A)		135.13	475.7541	950.502	-0.0006	-0.7	5.83	7781.8	6.82	HUMAN	E9PE20	Signal recognition particle 9 kDa protein
1521	dirMS_041712_NAR_50mM_minus2.6740.6761.3	3	17.11	1	1.91E+05	M24m M2	(K)LAEQAE	(K)L/A|E|Q/A/E R Y D/D m/A/A/A/m K(A)	m:Oxidized methionine	104.88	615.6099	1812.825	31.9897	-0.1	4.32	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha

1522	dirMS_041712_NAR_60mM_minus.9506.9506.3	3	17.11	0	3.19E+05		(R)QLSQAG	(R)Q L/S\Q/A/G/S/F S/D G T H G G L R(Y)		113.52	573.2781	1717.825	-0.0055	-3.2	6.74	266161	5.68	HUMAN	E9PPU0	Epiplakin
1523	dirMS_041712_NAR_20mM_plus.15561.15561.2	2	17.11	0	2.37E+05		(K)TITLEVEI	(K)T I/T L E/V|E|P S D T I E N V K(A)		179.03	894.4658	1787.927	-0.003	-1.7	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
1524	dirMS_041712_NAR_40mM_plus2.13006.13088.3	3	17.11	0	2.26E+05		(R)VVLSVSS	(R)V V|L/S/V/S S G G Q/H T V/L/L/V K(D)		143.62	575.0089	1723.011	0.0009	0.5	8.73	45424.7	7.24	HUMAN	P18754	Regulator of chromosome condensation
1525	dirMS_041712_NAR_40mM_plus2.12422.12422.3	3	17.1	1	1.73E+05		(K)IINADSE	(K)I/I/N A/D/S/E D/P K Y I I N V K(Q)		139.07	611.3255	1831.98	-0.0181	-9.9	4.56	14693.3	4.69	HUMAN	C9JLS9	26S protease regulatory subunit 7 (Fragment)
1526	dirMS_041712_NAR_50mM_plus2.11362.11362.3	3	17.1	1	1.25E+06		(K)NQVAM	(K)N\Q|V|A\M/N P/T/N T V/F/D A K/R(L)		127.8	602.6354	1805.896	-0.0046	-2.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
1527	dirMS_041712_NAR_60mM_plus.12356.12356.3	3	17.1	1	7.68E+05		(K)YGQISEV	(K)Y/G\Q/I/S E V/V/V/V K/D/R(E)		121.22	497.9427	1491.817	-0.003	-2	6.07	28815.3	9.52	HUMAN	B4E2X2	Cold-inducible RNA-binding protein
1528	dirMS_041712_NAR_20mM_minus.10608.10694.2	2	17.09	0	2.00E+05		(R)TTPSYVA	(R)T T|P S/Y/V|A/F/T D/T E/R(L)		154.63	744.3547	1487.701	0.0009	0.6	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
1529	dirMS_041712_NAR_30mM_minus2.10248.10248.2	2	17.09	0	3.99E+05		(K)ATAVVD	(K)A T|A/V|V D G A\F K(E)		109.93	489.7645	978.525	-0.0037	-3.8	5.88	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
1530	dirMS_041712_NAR_30mM_minus2.7601.7601.2	2	17.09	0	8.10E+04		(R)SDEGQL	(R)S\D|E/G Q/L/S|P A T/R(G)		95.82	580.7788	1160.554	-0.0039	-3.3	4.37	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
1531	dirMS_041712_NAR_120mM_plus.19549.19708.4	4	17.09	1	3.15E+06		(R)DFNHIN	(R)D F N H\I N|V E|L/S/L/L/G K K(K)		155.95	432.4918	1726.949	-0.0033	-1.9	6.75	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
1532	dirMS_041712_NAR_30mM_plus2.17525.17570.2	2	17.09	0	1.64E+05		(R)ASLEAAI	(R)A S/L/E/A|A|I/A|D/A E Q/R(G)		145.03	672.8406	1344.675	-0.0015	-1.1	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1533	dirMS_041712_NAR_50mM_plus2.12434.12434.3	3	17.09	0	2.04E+05		(K)AIIKPQY	(K)A I|I/K/P Q Y V D/Q I/P K(A)		133.23	504.9637	1512.878	-0.0019	-1.3	8.54	47949	9.16	HUMAN	D6R9I9	ATP-binding cassette sub-family E member 1
1534	dirMS_041712_NAR_50mM_plus2.19845.19985.3	3	17.09	1	5.31E+05		(-)MDELQL	(-)M/D|E|L/Q L/F/R/G D T V/L/L/K(G)		173.25	593.3209	1777.952	-0.0035	-2	4.56	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
1535	dirMS_041712_NAR_60mM_plus.5351.5538.3	3	17.09	0	1.54E+06		(R)AEAEAG	(R)A/E|A|E/A/G S P R P D|P/R(E)		85.88	451.5555	1352.655	-0.0034	-2.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
1536	dirMS_041712_NAR_30mM_plus2.14311.14311.2	2	17.08	0	9.71E+05		(R)MGQMA	(R)M\G Q|M|A|M/G/G/A M/G I N N R(G)		127.33	769.8376	1538.67	-0.0015	-1	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
1537	dirMS_041712_NAR_30mM_plus2.15092.15374.2	2	17.08	0	9.84E+05		(K)LWNTLG	(K)L/W|N|T/L/G V/C/K(Y)	C:Carbamidomethylation	132.65	545.7923	1090.571	0.0059	5.5	8.75	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
1538	dirMS_041712_NAR_50mM_plus2.18985.19262.3	3	17.08	0	5.88E+05		(R)GFGFITF	(R)G F|G|F|I/T/F/T N/P E H A S V A M R(A)		168.7	661.3258	1981.959	0.004	2	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
1539	dirMS_041712_NAR_20mM_minus.12249.12487.3	3	17.07	0	8.33E+05	M73m	(R)AVLVDLI	(R)A V|L\V D L E/P/G/T/m/D/S V R(S)	m:Oxidized methionine	172.57	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
1540	dirMS_041712_NAR_50mM_minus2.16032.16300.3	3	17.07	1	4.43E+06		(R)VSFELFA	(R)V/S|F/E/L/F/A D K V/P K(T)		159.72	460.5908	1379.757	0.0009	0.7	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
1541	dirMS_041712_NAR_60mM_minus.6036.6047.3	3	17.07	1	2.71E+06		(K)DSYVGD	(K)D S/Y V/G/D/E/A/Q/S K R(G)		90.57	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
1542	dirMS_041712_NAR_20mM_plus.18352.18352.2	2	17.07	0	1.95E+05		(R)AAVEEG	(R)A A V E E\G\I|V|L|G|G G C A L/L/R(C)	C:Carbamidomethylation	197.9	842.9549	1684.905	-0.0025	-1.5	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
1543	dirMS_041712_NAR_30mM_plus2.17036.17145.2	2	17.07	0	3.76E+04	M185m	(K)LAVNm\	(K)L/A|V|N/m|V/P F P R(L)	m:Oxidized methionine	142.12	580.3176	1143.634	15.9936	-1.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1544	dirMS_041712_NAR_50mM_minus2.14186.14245.3	3	17.06	0	2.61E+05		(R)TIQVENS	(R)T I|Q|V/E N\S H L/I/L/T/G A G A L N K(V)		149.02	660.367	1979.092	-0.0056	-2.8	6.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
1545	dirMS_041712_NAR_50mM_minus2.8713.8713.3	3	17.06	1	2.14E+05		(R)VAIEPGA	(R)V/A|I|E/P/G A P R E/N D E F C K(M)	C:Carbamidomethylation	117.37	611.2923	1831.864	-0.002	-1.1	4.41	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
1546	dirMS_041712_NAR_60mM_minus.16774.16774.3	3	17.06	1	2.85E+05		(R)GQFSTD	(R)G Q|F/S T D E L/V/A/E V E/K R(N)		153.92	569.9569	1707.855	0.0013	0.8	4.41	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
1547	dirMS_041712_NAR_30mM_plus2.6894.6894.2	2	17.06	0	7.31E+04		(R)ENPYYD	(R)E N|P/Y/Y/D/S R(V)		90.4	522.2255	1043.443	0.0009	0.8	4.37	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
1548	dirMS_041712_NAR_20mM_minus.13984.13984.2	2	17.05	0	6.81E+05		(R)VLITTDL	(R)V L|I/T|T D/L/L A R(G)		192.22	557.8438	1114.683	-0.0027	-2.4	5.81	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
1549	dirMS_041712_NAR_30mM_plus2.19782.19782.2	2	17.05	0	3.53E+05		(K)SNNVEM	(K)S N/N/V|E\M D W/V L\K(H)		156.98	667.8205	1334.641	-0.0072	-5.4	4.37	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
1550	dirMS_041712_NAR_40mM_plus2.17732.17732.3	3	17.05	1	1.96E+05		(R)LKLPSIPI	(R)L K\L P\S I\P L|V|P V/S A Q K(R)		170.73	530.671	1589.999	-0.0004	-0.3	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
1551	dirMS_041712_NAR_60mM_plus.13079.13542.3	3	17.05	1	8.86E+05		(R)VIDRELY	(R)V/I|D R E L|Y\Q|Q/L/Q/R(G)		125.78	520.952	1560.849	-0.0078	-5	6.04	533778	5.74	HUMAN	Q15149	Plectin
1552	dirMS_041712_NAR_20mM_minus.12216.12552.3	3	17.04	0	8.33E+05	M73m	(R)AVLVDLI	(R)A V\L\V D\L E/P/G T|m/D S V R(S)	m:Oxidized methionine	172.57	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
1553	dirMS_041712_NAR_50mM_minus2.14263.14263.3	3	17.04	1	6.62E+05		(R)VEKIPG(	(R)V E/K\I\P G G\I|I|E/D/S/C V|L/R(G)	C:Carbamidomethylation	149.1	595.6534	1784.958	-0.0118	-6.6	4.68	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
1554	dirMS_041712_NAR_60mM_minus.8231.8231.3	3	17.04	1	1.42E+05		(R)LSQIGVE	(R)L/S/Q/I/G V/E N/T E E N R R(L)		106.07	548.9481	1644.83	-0.0002	-0.1	4.79	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
1555	dirMS_041712_NAR_30mM_plus2.19187.19670.2	2	17.04	0	4.11E+06		(K)TLGILGL	(K)T/L|G|I|L|G/L|G R(I)		156.62	450.2857	899.567	-0.0032	-3.5	9.41	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
1556	dirMS_041712_NAR_30mM_minus2.13847.13890.2	2	17.03	0	3.08E+05	M313m	(K)NSLESYA	(K)N S|L|E|S/Y/A/F/N m K(A)	m:Oxidized methionine	128.9	660.3011	1303.599	15.9962	1	6	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
1557	dirMS_041712_NAR_40mM_minus2.12336.12461.3	3	17.03	1	2.87E+05		(K)DVAIKEF	(K)D V|A|I|K E/P\L|V/D V|V D/P K(Q)		156.13	546.3068	1636.916	-0.0098	-6	4.23	24376.8	6.08	HUMAN	E9PIX6	Protein arginine N-methyltransferase 1 (Fragment)
1558	dirMS_041712_NAR_120mM_plus.20505.21040.4	4	17.03	1	3.77E+06		(R)DYLHLPI	(R)D Y\L H|L\P|P/E\I/V/P A T L R R(S)		162.23	473.2689	1890.06	-0.0058	-3.1	6.75	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
1559	dirMS_041712_NAR_50mM_plus2.14636.14797.3	3	17.03	1	4.12E+06		(R)ELISNAS	(R)E L|I/S/N/A/S|D|A L/D K I R(L)		145.58	515.6136	1544.828	-0.0016	-1	4.56	5582.4	4.81	HUMAN	F8W026	Endoplasmin (Fragment)
1560	dirMS_041712_NAR_60mM_plus.15773.16290.3	3	17.03	1	3.36E+06		(R)MSMKE'	(R)M/S M K E V\D\E\Q|M|L/N/V/Q/N K(N)		141.48	641.9696	1923.897	-0.003	-1.6	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
1561	dirMS_041712_NAR_30mM_minus2.14863.14863.2	2	17.02	0	2.59E+04		(R)LSLYQAI	(R)L/S|L/Y/Q A/M/R(Q)		134.33	491.2611	981.519	-0.0037	-3.8	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
1562	dirMS_041712_NAR_50mM_minus2.10450.10963.3	3	17.02	1	7.18E+06	M72m	(R)TEmENE	(R)T\E|m/E N E|F/V L/I/K/K(D)	m:Oxidized methionine	129.07	499.5937	1480.772	15.995	0	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
1563	dirMS_041712_NAR_50mM_minus2.15952.15952.3	3	17.02	1	8.21E+04		(K)DANAKL	(K)D A/N/A K L\S E\L|E/A/A|L/Q R(A)		158.97	543.6248	1628.86	-0.0004	-0.2	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1564	dirMS_041712_NAR_50mM_minus2.16991.16991.3	3	17.02	1	3.18E+05		(K)AILILDNI	(K)A I|L/I/L/D/N D/G D R L F A K(Y)		165.27	558.6442	1673.922	-0.004	-2.4	4.43	18430.9	4.79	HUMAN	F8VS17	Coatomer subunit zeta-1
1565	dirMS_041712_NAR_60mM_minus.9237.9237.3	3	17.02	0	2.84E+05		(K)ATAGDT	(K)A/T|A/G D/T/H|L G G E D/F D N R(L)		111.4	559.2488	1675.731	0.0012	0.7	4.22	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
1566	dirMS_041712_NAR_30mM_plus2.13940.14058.2	2	17.02	0	8.38E+05		(R)AFFSEVE	(R)A/F|F|S/E/V/E/R(R)		126.17	492.7436	984.479	0.0014	1.4	4.53	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
1567	dirMS_041712_NAR_30mM_plus2.7403.7423.2	2	17.02	0	1.76E+05		(K)TTTAAA'	(K)T T|T/A|A|A|V/A S/T/G|P S S R(S)		93.25	689.3507	1377.697	-0.0027	-2	9.41	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
1568	dirMS_041712_NAR_40mM_plus2.17456.17834.3	3	17.02	1	5.62E+05		(R)GLLPGLI	(R)G L|L|P|G L/L/P\A/P A D K L T P K(G)		170.58	567.6811	1701.031	-0.0022	-1.3	8.59	153084.9	5.55	HUMAN	Q6P2E9	Enhancer of mRNA-decapping protein 4
1569	dirMS_041712_NAR_40mM_plus2.18529.18788.3	3	17.02	0	4.34E+05		(K)ALIEVLQ	(K)A L|I/E|V/L/Q/P L I/A E H Q A R(R)		176.12	601.0146	1801.033	-0.0038	-2.1	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
1570	dirMS_041712_NAR_30mM_plus2.21715.21864.2	2	17.01	0	3.31E+05		(R)IIWELIK(	(R)I/I|W/E|L/I/K(E)		169.42	457.7881	914.571	-0.002	-2.2	6	17833.3	8.73	HUMAN	C9J4N6	Isocitrate dehydrogenase [NADP] cytoplasmic (Fragment)
1571	dirMS_041712_NAR_60mM_plus.6354.6354.3	3	17.01	0	9.24E+04		(R)HNGAAE	(R)H N G A A E|P E|P E/A E T A/R(G)		91.8	526.9106	1578.714	0.003	1.9	4.48	87537	9.67	HUMAN	Q9Y446	Plakophilin-3
1572	dirMS_041712_NAR_50mM_minus2.15713.15799.3	3	17	0	1.29E+05		(K)FTISDHP	(K)F/T|I/S D/H P Q/P I D/P L/L/K(N)		157.77	574.3122	1720.927	-0.0048	-2.8	5.21	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
1573	dirMS_041712_NAR_60mM_minus.6937.7030.3	3	17	1	2.74E+05		(R)IVDGKV'	(R)I/V|D/G K/V/V/S E/T N D\T K(V)		97.95	502.2642	1504.785	-0.0073	-4.8	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
1574	dirMS_041712_NAR_20mM_plus.16772.16772.2	2	17	0	3.05E+05		(K)VQIAVA	(K)V Q|I/A|V/A/N A/Q E L/L Q R(M)		186.97	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
1575	dirMS_041712_NAR_40mM_minus2.9011.9011.3	3	16.99	0	2.56E+04		(K)AASAGV	(K)A/A/S/A/G V/P Y H G E V/P V S L A R(A)		135.53	594.3141	1780.934	-0.0063	-3.5	6.79	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
1576	dirMS_041712_NAR_50mM_minus2.14841.14901.3	3	16.99	1	2.45E+05		(K)IIVDELK(	(K)I/I|V/D E/L K/Q E/V/I/S T/S S K(A)		152.52	597.0016	1788.995	-0.0051	-2.8	4.68	30149.5	5.96	HUMAN	D6RAC2	Guanine nucleotide-binding protein subunit beta-2-like 1
1577	dirMS_041712_NAR_50mM_minus2.8634.8716.3	3	16.99	0	1.65E+05	M180m	(R)VVVLmG	(R)V V|V|L/m/G S/T/S/D L/G H C E K(I)	C:Carbamidomethylation m:Oxid	117.55	583.2829	1731.84	15.9937	-0.7	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
1578	dirMS_041712_NAR_60mM_minus.13610.13610.3	3	16.99	0	3.60E+05		(K)ILQGGV(	(K)I/L|Q/G/G V/G/I/P H I/R(S)		136.02	420.5931	1259.758	0.0065	5.1	9.75	9772.1	9.6	HUMAN	D6RGE5	Casein kinase I isoform alpha
1579	dirMS_041712_NAR_120mM_plus.12512.12970.3	3	16.99	1	9.33E+05		(R)LTPYEVD	(R)L/T|P/Y E|V D/E/L R/R(K)		119.82	464.2488	1390.733	-0.0007	-0.5	4.68	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
1580	dirMS_041712_NAR_120mM_plus.13692.14009.3	3	16.99	1	3.64E+06		(K)ASLENSI	(K)A/S|L/E/N S/L/R E V/E/A/R(Y)		125.98	491.9278	1473.766	0.0033	2.2	4.79	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1581	dirMS_041712_NAR_20mM_plus.11302.11302.2	2	16.99	0	2.56E+04		(R)IVLQIDN	(R)I/V|L|Q/I/D N A R(L)		150.32	521.3056	1041.605	-0.0012	-1.1	5.84	20842.9	5.32	HUMAN	C9JM50	Keratin, type I cytoskeletal 19 (Fragment)
1582	dirMS_041712_NAR_20mM_plus.15525.15608.2	2	16.99	0	2.37E+05		(K)TITLEVEI	(K)T I|T/L|E/V|E|P S D T I E/N V K(A)		179.03	894.4658	1787.927	-0.003	-1.7	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
1583	dirMS_041712_NAR_20mM_plus.17082.17431.2	2	16.99	0	1.44E+06		(R)VLITTDL	(R)V/L|I|T|T/D/L L/A R(G)		191	557.8442	1114.683	-0.0019	-1.7	5.81	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
1584	dirMS_041712_NAR_30mM_plus2.16108.16255.2	2	16.99	0	5.14E+05		(R)ALQALEI	(R)A/L|Q|A|L/E/E/L/R(L)		137.4	521.7961	1042.589	-0.0042	-4	4.53	533778	5.74	HUMAN	Q15149	Plectin
1585	dirMS_041712_NAR_30mM_plus2.17016.17016.2	2	16.99	0	2.20E+05		(R)GLGLDD	(R)G L/G|L/D/D/A/L/E/P R(Q)		142.2	578.3042	1155.6	0.0007	0.6	4.03	51326.8	5.49	HUMAN	Q9Y230	RuvB-like 2
1586	dirMS_041712_NAR_50mM_plus2.15918.15935.3	3	16.99	1	1.60E+06		(R)DVDFELI	(R)D V|D/F/E/L/I/K V E G/K(V)		152	464.5859	1391.742	0.0015	1.1	4.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
1587	dirMS_041712_NAR_60mM_plus.12503.12707.3	3	16.99	1	8.88E+05		(K)NKTGAA	(K)N K T G A A|P|I|I/D/V/V/R(S)		122.72	451.9377	1353.785	0.0137	10.1	8.75	10240.9	10.46	HUMAN	E9PJD9	60S ribosomal protein L27a
1588	dirMS_041712_NAR_50mM_minus2.13648.13648.3	3	16.98	0	4.59E+04		(K)MLDAED	(K)M/L/D/A E/D I/V N T A R P D/E K(A)		144.98	606.2965	1816.875	0.0004	0.2	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
1589	dirMS_041712_NAR_60mM_minus.13309.13309.3	3	16.98	1	8.97E+05		(R)ELISNSSI	(R)E L/I/S/N/S/S D/A\L D K I R(Y)		134.7	520.9443	1560.823	-0.0044	-2.8	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
1590	dirMS_041712_NAR_40mM_minus2.13145.13145.3	3	16.97	1	9.20E+04		(K)VLDSGA	(K)V L|D|S/G A/P I K/I/P V/G P E T L G R(I)		160.87	640.3618	1919.096	-0.0252	-13.1	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
1591	dirMS_041712_NAR_30mM_plus2.11036.11074.2	2	16.97	0	5.95E+04		(K)FAAATG	(K)F A|A|A|T|G/A|T/P I A G R(F)		111.33	602.3261	1203.648	-0.0031	-2.6	9.75	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
1592	dirMS_041712_NAR_30mM_plus2.21540.21863.2	2	16.97	0	6.04E+05		(R)IIWQFIK	(R)I/I|W/Q/F/I/K(E)		169.2	474.2886	947.571	-0.0014	-1.5	8.75	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
1593	dirMS_041712_NAR_50mM_plus2.10688.10688.3	3	16.97	1	2.00E+05		(K)GLESTTL	(K)G L/E/S T T L/A D K/D/G E I Y C/K(G)	C:Carbamidomethylation	123.87	633.9707	1899.9	-0.0029	-1.5	4.32	16685.6	9.7	HUMAN	E9PND2	Cysteine and glycine-rich protein 1 (Fragment)
1594	dirMS_041712_NAR_20mM_minus.13933.14086.2	2	16.96	0	6.81E+05		(R)VLITTDL	(R)V/L|I|T|T/D/L L/A R(G)		192.22	557.8438	1114.683	-0.0027	-2.4	5.81	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
1595	dirMS_041712_NAR_30mM_minus2.12031.12561.2	2	16.96	0	4.46E+06		(R)EYQELM	(R)E Y|Q/E/L/M/N V/K(L)		122.25	577.2825	1153.556	0.0019	1.7	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1596	dirMS_041712_NAR_30mM_minus2.12934.13436.2	2	16.96	0	1.86E+07		(R)IVLQIDN	(R)I/V|L|Q|I|D/N A R(L)		125.43	521.3062	1041.605	0	0	5.84	20842.9	5.32	HUMAN	C9JM50	Keratin, type I cytoskeletal 19 (Fragment)
1597	dirMS_041712_NAR_40mM_minus2.14645.14881.3	3	16.96	0	1.19E+06		(K)ISSIQSIV	(K)I/S|S I/Q/S I/V/P A L/E I/A/N/A H R(K)		172.1	640.3618	1919.071	0	0	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
1598	dirMS_041712_NAR_120mM_minus.7012.7340.2	2	16.95	1	3.10E+06		(K)IIAPPERI	(K)I/I|A|P/P E/R K(Y)		93.48	462.2871	923.567	-0.0004	-0.4	8.75	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
1599	dirMS_041712_NAR_40mM_minus2.9420.9420.3	3	16.95	1	2.72E+04		(K)IINADSE	(K)I/I/N/A/D S E D/P K/Y I I N V K(Q)		138.1	611.3244	1831.98	-0.0214	-11.7	4.56	14693.3	4.69	HUMAN	C9JLS9	26S protease regulatory subunit 7 (Fragment)
1600	dirMS_041712_NAR_60mM_minus.10046.10046.3	3	16.95	1	1.94E+05		(R)VEVGKD	(R)V/E|V G K D Q E F T/V/D/T R(G)		115.57	541.6051	1622.802	-0.0013	-0.8	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
1601	dirMS_041712_NAR_40mM_plus2.16561.16612.3	3	16.95	1	2.47E+05		(R)VTFSGLF	(R)V/T|F/S/G L/R D T\V T/P G E L/L/K(A)		163.87	611.6744	1833.012	-0.003	-1.6	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
1602	dirMS_041712_NAR_50mM_plus2.10746.10746.3	3	16.95	1	8.49E+05		(R)DISTNK\	(R)D I|S/T/N K V E Q|I/P/Y/G\E R(I)		124.08	583.6304	1748.881	-0.0047	-2.7	4.68	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
1603	dirMS_041712_NAR_50mM_plus2.5182.5260.3	3	16.95	0	1.37E+06		(K)TATPQQ	(K)T A|T/P/Q|Q A/Q E/V/H E K(L)		86.38	489.5774	1466.723	-0.0057	-3.9	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
1604	dirMS_041712_NAR_50mM_plus2.7203.7203.3	3	16.95	0	1.68E+05		(R)SGSSQEI	(R)S/G/S/S/Q/E L D/V K/P/S A S P Q E R(S)		103.85	634.6443	1901.92	-0.0016	-0.8	4.68	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
1605	dirMS_041712_NAR_60mM_plus.11512.11802.3	3	16.95	1	7.92E+05		(K)TAVCDIF	(K)T|A|V/C D I/P P/R G L K(M)	C:Carbamidomethylation	119.07	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
1606	dirMS_041712_NAR_60mM_plus.6500.6501.3	3	16.95	0	7.31E+04		(K)TVEAEA	(K)T|V|E/A/E A/A/H/G T V T R(H)		92.38	447.892	1341.676	-0.0143	-10.6	5.37	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
1607	dirMS_041712_NAR_50mM_minus2.15525.15796.3	3	16.94	0	1.90E+06		(R)VSLDVN	(R)V/S|L/D/V N/H/F|A/P D E L T V K(T)		157.4	595.3104	1783.922	-0.0058	-3.3	4.54	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
1608	dirMS_041712_NAR_60mM_minus.11563.11564.3	3	16.94	0	7.51E+05		(K)TKPYIQV	(K)T K|P Y\I Q|V/D|I/G/G G Q/T K(T)		124.67	535.6216	1604.864	-0.014	-8.7	8.17	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
1609	dirMS_041712_NAR_120mM_plus.18048.18396.3	3	16.94	1	4.47E+06		(R)ARFEELN	(R)A R\F E\E\L|N|A|D/L/F/R(G)		149.05	494.2571	1480.754	0.0024	1.7	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
1610	dirMS_041712_NAR_30mM_plus2.14346.14553.2	2	16.94	0	1.32E+07		(K)LLIEMEC	(K)L/L|I|E/M/E/Q/R(L)		130.35	516.2816	1031.555	0.0005	0.5	4.53	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
1611	dirMS_041712_NAR_20mM_minus.11231.11231.2	2	16.93	0	2.79E+05		(K)LSELEAA	(K)L/S|E|L|E A/A\L Q R(A)		159.5	565.3134	1129.621	-0.0016	-1.5	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1612	dirMS_041712_NAR_30mM_minus2.13416.13501.2	2	16.93	0	2.86E+05		(R)VFNYNT	(R)V/F|N|Y/N/T/L/E|R(V)		126.75	578.299	1155.579	0.0114	9.9	5.97	99900.1	5.04	HUMAN	B4DZI8	Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b
1613	dirMS_041712_NAR_30mM_minus2.9489.9671.2	2	16.93	0	4.78E+05		(R)TSLGPN(	(R)T/S|L/G/P N/G L/D K(M)		106.28	501.2667	1001.526	-0.0001	-0.1	5.5	55804.4	5.33	HUMAN	B7ZAR1	T-complex protein 1 subunit epsilon
1614	dirMS_041712_NAR_120mM_plus.19980.20516.4	4	16.93	1	3.55E+07		(K)AAIDWF	(K)A/A\I D/W/F/D/G K E F/H/G N I I/K(V)		159.08	491.0027	1960.992	-0.0026	-1.3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
1615	dirMS_041712_NAR_50mM_plus2.15620.15704.3	3	16.93	1	7.69E+05		(R)AITGASI	(R)A I|T|G A/S L/A/D I/M/A K/R(N)		150.25	473.2658	1417.783	-0.0003	-0.2	8.79	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
1616	dirMS_041712_NAR_50mM_plus2.20815.21201.3	3	16.93	0	8.65E+06		(R)LHFFMP	(R)L H\F\F\M|P/G|F|A|P\L/T S R(G)		181.48	540.9498	1620.835	-0.0007	-0.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1617	dirMS_041712_NAR_120mM_minus.14609.14609.3	3	16.92	1	2.59E+05		(K)LDKSQIH	(K)L D/K/S Q I H\D\I|V|L\V|G\G S T R(I)		133.85	613.3393	1838.013	-0.0097	-5.3	6.75	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
1618	dirMS_041712_NAR_30mM_plus2.15023.15626.2	2	16.92	0	3.59E+06		(R)QITVND	(R)Q I|T|V/N/D/L/P V/G R(S)		133.02	606.3403	1211.674	-0.0009	-0.8	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
1619	dirMS_041712_NAR_30mM_plus2.15873.15892.2	2	16.92	0	5.53E+05		(K)LLYNNV!	(K)L/L|Y|N/N/V|S/N F/G R(L)		136.27	648.8354	1296.67	-0.006	-4.6	8.75	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
1620	dirMS_041712_NAR_50mM_plus2.10681.10824.3	3	16.92	1	8.49E+05		(R)DISTNK\	(R)D I|S/T N K/V|E/Q|I|P Y G E R(I)		124.08	583.6304	1748.881	-0.0047	-2.7	4.68	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
1621	dirMS_041712_NAR_60mM_plus.10476.10476.2	2	16.92	1	4.41E+06		(R)LQAEIEG	(R)L Q|A/E|I/E|G L K/G Q R(A)		112.33	671.3774	1341.748	-0.001	-0.7	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1622	dirMS_041712_NAR_60mM_plus.13773.14096.2	2	16.92	1	2.17E+06		(K)FASFIDK	(K)F/A|S|F/I/D/K V/R(F)		129.18	541.8029	1082.599	-0.0008	-0.7	8.75	19569.8	9.88	HUMAN	F8VRG4	Keratin, type II cytoskeletal 8 (Fragment)
1623	dirMS_041712_NAR_60mM_plus.18288.18307.3	3	16.92	1	9.14E+05		(K)EVNKFQ	(K)E V|N K F Q/M/A|Y/S/N/L/L R(A)		152.85	571.6293	1712.879	-0.0055	-3.2	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
1624	dirMS_041712_NAR_120mM_minus.9832.9875.3	3	16.91	1	6.96E+05		(R)GSNKLV	(R)G S N K L\V|I|E/E/A/E/R(S)		108.1	448.9032	1344.712	-0.0167	-12.4	4.79	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
1625	dirMS_041712_NAR_50mM_minus2.10967.11007.3	3	16.91	1	6.21E+05		(R)ISVYYNE	(R)I/S|V|Y/Y N/E A/T/G G K Y V/P R(A)		131.08	606.3119	1816.923	-0.0017	-0.9	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
1626	dirMS_041712_NAR_50mM_minus2.15019.15040.3	3	16.91	1	1.08E+06		(R)DVDFELI	(R)D V|D/F/E/L/I/K V E/G K(V)		153.95	464.5852	1391.742	-0.0006	-0.4	4.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
1627	dirMS_041712_NAR_60mM_minus.13968.14218.3	3	16.91	1	1.28E+06		(K)VKEGMI	(K)V K E G\M N\I|V/E/A/M/E/R(F)		138.52	502.5858	1505.745	-0.0022	-1.5	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
1628	dirMS_041712_NAR_30mM_plus2.18482.18482.2	2	16.91	0	2.36E+05		(K)GNFNYII	(K)G N|F|N/Y/I/E/F T R(I)		150.27	630.8035	1260.601	-0.001	-0.8	6	20513.6	4.62	HUMAN	J3QRS3	Myosin regulatory light chain 12A
1629	dirMS_041712_NAR_40mM_plus2.11418.11436.3	3	16.91	0	3.79E+05		(R)MPLPAP	(R)M/P|L|P A/P S L S H Q|P/P P A P R(V)		133.63	598.3202	1792.953	-0.0066	-3.7	9.52	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
1630	dirMS_041712_NAR_40mM_plus2.14730.14810.3	3	16.91	1	2.59E+05		(K)DVAIKEF	(K)D V|A|I/K E|P\L|V/D\V/V D/P K(Q)		153.82	546.3096	1636.916	-0.0014	-0.8	4.23	24376.8	6.08	HUMAN	E9PIX6	Protein arginine N-methyltransferase 1 (Fragment)

1631	dirMS_041712_NAR_50mM_minus2.13426.13510.3	3	16.9	1	1.91E+05		(K)TITLEVEI	(K)T I|T|L E/V/E/P S D T I/E N V K A K(I)		144.63	663.0226	1987.059	-0.0061	-3.1	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
1632	dirMS_041712_NAR_50mM_minus2.8527.8570.3	3	16.9	1	2.43E+05		(R)AGTGVD	(R)A/G/T|G/V/D/N V/D L/E/A/A T R K(G)		116.55	539.6119	1616.824	-0.0027	-1.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
1633	dirMS_041712_NAR_60mM_minus.16779.17051.3	3	16.9	0	1.02E+06		(K)ICDQWD	(K)I/C|D Q/W D A|L/G S L/T H S R(R)	C:Carbamidomethylation	154.87	586.9446	1758.823	-0.0035	-2	5.21	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
1634	dirMS_041712_NAR_120mM_plus.20691.21229.4	4	16.9	2	1.12E+07		(R)TLAEIAK	(R)T/L\A E/I/A/K/V E L D N M/P L R G K(Q)		163.07	500.2814	1998.105	-0.0015	-0.7	5.85	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
1635	dirMS_041712_NAR_50mM_plus2.20771.20807.3	3	16.9	1	2.60E+05		(R)NLQNLL	(R)N L|Q|N/L/L/I/L/T/A I K/A D R(T)		178.05	566.0067	1696.012	-0.006	-3.6	8.75	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
1636	dirMS_041712_NAR_60mM_plus.14448.14449.3	3	16.9	1	6.02E+05		(K)SLERAEA	(K)S L|E R A E\A\G D\N|L|G/A/L|V/R(G)		131.97	557.6331	1670.882	0.0027	1.6	4.68	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
1637	dirMS_041712_NAR_60mM_minus.6725.7214.3	3	16.89	0	1.27E+06	M437m	(R)LESGMC	(R)L/E|S G/M Q/N m/S I/H/T/K(T)	m:Oxidized methionine	97.23	497.9023	1475.698	15.9942	-0.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1638	dirMS_041712_NAR_50mM_plus2.10973.10995.3	3	16.89	1	3.72E+05		(K)LAEQAE	(K)L/A|E/Q/A/E R Y D/D\M|A/A C M K(S)	C:Carbamidomethylation	125.2	634.6126	1901.819	0.0042	2.2	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
1639	dirMS_041712_NAR_120mM_minus.10984.11410.3	3	16.88	1	8.74E+05		(R)RFDDAV	(R)R F D D\A\V|V|Q/S/D/M/K(H)		115.2	470.8939	1410.668	-0.001	-0.7	4.43	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
1640	dirMS_041712_NAR_30mM_minus2.16571.16571.3	3	16.88	0	7.43E+05		(R)ASLEAAI	(R)A S\L E A A I/A/D/A E/Q R(G)		143.82	448.8965	1344.675	-0.0004	-0.3	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1641	dirMS_041712_NAR_30mM_minus2.7386.7386.2	2	16.88	0	1.44E+05		(R)FGGSGS	(R)F/G|G\S/G/S/Q/V/D/S A R(M)		94.65	584.2729	1167.539	-0.0004	-0.3	5.84	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
1642	dirMS_041712_NAR_50mM_minus2.10622.10622.3	3	16.88	0	1.73E+05		(R)LLELGPK	(R)L/L/E|L/G/P K/P E V A Q Q T R(K)		128.68	560.3182	1678.949	-0.0086	-5.1	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
1643	dirMS_041712_NAR_50mM_minus2.8432.8432.3	3	16.88	1	2.36E+05		(R)AGTGVD	(R)A G/T|G/V/D/N V D/L/E A/A T R\K(G)		116.53	539.6119	1616.824	-0.0027	-1.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
1644	dirMS_041712_NAR_120mM_plus.7170.7233.3	3	16.88	1	4.42E+05		(K)AQLEPV.	(K)A Q|L/E/P V/A/S/P A K K/P K(V)		91.1	488.6234	1463.858	-0.0024	-1.6	9.7	533778	5.74	HUMAN	Q15149	Plectin
1645	dirMS_041712_NAR_50mM_plus2.12896.13141.3	3	16.88	1	1.61E+06		(K)LIADVAF	(K)L/I|A/D/V/A/P S A I R E N D/I/K(S)		136.73	575.6533	1724.954	-0.0088	-5.1	4.56	18388.8	6.85	HUMAN	F5H1Y3	Flap endonuclease 1 (Fragment)
1646	dirMS_041712_NAR_30mM_minus2.18843.18931.2	2	16.87	0	2.45E+05		(K)LLQDFFN	(K)L/L|Q|D/F/F/N G/R(D)		157.37	555.2906	1109.574	0.0001	0.1	5.84	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
1647	dirMS_041712_NAR_50mM_plus2.7160.7223.3	3	16.87	0	1.04E+06		(R)EATNPP	(R)E A|T/N/P/P V/I Q/E E K/P K(K)		103.55	527.282	1579.833	-0.0012	-0.7	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
1648	dirMS_041712_NAR_60mM_plus.10333.10507.3	3	16.87	0	4.39E+06		(R)SSGPYG	(R)S S|G/P/Y/G G/G G Q/Y/F/A/K/P\R(N)		112.17	543.6023	1628.782	0.0108	6.6	9.7	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
1649	dirMS_041712_NAR_120mM_minus.6846.7155.2	2	16.86	1	2.88E+06		(R)TKTEISEI	(R)T/K|T|E|I|S/E/M N/R(N)		92.53	604.8012	1208.594	0.0012	1	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
1650	dirMS_041712_NAR_30mM_minus2.10870.11050.2	2	16.86	0	5.46E+05		(R)FASGGC	(R)F/A|S|G/G/C/D N L/I/K(L)	C:Carbamidomethylation	113.6	591.2858	1181.562	0.0024	2	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
1651	dirMS_041712_NAR_30mM_minus2.14109.14499.2	2	16.86	0	8.44E+05		(R)GLFDEY(	(R)G L|F|D/E/Y/G/S/K(K)		131.28	508.2442	1015.473	0.008	7.9	4.37	92752.5	4.76	HUMAN	P14625	Endoplasmin
1652	dirMS_041712_NAR_40mM_minus2.13608.13608.3	3	16.86	1	1.19E+05		(R)CITDPQT	(R)C/I|T/D/P Q T G L C L L/P L/K/E K(K)	C:Carbamidomethylation	164.02	662.684	1986.04	-0.0024	-1.2	6.07	533778	5.74	HUMAN	Q15149	Plectin
1653	dirMS_041712_NAR_60mM_minus.13268.13540.3	3	16.86	1	7.33E+06		(K)KVPQVS	(K)K\V\P\Q\V\S\T|P T|L|V/E V S R(N)		134.78	547.317	1639.938	-0.0013	-0.8	8.75	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
1654	dirMS_041712_NAR_30mM_plus2.12350.12818.2	2	16.86	0	7.35E+05		(K)NAGVEG	(K)N/A|G|V|E|G S L/I/V/E K(I)		118.18	608.3313	1215.658	-0.0026	-2.2	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
1655	dirMS_041712_NAR_30mM_plus2.13055.13055.2	2	16.86	0	4.73E+05		(K)QSLPPG	(K)Q S L/P/P G L/A/V K(E)		121.9	505.3008	1009.604	-0.0097	-9.6	8.75	8274.8	10.19	HUMAN	P63173	60S ribosomal protein L38
1656	dirMS_041712_NAR_50mM_plus2.14641.14662.3	3	16.86	0	5.16E+05		(K)MLDAED	(K)M/L|D|A/E/D/I/V/N T A R P D/E K(A)		144.95	606.2972	1816.875	0.0025	1.4	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
1657	dirMS_041712_NAR_50mM_minus2.17010.17476.3	3	16.85	0	2.11E+07		(R)IHFPLAT	(R)I H F\P L\A\T\Y|A|P/V/I S A E K(A)		167.2	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
1658	dirMS_041712_NAR_60mM_minus.16805.17138.3	3	16.85	1	2.04E+06		(K)LLQDFFN	(K)L/L|Q/D/F/F/N/G K/E L N K(S)		155.22	522.6138	1565.832	-0.0054	-3.4	6.07	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
1659	dirMS_041712_NAR_50mM_plus2.7651.7651.3	3	16.85	1	1.64E+05		(K)VDDSSEI	(K)V/D|D/S/S E D K T E F T V/K(N)		106.45	533.9169	1599.738	-0.0023	-1.4	4.11	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
1660	dirMS_041712_NAR_120mM_minus.11387.11485.3	3	16.84	0	5.06E+06		(R)GSAVHC	(R)G S|A/V/H/Q/L/S/E E/L/R(C)		116.67	442.565	1325.681	-0.0004	-0.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
1661	dirMS_041712_NAR_20mM_plus.12564.12629.2	2	16.84	0	2.52E+05		(K)DVNAAI.	(K)D V|N|A/A/I/A/A I/K(T)		159.55	493.2863	985.568	-0.0023	-2.4	5.84	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
1662	dirMS_041712_NAR_20mM_plus.14983.14984.2	2	16.84	0	1.45E+05		(K)VLEQLT(	(K)V L|E/Q|L|T|G\Q|T/P V/F/S K(A)		174.65	773.9244	1546.848	-0.006	-3.9	5.97	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
1663	dirMS_041712_NAR_20mM_plus.16906.16906.2	2	16.84	0	3.11E+05		(K)VQIAVA	(K)V Q|I/A|V|A/N\A Q/E L L/Q R(M)		187.77	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
1664	dirMS_041712_NAR_30mM_plus2.19807.19923.2	2	16.84	0	5.28E+05		(K)MAILQIN	(K)M/A|I/L/Q|I/M/K(E)		158.22	474.2739	947.542	-0.0011	-1.2	8.5	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
1665	dirMS_041712_NAR_30mM_plus2.6326.6326.2	2	16.84	0	1.43E+05		(R)FGGSGS	(R)F/G/G/S/G|S Q V/D/S A/R(M)		87.52	584.2731	1167.539	0	0	5.84	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
1666	dirMS_041712_NAR_30mM_minus2.17646.17852.2	2	16.83	0	1.51E+06		(K)AILFVPR	(K)A/I|L|F/V/P/R(R)		149.97	408.2606	815.514	0.0001	0.2	9.79	57660.2	6.38	HUMAN	Q9NQH7	Probable Xaa-Pro aminopeptidase 3
1667	dirMS_041712_NAR_50mM_minus2.15523.15761.3	3	16.83	1	6.45E+05		(K)LLQDFFN	(K)L/L|Q/D/F/F/N/G K E L/N/K(S)		157.4	522.6138	1565.832	-0.0054	-3.4	6.07	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
1668	dirMS_041712_NAR_60mM_minus.8304.8479.3	3	16.83	1	1.25E+06	M2747m	(K)TLQEVTI	(K)T L|Q/E/V/T E/m D/S V K/R(Y)	m:Oxidized methionine	106.78	517.927	1535.773	15.9931	-1.2	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
1669	dirMS_041712_NAR_120mM_plus.10377.10926.3	3	16.83	0	1.90E+06		(R)GFCLPPI	(R)G F|C\L/P/P/H C S R(G)	C:Carbamidomethylation	108.8	410.8593	1230.551	0.0127	10.3	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
1670	dirMS_041712_NAR_20mM_plus.16773.16773.2	2	16.83	0	3.05E+05		(K)VQIAVA	(K)V Q|I A/V/A/N/A Q E/L/L Q R(M)		186.97	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
1671	dirMS_041712_NAR_50mM_plus2.18499.18829.3	3	16.83	1	9.58E+06		(R)LFVGNLI	(R)L F|V|G/N/L/P A/D I/T E D E F K R(L)		166.67	655.3417	1964.012	-0.0018	-0.9	4.32	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
1672	dirMS_041712_NAR_50mM_plus2.6022.6042.3	3	16.83	1	2.93E+05		(K)TGQAPG	(K)T/G|Q|A|P/G Y S Y/T/A A/N K N K(G)		95.93	557.6102	1670.813	0.0028	1.7	9.52	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
1673	dirMS_041712_NAR_30mM_minus2.18342.18342.2	2	16.82	0	4.39E+05		(R)QAQEYE	(R)Q A/Q E|Y|E/A L/L/N/I/K(V)		154.65	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1674	dirMS_041712_NAR_50mM_minus2.9207.9207.3	3	16.82	0	1.89E+05	M778m	(R)mLTGPV	(R)m/L/T G/P V Y S Q/S T A L T H/K(Q)	m:Oxidized methionine	121.02	583.963	1733.889	15.9854	-5.5	8.37	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
1675	dirMS_041712_NAR_60mM_minus.13697.13792.3	3	16.82	0	4.30E+05		(K)IVLDNSV	(K)I/V|L/D\N/S/V/F/S/E/H R(N)		136.55	472.5814	1415.728	0.0019	1.3	5.32	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
1676	dirMS_041712_NAR_120mM_plus.8466.8466.3	3	16.82	1	3.33E+05		(R)LAEDEAI	(R)L/A|E/D/E A F Q R R(R)		97.8	412.2128	1234.618	0.0064	5.2	4.68	533778	5.74	HUMAN	Q15149	Plectin
1677	dirMS_041712_NAR_20mM_plus.12257.12257.2	2	16.82	0	1.17E+05		(K)VNQIGS'	(K)V N Q|I|G/S/V/T E S I/Q A C K(L)	C:Carbamidomethylation	157.67	817.4114	1633.821	-0.0059	-3.6	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
1678	dirMS_041712_NAR_30mM_plus2.11042.11346.2	2	16.82	0	2.26E+06		(R)VEFMDD	(R)V/E|F|M/D/D/T S/R(S)		111.32	550.2401	1099.473	0.0005	0.4	4.03	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
1679	dirMS_041712_NAR_60mM_plus.9291.9291.3	3	16.82	1	1.31E+06		(R)FNEVAA	(R)F/N|E/V|A A/Q/Y/S E\D K A R(Q)		106.1	543.2616	1627.771	-0.0008	-0.5	4.68	14236.2	10.25	HUMAN	F5H1P5	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4
1680	dirMS_041712_NAR_60mM_minus.11650.11650.3	3	16.81	1	2.96E+06		(K)VKLEAEI	(K)V/K L E A E|I/A/T/Y/R(R)		125.33	431.5779	1292.721	-0.0017	-1.3	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1681	dirMS_041712_NAR_60mM_minus.15793.16068.3	3	16.81	1	5.23E+05		(R)IFDSEEIL	(R)I/F\D/S/E E I/L/A/G Y K/R(E)		148.88	514.2713	1540.801	-0.0012	-0.8	4.68	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
1682	dirMS_041712_NAR_20mM_plus.6462.6462.2	2	16.81	0	2.02E+05	M216m	(R)DLmACA	(R)D L/m|A/C A/Q T G S\G K(T)	C:Carbamidomethylation m:Oxid	107.72	627.776	1238.55	15.9943	-0.5	5.84	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
1683	dirMS_041712_NAR_30mM_plus2.13546.13691.2	2	16.81	0	1.10E+06		(R)ANTFVA	(R)A N|T|F/V/A/E/L/K(G)		124.65	496.774	992.541	-0.0004	-0.4	6.05	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
1684	dirMS_041712_NAR_50mM_minus2.11513.11513.3	3	16.8	1	2.41E+04		(R)ESDVPLI	(R)E S D/V/P L/K/T/E E F E V/T K(T)		133.62	584.3049	1750.874	0.0256	14.6	4.25	18909	6.21	HUMAN	Q969H8	UPF0556 protein C19orf10
1685	dirMS_041712_NAR_20mM_plus.18729.18729.2	2	16.8	0	2.00E+05		(R)VFIGNLN	(R)V/F|I/G/N L|N T L V/V/K(K)		200.13	658.8999	1316.794	-0.0011	-0.9	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
1686	dirMS_041712_NAR_30mM_plus2.17969.18269.2	2	16.8	0	6.54E+05		(R)EQLAIAE	(R)E Q|L|A|I/A/E/F/A/R(S)		148.3	574.3083	1147.611	-0.0013	-1.1	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
1687	dirMS_041712_NAR_40mM_plus2.18107.18107.3	3	16.8	0	9.77E+04	M159m	(R)SVAAIHF	(R)S V|A\A I/H/P S L E\I P m L I/P K(E)	m:Oxidized methionine	172.8	611.3472	1816.04	15.9869	-4.4	6.47	31606.3	6.72	HUMAN	B4E329	Phosphoribosyl pyrophosphate synthase-associated protein 2
1688	dirMS_041712_NAR_50mM_plus2.19469.19469.3	3	16.8	1	6.92E+05		(K)AIDLFTD	(K)A I|D L/F T D/A I/K/L N/P R(L)		170.07	529.6346	1586.89	-0.0008	-0.5	6	18141.9	4.7	HUMAN	F6VDH7	Hsc70-interacting protein (Fragment)
1689	dirMS_041712_NAR_50mM_plus2.20968.21319.3	3	16.8	0	8.90E+06		(R)LHFFMP	(R)L H\F\F\M\P G\F|A|P|L/T S R(G)		181.53	540.9498	1620.835	-0.0007	-0.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1690	dirMS_041712_NAR_60mM_plus.17932.17997.3	3	16.8	1	4.10E+05		(K)ESQAKD	(K)E S Q/A K D\V|I/E/E/Y F/K(C)		151.17	529.2635	1585.774	0.0015	1	4.41	14914.1	6.84	HUMAN	P25398	40S ribosomal protein S12
1691	dirMS_041712_NAR_30mM_minus2.9449.9449.2	2	16.79	0	1.21E+06		(K)VFGPGV	(K)V/F|G/P/G V\E R(S)		105.38	430.7364	860.462	0.003	3.5	5.97	258215.9	5.48	HUMAN	E7EN95	Filamin-B
1692	dirMS_041712_NAR_60mM_minus.13519.13625.3	3	16.79	0	6.79E+05		(K)YYVTIID/	(K)Y Y|V/T/I/I/D/A P G H R(D)		135.67	468.9136	1404.727	-0.0008	-0.6	6.74	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
1693	dirMS_041712_NAR_30mM_plus2.12834.12834.2	2	16.79	0	3.14E+05		(K)QQIQSI(	(K)Q Q|I/Q/S I/Q/Q S I/E/R(L)		120.75	729.3893	1457.771	0.0006	0.4	6	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
1694	dirMS_041712_NAR_50mM_plus2.16993.16993.3	3	16.79	1	1.06E+06		(K)LFTAESL	(K)L/F/T/A E S L I/G L K/N P E K(S)		157.68	553.9791	1659.932	-0.0089	-5.3	6.14	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
1695	dirMS_041712_NAR_60mM_plus.9537.9895.3	3	16.79	1	3.28E+06		(K)LEAEIAT	(K)L/E|A|E/I/A T Y R/R(L)		108.77	407.889	1221.659	-0.0062	-5	6.14	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1696	dirMS_041712_NAR_120mM_minus.5438.5554.2	2	16.78	0	5.16E+06	M49m	(R)HQGVM	(R)H/Q|G V|M|V|G m/G Q|K(D)	m:Oxidized methionine	83.28	594.2863	1171.571	15.9943	-0.5	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
1697	dirMS_041712_NAR_50mM_minus2.9303.9303.3	3	16.78	0	2.64E+05	M167m	(R)ImLFTNI	(R)I m/L\F/T/N E D N P H|G N D/S/A/K(A)	m:Oxidized methionine	121.37	640.2914	1902.865	15.9946	-0.2	4.54	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
1698	dirMS_041712_NAR_60mM_minus.14428.14428.3	3	16.78	1	2.64E+05		(R)VEVERD	(R)V/E|V/E R D N\L|A/E D I M R(L)		139.98	563.6139	1688.827	-0.0001	0	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
1699	dirMS_041712_NAR_60mM_minus.17398.17625.3	3	16.78	1	4.55E+06		(R)VSFELFA	(R)V/S|F/E/L/F A D K\V/P K(T)		157.68	460.5911	1379.757	0.0018	1.3	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
1700	dirMS_041712_NAR_20mM_plus.15649.15751.2	2	16.78	0	5.10E+05		(R)GVVDSE	(R)G V V/D|S|E|D|I|P L N/L/S R(E)		179.4	757.3956	1513.786	-0.0017	-1.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
1701	dirMS_041712_NAR_20mM_plus.18631.18631.2	2	16.78	0	1.56E+05		(R)IITLTGPT	(R)I\I/T/L/T/G|P T N A I F K(A)		200.3	694.9091	1388.815	-0.0039	-2.8	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
1702	dirMS_041712_NAR_20mM_plus.8910.8910.2	2	16.78	0	1.30E+05		(K)VLEEAN(	(K)V L|E/E|A/N Q\A|I/N/P/K(L)		131.6	663.353	1325.706	-0.0072	-5.5	4.53	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
1703	dirMS_041712_NAR_50mM_plus2.17552.17552.3	3	16.78	1	5.87E+05		(R)LNRLPA/	(R)L N R\L P A A/G\V|G|D/M|V/M A T V K(K)		160.33	614.9984	1842.993	-0.0122	-6.6	8.75	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
1704	dirMS_041712_NAR_60mM_plus.13954.13954.3	3	16.78	0	1.56E+06		(K)LAQANG	(K)L/A|Q/A/N/G W/G/V/M\V/S H R(S)		129.07	509.2606	1525.769	-0.002	-1.3	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
1705	dirMS_041712_NAR_120mM_minus.14585.14625.3	3	16.77	1	6.69E+05		(K)NKDQGT	(K)N K D Q G T\Y|E/D|Y|V/E/G L/R(V)		133.68	596.2795	1786.824	-0.0003	-0.2	4.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
1706	dirMS_041712_NAR_120mM_minus.7924.7924.2	2	16.77	1	6.37E+04		(K)VAAYDK	(K)V/A|A/Y D K L E K(T)		97.5	518.7878	1036.567	0.001	1	6.04	227783.5	5.5	HUMAN	P35579	Myosin-9
1707	dirMS_041712_NAR_120mM_minus.9962.9999.3	3	16.77	1	1.83E+06		(K)LEAEIAT	(K)L/E|A/E/I/A T Y R/R(L)		109.02	407.8893	1221.659	-0.0053	-4.3	6.14	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1708	dirMS_041712_NAR_20mM_minus.14657.14657.2	2	16.77	0	2.10E+05		(K)LAVEALS	(K)L A V E|A|L/S/S L/D/G D/L A G/R(Y)		201.28	793.922	1586.838	-0.0017	-1.1	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
1709	dirMS_041712_NAR_30mM_plus2.12173.12320.2	2	16.77	0	5.52E+05		(R)AQPSVS	(R)A Q|P/S/V|S/L|G A A Y/R(A)		117.42	610.3242	1219.643	-0.0018	-1.5	8.79	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
1710	dirMS_041712_NAR_40mM_plus2.17737.17737.3	3	16.77	0	3.79E+04		(R)AGLGSG	(R)A G/L/G/S/G L/S L/S G L/V/H P E\L S R(S)		170.98	617.3431	1850.013	0.0017	0.9	6.79	73325.2	9.19	HUMAN	F5H2A9	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial
1711	dirMS_041712_NAR_40mM_plus2.17749.17749.3	3	16.77	1	1.96E+05		(R)LKLPSIPI	(R)L K L|P S I|P L\V/P V/S A Q K(R)		170.73	530.671	1589.999	-0.0004	-0.3	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
1712	dirMS_041712_NAR_50mM_plus2.21906.22110.3	3	16.77	1	8.66E+06		(R)KEGGLG	(R)K\E G G L G\P L\N\I|P/L/L/A/D/V T R(R)		188.23	621.6925	1863.07	-0.0069	-3.7	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
1713	dirMS_041712_NAR_30mM_minus2.5897.5897.2	2	16.76	0	5.74E+04		(R)LAEAEET	(R)L/A|E/A|E E T/A R(T)		86.62	495.2478	989.49	-0.0015	-1.5	4.25	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
1714	dirMS_041712_NAR_120mM_plus.11467.11488.3	3	16.76	2	7.36E+05		(K)QAGPAS	(K)Q/A|G/P/A/S/V/P L R T E E E F\K K(F)		113.4	629.6702	1886.997	-0.001	-0.5	6.23	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
1715	dirMS_041712_NAR_30mM_plus2.19571.19873.2	2	16.76	0	8.13E+05		(-)MDELQL	(-)M/D|E|L|Q/L/F/R(G)		156.65	526.2726	1051.524	0.0138	13.2	4.37	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
1716	dirMS_041712_NAR_60mM_minus.8963.8963.2	2	16.75	0	9.67E+05		(K)QEYDES(	(K)Q/E|Y|D|E S/G P S I/V/H|R(K)		110.35	758.8539	1516.703	-0.0021	-1.4	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
1717	dirMS_041712_NAR_20mM_plus.18645.18645.2	2	16.75	0	2.00E+05		(R)VFIGNLN	(R)V/F|I/G\N L/N T L\V V K(K)		200.13	658.8999	1316.794	-0.0011	-0.9	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
1718	dirMS_041712_NAR_50mM_plus2.11381.11399.3	3	16.75	0	4.19E+05		(K)GFVEFA/	(K)G F|V/E/F/A/A/K/P P A R(K)		127.83	430.5716	1289.7	0.0002	0.1	8.75	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
1719	dirMS_041712_NAR_50mM_plus2.16543.16924.3	3	16.75	1	6.78E+06		(K)QLDDLK'	(K)Q L/D/D/L/K/V/E/L/S/Q L R(V)		155.75	519.6261	1556.864	-0.0005	-0.3	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
1720	dirMS_041712_NAR_60mM_plus.7196.7373.3	3	16.75	1	8.06E+05		(R)IQFKQD	(R)I/Q/F/K/Q/D D/G/T/G P E/K(I)		96.18	488.2441	1462.717	0.0005	0.3	4.56	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
1721	dirMS_041712_NAR_40mM_minus2.11103.11103.3	3	16.73	0	7.92E+05		(R)QVSASE	(R)Q V|S A/S E L H/T/S/G I L/G/P E T L R(D)		148.75	665.6822	1995.051	-0.0185	-9.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
1722	dirMS_041712_NAR_50mM_minus2.18081.18176.3	3	16.73	1	6.74E+05		(R)VLEALLP	(R)V/L|E/A/L L/P/L/K G L E E/R(V)		172.47	527.3171	1579.942	-0.005	-3.2	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
1723	dirMS_041712_NAR_50mM_minus2.18373.18373.3	3	16.73	0	4.62E+05		(K)ALIEVLQ	(K)A L|I/E/V|L Q/P L I/A E/H Q A/R(R)		175.42	601.0139	1801.033	-0.0059	-3.3	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
1724	dirMS_041712_NAR_30mM_plus2.13814.13837.2	2	16.73	0	7.43E+05		(R)GDFCIQ'	(R)G D/F/C|I|Q/V|G R(-)	C:Carbamidomethylation	125.57	526.2542	1051.499	0.0022	2.1	5.84	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
1725	dirMS_041712_NAR_30mM_plus2.20504.20504.2	2	16.73	0	1.71E+05		(K)GSFSEQ(	(K)G S/F/S E/Q|G\I/N\E/F L/R(E)		161.05	742.362	1483.718	-0.0009	-0.6	4.53	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
1726	dirMS_041712_NAR_30mM_plus2.5695.5695.2	2	16.73	0	2.46E+05		(R)QSSGAS	(R)Q S\S/G/A|S/S/S S F/S S S R(A)		84.3	681.3013	1361.593	0.0025	1.9	9.75	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
1727	dirMS_041712_NAR_50mM_plus2.14703.14799.3	3	16.73	1	1.32E+06		(K)VIDPATA	(K)V/I|D|P/A/T A/T/S V D L R D/I/K(I)		145.65	571.9848	1713.938	0.0017	1	4.43	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
1728	dirMS_041712_NAR_120mM_minus.11966.12066.3	3	16.72	1	5.17E+05		(R)ARQEEL'	(R)A R Q E E\L|Y|S|E|L/Q/A R(E)		119.52	531.6052	1592.803	-0.0017	-1	4.79	533778	5.74	HUMAN	Q15149	Plectin
1729	dirMS_041712_NAR_30mM_minus2.16608.17015.2	2	16.72	0	1.63E+05		(R)FFMGN(	(R)F/F|M/G/N/Q V/L/K(V)		146.13	542.2866	1083.566	0.0004	0.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
1730	dirMS_041712_NAR_30mM_minus2.7410.7410.2	2	16.72	0	2.50E+03		(R)TPEEYPE	(R)T/P/E/E/Y/P E S/A/K(V)		93.4	575.7705	1150.526	0.0075	6.5	4.25	21580.5	5.38	HUMAN	B4DGT0	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1
1731	dirMS_041712_NAR_40mM_minus2.16006.16013.3	3	16.72	0	1.60E+06	M166m	(K)VLDFEHI	(K)V/L|D\F E/H F\L|P m/L Q/T V A K(N)	m:Oxidized methionine	187.72	635.3376	1888.004	15.9945	-0.2	5.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
1732	dirMS_041712_NAR_50mM_minus2.12163.12204.3	3	16.72	1	2.39E+05		(K)LIADVAF	(K)L/I|A/D/V/A/P S A I R E N D/I/K(S)		137.7	575.6545	1724.954	-0.0052	-3	4.56	18388.8	6.85	HUMAN	F5H1Y3	Flap endonuclease 1 (Fragment)
1733	dirMS_041712_NAR_50mM_minus2.9183.9345.3	3	16.72	0	3.48E+05		(R)TIVITSHI	(R)T I|V|I/T/S H/P G Q I V/K(H)		120.98	464.9452	1392.821	0.0001	0.1	8.44	27999.4	5.61	HUMAN	B7Z5C0	DnaJ homolog subfamily A member 1
1734	dirMS_041712_NAR_40mM_plus2.18608.18666.3	3	16.72	1	4.00E+05		(R)TLAEIAK	(R)T/L\A/E/I/A/K/V E\L/D/N M/P L R(G)		176.57	604.9967	1812.989	-0.0132	-7.3	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
1735	dirMS_041712_NAR_60mM_plus.13848.13864.3	3	16.72	1	8.35E+05		(R)IAWDDE	(R)I/A|W|D/D/E E/T R D/G F/R(L)		129.13	537.2476	1609.724	0.0041	2.6	4.11	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
1736	dirMS_041712_NAR_120mM_minus.12140.12178.3	3	16.71	0	1.58E+06		(R)HVFGES	(R)H V\F\G E|S/D|E|L|I/G Q/K(V)		120.68	486.9119	1458.722	-0.0012	-0.8	4.65	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
1737	dirMS_041712_NAR_30mM_minus2.20229.20242.2	2	16.71	0	6.49E+05		(K)IGFPWSI	(K)I/G|F|P/W/S E I/R(N)		171.88	552.7932	1104.584	-0.0045	-4.1	6	71218.8	6.3	HUMAN	A7YIJ8	Radixin
1738	dirMS_041712_NAR_40mM_minus2.11001.11001.3	3	16.71	0	4.81E+05		(R)DAGEGL	(R)D A|G\E/G L/L A V Q I/T/D Q E G K P K(R)		148	657.0157	1969.024	0.0089	4.5	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
1739	dirMS_041712_NAR_60mM_minus.12088.12088.3	3	16.71	1	3.03E+06	M72m	(R)TEmENE	(R)T/E/m/E N E F/V/L/I/K K(D)	m:Oxidized methionine	126.87	499.5941	1480.772	15.9962	0.8	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)

1740	dirMS_041712_NAR_60mM_minus.13253.13253.3	3	16.71	1	2.81E+05	M194m	(R)KLQEEEL	(R)K L Q E E E L L|A|T/Q/V/D|m R(A)	m:Oxidized methionine	133.93	606.9793	1802.932	15.9917	-1.8	4.41	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
1741	dirMS_041712_NAR_50mM_plus2.14846.14889.3	3	16.71	1	9.00E+05		(R)LYSILGT	(R)L/Y|S/I/L/G T T L/K D E/G K(L)		145.9	513.2859	1537.847	-0.0041	-2.6	6.07	66876.9	6.17	HUMAN	O75083	WD repeat-containing protein 1
1742	dirMS_041712_NAR_50mM_plus2.15994.16043.3	3	16.71	1	1.41E+06		(R)VCENIPI	(R)V/C/E|N|I|P I V L/C G N K V D|I/K(D)	C:Carbamidomethylation	152.08	657.6802	1971.04	-0.0141	-7.2	6.04	14844.8	5.89	HUMAN	B4DV51	GTP-binding nuclear protein Ran
1743	dirMS_041712_NAR_120mM_plus.10044.10539.3	3	16.7	1	1.60E+07		(R)VKYETEL	(R)V/K Y E T|E|L/A/M/R(Q)		107.58	413.8849	1239.64	0	0	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1744	dirMS_041712_NAR_60mM_plus.19435.19435.3	3	16.7	1	5.59E+05		(K)TVTAMD	(K)T/V|T/A/M D/V/V/Y A L K R(Q)		160.4	489.6071	1466.804	0.0032	2.2	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
1745	dirMS_041712_NAR_120mM_minus.7830.8060.3	3	16.69	1	9.87E+05		(K)IQDKEGI	(K)I Q/D\K E G|I|P/P/D Q Q R(L)		97.6	508.5981	1523.781	-0.0015	-1	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
1746	dirMS_041712_NAR_50mM_minus2.14963.14963.3	3	16.69	0	4.22E+05		(K)IAILTCPF	(K)I/A/I|L/T C\P F E/P P K/P K(T)	C:Carbamidomethylation	153.37	537.6375	1610.898	0.0005	0.3	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
1747	dirMS_041712_NAR_50mM_plus2.19264.19400.3	3	16.69	1	3.94E+05		(K)ILDVASL	(K)I/L|D|V/A/S/L/E/V L N E V N R R(S)		169.97	614.0109	1840.029	-0.0105	-5.7	4.68	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
1748	dirMS_041712_NAR_50mM_plus2.20255.20368.3	3	16.69	0	1.29E+05		(R)AFIDPL	(R)A F|I|D/P/L/G/L/P D|R P F Y R(H)		175.4	592.986	1776.943	0.0003	0.2	6	84557.3	6.5	HUMAN	Q04609	Glutamate carboxypeptidase 2
1749	dirMS_041712_NAR_30mM_minus2.7668.7668.2	2	16.68	0	9.48E+04		(R)FYQQVT	(R)F/Y|Q/Q|V T/K(D)		96.08	457.2426	913.478	0.0001	0.1	8.59	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
1750	dirMS_041712_NAR_120mM_plus.8540.8943.3	3	16.68	0	2.74E+06		(K)HTGPNS	(K)H T G P N\S P/D|T|A/N/D/G/F V/R(L)		99.25	562.26	1684.767	-0.0019	-1.2	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
1751	dirMS_041712_NAR_20mM_plus.15501.15825.3	3	16.68	0	7.37E+05		(K)VGINYQ	(K)V G I N Y Q|P P T\V|V|P/G G D L A K(V)		179.22	608.9991	1824.985	-0.0027	-1.5	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
1752	dirMS_041712_NAR_20mM_plus.9664.9924.2	2	16.68	0	2.26E+05		(K)IVVVTA	(K)I/V|V|V|T/A/G/V/R(Q)		139.2	457.2945	913.583	-0.0012	-1.3	9.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
1753	dirMS_041712_NAR_30mM_plus2.18477.18497.2	2	16.68	0	5.13E+05		(R)GFVDDII	(R)G F|V/D|D|I|I|Q|P S S T R(A)		150.37	717.8617	1434.722	-0.0062	-4.3	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
1754	dirMS_041712_NAR_60mM_plus.11426.11577.3	3	16.68	1	1.25E+06		(K)FGQYNK	(K)F/G|Q|Y/N K/E D|P T/S F R(L)		117.23	530.2507	1588.739	-0.0015	-0.9	6.07	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
1755	dirMS_041712_NAR_20mM_plus.18158.18158.2	2	16.67	0	1.70E+05		(R)LTGQLF	(R)L T|G Q/L/F/L G G S I/V/K(G)		197.02	666.8962	1332.789	-0.0034	-2.6	8.75	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
1756	dirMS_041712_NAR_30mM_plus2.12257.12257.2	2	16.67	0	2.21E+05		(K)VLQATV	(K)V L/Q|A/T/V|V/A V/G S G S K(G)		117.57	658.3806	1315.758	-0.0041	-3.1	8.72	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
1757	dirMS_041712_NAR_30mM_plus2.13994.14284.2	2	16.67	0	1.37E+06		(R)NLVDNI	(R)N L|V|D|N/I|T/G Q/R(L)		127.05	565.3018	1129.596	0.0003	0.3	5.84	533778	5.74	HUMAN	Q15149	Plectin
1758	dirMS_041712_NAR_30mM_plus2.19827.19870.2	2	16.67	0	2.35E+05		(K)GFAFVQ	(K)G F|A|F|V|Q/Y V/N E R(N)		157.57	665.3326	1329.659	-0.0007	-0.5	6	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
1759	dirMS_041712_NAR_30mM_plus2.21773.21773.2	2	16.67	0	2.02E+05		(R)NSILAQ	(R)N S\I|L|A/Q\V L/D/Q S A R(A)		170.1	707.8889	1414.765	0.0057	4	5.84	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
1760	dirMS_041712_NAR_50mM_plus2.8911.8911.3	3	16.67	0	1.99E+05		(K)VVQVSA	(K)V V|Q|V/S/A G D S H T A A L T\D D G R(V)		113.48	633.6509	1898.92	0.0179	9.4	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
1761	dirMS_041712_NAR_30mM_minus2.15972.16283.2	2	16.66	0	5.16E+05		(K)LIINSLYK	(K)L/I|I|N/S/L/Y K(N)		141.27	482.2955	963.587	-0.0036	-3.8	8.59	5582.4	4.81	HUMAN	F8W026	Endoplasmin (Fragment)
1762	dirMS_041712_NAR_30mM_minus2.17025.17186.2	2	16.66	0	1.94E+05		(R)IYNVIGT	(R)I/Y|N|V|I|G/T L R(G)		146.9	524.8092	1048.615	-0.0038	-3.7	8.75	84557.3	6.5	HUMAN	Q04609	Glutamate carboxypeptidase 2
1763	dirMS_041712_NAR_30mM_minus2.18724.18901.2	2	16.66	0	2.79E+05		(R)LDFNLIR	(R)L/D|F/N/L/I/R(V)		157.08	445.759	890.509	0.0013	1.5	5.84	18956.4	6.97	HUMAN	C9JLK0	Phosphoribosylaminoimidazolecarboxamide formyltransferase (Fragment)
1764	dirMS_041712_NAR_60mM_minus.17201.17688.3	3	16.66	1	1.28E+07	M148m	(R)LDLAGR	(R)L/D|L|A/G R D L T/D/Y L/m K(I)	m:Oxidized methionine	157.95	547.2829	1623.841	15.9931	-1.1	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
1765	dirMS_041712_NAR_120mM_plus.19016.19133.4	4	16.66	0	9.03E+05		(R)EVPIPEH	(R)E V P I/P/E/H\I/D/I/Y|H/L T/R(E)		153.55	458.7454	1831.97	-0.0103	-5.6	5.28	27043.5	6.34	HUMAN	C9JHK9	ATP-binding cassette sub-family F member 2 (Fragment)
1766	dirMS_041712_NAR_40mM_plus2.13530.13694.3	3	16.66	0	6.25E+05		(R)TIQVEN	(R)T/I|Q|V/E N\S H L/I/L/T/G A G A L N K(V)		146.55	660.3654	1979.092	-0.0104	-5.2	6.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
1767	dirMS_041712_NAR_60mM_plus.6869.6869.3	3	16.66	1	7.28E+05		(R)SGAPAA	(R)S/G|A/P A/A E S/K E I V R(G)		94.78	438.904	1314.701	-0.0038	-2.9	5.87	14003.4	5.66	HUMAN	Q9NRX4	14 kDa phosphohistidine phosphatase
1768	dirMS_041712_NAR_120mM_minus.20139.20139.4	4	16.65	0	4.49E+05		(K)LAFPSPF	(K)L A|F|P/S/P F G H L S/E G F S/H S/R(W)		166.17	493.9968	1972.966	-0.0011	-0.5	6.92	16196.2	9.92	HUMAN	C9JRJ8	Sequestosome-1 (Fragment)
1769	dirMS_041712_NAR_30mM_minus2.18449.18556.2	2	16.65	0	2.28E+05		(K)YPQLLP	(K)Y/P/Q/L|L|P G I R(G)		154.92	528.816	1056.62	0.0047	4.4	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
1770	dirMS_041712_NAR_30mM_minus2.19113.19502.2	2	16.65	0	9.37E+06		(R)YLTVAA	(R)Y/L|T|V/A/A|V/F R(G)		161.02	520.2998	1039.593	-0.0012	-1.1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
1771	dirMS_041712_NAR_20mM_plus.10907.10907.2	2	16.65	0	2.19E+05	M33m	(K)VAGmD	(K)V A/G|m|D/V/E L/T V E E R(N)	m:Oxidized methionine	147.28	732.3555	1447.71	15.994	-0.6	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
1772	dirMS_041712_NAR_30mM_plus2.19593.19593.2	2	16.65	0	1.98E+04		(K)NQALFP	(K)N Q|A|L/F|P A C V L K(N)	C:Carbamidomethylation	157.7	630.8399	1260.677	-0.0044	-3.5	8.75	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
1773	dirMS_041712_NAR_30mM_plus2.21623.22005.2	2	16.65	0	1.49E+06		(K)EIIDLVL	(K)E I|I/D|L|V/L/D/R(I)		169.95	543.3133	1085.62	-0.0008	-0.7	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
1774	dirMS_041712_NAR_40mM_plus2.10633.10772.3	3	16.65	0	1.77E+05		(K)MAPVPL	(K)M A|P/V/P/L D/D S N R P A S L T/K(D)		128.32	604.6467	1811.932	-0.0065	-3.6	5.71	53030.7	11.3	HUMAN	E9PJA7	Bcl-2-associated transcription factor 1
1775	dirMS_041712_NAR_50mM_plus2.20291.20567.3	3	16.65	1	4.12E+05		(R)VISGVL	(R)V/I|S/G/V|L Q/L/G N I V/F K K(E)		176.1	539.0011	1614.994	-0.0054	-3.3	10	227783.5	5.5	HUMAN	P35579	Myosin-9
1776	dirMS_041712_NAR_60mM_plus.7442.7499.3	3	16.65	1	5.05E+05		(K)SSGGRE	(K)S/S|G/G R E D\L\E|S|S/G L Q\R(R)		97.3	526.5897	1577.751	0.0031	2	4.68	11625.5	8.01	HUMAN	B8ZZT7	Hematological and neurological-expressed 1 protein
1777	dirMS_041712_NAR_30mM_minus2.11952.12357.2	2	16.64	0	7.64E+05		(K)SIYYITGE	(K)S I|Y|Y/I/T/G E/S/K(E)		119.17	580.7949	1160.583	-0.0009	-0.7	5.72	16789.1	8.77	HUMAN	H0Y5S7	Heat shock protein HSP 90-beta (Fragment)
1778	dirMS_041712_NAR_30mM_plus2.21435.21565.2	2	16.64	0	3.50E+05		(K)FDGILGN	(K)F/D/G\I|L|G/M/A/Y|P R(I)		167.42	620.3199	1239.619	0.0135	10.9	5.83	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
1779	dirMS_041712_NAR_20mM_minus.13233.13233.2	2	16.63	0	2.34E+05		(R)GVVDSE	(R)G V/V|D/S|E/D I/P L/N L\S R(E)		183.02	757.3944	1513.786	-0.0041	-2.7	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
1780	dirMS_041712_NAR_30mM_minus2.12658.12739.2	2	16.63	0	3.27E+05		(R)GGAEQF	(R)G G A|E|Q|F|M|E/E|T E/R(S)		122.7	692.2961	1383.584	0.0004	0.3	4.09	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
1781	dirMS_041712_NAR_30mM_minus2.13604.13643.2	2	16.63	0	3.31E+05		(R)ISGLIYEE	(R)I/S|G|L|I|Y/E E/T/R(G)		127.68	590.8127	1180.621	-0.0027	-2.3	4.53	11367.1	11.36	HUMAN	P62805	Histone H4
1782	dirMS_041712_NAR_30mM_plus2.18806.18868.2	2	16.63	0	1.53E+05		(K)FGAYIVD	(K)F/G|A|Y|I/V/D/G L/R(Q)		152.32	555.8011	1110.594	0.0007	0.6	5.83	269989.9	5.92	HUMAN	F8W8T8	Acetyl-CoA carboxylase 2
1783	dirMS_041712_NAR_60mM_plus.12101.12121.3	3	16.63	1	6.89E+05		(R)MGIVGP	(R)M/G I/V/G/P E/F K D/K(L)		120.63	407.5532	1220.634	0.0107	8.7	5.82	533778	5.74	HUMAN	Q15149	Plectin
1784	dirMS_041712_NAR_50mM_minus2.7190.7255.3	3	16.62	1	1.49E+05		(R)IAECSSQ	(R)I/A|E/C/S S Q L/A/E E/E E K/A K(N)	C:Carbamidomethylation	108.03	607.9557	1821.853	-0.0009	-0.5	4.32	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
1785	dirMS_041712_NAR_60mM_minus.11637.11878.3	3	16.62	1	2.96E+06		(K)VKLEAEI	(K)V K L E A E|I|A/T/Y/R(R)		125.33	431.5779	1292.721	-0.0017	-1.3	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1786	dirMS_041712_NAR_50mM_plus2.12031.12161.3	3	16.62	0	2.97E+05		(R)VVVLM	(R)V V|V|L/M/G S T S D L/G H/C E/K(I)	C:Carbamidomethylation	131.5	577.9512	1731.84	-0.0014	-0.8	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
1787	dirMS_041712_NAR_120mM_minus.18644.18666.3	3	16.61	1	3.30E+05		(R)ARFEEL	(R)A R F E E\L|C|S/D/L|F R(S)	C:Carbamidomethylation	156.88	514.9175	1542.737	0.001	0.7	4.68	25598.3	6.45	HUMAN	E7EP11	Heat shock 70 kDa protein 1A/1B
1788	dirMS_041712_NAR_50mM_minus2.15296.15462.3	3	16.61	0	5.45E+05		(R)DGLAFN	(R)D|G L|A/F/N/A/L/I/H/R(H)		155.45	409.5594	1226.664	-0.0004	-0.3	6.74	146974	5.55	HUMAN	C9JRP8	Spectrin beta chain, non-erythrocytic 4
1789	dirMS_041712_NAR_30mM_plus2.13563.13657.2	2	16.61	0	4.63E+05		(K)NLQYYD	(K)N/L|Q|Y|Y/D/I/S A K(S)		124.33	607.8058	1214.605	-0.0009	-0.7	5.83	14844.8	5.89	HUMAN	B4DV51	GTP-binding nuclear protein Ran
1790	dirMS_041712_NAR_50mM_plus2.13335.13336.3	3	16.61	0	6.82E+05		(K)AASDIA	(K)A A|S D|I|A|M/T E L/P/P T H P I R(L)		138.7	607.3177	1819.937	0.0015	0.8	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
1791	dirMS_041712_NAR_60mM_minus.17165.17260.3	3	16.6	1	3.81E+05		(R)KAPSDL	(R)K\A/P S D\L|Y/Q I I/L/K(A)		156.22	463.6095	1388.815	-0.0008	-0.6	8.5	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
1792	dirMS_041712_NAR_60mM_minus.5107.5335.3	3	16.6	0	4.24E+06	M434m M	(R)LESGm	(R)L/E|S/G m Q/N m/S I/H/T/K(T)	m:Oxidized methionine	84.33	503.2336	1475.698	31.9881	-1.1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1793	dirMS_041712_NAR_120mM_plus.8433.8433.3	3	16.6	1	1.83E+05		(K)ALSRQE	(K)A L/S R Q E\M|Q|E|V/Q/S S/R(S)		97.45	550.2746	1648.807	0.0021	1.3	6.19	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
1794	dirMS_041712_NAR_20mM_plus.13703.13851.2	2	16.6	0	2.08E+05		(K)APILIAT	(K)A/P|I/L|I|A/T/D V A S R(G)		166.65	613.8559	1226.71	-0.0058	-4.7	5.88	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
1795	dirMS_041712_NAR_20mM_plus.16254.16499.2	2	16.6	0	2.45E+05		(R)ADLIAYL	(R)A/D|L|I|A/Y/L/K(K)		184.42	453.7678	906.529	-0.0012	-1.3	5.88	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
1796	dirMS_041712_NAR_20mM_plus.7627.7633.2	2	16.6	0	1.57E+05		(K)IAVAAQ	(K)I/A|V/A|A/Q/N C Y\K(V)	C:Carbamidomethylation	122.43	569.2902	1137.572	0.001	0.9	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
1797	dirMS_041712_NAR_30mM_plus2.17548.17548.2	2	16.6	0	1.64E+05		(R)ASLEAAI	(R)A S L E/A/A|I/A|D/A E Q R(G)		145.03	672.8406	1344.675	-0.0015	-1.1	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1798	dirMS_041712_NAR_60mM_plus.11721.11721.3	3	16.6	0	2.19E+05		(K)TGNLGN	(K)T G|N|L/G N V/V/H/I E R(F)		118.37	436.9042	1308.702	-0.0038	-2.9	6.41	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
1799	dirMS_041712_NAR_60mM_plus.12239.12296.3	3	16.6	1	8.16E+05		(K)NQLTSN	(K)N Q|L|T/S/N/P E/N T V/F D A K/R(L)		121.12	611.9737	1833.909	-0.0024	-1.3	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
1800	dirMS_041712_NAR_30mM_minus2.18426.18469.2	2	16.59	0	4.47E+05		(R)QAQEYE	(R)Q A|Q|E/Y/E/A/L/L/N I K(V)		154.67	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1801	dirMS_041712_NAR_50mM_minus2.9448.9448.2	2	16.59	1	7.15E+05		(R)DGKLVS	(R)D/G K|L/V|S E S S D V L|P/K(-)		121.97	737.3927	1473.78	-0.0014	-0.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1802	dirMS_041712_NAR_30mM_plus2.16221.16221.2	2	16.59	0	7.14E+05		(R)GLCAIA	(R)G L/C|A|I|A/Q/A/E/S L R(Y)	C:Carbamidomethylation	138.47	644.8372	1288.668	-0.0007	-0.5	6	18529.2	9.98	HUMAN	E9PL45	40S ribosomal protein S3
1803	dirMS_041712_NAR_30mM_plus2.16582.16880.2	2	16.59	0	5.48E+05		(R)FNVPVS	(R)F/N|V|P/V/S L E/S K(K)		140.52	560.3022	1119.604	-0.0073	-6.5	6	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
1804	dirMS_041712_NAR_20mM_minus.12183.12189.2	2	16.58	0	5.41E+05	M185m	(K)LAVNm	(K)L/A|V/N|m|V/P F/P R(L)	m:Oxidized methionine	171.12	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1805	dirMS_041712_NAR_50mM_minus2.14855.14855.3	3	16.58	1	2.91E+05		(R)EAVTEIL	(R)E A/V/T/E/I/L/G I/E/P D R E K(G)		152.33	566.9683	1698.891	-0.0005	-0.3	4.25	25685.9	6.4	HUMAN	E9PGT1	Translin
1806	dirMS_041712_NAR_20mM_plus.17624.17624.2	2	16.58	0	1.55E+05		(K)DVDLEF	(K)D V|D|L|E F L A\K(M)		192.7	525.2795	1049.551	0.0004	0.4	4.03	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
1807	dirMS_041712_NAR_20mM_plus.9312.9529.2	2	16.58	0	5.64E+05		(K)TIAPALV	(K)T I|A|P/A L/V/S K(K)		136.25	450.2814	899.556	-0.0005	-0.6	8.41	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
1808	dirMS_041712_NAR_30mM_plus2.16224.16390.2	2	16.58	0	1.72E+05		(K)YIQELW	(K)Y/I|Q/E/L/W/R(K)		138.08	504.2687	1007.531	-0.0008	-0.8	6	20608.6	11.48	HUMAN	E7ENU7	Ribosomal protein L15 (Fragment)
1809	dirMS_041712_NAR_50mM_plus2.13400.13400.3	3	16.58	0	6.77E+05		(R)VLVVHD	(R)V/L|V/V/H/D G F E G L/A/K(G)		139.17	461.9229	1383.763	-0.0089	-6.5	5.32	18719.9	6.91	HUMAN	F8VP00	6-phosphofructokinase, muscle type (Fragment)
1810	dirMS_041712_NAR_50mM_plus2.18522.18641.3	3	16.58	0	9.87E+05		(K)VAHALA	(K)V A H A L\A E\G\L|G|V|I/A/C/I G E K(L)	C:Carbamidomethylation	166.15	603.3265	1807.974	-0.0085	-4.7	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
1811	dirMS_041712_NAR_60mM_minus.9607.9607.3	3	16.57	1	4.95E+05		(R)LQAEIE	(R)L Q|A/E/I E/G L/K G Q R(A)		113.32	447.9164	1341.748	-0.0138	-10.3	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1812	dirMS_041712_NAR_20mM_plus.15350.15769.3	3	16.57	0	1.92E+06	M73m	(R)AILVDLE	(R)A I\L\V D\L E/P/G T/m/D S V R(S)	m:Oxidized methionine	179.15	544.6139	1615.836	15.9912	-2.3	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
1813	dirMS_041712_NAR_30mM_plus2.17064.17064.2	2	16.57	0	1.82E+05		(K)GVVDSD	(K)G V|V|D|S/D D L|P L N V/S R(E)		142.53	743.3807	1485.754	-0.0002	-0.2	3.93	92752.5	4.76	HUMAN	P14625	Endoplasmin
1814	dirMS_041712_NAR_50mM_plus2.14739.14739.3	3	16.57	1	1.88E+05		(R)ALSNLES	(R)A L|S|N/L/E/S I/P G G Y N A L R\R(M)		146.72	610.9972	1830.982	-0.005	-2.7	8.79	16443.8	5	HUMAN	H0YDS0	Ubiquilin-1 (Fragment)
1815	dirMS_041712_NAR_50mM_plus2.15943.15963.3	3	16.57	1	3.72E+05		(K)TQLLQD	(K)T Q|L|L/Q/D V/Q/D E N K/L/F/K(S)		151.8	606.9845	1818.96	-0.0207	-11.4	4.55	69285	5.2	HUMAN	G3V4Y7	Kinectin
1816	dirMS_041712_NAR_60mM_plus.19366.19556.3	3	16.57	1	6.73E+05		(R)TRIEGLL	(R)T R I E G\L|L|A/A/F/P/K(L)		159.8	439.262	1315.773	-0.0018	-1.4	8.41	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
1817	dirMS_041712_NAR_20mM_minus.7866.7866.2	2	16.56	0	1.69E+05		(K)SVEAAA	(K)S V|E/A/A/A/E L S A K(D)		128.45	538.2838	1075.563	-0.0027	-2.5	4.53	12131.5	11.14	HUMAN	F5GXR3	Parathymosin
1818	dirMS_041712_NAR_30mM_plus2.19581.19581.2	2	16.56	0	2.14E+05		(K)TVDNFV	(K)T V|D|N/F|V/A L/A T G E K(G)		155.58	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
1819	dirMS_041712_NAR_40mM_minus2.12009.12090.3	3	16.55	1	9.22E+04		(K)IIVDELK	(K)I/I|V|D/E L K/Q E\V/I/S T S S/K(A)		154.43	597.0023	1788.995	-0.003	-1.7	4.68	30149.5	5.96	HUMAN	D6RAC2	Guanine nucleotide-binding protein subunit beta-2-like 1
1820	dirMS_041712_NAR_30mM_plus2.16492.16492.2	2	16.55	0	1.38E+05		(R)STLNEIY	(R)S T/L/N/E/I|Y/F G K(T)		139.07	586.3039	1171.599	0.0012	1	5.72	29580	6.46	HUMAN	B1AK87	Capping protein (Actin filament) muscle Z-line, beta
1821	dirMS_041712_NAR_30mM_plus2.17843.17860.2	2	16.55	0	1.29E+05		(K)FAEAFE	(K)F/A|E|A|F/E/A/I/P R(A)		146.62	575.798	1150.589	-0.0004	-0.4	4.53	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
1822	dirMS_041712_NAR_60mM_plus.17088.17088.3	3	16.55	1	7.26E+06		(K)LKVPEW	(K)L/K V\P E/W|V/D/T V/K(L)		145.72	438.5872	1313.746	0.0007	0.5	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
1823	dirMS_041712_NAR_60mM_plus.5154.5154.3	3	16.55	1	4.46E+04		(K)GNSPPS	(K)G N/S|P/P/S S G E A C R E E K(G)	C:Carbamidomethylation	84.52	535.5678	1604.697	-0.0081	-5	4.79	24954.4	5.33	HUMAN	A6NM98	ARD1 homolog A, N-acetyltransferase (S. cerevisiae), isoform CRA_b
1824	dirMS_041712_NAR_30mM_minus2.8998.9018.2	2	16.54	0	2.70E+05		(K)TNEAQA	(K)T/N|E|A|Q/A|I|E/T A R(A)		103.52	602.3015	1203.596	-0.0007	-0.6	4.53	10145.6	9.15	HUMAN	F8VQQ8	Ubiquitin-conjugating enzyme E2 N
1825	dirMS_041712_NAR_50mM_minus2.12363.12541.3	3	16.54	0	6.64E+05		(K)AGVVG	(K)A/G\V|V|G/P E/L/H/E Q L L/S A E K(A)		139.27	592.9866	1776.949	-0.0038	-2.1	4.75	533778	5.74	HUMAN	Q15149	Plectin
1826	dirMS_041712_NAR_50mM_minus2.12471.12524.3	3	16.54	0	1.98E+05		(R)VLVVHD	(R)V/L/V/V/H/D/G F E G L/A K(G)		139.7	461.9238	1383.763	-0.0062	-4.5	5.32	18719.9	6.91	HUMAN	F8VP00	6-phosphofructokinase, muscle type (Fragment)
1827	dirMS_041712_NAR_50mM_minus2.8472.8673.3	3	16.54	0	1.58E+06		(R)EIVHIQA	(R)E/I\V H I Q\A G/Q|C/G N Q I/G A/K(F)	C:Carbamidomethylation	116.8	608.3087	1822.923	-0.0113	-6.2	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
1828	dirMS_041712_NAR_20mM_plus.15454.15790.3	3	16.54	0	1.92E+06	M73m	(R)AILVDLE	(R)A I|L\V D L E|P/G T m/D/S V R(S)	m:Oxidized methionine	179.15	544.6139	1615.836	15.9912	-2.3	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
1829	dirMS_041712_NAR_20mM_plus.16449.16449.2	2	16.54	0	1.66E+05		(R)LLEAQIA	(R)L L E/A/Q I|A|T G G I/I\D|P K(E)		185.07	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
1830	dirMS_041712_NAR_20mM_plus.19355.19355.2	2	16.54	0	8.40E+04		(R)ALIAGG	(R)A/L/I|A|G G G\A|P E I E\L A L R(L)		205.1	775.9467	1550.89	-0.0039	-2.5	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
1831	dirMS_041712_NAR_30mM_plus2.12078.12110.2	2	16.54	0	2.57E+05		(R)ENVNLA	(R)E N|V|N/L/A/Q/I/R(T)		116.4	528.7932	1056.58	-0.0005	-0.5	6.1	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
1832	dirMS_041712_NAR_30mM_plus2.12353.12425.2	2	16.54	0	8.33E+04		(K)MADEAI	(K)M/A|D|E|A|I|L/Q E/R(E)		116.57	588.2906	1175.573	0.0014	1.2	4.14	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
1833	dirMS_041712_NAR_60mM_plus.21571.21571.3	3	16.54	1	5.98E+05		(K)EIIDLVL	(K)E I/I/D/L V L/D/R I/R(K)		180.57	452.2733	1354.805	0.0001	0.1	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
1834	dirMS_041712_NAR_60mM_minus.14146.14243.3	3	16.53	0	1.14E+05		(K)GVGISV	(K)G V|G I/S/V/L/E/M S H/R(S)		139.12	428.9004	1284.673	0.0138	10.7	6.75	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
1835	dirMS_041712_NAR_20mM_plus.13897.13897.2	2	16.53	0	6.90E+04		(K)LLDLVQ	(K)L/L\D\L/V/Q/Q/S C N Y K(Q)	C:Carbamidomethylation	167.73	740.8757	1480.746	-0.0023	-1.6	5.83	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
1836	dirMS_041712_NAR_30mM_plus2.9737.9775.2	2	16.53	0	5.42E+05		(K)FESPEV	(K)F/E|S|P/E/V/A E R(A)		104.78	532.2579	1063.506	0.0031	2.9	4.25	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
1837	dirMS_041712_NAR_60mM_plus.14919.14951.3	3	16.53	1	7.41E+05		(R)ELAFQIS	(R)E L/A/F/Q/I/S K/E/Y E R(F)		134.78	504.9258	1512.769	-0.0064	-4.3	4.79	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
1838	dirMS_041712_NAR_60mM_plus.5085.5085.3	3	16.53	1	3.95E+05		(R)AAEDDE	(R)A/A|E D/D E/D/D D V/D T K K(Q)		83.53	522.5529	1565.645	-0.0008	-0.5	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
1839	dirMS_041712_NAR_60mM_minus.10597.10597.3	3	16.52	0	5.02E+05	M368m	(K)LAQAN	(K)L/A|Q\A N/G W/G V/m\V/S H R(S)	m:Oxidized methionine	119	514.591	1525.769	15.9892	-3.7	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
1840	dirMS_041712_NAR_20mM_plus.18693.18693.2	2	16.52	0	2.74E+05		(K)TAVETA	(K)T A|V/E/T/A/V L\L/L R(I)		200	593.3625	1185.72	-0.0024	-2	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
1841	dirMS_041712_NAR_30mM_plus2.16018.16039.2	2	16.52	0	2.68E+06		(R)INEILSN	(R)I/N|E|I|L/S N/A L K(R)		137.82	557.8307	1114.647	0.0075	6.7	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
1842	dirMS_041712_NAR_30mM_plus2.17129.17318.2	2	16.52	0	3.45E+05		(K)TVFGVE	(K)T V|F/G|V/E/P\D L T R(E)		143.35	617.3263	1233.647	-0.0021	-1.7	4.37	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
1843	dirMS_041712_NAR_40mM_plus2.16880.16880.3	3	16.52	0	8.98E+04		(R)LLEVLSG	(R)L/L/E V/L/S G E/I/L/P K P T K(G)		166	546.3323	1636.988	-0.006	-3.7	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
1844	dirMS_041712_NAR_50mM_plus2.21733.21849.3	3	16.52	0	9.49E+05		(K)GLAPDL	(K)G L|A|P/D/L/P E\D L/Y/H L I/K(K)		185.65	565.3101	1693.916	-0.0002	-0.1	4.54	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
1845	dirMS_041712_NAR_60mM_plus.9449.9450.3	3	16.52	0	2.84E+06		(K)SYCAEIA	(K)S Y|C/A E/I/A H N V S/S/K(N)	C:Carbamidomethylation	107.38	489.235	1465.674	0.0164	11.2	6.47	15730.4	11.67	HUMAN	D3YTB1	60S ribosomal protein L32 (Fragment)
1846	dirMS_041712_NAR_30mM_minus2.18036.18280.2	2	16.51	0	4.30E+05		(R)GLFIIDD	(R)G L|F|I|I/D/D/K(G)		153.47	460.7585	920.509	0.001	1	4.21	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
1847	dirMS_041712_NAR_30mM_minus2.18323.18323.2	2	16.51	0	4.28E+05		(R)QAQEYE	(R)Q A/Q/E|Y/E/A/L/L/N I K(V)		154.63	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1848	dirMS_041712_NAR_30mM_minus2.7471.7471.2	2	16.51	0	5.49E+04		(R)GAEQLA	(R)G A|E|Q/L A|E/G G R(M)		95.05	494.2466	987.485	0.0005	0.5	4.53	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b

1849	dirMS_041712_NAR_60mM_minus.10287.10543.3	3	16.51	1	6.05E+05	M88m	(K)DVDEAY	(K)D V\D|E/A/Y m N K/V/E/L/E/S R(L)	m:Oxidized methionine	118.37	605.2791	1797.832	15.9904	-2.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
1850	dirMS_041712_NAR_60mM_minus.11906.11906.3	3	16.51	1	3.74E+05		(K)NQVAM	(K)N Q|V/A|M/N/P T N T V F/D A K R(L)		126.55	602.6357	1805.896	-0.0037	-2.1	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
1851	dirMS_041712_NAR_30mM_plus2.22336.22336.3	3	16.51	0	5.20E+05		(R)VGNLGL	(R)V G N L\G L\A\T/S/F/F|N E R(N)		172.8	508.9306	1524.781	-0.0033	-2.1	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
1852	dirMS_041712_NAR_40mM_plus2.16866.16866.3	3	16.51	1	1.02E+05		(R)ALGTEVI	(R)A L|G T/E/V/I Q L/F/P E K G N M G/K(I)		165.6	644.6779	1932.026	-0.0068	-3.5	6.18	67184.7	9.24	HUMAN	O95831	Apoptosis-inducing factor 1, mitochondrial
1853	dirMS_041712_NAR_40mM_plus2.19240.19240.3	3	16.51	1	1.93E+05		(K)TSAQVV	(K)T S/A/Q/V/V/L|D G L V D K I G D/V/K(C)		180.37	619.6811	1857.033	-0.004	-2.2	4.43	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
1854	dirMS_041712_NAR_50mM_plus2.6005.6005.3	3	16.51	1	3.38E+04		(K)SAVEAQ	(K)S A/V|E/A/Q/N E V T E N/P K/Q K(I)		95.67	591.3073	1771.882	0.0253	14.3	4.78	89879.1	4.58	HUMAN	Q32MZ4	Leucine-rich repeat flightless-interacting protein 1
1855	dirMS_041712_NAR_120mM_minus.8095.8115.3	3	16.5	0	1.23E+06		(K)HSGPNS	(K)H S G P N\S\A/D|S|A|N/D/G F V/R(L)		98.42	544.2477	1630.72	0.0081	5	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
1856	dirMS_041712_NAR_120mM_minus.8350.8473.3	3	16.5	1	1.00E+06		(K)KGTVEG	(K)K\G T V E\G\F|E|P/A/D/N K(C)		100.1	464.5648	1391.68	-0.0003	-0.2	4.68	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
1857	dirMS_041712_NAR_20mM_plus.6868.6868.2	2	16.5	0	4.23E+05	M132m	(R)DmVGIA	(R)D m|V|G/I|A Q/T/G S G K(T)	m:Oxidized methionine	112.85	590.2864	1163.573	15.993	-1.6	5.84	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
1858	dirMS_041712_NAR_40mM_plus2.10727.10727.3	3	16.5	0	1.85E+05		(K)VGSLDN	(K)V/G/S\L D N V/G H/L P/A G G A V/K(I)		128.15	530.9567	1590.86	-0.0043	-2.7	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
1859	dirMS_041712_NAR_40mM_plus2.13783.13783.3	3	16.5	1	2.45E+05		(R)GDVVPK	(R)G D/V|V|P/K/D\V N/A A I A/T/I K(T)		147.4	537.6381	1610.911	-0.0115	-7.1	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
1860	dirMS_041712_NAR_120mM_plus.13414.13435.3	3	16.49	1	4.93E+05		(R)VIDRELY	(R)V/I/D/R E L\Y|Q/Q|L Q/R(G)		123.58	520.9543	1560.849	-0.0009	-0.6	6.04	533778	5.74	HUMAN	Q15149	Plectin
1861	dirMS_041712_NAR_20mM_plus.18612.18772.2	2	16.49	0	2.00E+05		(R)VFIGNLN	(R)V/F|I|G/N/L/N T/L/V\V/K(K)		200.13	658.8999	1316.794	-0.0011	-0.9	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
1862	dirMS_041712_NAR_30mM_plus2.11204.11509.2	2	16.49	0	8.39E+05		(K)LTVDSAI	(K)L/T|V/D/S/A/I A R(D)		112.58	473.2687	945.536	-0.0062	-6.6	5.84	334221.3	6.44	HUMAN	P15924	Desmoplakin
1863	dirMS_041712_NAR_120mM_minus.6664.6667.2	2	16.48	1	8.10E+04		(K)DSYVGD	(K)D/S/Y|V/G/D/E A Q S K/R(G)		90.67	677.8145	1354.623	-0.0016	-1.2	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
1864	dirMS_041712_NAR_30mM_minus2.16073.16073.2	2	16.48	0	1.16E+05		(K)EQFLDG	(K)E Q|F|L/D/G D/G W/T|S R(W)		141.08	705.8174	1410.628	-0.0009	-0.6	4.03	28545.1	4.5	HUMAN	K7EJB9	Calreticulin (Fragment)
1865	dirMS_041712_NAR_60mM_minus.14221.14222.3	3	16.48	0	1.14E+05		(K)GVGISVL	(K)G V|G I/S V/L/E/M/S H R(S)		139.12	428.9004	1284.673	0.0138	10.7	6.75	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
1866	dirMS_041712_NAR_20mM_plus.14298.14298.2	2	16.48	0	3.41E+04		(R)IALTDNA	(R)I/A|L\T/D/N/A L I/A R(S)		170.65	585.8432	1170.684	-0.005	-4.2	5.84	24489.6	10.74	HUMAN	A8MUD9	60S ribosomal protein L7
1867	dirMS_041712_NAR_20mM_plus.8335.8335.2	2	16.48	0	1.32E+04		(R)LAAVDV	(R)L/A|A|V/D\V S A/R(A)		127.57	451.2557	901.51	-0.006	-6.7	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin
1868	dirMS_041712_NAR_20mM_plus.10616.10616.2	2	16.47	0	7.50E+04		(K)TTTLSGT	(K)T T T|L/S/G/T/A|P A A/G V V|P S R(V)		145.97	793.4284	1585.854	-0.0049	-3.1	9.41	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
1869	dirMS_041712_NAR_30mM_plus2.14555.14760.2	2	16.47	0	4.73E+06		(R)FPGQLN	(R)F/P|G/Q/L/N/A|D|L R(K)		130.65	565.801	1130.595	-0.0006	-0.5	5.84	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1870	dirMS_041712_NAR_40mM_plus2.15007.15402.3	3	16.47	0	6.93E+05		(K)IEVIKPG	(K)I/E|V I/K/P G D|L/G V D/L T S K(L)		156.1	561.9876	1683.953	-0.0045	-2.7	4.56	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
1871	dirMS_041712_NAR_40mM_plus2.16567.16593.3	3	16.47	0	1.95E+05		(R)VAAGLP	(R)V A|A|G/L|P/P I L V H/T D A A/Q A L G K(Q)		164.1	648.041	1942.112	-0.0036	-1.8	6.71	17974.2	4.97	HUMAN	C9JNL5	Selenocysteine lyase (Fragment)
1872	dirMS_041712_NAR_40mM_plus2.6678.6678.2	2	16.47	0	4.08E+05		(K)AGFAGD	(K)A G/F/A/G/D/D/A/P R(A)		99.45	488.728	976.448	0.0004	0.4	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
1873	dirMS_041712_NAR_50mM_plus2.14466.14598.3	3	16.47	0	1.06E+06		(R)ETHSALG	(R)E T H S A\L|G|P|A|L|Q/A A F/K(L)		144.3	514.2745	1540.812	-0.0029	-1.9	6.85	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
1874	dirMS_041712_NAR_120mM_minus.15982.16391.4	4	16.46	2	1.46E+06		(K)KQGGLG	(K)K Q G G\L G\P M|N\I/P/L/V/S D/P K R(T)		143.48	477.5179	1907.053	-0.0034	-1.8	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
1875	dirMS_041712_NAR_20mM_minus.11224.11224.2	2	16.46	0	2.79E+05		(K)LSELEAA	(K)L/S/E/L|E A A|L/Q R(A)		159.5	565.3134	1129.621	-0.0016	-1.5	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1876	dirMS_041712_NAR_20mM_minus.8134.8445.2	2	16.46	0	6.77E+06	M239m	(K)EITALAP	(K)E I|T/A|L|A|P/S T m K(I)	m:Oxidized methionine	132.6	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
1877	dirMS_041712_NAR_50mM_minus2.5675.5675.3	3	16.46	1	3.66E+05		(K)DSYVGD	(K)D/S|Y/V/G D E/A/Q S K/R(G)		92.95	452.2119	1354.623	-0.0022	-1.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
1878	dirMS_041712_NAR_60mM_minus.18853.19112.3	3	16.46	1	4.12E+06		(R)LDLAGR	(R)L/D|L/A/G R D L/T D/Y L/M/K(I)		167.95	541.9507	1623.841	-0.0035	-2.2	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
1879	dirMS_041712_NAR_60mM_minus.8253.8253.3	3	16.46	1	1.45E+05		(R)LSQIGVE	(R)L/S/Q/I/G/V E N T E E N R R(L)		106.1	548.9481	1644.83	-0.0002	-0.1	4.79	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
1880	dirMS_041712_NAR_120mM_plus.16292.16763.4	4	16.46	2	4.59E+06		(K)KQGGLG	(K)K Q G G\L G\P M|N\I/P/L/V/S D/P K R(T)		140.23	477.5186	1907.053	-0.0006	-0.3	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
1881	dirMS_041712_NAR_30mM_plus2.13928.14038.2	2	16.46	0	3.99E+05		(R)LLQLQEQ	(R)L L|Q|L/Q\E/Q/M/R(A)		126.32	579.8193	1158.63	0.0014	1.2	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
1882	dirMS_041712_NAR_50mM_plus2.11437.11437.3	3	16.46	1	7.45E+05		(K)LAEQAE	(K)L/A|E/Q/A/E R Y D D/M A A A M K(A)		127.98	604.9469	1812.825	0.0007	0.4	4.32	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
1883	dirMS_041712_NAR_40mM_minus2.13812.13812.3	3	16.45	1	4.48E+04		(K)FGEVVD	(K)F/G/E/V/V/D C T L K/L D/P I\T G R(S)	C:Carbamidomethylation	165.3	640.6656	1919.989	-0.0073	-3.8	4.56	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
1884	dirMS_041712_NAR_60mM_minus.12725.13235.3	3	16.45	0	1.39E+07		(R)NLDIERP	(R)N/L|D|I/E R/P T Y/T/N/L N R(L)		130.23	573.6304	1718.882	-0.0054	-3.1	6.07	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
1885	dirMS_041712_NAR_20mM_plus.18802.19183.2	2	16.45	0	1.21E+06		(K)EIIDLVLD	(K)E I|I/D|L/V/L/D/R(I)		202.38	543.313	1085.62	-0.0014	-1.3	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
1886	dirMS_041712_NAR_30mM_plus2.19929.20072.2	2	16.45	0	3.53E+05		(R)LNILDTL	(R)L/N|I|L/D/T/L/S/K(F)		158.72	508.8023	1016.599	-0.0013	-1.3	5.84	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
1887	dirMS_041712_NAR_50mM_plus2.16044.16044.3	3	16.45	0	1.05E+06		(R)LSFQHD	(R)L/S/F Q H/D|P E/T S V/L/V L/R(K)		152.42	580.9801	1740.928	-0.0022	-1.2	5.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
1888	dirMS_041712_NAR_60mM_plus.11495.11495.3	3	16.45	0	1.11E+06		(R)SIFQHIQ	(R)S I/F Q/H I/Q/S/A/Q/S Q/R(S)		117.93	510.6056	1529.782	0.0203	13.3	9.49	108720.9	10.17	HUMAN	Q9Y2W1	Thyroid hormone receptor-associated protein 3
1889	dirMS_041712_NAR_60mM_minus.13591.13918.3	3	16.44	1	2.50E+07		(R)GYSFTTT	(R)G Y|S|F/T T/T/A E R E I V/R(D)		136.28	543.9458	1629.823	-0.0003	-0.2	6.14	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
1890	dirMS_041712_NAR_30mM_plus2.13778.13793.2	2	16.44	0	8.29E+05		(R)GIVDSIT	(R)G I|V|D/S/I/T/G Q/R(L)		125.5	523.2797	1045.564	-0.0115	-11	5.84	334221.3	6.44	HUMAN	P15924	Desmoplakin
1891	dirMS_041712_NAR_30mM_plus2.9894.9910.2	2	16.44	0	1.51E+06		(R)LTVDEAV	(R)L/T|V/D/E/A V/R(A)		105.73	451.7509	902.494	0.0004	0.4	4.37	533778	5.74	HUMAN	Q15149	Plectin
1892	dirMS_041712_NAR_30mM_minus2.15071.15198.2	2	16.43	0	7.18E+05	M2249m	(K)MSIYQA	(K)M/S|I|Y/Q/A/m W/K(G)	m:Oxidized methionine	135.72	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
1893	dirMS_041712_NAR_40mM_minus2.14514.14781.3	3	16.43	1	1.50E+06	M116m	(R)ELAILLG	(R)E L|A|I/L/L/G m L/D/P A/E K D E K(G)	m:Oxidized methionine	171.22	634.338	1884.999	16.0008	3.1	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
1894	dirMS_041712_NAR_60mM_minus.11523.11523.3	3	16.43	1	2.94E+05		(R)VFDKEG	(R)V/F|D K E G\N G\T\V/M/G A E/I R(H)		124.35	574.9539	1722.848	-0.0008	-0.5	4.68	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
1895	dirMS_041712_NAR_60mM_minus.12199.12724.3	3	16.43	1	3.18E+06		(K)ASLENSL	(K)A/S|L/E/N S/L/R E V E/A/R(Y)		128.3	491.927	1473.766	0.0009	0.6	4.79	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1896	dirMS_041712_NAR_40mM_plus2.18201.18391.3	3	16.43	0	3.43E+05		(R)EAVELPL	(R)E A|V/E/L/P/L/T/H F E/L/Y/K(Q)		173.8	563.6336	1688.889	-0.0032	-1.9	4.75	47479.5	5.09	HUMAN	P43686	26S protease regulatory subunit 6B
1897	dirMS_041712_NAR_50mM_plus2.10638.10806.3	3	16.43	1	6.61E+05		(K)GCGVVK	(K)G C|G V|V K/F E/S/P/E/V A E R(A)	C:Carbamidomethylation	123.88	555.2753	1663.811	0.0005	0.3	4.79	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
1898	dirMS_041712_NAR_120mM_minus.11584.12119.3	3	16.42	1	5.12E+06		(R)FPGQLN	(R)F/P/G Q|L/N/A/D/L R K(L)		118.65	420.2348	1258.69	-0.0004	-0.3	8.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1899	dirMS_041712_NAR_20mM_minus.13093.13151.3	3	16.42	0	1.85E+06	M73m	(R)AILVDLE	(R)A I\L\V D\L E|P/G T/m D/S V R(S)	m:Oxidized methionine	182.72	544.6138	1615.836	15.9909	-2.5	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
1900	dirMS_041712_NAR_120mM_plus.11430.11448.3	3	16.42	0	7.46E+05		(K)TGNLGN	(K)T/G|N|L/G N V/V/H/I/E R(F)		113.42	436.9054	1308.702	-0.0002	-0.2	6.41	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
1901	dirMS_041712_NAR_20mM_plus.15524.15524.2	2	16.42	0	4.33E+05		(R)GVVDSE	(R)G V\V/D/S/E/D/I|P L N/L/S/R(E)		179.2	757.3956	1513.786	-0.0017	-1.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
1902	dirMS_041712_NAR_20mM_plus.18677.18677.2	2	16.42	0	2.87E+05		(K)LAVEALS	(K)L A V/E A|L|S/S L|D|G D L/A/G R(Y)		200.48	793.9214	1586.838	-0.0029	-1.8	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
1903	dirMS_041712_NAR_30mM_plus2.19467.19529.2	2	16.42	0	7.16E+05		(R)LDFNLIR	(R)L/D|F|N|L/I/R(V)		156.18	445.759	890.509	0.0013	1.5	5.84	18956.4	6.97	HUMAN	C9JLK0	Phosphoribosylaminoimidazolecarboxamide formyltransferase (Fragment)
1904	dirMS_041712_NAR_50mM_plus2.14343.14343.3	3	16.42	1	1.80E+05		(K)TITLEVEI	(K)T I|T L/E/V/E/P S/D T I E/N V K/A K(I)		143.57	663.0232	1987.059	-0.0043	-2.2	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
1905	dirMS_041712_NAR_120mM_minus.10767.10788.3	3	16.41	0	9.41E+05		(R)GFCLPPH	(R)G F|C/L/P/P/H C S R(G)	C:Carbamidomethylation	113.53	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
1906	dirMS_041712_NAR_30mM_minus2.18980.19254.2	2	16.41	0	1.32E+06		(K)LAVNMV	(K)L A|V/N|M|V|P F/P R(L)		159.15	572.3143	1143.634	-0.013	-11.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1907	dirMS_041712_NAR_60mM_minus.11928.12008.3	3	16.41	0	3.17E+05		(K)VFEGNR	(K)V/F|E/G N R P T N S I/V/F/T/K(L)		126.65	570.304	1708.902	-0.0042	-2.5	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
1908	dirMS_041712_NAR_20mM_plus.13915.13915.2	2	16.41	0	6.90E+04		(K)LLDLVQQ	(K)L L|D|L/V/Q/Q/S/C/N Y K(Q)	C:Carbamidomethylation	167.73	740.8757	1480.746	-0.0023	-1.6	5.83	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
1909	dirMS_041712_NAR_20mM_plus.18331.18331.2	2	16.41	0	1.95E+05		(R)AAVEEG	(R)A A V E\E\G/I|V|L/G G/G C/A L L R(C)	C:Carbamidomethylation	197.9	842.9549	1684.905	-0.0025	-1.5	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
1910	dirMS_041712_NAR_30mM_plus2.11479.11529.2	2	16.41	0	4.70E+05		(K)IVVVTAG	(K)I/V|V|V/T/A G V/R(Q)		113.82	457.2931	913.583	-0.004	-4.4	9.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
1911	dirMS_041712_NAR_30mM_plus2.13171.13478.2	2	16.41	0	5.84E+06		(R)YLYEIAR	(R)Y/L|Y/E/I/A/R(R)		123.2	464.2507	927.493	0.0007	0.7	6	53112	6.64	HUMAN	H0YA55	Serum albumin (Fragment)
1912	dirMS_041712_NAR_30mM_minus2.16596.16596.2	2	16.4	0	2.83E+05		(R)ASLEAAI	(R)A S/L E/A/A|I/A/D/A\E Q/R(G)		143.85	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1913	dirMS_041712_NAR_30mM_minus2.18749.19104.2	2	16.4	0	1.14E+06		(R)ALLFIPR	(R)A/L|L|F|I/P/R(R)		157.52	415.2685	829.529	0.0003	0.3	9.79	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
1914	dirMS_041712_NAR_50mM_minus2.6231.6231.3	3	16.4	0	2.41E+05	M434m	(R)LESGmQ	(R)L/E|S\G m/Q N/M/S\I H/T/K(T)	m:Oxidized methionine	98.83	497.9018	1475.698	15.9927	-1.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1915	dirMS_041712_NAR_60mM_minus.5063.5314.3	3	16.4	0	3.20E+06		(R)AEAEAG	(R)A E|A|E|A/G S P R P D|P/R(E)		83.35	451.5562	1352.655	-0.0013	-0.9	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
1916	dirMS_041712_NAR_120mM_plus.9732.9761.3	3	16.4	0	2.73E+06		(R)QSVEND	(R)Q S/V/E N/D/I/H/G L/R(K)		104.47	423.2188	1267.639	0.0029	2.3	5.32	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1917	dirMS_041712_NAR_20mM_plus.17590.17590.2	2	16.4	0	8.72E+04	M148m	(K)TFAPEEI	(K)T F|A/P E E I/S A m/V L\T K(M)	m:Oxidized methionine	193.43	776.8996	1536.798	15.9941	-0.5	4.53	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
1918	dirMS_041712_NAR_20mM_plus.18813.19032.2	2	16.4	0	1.21E+06		(K)EIIDLVLD	(K)E I|I|D|L/V/L/D/R(I)		202.38	543.313	1085.62	-0.0014	-1.3	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
1919	dirMS_041712_NAR_50mM_plus2.12287.12287.3	3	16.4	1	3.20E+05		(K)LSAEKVE	(K)L/S\A/E K/V E/I/A/T/L/T R(E)		132.33	477.6113	1430.821	-0.002	-1.4	6.14	26661.1	7.81	HUMAN	H0YL69	Proteasome subunit alpha type (Fragment)
1920	dirMS_041712_NAR_50mM_plus2.16428.16428.3	3	16.4	0	5.57E+05		(R)QVVQGI	(R)Q V|V/Q|G|L\L S/E T/Y/L|E/A H R(I)		154.53	614.9984	1842.971	0.0098	5.3	5.4	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
1921	dirMS_041712_NAR_50mM_plus2.8224.8224.3	3	16.4	1	3.71E+05		(R)VLVNDA	(R)V/L/V/N/D A Q/K V/T E\G Q Q E R(L)		109.88	605.3151	1813.94	-0.0095	-5.2	4.68	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
1922	dirMS_041712_NAR_60mM_plus.9167.9167.3	3	16.4	1	8.85E+05		(K)AQAEVE	(K)A Q|A|E|V/E/G/L G K/G V A R(L)		105.75	462.2549	1384.754	-0.0042	-3	6.19	533778	5.74	HUMAN	Q15149	Plectin
1923	dirMS_041712_NAR_20mM_minus.14706.14880.2	2	16.39	0	3.01E+06		(K)EIIDLVLD	(K)E I|I|D|L/V/L/D/R(I)		203.67	543.3133	1085.62	-0.0008	-0.7	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
1924	dirMS_041712_NAR_30mM_minus2.10956.11131.2	2	16.39	0	6.58E+05		(K)VAGQDG	(K)V/A|G\Q/D|G/S V/V/Q\F K(I)		114	617.824	1234.643	-0.0019	-1.5	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
1925	dirMS_041712_NAR_30mM_minus2.12237.12720.2	2	16.39	0	5.64E+05		(K)GDYPLEA	(K)G D/Y|P/L/E/A/V/R(M)		122.22	510.2598	1019.516	-0.0033	-3.2	4.37	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
1926	dirMS_041712_NAR_30mM_minus2.13683.13683.2	2	16.39	0	6.08E+05		(K)NLVTEDV	(K)N L|V|T/E D/V M\R(M)		127.03	538.7747	1076.541	0.0017	1.5	4.37	12797.5	10.58	HUMAN	K7EIL4	Glucose-6-phosphate isomerase (Fragment)
1927	dirMS_041712_NAR_30mM_minus2.9615.9795.2	2	16.39	1	9.31E+05		(K)AIYKGPG	(K)A I|Y/K/G P G S E|A|G|P(-)		107.28	573.7932	1146.579	0.0002	0.1	6.04	30492.9	5.26	HUMAN	P21964	Catechol O-methyltransferase
1928	dirMS_041712_NAR_120mM_plus.10866.11191.3	3	16.39	0	1.51E+06		(R)GSAVHQ	(R)G S|A/V/H/Q/L/S/E/E/L/R(C)		111.13	442.5657	1325.681	0.0017	1.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
1929	dirMS_041712_NAR_120mM_plus.9689.9729.3	3	16.39	1	4.94E+05		(K)LTRDETN	(K)L T R D E/T\N|Y/G|I|P Q/R(A)		104.2	521.6023	1562.792	0.0002	0.1	6.07	13083.6	6.26	HUMAN	D6R909	Guanine nucleotide-binding protein subunit beta-2-like 1
1930	dirMS_041712_NAR_20mM_plus.10627.10708.2	2	16.39	0	2.04E+05		(K)NAGVEG	(K)N A|G|V|E|G S L/I/V/E/K(I)		146.07	608.3304	1215.658	-0.0044	-3.6	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
1931	dirMS_041712_NAR_30mM_plus2.10697.10698.2	2	16.39	0	2.62E+05		(K)DQVANS	(K)D Q|V|A|N/S/A/F/V/E/R(L)		109.43	618.3057	1235.602	0.0026	2.1	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
1932	dirMS_041712_NAR_30mM_plus2.8255.8569.2	2	16.39	0	1.33E+06		(K)YICENQD	(K)Y/I|C|E N Q D S/I|S/S K(L)	C:Carbamidomethylation	97.88	722.3239	1443.642	-0.0015	-1	4.37	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
1933	dirMS_041712_NAR_50mM_plus2.17639.17639.3	3	16.39	1	8.31E+05		(R)DSEQVA	(R)D S|E/Q/V/A E/L K Q E L A T L K(S)		161.07	601.322	1801.954	-0.0027	-1.5	4.41	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
1934	dirMS_041712_NAR_60mM_plus.18347.18410.3	3	16.39	1	1.76E+06		(K)QLDDLKV	(K)Q L/D/D/L/K/V/E/L/S Q/L R(V)		154.27	519.6254	1556.864	-0.0026	-1.7	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
1935	dirMS_041712_NAR_60mM_plus.9791.9791.3	3	16.39	0	7.66E+05		(R)QQEGFK	(R)Q Q/E/G/F K/P N/Y M E/N/R(E)		109.3	547.5879	1640.749	0.0006	0.4	6.14	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
1936	dirMS_041712_NAR_50mM_minus2.16353.16353.3	3	16.38	1	5.41E+04		(K)SELVAM	(K)S E|L|V/A M/L E/E E E L/R K(A)		161.32	559.2917	1675.857	0.0034	2	4.32	18679.2	5.61	HUMAN	B4DWW1	ADP-ribosylation factor-like protein 1
1937	dirMS_041712_NAR_20mM_plus.18330.18446.3	3	16.38	0	3.15E+05		(R)AAVEEG	(R)A A\V E E\G I\V|L/G|G/G/C/A L L R(C)	C:Carbamidomethylation	198.02	562.3058	1684.905	-0.0022	-1.3	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
1938	dirMS_041712_NAR_30mM_plus2.8094.8384.2	2	16.38	0	1.36E+06		(K)QGGGGG	(K)Q G\G G/G|G/G/G/S/V|P G I/E/R(M)		97.17	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
1939	dirMS_041712_NAR_40mM_plus2.11892.12028.3	3	16.38	1	2.81E+05		(K)LIADVAP	(K)L/I|A|D|V|A/P S A I R E N D/I/K(S)		136.47	575.6528	1724.954	-0.0103	-6	4.56	18388.8	6.85	HUMAN	F5H1Y3	Flap endonuclease 1 (Fragment)
1940	dirMS_041712_NAR_50mM_plus2.10749.10749.3	3	16.38	1	5.26E+05		(R)VAVEEV	(R)V/A|V/E/E/V/D E E/G K F V/R(L)		124.4	535.9422	1605.812	0.0002	0.1	4.25	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
1941	dirMS_041712_NAR_50mM_plus2.11372.11372.3	3	16.38	1	1.25E+06		(K)NQVAM	(K)N Q|V|A M/N/P T/N T V/F D A K R(L)		127.8	602.6354	1805.896	-0.0046	-2.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
1942	dirMS_041712_NAR_50mM_minus2.11477.11477.3	3	16.37	0	2.35E+04		(R)LIAEQPP	(R)L/I/A E Q/P P H L/T P/G I R(E)		133.68	514.6309	1541.88	-0.0017	-1.1	6.75	20915.7	6.45	HUMAN	C9JBI3	Phosphoserine phosphatase (Fragment)
1943	dirMS_041712_NAR_50mM_minus2.17753.17753.3	3	16.37	1	3.97E+05		(R)LKLPSIPL	(R)L K L P S I|P|L|V/P V/S A Q K(R)		169.73	530.669	1589.999	-0.0064	-4.1	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
1944	dirMS_041712_NAR_50mM_minus2.9052.9090.3	3	16.37	0	2.39E+05		(R)GISEETT	(R)G I|S/E/E/T/T/T/G V/H N L Y K(M)		119.9	550.2763	1648.818	-0.0033	-2	5.4	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
1945	dirMS_041712_NAR_20mM_plus.16612.16905.2	2	16.37	0	4.12E+05		(K)VQIAVA	(K)V Q|I\A/V|A|N A/Q/E/L L/Q R(M)		187.28	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
1946	dirMS_041712_NAR_30mM_plus2.14075.14325.3	3	16.37	0	1.32E+06		(R)MGQMA	(R)M/G\Q\M A\M/G G\A|M/G|I/N/N R(G)		127.32	513.5611	1538.67	-0.0007	-0.5	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
1947	dirMS_041712_NAR_50mM_plus2.16209.16209.3	3	16.37	0	2.89E+05		(K)ACQSIYP	(K)A C/Q S/I/Y/P L/H/D V F V R(K)	C:Carbamidomethylation	154.4	568.9562	1704.853	0.0014	0.8	6.79	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
1948	dirMS_041712_NAR_20mM_minus.13918.13952.2	2	16.36	0	8.14E+05		(K)VLTPELY	(K)V L|T|P/E/L Y A E/L R(A)		191.32	652.3653	1303.726	-0.0023	-1.8	4.53	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
1949	dirMS_041712_NAR_20mM_plus.14296.14643.3	3	16.36	0	8.76E+05	M73m	(R)AVLVDLI	(R)A V|L\V D L\E/P/G/T/m/D S V R(S)	m:Oxidized methionine	171.03	539.9421	1601.82	15.9914	-2.2	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
1950	dirMS_041712_NAR_50mM_plus2.12011.12046.3	3	16.36	0	1.29E+06		(R)VYNVTQ	(R)V/Y/N/V/T/Q/H A\V/G I V/V/N K(Q)		131.48	547.6436	1640.912	0.0044	2.7	8.57	10000.5	10.56	HUMAN	G3V1B3	60S ribosomal protein L21
1951	dirMS_041712_NAR_50mM_plus2.16888.16888.3	3	16.36	1	8.57E+05		(K)LFTAESL	(K)L/F|T\A/E S L/I/G L K/N P E/K(S)		157.48	553.9791	1659.932	-0.0089	-5.3	6.14	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
1952	dirMS_041712_NAR_50mM_plus2.19676.20162.3	3	16.35	1	3.18E+06		(R)KAIIIFVP	(R)K\A I I\I\F|V|P/V P Q/L K(S)		173.15	489.3212	1465.95	-0.0014	-1	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
1953	dirMS_041712_NAR_60mM_plus.13044.13045.3	3	16.35	1	1.81E+05		(R)GLAGLG	(R)G L|A/G/L/G D/V/A E/V R/K(S)		124.92	428.9129	1284.727	-0.0029	-2.2	6.07	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
1954	dirMS_041712_NAR_60mM_plus.6820.6820.3	3	16.35	0	5.16E+05		(R)ATAPQT	(R)A T|A/P Q T Q/H/V/S/P M R(Q)		94.17	475.2423	1423.711	0.0013	0.9	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
1955	dirMS_041712_NAR_20mM_minus.12302.12511.2	2	16.34	0	5.88E+05	M73m	(R)AVLVDLI	(R)A V/L|V/D/L|E|P/G T\m D S V R(S)	m:Oxidized methionine	172.52	809.4088	1601.82	15.99	-3	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
1956	dirMS_041712_NAR_30mM_minus2.17806.17945.2	2	16.34	0	2.89E+05		(R)NNLAGA	(R)N N|L|A|G/A/E E/L/F A/R(K)		151.62	652.8358	1304.659	0.005	3.8	4.53	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
1957	dirMS_041712_NAR_40mM_minus2.14772.14772.3	3	16.34	1	1.48E+06	M116m	(R)ELAILLG	(R)E L/A/I/L L/G m L D/P A E/K D/E K(G)	m:Oxidized methionine	171.23	634.338	1884.999	16.0008	3.1	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6

1958	dirMS_041712_NAR_50mM_minus2.17273.17273.3	3	16.34	0	1.05E+06	M195m	(R)LHFFmP	(R)L H F F m|P G|F|A/P L T S R(G)	m:Oxidized methionine	167.33	546.2872	1620.835	16.0115	10.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1959	dirMS_041712_NAR_60mM_minus.11605.11605.3	3	16.34	0	7.51E+05		(K)TKPYIQV	(K)T K\P Y I Q\V|D|I/G G G Q T K(T)		124.67	535.6216	1604.864	-0.014	-8.7	8.17	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
1960	dirMS_041712_NAR_60mM_minus.18465.18465.3	3	16.34	0	5.02E+04	M195m	(R)LHFFmP	(R)L H\F F m/P G|F/A|P L/T S R(G)	m:Oxidized methionine	164.37	546.2843	1620.835	16.0028	4.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
1961	dirMS_041712_NAR_20mM_plus.9325.9325.2	2	16.34	0	1.86E+05		(K)SVTNED	(K)S V/T/N|E|D V/T Q/E E/L/G G A K(T)		136	838.9014	1676.797	-0.0018	-1.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
1962	dirMS_041712_NAR_40mM_plus2.7506.7506.2	2	16.34	0	3.99E+05		(K)ASLENSL	(K)A S/L/E/N/S L/R(E)		105.08	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1963	dirMS_041712_NAR_50mM_plus2.15498.15498.3	3	16.34	1	9.99E+05		(R)KVPGVT	(R)K\V\P G V T A I\E\L/D/E/D/T/G T F R(I)		149.85	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
1964	dirMS_041712_NAR_60mM_plus.12958.13020.3	3	16.34	1	1.36E+06		(K)NQVAM	(K)N Q|V|A/M/N/P T/N/T/V/F D A K R(L)		124.48	602.6367	1805.896	-0.0007	-0.4	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
1965	dirMS_041712_NAR_60mM_plus.16347.16465.3	3	16.34	0	4.79E+05		(R)EAYPGD	(R)E A/Y/P/G D V/F Y L/H/S R(L)		142.62	518.5855	1553.738	0.0036	2.3	5.32	48851.3	9.2	HUMAN	K7EK63	ATP synthase subunit alpha, mitochondrial
1966	dirMS_041712_NAR_30mM_minus2.19569.19627.2	2	16.33	0	4.70E+05		(R)ASLSLW	(R)A S/L/S/L|W/Q/A/M E K(G)		162.75	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
1967	dirMS_041712_NAR_30mM_plus2.17524.17549.2	2	16.33	0	1.64E+05		(R)ASLEAAI	(R)A S L|E/A|A|I/A|D\A/E Q R(G)		145.03	672.8406	1344.675	-0.0015	-1.1	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
1968	dirMS_041712_NAR_30mM_plus2.7606.7646.2	2	16.33	0	9.52E+05		(K)STCIYGG	(K)S/T|C|I/Y/G G A/P/K(G)	C:Carbamidomethylation	94.2	527.2559	1053.503	0.0012	1.1	8.31	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
1969	dirMS_041712_NAR_50mM_plus2.15971.16027.3	3	16.33	1	7.23E+05		(R)EGLTSIE	(R)E/G/L|T/S/I/E E/V/T K/N L Q/K(F)		152.15	563.6357	1688.907	-0.014	-8.3	4.79	533778	5.74	HUMAN	Q15149	Plectin
1970	dirMS_041712_NAR_50mM_plus2.21792.21792.3	3	16.33	1	1.26E+05		(K)TENPLIL	(K)T E|N/P L/I/L I/D E V/D/K\I/G R(G)		185.57	609.0045	1825.007	-0.0076	-4.2	4.32	86039.3	5.74	HUMAN	F5GZ27	Lon protease homolog
1971	dirMS_041712_NAR_60mM_plus.18327.18552.3	3	16.33	1	2.81E+06		(K)QLDDLK	(K)Q L|D/D/L/K/V/E/L/S/Q L R(V)		154.67	519.6254	1556.864	-0.0026	-1.7	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
1972	dirMS_041712_NAR_50mM_minus2.6821.6822.3	3	16.32	0	5.92E+05		(R)EATNPP	(R)E A|T/N/P/P V/I Q E/E K/P K(K)		105.52	527.2846	1579.833	0.0066	4.2	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
1973	dirMS_041712_NAR_30mM_plus2.8034.8610.2	2	16.32	0	7.03E+06		(K)ASLENSL	(K)A/S|L/E/N/S/L/R(E)		99.25	445.2405	889.474	0	-0.1	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1974	dirMS_041712_NAR_40mM_plus2.13963.13963.3	3	16.32	0	2.92E+05		(R)LASTLVH	(R)L/A|S/T L/V/H L G E|Y Q A|A|V\D G A R(K)		148.43	657.6841	1971.029	0.0083	4.2	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
1975	dirMS_041712_NAR_50mM_plus2.20117.20118.3	3	16.32	0	3.51E+05		(R)NEVSFVI	(R)N E|V/S/F V/I/H|N L P\V/L A K(M)		174.32	560.6531	1679.948	-0.0032	-1.9	6.75	35663.7	5.91	HUMAN	B4DWK0	Selenide, water dikinase 1
1976	dirMS_041712_NAR_40mM_minus2.11652.11652.3	3	16.31	1	1.06E+05		(R)IINEPTA	(R)I I/N\E/P T/A A/A I A Y/G L/D/K K(V)		152.32	596.6671	1787.99	-0.0034	-1.9	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
1977	dirMS_041712_NAR_50mM_minus2.13447.13447.3	3	16.31	0	3.52E+05		(R)AVAIDLF	(R)A V\A/I/D L/P/G L G/H/S K(E)		144.57	426.5785	1277.721	-0.0003	-0.2	6.79	19983.6	8.14	HUMAN	B4DQI4	Alpha/beta hydrolase domain-containing protein 14B
1978	dirMS_041712_NAR_50mM_minus2.14267.14267.3	3	16.31	0	2.61E+05		(R)TIQVENS	(R)T I|Q/V/E N S H L I L/T/G A G A L N K(V)		149.02	660.367	1979.092	-0.0056	-2.8	6.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
1979	dirMS_041712_NAR_60mM_minus.10027.10069.3	3	16.31	0	1.56E+06		(R)EIVHIQA	(R)E/I\V H I Q A G/Q|C|G N Q I/G A/K(F)	C:Carbamidomethylation	115.57	608.3099	1822.923	-0.0077	-4.2	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
1980	dirMS_041712_NAR_120mM_plus.10407.10407.3	3	16.31	0	4.82E+05		(K)NLPLAD	(K)N L/P/L/A D/Q/G S/S H H I T V K(I)		107.58	572.9712	1716.903	-0.0037	-2.2	6.92	334221.3	6.44	HUMAN	P15924	Desmoplakin
1981	dirMS_041712_NAR_60mM_plus.6427.6444.3	3	16.31	1	2.97E+05		(K)VATQEG	(K)V/A|T/Q/E/G K/E I/T/C R(S)	C:Carbamidomethylation	92.3	464.5649	1391.695	-0.0146	-10.5	6.11	18626.5	5.64	HUMAN	B8ZZK2	Gamma-glutamylcyclotransferase
1982	dirMS_041712_NAR_20mM_minus.13261.13261.3	3	16.3	0	2.65E+05		(K)VGINYQ	(K)V G I N Y Q|P P T\V/V/P/G/G D L A K(V)		183.15	608.9971	1824.985	-0.0087	-4.8	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
1983	dirMS_041712_NAR_50mM_minus2.12995.13237.3	3	16.3	1	3.35E+05		(R)ALPAVQ	(R)A L|P/A/V/Q/Q N N L/D/E D/L I R K(L)		142.8	646.3522	1937.045	-0.003	-1.6	4.56	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
1984	dirMS_041712_NAR_50mM_minus2.8670.8670.3	3	16.3	0	1.55E+06		(R)EIVHIQA	(R)E/I/V H I Q A G\Q/C|G N Q I/G A K(F)	C:Carbamidomethylation	116.82	608.3087	1822.923	-0.0113	-6.2	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
1985	dirMS_041712_NAR_20mM_plus.10512.10626.2	2	16.3	0	3.12E+05		(K)VLQATV	(K)V/L/Q|A|T|V/V/A V/G S\G S K(G)		145.67	658.3823	1315.758	-0.0007	-0.5	8.72	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
1986	dirMS_041712_NAR_20mM_plus.18841.18841.2	2	16.3	0	1.01E+05		(K)LTVYTTL	(K)L T/V|Y/T/T L\I/D/V T K(G)		200.87	683.8948	1366.783	-0.0005	-0.4	5.83	42194.9	8.75	HUMAN	E7EMM4	Acid ceramidase
1987	dirMS_041712_NAR_50mM_minus2.14835.14835.3	3	16.29	1	2.96E+05		(R)EAVTEIL	(R)E/A|V/T/E/I L G I/E/P D R E K(G)		152.32	566.9683	1698.891	-0.0005	-0.3	4.25	25685.9	6.4	HUMAN	E9PGT1	Translin
1988	dirMS_041712_NAR_120mM_plus.5719.6114.3	3	16.29	1	1.19E+06		(R)TAQEVE	(R)T/A|Q/E V/E/T Y R/R(S)		84.27	418.2137	1252.628	-0.0015	-1.2	5.81	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
1989	dirMS_041712_NAR_120mM_plus.9444.9476.3	3	16.29	1	3.69E+05		(R)SRSGEG	(R)S R S G E\G\E|V|S/G/L/M/R(K)		102.8	455.5574	1364.659	-0.001	-0.8	5.87	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
1990	dirMS_041712_NAR_20mM_plus.6946.6946.2	2	16.29	0	8.44E+04	M29m	(K)IVQmTE	(K)I/V|Q|m/T E/A/E V R(G)	m:Oxidized methionine	114.35	596.3035	1175.609	15.9908	-3.4	4.53	14493.5	5.23	HUMAN	C9J9S3	Serine/threonine-protein phosphatase (Fragment)
1991	dirMS_041712_NAR_30mM_plus2.9548.9559.2	2	16.29	0	4.96E+05		(K)TAVCDIF	(K)T A|V|C/D|I|P|P/R(G)	C:Carbamidomethylation	105.07	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
1992	dirMS_041712_NAR_50mM_plus2.10075.10075.3	3	16.29	1	5.94E+04		(K)ITIKNDP	(K)I/T|I/K\N D P S L P/E/P K(C)		120.53	484.6079	1451.81	-0.0013	-0.9	6.07	20203.8	9.79	HUMAN	B4DG16	Asparagine--tRNA ligase, cytoplasmic
1993	dirMS_041712_NAR_60mM_plus.17903.18000.3	3	16.29	1	3.14E+04		(K)MFGIDR	(K)M/F|G/I/D/R D A\I/A/Q/A V R(G)		152.45	521.6038	1562.811	-0.0139	-8.9	5.71	63448.4	7.29	HUMAN	B4E022	Transketolase
1994	dirMS_041712_NAR_20mM_minus.9260.9260.2	2	16.28	0	2.79E+05		(R)AQIFAN	(R)A Q|I|F/A/N/T\V D N/A R(I)		142.32	660.3388	1319.67	0.0001	0.1	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
1995	dirMS_041712_NAR_50mM_minus2.9723.9742.3	3	16.28	0	3.73E+05		(R)EALLSSA	(R)E A|L/L/S/S A\V\D/H G S D E/V/K(F)		123.88	552.9403	1656.807	-0.0012	-0.7	4.31	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
1996	dirMS_041712_NAR_50mM_plus2.11438.11438.3	3	16.28	1	7.45E+05		(K)LAEQAE	(K)L/A|E/Q/A/E R Y D D M/A A A M/K(A)		127.98	604.9469	1812.825	0.0007	0.4	4.32	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
1997	dirMS_041712_NAR_20mM_plus.14233.14379.3	3	16.27	0	6.16E+05	M256m	(R)SLDmDS	(R)S L\D\m\D S|I|I A E/V/K(A)	m:Oxidized methionine	170.42	446.2266	1320.671	15.9937	-0.9	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
1998	dirMS_041712_NAR_30mM_plus2.16578.16764.2	2	16.27	0	3.64E+05		(R)FLICTDV	(R)F/L|I|C/T D/V A A/R(G)	C:Carbamidomethylation	140.02	583.3055	1165.603	0.0003	0.3	5.84	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
1999	dirMS_041712_NAR_30mM_plus2.23357.23527.2	2	16.27	0	2.11E+06		(R)DLPLLLF	(R)D L|P|L|L|L/F/R(T)		189.25	493.8049	986.603	-0.0008	-0.8	5.84	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
2000	dirMS_041712_NAR_40mM_plus2.12921.13214.3	3	16.27	1	9.95E+05		(K)TITLEVEI	(K)T I|T|L/E/V/E/P S D T I/E N V K A K(I)		143.45	663.0201	1987.059	-0.0136	-6.9	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
2001	dirMS_041712_NAR_50mM_plus2.18614.18749.3	3	16.27	1	9.79E+05		(R)LKLPSIPI	(R)L K L/P S I|P\L\V|P V/S A Q K(R)		166.8	530.6702	1589.999	-0.0028	-1.8	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
2002	dirMS_041712_NAR_50mM_plus2.9775.9775.3	3	16.27	1	1.99E+05		(R)AGTGVD	(R)A/G/T|G/V/D N V D/L E/A A/T R K(G)		118.75	539.6108	1616.824	-0.006	-3.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
2003	dirMS_041712_NAR_60mM_plus.7130.7130.3	3	16.27	0	3.22E+05		(K)IFSGSSH	(K)I/F|S/G/S S H/Q D L/S Q K(I)		95.45	478.5718	1433.702	-0.0011	-0.8	6.74	18741.7	9.49	HUMAN	B1ALA7	Phosphoribosyl pyrophosphate synthetase 1
2004	dirMS_041712_NAR_50mM_minus2.16845.16948.3	3	16.26	0	4.60E+05		(K)NILFVIT	(K)N I|L|F/V/I T/K/P D V/Y K(S)		164.12	517.2991	1549.899	-0.0161	-10.4	8.5	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
2005	dirMS_041712_NAR_20mM_plus.10467.10486.2	2	16.26	0	2.32E+05		(R)AQIFAN	(R)A Q|I|F/A|N/T/V/D N A R(I)		145.25	660.3343	1319.67	-0.0089	-6.8	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2006	dirMS_041712_NAR_30mM_plus2.16021.16299.2	2	16.26	0	1.14E+06		(R)GDLGIEI	(R)G D/L|G|I|E|I|P A E K(V)		137.55	571.3087	1141.61	0.0002	0.2	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
2007	dirMS_041712_NAR_20mM_minus.12520.12520.2	2	16.25	0	4.31E+05	M185m	(K)LAVNm	(K)L/A/V/N/m/V/P F P/R(L)	m:Oxidized methionine	172.88	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
2008	dirMS_041712_NAR_30mM_minus2.14121.14121.2	2	16.25	0	3.83E+05		(R)NLVDNI	(R)N L|V|D N/I/T/G Q/R(L)		129.95	565.3015	1129.596	-0.0003	-0.3	5.84	533778	5.74	HUMAN	Q15149	Plectin
2009	dirMS_041712_NAR_30mM_plus2.20271.20766.2	2	16.25	0	1.40E+06		(R)ILVATNL	(R)I/L|V|A/T/N/L F/G R(G)		162.17	552.331	1103.657	-0.0024	-2.2	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
2010	dirMS_041712_NAR_50mM_plus2.14422.14422.3	3	16.25	1	9.68E+05		(R)LAIKLPD	(R)L/A/I/K\L/P D D Q I P K(T)		144.23	450.9373	1350.799	-0.0018	-1.3	5.96	26413	9.18	HUMAN	B1APP6	6-phosphofructokinase type C (Fragment)
2011	dirMS_041712_NAR_60mM_plus.18372.18372.3	3	16.25	1	5.97E+05		(R)IRIDSLS	(R)I R I D S L\S A|Q\L|S Q L/Q/K(Q)		153.73	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
2012	dirMS_041712_NAR_30mM_minus2.14401.14851.2	2	16.24	0	4.42E+06		(R)NLLSVA	(R)N/L|L|S/V/A/Y|K(N)		133.37	454.2604	907.525	-0.0112	-12.4	8.59	18789.1	6.77	HUMAN	A2IDB2	14-3-3 protein eta (Fragment)
2013	dirMS_041712_NAR_50mM_minus2.15535.15779.3	3	16.24	1	4.93E+05		(K)QGGLGF	(K)Q/G/G L/G/P M N\I/P/L/V/S D/P K R(T)		157.5	593.6566	1778.958	-0.0029	-1.6	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
2014	dirMS_041712_NAR_60mM_minus.9834.10013.3	3	16.24	0	1.71E+06		(R)ISNRPAF	(R)I/S/N R P A\F\M|P/S/E/G K(M)		115.08	478.5785	1433.721	0.0004	0.3	8.75	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
2015	dirMS_041712_NAR_120mM_plus.17377.17678.4	4	16.24	1	1.48E+05		(R)GFGHIG	(R)G F G H I G I|A\V|P/D/V/Y/S A C K R(F)	C:Carbamidomethylation	146.95	487.5024	1946.991	-0.0028	-1.4	8.6	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
2016	dirMS_041712_NAR_20mM_plus.16439.16439.2	2	16.24	0	1.40E+05		(R)QAQEYE	(R)Q A/Q|E Y/E/A L/L/N I/K(V)		184.52	710.3754	1419.748	-0.0043	-3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2017	dirMS_041712_NAR_30mM_plus2.22606.22606.2	2	16.24	0	1.01E+06		(R)FLTWILN	(R)F L|T/W I L/N R(Y)		175.88	531.8078	1062.61	-0.0012	-1.1	9.75	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
2018	dirMS_041712_NAR_60mM_plus.5622.5622.3	3	16.24	1	1.91E+05		(R)SGGGYG	(R)S G G G\Y/G/G D R S S G/G G/Y|S G D/R(S)		88.07	583.5777	1748.722	-0.0033	-1.9	5.68	21563.9	10.01	HUMAN	K7EKB2	TATA-binding protein-associated factor 2N (Fragment)
2019	dirMS_041712_NAR_60mM_plus.8339.8374.3	3	16.24	0	2.22E+06		(K)HTGPNS	(K)H T G\P N\S P/D|T|A/N/D/G F/V/R(L)		102.07	562.2601	1684.767	-0.0016	-1	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
2020	dirMS_041712_NAR_30mM_minus2.12971.13439.2	2	16.23	0	5.54E+06		(K)FASFIDK	(K)F/A|S|F/I/D|K(V)		125.32	414.2189	827.43	0.0007	0.9	5.84	54364	5.73	HUMAN	F5H8K9	Keratin, type II cytoskeletal 4
2021	dirMS_041712_NAR_30mM_minus2.15879.15879.2	2	16.23	0	3.79E+05		(R)FGLNVS	(R)F/G\L|N|V/S/S I S R(K)		139.97	540.2895	1079.584	-0.0127	-11.7	9.75	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
2022	dirMS_041712_NAR_30mM_plus2.17533.17533.3	3	16.23	0	8.69E+05		(R)ASLEAAI	(R)A S L E A\A|I/A/D/A/E/Q R(G)		144.75	448.8963	1344.675	-0.001	-0.8	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2023	dirMS_041712_NAR_30mM_plus2.6102.6102.2	2	16.23	0	7.31E+04		(K)SCCSCCF	(K)S C|C/S\C|C/P V/G\C A K(C)	C:Carbamidomethylation	86.22	723.2586	1445.51	0.0001	0	8.47	7183.2	9.78	HUMAN	P02795	Metallothionein-2
2024	dirMS_041712_NAR_30mM_plus2.6342.6342.2	2	16.23	0	1.43E+05		(R)FGGSGS	(R)F/G|G/S/G S Q/V/D|S A R(M)		87.52	584.2731	1167.539	0	0	5.84	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
2025	dirMS_041712_NAR_50mM_plus2.15390.15441.3	3	16.23	1	4.11E+05		(R)LAAELNI	(R)L/A|A/E/L N/K F/M L E/K(V)		149.03	469.5948	1406.771	-0.0014	-1	6.14	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
2026	dirMS_041712_NAR_50mM_plus2.6754.6754.3	3	16.23	1	1.72E+05		(R)EGVLTG	(R)E G\V/L/T/G S/P E Q K E E A/A K(A)		100.87	558.2837	1672.839	-0.0023	-1.4	4.49	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
2027	dirMS_041712_NAR_20mM_minus.10619.10619.2	2	16.22	0	2.00E+05		(R)TTPSYV	(R)T T|P S Y/V|A/F T D/T E/R(L)		154.63	744.3547	1487.701	0.0009	0.6	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
2028	dirMS_041712_NAR_40mM_minus2.13511.13511.3	3	16.22	0	3.00E+04		(K)YVDTPF	(K)Y V|D T/P F G K/P S D/A L/I/L G K(I)		163.33	607.6637	1820.979	-0.0027	-1.5	5.96	33699.1	7.18	HUMAN	B4DUC8	S-methyl-5'-thioadenosine phosphorylase
2029	dirMS_041712_NAR_50mM_minus2.16098.16303.3	3	16.22	1	4.74E+05		(K)LFTAESL	(K)L/F|T/A/E S L I/G/L K N/P E/K(S)		160.67	553.9759	1659.932	-0.0185	-11.1	6.14	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
2030	dirMS_041712_NAR_50mM_minus2.7668.7668.3	3	16.22	0	5.25E+04	M151m	(R)AYADSY	(R)A/Y|A/D/S Y/Y Y/E D/G G m K P R(V)	m:Oxidized methionine	110.73	634.6139	1885.806	16.021	13.7	4.56	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
2031	dirMS_041712_NAR_50mM_minus2.9323.9344.3	3	16.22	0	1.54E+05		(R)TPVIDAI	(R)T/P|V|I/D\A D K|P/V/S S Q L/R(V)		121.28	542.6354	1625.886	0.0059	3.7	5.62	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
2032	dirMS_041712_NAR_30mM_minus2.7659.7718.2	2	16.21	0	2.91E+06		(K)TEISEM	(K)T/E|I|S/E/M/N/R(N)		96.23	490.2292	979.451	-0.0002	-0.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
2033	dirMS_041712_NAR_50mM_minus2.18041.18041.3	3	16.21	1	1.56E+04		(K)TFVNITP	(K)T F|V/N I/T/P A E V G V L\V/G\K D R(S)		171.78	639.0247	1915.065	-0.0052	-2.7	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
2034	dirMS_041712_NAR_20mM_plus.10797.10797.2	2	16.21	0	1.18E+05		(R)AGTGVD	(R)A G T G V/D/N/V|D|L E A/A/T R(K)		146.88	744.8731	1488.729	0.01	6.7	4.03	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
2035	dirMS_041712_NAR_30mM_plus2.11513.11557.2	2	16.21	0	5.15E+05		(R)SGEGEV	(R)S G|E|G|E|V S|G L/M/R(K)		114.07	561.2662	1121.526	-0.0004	-0.4	4.53	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
2036	dirMS_041712_NAR_30mM_plus2.16012.16256.2	2	16.21	0	7.42E+05		(R)GALQNI	(R)G A/L|Q|N|I|I\P A/S T G\A/A K(A)		137.53	706.3979	1411.79	-0.0018	-1.3	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
2037	dirMS_041712_NAR_30mM_plus2.17772.17772.2	2	16.21	0	4.92E+05		(K)LLGELLQ	(K)L/L|G\E/L/L/Q D N/A K(L)		145.8	607.3423	1213.679	-0.0014	-1.1	4.37	35556.4	9.3	HUMAN	F2Z393	Transaldolase
2038	dirMS_041712_NAR_30mM_plus2.20438.20438.2	2	16.21	0	3.06E+05		(R)YISPDQL	(R)Y I|S|P D Q L A D L Y K(S)		161.52	713.3669	1425.726	0.0005	0.4	4.21	47510.4	7.04	HUMAN	P06733	Alpha-enolase
2039	dirMS_041712_NAR_30mM_plus2.9010.9553.2	2	16.21	0	3.27E+06		(R)MGYMD	(R)M/G|Y|M/D|P/R(E)		101.28	435.186	869.364	0.0003	0.3	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
2040	dirMS_041712_NAR_50mM_plus2.15077.15618.3	3	16.21	1	9.32E+06		(R)IINEPTA	(R)I/I|N\E|P T A A/A/I/A/Y G L D K K(V)		149.67	596.6673	1787.99	-0.0028	-1.6	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
2041	dirMS_041712_NAR_60mM_plus.16344.16344.3	3	16.21	1	1.84E+05		(K)KAPDFV	(K)K A P D\F V|F/Y/A/P/R(L)		141.8	437.5685	1310.689	0.0018	1.3	8.59	71218.8	6.3	HUMAN	A7YIJ8	Radixin
2042	dirMS_041712_NAR_60mM_plus.9825.9825.3	3	16.21	1	1.31E+06		(K)LAELKQ	(K)L/A/E/L/K/Q/E C/L A R(G)	C:Carbamidomethylation	109.57	444.2368	1330.715	-0.0189	-14.2	6.14	6106	9.22	HUMAN	F8VS12	SAP domain-containing ribonucleoprotein
2043	dirMS_041712_NAR_30mM_minus2.10473.10473.2	2	16.2	0	1.68E+06		(K)TAVCDIF	(K)T A|V|C/D/I/P|P R(G)	C:Carbamidomethylation	110.87	514.7641	1028.519	0.0016	1.5	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
2044	dirMS_041712_NAR_50mM_minus2.12725.12902.3	3	16.2	1	3.91E+05		(R)LSEDYG	(R)L/S|E/D/Y/G V/L K/T D/E/G I A Y R(G)		141.52	643.6561	1928.96	-0.0063	-3.2	4.32	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
2045	dirMS_041712_NAR_120mM_plus.7940.8118.4	4	16.2	1	6.41E+05		(K)VLATVTI	(K)V/L\A/T/V/T K/P V G G D/K/N G G T R(V)		95.57	443.251	1769.987	-0.0047	-2.6	9.99	12738	10.72	HUMAN	F8VWR1	60S ribosomal protein L6 (Fragment)
2046	dirMS_041712_NAR_20mM_plus.10796.10796.2	2	16.2	0	3.14E+04		(K)IGGIGTV	(K)I/G/G\I/G/T/V/P V G R(V)		146.8	513.3057	1025.61	-0.0061	-5.9	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
2047	dirMS_041712_NAR_120mM_minus.5124.5147.3	3	16.19	0	1.86E+05		(R)YINTEH	(R)Y/I/N/T/E/H/G G S Q A/R(F)		80.6	444.8813	1332.629	0.0002	0.2	6.75	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
2048	dirMS_041712_NAR_20mM_minus.14676.14676.2	2	16.19	0	2.10E+05		(K)LAVEALS	(K)L A/V|E/A|L/S/S L|D\G D L A/G R(Y)		201.28	793.922	1586.838	-0.0017	-1.1	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
2049	dirMS_041712_NAR_30mM_minus2.10933.10933.2	2	16.19	0	5.26E+05		(K)VAGQD	(K)V/A|G/Q/D|G S/V/V Q|F K(I)		113.68	617.824	1234.643	-0.0019	-1.5	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
2050	dirMS_041712_NAR_30mM_minus2.18340.18467.3	3	16.19	0	5.33E+05		(R)QAQEYE	(R)Q A Q\E\Y|E|A/L/L/N/I K(V)		154.7	473.9196	1419.748	-0.0036	-2.5	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2051	dirMS_041712_NAR_50mM_minus2.7914.7930.3	3	16.19	1	3.13E+05		(R)LQAEIEG	(R)L/Q|A/E/I/E/G L/K/G Q R(A)		112.3	447.921	1341.748	0	0	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2052	dirMS_041712_NAR_20mM_plus.16674.16674.2	2	16.19	0	5.10E+05		(K)LGGSAV	(K)L G G S A/V|I/S L/E/G\K|P L(-)		185.82	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
2053	dirMS_041712_NAR_30mM_plus2.19892.20176.2	2	16.19	0	8.41E+05		(K)MSIYQA	(K)M/S|I/Y/Q/A/M/W/K(G)		158.83	579.2783	1157.548	0.0011	1	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
2054	dirMS_041712_NAR_60mM_plus.7525.7730.3	3	16.19	1	1.56E+06		(K)IVADKD	(K)I/V|A D/K/D/Y/S V/T/A N S K(I)		97.95	504.2625	1510.775	-0.0018	-1.2	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
2055	dirMS_041712_NAR_20mM_minus.12232.12473.3	3	16.18	0	8.33E+05	M73m	(R)AVLVDLI	(R)A V L\V D\L\E/P G T|m/D S V R(S)	m:Oxidized methionine	172.57	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
2056	dirMS_041712_NAR_30mM_minus2.13306.13558.2	2	16.18	0	9.82E+05		(K)DVNAAI	(K)D V|N/A|A/I/A/T/I/K(T)		126.43	508.2928	1015.578	0.0001	0.1	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
2057	dirMS_041712_NAR_30mM_minus2.6842.6898.2	2	16.18	0	3.65E+05		(K)AMEAV	(K)A M|E|A|V/A|A|Q/G K(A)		91.98	488.2495	975.493	-0.0011	-1.1	6.05	28936.8	9.22	HUMAN	P15259	Phosphoglycerate mutase 2
2058	dirMS_041712_NAR_50mM_plus2.19281.19281.3	3	16.18	0	4.12E+05		(R)GFGFITF	(R)G F G\F/I/T/F T/N/P E H A/S V/A M R(A)		169.22	661.3258	1981.959	0.004	2	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
2059	dirMS_041712_NAR_60mM_plus.7880.7880.3	3	16.18	1	5.18E+05		(K)FAAKGE	(K)F/A|A/K/G E G Q|L/G|P/A E R(A)		99.2	477.5865	1430.739	0.0063	4.4	6.14	96306.4	6.41	HUMAN	P13639	Elongation factor 2
2060	dirMS_041712_NAR_50mM_minus2.10513.10844.3	3	16.17	1	4.28E+05		(R)DVVICPI	(R)D V|V|I/C/P D/A S L E D A K K(E)	C:Carbamidomethylation	128.55	553.9474	1659.826	0.0018	1.1	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
2061	dirMS_041712_NAR_120mM_plus.18692.18815.3	3	16.17	1	6.76E+05		(R)ARFEEL	(R)A R F E E\L|C/S/D/L/F R(S)	C:Carbamidomethylation	151.33	514.9165	1542.737	-0.002	-1.3	4.68	25598.3	6.45	HUMAN	E7EP11	Heat shock 70 kDa protein 1A/1B
2062	dirMS_041712_NAR_120mM_plus.6761.6806.3	3	16.17	1	6.52E+05		(R)NKQTYS	(R)N K Q T\Y|S|T/E/P/N N L K(A)		88.83	512.9261	1536.765	-0.0015	-1	8.5	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
2063	dirMS_041712_NAR_30mM_plus2.11626.11923.2	2	16.17	0	2.78E+06		(K)LSDGVA	(K)L/S|D|G V A/V|L/K(V)		115.52	451.2712	901.535	-0.0002	-0.2	5.84	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
2064	dirMS_041712_NAR_30mM_plus2.18758.18942.2	2	16.17	0	1.19E+06		(R)LSNIFVI	(R)L/S|N|I|F/V|I/G/K(G)		151.42	495.8019	990.598	-0.0017	-1.7	8.75	29825.4	10.37	HUMAN	P62701	40S ribosomal protein S4, X isoform
2065	dirMS_041712_NAR_30mM_minus2.11002.11002.2	2	16.16	0	5.91E+05		(K)VAGQD	(K)V A|G|Q/D|G S/V V Q|F K(I)		113.82	617.824	1234.643	-0.0019	-1.5	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
2066	dirMS_041712_NAR_30mM_plus2.14608.14910.2	2	16.16	0	2.26E+06		(K)DLAGSII	(K)D/L|A|G/S I/I/G/K(G)		130.5	437.2557	873.504	0.0001	0.1	5.84	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K

2067	dirMS_041712_NAR_60mM_plus.14390.14468.3	3	16.16	1	9.50E+05		(K)TKEVYEL	(K)T K/E V Y\E|L|L/D/S/P G/K(V)		131.9	493.5959	1478.774	-0.0006	-0.4	4.68	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
2068	dirMS_041712_NAR_60mM_plus.16256.16564.3	3	16.16	1	3.69E+05		(-)MKLNISF	(-)M K L N I S\F|P/A/T/G C Q K(L)	C:Carbamidomethylation	142.85	532.2733	1594.808	-0.0026	-1.7	10	10471.9	5.4	HUMAN	A2A3R7	40S ribosomal protein S6
2069	dirMS_041712_NAR_60mM_plus.21545.21709.3	3	16.16	0	9.30E+06		(R)LHFFMP	(R)L H\F\F\M|P/G\F|A|P\L/T S R(G)		180.4	540.9492	1620.835	-0.0025	-1.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
2070	dirMS_041712_NAR_60mM_plus.7177.7408.3	3	16.16	1	1.57E+07		(R)AAPGAE	(R)A A|P/G A E/F A/P N K/R(R)		96.3	410.2195	1228.643	0.0007	0.5	8.79	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
2071	dirMS_041712_NAR_120mM_minus.5379.5379.3	3	16.15	1	9.04E+05		(R)NDDDEE	(R)N/D|D/D/E/E A A\R E R(R)		82.93	483.5345	1448.588	0.0005	0.4	3.95	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
2072	dirMS_041712_NAR_30mM_minus2.10523.10566.2	2	16.15	0	3.17E+05		(R)SGSYSYL	(R)S G|S|Y/S/Y/L/E/E/R(K)		111.13	595.7696	1190.532	-0.0005	-0.4	4.53	22046.7	5.8	HUMAN	H0YIM2	Protein phosphatase 1 regulatory subunit 12A (Fragment)
2073	dirMS_041712_NAR_50mM_minus2.8555.8756.3	3	16.15	1	4.24E+05	M244m	(K)ILIANTG	(K)I/L|I/A/N/T/G m D T D/K I/K(I)	m:Oxidized methionine	117.38	516.9426	1532.835	15.978	-10.9	5.96	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
2074	dirMS_041712_NAR_60mM_minus.18628.18755.3	3	16.15	1	1.31E+05		(K)IILDLISE	(K)I I|L D/L/I/S E/S/P I K G R(A)		166.17	518.6442	1553.926	-0.0081	-5.2	6.07	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
2075	dirMS_041712_NAR_20mM_plus.13793.13793.2	2	16.15	0	5.65E+04	M33m	(R)LVQSPN	(R)L V|Q|S|P N S/Y/F m D V/K(C)	m:Oxidized methionine	167.07	772.3772	1527.751	15.9959	0.7	5.83	11227.9	9.22	HUMAN	C9JLI6	40S ribosomal protein S27
2076	dirMS_041712_NAR_30mM_plus2.11949.12010.2	2	16.15	0	6.83E+05		(K)CGDLVF	(K)C/G/D|L/V/F|A/K(M)	C:Carbamidomethylation	116.12	455.2298	909.45	0.0025	2.7	5.84	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
2077	dirMS_041712_NAR_30mM_plus2.8624.8920.2	2	16.15	0	4.02E+06		(R)ELNITAA	(R)E L/N/I/T/A/A/K(E)		100.15	430.2487	859.488	0.0018	2.1	6.1	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
2078	dirMS_041712_NAR_20mM_minus.10615.10615.2	2	16.14	0	2.00E+05		(R)TTPSYV	(R)T T/P S Y/V/A/F T D/T E/R(L)		154.63	744.3547	1487.701	0.0009	0.6	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
2079	dirMS_041712_NAR_40mM_minus2.14534.14534.3	3	16.14	1	1.17E+06	M116m	(R)ELAILLG	(R)E L/A I/L/L/G m L D/P A E K D E/K(G)	m:Oxidized methionine	171.02	634.338	1884.999	16.0008	3.1	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
2080	dirMS_041712_NAR_20mM_plus.18175.18175.2	2	16.14	0	1.13E+05		(K)LVLPSLI	(K)L V|L/P S L/I S S R(I)		196.6	542.8388	1084.672	-0.0021	-2	9.75	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
2081	dirMS_041712_NAR_30mM_plus2.17864.17868.2	2	16.14	0	2.68E+05		(K)FEDENFI	(K)F/E|D E/N|F/I/L/K(H)		147.02	577.7904	1154.573	0.0007	0.6	4.14	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
2082	dirMS_041712_NAR_60mM_plus.12668.12668.3	3	16.14	1	8.35E+05		(R)DLDRIA	(R)D L/D R\I\A/G Q\V/A|A/A N K(K)		123.38	481.263	1441.776	-0.0013	-0.9	5.96	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
2083	dirMS_041712_NAR_30mM_minus2.10563.10588.2	2	16.13	0	3.30E+05		(K)FADLSE	(K)F/A|D|L|S/E/A/A N R(N)		111.48	547.265	1093.527	-0.0045	-4.2	4.37	49709.6	5.19	HUMAN	B0YJC4	Vimentin
2084	dirMS_041712_NAR_50mM_minus2.12273.12349.3	3	16.13	0	1.08E+06		(K)LGDVYV	(K)L/G/D|V/Y V/N/D A/F G T A\H/R(A)		138.38	545.6023	1634.792	0.0002	0.1	5.21	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
2085	dirMS_041712_NAR_60mM_minus.9391.9403.3	3	16.13	1	1.78E+05		(K)IFRDGEE	(K)I/F/R D G E\E\A|G|A|Y/D/G P R(T)		112.25	551.5934	1652.766	-0.0007	-0.4	4.32	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
2086	dirMS_041712_NAR_30mM_plus2.6095.6118.2	2	16.13	0	3.26E+05		(K)ISSPTET	(K)I/S|S|P/T E T E R(C)		86.23	510.2497	1019.5	-0.0083	-8.1	4.53	11854.4	6.57	HUMAN	P31949	Protein S100-A11
2087	dirMS_041712_NAR_40mM_plus2.19128.19128.3	3	16.13	1	3.14E+05		(R)GGPNIIT	(R)G G/P\N/I|I/T/L A D I/V/K D P V S R(T)		178.97	622.3522	1865.049	-0.007	-3.8	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
2088	dirMS_041712_NAR_50mM_plus2.6020.6020.3	3	16.13	0	1.14E+05		(R)AGAAG	(R)A/G\A|A/G|G/P E E E A E/K P V\K(T)		95.73	513.9259	1539.765	-0.0018	-1.2	4.49	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
2089	dirMS_041712_NAR_30mM_minus2.13259.13259.2	2	16.12	0	3.00E+05		(K)STYGWT	(K)S T|Y/G|W/T A/N M E/R(I)		125.7	658.2918	1315.574	0.0028	2.1	5.72	47825.1	5.07	HUMAN	Q58FG1	Putative heat shock protein HSP 90-alpha A4
2090	dirMS_041712_NAR_50mM_minus2.14392.14539.3	3	16.12	1	1.07E+06		(K)EAFSLFD	(K)E A|F|S/L F/D/K/D/G D/G T I T T K(E)		149.97	615.6336	1844.891	-0.005	-2.7	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
2091	dirMS_041712_NAR_30mM_plus2.21467.21467.2	2	16.12	0	3.90E+05		(R)VNQAIW	(R)V N Q A/I/W|L|L/C/T/G A R(E)	C:Carbamidomethylation	166.88	751.3976	1501.794	-0.0065	-4.3	9.72	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
2092	dirMS_041712_NAR_30mM_plus2.7182.7182.2	2	16.12	0	1.83E+04		(R)SGGGG	(R)S G|G G G/G/G G L/G S G G/S I/R(S)		92.03	616.8023	1232.598	-0.0005	-0.4	9.47	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
2093	dirMS_041712_NAR_40mM_plus2.6150.6192.2	2	16.12	0	2.76E+05		(R)MGANS	(R)M/G|A|N/S L/E/R(M)		95.23	439.2183	877.42	0.0097	11.1	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
2094	dirMS_041712_NAR_40mM_minus2.8617.8630.3	3	16.11	0	2.84E+05		(R)SVIDPV	(R)S V\I D/P V/P A/P V G/D/S H V D G A A K(S)		132.52	644.3329	1930.987	-0.0027	-1.4	4.41	58326.8	5.7	HUMAN	Q13177	Serine/threonine-protein kinase PAK 2
2095	dirMS_041712_NAR_50mM_minus2.8265.8280.3	3	16.11	1	2.19E+05		(K)GILAADE	(K)G I|L/A/A/D/E/S T/G S I A K/R(L)		114.78	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
2096	dirMS_041712_NAR_120mM_plus.20630.20630.4	4	16.11	2	6.22E+05		(K)LTVEDLE	(K)L/T/V/E/D|L/E/K E R D F Y F G K(L)		160.9	498.0043	1988.996	-0.001	-0.5	4.51	30169.7	5.02	HUMAN	Q15691	Microtubule-associated protein RP/EB family member 1
2097	dirMS_041712_NAR_30mM_plus2.10950.11051.2	2	16.11	0	5.82E+05		(R)QLYEEEI	(R)Q/L|Y/E/E/E/I/R(E)		110.97	540.2736	1079.537	0.0032	2.9	4.25	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
2098	dirMS_041712_NAR_30mM_plus2.20756.20756.2	2	16.11	0	2.60E+05		(R)ASLSLW	(R)A S/L/S/L/W\Q A/M E K(G)		162.9	632.3231	1263.64	-0.0013	-1	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
2099	dirMS_041712_NAR_30mM_plus2.9980.10438.2	2	16.11	0	3.14E+06		(K)DVNQQ	(K)D V|N|Q|Q E/F/V/R(A)		106.65	567.7813	1134.554	0.0015	1.3	4.37	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
2100	dirMS_041712_NAR_40mM_plus2.12271.12447.2	2	16.11	0	1.06E+05		(R)VLQALE	(R)V/L|Q|A/L E/G L/K(M)		138.8	485.8002	970.593	0	0	5.97	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
2101	dirMS_041712_NAR_50mM_plus2.14002.14171.3	3	16.11	1	1.21E+06		(K)ALQQGL	(K)A L|Q/Q/G L/V/G L/E L K\E K(L)		142.02	509.3022	1525.895	-0.0028	-1.8	6.18	266161	5.68	HUMAN	E9PPU0	Epiplakin
2102	dirMS_041712_NAR_50mM_plus2.17856.17900.3	3	16.11	0	2.57E+05		(K)YAPLHL	(K)Y A|P L/H/L|V|P/L I E R(L)		162.08	474.2819	1420.831	0.0001	0	6.75	147553.6	6.73	HUMAN	E7EVF4	Cytoplasmic FMR1-interacting protein 2
2103	dirMS_041712_NAR_120mM_minus.18058.18210.3	3	16.1	1	3.33E+06		(R)ARFEELN	(R)A R\F E\E\L|N|A|D/L/F/R(G)		154.37	494.2561	1480.754	-0.0006	-0.4	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
2104	dirMS_041712_NAR_60mM_minus.10011.10011.3	3	16.1	0	2.95E+04		(R)ISNRPAF	(R)I/S|N R P A F|M/P S/E G/K(M)		115.67	478.5785	1433.721	0.0004	0.3	8.75	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
2105	dirMS_041712_NAR_60mM_minus.15202.15202.2	2	16.1	0	4.20E+05		(R)EHALLA	(R)E/H/A|L|L/A/Y T L G V K(Q)		144.65	657.873	1314.742	-0.0029	-2.2	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
2106	dirMS_041712_NAR_60mM_minus.7338.7744.3	3	16.1	1	1.38E+06		(K)IQDKEGI	(K)I Q D K E G\I|P/P/D/Q Q R(L)		100.07	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
2107	dirMS_041712_NAR_120mM_plus.8216.8254.3	3	16.1	1	8.15E+05		(R)AVVIVD	(R)A/V|V|I/V/D/D/R G/R P S G K(G)		96.73	490.2792	1468.823	0	0	8.79	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
2108	dirMS_041712_NAR_20mM_plus.11303.11558.2	2	16.1	0	2.93E+05		(K)LITPAVV	(K)L I|T|P/A/V/V S E/R(L)		150.83	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
2109	dirMS_041712_NAR_30mM_plus2.8235.8533.2	2	16.1	0	1.06E+06		(R)ALANSL	(R)A L|A|N/S|L A/C/Q/G K(Y)	C:Carbamidomethylation	97.87	566.7922	1132.578	-0.0008	-0.7	8.8	13951.6	9.48	HUMAN	H3BR68	Fructose-bisphosphate aldolase A (Fragment)
2110	dirMS_041712_NAR_40mM_plus2.19392.19532.3	3	16.1	1	4.58E+05		(K)ALFEEV	(K)A L|F/E/E/V/P E L L/T E A E K K(E)		181.77	615.9991	1845.984	-0.0017	-0.9	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
2111	dirMS_041712_NAR_50mM_plus2.14829.14829.3	3	16.1	1	4.71E+05	M93m	(K)SELVAm	(K)S E|L|V/A/m L E/E E E/L R/K(A)	m:Oxidized methionine	146.08	564.6211	1675.857	15.9916	-1.9	4.32	18679.2	5.61	HUMAN	B4DWW1	ADP-ribosylation factor-like protein 1
2112	dirMS_041712_NAR_60mM_plus.15623.15623.3	3	16.1	0	1.71E+05		(R)ILHGLGF	(R)I L H G L G F|T|P/A M Q R(K)		138.35	480.9305	1440.778	-0.0011	-0.7	9.75	27043.5	6.34	HUMAN	C9JHK9	ATP-binding cassette sub-family F member 2 (Fragment)
2113	dirMS_041712_NAR_60mM_plus.7115.7115.2	2	16.1	0	1.72E+06		(K)STTTGHI	(K)S/T|T/T/G/H L\I/Y/K(C)		95.58	560.8031	1120.6	-0.0008	-0.7	8.34	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
2114	dirMS_041712_NAR_120mM_minus.12126.12437.3	3	16.09	0	1.58E+06		(R)HVFGES	(R)H V\F G\E|S|D|E|L|I/G Q/K(V)		120.68	486.9119	1458.722	-0.0012	-0.8	4.65	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
2115	dirMS_041712_NAR_30mM_minus2.9172.9172.2	2	16.09	0	4.11E+04		(R)TYQASS	(R)T Y|Q/A/S S\A\A F/R(Y)		104.48	551.2778	1101.532	0.016	14.5	8.41	26240.9	9.1	HUMAN	Q92567	Protein FAM168A
2116	dirMS_041712_NAR_120mM_plus.20441.20958.4	4	16.09	1	3.77E+06		(R)DYLHLP	(R)D Y L H L|P\P/E I/V/P A T L R/R(S)		162.23	473.2689	1890.06	-0.0058	-3.1	6.75	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
2117	dirMS_041712_NAR_20mM_plus.18627.18793.2	2	16.09	0	3.00E+05		(K)TAVETA	(K)T\A\V|E/T/A/V/L|L L R(I)		199.87	593.3625	1185.72	-0.0024	-2	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
2118	dirMS_041712_NAR_30mM_plus2.14339.14339.2	2	16.09	0	5.73E+05		(K)CCSGAII	(K)C C|S/G A I|I/V|L\T K(S)	C:Carbamidomethylation	128.2	611.3189	1221.633	-0.0025	-2	8.75	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
2119	dirMS_041712_NAR_30mM_minus2.12766.12766.2	2	16.08	0	3.27E+05		(R)GGAEQF	(R)G G A\E/Q|F|M/E E/T/E R(S)		122.7	692.2961	1383.584	0.0004	0.3	4.09	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
2120	dirMS_041712_NAR_30mM_minus2.18870.18870.2	2	16.08	0	5.41E+04		(R)CGGIQY	(R)C G/G\I|Q|Y/L\Q\N/A I/E/S/R(Q)	C:Carbamidomethylation	157.12	804.8951	1608.78	0.0031	1.9	6	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
2121	dirMS_041712_NAR_30mM_minus2.7406.7552.2	2	16.08	0	9.71E+05		(R)EMDEQI	(R)E/M/D/E/Q/I/R(L)		95.1	460.7171	920.414	0.0127	13.8	4.14	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
2122	dirMS_041712_NAR_60mM_minus.15853.16095.3	3	16.08	1	5.23E+05		(R)IFDSEEIL	(R)I/F\D/S E/E/I/L/A/G Y K/R(E)		148.88	514.2713	1540.801	-0.0012	-0.8	4.68	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
2123	dirMS_041712_NAR_20mM_plus.13230.13644.2	2	16.08	0	4.95E+05	M148m	(R)DLTDYL	(R)D/L|T/D/Y/L/m/K(I)	m:Oxidized methionine	164.77	507.7439	998.486	15.9942	-0.7	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
2124	dirMS_041712_NAR_20mM_plus.16417.16417.2	2	16.08	0	1.40E+05		(R)QAQEYE	(R)Q A|Q/E Y/E/A L/L/N/I/K(V)		184.52	710.3754	1419.748	-0.0043	-3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2125	dirMS_041712_NAR_30mM_plus2.12798.13079.2	2	16.08	0	1.75E+06		(R)LQAEIEG	(R)L/Q|A|E/I/E/G/L/K(G)		121.42	500.7889	1000.567	0.0032	3.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
2126	dirMS_041712_NAR_50mM_plus2.14407.14407.3	3	16.08	1	9.68E+05		(R)LAIKLPD	(R)L/A/I K L/P D D/Q I/P K(T)		144.23	450.9373	1350.799	-0.0018	-1.3	5.96	26413	9.18	HUMAN	B1APP6	6-phosphofructokinase type C (Fragment)
2127	dirMS_041712_NAR_60mM_plus.14918.15248.3	3	16.08	0	2.92E+06		(-)MVNHFI	(-)M/V/N/H/F/I A E/F/K(R)		135.18	412.5464	1235.624	0.0005	0.4	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
2128	dirMS_041712_NAR_120mM_minus.20119.20119.3	3	16.07	0	5.07E+05	M195m	(R)LHFFmP	(R)L H F F m\P G|F/A/P/L/T S R(G)	m:Oxidized methionine	166.18	546.2809	1620.835	15.9926	-1.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
2129	dirMS_041712_NAR_120mM_plus.7602.7602.2	2	16.07	1	1.19E+06		(R)AQYDEL	(R)A/Q|Y/D/E/L A/R K(N)		93.32	547.2874	1093.564	0.0039	3.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2130	dirMS_041712_NAR_30mM_plus2.19075.19616.2	2	16.07	0	1.20E+06		(R)LIDFLEC	(R)L/I|D|F|L/E/C/G/K(T)	C:Carbamidomethylation	155.15	547.7808	1094.555	-0.0007	-0.7	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
2131	dirMS_041712_NAR_30mM_plus2.19535.19535.2	2	16.07	0	1.85E+04		(K)MNEFLE	(K)M/N/E|F|L/E N F E K(N)		155.87	650.7974	1300.588	-0.0003	-0.2	4.25	28580.2	9.35	HUMAN	Q9UFN0	Protein NipSnap homolog 3A
2132	dirMS_041712_NAR_30mM_plus2.19653.19868.2	2	16.07	0	7.76E+05		(K)VLTPELY	(K)V L|T|P/E/L Y/A E/L R(A)		157.2	652.3617	1303.726	-0.0095	-7.3	4.53	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
2133	dirMS_041712_NAR_40mM_plus2.12440.12440.3	3	16.07	0	3.39E+05		(K)AASDIA	(K)A A\S D\I/A|M/T E L/P/P/T H P I R(L)		139.6	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
2134	dirMS_041712_NAR_40mM_plus2.5423.5458.2	2	16.07	0	2.45E+05	M300m	(K)NMmAA	(K)N|M|m|A|A/C/D|P/R(H)	C:Carbamidomethylation m:Oxid	89.2	541.2145	1065.427	15.9943	-0.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
2135	dirMS_041712_NAR_50mM_plus2.11628.11988.3	3	16.07	1	1.78E+06		(K)TGQPMI	(K)T G\Q|P/M/I/N L Y/T/D R E|T G K(L)		130.72	608.6361	1823.896	-0.0019	-1	5.73	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
2136	dirMS_041712_NAR_120mM_minus.5401.5423.3	3	16.06	1	2.17E+05		(R)KQQTLE	(R)K\Q Q\T\L|E/A/E E/A/K(R)		82.88	425.5623	1274.659	0.0137	10.7	4.79	76925.9	4.46	HUMAN	A8MV58	Drebrin
2137	dirMS_041712_NAR_50mM_minus2.8545.8652.3	3	16.06	0	1.58E+06		(R)EIVHIQA	(R)E/I|V H I Q\A\G/Q|C/G N Q\I/G A/K(F)	C:Carbamidomethylation	116.8	608.3087	1822.923	-0.0113	-6.2	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
2138	dirMS_041712_NAR_20mM_plus.17952.17969.2	2	16.06	0	1.63E+05		(R)TVQSLEI	(R)T V|Q|S/L/E|I\D L D/S M R(N)		195.05	753.8776	1506.747	0.0011	0.7	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2139	dirMS_041712_NAR_30mM_plus2.11112.11174.2	2	16.06	0	6.16E+05		(R)AQPSAS	(R)A Q|P/S/A/S/L/G V/G Y R(T)		111.58	603.3192	1205.627	0.0038	3.2	8.79	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
2140	dirMS_041712_NAR_30mM_plus2.18436.18585.2	2	16.06	0	5.82E+05		(R)NNLAGA	(R)N N|L|A|G/A/E E/L/F/A R(K)		150.42	652.8322	1304.659	-0.0022	-1.7	4.53	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
2141	dirMS_041712_NAR_30mM_plus2.9578.9701.2	2	16.06	0	4.97E+05		(R)LAPEYE	(R)L/A|P/E/Y/E/A/A A T R(L)		104.48	596.3026	1191.6	-0.0025	-2.1	4.53	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
2142	dirMS_041712_NAR_40mM_plus2.14722.14868.3	3	16.06	1	1.15E+06		(R)IIAFVGS	(R)I/I|A|F/V/G/S/P V E D N E K D L V/K(L)		153.98	658.3499	1973.059	-0.0238	-12.1	4.32	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
2143	dirMS_041712_NAR_20mM_minus.11273.11479.2	2	16.05	0	1.17E+07	M148m	(R)DLTDYL	(R)D L|T|D/Y/L/m/K(I)	m:Oxidized methionine	162.17	507.7443	998.486	15.995	0.1	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
2144	dirMS_041712_NAR_30mM_minus2.17120.17120.2	2	16.05	0	1.88E+05		(R)SIQEEL	(R)S I|Q/E/E L/Q Q/L/R(Q)		146.55	622.3359	1243.664	0.0004	0.3	4.53	533778	5.74	HUMAN	Q15149	Plectin
2145	dirMS_041712_NAR_30mM_minus2.18180.18198.2	2	16.05	0	1.57E+05		(K)FGAYIVD	(K)F/G|A|Y|I/V/D G L/R(Q)		153.6	555.7984	1110.594	-0.0047	-4.2	5.83	269989.9	5.92	HUMAN	F8W8T8	Acetyl-CoA carboxylase 2
2146	dirMS_041712_NAR_50mM_minus2.16754.16754.3	3	16.05	1	2.96E+05		(R)SELELTL	(R)S E|L|E L T L/G K L E/Q V R(S)		163.72	538.9725	1614.906	-0.0032	-2	4.78	533778	5.74	HUMAN	Q15149	Plectin
2147	dirMS_041712_NAR_50mM_minus2.8993.8993.3	3	16.05	0	2.22E+05		(R)VMLGET	(R)V M|L/G E/T/N/P A D S K/P G T/I R(G)		118.33	595.9744	1785.916	-0.0077	-4.3	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
2148	dirMS_041712_NAR_60mM_minus.10790.10790.3	3	16.05	1	5.44E+05	M239m	(R)MSMKE	(R)M/S|M K E V D E|Q|m|L N/V/Q N K(N)	m:Oxidized methionine	119.9	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
2149	dirMS_041712_NAR_40mM_plus2.17752.17752.3	3	16.05	0	3.79E+04		(R)AGLGSG	(R)A G L|G/S/G L/S L/S G L V/H P E\L S\R(S)		170.98	617.3431	1850.013	0.0017	0.9	6.79	73325.2	9.19	HUMAN	F5H2A9	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial
2150	dirMS_041712_NAR_50mM_plus2.13312.13600.3	3	16.05	0	2.57E+06		(K)AGVVG	(K)A/G V|V|G/P E L/H/E Q L L/S A E K(A)		138.58	592.986	1776.949	-0.0056	-3.1	4.75	533778	5.74	HUMAN	Q15149	Plectin
2151	dirMS_041712_NAR_50mM_plus2.15907.15954.3	3	16.05	1	1.60E+06		(R)DVDFELI	(R)D V|D/F/E/L/I K/V E/G K(V)		152	464.5859	1391.742	0.0015	1.1	4.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
2152	dirMS_041712_NAR_50mM_plus2.5647.5730.3	3	16.05	1	1.06E+06		(K)TAGPIAS	(K)T/A|G/P I/A/S\A/Q\K Q/P A/G K(V)		91.9	475.5987	1424.786	-0.0041	-2.8	10	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
2153	dirMS_041712_NAR_30mM_minus2.7672.7680.2	2	16.04	0	2.56E+05		(K)LAGESES	(K)L/A|G|E|S/E/S N/L/R(K)		96.3	538.273	1075.538	0.0009	0.8	4.53	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
2154	dirMS_041712_NAR_50mM_minus2.15439.15439.3	3	16.04	0	3.28E+05		(R)LSFQHD	(R)L/S/F Q/H D P E|T S/V/L/V/L R(K)		156.07	580.9793	1740.928	-0.0046	-2.6	5.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
2155	dirMS_041712_NAR_20mM_plus.13810.13810.2	2	16.04	0	6.96E+04		(R)VEVTEFE	(R)V E|V/T E F E D/I/K(S)		167.18	604.8056	1208.604	-0.0006	-0.5	4	30992.3	4.14	HUMAN	B2REB8	Protein SET
2156	dirMS_041712_NAR_30mM_plus2.11766.11766.2	2	16.04	0	5.40E+05		(K)VASGCLI	(K)V A|S/G/C/L/D I N S S V/K(G)	C:Carbamidomethylation	114.82	675.3393	1349.673	-0.0016	-1.2	5.81	56837	7.19	HUMAN	E7ETT1	Propionyl-CoA carboxylase beta chain, mitochondrial
2157	dirMS_041712_NAR_20mM_minus.10042.10042.2	2	16.03	0	8.73E+05		(R)IVLQIDN	(R)I/V|L/Q/I|D/N/A R(L)		149.7	521.3059	1041.605	-0.0006	-0.6	5.84	20842.9	5.32	HUMAN	C9JM50	Keratin, type I cytoskeletal 19 (Fragment)
2158	dirMS_041712_NAR_50mM_minus2.15319.15465.3	3	16.03	1	4.51E+05		(K)GADFLV	(K)G A\D|F|L|V/T/E V E/N G G S L G S K K(G)		155.55	636.662	1907.971	0.0005	0.3	4.68	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
2159	dirMS_041712_NAR_60mM_minus.7087.7148.3	3	16.03	1	3.04E+05		(R)ELFESST	(R)E L|F/E/S/S T N N N K D/T/K(Q)		98.72	542.9247	1626.761	-0.001	-0.6	4.68	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
2160	dirMS_041712_NAR_30mM_plus2.10005.10024.2	2	16.03	0	2.67E+05		(R)ELSEQLG	(R)E L|S E|Q/L|G/Q/A E/R(A)		105.82	630.3143	1259.623	-0.0013	-1	4.25	266161	5.68	HUMAN	E9PPU0	Epiplakin
2161	dirMS_041712_NAR_50mM_plus2.20408.20551.3	3	16.03	1	4.12E+05		(R)VISGVL	(R)V/I|S G/V/L/Q/L/G N I|V F K K(E)		176.1	539.0011	1614.994	-0.0054	-3.3	10	227783.5	5.5	HUMAN	P35579	Myosin-9
2162	dirMS_041712_NAR_50mM_plus2.7501.7501.3	3	16.03	0	2.12E+05		(R)SAEEEA	(R)S A|E/E/E A A/D/L P T K P T K(I)		105.3	529.5984	1586.791	-0.0102	-6.4	4.41	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
2163	dirMS_041712_NAR_120mM_minus.10608.10643.3	3	16.02	1	2.46E+05		(R)YLAEFAT	(R)Y/L|A E/F/A/T/G N D R K(E)		111.73	462.2338	1384.686	0.0013	0.9	6.07	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
2164	dirMS_041712_NAR_30mM_minus2.16902.16902.2	2	16.02	0	1.48E+05		(R)ASLEAAI	(R)A S/L E/A|A/I/A/D A/E Q R(G)		145.03	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2165	dirMS_041712_NAR_30mM_minus2.5645.5686.2	2	16.02	0	1.73E+05		(R)LYQAGE	(R)L/Y|Q|A/G E/G R(L)		84.73	447.2217	893.448	-0.0114	-12.8	6	38089.6	6.79	HUMAN	B4DT77	Annexin
2166	dirMS_041712_NAR_50mM_minus2.14781.14781.3	3	16.02	0	3.07E+04		(K)GQYFGE	(K)G Q/Y/F/G E|L A L/V T/N K P R(A)		152.52	564.9709	1692.907	-0.0086	-5.1	8.59	10305.6	6.94	HUMAN	H7C330	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
2167	dirMS_041712_NAR_50mM_minus2.15148.15341.3	3	16.02	1	3.90E+05		(R)VVVDAL	(R)V/V|V/D/A/L/S/G L K/G D L A G R(Y)		154.87	523.9677	1569.896	-0.0073	-4.7	5.93	26949.2	7.99	HUMAN	C9JSQ1	Creatine kinase U-type, mitochondrial (Fragment)
2168	dirMS_041712_NAR_20mM_plus.13936.13936.2	2	16.02	0	6.12E+04		(K)IVPNVLL	(K)I/V|P N V/L/L/E Q/G K(A)		167.72	605.3616	1209.72	-0.0042	-3.5	6	50659.2	7.87	HUMAN	B4DJV2	Citrate synthase
2169	dirMS_041712_NAR_30mM_plus2.20844.21209.2	2	16.02	0	3.43E+05		(K)FIIPQIV	(K)F/I|I|P Q/I\V/K(Y)		164.53	479.3092	957.613	-0.002	-2.1	8.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
2170	dirMS_041712_NAR_30mM_plus2.22352.22352.2	2	16.02	0	3.76E+05		(R)VGNLGL	(R)V G N|L|G/L/A/T/S F F N/E R(N)		172.82	762.8926	1524.781	-0.0026	-1.7	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
2171	dirMS_041712_NAR_30mM_plus2.6845.6970.2	2	16.02	0	4.77E+05		(R)VISSIEQ	(R)V/I|S/S/I/E/Q/K(T)		90.68	452.2602	903.515	-0.0014	-1.6	5.97	18789.1	6.77	HUMAN	A2IDB2	14-3-3 protein eta (Fragment)
2172	dirMS_041712_NAR_40mM_plus2.15544.15584.3	3	16.02	1	3.51E+04		(R)IILPPEKE	(R)I I|L|P/P E K E L|A|M/P G E D/L/K(F)		158.55	631.6874	1893.04	0.0075	4	4.41	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
2173	dirMS_041712_NAR_50mM_plus2.18796.18796.3	3	16.02	1	4.32E+05		(K)ITQDIFQ	(K)I/T/Q/D|I/F/Q Q L/L K/R(G)		167.02	501.627	1502.869	-0.0025	-1.7	8.75	72796.9	6.75	HUMAN	A6NC17	Methionine--tRNA ligase, cytoplasmic
2174	dirMS_041712_NAR_50mM_minus2.14331.14665.3	3	16.01	1	3.52E+06		(R)IINEPTA	(R)I/I|N|E|P T A A/A/I/A Y G L D K K(V)		151.02	596.6655	1787.99	-0.0082	-4.6	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
2175	dirMS_041712_NAR_50mM_minus2.14474.14474.3	3	16.01	1	3.52E+06		(R)IINEPTA	(R)I/I|N\E/P T A A A I/A/Y/G L D/K K(V)		151.02	596.6655	1787.99	-0.0082	-4.6	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)

2176	dirMS_041712_NAR_60mM_minus.15625.15806.3	3	16.01	1	6.80E+05		(R)FLQDYFI	(R)F/L|Q/D Y/F/D/G N L K R(Y)		147.7	505.924	1515.759	-0.0016	-1.1	5.96	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
2177	dirMS_041712_NAR_30mM_plus2.6193.6194.2	2	16.01	0	1.67E+05		(K)VQEQEL	(K)V/Q|E|Q/E/L/T/R(L)		86.78	501.7639	1002.521	-0.0009	-0.9	4.53	334221.3	6.44	HUMAN	P15924	Desmoplakin
2178	dirMS_041712_NAR_50mM_plus2.18292.18292.3	3	16.01	0	1.35E+06		(K)ALSAIAD	(K)A L/S\A/I/A D/L/L T N E H E R(V)		163.85	551.6254	1652.86	0.0014	0.9	4.65	105417.2	6.41	HUMAN	C9JZR2	Catenin delta-1
2179	dirMS_041712_NAR_120mM_minus.17700.18190.3	3	16	1	1.19E+06		(R)RAPFDLI	(R)R A\P\F|D|L|F E/N/R(K)		153.2	422.2193	1264.643	0.0001	0	6.07	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
2180	dirMS_041712_NAR_20mM_minus.13751.13751.2	2	16	0	3.99E+05		(K)LGGSAV	(K)L G\G S\A V|I/S L E G|K|P L(-)		188.68	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
2181	dirMS_041712_NAR_50mM_minus2.8266.8324.3	3	16	1	2.27E+05		(K)GILAADE	(K)G I|L/A/A/D E/S T/G S I/A/K R(L)		114.85	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
2182	dirMS_041712_NAR_120mM_plus.10877.11044.4	4	16	1	1.33E+06		(K)VVQHLG	(K)V/V Q H L G/P/A T/D/F/Y K K(L)		110.45	401.4712	1602.864	-0.0009	-0.6	8.48	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
2183	dirMS_041712_NAR_20mM_plus.9952.10195.2	2	16	0	1.43E+06		(K)LVSESSD	(K)L/V|S/E|S/S D\V L/P K(-)		143.17	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2184	dirMS_041712_NAR_30mM_plus2.12440.12602.2	2	16	0	9.27E+05		(R)YSGSYNI	(R)Y/S|G S|Y/N/D/Y/L/R(A)		119.1	619.2776	1237.548	-0.0005	-0.4	5.83	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
2185	dirMS_041712_NAR_30mM_plus2.13174.13307.2	2	16	0	1.30E+06		(K)NDLAVV	(K)N/D|L|A/V/V/D/V/R(I)		121.68	500.7769	1000.542	0.0043	4.3	4.21	76670.1	4.6	HUMAN	P19338	Nucleolin
2186	dirMS_041712_NAR_40mM_plus2.12539.12559.3	3	16	0	3.96E+05		(K)AASDIAI	(K)A A|S/D I/A/M T/E/L/P P T H P I R(L)		140	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
2187	dirMS_041712_NAR_50mM_plus2.13638.13732.3	3	16	0	1.81E+06		(K)DLAGCIH	(K)D L|A/G/C/I H/G L S N V/K(L)	C:Carbamidomethylation	140.17	461.9121	1383.705	0.0168	12.2	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
2188	dirMS_041712_NAR_50mM_plus2.18594.18814.3	3	16	1	9.79E+05		(R)LKLPSIPI	(R)L K L P S I|P\L|V|P V/S A Q K(R)		166.8	530.6702	1589.999	-0.0028	-1.8	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
2189	dirMS_041712_NAR_60mM_plus.12229.12229.3	3	16	1	1.21E+06		(R)LNDSILC	(R)L/N/D/S|I/L Q A T E Q R R(R)		120.48	515.2771	1543.819	-0.0019	-1.3	6.07	334221.3	6.44	HUMAN	P15924	Desmoplakin
2190	dirMS_041712_NAR_120mM_minus.20169.20169.3	3	15.99	0	3.74E+05		(K)VHLVGII	(K)V H L\V G\I/D|I/F T/G/K(K)		166.4	433.5866	1298.747	-0.0015	-1.1	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
2191	dirMS_041712_NAR_120mM_minus.5198.5198.3	3	15.99	1	3.17E+05		(R)LRAETEC	(R)L R\A E T\E|Q|G/E/Q/Q R(Q)		81.13	482.2432	1444.714	0.0012	0.8	4.79	533778	5.74	HUMAN	Q15149	Plectin
2192	dirMS_041712_NAR_50mM_minus2.13381.13509.3	3	15.99	0	2.46E+05		(K)VIQYLAY	(K)V/I/Q|Y/L/A|Y V/A/S S/H K(S)		144.78	493.6043	1478.8	-0.0018	-1.2	8.48	227783.5	5.5	HUMAN	P35579	Myosin-9
2193	dirMS_041712_NAR_20mM_plus.15506.15506.2	2	15.99	0	4.20E+05		(R)GVVDSE	(R)G/V\V D/S|E/D/I|P L/N/L\S R(E)		179.18	757.3956	1513.786	-0.0017	-1.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
2194	dirMS_041712_NAR_20mM_plus.7264.7264.2	2	15.99	0	2.85E+04		(R)VLEEGS\	(R)V/L|E/E/G/S V E/A R(T)		118.03	544.7829	1088.558	0.0003	0.3	4.25	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
2195	dirMS_041712_NAR_30mM_plus2.10023.10292.2	2	15.99	0	7.41E+05		(K)EQVANS	(K)E Q|V|A/N/S/A/F/V/E R(C)		106.63	625.311	1249.617	-0.0024	-1.9	4.53	17664	8.77	HUMAN	H0Y6E4	Heat shock protein HSP 90-beta (Fragment)
2196	dirMS_041712_NAR_30mM_plus2.7444.7474.2	2	15.99	0	5.37E+05		(K)TQLAVC	(K)T Q|L|A|V/C/Q/Q/R(I)	C:Carbamidomethylation	93.53	552.2842	1103.563	-0.0015	-1.3	9.41	9740.1	10.08	HUMAN	H0YFG2	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed (Fragment)
2197	dirMS_041712_NAR_50mM_plus2.19891.20031.3	3	15.99	0	4.71E+05		(K)HSQFIG\	(K)H S Q\F\I|G\Y|P/I/T L/Y L E/K(E)		173.82	603.6541	1808.958	-0.0104	-5.7	6.75	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
2198	dirMS_041712_NAR_60mM_plus.11216.11216.3	3	15.99	0	1.50E+06		(K)YIQQTKI	(K)Y/I|Q Q T/K/P L T/L E/R(T)		115.95	497.2818	1489.837	-0.0065	-4.3	8.59	26283.8	8.96	HUMAN	O43809	Cleavage and polyadenylation specificity factor subunit 5
2199	dirMS_041712_NAR_20mM_minus.12289.12537.2	2	15.98	0	5.88E+05	M73m	(R)AVLVDLI	(R)A V\L|V|D|L|E|P G T\m D S V R(S)	m:Oxidized methionine	172.52	809.4088	1601.82	15.99	-3	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
2200	dirMS_041712_NAR_20mM_minus.14714.14884.2	2	15.98	0	3.01E+06		(K)EIIDLVLI	(K)E I|I/D|L/V/L/D/R(I)		203.67	543.3133	1085.62	-0.0008	-0.7	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
2201	dirMS_041712_NAR_50mM_minus2.9044.9044.3	3	15.98	0	7.04E+04		(R)EANALA	(R)E A\N\A/L/A A G H/P A Q A V A I N A R(L)		119.77	615.6611	1844.973	-0.0038	-2.1	6.85	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
2202	dirMS_041712_NAR_30mM_plus2.21319.21319.2	2	15.98	0	2.71E+05		(R)GVVQEL	(R)G V|V/Q/E|L/Q/Q A/I/S/K(L)		166.02	650.3632	1299.727	-0.0076	-5.8	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
2203	dirMS_041712_NAR_30mM_plus2.6022.6025.2	2	15.98	0	2.12E+06	M300m	(K)NMmAA	(K)N/M|m|A|A/C\D|P R(H)	C:Carbamidomethylation m:Oxid	86.02	541.2163	1065.427	15.9979	2.8	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
2204	dirMS_041712_NAR_50mM_plus2.13260.13285.3	3	15.98	0	2.96E+06		(K)LGDVYV	(K)L/G|D\V/Y V/N D/A/F G T A\H/R(A)		138.15	545.6029	1634.792	0.002	1.2	5.21	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
2205	dirMS_041712_NAR_50mM_plus2.20290.20606.3	3	15.98	1	4.12E+05		(R)VISGVLC	(R)V/I|S/G V/L Q/L/G N I V F/K/K(E)		176.1	539.0011	1614.994	-0.0054	-3.3	10	227783.5	5.5	HUMAN	P35579	Myosin-9
2206	dirMS_041712_NAR_120mM_minus.10135.10298.3	3	15.97	1	6.25E+05	M142m	(K)VKEGMI	(K)V K E G M N|I|V/E/A m E/R(F)	m:Oxidized methionine	110.08	507.9186	1505.745	15.9962	0.8	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
2207	dirMS_041712_NAR_30mM_minus2.17317.17317.2	2	15.97	0	2.42E+05		(R)NGGQIL	(R)N/G\G Q|I/L I\A/D L R(G)		148.4	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
2208	dirMS_041712_NAR_20mM_plus.15054.15054.2	2	15.97	0	1.40E+05		(K)VLEQLT(	(K)V/L|E/Q\L|T/G/Q/T/P V/F\S K(A)		174.68	773.9244	1546.848	-0.006	-3.9	5.97	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
2209	dirMS_041712_NAR_20mM_plus.16649.16649.2	2	15.97	0	1.58E+05		(R)LLEAQIA	(R)L/L/E\A/Q|I\A|T G G I I D|P K(E)		185.68	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
2210	dirMS_041712_NAR_20mM_plus.18757.18757.2	2	15.97	0	2.40E+05		(K)IYVDDGI	(K)I Y|V/D/D G/L/I/S L/Q V K(Q)		200.68	731.9068	1462.815	-0.0088	-6	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
2211	dirMS_041712_NAR_50mM_plus2.11270.11270.3	3	15.97	0	9.26E+05		(R)TFIAIKPI	(R)T F/I A I/K/P/D/G V Q R(G)		126.32	448.9241	1344.763	-0.0057	-4.2	8.41	6640.6	8.25	HUMAN	C9K028	Nucleoside diphosphate kinase A (Fragment)
2212	dirMS_041712_NAR_60mM_plus.16395.16772.3	3	15.97	0	1.39E+07		(R)EHALLA\	(R)E H\A\L\L|A|Y|T/L/G V/K(Q)		144.08	438.9179	1314.742	-0.0025	-1.9	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
2213	dirMS_041712_NAR_60mM_minus.15408.15408.3	3	15.96	0	1.03E+06		(R)LSDQFH	(R)L/S/D/Q/F/H/D I L I/R(K)		145.65	452.9148	1356.727	0.0028	2.1	5.21	12284.6	4.89	HUMAN	H0Y9X3	Programmed cell death protein 6 (Fragment)
2214	dirMS_041712_NAR_60mM_minus.9526.9526.3	3	15.96	0	3.33E+05		(R)QLSQAG	(R)Q\L/S Q/A/G/S F/S D/G T H G\G L/R(Y)		113.55	573.2781	1717.825	-0.0055	-3.2	6.74	266161	5.68	HUMAN	E9PPU0	Epiplakin
2215	dirMS_041712_NAR_120mM_plus.10867.11152.3	3	15.96	0	1.47E+06		(R)GSAVHC	(R)G S|A/V/H/Q/L/S/E E/L/R(C)		111.08	442.5657	1325.681	0.0017	1.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
2216	dirMS_041712_NAR_30mM_plus2.21716.21716.2	2	15.96	0	3.41E+05		(R)FSWNV\	(R)F/S\W/N/V W/P S S R(L)		169.22	633.3085	1265.606	0.0035	2.8	9.75	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
2217	dirMS_041712_NAR_40mM_plus2.13540.13798.3	3	15.96	1	1.93E+06		(K)TVGVEP.	(K)T V\G|V/E/P A A D G K/G V V V V/I/K(R)		147.37	580.0077	1738.011	-0.0024	-1.4	5.73	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
2218	dirMS_041712_NAR_120mM_minus.11894.12056.3	3	15.95	1	2.55E+06		(R)NLKASLE	(R)N L/K A S\L|E/N/S/L/R(E)		119.45	415.5698	1244.696	-0.0009	-0.7	8.75	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2219	dirMS_041712_NAR_120mM_minus.14729.14791.3	3	15.95	1	1.31E+06		(R)GYSFTTI	(R)G Y|S|F/T T/T A E/R E/I V/R(D)		134.73	543.9428	1629.823	-0.0093	-5.7	6.14	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
2220	dirMS_041712_NAR_120mM_minus.14793.14860.4	4	15.95	2	6.23E+05		(R)KLVIIESI	(R)K L V\I\I|E/S/D L/E R/A E/E/R(A)		134.88	450.7512	1799.986	-0.0032	-1.8	4.58	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
2221	dirMS_041712_NAR_60mM_minus.13716.13716.3	3	15.95	0	3.78E+05		(-)MVNHFI.	(-)M/V|N H|F\I/A E/F K(R)		136.52	412.5461	1235.624	-0.0004	-0.3	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
2222	dirMS_041712_NAR_30mM_plus2.18895.19194.2	2	15.95	0	1.39E+06		(K)FIIPNVV	(K)F/I|I|P N V V/K(Y)		153.13	465.2943	929.582	-0.0005	-0.6	8.75	17529.3	9.3	HUMAN	F5GXY2	L-lactate dehydrogenase A chain (Fragment)
2223	dirMS_041712_NAR_60mM_plus.7086.7086.3	3	15.95	1	2.94E+05		(R)ARQENG	(R)A R Q\E N G\M|P E E/P/A/T T A R(G)		95.2	586.6118	1757.824	-0.0027	-1.5	4.79	64356.2	9.96	HUMAN	O96013	Serine/threonine-protein kinase PAK 4
2224	dirMS_041712_NAR_120mM_minus.13668.13984.3	3	15.94	0	2.04E+06		(R)NLDIERI	(R)N/L|D|I/E R/P T Y/T/N L N R(L)		129.73	573.6313	1718.882	-0.0027	-1.6	6.07	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
2225	dirMS_041712_NAR_30mM_minus2.11003.11003.2	2	15.94	0	5.91E+05		(K)VAGQD(	(K)V A|G/Q/D|G S/V V Q\F K(I)		113.82	617.824	1234.643	-0.0019	-1.5	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
2226	dirMS_041712_NAR_50mM_minus2.10392.10392.3	3	15.94	0	3.38E+04		(R)GITINAA	(R)G I/T/I/N A A H/V/E/Y S T A/A R(H)		127.28	558.6229	1673.861	-0.0064	-3.8	6.75	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
2227	dirMS_041712_NAR_50mM_minus2.13471.13828.3	3	15.94	0	3.04E+05		(R)DLSHIGI	(R)D L S H\I G D\A\V|V|I/S/C/A K(D)	C:Carbamidomethylation	146.72	528.9397	1584.805	-0.0005	-0.3	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
2228	dirMS_041712_NAR_50mM_minus2.9510.9945.3	3	15.94	1	2.86E+06		(R)MQKEIT	(R)M Q|K E I T/A|L|A|P/S T M K(I)		123.52	516.9426	1548.812	0.0008	0.5	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
2229	dirMS_041712_NAR_20mM_plus.18207.18207.2	2	15.94	0	1.70E+05		(R)LTGQLFI	(R)L T|G/Q|L|F L\G/G S I/V\K(G)		197.02	666.8962	1332.789	-0.0034	-2.6	8.75	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
2230	dirMS_041712_NAR_30mM_plus2.12478.12478.2	2	15.94	0	5.26E+05		(R)LLVVTDI	(R)L L|V/V/T D/P R(A)		118.67	456.779	912.551	-0.0006	-0.6	5.84	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
2231	dirMS_041712_NAR_40mM_plus2.13722.13925.3	3	15.94	1	2.67E+05		(R)GDVVPK	(R)G D|V|V|P/K/D\V N/A|A/I A T I K(T)		147.25	537.6381	1610.911	-0.0115	-7.1	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
2232	dirMS_041712_NAR_50mM_plus2.16309.16478.3	3	15.94	1	4.20E+06		(K)LLQDFFI	(K)L/L|Q/D|F/F/N G K E L N/K(S)		154.6	522.6137	1565.832	-0.0057	-3.6	6.07	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
2233	dirMS_041712_NAR_50mM_plus2.19803.19864.3	3	15.94	0	1.72E+05		(R)QLPAMT	(R)Q L|P/A/M T A/L/Q/T L/H/L R(S)		172.75	531.635	1592.894	-0.0037	-2.3	9.75	78827.3	5.92	HUMAN	J3KS54	Protein flightless-1 homolog
2234	dirMS_041712_NAR_120mM_minus.6321.6321.3	3	15.93	1	9.86E+05		(R)TEERAEI	(R)T|E/E/R A E/L/A E/S R(C)		88.93	430.8806	1290.628	-0.0012	-0.9	4.49	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
2235	dirMS_041712_NAR_30mM_minus2.18072.18302.2	2	15.93	0	3.80E+05		(K)GLIPWE(	(K)G/L|I|P/W/E Q/A A R(L)		153.42	570.8106	1140.616	-0.0021	-1.8	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
2236	dirMS_041712_NAR_50mM_minus2.14125.14125.3	3	15.93	1	1.24E+06		(R)LLDAQL/	(R)L/L/D/A/Q/L/A T G G L V C P A R R(L)	C:Carbamidomethylation	149.03	604.3359	1810.996	-0.0025	-1.4	9.6	266161	5.68	HUMAN	E9PPU0	Epiplakin
2237	dirMS_041712_NAR_40mM_plus2.11540.11540.3	3	15.93	0	3.79E+05		(R)MPLPAP	(R)M/P L/P/A/P S L S H Q|P/P P A P R(V)		133.63	598.3202	1792.953	-0.0066	-3.7	9.52	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
2238	dirMS_041712_NAR_60mM_plus.15620.15620.2	2	15.93	1	4.11E+05		(R)TEMENE	(R)T/E|M/E/N E/F V/L I/K K(D)		138.27	740.8875	1480.772	-0.0039	-2.6	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
2239	dirMS_041712_NAR_20mM_minus.7692.7692.2	2	15.92	0	5.17E+05	M239m	(K)EVDEQm	(K)E V/D/E Q m L/N|V Q/N K(N)	m:Oxidized methionine	125.37	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
2240	dirMS_041712_NAR_30mM_minus2.10941.11254.2	2	15.92	0	5.89E+05		(K)IVVVTA(	(K)I/V|V|V|T/A G V/R(Q)		114.07	457.2948	913.583	-0.0006	-0.7	9.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
2241	dirMS_041712_NAR_30mM_minus2.16670.16670.2	2	15.92	0	8.67E+04		(R)IMNTFS\	(R)I M/N\T|F/S V/V/P S/P K(V)		144.65	660.3534	1319.703	-0.0033	-2.5	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
2242	dirMS_041712_NAR_30mM_minus2.18263.18344.2	2	15.92	0	2.33E+05		(K)ALQFLEE	(K)A/L|Q/F/L E/E V/K(V)		153.82	538.7985	1076.599	-0.0089	-8.3	4.53	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
2243	dirMS_041712_NAR_50mM_minus2.12749.12749.3	3	15.92	0	3.41E+06	M84m	(K)YPIEHGI	(K)Y/P/I E H G I I/T/N/W/D D m E K(I)	m:Oxidized methionine	141.47	659.6398	1960.911	15.9939	-0.5	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
2244	dirMS_041712_NAR_120mM_plus.21491.21594.4	4	15.92	2	4.53E+05	M145m	(R)RGVmL/	(R)R G V\m|L\A|V/D A V I/A/E L/K K(Q)	m:Oxidized methionine	166.22	433.0059	1713.009	15.9926	-1.3	8.59	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
2245	dirMS_041712_NAR_50mM_plus2.17936.18222.3	3	15.92	1	1.81E+06		(R)ELIKVLEI	(R)E L\I K V L E E A/N/Q|A/I/N/P K(L)		163.53	603.6741	1809.012	-0.0039	-2.2	4.79	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
2246	dirMS_041712_NAR_20mM_minus.10714.10714.2	2	15.91	0	1.92E+05		(R)TTPSYV/	(R)T T|P/S Y/V/A/F T D/T E R(L)		154.67	744.3547	1487.701	0.0009	0.6	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
2247	dirMS_041712_NAR_60mM_minus.7586.7630.3	3	15.91	1	6.66E+05		(K)IVADKD\	(K)I/V|A D/K/D Y/S/V T/A/N S K(I)		102.58	504.2624	1510.775	-0.0021	-1.4	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
2248	dirMS_041712_NAR_60mM_minus.9384.9401.3	3	15.91	1	2.76E+05	M198m	(R)VFDKEG	(R)V/F|D K E G N\G T|V/m/G A/E/I R(H)	m:Oxidized methionine	112.15	580.2853	1722.848	15.9934	-0.9	4.68	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
2249	dirMS_041712_NAR_20mM_plus.10668.10668.2	2	15.91	0	6.90E+04	M61m	(K)NQVAm	(K)N Q/V|A/m|N/P T N T/V F D/A K(R)	m:Oxidized methionine	146.22	833.3977	1649.795	15.9929	-1.2	5.84	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
2250	dirMS_041712_NAR_40mM_plus2.15955.15955.3	3	15.91	0	2.95E+05		(K)VAIVKP(	(K)V/A\I/V K/P G|V|P/M E I V L N K(E)		160.92	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
2251	dirMS_041712_NAR_60mM_plus.7455.7477.3	3	15.91	1	5.05E+05		(K)SSGGREI	(K)S/S/G G R E D\L|E|S/S/G L Q|R(R)		97.3	526.5897	1577.751	0.0031	2	4.68	11625.5	8.01	HUMAN	B8ZZT7	Hematological and neurological-expressed 1 protein
2252	dirMS_041712_NAR_30mM_minus2.19043.19043.2	2	15.9	0	1.18E+06		(K)LAVNM\	(K)L A|V/N|M|V/P F P R(L)		159.03	572.3143	1143.634	-0.013	-11.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
2253	dirMS_041712_NAR_50mM_minus2.15906.15906.3	3	15.9	0	3.64E+05		(K)LYGPTNI	(K)L/Y/G/P T N|F/S/P\I I N H V A R(F)		158.22	600.3221	1798.96	-0.0081	-4.5	8.75	60985.3	5.6	HUMAN	O75131	Copine-3
2254	dirMS_041712_NAR_60mM_minus.7330.7759.3	3	15.9	1	1.38E+06		(K)IQDKEGI	(K)I/Q\D K E G|I|P/P D/Q Q/R(L)		100.07	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
2255	dirMS_041712_NAR_20mM_plus.16379.16461.3	3	15.9	0	1.68E+05		(K)TVTNAV	(K)T V\T N A V\V T V/P/A/Y/F/N D S Q R(Q)		184.78	661.3368	1981.998	-0.0019	-1	5.5	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
2256	dirMS_041712_NAR_30mM_plus2.7530.7530.2	2	15.9	0	3.61E+05		(R)MNEAF(	(R)M/N|E|A/F/G D/T K(F)		93.75	506.7256	1012.44	0.0035	3.5	4.37	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
2257	dirMS_041712_NAR_40mM_plus2.16896.16918.3	3	15.9	0	8.98E+04		(R)LLEVLSG	(R)L/L|E|V\L S/G E/I/L/P K/P T K(G)		166	546.3323	1636.988	-0.006	-3.7	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
2258	dirMS_041712_NAR_50mM_plus2.18484.18650.3	3	15.9	1	3.94E+05		(K)VCSTND	(K)V/C|S T N D/L K/E L L/I/F/N/K(Q)	C:Carbamidomethylation	166.02	598.6527	1793.947	-0.0031	-1.7	6.04	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
2259	dirMS_041712_NAR_60mM_plus.14465.14613.3	3	15.9	1	1.26E+06		(K)FSIEDLK.	(K)F/S|I/E/D/L K/A Q/P K(Q)		132.38	425.898	1275.694	-0.0149	-11.7	6.07	13579.2	9.99	HUMAN	E9PPQ6	Thymocyte nuclear protein 1 (Fragment)
2260	dirMS_041712_NAR_50mM_minus2.12922.12922.3	3	15.89	0	3.06E+05		(R)ETNLDSI	(R)E T N/L/D/S L/P/L/V/D T H S K(R)		142.27	556.9529	1668.844	0.0002	0.1	4.53	53707.8	5.06	HUMAN	P08670	Vimentin
2261	dirMS_041712_NAR_120mM_plus.11511.11511.3	3	15.89	2	7.36E+05		(K)QAGPAS	(K)Q A|G/P/A/S/V/P L R T E E E F K/K(F)		113.4	629.6702	1886.997	-0.001	-0.5	6.23	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
2262	dirMS_041712_NAR_30mM_plus2.21984.21984.2	2	15.89	0	2.09E+05		(K)QSLGELI	(K)Q S|L/G|E|L/I|G/T L N A/A K(V)		170.25	707.8889	1414.79	-0.0195	-13.8	6	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
2263	dirMS_041712_NAR_30mM_plus2.22156.22156.2	2	15.89	0	2.10E+05		(K)NSSYFVE	(K)N S S Y/F/V/E/W/I|P N N V/K(V)		171.87	848.9189	1696.833	-0.0024	-1.4	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
2264	dirMS_041712_NAR_30mM_plus2.22577.22703.2	2	15.89	0	1.01E+06		(R)FLTWILN	(R)F/L|T|W I/L/N/R(Y)		175.88	531.8078	1062.61	-0.0012	-1.1	9.75	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
2265	dirMS_041712_NAR_30mM_minus2.12598.12598.2	2	15.88	0	2.70E+05		(R)TLSGME	(R)T L|S/G M/E/S Y C V/R(A)	C:Carbamidomethylation	122.03	651.795	1302.582	0.001	0.8	5.66	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
2266	dirMS_041712_NAR_20mM_plus.13244.13665.2	2	15.88	0	8.91E+05		(R)VLQALE(	(R)V/L|Q/A/L/E|G L K(M)		164.68	485.8004	970.593	0.0004	0.4	5.97	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
2267	dirMS_041712_NAR_30mM_plus2.11794.11794.2	2	15.88	0	4.85E+05		(R)AMGEQ.	(R)A M/G E|Q/A/V|A L A/R(A)		114.22	558.7944	1116.583	-0.0015	-1.3	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
2268	dirMS_041712_NAR_40mM_plus2.13130.13278.3	3	15.88	0	3.31E+05		(K)LQMEAI	(K)L/Q|M E A/P H/I/I/V/G T/P G R(V)		144.07	540.2954	1618.873	-0.0017	-1.1	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
2269	dirMS_041712_NAR_50mM_plus2.19370.19370.3	3	15.88	0	3.55E+05		(-)MKPLVV	(-)M K P L V V F V|L/G/G/P G A G|K(G)		169.73	523.9715	1569.919	-0.0186	-11.8	10	22450.2	5.44	HUMAN	P30085	UMP-CMP kinase
2270	dirMS_041712_NAR_30mM_minus2.11584.11733.2	2	15.87	0	9.25E+05		(K)SSLGPV(	(K)S S|L/G|P V/G L/D K(M)		117.13	486.7751	972.536	0.0069	7.1	5.55	47423	5.43	HUMAN	E7ERF2	T-complex protein 1 subunit alpha
2271	dirMS_041712_NAR_30mM_minus2.11632.11667.2	2	15.87	0	5.59E+05	M64m	(K)VmYGF(	(K)V/m|Y|G/F/C S V/K(D)	C:Carbamidomethylation m:Oxid	117.33	553.7611	1090.506	16.0089	12.7	8.56	76925.9	4.46	HUMAN	A8MV58	Drebrin
2272	dirMS_041712_NAR_120mM_plus.9417.9417.4	4	15.87	1	2.90E+05		(K)MCKQDI	(K)M/C K Q D|P/S V L H/T E E|M/R(F)	C:Carbamidomethylation	102.68	465.966	1860.84	0.0021	1.1	5.43	4776.5	8.27	HUMAN	F8WAQ7	Hsc70-interacting protein
2273	dirMS_041712_NAR_20mM_plus.7900.7900.3	3	15.87	0	1.18E+05		(K)VEIIAND	(K)V E\I\I A/N|D/Q/G N/R(T)		124.5	410.2139	1228.628	-0.0009	-0.7	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
2274	dirMS_041712_NAR_30mM_plus2.19998.20177.2	2	15.87	0	2.43E+05		(K)LYNLFLK	(K)L/Y/N|L|F/L K(I)		159.32	455.7738	910.54	0.0007	0.7	8.59	41666	7.73	HUMAN	E9PDQ8	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial
2275	dirMS_041712_NAR_50mM_plus2.18773.18835.3	3	15.87	1	2.23E+05		(K)IGEEFLT	(K)I/G|E/E/F L/T/D L/S Q/L K/K(L)		167.02	540.965	1620.884	-0.0039	-2.4	4.68	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
2276	dirMS_041712_NAR_30mM_minus2.18028.18028.2	2	15.86	0	4.12E+05		(R)LLLNNDI	(R)L L|L/N/N D N L/L/R(E)		153.13	599.3487	1197.695	-0.0049	-4.1	5.84	19945.8	4.97	HUMAN	B4DG50	F-actin-capping protein subunit alpha-2
2277	dirMS_041712_NAR_50mM_minus2.16852.16852.3	3	15.86	0	4.60E+05		(K)NILFVITI	(K)N\I/L/F/V/I/T K/P D V/Y K(S)		164.12	517.2991	1549.899	-0.0161	-10.4	8.5	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
2278	dirMS_041712_NAR_20mM_plus.6022.6022.3	3	15.86	0	1.02E+06	M295m M.	(R)mGQmA	(R)m G Q m A\m/G\G|A|m/G I N N R(G)	m:Oxidized methionine	100.27	534.8861	1538.67	63.9743	-3.4	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
2279	dirMS_041712_NAR_30mM_plus2.20250.20583.2	2	15.86	0	2.89E+05		(R)FLIQNVL	(R)F/L|I|Q N/V L/R(L)		160.97	501.8112	1002.61	0.0056	5.6	9.75	132902.3	5.82	HUMAN	J3KR24	Isoleucine--tRNA ligase, cytoplasmic
2280	dirMS_041712_NAR_30mM_plus2.21455.21862.2	2	15.86	0	8.57E+05		(R)LFFLQVI	(R)L/F|F|L/Q/V/K(E)		169.12	447.7756	894.545	-0.0008	-0.9	8.75	71218.8	6.3	HUMAN	A7YIJ8	Radixin
2281	dirMS_041712_NAR_50mM_plus2.15945.15978.3	3	15.86	1	7.30E+05		(R)LKLPAV\	(R)L K L P A\V|V|T|A/D/L/R(L)		152.03	432.6039	1295.805	-0.0074	-5.7	8.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
2282	dirMS_041712_NAR_50mM_plus2.17493.17493.3	3	15.86	1	7.15E+05		(R)CITDPQ1	(R)C/I|T|D/P Q\T G L C L/L P L K E K(K)	C:Carbamidomethylation	160.15	662.6825	1986.04	-0.0069	-3.5	6.07	533778	5.74	HUMAN	Q15149	Plectin
2283	dirMS_041712_NAR_50mM_plus2.19630.19630.3	3	15.86	1	7.20E+05		(R)VLEALLP	(R)V/L|E/A L L/P/L K G L E E R(V)		171.8	527.318	1579.942	-0.0023	-1.5	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
2284	dirMS_041712_NAR_50mM_plus2.20180.20201.3	3	15.86	0	4.67E+05		(K)ALIEVLQ	(K)A L\I|E/V/L Q/P L/I/A/E H Q A R(R)		174.23	601.0191	1801.033	0.0097	5.4	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic

2285	dirMS_041712_NAR_30mM_minus2.7747.7850.2	2	15.85	0	4.23E+05		(K)TDEGIA	(K)T/D|E|G|I|A/Y/R(G)		96.7	462.7203	924.442	-0.0088	-9.5	4.37	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
2286	dirMS_041712_NAR_60mM_minus.8979.8979.2	2	15.85	0	9.67E+05		(K)QEYDES	(K)Q\E|Y D E/S/G/P S I/V/H/R(K)		110.35	758.8539	1516.703	-0.0021	-1.4	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
2287	dirMS_041712_NAR_20mM_plus.8314.8361.2	2	15.85	0	1.23E+05		(K)SVEAAA	(K)S V|E|A|A/A/E/L/S A K(D)		127.72	538.2834	1075.563	-0.0035	-3.2	4.53	12131.5	11.14	HUMAN	F5GXR3	Parathymosin
2288	dirMS_041712_NAR_30mM_plus2.13303.13401.2	2	15.85	0	4.96E+05		(K)ISITEGIE	(K)I/S|I/T/E/G I E/R(G)		123.28	509.2827	1017.558	0.0006	0.6	4.53	334221.3	6.44	HUMAN	P15924	Desmoplakin
2289	dirMS_041712_NAR_50mM_plus2.21947.22124.3	3	15.85	1	8.66E+06		(R)KEGGLG	(R)K\E G G L\G P\L\N\I|P|L/L/A/D V T R(R)		188.23	621.6925	1863.07	-0.0069	-3.7	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
2290	dirMS_041712_NAR_60mM_plus.12175.12217.3	3	15.85	1	1.99E+06		(R)MQKEIT	(R)M Q K E I T/A|L/A/P S/T/M K(I)		120.7	516.9402	1548.812	-0.0064	-4.1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
2291	dirMS_041712_NAR_60mM_plus.20058.20138.3	3	15.85	1	5.36E+05		(R)AKFEEL	(R)A K\F E E\L/N|M/D/L/F/R(S)		165.08	504.9258	1512.752	0.0113	7.5	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
2292	dirMS_041712_NAR_120mM_minus.13538.13538.4	4	15.84	1	7.85E+05		(K)SVHSSV	(K)S V H S S V|P L/L/N S K D/P I D|R(I)		127.8	466.7525	1863.992	-0.0041	-2.2	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
2293	dirMS_041712_NAR_120mM_minus.7490.7512.3	3	15.84	1	2.23E+05		(R)KTGQAP	(R)K\T G Q A|P/G\Y|S|Y\T/A A/N K(N)		95.17	519.5935	1556.77	-0.0044	-2.8	9.53	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
2294	dirMS_041712_NAR_20mM_minus.13199.13274.3	3	15.84	0	4.00E+05		(K)TITLEVE	(K)T\I\T L E\V E/P/S/D/T I/E N V\K(A)		183.03	596.6453	1787.927	-0.006	-3.3	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
2295	dirMS_041712_NAR_30mM_minus2.16115.16115.2	2	15.84	0	1.16E+05		(K)EQFLDG	(K)E Q|F|L/D/G D G W T S R(W)		141.08	705.8174	1410.628	-0.0009	-0.6	4.03	28545.1	4.5	HUMAN	K7EJB9	Calreticulin (Fragment)
2296	dirMS_041712_NAR_30mM_minus2.7596.7596.2	2	15.84	0	1.75E+05		(K)YTQSNS	(K)Y/T|Q/S/N/S V C/Y/A/K(N)	C:Carbamidomethylation	95.73	660.7969	1320.589	-0.0024	-1.8	8.5	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
2297	dirMS_041712_NAR_50mM_minus2.13364.13364.3	3	15.84	1	1.91E+05		(K)TITLEVE	(K)T I/T/L/E V E/P S/D/T I/E N V K A K(I)		144.63	663.0226	1987.059	-0.0061	-3.1	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
2298	dirMS_041712_NAR_120mM_plus.10633.10837.3	3	15.84	1	1.21E+06		(R)QQEGF	(R)Q Q/E/G F/K/G T/F/P/D/A R(E)		109.43	494.2435	1480.718	-0.002	-1.3	6.07	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
2299	dirMS_041712_NAR_30mM_plus2.13704.13761.2	2	15.84	0	2.11E+05		(R)VFNYNT	(R)V/F|N|Y/N/T L/E/R(V)		124.98	578.2929	1155.579	-0.0008	-0.7	5.97	99900.1	5.04	HUMAN	B4DZI8	Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b
2300	dirMS_041712_NAR_30mM_plus2.16477.16968.2	2	15.84	0	1.10E+06		(K)LIINSLY	(K)L/I|I|N/S L/Y/K(N)		140.43	482.2971	963.587	-0.0004	-0.4	8.59	5582.4	4.81	HUMAN	F8W026	Endoplasmin (Fragment)
2301	dirMS_041712_NAR_40mM_plus2.19639.19639.3	3	15.84	1	1.67E+05		(K)LGFAGL	(K)L G|F|A/G L/V Q\E/I/S F/G T T K D K(M)		183.78	637.673	1911.022	-0.0178	-9.3	6.07	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
2302	dirMS_041712_NAR_30mM_minus2.13012.13238.2	2	15.83	0	5.66E+05		(K)ALMDE	(K)A/L|M/D/E/V/V/K(A)		125.2	452.7446	904.481	0.0011	1.2	4.37	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
2303	dirMS_041712_NAR_50mM_minus2.14460.14460.3	3	15.83	1	1.40E+05		(R)GDVVP	(R)G D/V|V|P/K D\V/N A\A I/A T I K(T)		150.42	537.6375	1610.911	-0.0133	-8.2	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
2304	dirMS_041712_NAR_60mM_minus.9349.9350.3	3	15.83	1	1.46E+05		(R)KIQVLQ	(R)K\I Q\V L\Q\Q|Q|A/D/D/A/E\E R(A)		112	590.9696	1770.898	-0.0038	-2.2	4.32	11017	4.8	HUMAN	D6R904	Tropomyosin alpha-3 chain
2305	dirMS_041712_NAR_120mM_plus.17568.18101.3	3	15.83	1	2.34E+06		(R)RAPFDL	(R)R\A\P\F\D|L|F E/N/R(K)		146.97	422.22	1264.643	0.0022	1.7	6.07	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
2306	dirMS_041712_NAR_20mM_plus.14264.14665.2	2	15.83	0	6.81E+05	M73m	(R)AVLVDL	(R)A V|L|V|D|L|E|P G/T\m D S V R(S)	m:Oxidized methionine	171.03	809.4082	1601.82	15.9888	-3.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
2307	dirMS_041712_NAR_20mM_plus.7429.7429.2	2	15.83	0	7.63E+04		(K)SNVSDA	(K)S N|V/S D A/V/A Q/S|T/R(I)		119.48	617.8019	1234.602	-0.0057	-4.6	5.55	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
2308	dirMS_041712_NAR_40mM_plus2.11872.11872.3	3	15.83	0	4.24E+04		(K)AASAGV	(K)A A|S A/G/V/P Y/H G E V/P V S L A R(A)		136.07	594.314	1780.934	-0.0066	-3.7	6.79	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
2309	dirMS_041712_NAR_40mM_plus2.15562.15562.3	3	15.83	1	7.33E+04		(K)VLDSGA	(K)V L|D\S/G A/P I K/I|P V G/P E T L/G R(I)		158.12	640.3668	1919.096	-0.0102	-5.3	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
2310	dirMS_041712_NAR_20mM_minus.8145.8281.2	2	15.82	0	6.77E+06	M239m	(K)EITALAP	(K)E I|T|A|L|A/P/S T m K(I)	m:Oxidized methionine	132.6	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
2311	dirMS_041712_NAR_30mM_minus2.8095.8095.2	2	15.82	0	1.83E+05		(K)GSGTAE	(K)G S|G T|A/E V/E/L K(K)		98.32	495.7528	990.51	-0.0119	-12	4.53	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
2312	dirMS_041712_NAR_40mM_minus2.14317.14317.3	3	15.82	1	1.61E+05		(K)TGISDV	(K)T G/I/S D/V F A K\N D L/A/V V D/V R(I)		168.48	640.3454	1919.023	-0.0016	-0.8	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
2313	dirMS_041712_NAR_60mM_minus.9737.9737.2	2	15.82	1	4.41E+05		(R)LQAEIE	(R)L/Q|A|E|I/E G L K/G Q R(A)		114.13	671.3768	1341.748	-0.0022	-1.6	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2314	dirMS_041712_NAR_20mM_plus.18728.18728.3	3	15.82	0	5.22E+05		(K)LAVEAL	(K)L A V E A L\S\S/L/D/G D/L/A/G R(Y)		200.47	529.6164	1586.838	-0.0038	-2.4	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
2315	dirMS_041712_NAR_40mM_plus2.15332.15332.3	3	15.82	0	6.25E+05		(K)IEVIKPG	(K)I/E|V I/K P/G D\L G V D L T S K(L)		156.2	561.9876	1683.953	-0.0045	-2.7	4.56	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
2316	dirMS_041712_NAR_30mM_minus2.18391.18795.2	2	15.81	0	1.87E+06		(R)DLTDYL	(R)D L|T|D/Y/L/M/K(I)		155.93	499.7499	998.486	0.0062	6.2	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
2317	dirMS_041712_NAR_50mM_minus2.13141.13141.3	3	15.81	0	3.75E+05		(K)VTHAVV	(K)V T H A\V V\T\V/P\A/Y/F/N D A Q R(Q)		143.35	629.9954	1887.971	0.0005	0.3	6.71	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
2318	dirMS_041712_NAR_30mM_plus2.7037.7179.2	2	15.81	0	2.83E+05		(K)ALLQSS	(K)A/L|L|Q/S/S\A/S/R(K)		91.82	466.7618	932.516	0.0004	0.4	9.79	44128.4	6.13	HUMAN	Q9UQ80	Proliferation-associated protein 2G4
2319	dirMS_041712_NAR_30mM_plus2.9432.9555.2	2	15.81	0	8.52E+04		(K)VCNPIIT	(K)V/C|N/P I/I/T/K(L)	C:Carbamidomethylation	104.22	472.7711	944.523	0.0116	12.2	8.72	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
2320	dirMS_041712_NAR_40mM_plus2.18885.18885.3	3	15.81	1	4.04E+05		(R)TLAEIAK	(R)T L|A/E I/A K V|E L/D N M/P L R(G)		176.78	604.9967	1812.989	-0.0132	-7.3	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
2321	dirMS_041712_NAR_30mM_minus2.10166.10166.2	2	15.8	0	5.85E+05		(K)FGVQM	(K)F/G|V/Q M D/R(V)		109.88	426.7012	852.403	-0.0081	-9.5	5.84	25153.2	6.6	HUMAN	H7C314	Src substrate cortactin (Fragment)
2322	dirMS_041712_NAR_30mM_minus2.18343.18448.2	2	15.8	0	4.47E+05		(R)QAQEYE	(R)Q A|Q/E/Y/E/A/L/L/N I K(V)		154.67	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2323	dirMS_041712_NAR_30mM_minus2.7754.7754.2	2	15.8	0	1.29E+05		(K)VTQVD	(K)V/T|Q/V/D/G N/S P V R(F)		96.45	586.3085	1171.607	0.0031	2.7	5.81	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
2324	dirMS_041712_NAR_40mM_minus2.13124.13144.3	3	15.8	1	9.20E+04		(K)VLDSGA	(K)V/L|D|S/G A/P I K I/P/V G/P E T L G R(I)		160.87	640.3618	1919.096	-0.0252	-13.1	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
2325	dirMS_041712_NAR_50mM_minus2.11257.11257.3	3	15.8	0	1.44E+06		(R)NLDIER	(R)N/L|D|I/E R P T Y T N L N R(L)		131.95	573.6313	1718.882	-0.0027	-1.6	6.07	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
2326	dirMS_041712_NAR_60mM_minus.15159.15159.2	2	15.8	0	4.20E+05		(R)EHALLA	(R)E H|A/L/L/A Y/T\L G V K(Q)		144.65	657.873	1314.742	-0.0029	-2.2	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
2327	dirMS_041712_NAR_60mM_minus.17181.17181.3	3	15.8	1	6.23E+05		(K)EVNKFQ	(K)E V/N K F Q M/A/Y/S/N/L/L R(A)		155.47	571.6279	1712.879	-0.0097	-5.7	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
2328	dirMS_041712_NAR_120mM_plus.21471.21538.3	3	15.8	1	2.33E+05		(R)GLFIIDD	(R)G L|F/I/I/D/D K/G I L R(Q)		165.98	453.9377	1359.8	-0.0009	-0.7	5.96	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
2329	dirMS_041712_NAR_20mM_plus.17520.17520.2	2	15.8	0	3.08E+05		(K)SYELPD	(K)S Y\E|L|P D G Q V/I|T I/G N E R(F)		193.17	895.9492	1790.892	-0.0008	-0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
2330	dirMS_041712_NAR_60mM_plus.7439.7530.3	3	15.8	0	5.01E+05		(R)SSGHSS	(R)S/S G H S S S\E|L|S|P D A/V/E/K(A)		96.95	539.584	1616.74	-0.0024	-1.5	4.65	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
2331	dirMS_041712_NAR_60mM_plus.9511.9878.3	3	15.8	1	1.21E+06		(K)ILVANR	(K)I/L|V/A/N R/G E I/A C/R(V)	C:Carbamidomethylation	107.78	457.9222	1371.753	-0.0005	-0.4	9.6	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
2332	dirMS_041712_NAR_120mM_minus.8006.8101.2	2	15.79	0	5.03E+05		(K)IGHPAP	(K)I/G/H|P/A/P N\F/K(A)		98.13	490.7694	980.531	0.0003	0.3	8.76	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
2333	dirMS_041712_NAR_20mM_minus.10350.10350.2	2	15.79	0	4.24E+04		(K)AVLSLY	(K)A V/L|S L/Y/A S G/R(T)		152.4	518.7929	1036.579	0	0	8.79	14579.3	5.13	HUMAN	K7EM38	Actin, cytoplasmic 2, N-terminally processed (Fragment)
2334	dirMS_041712_NAR_50mM_minus2.10395.10395.3	3	15.79	0	7.23E+04		(R)LTSPIVS	(R)L\T|S/P I/V/S/T/H L D/T R(N)		127.37	480.6	1439.785	0.0002	0.1	6.74	58760.2	5.26	HUMAN	Q6ZTN6	Ankyrin repeat domain-containing protein 13D
2335	dirMS_041712_NAR_50mM_minus2.10568.10568.3	3	15.79	0	1.60E+05		(R)LLELGPK	(R)L L|E|L/G P K/P E V A|Q Q T R(K)		128.52	560.3182	1678.949	-0.0086	-5.1	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
2336	dirMS_041712_NAR_20mM_plus.16611.16611.2	2	15.79	0	1.91E+05		(K)VQIAVA	(K)V Q\I|A/V/A/N A Q E L/L\Q|R(M)		186.22	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
2337	dirMS_041712_NAR_30mM_plus2.12388.12908.2	2	15.79	0	2.48E+06		(R)LQIDEQ	(R)L/Q|I|D/E/Q L/R(Q)		118.98	507.7822	1014.558	-0.0007	-0.7	4.37	66105.7	7.3	HUMAN	A8MQB8	Fragile X mental retardation protein 1
2338	dirMS_041712_NAR_30mM_plus2.21157.21398.2	2	15.79	0	2.85E+05		(R)FDAMP	(R)F/D|A|M|P/F/T L/R(A)		166.32	549.276	1097.545	-0.0001	-0.1	5.84	42088	5.39	HUMAN	F8VTY8	Proliferation-associated protein 2G4
2339	dirMS_041712_NAR_50mM_plus2.14381.14403.3	3	15.79	0	5.99E+05		(R)AVAIDL	(R)A V|A I/D L/P/G L G H S K(E)		143.8	426.5786	1277.721	0	0	6.79	19983.6	8.14	HUMAN	B4DQI4	Alpha/beta hydrolase domain-containing protein 14B
2340	dirMS_041712_NAR_50mM_plus2.15238.15238.3	3	15.79	1	6.82E+05		(K)TVGVEP	(K)T V|G V/E/P A A D/G K G V V V V I K(R)		147.9	580.0056	1738.011	-0.0087	-5	5.73	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
2341	dirMS_041712_NAR_50mM_plus2.17722.17872.3	3	15.79	0	8.69E+05		(K)NILFVIT	(K)N I|L/F/V/I/T K/P D V Y K(S)		161.55	517.3015	1549.899	-0.0089	-5.7	8.5	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
2342	dirMS_041712_NAR_60mM_plus.14375.14425.3	3	15.79	1	8.33E+05		(R)TIRYPDP	(R)T/I/R\Y P D|P/L/I/K(V)		131.87	405.9078	1215.71	-0.0007	-0.6	8.25	29825.4	10.37	HUMAN	P62701	40S ribosomal protein S4, X isoform
2343	dirMS_041712_NAR_20mM_plus.7173.7173.2	2	15.78	0	3.06E+05	M532m M	(R)mVPAG	(R)m V|P/A/G m G A G L E R(M)	m:Oxidized methionine	117.37	610.7907	1188.586	31.9877	-1.7	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
2344	dirMS_041712_NAR_30mM_plus2.10513.10513.2	2	15.78	0	1.78E+05		(R)DGYDY	(R)D G Y/D/Y/D/G Y R(L)		108.43	562.2211	1123.433	0.0022	2	3.93	28442.8	10.22	HUMAN	J3KTL2	Serine/arginine-rich-splicing factor 1
2345	dirMS_041712_NAR_30mM_plus2.14272.14272.2	2	15.78	0	2.49E+05		(R)IYGFYDE	(R)I/Y|G|F Y D E/C K(R)	C:Carbamidomethylation	127.52	597.761	1194.514	0.0011	1	4.37	33222.3	5.74	HUMAN	A6NNR3	Serine/threonine-protein phosphatase
2346	dirMS_041712_NAR_50mM_plus2.13401.13526.3	3	15.78	0	1.54E+06		(R)VLVVHD	(R)V/L|V/V/H/D G F E G L A/K(G)		139.83	461.9229	1383.763	-0.0089	-6.5	5.32	18719.9	6.91	HUMAN	F8VP00	6-phosphofructokinase, muscle type (Fragment)
2347	dirMS_041712_NAR_40mM_minus2.13615.13753.3	3	15.77	1	3.98E+05		(R)VTFSGL	(R)V T|F/S/G L R D T\V/T/P G E L L K(A)		164.73	611.6742	1833.012	-0.0036	-2	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
2348	dirMS_041712_NAR_50mM_minus2.12436.12436.3	3	15.77	0	2.71E+05		(K)AASDIA	(K)A A/S D I/A/M/T E L/P/P T H/P I R(L)		139.15	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
2349	dirMS_041712_NAR_50mM_minus2.15419.15419.3	3	15.77	0	3.28E+05		(R)LSFQHD	(R)L/S/F Q H D\P\E\T|S/V/L/V L/R(K)		156.07	580.9793	1740.928	-0.0046	-2.6	5.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
2350	dirMS_041712_NAR_30mM_plus2.15018.15018.2	2	15.77	0	7.43E+05		(R)LSLYQA	(R)L/S|L/Y/Q A/M R(Q)		131.28	491.2638	981.519	0.0017	1.7	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
2351	dirMS_041712_NAR_50mM_plus2.10370.10371.3	3	15.77	1	2.76E+05		(K)IQVLQQ	(K)I/Q|V|L/Q/Q/Q/A D/D/A E E R A E R(L)		121.95	666.999	1998.984	-0.0015	-0.7	4.18	26611.3	4.47	HUMAN	A6NL28	Putative tropomyosin alpha-3 chain-like protein
2352	dirMS_041712_NAR_50mM_plus2.11351.11370.3	3	15.77	0	5.94E+05		(R)ITLRPDP	(R)I/T|L/R P D|P\L/P E/R(S)		127.35	436.2535	1306.748	-0.0018	-1.4	6.07	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
2353	dirMS_041712_NAR_50mM_plus2.13324.13476.3	3	15.77	0	9.05E+05		(R)TVVTGI	(R)T/V|V|T/G I/E M/F/H K(S)		138.55	421.225	1261.661	-0.0005	-0.4	6.41	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
2354	dirMS_041712_NAR_60mM_plus.8093.8235.3	3	15.77	1	6.15E+05		(R)KQSTDE	(R)K\Q S T D\E|E|V/T|S L/A/K(S)		100.87	479.2461	1435.728	-0.0037	-2.6	4.68	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
2355	dirMS_041712_NAR_30mM_minus2.16414.16851.2	2	15.76	0	3.42E+05		(R)ASLEAA	(R)A S/L/E/A|A|I/A|D/A/E Q R(G)		144.08	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2356	dirMS_041712_NAR_50mM_minus2.13489.13719.3	3	15.76	0	3.04E+05		(R)DLSHIG	(R)D L S H\I\G D\A\V|V|I/S/C/A K(D)	C:Carbamidomethylation	146.72	528.9397	1584.805	-0.0005	-0.3	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
2357	dirMS_041712_NAR_40mM_plus2.17300.17300.3	3	15.76	1	1.93E+05		(R)GDSVIV	(R)G D/S/V/I|V V L R N/P L I A\G K(-)		168.72	551.0007	1650.99	-0.0026	-1.6	8.75	6144.3	10.23	HUMAN	K7EJB5	Small nuclear ribonucleoprotein Sm D2
2358	dirMS_041712_NAR_120mM_minus.13514.13514.3	3	15.75	2	9.83E+05		(R)AQKDEE	(R)A Q/K/D E E K|M E/I/Q\E I Q\L K(E)		128.13	654.0058	1960.006	-0.0027	-1.4	4.58	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
2359	dirMS_041712_NAR_30mM_minus2.17161.17161.2	2	15.75	0	2.76E+05		(R)LLNTFLE	(R)L/L|N/T/F L E/R(L)		146.9	503.2871	1005.573	-0.0058	-5.8	6	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
2360	dirMS_041712_NAR_60mM_minus.10632.10662.3	3	15.75	1	1.21E+05		(R)VLTVIN	(R)V/L|T/V/I/N Q T Q K/E/N L R(K)		119.27	552.6501	1655.944	-0.0081	-4.9	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
2361	dirMS_041712_NAR_60mM_minus.7060.7224.3	3	15.75	1	3.04E+05		(R)ELFESST	(R)E L|F/E/S S/T N N N K D/T/K(Q)		98.72	542.9247	1626.761	-0.001	-0.6	4.68	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
2362	dirMS_041712_NAR_120mM_plus.5514.5553.3	3	15.75	1	6.20E+05		(R)GGGYG	(R)G G|G|Y/G/G D R\G/G G Y/G G D/R(G)		82.03	486.5431	1457.615	-0.0005	-0.3	5.96	21563.9	10.01	HUMAN	K7EKB2	TATA-binding protein-associated factor 2N (Fragment)
2363	dirMS_041712_NAR_30mM_plus2.12278.12542.2	2	15.75	0	1.00E+06		(R)SGYLLP	(R)S G/Y|L|L|P D/T/K(A)		117.57	497.2641	993.525	-0.0042	-4.2	5.55	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
2364	dirMS_041712_NAR_40mM_plus2.8220.8270.2	2	15.75	0	2.86E+05		(R)FGSGM	(R)F/G|S/G/M N/M|G/R(I)		109.45	478.706	956.408	-0.003	-3.1	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
2365	dirMS_041712_NAR_60mM_plus.11936.11949.3	3	15.75	1	3.80E+05		(K)VTVAGL	(K)V/T|V/A/G/L/A/G K/D/P V Q C S R(D)	C:Carbamidomethylation	119.65	553.2934	1657.869	-0.0034	-2	8.72	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
2366	dirMS_041712_NAR_60mM_plus.16486.16486.2	2	15.75	0	6.93E+05		(R)EHALLA	(R)E/H|A/L|L|A Y/T/L G V K(Q)		143.63	657.8735	1314.742	-0.0019	-1.4	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
2367	dirMS_041712_NAR_20mM_minus.11225.11468.2	2	15.74	0	1.17E+07	M148m	(R)DLTDYL	(R)D L|T|D|Y/L/m/K(I)	m:Oxidized methionine	162.17	507.7443	998.486	15.995	0.1	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
2368	dirMS_041712_NAR_30mM_minus2.14569.14665.2	2	15.74	0	2.99E+05		(R)SLSAIYL	(R)S L|S|A|I/Y/L/E/K(L)		133.4	512.2885	1023.572	-0.0024	-2.3	5.72	533778	5.74	HUMAN	Q15149	Plectin
2369	dirMS_041712_NAR_50mM_minus2.13261.13378.3	3	15.74	1	5.24E+05		(K)ATLPSP	(K)A/T|L/P/S/P D K L/P G F/K(M)		144.18	457.5912	1370.768	-0.0088	-6.4	8.64	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
2370	dirMS_041712_NAR_60mM_minus.7691.7691.3	3	15.74	1	6.25E+05		(K)IQDKEG	(K)I Q D K E/G I|P/P/D/Q Q/R(L)		102.15	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
2371	dirMS_041712_NAR_60mM_minus.8289.8354.3	3	15.74	1	2.41E+05		(K)MIYASS	(K)M/I/Y/A/S/S K D/A I/K(K)		106.4	409.5576	1226.645	0.0133	10.9	8.26	22956	8.8	HUMAN	E9PK25	Cofilin-1
2372	dirMS_041712_NAR_20mM_plus.10801.10801.2	2	15.74	0	8.63E+04		(R)FLEQQN	(R)F L|E\Q/Q N Q/V/L|Q/T\K(W)		146.73	738.3942	1475.785	-0.0041	-2.8	6	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
2373	dirMS_041712_NAR_20mM_plus.17535.17535.2	2	15.74	0	2.22E+05		(K)LLYAFAE	(K)L L|Y/A/F A E/A\T V/P K(V)		192.97	661.8712	1322.736	-0.0003	-0.3	6	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
2374	dirMS_041712_NAR_30mM_plus2.6659.6659.2	2	15.74	0	2.92E+05		(R)EAGEQ	(R)E\A|G|E/Q\G D/I|E/P R(R)		89.77	600.7772	1200.549	-0.002	-1.7	4	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
2375	dirMS_041712_NAR_30mM_plus2.9303.9891.2	2	15.74	0	9.85E+06		(R)LASYLD	(R)L/A|S|Y L/D|R(V)		104.55	419.2286	837.447	0.0034	4.1	5.83	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2376	dirMS_041712_NAR_50mM_plus2.8689.8689.3	3	15.74	0	1.95E+04		(R)TVAIYSE	(R)T V|A|I/Y S E Q/D T/G Q/M/H R(Q)		113.87	579.2737	1735.807	-0.0003	-0.2	5.29	58266.4	9.46	HUMAN	B4DN00	Pyruvate carboxylase, mitochondrial
2377	dirMS_041712_NAR_60mM_plus.15640.15683.3	3	15.74	1	3.43E+06		(R)TEMENE	(R)T|E|M/E N E|F/V/L/I/K K(D)		138.23	494.2622	1480.772	0.0005	0.3	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
2378	dirMS_041712_NAR_60mM_plus.20147.20161.3	3	15.74	0	2.10E+06		(K)VHLVGI	(K)V H\L\V G|I/D|I/F/T/G K(K)		166.1	433.5839	1298.747	-0.0096	-7.4	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
2379	dirMS_041712_NAR_120mM_plus.10363.10740.3	3	15.73	1	1.62E+06		(R)FLRENP	(R)F L/R E N|P|Y|Y/D/S|R(V)		108.55	487.239	1459.697	0.006	4.1	6.07	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
2380	dirMS_041712_NAR_20mM_plus.14479.14479.2	2	15.73	0	6.07E+05	M185m	(K)LAVNm	(K)L/A/V|N m/V|P F\P R(L)	m:Oxidized methionine	170.72	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
2381	dirMS_041712_NAR_20mM_plus.16203.16496.3	3	15.73	0	1.17E+06	M221m	(R)ALTVPE	(R)A L\T|V P E/L/T/Q/Q/m/F D/A K(N)	m:Oxidized methionine	184.35	569.9583	1691.867	15.9931	-1.1	4.37	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
2382	dirMS_041712_NAR_20mM_plus.16477.16477.2	2	15.73	0	4.51E+05		(K)LGGSAV	(K)L/G\G S A\V|I/S L E/G K|P L(-)		185.52	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
2383	dirMS_041712_NAR_50mM_plus2.13332.13332.3	3	15.73	0	4.70E+05		(K)QLTEED	(K)Q L/T/E/E/D/G V/H S V/I E E N I K(C)		138.32	647.3311	1939.961	0.018	9.3	4.25	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
2384	dirMS_041712_NAR_50mM_plus2.18603.18603.3	3	15.73	1	5.52E+05		(K)NAAGAL	(K)N A|A|G/A/L/D L/L K/E L/K(N)		165.92	452.601	1355.789	-0.0008	-0.6	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
2385	dirMS_041712_NAR_120mM_minus.19502.19502.3	3	15.72	1	3.72E+05		(K)NLRDID	(K)N L R\D I D/E|V|S/S/L L R(T)		161.42	510.614	1529.828	-0.0007	-0.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
2386	dirMS_041712_NAR_50mM_minus2.16891.16891.3	3	15.72	1	2.84E+05		(R)SELELTL	(R)S E|L/E L T/L/G K L E Q V R(S)		163.78	538.9725	1614.906	-0.0032	-2	4.78	533778	5.74	HUMAN	Q15149	Plectin
2387	dirMS_041712_NAR_20mM_plus.15400.15400.2	2	15.72	0	7.60E+05		(K)LLCGLLA	(K)L L/C/G L L/A E R(L)	C:Carbamidomethylation	177.75	522.7971	1044.587	-0.0001	-0.1	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
2388	dirMS_041712_NAR_30mM_plus2.16147.16147.2	2	15.72	0	7.42E+05		(R)GALQNI	(R)G A L\Q/N|I|I\P A S/T/G A A K(A)		137.53	706.3979	1411.79	-0.0018	-1.3	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
2389	dirMS_041712_NAR_30mM_plus2.6277.6277.2	2	15.72	0	3.51E+05		(K)NQCTQ	(K)N Q|C|T/Q V/V/Q E R(E)	C:Carbamidomethylation	87	631.3039	1261.595	0.0052	4.1	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
2390	dirMS_041712_NAR_60mM_plus.17743.17743.3	3	15.72	1	2.42E+05		(K)IIVDELK	(K)I/I|V/D E/L K Q|E/V\I S\T S S K(A)		149.47	597.0009	1788.995	-0.0072	-4	4.68	30149.5	5.96	HUMAN	D6RAC2	Guanine nucleotide-binding protein subunit beta-2-like 1
2391	dirMS_041712_NAR_30mM_minus2.9610.9610.2	2	15.71	0	8.22E+05		(K)EASSPF	(K)E A|E/S/S/P F V/E R(L)		107.22	575.7705	1150.537	-0.0038	-3.3	4.25	92752.5	4.76	HUMAN	P14625	Endoplasmin
2392	dirMS_041712_NAR_40mM_minus2.11984.11984.3	3	15.71	1	1.80E+05		(K)AGTQIE	(K)A/G T|Q/I/E N I/D E D/F R D/G L/K(L)		153.87	640.9843	1920.93	0.0086	4.5	4.11	59872.5	4.85	HUMAN	F5GXS2	Alpha-actinin-4
2393	dirMS_041712_NAR_60mM_minus.11484.11630.3	3	15.71	0	7.51E+05		(K)TKPYIQ	(K)T K|P Y\I\Q\V/D|I/G/G G Q/T K(T)		124.67	535.6216	1604.864	-0.014	-8.7	8.17	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein

2394	dirMS_041712_NAR_60mM_minus.6102.6102.3	3	15.71	1	1.53E+06		(K)DSYVGD	(K)D S/Y|V/G D/E/A Q S K/R(G)		90.97	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
2395	dirMS_041712_NAR_30mM_plus2.8326.8885.2	2	15.71	0	2.01E+06		(K)TAVCDIF	(K)T A|V|C/D/I|P|P/R(G)	C:Carbamidomethylation	100.2	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
2396	dirMS_041712_NAR_50mM_plus2.14115.14115.3	3	15.71	1	7.81E+05		(R)MSMKE	(R)M/S/M K E V D E Q/M/L N|V|Q N K(N)		142.88	641.9706	1923.897	0	0	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
2397	dirMS_041712_NAR_50mM_plus2.16417.16417.3	3	15.71	1	2.02E+06		(K)QGGLGF	(K)Q G G L/G/P M/N\I|P L V/S D/P K R(T)		154.68	593.6536	1778.958	-0.0119	-6.7	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
2398	dirMS_041712_NAR_60mM_plus.18266.18266.3	3	15.71	1	9.23E+05		(K)EVNKFQ	(K)E V N K F Q\M|A|Y/S/N/L L R(A)		152.83	571.6293	1712.879	-0.0055	-3.2	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
2399	dirMS_041712_NAR_120mM_minus.8998.8998.3	3	15.7	0	9.66E+05		(K)HTGPNS	(K)H T G P N S P D\T|A/N/D G F V/R(L)		103.18	562.2599	1684.767	-0.0022	-1.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
2400	dirMS_041712_NAR_30mM_minus2.10500.10609.2	2	15.7	0	3.43E+05		(K)SAVGFD	(K)S A|V|G|F/D/Y/Q/G K(T)		111.15	536.2608	1071.511	0.0038	3.5	5.55	25153.2	6.6	HUMAN	H7C314	Src substrate cortactin (Fragment)
2401	dirMS_041712_NAR_30mM_minus2.18138.18138.2	2	15.7	0	2.25E+05		(K)EGMNIV	(K)E G\M/N|I/V E/A/M E R(F)		152.4	639.7955	1278.582	0.002	1.6	4.25	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
2402	dirMS_041712_NAR_50mM_minus2.15570.15570.3	3	15.7	0	2.05E+05		(R)QVVQGI	(R)Q V\V/Q|G\L\L/S\E T Y/L/E A H R(I)		156.73	614.9953	1842.971	0.0005	0.3	5.4	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
2403	dirMS_041712_NAR_20mM_plus.18814.18930.2	2	15.7	0	1.09E+06		(K)EIIDLVL	(K)E I|I/D|L/V/L/D/R(I)		202.28	543.313	1085.62	-0.0014	-1.3	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
2404	dirMS_041712_NAR_30mM_plus2.16266.16266.2	2	15.7	0	2.25E+05		(K)IIIPEIQK	(K)I I|I/P/E/I/Q/K(V)		137.62	477.3031	953.603	-0.0041	-4.3	6	86098.8	5.31	HUMAN	B4DUC5	Exportin-2
2405	dirMS_041712_NAR_30mM_plus2.16302.16302.2	2	15.7	0	1.18E+06		(R)FGLNVS	(R)F G|L/N/V/S/S I S/R(K)		139.02	540.3016	1079.584	0.0115	10.7	9.75	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
2406	dirMS_041712_NAR_30mM_plus2.16766.16793.2	2	15.7	0	4.37E+04		(R)AALQELI	(R)A/A/L/Q/E/L L|S/K(G)		140.85	486.7894	972.572	-0.0009	-0.9	6.05	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
2407	dirMS_041712_NAR_60mM_plus.16698.16800.3	3	15.7	1	5.39E+05		(K)AKLEQL	(K)A K L E Q\L|F|Q/D E\V/A/K(A)		144.23	506.9426	1518.816	-0.003	-2	4.68	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
2408	dirMS_041712_NAR_60mM_plus.8313.8313.3	3	15.7	1	7.22E+05		(R)DSFDGR	(R)D S|F/D/G R G P/P G P\E/S Q S R(A)		101.7	563.5923	1688.762	0	0	4.56	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
2409	dirMS_041712_NAR_60mM_minus.14874.14874.3	3	15.69	1	2.10E+05		(K)IDSRLEQ	(K)I/D/S R L E Q/Y\T|S/A/I/E G T K(S)		142.88	604.3095	1810.918	-0.0042	-2.3	4.68	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
2410	dirMS_041712_NAR_30mM_plus2.18588.18588.2	2	15.69	0	1.90E+05		(-)SDVLELT	(-)S D V/L/E|L/T/D D\N F/E S R(I)		150.83	820.3752	1639.745	-0.0015	-0.9	3.77	13747.3	6.8	HUMAN	H7BZJ3	Thioredoxin (Fragment)
2411	dirMS_041712_NAR_30mM_plus2.7276.7291.2	2	15.69	0	1.84E+05		(K)AAAAAA	(K)A A|A|A|A|A|A L Q/A K(S)		92.88	478.7844	956.552	0.0092	9.6	8.8	37884.5	11.27	HUMAN	H3BM89	60S ribosomal protein L4
2412	dirMS_041712_NAR_50mM_plus2.11443.11443.3	3	15.69	1	2.61E+05		(K)CATITPD	(K)C/A|T I/T/P D/E A R V E E/F/K(L)	C:Carbamidomethylation	127.75	589.2842	1765.843	-0.0045	-2.5	4.41	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
2413	dirMS_041712_NAR_40mM_minus2.13831.13831.3	3	15.68	0	1.24E+05		(R)VAAGLP	(R)V A|A/G L|P P I L V H/T D A A Q A/L G K(Q)		165.12	648.0401	1942.112	-0.0063	-3.2	6.71	17974.2	4.97	HUMAN	C9JNL5	Selenocysteine lyase (Fragment)
2414	dirMS_041712_NAR_120mM_plus.4091.4306.3	3	15.68	1	2.05E+06	M54m	(K)SLDEmE	(K)S/L|D/E/m/E/K/Q/Q R(E)	m:Oxidized methionine	70.2	427.2032	1263.6	15.9953	0.3	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
2415	dirMS_041712_NAR_50mM_plus2.15514.15514.3	3	15.68	0	1.51E+06		(R)LASTLVH	(R)L A|S/T L V/H\L|G E Y Q A\A/V/D G A R(K)		149.68	657.6802	1971.029	-0.0034	-1.7	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
2416	dirMS_041712_NAR_50mM_minus2.10984.10985.3	3	15.67	1	2.77E+06	M72m	(R)TEmENE	(R)T|E|m E N E\F|V/L/I/K K(D)	m:Oxidized methionine	129.93	499.5937	1480.772	15.995	0	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
2417	dirMS_041712_NAR_20mM_plus.17541.17558.2	2	15.67	0	3.08E+05		(K)SYELPD	(K)S Y E/L|P D\G Q/V|I|T/I/G N E R(F)		193.17	895.9492	1790.892	-0.0008	-0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
2418	dirMS_041712_NAR_40mM_plus2.13928.13946.3	3	15.67	0	3.53E+05		(K)LVEALC	(K)L/V|E|A/L/C A E/H Q I N L I/K(V)	C:Carbamidomethylation	148.62	584.3205	1750.952	-0.0051	-2.9	5.4	14914.1	6.84	HUMAN	P25398	40S ribosomal protein S12
2419	dirMS_041712_NAR_50mM_plus2.15734.15734.3	3	15.67	0	1.18E+05		(K)NLDYVA	(K)N L|D|Y V/A/T/S I/H E A V/T K(I)		150.87	554.2887	1660.854	-0.0025	-1.5	5.32	44431.6	8.52	HUMAN	B7Z7E9	Aspartate aminotransferase
2420	dirMS_041712_NAR_60mM_plus.11804.11804.3	3	15.67	1	3.83E+05		(R)LAEVEA	(R)L/A|E/V/E/A A L E|K Q R(Q)		118.88	452.9164	1356.748	-0.0135	-10	4.79	533778	5.74	HUMAN	Q15149	Plectin
2421	dirMS_041712_NAR_120mM_minus.13545.13579.3	3	15.66	1	2.25E+05		(R)VIDRELY	(R)V/I/D/R E L|Y|Q/Q/L Q R(G)		128.15	520.955	1560.849	0.0012	0.8	6.04	533778	5.74	HUMAN	Q15149	Plectin
2422	dirMS_041712_NAR_20mM_minus.8320.8320.2	2	15.66	0	1.25E+05		(K)VTADVI	(K)V/T|A/D\V/I/N A A E/K(L)		132.47	565.8065	1130.605	0.0005	0.5	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
2423	dirMS_041712_NAR_50mM_minus2.17714.17770.3	3	15.66	1	3.97E+05		(R)LKLPSIPI	(R)L K L/P S I|P\L\V|P V/S A Q K(R)		169.73	530.669	1589.999	-0.0064	-4.1	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
2424	dirMS_041712_NAR_60mM_minus.14913.14913.3	3	15.66	0	4.33E+05		(K)WIGLDL	(K)W\I|G L D/L/S/N/G K/P R(D)		143.53	452.5849	1355.743	-0.0029	-2.1	8.75	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
2425	dirMS_041712_NAR_60mM_minus.15742.15742.3	3	15.66	1	1.58E+06		(R)KDDPVT	(R)K D D\P\V\T\N\L N/N/A/F E V/A E K(Y)		147.43	635.317	1903.94	-0.0032	-1.7	4.32	21601.4	6.27	HUMAN	K7EJH8	Alpha-actinin-4 (Fragment)
2426	dirMS_041712_NAR_60mM_minus.9452.9452.3	3	15.66	1	2.04E+05	M118m	(R)LSFDKD	(R)L/S/F/D K/D A m/V A R(A)	m:Oxidized methionine	112.4	423.5497	1252.635	15.9991	3.3	5.96	35556.4	9.3	HUMAN	F2Z393	Transaldolase
2427	dirMS_041712_NAR_120mM_plus.12464.12908.3	3	15.66	1	1.16E+06		(K)LFNLSKE	(K)L/F|N/L/S/K/E D D/V/R(Q)		119.35	445.9007	1335.69	-0.0028	-2.1	4.56	25082	11.29	HUMAN	A2A3R5	40S ribosomal protein S6
2428	dirMS_041712_NAR_120mM_plus.21512.21533.4	4	15.66	2	4.53E+05	M145m	(R)RGVmLA	(R)R G V\m\L|A|V D/A V/I/A E L K/K(Q)	m:Oxidized methionine	166.22	433.0059	1713.009	15.9926	-1.3	8.59	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
2429	dirMS_041712_NAR_30mM_plus2.19472.19874.2	2	15.66	0	8.20E+05		(-)MDELQL	(-)M/D|E|L|Q/L/F/R(G)		156.63	526.2726	1051.524	0.0138	13.2	4.37	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
2430	dirMS_041712_NAR_30mM_plus2.19956.19956.2	2	15.66	0	8.31E+04		(R)FEELTNL	(R)F/E|E|L/T N L\I R(T)		158.62	567.8152	1134.615	0.0078	6.9	4.53	106155.7	5.45	HUMAN	B5ME19	Eukaryotic translation initiation factor 3 subunit C
2431	dirMS_041712_NAR_50mM_plus2.5963.5963.3	3	15.66	0	3.79E+04		(R)ITAAQH	(R)I/T|A/A Q H\S V T G S A V S K(T)		95.48	486.2644	1456.775	0.0032	2.2	8.76	5282	9.4	HUMAN	E9PJT1	Phosphatidylinositol-binding clathrin assembly protein
2432	dirMS_041712_NAR_50mM_plus2.7946.7946.3	3	15.66	1	5.05E+04		(K)ELQAAG	(K)E L/Q|A/A G/K S/P E/D/L E R(L)		108.27	514.9321	1542.776	0.0059	3.8	4.41	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
2433	dirMS_041712_NAR_50mM_plus2.9304.9304.3	3	15.66	1	2.75E+05		(R)TNAENE	(R)T|N/A/E N E F/V/T I/K K(D)		115.83	465.2518	1393.732	0.0087	6.2	5.81	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
2434	dirMS_041712_NAR_50mM_minus2.13882.13882.3	3	15.65	0	3.00E+04		(K)TGEEIFG	(K)T/G|E/E|I/F G T I/G M R P N A K(N)		146.93	574.2947	1720.869	0.0009	0.5	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
2435	dirMS_041712_NAR_120mM_plus.7268.7310.3	3	15.65	1	5.17E+05		(K)SKAEAE	(K)S K\A E A\E|S|L/Y/Q/S/K(Y)		91.33	447.5614	1340.669	0.0004	0.3	5.86	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
2436	dirMS_041712_NAR_60mM_plus.8292.8332.3	3	15.65	1	1.52E+06		(K)MIYASS	(K)M/I/Y/A/S/S K/D A I/K(K)		101.88	409.553	1226.645	-0.0005	-0.4	8.26	22956	8.8	HUMAN	E9PK25	Cofilin-1
2437	dirMS_041712_NAR_30mM_minus2.12330.12623.2	2	15.64	0	1.76E+06		(R)LQAEIE	(R)L/Q|A|E/I E/G L/K(G)		121.93	500.7842	1000.567	-0.0062	-6.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
2438	dirMS_041712_NAR_60mM_minus.6666.6884.3	3	15.64	1	4.60E+05		(R)LQSIGTE	(R)L/Q|S|I/G T/E N T/E E/N R/R(F)		96.57	549.6071	1646.809	-0.0025	-1.5	4.79	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
2439	dirMS_041712_NAR_120mM_plus.20656.20736.3	3	15.64	0	3.63E+05		(K)VHLVGI	(K)V H\L\V\G\I|D|I/F/T/G K(K)		161.62	433.5874	1298.747	0.0009	0.7	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
2440	dirMS_041712_NAR_50mM_plus2.11394.11394.3	3	15.64	1	9.91E+05		(K)VIQEIVD	(K)V I/Q/E/I V D K/S G V V R(V)		127.82	481.2834	1441.837	-0.0017	-1.1	6.04	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
2441	dirMS_041712_NAR_50mM_minus2.17715.17715.3	3	15.63	0	6.40E+04		(R)IHFPLAT	(R)I H F P L\A\T\Y A/P/V/I S A E K(A)		169.52	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
2442	dirMS_041712_NAR_50mM_minus2.9056.9056.3	3	15.63	0	7.04E+04		(R)EANALA	(R)E A/N A/L/A/A G H/P A Q A/V/A I N A R(L)		119.77	615.6611	1844.973	-0.0038	-2.1	6.85	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
2443	dirMS_041712_NAR_60mM_minus.9980.10285.3	3	15.63	1	6.51E+05		(K)VIADNV	(K)V/I|A/D/N V/K D W S/K(V)		116.02	425.5679	1274.674	0.0152	11.9	5.93	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
2444	dirMS_041712_NAR_120mM_plus.7475.7688.3	3	15.63	1	2.02E+06	M281m	(R)SRAEAE	(R)S R\A E\A\E|S/m/Y Q/I/K(Y)	m:Oxidized methionine	93.02	476.8977	1412.684	15.9947	-0.1	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
2445	dirMS_041712_NAR_20mM_plus.15764.15764.2	2	15.63	0	2.05E+05		(K)TITLEVEI	(K)T I/T|L E/V/E|P S D T I/E N V K(A)		179.13	894.4658	1787.927	-0.003	-1.7	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
2446	dirMS_041712_NAR_30mM_plus2.18017.18017.2	2	15.63	0	6.21E+05		(R)EQLAIAE	(R)E Q L/A/I/A E/F A R(S)		148.23	574.3083	1147.611	-0.0013	-1.1	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
2447	dirMS_041712_NAR_30mM_plus2.6153.6169.2	2	15.63	0	2.13E+05		(R)ETQSQL	(R)E T|Q/S/Q/L/E/T/E/R(S)		86.58	610.8002	1220.575	0.0178	14.6	4.25	334221.3	6.44	HUMAN	P15924	Desmoplakin
2448	dirMS_041712_NAR_30mM_plus2.7246.7287.2	2	15.63	0	1.31E+06		(R)VTDALN	(R)V/T|D|A|L/N/A T/R(A)		92.9	480.759	960.511	-0.0002	-0.2	5.81	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
2449	dirMS_041712_NAR_30mM_plus2.9598.9804.2	2	15.63	0	1.23E+06		(R)FGSGM	(R)F/G|S|G/M N/M|G R(I)		104.72	478.7075	956.408	0	0	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
2450	dirMS_041712_NAR_50mM_plus2.10972.10972.3	3	15.63	1	3.72E+05		(K)LAEQAE	(K)L A|E/Q/A E R Y D|D M/A|A C M K(S)	C:Carbamidomethylation	125.2	634.6126	1901.819	0.0042	2.2	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
2451	dirMS_041712_NAR_120mM_minus.10006.10091.2	2	15.62	0	5.19E+05		(K)HIYYITG	(K)H|I|Y|Y|I|T\G E|T/K(D)		109.03	612.8167	1224.626	0.0002	0.2	6.75	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
2452	dirMS_041712_NAR_120mM_minus.13577.13597.4	4	15.62	2	8.32E+05	M100m	(K)KQGGLG	(K)K\Q G G L\G P\m/N\I/P L/V/S D/P K R(T)	m:Oxidized methionine	128.55	481.5173	1907.053	15.9942	-0.3	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
2453	dirMS_041712_NAR_30mM_minus2.10408.10408.2	2	15.62	0	1.88E+06		(K)TAVCDIF	(K)T/A|V/C D/I|P\P R(G)	C:Carbamidomethylation	110.4	514.7641	1028.519	0.0016	1.5	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
2454	dirMS_041712_NAR_60mM_minus.11174.11479.3	3	15.62	1	3.02E+06		(R)MQKEIT	(R)M Q\K E I T/A|L|A/P S/T M/K(I)		123.32	516.9421	1548.812	-0.0007	-0.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
2455	dirMS_041712_NAR_60mM_minus.8508.8508.3	3	15.62	1	5.78E+04		(K)GAVAED	(K)G A/V|A/E|D G D E L R T E P E/A K(K)		107.4	596.2923	1786.845	0.017	9.5	4.08	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
2456	dirMS_041712_NAR_30mM_plus2.9877.9916.2	2	15.62	0	6.65E+05		(K)NNTQVL	(K)N N|T/Q|V|L|I/N\C/R(N)	C:Carbamidomethylation	105.42	616.3143	1231.621	0.0001	0.1	9.75	8948	9.6	HUMAN	K7ERG4	Small nuclear ribonucleoprotein Sm D2
2457	dirMS_041712_NAR_50mM_plus2.11446.11483.3	3	15.62	1	3.27E+05		(K)ELALQP	(K)E/L/A L Q/P/K/D D I/V/D/R(A)		128.03	504.606	1511.806	-0.003	-2	4.23	83905.8	6.62	HUMAN	P41250	Glycine--tRNA ligase
2458	dirMS_041712_NAR_60mM_plus.12936.12936.3	3	15.62	0	1.26E+06		(K)VNGRPL	(K)V/N/G R P L E/M|I/E/P/R(T)		124.65	470.9225	1410.752	0.0008	0.5	6.11	16559.1	10.36	HUMAN	P62249	40S ribosomal protein S16
2459	dirMS_041712_NAR_30mM_minus2.10551.10614.2	2	15.61	0	1.33E+06		(R)QLYEEEI	(R)Q L|Y/E/E/E/I/R(E)		111.58	540.2725	1079.537	0.001	0.9	4.25	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
2460	dirMS_041712_NAR_40mM_minus2.14870.14870.3	3	15.61	0	1.16E+06		(K)ISSIQSIV	(K)I S\S I/Q/S I/V/P A L E/I/A N/A H R(K)		172.13	640.3618	1919.071	0	0	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
2461	dirMS_041712_NAR_60mM_minus.11082.11082.3	3	15.61	1	6.02E+05		(K)IQVLQQ	(K)I Q|V/L/Q/Q Q A D D A E E/R A E R(L)		121.07	666.9983	1998.984	-0.0036	-1.8	4.18	26611.3	4.47	HUMAN	A6NL28	Putative tropomyosin alpha-3 chain-like protein
2462	dirMS_041712_NAR_60mM_minus.18417.18460.3	3	15.61	1	3.37E+05		(R)GFKDQI	(R)G F\K D\Q\I|Y/D/I/F/Q/K(L)		164.1	501.2584	1501.769	-0.0079	-5.3	5.96	26945.8	8.07	HUMAN	J3KSZ0	Eukaryotic initiation factor 4A-I (Fragment)
2463	dirMS_041712_NAR_120mM_plus.17297.17297.3	3	15.61	2	9.50E+05		(R)NLKASLE	(R)N L/K/A/S L/E N S L R E V E|A R(Y)		143.52	610.332	1828.988	-0.0061	-3.3	6.23	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2464	dirMS_041712_NAR_30mM_plus2.11962.11962.2	2	15.61	0	8.69E+04		(K)VGDPQE	(K)V/G/D|P Q/E|L/N G I T R(A)		115.82	649.8373	1298.67	-0.0026	-2	4.37	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
2465	dirMS_041712_NAR_30mM_plus2.19784.20117.2	2	15.61	0	5.28E+05		(K)MAILQI	(K)M/A|I|L/Q/I M/K(E)		158.22	474.2739	947.542	-0.0011	-1.2	8.5	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
2466	dirMS_041712_NAR_30mM_plus2.8558.8558.2	2	15.61	0	8.96E+05		(R)LGLGEG.	(R)L/G/L/G E G/A E E|K(S)		99.07	501.7639	1002.51	0.0103	10.3	4.25	40096.8	9.24	HUMAN	C9JW69	Regulator of chromosome condensation (Fragment)
2467	dirMS_041712_NAR_40mM_plus2.11024.11024.3	3	15.61	1	6.32E+04		(K)VAVVAG	(K)V A|V/V/A/G/Y G D V/G/K G C A Q A L R(G)	C:Carbamidomethylation	131.05	630.9981	1890.985	-0.0057	-3	8.56	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
2468	dirMS_041712_NAR_40mM_plus2.11226.11226.3	3	15.61	0	1.03E+05		(R)VLVASS	(R)V L|V/A/S/S V V A G E S Q K P E/L K(A)		132.08	614.3443	1841.038	-0.0195	-10.6	6.11	61441.6	5.93	HUMAN	G8JLE9	Fragile X mental retardation protein 1
2469	dirMS_041712_NAR_120mM_minus.11964.11974.3	3	15.6	0	3.85E+05		(R)HSSLAG	(R)H S\S L\A G|C|Q|I/I/N\Y R(T)	C:Carbamidomethylation	119.48	506.9192	1518.748	-0.0051	-3.4	8.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
2470	dirMS_041712_NAR_120mM_minus.8225.8305.3	3	15.6	1	5.91E+05		(K)SSGGREI	(K)S/S|G G R E D\L\E|S/S/G/L/Q\R(R)		99.45	526.5882	1577.751	-0.0014	-0.9	4.68	11625.5	8.01	HUMAN	B8ZZT7	Hematological and neurological-expressed 1 protein
2471	dirMS_041712_NAR_60mM_minus.15075.15075.3	3	15.6	0	2.16E+05		(K)MLDAED	(K)M/L/D/A E D/I/V/N T/A R P D/E K(A)		143.72	606.2986	1816.875	0.0067	3.7	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
2472	dirMS_041712_NAR_30mM_plus2.13839.13903.2	2	15.6	0	5.28E+05		(K)YLVLDEA	(K)Y/L|V|L/D/E/A D/R(M)		125.72	547.2819	1093.552	0.0041	3.8	4.03	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
2473	dirMS_041712_NAR_30mM_plus2.21018.21018.2	2	15.6	0	2.03E+05		(R)GVVQEL	(R)G V/V/Q/E L|Q/Q A I/S\K(L)		165.2	650.3632	1299.727	-0.0076	-5.8	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
2474	dirMS_041712_NAR_50mM_plus2.15068.15068.3	3	15.6	0	4.74E+05		(K)TTISVAH	(K)T T|I/S V/A/H L\L A A/R(Q)		146.48	418.2499	1252.737	-0.002	-1.6	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
2475	dirMS_041712_NAR_30mM_minus2.16476.16476.2	2	15.59	0	2.61E+05		(R)ASLEAAI	(R)A S L E/A\A/I/A/D/A E Q/R(G)		143.62	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2476	dirMS_041712_NAR_30mM_minus2.19142.19142.2	2	15.59	0	2.58E+05		(K)SYELPD	(K)S Y\E|L/P/D G Q/V|I/T I G N E R(F)		158.9	895.9492	1790.892	-0.0008	-0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
2477	dirMS_041712_NAR_50mM_minus2.8682.8714.3	3	15.59	1	4.19E+04	M88m	(K)DVDEAY	(K)D V|D/E/A|Y/m N K V/E L E/S R(L)	m:Oxidized methionine	117.5	605.2817	1797.832	15.9982	1.8	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
2478	dirMS_041712_NAR_20mM_plus.6866.6866.2	2	15.59	0	4.25E+05	M132m	(R)DmVGIA	(R)D m|V/G/I|A/Q T\G S G K(T)	m:Oxidized methionine	112.83	590.2864	1163.573	15.993	-1.6	5.84	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
2479	dirMS_041712_NAR_120mM_minus.5618.5618.3	3	15.58	1	1.23E+05		(K)CDSSPD	(K)C D/S S/P D/S/A E D/V R K(V)	C:Carbamidomethylation	83.98	489.2132	1465.622	0.0027	1.8	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
2480	dirMS_041712_NAR_120mM_minus.8432.8515.3	3	15.58	1	4.37E+05		(K)NGRVEII	(K)N G R V E\I|I|A|N/D/Q/G N/R(I)		100.53	519.269	1555.794	-0.0011	-0.7	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
2481	dirMS_041712_NAR_30mM_minus2.10094.10291.2	2	15.58	0	6.09E+05	M239m	(K)EITALAP	(K)E I|T|A|L/A|P/S T m K(I)	m:Oxidized methionine	109.48	589.3092	1161.618	15.9927	-1.8	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
2482	dirMS_041712_NAR_30mM_minus2.17946.18008.2	2	15.58	0	2.20E+05		(K)EGMNIV	(K)E G/M/N\I|V\E/A/M/E/R(F)		152.3	639.7955	1278.582	0.002	1.6	4.25	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
2483	dirMS_041712_NAR_50mM_minus2.13531.13531.3	3	15.58	0	3.38E+05		(K)MLDAED	(K)M/L|D|A/E|D\I/V N T A R P D E K(A)		145.72	606.2965	1816.875	0.0004	0.2	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
2484	dirMS_041712_NAR_60mM_minus.14267.14267.3	3	15.58	1	2.87E+05		(K)VFGPGIE	(K)V/F/G/P G/I E/G K D V F R(E)		139.95	474.2636	1420.758	0.0179	12.6	6.04	258215.9	5.48	HUMAN	E7EN95	Filamin-B
2485	dirMS_041712_NAR_60mM_minus.17868.18131.3	3	15.58	0	1.33E+06		(K)VSHLLGI	(K)V S H\L\L\G\I|N|V|T/D/F T R(G)		161.62	524.623	1571.854	0.0004	0.3	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
2486	dirMS_041712_NAR_20mM_plus.8364.8364.2	2	15.58	0	4.09E+04	M105m	(K)mADEA	(K)m A\D/E/A|V/C V/G P A/P T S K(S)	C:Carbamidomethylation m:Oxid	127.8	774.8589	1532.708	16.0022	4.7	4.37	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
2487	dirMS_041712_NAR_30mM_plus2.13358.13358.2	2	15.58	0	5.70E+05		(K)CPFTGN	(K)C/P/F|T/G/N V S I/R(G)	C:Carbamidomethylation	122.88	575.7876	1150.567	0.0006	0.5	9.75	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
2488	dirMS_041712_NAR_30mM_plus2.23513.23513.2	2	15.58	0	1.80E+05		(R)IAIYELLF	(R)I/A/I\Y/E\L|L F K(E)		190.25	555.3331	1109.661	-0.0016	-1.4	6	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
2489	dirMS_041712_NAR_30mM_plus2.6114.6114.2	2	15.58	0	8.14E+05		(R)NQGGY	(R)N/Q|G/G Y\G/G S/S S S S/S Y/G S G R(R)		86.18	847.8524	1694.7	-0.0026	-1.5	8.59	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
2490	dirMS_041712_NAR_30mM_plus2.9987.10063.2	2	15.58	0	3.63E+05		(R)GNIPTL	(R)G N|I|P/T/L/N/R(M)		105.65	442.7515	884.495	0.0009	1	9.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
2491	dirMS_041712_NAR_40mM_plus2.12896.12916.3	3	15.58	0	4.96E+05		(R)VAPDEH	(R)V/A|P D E H\P I L/L/T/E A/P L N/P K(I)		142.93	652.0252	1954.064	-0.0034	-1.7	4.65	42344.8	5.39	HUMAN	Q562R1	Beta-actin-like protein 2
2492	dirMS_041712_NAR_20mM_minus.7310.7310.2	2	15.57	0	3.99E+04		(K)AVTEQG	(K)A V/T E/Q G/A|E L|S/N E/E/R(N)		120.98	766.8612	1532.719	-0.0036	-2.3	4.09	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
2493	dirMS_041712_NAR_30mM_minus2.18228.18532.3	3	15.57	0	5.33E+05		(R)QAQEYE	(R)Q A\Q\E\Y|E|A|L/L/N I K(V)		154.7	473.9196	1419.748	-0.0036	-2.5	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2494	dirMS_041712_NAR_30mM_minus2.7922.8099.2	2	15.57	0	1.14E+06		(R)SLQAVP	(R)S/L|Q|A/V/P/G\A K(D)		97.65	435.7524	870.504	-0.0068	-7.8	8.47	266161	5.68	HUMAN	E9PPU0	Epiplakin
2495	dirMS_041712_NAR_60mM_minus.14783.14783.3	3	15.57	0	2.66E+05		(K)YYITIIDA	(K)Y Y/I/T I/I/D/A/P/G H R(D)		142.87	473.5815	1418.743	-0.0127	-9	6.74	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
2496	dirMS_041712_NAR_20mM_plus.10647.10647.2	2	15.57	0	7.50E+04		(K)TTTLSGT	(K)T T/T L/S/G/T A/P A A G V/V/P S R(V)		145.97	793.4284	1585.854	-0.0049	-3.1	9.41	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
2497	dirMS_041712_NAR_30mM_plus2.9952.9979.2	2	15.57	0	1.48E+05		(R)LTPEEIEI	(R)L/T|P/E/E/I E/R(M)		105.78	493.7641	986.515	0.0056	5.7	4.25	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
2498	dirMS_041712_NAR_30mM_minus2.6544.6544.2	2	15.56	0	4.22E+05		(K)VLEEEEC	(K)V/L|E/E/E E Q/R(R)		90.3	516.2552	1031.5	0.0027	2.7	4.09	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
2499	dirMS_041712_NAR_40mM_minus2.10966.11252.3	3	15.56	0	7.92E+05		(R)QVSASE	(R)Q V/S/A/S E L H/T/S/G I/L/G P E/T L R(D)		148.75	665.6822	1995.051	-0.0185	-9.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
2500	dirMS_041712_NAR_50mM_minus2.10945.11068.3	3	15.56	1	6.21E+05		(R)ISVYYNE	(R)I S|V/Y/Y/N E A/T/G G K Y V P R(A)		131.08	606.3119	1816.923	-0.0017	-0.9	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
2501	dirMS_041712_NAR_50mM_minus2.8925.8925.3	3	15.56	1	1.31E+05	M227m	(R)mQKEIT.	(R)m Q K E I T|A|L/A/P S T M K(I)	m:Oxidized methionine	119.48	522.2727	1548.812	15.9911	-2.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
2502	dirMS_041712_NAR_120mM_plus.17339.17613.3	3	15.56	1	6.08E+05		(R)RAPFDLI	(R)R A\P\F|D|L|F/E/N K(K)		144.5	412.8845	1236.637	0.0018	1.5	6.07	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta

2503	dirMS_041712_NAR_30mM_plus2.16665.17073.2	2	15.56	0	8.08E+05		(K)FSIEDLK	(K)F/S|I/E/D|L/K(A)		141.68	426.2291	851.451	0	0	4.37	13579.2	9.99	HUMAN	E9PPQ6	Thymocyte nuclear protein 1 (Fragment)
2504	dirMS_041712_NAR_30mM_plus2.7673.7804.2	2	15.56	0	1.67E+06		(K)VTLTSEE	(K)V/T|L|T/S/E E E/A R(L)		94.47	567.7813	1134.564	-0.0084	-7.4	4.25	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
2505	dirMS_041712_NAR_50mM_plus2.19277.19277.3	3	15.56	1	3.94E+05		(K)ILDVASL	(K)I/L|D|V/A/S L/E V L N E V N R R(S)		169.97	614.0109	1840.029	-0.0105	-5.7	4.68	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
2506	dirMS_041712_NAR_60mM_plus.6676.6741.3	3	15.56	1	4.94E+05		(K)IYEDGD	(K)I/Y|E/D/G D/D D/M/K/R(T)		93.68	452.8641	1356.574	0.0041	3	4.03	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
2507	dirMS_041712_NAR_60mM_plus.7475.7476.3	3	15.56	1	7.87E+06		(R)VITEEEK	(R)V/I/T/E E E/K N F/K(A)		97.9	412.8904	1236.647	0.0096	7.8	4.79	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
2508	dirMS_041712_NAR_60mM_minus.11995.12037.3	3	15.55	1	2.62E+05		(R)GLAGLG	(R)G L|A|G/L/G/D/V/A/E V R K(S)		126.95	428.9126	1284.727	-0.0038	-2.9	6.07	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
2509	dirMS_041712_NAR_50mM_plus2.19301.19324.3	3	15.55	0	3.59E+05		(-)MKPLVV	(-)M K P L V V|F|V|L|G/G/P G A G K(G)		169.73	523.9715	1569.919	-0.0186	-11.8	10	22450.2	5.44	HUMAN	P30085	UMP-CMP kinase
2510	dirMS_041712_NAR_50mM_plus2.9884.9884.3	3	15.55	1	1.04E+06		(K)LKGEAT	(K)L K G E A\T\V|S|F D/D/P/P S A K(A)		119.12	554.6155	1661.838	-0.0061	-3.7	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
2511	dirMS_041712_NAR_60mM_plus.11051.11099.3	3	15.55	1	9.67E+05		(R)KTEELEE	(R)K\T E E\L E|E|E/S/F/P E/R(S)		115.75	541.5897	1622.754	0.0001	0.1	4.2	108720.9	10.17	HUMAN	Q9Y2W1	Thyroid hormone receptor-associated protein 3
2512	dirMS_041712_NAR_60mM_plus.15044.15044.3	3	15.55	1	2.99E+04		(R)ELAFQIS	(R)E L/A/F/Q/I/S K E/Y E/R(F)		135.27	504.9258	1512.769	-0.0064	-4.3	4.79	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
2513	dirMS_041712_NAR_60mM_plus.7002.7017.3	3	15.55	1	2.95E+05		(R)DSGRGD	(R)D S\G R G D S\V|S|D|S/G S/D/A L R(S)		95	560.9181	1680.742	-0.0022	-1.3	4.14	50974.6	5.31	HUMAN	B5ME91	Programmed cell death protein 4
2514	dirMS_041712_NAR_120mM_minus.12012.12073.3	3	15.54	1	2.38E+06		(K)MKEIAE	(K)M/K E I A\E|A/Y/L/G/K(T)		119.63	418.2252	1252.661	0.0005	0.4	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
2515	dirMS_041712_NAR_20mM_minus.12366.12386.2	2	15.54	0	5.77E+05	M73m	(R)AVLVDL	(R)A V|L\V|D|L|E|P G T|m D S V R(S)	m:Oxidized methionine	172.48	809.4088	1601.82	15.99	-3	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
2516	dirMS_041712_NAR_30mM_minus2.10120.10187.2	2	15.54	0	5.79E+05		(K)TGTVSL	(K)T/G|T|V/S/L E/V/R(L)		109.52	481.2669	961.531	-0.0048	-5	5.66	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
2517	dirMS_041712_NAR_50mM_minus2.17775.17775.3	3	15.54	0	1.26E+05		(R)CRPDQL	(R)C R\P D Q\L T/G|L/S L/L/P L S E K(A)	C:Carbamidomethylation	170.07	643.0129	1927.032	-0.0076	-3.9	6.07	533778	5.74	HUMAN	Q15149	Plectin
2518	dirMS_041712_NAR_120mM_plus.17857.17857.3	3	15.54	0	7.30E+05		(R)HLLQAP	(R)H L|L Q\A|P V/D D A/Q E/I L/H\S R(F)		146.82	648.0088	1942.014	-0.0023	-1.2	5.21	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
2519	dirMS_041712_NAR_20mM_plus.18934.18934.2	2	15.54	0	2.17E+05		(R)IITLAGP	(R)I/I|T L/A/G/P T N A I F K(A)		201.03	679.9039	1358.804	-0.0037	-2.7	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
2520	dirMS_041712_NAR_30mM_plus2.18244.18512.2	2	15.54	0	2.76E+05		(R)TEMDW	(R)T/E|M/D/W/V/L/K(H)		149.6	511.2577	1021.502	0.0058	5.7	4.37	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
2521	dirMS_041712_NAR_40mM_plus2.13757.13757.3	3	15.54	1	3.43E+05		(R)QVFGEA	(R)Q V|F/G/E A T K Q/P G I T F I A A K(F)		147.45	636.0176	1906.043	-0.005	-2.6	8.59	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
2522	dirMS_041712_NAR_30mM_minus2.11322.11322.2	2	15.53	0	1.40E+05		(R)AATSPA	(R)A A|T\S/P/A L F N R(C)		115.4	524.2789	1047.558	-0.0076	-7.3	9.79	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
2523	dirMS_041712_NAR_50mM_minus2.15934.16407.3	3	15.53	1	3.24E+07	M148m	(R)LDLAGR	(R)L/D|L|A/G R D L/T/D/Y L/m K(I)	m:Oxidized methionine	160.03	547.2838	1623.841	15.9958	0.5	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
2524	dirMS_041712_NAR_120mM_plus.7648.7817.3	3	15.53	0	5.16E+05		(R)SGSMDF	(R)S G|S|M/D/P/S G A/H P S V/R(Q)		94.08	462.218	1384.627	0.0121	8.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
2525	dirMS_041712_NAR_30mM_plus2.8262.8262.2	2	15.53	0	2.73E+05		(K)EIAENAL	(K)E I|A/E/N A/L/G/K(H)		96.92	472.755	944.505	-0.002	-2.1	4.53	36982.9	6.37	HUMAN	P31942	Heterogeneous nuclear ribonucleoprotein H3
2526	dirMS_041712_NAR_50mM_plus2.10365.10677.3	3	15.53	1	2.20E+07		(R)DGKLVS	(R)D G K\L\V\S\E|S/S/D/V/L/P/K(-)		122.83	491.9313	1473.78	-0.0002	-0.1	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2527	dirMS_041712_NAR_60mM_plus.13209.13605.3	3	15.53	1	1.02E+06		(R)ISVYYNE	(R)I/S|V/Y/Y N/E A/T/G G K/Y V/P R(A)		125.95	606.3113	1816.923	-0.0035	-1.9	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
2528	dirMS_041712_NAR_50mM_minus2.18364.18364.3	3	15.52	0	4.62E+05		(K)ALIEVLQ	(K)A L|I/E/V L Q/P L/I A E H Q A R(R)		175.42	601.0139	1801.033	-0.0059	-3.3	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
2529	dirMS_041712_NAR_20mM_plus.18985.19149.3	3	15.52	0	1.11E+05		(R)VCTLAII	(R)V C T L\A I\I/D|P/G/D/S D I I R(S)	C:Carbamidomethylation	202.28	586.641	1757.91	-0.0018	-1	3.93	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
2530	dirMS_041712_NAR_30mM_plus2.16988.17489.2	2	15.52	0	3.76E+06		(K)MIFVGI	(K)M/I|F/V/G/I/K(K)		144.32	404.2433	807.48	-0.0004	-0.5	8.5	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
2531	dirMS_041712_NAR_60mM_plus.17877.17971.3	3	15.52	1	1.04E+06		(R)ARFEEL	(R)A R F E\E\L|N|A/D/L/F/R(G)		150.85	494.2554	1480.754	-0.0027	-1.8	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
2532	dirMS_041712_NAR_60mM_plus.20562.20664.3	3	15.52	1	7.14E+05		(R)LDLAGR	(R)L/D|L|A/G R D L/T/D/Y L/M/K(I)		168.28	541.9516	1623.841	-0.0008	-0.5	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
2533	dirMS_041712_NAR_60mM_plus.7940.8003.3	3	15.52	1	3.68E+05		(K)DISTNYY	(K)D I|S|T/N/Y/Y/A S Q K K(T)		99.77	473.2367	1417.696	-0.0002	-0.2	8.43	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
2534	dirMS_041712_NAR_20mM_minus.13781.13781.2	2	15.51	0	2.36E+05		(R)IVLLDSS	(R)I V|L/L/D/S S L\E Y K(K)		189.15	640.3594	1279.714	-0.0029	-2.2	4.37	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
2535	dirMS_041712_NAR_20mM_plus.18969.18969.2	2	15.51	0	2.13E+04		(K)LLVYEAL	(K)L/L|V/Y/E A/L E|Y A/K(R)		201.67	656.3664	1311.719	0.006	4.6	4.53	32535.6	9.19	HUMAN	B4DZW6	Regulator of microtubule dynamics protein 1
2536	dirMS_041712_NAR_30mM_plus2.21578.21578.2	2	15.51	0	3.32E+05		(K)FDGILG	(K)F/D|G I/L|G/M A\Y P R(I)		167.47	620.3199	1239.619	0.0135	10.9	5.83	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
2537	dirMS_041712_NAR_40mM_plus2.18463.18463.3	3	15.51	1	2.56E+04		(R)IAEVGG	(R)I A/E/V/G/G V/P Y L L P L V N Q K K(V)		174.58	646.716	1938.142	-0.0088	-4.5	8.5	18803.3	5.55	HUMAN	E9PIP1	Ester hydrolase C11orf54 (Fragment)
2538	dirMS_041712_NAR_60mM_plus.10080.10330.2	2	15.51	0	2.03E+06		(K)GIVEFSG	(K)G I|V/E/F/S G/K/P A A/R(K)		111.3	616.3425	1231.679	-0.0016	-1.3	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
2539	dirMS_041712_NAR_120mM_minus.10162.10162.3	3	15.5	1	1.07E+06		(K)IFRDGEE	(K)I/F R D G E E\A|G|A/Y/D/G P R(T)		110.25	551.5928	1652.766	-0.0025	-1.5	4.32	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
2540	dirMS_041712_NAR_120mM_minus.11184.11184.3	3	15.5	0	2.93E+05		(K)SAKPTK	(K)S A/K/P T K\P A A/S D|L|P V|P A E G V R(N)		115.03	664.3662	1991.092	-0.008	-4	8.31	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
2541	dirMS_041712_NAR_30mM_minus2.6878.6902.2	2	15.5	0	1.55E+05	M697m	(K)EGALCE	(K)E G A|L/C|E/E/N\m R(G)	C:Carbamidomethylation m:Oxid	91.9	612.7538	1208.503	15.9969	1.6	4.25	96306.4	6.41	HUMAN	P13639	Elongation factor 2
2542	dirMS_041712_NAR_30mM_plus2.14243.14466.2	2	15.5	0	5.73E+05		(K)CCSGAI	(K)C C|S|G/A|I/I V|L/T/K(S)	C:Carbamidomethylation	128.2	611.3189	1221.633	-0.0025	-2	8.75	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
2543	dirMS_041712_NAR_30mM_plus2.16007.16007.2	2	15.5	0	5.88E+05		(R)YLCGLG	(R)Y L/C/G/L/G A V G G V/R(L)	C:Carbamidomethylation	137.22	611.3189	1221.641	-0.0103	-8.5	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
2544	dirMS_041712_NAR_40mM_plus2.11023.11023.3	3	15.5	1	6.32E+04		(K)VAVVAG	(K)V A|V/V/A|G Y G D V/G K G C A Q A L R(G)	C:Carbamidomethylation	131.05	630.9981	1890.985	-0.0057	-3	8.56	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
2545	dirMS_041712_NAR_60mM_plus.12372.12372.3	3	15.5	1	9.36E+05		(R)LSFDKD	(R)L/S/F D/K D A/M/V A R(A)		121.18	418.2158	1252.635	-0.0026	-2.1	5.96	35556.4	9.3	HUMAN	F2Z393	Transaldolase
2546	dirMS_041712_NAR_120mM_minus.17386.17443.3	3	15.49	1	3.94E+05		(R)RTVQSLI	(R)R T V Q\S\L|E|I|D|L/D/S M R(N)		149.48	554.9552	1662.848	0.0031	1.9	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2547	dirMS_041712_NAR_20mM_minus.9816.9887.2	2	15.49	0	8.73E+05		(R)IVLQIDN	(R)I V|L|Q/I/D/N/A R(L)		149.7	521.3059	1041.605	-0.0006	-0.6	5.84	20842.9	5.32	HUMAN	C9JM50	Keratin, type I cytoskeletal 19 (Fragment)
2548	dirMS_041712_NAR_50mM_minus2.14501.14501.3	3	15.49	1	2.03E+05		(R)IIDSLFN	(R)I/I/D S L/F/N T V/T D K K(I)		150.6	498.612	1493.821	0.0005	0.3	5.96	44813.4	7.79	HUMAN	B4DN25	UDP-glucose 6-dehydrogenase
2549	dirMS_041712_NAR_120mM_plus.6259.6364.3	3	15.49	1	5.04E+05		(R)ARSDEG	(R)A R S D E/G\Q|L|S|P/A T/R(G)		86.7	463.2395	1387.692	0.0115	8.3	6.12	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
2550	dirMS_041712_NAR_20mM_plus.14735.14735.2	2	15.49	0	1.06E+05		(K)LLGELLQ	(K)L L/G E|L/L Q/D N A K(L)		173.62	607.3421	1213.679	-0.0018	-1.4	4.37	35556.4	9.3	HUMAN	F2Z393	Transaldolase
2551	dirMS_041712_NAR_30mM_plus2.18953.18953.2	2	15.49	0	3.33E+05		(R)LTAEDLF	(R)L/T|A/E|D\L/F/E A R(I)		153.07	582.796	1164.59	-0.0048	-4.1	4.14	533778	5.74	HUMAN	Q15149	Plectin
2552	dirMS_041712_NAR_40mM_plus2.10704.10704.3	3	15.49	0	1.85E+05		(K)VGSLDN	(K)V/G|S L/D\N V G/H L/P A G G A V K(I)		128.15	530.9567	1590.86	-0.0043	-2.7	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
2553	dirMS_041712_NAR_50mM_plus2.15478.15478.3	3	15.49	1	8.15E+05		(K)EAFSLFD	(K)E A|F S/L/F/D/K D G D G/T I/T T K(E)		149.52	615.6348	1844.891	-0.0014	-0.8	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
2554	dirMS_041712_NAR_30mM_minus2.14878.14924.2	2	15.48	0	1.75E+05		(K)SLAEGYF	(K)S L|A|E|G/Y/F/D/A A G R(L)		134.77	628.7988	1256.591	-0.0003	-0.2	4.37	22270.1	8.67	HUMAN	E9PHS0	LanC-like protein 1 (Fragment)
2555	dirMS_041712_NAR_30mM_minus2.7345.7368.2	2	15.48	0	1.25E+05		(K)VQYPQS	(K)V Q|Y|P Q/S Q/A/C/K(M)	C:Carbamidomethylation	94.43	604.7902	1208.573	0.0003	0.2	8.56	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
2556	dirMS_041712_NAR_120mM_plus.8887.8887.2	2	15.48	0	5.69E+05		(R)NGVMP	(R)N G V|M/P S H F S R(G)		99.85	566.274	1131.536	0.0043	3.8	9.75	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
2557	dirMS_041712_NAR_30mM_plus2.16303.16303.2	2	15.48	0	1.18E+06		(R)FGLNVS	(R)F/G/L|N/V/S/S I S R(K)		139.02	540.3016	1079.584	0.0115	10.7	9.75	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
2558	dirMS_041712_NAR_30mM_plus2.17254.17798.2	2	15.48	0	1.17E+06		(R)IMNTFS	(R)I M|N|T|F|S V/V/P S/P K(V)		145.38	660.3537	1319.703	-0.0027	-2	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
2559	dirMS_041712_NAR_120mM_minus.19438.19439.3	3	15.47	1	3.72E+05		(K)NLRDIDE	(K)N L/R D I D\E|V|S/S/L/L R(T)		161.42	510.614	1529.828	-0.0007	-0.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
2560	dirMS_041712_NAR_20mM_minus.10310.10310.2	2	15.47	0	7.05E+04		(K)AVLSLYA	(K)A V|L/S|L/Y A/S G R(T)		152.45	518.7929	1036.579	0	0	8.79	14579.3	5.13	HUMAN	K7EM38	Actin, cytoplasmic 2, N-terminally processed (Fragment)
2561	dirMS_041712_NAR_30mM_minus2.17821.17821.2	2	15.47	0	3.07E+05		(K)EAFQLFI	(K)E A/F|Q/L/F D/R(T)		151.65	513.2571	1025.505	0.0019	1.8	4.37	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
2562	dirMS_041712_NAR_60mM_minus.14849.14887.3	3	15.47	1	2.72E+05		(R)KLQEEEI	(R)K L Q E/E E\L\L|A|T/Q/V/D\M R(A)		142.8	601.6438	1802.932	-0.0148	-8.2	4.41	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
2563	dirMS_041712_NAR_120mM_plus.12384.12541.4	4	15.47	2	9.28E+05		(K)KGTVEG	(K)K G T V E G\F\E|P/A/D/N K/C/L L R(A)	C:Carbamidomethylation	118.9	484.2468	1933.98	-0.0147	-7.6	6.18	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
2564	dirMS_041712_NAR_20mM_plus.16430.16430.2	2	15.47	0	1.63E+05		(R)LLEAQIA	(R)L L|E\A Q/I|A T/G/G/I I/D/P K(E)		185	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
2565	dirMS_041712_NAR_40mM_plus2.14766.14874.3	3	15.47	0	3.03E+05		(R)IEGDMI	(R)I/E|G D\M I/V/C/A A Y A H E L/P K(Y)	C:Carbamidomethylation	153.93	639.6498	1916.925	0.0104	5.4	4.65	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
2566	dirMS_041712_NAR_60mM_plus.10477.10477.2	2	15.47	1	4.41E+06		(R)LQAEIEG	(R)L/Q|A/E/I\E/G\L K/G Q/R(A)		112.33	671.3774	1341.748	-0.001	-0.7	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2567	dirMS_041712_NAR_30mM_minus2.11353.11353.2	2	15.46	0	1.22E+06		(K)FSASGEL	(K)F S|A/S|G E|L/G N/G N I/K(L)		114.95	647.3253	1293.643	0	0	6	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
2568	dirMS_041712_NAR_50mM_minus2.14289.14481.3	3	15.46	0	3.62E+05		(K)LHIIEVG	(K)L H I\I E V\G\T|P/P/T/G N Q/P F/P K(K)		150.02	649.0215	1945.054	-0.0042	-2.2	6.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
2569	dirMS_041712_NAR_60mM_minus.10091.10091.3	3	15.46	0	1.56E+06		(R)EIVHIQA	(R)E/I V H I Q\A\G/Q/C/G/N Q\I/G A/K(F)	C:Carbamidomethylation	115.57	608.3099	1822.923	-0.0077	-4.2	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
2570	dirMS_041712_NAR_60mM_minus.6559.6559.3	3	15.46	1	9.46E+04	M436m	(R)TPGKEA	(R)T/P/G K E A V A m/E/S Y/A/K(A)	m:Oxidized methionine	95.08	499.9146	1481.73	15.9988	2.6	5.81	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
2571	dirMS_041712_NAR_120mM_plus.11710.12026.3	3	15.46	0	2.30E+05		(K)VYNYNH	(K)V/Y/N/Y/N/H/L/M/P T|R(Y)		114.35	469.8997	1407.684	0.0008	0.5	8.57	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
2572	dirMS_041712_NAR_20mM_plus.11340.11340.2	2	15.46	0	2.96E+05		(K)LITPAVV	(K)L I/T|P A V V/S\E R(L)		150.53	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
2573	dirMS_041712_NAR_30mM_plus2.6215.6256.2	2	15.46	0	3.51E+05		(K)NQCTQ	(K)N|Q|C|T|Q V/V/Q/E/R(E)	C:Carbamidomethylation	87	631.3039	1261.595	0.0052	4.1	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
2574	dirMS_041712_NAR_40mM_plus2.10387.10558.2	2	15.46	0	4.25E+05		(R)YLYEIAR	(R)Y/L|Y/E/I/A/R(R)		126.83	464.2502	927.493	-0.0003	-0.3	6	53112	6.64	HUMAN	H0YA55	Serum albumin (Fragment)
2575	dirMS_041712_NAR_40mM_plus2.9027.9027.2	2	15.46	0	8.93E+04		(K)GSDFDC	(K)G S|D/F/D/C E/L/R(L)	C:Carbamidomethylation	115.47	549.7296	1098.452	-0.0001	-0.1	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
2576	dirMS_041712_NAR_50mM_plus2.13234.13254.3	3	15.46	0	2.27E+06		(R)SCTVNI	(R)S C|T|V/N I/M|F|G/T/P\Q E H R(N)	C:Carbamidomethylation	138.43	592.9438	1776.816	0.0012	0.7	6.47	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
2577	dirMS_041712_NAR_50mM_plus2.8947.8947.3	3	15.46	0	6.04E+05		(R)AALAHS	(R)A A|L A H S/E E\V\T|A/S/Q/V/A A/T K(T)		113.75	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
2578	dirMS_041712_NAR_60mM_plus.9665.9952.3	3	15.46	0	4.99E+06		(R)QSVEND	(R)Q/S/V/E N D/I/H/G L/R(K)		109.7	423.2195	1267.639	0.005	4	5.32	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2579	dirMS_041712_NAR_120mM_minus.11929.11947.4	4	15.45	2	6.76E+05		(K)GTVIKVF	(K)G T|V I\K V/P L/K V/E Q/A/N/N A R(D)		119.27	460.021	1837.065	-0.0032	-1.8	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
2580	dirMS_041712_NAR_120mM_minus.14733.14900.3	3	15.45	0	1.01E+06		(-)MVNHFI	(-)M/V/N/H/F|I A E/F/K(R)		134.9	412.5458	1235.624	-0.0013	-1	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
2581	dirMS_041712_NAR_30mM_minus2.13577.13909.2	2	15.45	0	1.22E+06		(K)VMYGF	(K)V/M|Y/G/F/C/S V/K(D)	C:Carbamidomethylation	127.8	545.7611	1090.506	0.0089	8.2	8.56	76925.9	4.46	HUMAN	A8MV58	Drebrin
2582	dirMS_041712_NAR_30mM_minus2.13976.13976.2	2	15.45	0	1.66E+05		(K)NVIGLQI	(K)N V|I|G\L/Q\M G T N R(G)		129.38	601.8183	1202.631	-0.0017	-1.4	9.75	22562.2	8.8	HUMAN	P37802	Transgelin-2
2583	dirMS_041712_NAR_60mM_minus.14288.14529.3	3	15.45	0	3.65E+05		(R)VWYVSN	(R)V W|Y|V/S N I/D\G T H I A K(T)		140.38	534.9461	1602.828	-0.0037	-2.3	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
2584	dirMS_041712_NAR_120mM_plus.23690.23690.3	3	15.45	0	7.83E+05		(R)LHFFMP	(R)L H F F\M\P G\F|A/P\L/T S R(G)		179.12	540.9492	1620.835	-0.0025	-1.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
2585	dirMS_041712_NAR_30mM_plus2.13433.13433.2	2	15.45	0	2.78E+05		(K)SDFQVN	(K)S D F Q|V|N L/N N/A S R(S)		123.47	682.8318	1364.655	0.001	0.7	5.55	105417.2	6.41	HUMAN	C9JZR2	Catenin delta-1
2586	dirMS_041712_NAR_50mM_plus2.10850.10872.3	3	15.45	0	4.89E+05		(R)EALLSSA	(R)E A\L/L/S/S/A|V|D|H G S D E/V K(F)		124.7	552.9403	1656.807	-0.0012	-0.7	4.31	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
2587	dirMS_041712_NAR_20mM_minus.13206.13206.3	3	15.44	0	4.00E+05		(K)TITLEVEI	(K)T\I\T L E V E/P S/D/T I E/N V K(A)		183.03	596.6453	1787.927	-0.006	-3.3	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
2588	dirMS_041712_NAR_20mM_minus.8147.8188.2	2	15.44	0	6.38E+06	M239m	(K)EITALAP	(K)E I|T/A|L/A|P/S T m K(I)	m:Oxidized methionine	132.57	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
2589	dirMS_041712_NAR_40mM_minus2.8850.8850.3	3	15.44	1	2.33E+05		(R)IVLANDI	(R)I/V|L/A/N D P D A D R L A V A E K(Q)		134.3	603.9966	1809.97	0.0047	2.6	4.23	32837.5	6.16	HUMAN	B4E0G8	Phosphoglucomutase-2
2590	dirMS_041712_NAR_50mM_minus2.12270.12330.3	3	15.44	1	3.32E+05		(R)DGRGAL	(R)D G R G A L Q\N\I|I|P/A/S T G A A K(A)		138.33	580.6487	1739.94	-0.0083	-4.8	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
2591	dirMS_041712_NAR_60mM_minus.10397.10397.3	3	15.44	1	6.05E+05	M88m	(K)DVDEAY	(K)D V|D/E/A|Y m N/K V E L E S R(L)	m:Oxidized methionine	118.37	605.2791	1797.832	15.9904	-2.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
2592	dirMS_041712_NAR_60mM_minus.18962.18962.3	3	15.44	1	1.98E+05		(K)ITQDIFQ	(K)I/T|Q/D I/F/Q Q L L K R(G)		167.82	501.6268	1502.869	-0.0031	-2.1	8.75	72796.9	6.75	HUMAN	A6NC17	Methionine--tRNA ligase, cytoplasmic
2593	dirMS_041712_NAR_120mM_plus.6453.6592.3	3	15.44	1	1.74E+07		(R)TKTEISEI	(R)T\K\T E\I/S/E/M/N/R(N)		88.12	403.5365	1208.594	0.001	0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
2594	dirMS_041712_NAR_120mM_plus.9686.9686.3	3	15.44	0	6.06E+05		(K)STAGDT	(K)S T|A/G D/T H L/G G E|D F D/N R(M)		104.03	564.579	1691.726	-0.0031	-1.9	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
2595	dirMS_041712_NAR_20mM_plus.18808.18808.2	2	15.44	0	2.08E+05		(K)TAVETA	(K)T\A|V E|T/A/V/L\L/L/R(I)		200.28	593.3625	1185.72	-0.0024	-2	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
2596	dirMS_041712_NAR_30mM_plus2.19531.19531.2	2	15.44	0	2.30E+04		(K)NQALFP	(K)N Q|A|L|F/P A C V L K(N)	C:Carbamidomethylation	155.17	630.8399	1260.677	-0.0044	-3.5	8.75	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
2597	dirMS_041712_NAR_60mM_plus.12065.12220.3	3	15.44	1	2.25E+06		(K)GCGVVK	(K)G C|G V/V/K/F E\S|P/E/V/A E R(A)	C:Carbamidomethylation	120.45	555.2752	1663.811	0.0002	0.1	4.79	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
2598	dirMS_041712_NAR_60mM_plus.5672.5672.3	3	15.44	0	1.11E+06		(K)TATPQQ	(K)T/A|T|P/Q Q A/Q E V H E K(L)		87.6	489.5727	1466.723	-0.0198	-13.5	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
2599	dirMS_041712_NAR_120mM_plus.16796.16943.4	4	15.43	1	3.13E+05		(R)GHYTIGI	(R)G H\Y\T I G/K E I\I\D|P|V/L/D/R(I)		141.77	457.2493	1825.981	-0.0053	-2.9	5.38	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
2600	dirMS_041712_NAR_30mM_plus2.18637.18881.2	2	15.43	0	5.93E+05		(R)GLFIIDD	(R)G L|F|I|I/D/D/K(G)		151.82	460.7596	920.509	0.0032	3.4	4.21	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
2601	dirMS_041712_NAR_30mM_plus2.20368.20368.2	2	15.43	0	1.80E+05		(K)GSFSEQ	(K)G S/F/S/E/Q/G I|N E F\L R(E)		161	742.362	1483.718	-0.0009	-0.6	4.53	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
2602	dirMS_041712_NAR_50mM_plus2.9503.9799.3	3	15.43	1	1.99E+05		(R)AGTGVD	(R)A G/T/G/V/D N V/D L/E/A A/T R K(G)		118.75	539.6108	1616.824	-0.006	-3.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
2603	dirMS_041712_NAR_30mM_minus2.16043.16492.2	2	15.42	0	6.11E+05		(R)DFFLAN	(R)D F|F|L\A|N/A|S/R(A)		142.12	520.763	1040.516	0.0028	2.6	5.84	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
2604	dirMS_041712_NAR_50mM_minus2.12161.12208.3	3	15.42	1	2.66E+05		(K)LAEIGAF	(K)L/A\E|I|G/A/P I/Q/G N/R E E L V E R(L)		137.77	665.3584	1994.066	-0.0059	-2.9	4.49	38572.2	6.31	HUMAN	E9PJ04	Splicing factor 3B subunit 2 (Fragment)
2605	dirMS_041712_NAR_50mM_minus2.6705.6705.3	3	15.42	1	2.52E+05		(R)ASVDTK	(R)A S/V D/T/K E A E/G A/P Q/V E|A G K(R)		104.8	596.2904	1786.882	-0.0251	-14	4.41	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
2606	dirMS_041712_NAR_60mM_minus.15260.15282.3	3	15.42	1	1.56E+06		(R)TIPWLEI	(R)T I|P/W/L/E/D R V/P Q/K(T)		145.47	494.6084	1481.811	-0.0004	-0.3	5.74	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
2607	dirMS_041712_NAR_20mM_plus.15584.15584.3	3	15.42	0	2.07E+05		(K)TITLEVEI	(K)T I\T L E\V\E/P S/D/T I/E N V K(A)		179.07	596.6463	1787.927	-0.003	-1.7	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
2608	dirMS_041712_NAR_30mM_plus2.20352.20584.2	2	15.42	0	3.06E+05		(R)YISPDQL	(R)Y I|S|P/D Q/L/A D L/Y K(S)		161.52	713.3669	1425.726	0.0005	0.4	4.21	47510.4	7.04	HUMAN	P06733	Alpha-enolase
2609	dirMS_041712_NAR_50mM_plus2.12491.12491.3	3	15.42	0	3.93E+05		(R)LDDTVH	(R)L/D/D T V/H/V/V/I/A T\P G R(I)		133.35	498.2741	1492.812	-0.0041	-2.7	5.21	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
2610	dirMS_041712_NAR_20mM_minus.10600.10600.2	2	15.41	0	2.00E+05		(R)TTPSYV	(R)T T/P S/Y V/A/F T D/T E R(L)		154.63	744.3547	1487.701	0.0009	0.6	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
2611	dirMS_041712_NAR_20mM_minus.11232.11473.2	2	15.41	0	1.17E+07	M148m	(R)DLTDYL	(R)D/L|T|D|Y/L/m/K(I)	m:Oxidized methionine	162.17	507.7443	998.486	15.995	0.1	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle

2612	dirMS_041712_NAR_20mM_plus.12490.12490.2	2	15.41	0	1.78E+05		(R)GVEICIA	(R)G V E|I/C/I A/T/P/G R(L)	C:Carbamidomethylation	158.8	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
2613	dirMS_041712_NAR_30mM_plus2.19264.19756.2	2	15.41	0	2.25E+06		(R)ALLFIPR	(R)A L|L|F|I/P/R(R)		156.72	415.2703	829.529	0.0039	4.7	9.79	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
2614	dirMS_041712_NAR_30mM_plus2.6885.6927.2	2	15.41	0	3.28E+05		(R)FSNISAA	(R)F/S|N/I/S/A/A|K(A)		90.63	419.2286	837.447	0.0034	4.1	8.75	55232.1	8.4	HUMAN	F5H5W3	T-complex protein 1 subunit delta
2615	dirMS_041712_NAR_50mM_plus2.14992.14992.3	3	15.41	1	1.14E+05		(R)LLDAQL	(R)L/L|D A/Q|L|A T G G L V C/P A/R R(L)	C:Carbamidomethylation	147.2	604.3351	1810.996	-0.0049	-2.7	9.6	266161	5.68	HUMAN	E9PPU0	Epiplakin
2616	dirMS_041712_NAR_50mM_plus2.18688.18688.3	3	15.41	1	5.80E+05		(R)YLTAEET	(R)Y/L|T/A/E/E T D K I/I N Y L R(E)		166.65	614.662	1841.964	0.0071	3.8	4.68	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
2617	dirMS_041712_NAR_60mM_plus.10838.10960.3	3	15.41	1	6.41E+06		(R)QQEGFK	(R)Q Q/E G F K/G T/F/P/D|A/R(E)		115.52	494.2424	1480.718	-0.0053	-3.6	6.07	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
2618	dirMS_041712_NAR_60mM_plus.6130.6130.3	3	15.41	1	4.67E+04		(R)ALCDYK	(R)A/L/C D/Y K/Q D Q/K(I)	C:Carbamidomethylation	90.68	423.5361	1268.594	-0.0002	-0.2	6.01	334221.3	6.44	HUMAN	P15924	Desmoplakin
2619	dirMS_041712_NAR_60mM_plus.8351.8351.3	3	15.41	1	2.74E+05		(R)NVDSSG	(R)N/V|D/S/S/G N K S V/L/M E R(L)		102.1	512.5887	1535.748	0.0033	2.2	6.07	103309.5	5.34	HUMAN	A0AV56	SAFB protein
2620	dirMS_041712_NAR_120mM_minus.18180.18295.4	4	15.4	1	4.84E+05		(K)EMVELP	(K)E M V/E/L/P L R H/P A L/F/K(A)		154.6	420.737	1679.93	-0.004	-2.4	6.86	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
2621	dirMS_041712_NAR_120mM_minus.8136.8136.3	3	15.4	0	1.23E+06		(K)HSGPNS	(K)H S G\P N\S A|D\S\A/N/D/G F/V/R(L)		98.42	544.2477	1630.72	0.0081	5	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
2622	dirMS_041712_NAR_20mM_minus.12188.12188.2	2	15.4	0	1.08E+06	M313m	(R)TVQSLEI	(R)T V/Q|S L|E|I\D L D S m R(N)	m:Oxidized methionine	170.73	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2623	dirMS_041712_NAR_50mM_minus2.9378.9378.3	3	15.4	0	2.53E+05		(K)TGVAVN	(K)T/G|V/A V/N K/P A/E F T V D/A K(H)		121.95	549.6316	1646.875	0.0054	3.3	5.73	283472.4	5.71	HUMAN	P21333	Filamin-A
2624	dirMS_041712_NAR_120mM_plus.16287.16424.3	3	15.4	1	6.86E+05		(K)STFVLDE	(K)S T|F/V/L/D/E/F K/R(K)		138.87	414.5556	1241.652	-0.0002	-0.2	5.79	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
2625	dirMS_041712_NAR_20mM_plus.16610.16907.2	2	15.4	0	2.65E+05		(R)IVLLDSS	(R)I/V|L|L|D/S S L\E/Y K(K)		186.97	640.36	1279.714	-0.0017	-1.3	4.37	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
2626	dirMS_041712_NAR_20mM_plus.17051.17051.2	2	15.4	0	2.06E+05		(K)VQIAVA	(K)V Q|I|A|V/A/N A Q E\L/L\Q\R(M)		188.23	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
2627	dirMS_041712_NAR_30mM_plus2.11583.11584.2	2	15.4	0	3.50E+05		(K)YQAVTA	(K)Y/Q|A|V|T/A T L/E/E/K(R)		114.32	626.8237	1252.642	-0.0018	-1.5	4.53	23633.9	11.02	HUMAN	P40429	60S ribosomal protein L13a
2628	dirMS_041712_NAR_30mM_plus2.18491.18673.2	2	15.4	0	6.99E+05		(K)EGMNIV	(K)E G\M|N/I|V|E/A M/E/R(F)		150.78	639.7958	1278.582	0.0026	2.1	4.25	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
2629	dirMS_041712_NAR_30mM_minus2.20098.20137.2	2	15.39	0	1.49E+06		(R)VIFGLFG	(R)V/I|F/G L/F/G/K(T)		170.9	440.768	880.529	-0.0004	-0.4	8.72	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
2630	dirMS_041712_NAR_50mM_minus2.12132.12132.3	3	15.39	0	9.82E+04	M240m	(K)mLDAED	(K)m L|D/A/E D I V/N T A R P D|E K(A)	m:Oxidized methionine	137.35	611.6283	1816.875	15.9958	0.5	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
2631	dirMS_041712_NAR_30mM_plus2.7657.7691.2	2	15.39	0	4.27E+05		(R)VGQDP	(R)V/G|Q|D|P V L|R(Q)		94.27	442.2536	883.5	0.0003	0.4	5.81	14130.9	9.56	HUMAN	C9K0U8	Single-stranded DNA-binding protein (Fragment)
2632	dirMS_041712_NAR_40mM_plus2.16063.16063.3	3	15.39	1	1.85E+05		(K)LGVQVV	(K)L G V|Q/V/V|I/T D/P E K L D Q\I R(Q)		161.38	641.701	1923.091	-0.0025	-1.3	4.56	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
2633	dirMS_041712_NAR_30mM_minus2.11305.11378.2	2	15.38	0	3.66E+05		(K)TDGFGI	(K)T D|G|F|G/I/D/T C/R(S)	C:Carbamidomethylation	115.32	571.2521	1141.494	0.0027	2.3	4.21	21983.3	4.68	HUMAN	K7EIV0	Calpain small subunit 1
2634	dirMS_041712_NAR_50mM_minus2.11351.11351.3	3	15.38	1	9.59E+04		(R)LLIVSTT	(R)L L|I/V|S T T/P Y/S E K D T K(Q)		133.12	565.6428	1694.921	-0.0072	-4.3	6.07	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
2635	dirMS_041712_NAR_50mM_minus2.12360.12360.3	3	15.38	1	8.70E+03	M124m M	(K)SYLNmD	(K)S/Y|L/N m/D A I m E A I K/K(T)	m:Oxidized methionine	137.73	553.6091	1626.823	31.9898	0	5.79	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
2636	dirMS_041712_NAR_50mM_minus2.16033.16033.3	3	15.38	1	4.43E+06		(R)VSFELFA	(R)V/S/F E L/F/A D K|V P K(T)		159.72	460.5908	1379.757	0.0009	0.7	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
2637	dirMS_041712_NAR_30mM_plus2.20346.20496.2	2	15.38	0	1.13E+06		(R)ILVATNL	(R)I/L|V|A|T/N/L/F G R(G)		161.92	552.331	1103.657	-0.0024	-2.2	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
2638	dirMS_041712_NAR_50mM_plus2.14970.15142.3	3	15.38	0	9.16E+05		(K)LHIIEVG	(K)L H\I\I E\V\G\T|P/P/T/G N Q P F/P K(K)		147.17	649.0216	1945.054	-0.0039	-2	6.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
2639	dirMS_041712_NAR_60mM_plus.11414.11519.3	3	15.38	1	4.52E+05		(K)TCVFEKE	(K)T/C|V|F/E/K/E N D|P/S V M/R(S)	C:Carbamidomethylation	117.33	571.2635	1711.778	-0.0019	-1.1	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
2640	dirMS_041712_NAR_30mM_minus2.12849.12967.2	2	15.37	0	5.00E+05		(R)GGEPQG	(R)G G\E|P/Q|G/P P F I|K(Y)		124.6	563.7964	1126.589	-0.0036	-3.2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
2641	dirMS_041712_NAR_30mM_minus2.18297.18600.2	2	15.37	0	6.71E+05		(K)FIIPNVV	(K)F/I|I|P N V V/K(Y)		154.63	465.2877	929.582	-0.0137	-14.8	8.75	17529.3	9.3	HUMAN	F5GXY2	L-lactate dehydrogenase A chain (Fragment)
2642	dirMS_041712_NAR_40mM_minus2.11821.11821.3	3	15.37	0	1.02E+04		(K)LVEALCA	(K)L/V/E\A L C A/E/H Q I N L I K(V)	C:Carbamidomethylation	152.93	584.3199	1750.952	-0.0069	-3.9	5.4	14914.1	6.84	HUMAN	P25398	40S ribosomal protein S12
2643	dirMS_041712_NAR_60mM_plus.14407.14840.3	3	15.37	1	7.26E+06		(R)QLREYQ	(R)Q L/R E Y\Q/E/L/M/N V/K(L)		132.48	517.6044	1550.8	-0.0009	-0.6	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2644	dirMS_041712_NAR_30mM_minus2.13121.13121.2	2	15.36	0	3.22E+05		(K)LSELEPG	(K)L S/E/L/E/P G T\G D\L/R(F)		124.73	643.8325	1286.659	-0.0009	-0.7	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
2645	dirMS_041712_NAR_30mM_minus2.18427.18427.2	2	15.36	0	4.47E+05		(R)QAQEYE	(R)Q A Q|E/Y/E/A L/L|N/I K(V)		154.67	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2646	dirMS_041712_NAR_40mM_minus2.9153.9189.3	3	15.36	1	6.96E+05	M356m	(K)VGEVIVT	(K)V G|E|V|I|V/T K D D A m L/L K(G)	m:Oxidized methionine	136.93	549.6354	1630.908	15.9832	-7.1	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
2647	dirMS_041712_NAR_60mM_minus.5108.5206.3	3	15.36	0	4.24E+06	M434m M	(R)LESGmC	(R)L/E|S/G m Q/N m/S I/H/T K(T)	m:Oxidized methionine	84.33	503.2336	1475.698	31.9881	-1.1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2648	dirMS_041712_NAR_30mM_plus2.13677.13697.2	2	15.36	0	3.10E+05		(R)IASLEVE	(R)I A|S\L|E/V|E N Q S L/R(G)		124.87	679.867	1358.727	-0.0007	-0.5	4.53	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
2649	dirMS_041712_NAR_30mM_plus2.16027.16125.2	2	15.36	0	7.35E+05		(R)GALQNI	(R)G A/L|Q|N|I|I\P A S T G\A A\K(A)		137.52	706.3979	1411.79	-0.0018	-1.3	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
2650	dirMS_041712_NAR_30mM_plus2.19882.19882.2	2	15.36	0	5.28E+05		(K)MAILQI	(K)M/A|I|L Q I/M|K(E)		158.22	474.2739	947.542	-0.0011	-1.2	8.5	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
2651	dirMS_041712_NAR_30mM_plus2.21942.21942.2	2	15.36	0	1.55E+05		(K)ANFLQN	(K)A N|F\L/Q|N M/I/E/D/R(T)		170.25	675.8282	1350.647	0.0021	1.5	4.37	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
2652	dirMS_041712_NAR_120mM_minus.10768.11144.3	3	15.35	0	1.08E+06		(R)GFCLPP	(R)G F|C L/P/P H/C S/R(G)	C:Carbamidomethylation	113.72	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
2653	dirMS_041712_NAR_120mM_minus.19212.19212.3	3	15.35	1	2.76E+05	M148m	(R)LDLAGR	(R)L/D|L|A/G R D L T D/Y L m K(I)	m:Oxidized methionine	159.78	547.2876	1623.841	16.0072	7.5	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
2654	dirMS_041712_NAR_40mM_minus2.12893.12893.3	3	15.35	0	3.35E+05		(R)DVQIGD	(R)D V|Q|I/G/D/I/V/T V G E C R P L S K(T)	C:Carbamidomethylation	159.67	662.684	1986.033	0.005	2.5	4.56	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
2655	dirMS_041712_NAR_40mM_minus2.15432.15432.3	3	15.35	1	3.01E+05		(R)GGPNIIT	(R)G G/P N I|I/T L/A D I V K D/P V S R(T)		178.45	622.3523	1865.049	-0.0067	-3.6	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
2656	dirMS_041712_NAR_50mM_minus2.17479.17660.3	3	15.35	0	4.20E+05		(K)VAHALA	(K)V A H A L A E G\L|G\V|I|A/C/I/G E K(L)	C:Carbamidomethylation	168.75	603.3247	1807.974	-0.0139	-7.7	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
2657	dirMS_041712_NAR_50mM_minus2.9996.9996.3	3	15.35	0	5.74E+05	M147m	(K)LQmEA	(K)L Q/m\E A/P H\I|I/V G T P G R(V)	m:Oxidized methionine	125.45	545.6267	1618.873	15.9922	-1.7	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
2658	dirMS_041712_NAR_60mM_minus.9967.10009.3	3	15.35	0	1.64E+06		(R)DNIQGI	(R)D N|I|Q/G I/T K/P A/I/R(R)		116.53	442.5878	1325.754	-0.0047	-3.6	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
2659	dirMS_041712_NAR_20mM_plus.15483.15483.2	2	15.35	0	7.27E+04		(R)AVLNPL	(R)A V\L/N|P\L C/Q V D/Y/R(A)	C:Carbamidomethylation	178.62	724.3735	1447.736	0.0035	2.4	5.88	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
2660	dirMS_041712_NAR_30mM_plus2.7741.7773.2	2	15.35	0	3.78E+05		(R)VGFAEA	(R)V/G|F/A/E/A A/R(L)		94.65	410.7181	820.431	-0.0023	-2.7	5.97	20599.3	9.19	HUMAN	H7C1V0	Cathepsin D light chain (Fragment)
2661	dirMS_041712_NAR_50mM_plus2.14769.14813.3	3	15.35	1	1.58E+04		(K)KGVNLP	(K)K G V|N L P G\A\A|V/D|L|P A V/S E K(D)		145.08	588.999	1764.985	-0.003	-1.7	6.07	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
2662	dirMS_041712_NAR_50mM_plus2.18540.18560.3	3	15.35	0	9.87E+05		(K)VAHALA	(K)V A H A\L A E G|L/G\V|I/A/C/I G E K(L)	C:Carbamidomethylation	166.15	603.3265	1807.974	-0.0085	-4.7	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
2663	dirMS_041712_NAR_60mM_plus.16088.16088.3	3	15.35	0	1.09E+06		(K)SLTNDW	(K)S L/T/N/D/W/E D H/L/A/V K(H)		141.68	509.919	1527.744	-0.0014	-0.9	4.53	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
2664	dirMS_041712_NAR_120mM_minus.9371.9601.3	3	15.34	0	1.70E+06		(K)EFHLNE	(K)E\F H\L N\E/S/G/D/P/S/S K(S)		106.18	482.8881	1446.65	0.0002	0.1	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
2665	dirMS_041712_NAR_30mM_minus2.14145.14349.2	2	15.34	0	4.40E+05		(R)SVPTWL	(R)S V|P/T|W/L/K(L)		131.07	415.7421	830.477	-0.0001	-0.2	8.47	12573.5	10.39	HUMAN	E9PS50	40S ribosomal protein S13 (Fragment)
2666	dirMS_041712_NAR_30mM_minus2.15675.15731.2	2	15.34	0	2.02E+05		(K)ALELDS	(K)A/L|E|L|D/S N/L/Y/R(I)		138.85	597.3118	1193.616	0.0002	0.2	4.37	227783.5	5.5	HUMAN	P35579	Myosin-9
2667	dirMS_041712_NAR_60mM_minus.10259.10484.3	3	15.34	0	5.97E+05		(K)AQVARP	(K)A/Q|V/A/R P G G D/T I/F/G/K(I)		117.88	472.9235	1416.759	-0.0034	-2.4	8.79	7323.5	9.4	HUMAN	D6RC06	Histidine triad nucleotide-binding protein 1
2668	dirMS_041712_NAR_120mM_plus.19629.19688.3	3	15.34	1	2.18E+05		(K)RSIQFVD	(K)R S I Q\F\V|D|W/C/P T G F K(V)	C:Carbamidomethylation	156.15	580.9585	1740.853	0.0083	4.8	8.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
2669	dirMS_041712_NAR_20mM_plus.11005.11005.2	2	15.34	0	2.60E+04		(R)IVLQIDN	(R)I V|L/Q/I/D N/A R(L)		148.23	521.3056	1041.605	-0.0012	-1.1	5.84	20842.9	5.32	HUMAN	C9JM50	Keratin, type I cytoskeletal 19 (Fragment)
2670	dirMS_041712_NAR_30mM_plus2.17624.17684.2	2	15.34	0	4.73E+05		(R)LSYTQLL	(R)L/S|Y/T/Q/L/L/R(R)		145.87	497.2902	993.573	0.0004	0.4	8.75	533778	5.74	HUMAN	Q15149	Plectin
2671	dirMS_041712_NAR_40mM_plus2.13298.13400.3	3	15.34	0	6.01E+05		(R)QVSASE	(R)Q V\S/A/S E/L H T/S G I/L/G/P E T L R(D)		145.08	665.6807	1995.051	-0.023	-11.5	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
2672	dirMS_041712_NAR_60mM_plus.11514.11592.3	3	15.34	1	1.90E+06		(R)LMEEIM	(R)L/M|E/E I/M/S E K E N K(T)		118.2	494.2424	1480.702	0.0105	7.1	4.49	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
2673	dirMS_041712_NAR_60mM_plus.12298.12371.3	3	15.34	1	9.36E+05		(R)LSFDKD	(R)L/S|F D/K/D/A/M/V A/R(A)		121.18	418.2158	1252.635	-0.0026	-2.1	5.96	35556.4	9.3	HUMAN	F2Z393	Transaldolase
2674	dirMS_041712_NAR_50mM_minus2.15780.15780.3	3	15.33	0	3.64E+05		(K)LYGPTNI	(K)L Y|G/P/T N F/S P I I N/H V A R(F)		158.22	600.3221	1798.96	-0.0081	-4.5	8.75	60985.3	5.6	HUMAN	O75131	Copine-3
2675	dirMS_041712_NAR_50mM_minus2.18183.18183.3	3	15.33	1	2.42E+05		(K)LKEAELL	(K)L/K\E A E\L\L|E|P\L M/P A I R(A)		172.72	574.9957	1722.982	-0.0097	-5.6	4.79	56164.6	6.01	HUMAN	E9PP73	Coatomer subunit beta (Fragment)
2676	dirMS_041712_NAR_120mM_plus.18686.19009.3	3	15.33	1	2.43E+05		(K)SIYGEKF	(K)S I|Y/G E/K/F/E/D E N F I/L/K(H)		151.63	611.3079	1831.911	-0.0021	-1.2	4.41	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
2677	dirMS_041712_NAR_20mM_plus.14468.14468.3	3	15.33	0	1.30E+05		(R)LQEAGIL	(R)L Q E\A G\I\L|S A/E/E L/Q R(L)		171.58	519.6131	1556.828	-0.0031	-2	4.25	533778	5.74	HUMAN	Q15149	Plectin
2678	dirMS_041712_NAR_20mM_plus.15189.15564.2	2	15.33	0	8.10E+05		(K)LLCGLLA	(K)L/L|C|G/L/L/A E/R(L)	C:Carbamidomethylation	177.65	522.7971	1044.587	-0.0001	-0.1	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
2679	dirMS_041712_NAR_30mM_plus2.10865.11120.2	2	15.33	0	1.56E+06		(K)TIAPALV	(K)T I|A|P/A L/V S K(K)		110.98	450.2857	899.556	0.0081	9	8.41	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
2680	dirMS_041712_NAR_30mM_plus2.16993.16993.2	2	15.33	0	2.53E+05	M313m	(R)TVQSLEI	(R)T V/Q/S L/E|I D L/D S m R(N)	m:Oxidized methionine	142.07	761.8741	1506.747	15.9941	-0.5	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2681	dirMS_041712_NAR_30mM_plus2.6898.6958.2	2	15.33	0	1.33E+05		(R)TAPAAN	(R)T/A|P|A/A/N/L A S/R(I)		90.78	486.2674	971.527	0.0007	0.7	9.41	300351.7	12.1	HUMAN	Q9UQ35	Serine/arginine repetitive matrix protein 2
2682	dirMS_041712_NAR_20mM_minus.7535.7535.2	2	15.32	0	6.83E+05	M239m	(K)EVDEQ	(K)E V/D/E/Q/m\L/N|V/Q/N K(N)	m:Oxidized methionine	123.77	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
2683	dirMS_041712_NAR_30mM_minus2.7665.7665.2	2	15.32	0	1.21E+05		(R)SGGGG	(R)S G/G/G/G/G/G G L/G S G/G S I R(S)		96.1	616.8021	1232.598	-0.0009	-0.7	9.47	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
2684	dirMS_041712_NAR_60mM_minus.9338.9338.3	3	15.32	1	2.25E+05	M232m M	(R)MSmKE	(R)M S m K E V\D\E Q|m|L/N V/Q/N K(N)	m:Oxidized methionine	111.92	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
2685	dirMS_041712_NAR_60mM_minus.9351.9361.3	3	15.32	1	1.67E+05		(K)LAELKQ	(K)L/A|E/L/K/Q/E/C/L A R(G)	C:Carbamidomethylation	112.02	444.2455	1330.715	0.0072	5.4	6.14	6106	9.22	HUMAN	F8VS12	SAP domain-containing ribonucleoprotein
2686	dirMS_041712_NAR_120mM_plus.9473.9473.3	3	15.32	0	3.32E+05		(K)QEYDES	(K)Q E Y/D E S/G/P/S I/V/H/R(K)		102.88	506.2393	1516.703	0.0007	0.5	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
2687	dirMS_041712_NAR_20mM_plus.15706.15706.2	2	15.32	0	1.28E+06	M73m	(R)AILVDLE	(R)A I L V|D|L|E/P G T m D S V R(S)	m:Oxidized methionine	179.22	816.4181	1615.836	15.9929	-1.2	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
2688	dirMS_041712_NAR_20mM_plus.16031.16378.2	2	15.32	0	4.91E+05		(K)DAGTIA	(K)D A\G\T|I|A|G/L/N/V L R(I)		183.63	600.3422	1199.674	0.0029	2.4	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
2689	dirMS_041712_NAR_20mM_plus.18241.18241.2	2	15.32	0	1.70E+05		(R)LTGQLF	(R)L/T|G Q|L|F/L/G G S I V K(G)		197.02	666.8962	1332.789	-0.0034	-2.6	8.75	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
2690	dirMS_041712_NAR_30mM_plus2.6384.6384.2	2	15.32	0	3.31E+05	M367m	(R)FGSGm	(R)F/G|S|G m N M/G R(I)	m:Oxidized methionine	87.53	486.7048	956.408	15.9946	-0.3	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
2691	dirMS_041712_NAR_40mM_plus2.11915.11915.3	3	15.32	1	6.43E+04		(R)FGEVVD	(R)F/G|E/V/V/D C T I/K T D P/V T G R(S)	C:Carbamidomethylation	136.33	631.9821	1893.938	-0.0057	-3	4.56	46607.8	9.68	HUMAN	O14979	Heterogeneous nuclear ribonucleoprotein D-like
2692	dirMS_041712_NAR_30mM_minus2.7370.7404.2	2	15.31	0	5.41E+05		(K)AMDVY	(K)A/M|D|V/Y/Q/K(A)		94.8	427.7069	854.408	-0.0011	-1.3	5.88	60404.6	6.4	HUMAN	F5H0T1	Stress-induced-phosphoprotein 1
2693	dirMS_041712_NAR_50mM_minus2.9363.9702.3	3	15.31	1	1.07E+07		(R)DGKLVS	(R)D G K\L\V\S\E|S/S/D/V/L/P/K(-)		121.97	491.9322	1473.78	0.0025	1.7	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2694	dirMS_041712_NAR_60mM_minus.10048.10048.3	3	15.31	0	1.56E+06		(R)EIVHIQA	(R)E/I V H I Q A G Q/C/G N Q I|G A K(F)	C:Carbamidomethylation	115.57	608.3099	1822.923	-0.0077	-4.2	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
2695	dirMS_041712_NAR_30mM_plus2.16032.16032.2	2	15.31	0	4.04E+05		(K)MDQAII	(K)M D|Q/A|I/I/F/C R(T)	C:Carbamidomethylation	137.1	577.2809	1153.549	0.0053	4.6	5.59	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
2696	dirMS_041712_NAR_30mM_plus2.16890.17177.2	2	15.31	0	7.05E+05		(K)FFVGGN	(K)F/F|V/G/G N/W K(M)		142.57	477.7447	954.483	-0.0011	-1.1	8.75	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
2697	dirMS_041712_NAR_30mM_plus2.19404.19554.2	2	15.31	0	2.95E+05		(K)TVDNFV	(K)T V|D|N|F/V/A L/A/T/G E K(G)		155.22	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
2698	dirMS_041712_NAR_30mM_plus2.20798.20992.2	2	15.31	0	3.07E+05		(K)LVLPSLI	(K)L/V|L/P/S/L/I/S S/R(I)		163.97	542.8382	1084.672	-0.0033	-3.1	9.75	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
2699	dirMS_041712_NAR_50mM_plus2.20345.20345.3	3	15.31	1	3.35E+06		(R)TLAEIAK	(R)T L|A E/I/A/K/V/E\L/D N M P L R(G)		174.87	604.9965	1812.989	-0.0138	-7.6	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
2700	dirMS_041712_NAR_50mM_minus2.16905.16905.3	3	15.3	0	2.41E+05		(R)LGIEGLS	(R)L/G\I|E/G L/S L H N V L/K(L)		164.2	464.9452	1392.821	0.0001	0.1	6.75	177928	5.42	HUMAN	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1
2701	dirMS_041712_NAR_60mM_minus.10114.10114.3	3	15.3	0	3.39E+05		(K)LTPLSHE	(K)L/T/P L/S H/E V I/S R(Q)		115.77	417.9007	1251.706	-0.018	-14.4	6.75	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
2702	dirMS_041712_NAR_120mM_plus.10719.10719.3	3	15.3	0	8.43E+05		(R)YYDSRP	(R)Y/Y/D/S\R P/G G Y G Y/G Y G R(S)		108.75	577.5892	1730.756	-0.0027	-1.6	8.38	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
2703	dirMS_041712_NAR_30mM_plus2.13475.13496.2	2	15.3	0	1.03E+05		(R)TIYAGN	(R)T I|Y|A|G/N|A|L C T/V/K(C)	C:Carbamidomethylation	123.85	655.8414	1310.677	-0.0018	-1.4	8.26	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
2704	dirMS_041712_NAR_30mM_plus2.8995.8995.2	2	15.3	0	6.30E+05		(R)SSQSSS	(R)S S/Q|S S|S Q Q/F/S/G I|G\R(S)		101.03	728.345	1455.682	0.0005	0.3	9.47	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
2705	dirMS_041712_NAR_40mM_plus2.7020.7057.2	2	15.3	0	1.61E+05		(R)QLETLG	(R)Q/L/E/T/L/G Q/E/K(L)		101.52	523.282	1045.552	0.0043	4.1	4.53	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
2706	dirMS_041712_NAR_50mM_plus2.9533.9533.3	3	15.3	1	4.76E+05		(K)LTSDDVI	(K)L/T|S D/D V K/E Q I/Y/K(L)		117.47	480.2521	1438.742	-0.0007	-0.5	4.56	12573.5	10.39	HUMAN	E9PS50	40S ribosomal protein S13 (Fragment)
2707	dirMS_041712_NAR_60mM_plus.15578.15579.3	3	15.3	1	4.36E+05		(K)TLNNKF	(K)T/L|N N K/F/A/S/F I/D K(V)		138.13	466.5862	1397.742	0.0017	1.2	8.26	19569.8	9.88	HUMAN	F8VRG4	Keratin, type II cytoskeletal 8 (Fragment)
2708	dirMS_041712_NAR_60mM_plus.18454.18454.3	3	15.3	1	7.09E+05		(R)IRIDSLS	(R)I R I D S\L\S\A\Q|L/S/Q/L Q K(Q)		153.97	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
2709	dirMS_041712_NAR_50mM_minus2.16428.16720.3	3	15.29	1	1.07E+06		(R)VTFSGLF	(R)V/T|F/S/G L R D T V/T/P G E L/L/K(A)		162.5	611.672	1833.012	-0.0102	-5.6	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
2710	dirMS_041712_NAR_50mM_minus2.18067.18182.3	3	15.29	1	6.74E+05		(R)VLEALLP	(R)V/L|E|A/L L/P L/K G L E/E R(V)		172.47	527.3171	1579.942	-0.005	-3.2	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
2711	dirMS_041712_NAR_30mM_plus2.17038.17085.2	2	15.29	0	2.91E+05		(R)GLGLDD	(R)G L|G|L/D/D/A|L/E|P R(Q)		142.02	578.3042	1155.6	0.0007	0.6	4.03	51326.8	5.49	HUMAN	Q9Y230	RuvB-like 2
2712	dirMS_041712_NAR_30mM_plus2.20390.20390.2	2	15.29	0	6.53E+04		(K)SYELPD	(K)S Y\E|L/P D/G Q V I|T I/G N E R(F)		160.92	895.9487	1790.892	-0.0018	-1	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
2713	dirMS_041712_NAR_30mM_plus2.22258.22258.2	2	15.29	0	1.03E+06		(K)IGFPWS	(K)I G/F|P/W/S E I R(N)		173.07	552.8032	1104.584	0.0155	14	6	71218.8	6.3	HUMAN	A7YIJ8	Radixin
2714	dirMS_041712_NAR_50mM_plus2.18186.18186.3	3	15.29	1	1.08E+05		(K)DLEIKIP	(K)D L\E I K/I/P\V/V/V/R(L)		163.52	427.6021	1280.794	-0.0019	-1.5	6.07	44183.5	5.64	HUMAN	F5GXC8	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial
2715	dirMS_041712_NAR_60mM_plus.5038.5038.3	3	15.29	1	3.95E+05		(R)AAEDDE	(R)A A|E/D D/E/D D D/V D T K K(Q)		83.53	522.5529	1565.645	-0.0008	-0.5	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
2716	dirMS_041712_NAR_60mM_plus.5301.5301.3	3	15.29	1	1.18E+04	M117m	(K)EmQLR	(K)E\m/Q/L/R Q E/E/E/R(R)	m:Oxidized methionine	85.13	455.2157	1347.632	16.0004	4	4.49	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
2717	dirMS_041712_NAR_120mM_minus.11369.11369.3	3	15.28	0	2.31E+05		(R)GFCLPP	(R)G F|C/L/P/P/H C S R(G)	C:Carbamidomethylation	116.42	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
2718	dirMS_041712_NAR_120mM_minus.20102.20250.3	3	15.28	0	1.72E+05	M195m	(R)LHFFmP	(R)L H F F m|P G|F|A|P/L T S/R(G)	m:Oxidized methionine	165.67	546.2809	1620.835	15.9926	-1.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
2719	dirMS_041712_NAR_120mM_minus.9837.9894.3	3	15.28	0	8.69E+05		(K)STAGDT	(K)S/T|A/G D/T H/L/G G E D F D/N R(M)		108.4	564.5795	1691.726	-0.0016	-1	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
2720	dirMS_041712_NAR_20mM_plus.6956.6956.2	2	15.28	0	8.44E+04	M29m	(K)IVQmTE	(K)I/V|Q m|T/E A E/V R(G)	m:Oxidized methionine	114.35	596.3035	1175.609	15.9908	-3.4	4.53	14493.5	5.23	HUMAN	C9J9S3	Serine/threonine-protein phosphatase (Fragment)

2721	dirMS_041712_NAR_30mM_plus2.8833.8833.2	2	15.28	0	3.99E+05		(K)ITSEIPQ'	(K)I T|S/E|I/P Q T E R(M)		100.2	587.3094	1173.611	0.0005	0.5	4.53	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
2722	dirMS_041712_NAR_50mM_plus2.22484.22484.3	3	15.28	1	1.26E+06		(R)GVMLA\	(R)G V/M/L/A V/D A V I A E/L K K(Q)		195.7	519.6393	1556.908	-0.0047	-3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
2723	dirMS_041712_NAR_60mM_plus.7898.7933.3	3	15.28	0	1.02E+06		(K)EAYPDH	(K)E A|Y/P/D/H T Q F E/K(N)		99.42	455.5423	1364.612	0.0006	0.5	4.65	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1
2724	dirMS_041712_NAR_30mM_minus2.10689.10840.2	2	15.27	0	5.83E+05		(R)GYSFTT1	(R)G/Y|S|F/T/T/T/A E R(E)		112.3	566.7699	1132.527	0.0056	4.9	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
2725	dirMS_041712_NAR_30mM_minus2.12569.13070.2	2	15.27	1	3.16E+06		(K)KITIADC	(K)K\I\T\I|A|D\C\G\Q|L|E(-)	C:Carbamidomethylation	123.22	624.3176	1247.63	-0.0021	-1.7	4.75	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
2726	dirMS_041712_NAR_30mM_minus2.14875.14875.2	2	15.27	0	1.40E+05		(R)WALSQS	(R)W/A|L|S/Q/S N/P S A L R(E)		134.55	665.3481	1329.691	-0.0021	-1.5	9.75	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
2727	dirMS_041712_NAR_30mM_plus2.14583.14773.2	2	15.27	0	4.71E+05		(K)VPEWVI	(K)V/P|E/W/V/D/T V/K(L)		129.9	536.7859	1072.567	-0.0028	-2.6	4.37	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
2728	dirMS_041712_NAR_30mM_plus2.19089.19089.2	2	15.27	0	9.29E+05		(K)DAGTIA	(K)D A G/T|I/A/G L|N V L R(I)		152.63	600.3411	1199.674	0.0007	0.6	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
2729	dirMS_041712_NAR_30mM_plus2.8792.8931.2	2	15.27	0	7.50E+05		(R)GMGPG	(R)G M/G/P/G/T|P A/G Y/G R(G)		100.25	560.7657	1120.52	0.0037	3.3	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
2730	dirMS_041712_NAR_60mM_plus.16743.16761.3	3	15.27	1	8.72E+05		(R)STNKGT.	(R)S T N K\G T A\Y\T/F/F/T|P G N/L K(Q)		144.73	616.3117	1846.933	-0.0128	-7	9.7	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
2731	dirMS_041712_NAR_120mM_minus.17474.17760.3	3	15.26	1	3.32E+05		(R)RAPFDLI	(R)R A\P F|D|L|F/E/N/K(K)		150.82	412.8849	1236.637	0.003	2.4	6.07	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
2732	dirMS_041712_NAR_40mM_minus2.14113.14201.3	3	15.26	0	6.88E+05		(R)IHFPLAT	(R)I H F\P L A\T|Y|A|P V/I/S A E K(A)		167.82	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
2733	dirMS_041712_NAR_40mM_minus2.14162.14277.3	3	15.26	1	2.95E+05		(K)VIAATNI	(K)V/I|A|A/T N R V D I|L/D/P A L L R(S)		167.82	617.3653	1850.086	-0.0045	-2.4	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
2734	dirMS_041712_NAR_50mM_minus2.17073.17073.3	3	15.26	0	1.55E+05		(R)LLEVLSG	(R)L/L|E|V/L/S G E I L/P/K/P T K(G)		165.35	546.3329	1636.988	-0.0042	-2.6	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
2735	dirMS_041712_NAR_60mM_minus.15320.15320.3	3	15.26	1	3.71E+05		(R)LLDAQL/	(R)L L/D/A/Q L/A|T G/G L V C P A R R(L)	C:Carbamidomethylation	145.7	604.3344	1810.996	-0.007	-3.8	9.6	266161	5.68	HUMAN	E9PPU0	Epiplakin
2736	dirMS_041712_NAR_120mM_plus.10966.11258.3	3	15.26	0	1.15E+06		(K)NFYVEH	(K)N F/Y/V/E H/P E/V A/R(L)		111.23	454.2277	1360.664	0.0041	3	5.4	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
2737	dirMS_041712_NAR_20mM_plus.12409.12409.3	3	15.26	0	3.15E+04		(K)IISNASC'	(K)I I\S N\A|S/C T T N/C L|A/P L A K(V)	C:Carbamidomethylation	157.65	611.9768	1833.92	-0.0039	-2.1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
2738	dirMS_041712_NAR_30mM_plus2.12103.12104.2	2	15.26	0	3.92E+05		(R)GYFSEEI	(R)G Y|F|S/E E/M N/R(V)		116.33	566.7397	1132.473	-0.0007	-0.6	4.53	533778	5.74	HUMAN	Q15149	Plectin
2739	dirMS_041712_NAR_50mM_plus2.12236.12299.3	3	15.26	1	1.69E+06		(K)ILIANTG	(K)I/L|I|A N/T/G/M D T D K I K(I)		132.52	511.6172	1532.835	0.0018	1.2	5.96	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
2740	dirMS_041712_NAR_60mM_plus.8565.8565.3	3	15.26	1	1.32E+06		(K)MQASIE	(K)M/Q|A S I/E K/G G S L/P K(V)		103.15	449.2449	1345.714	0.0057	4.3	8.35	32745.6	4.64	HUMAN	P06748	Nucleophosmin
2741	dirMS_041712_NAR_60mM_minus.10051.10479.3	3	15.25	0	5.90E+06		(R)GSAVHC	(R)G S|A/V/H/Q/L/S/E/E/L/R(C)		117.4	442.5648	1325.681	-0.001	-0.7	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
2742	dirMS_041712_NAR_60mM_minus.11315.11315.3	3	15.25	1	1.43E+05		(R)DGKLVS	(R)D G K L V\S E/S/S/D V/L/P K(-)		123.12	491.927	1473.78	-0.0131	-8.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2743	dirMS_041712_NAR_120mM_plus.19474.19474.3	3	15.25	1	6.90E+05		(K)YNQLLRI	(K)Y/N/Q/L/L/R I E E E L G S K(A)		155.23	564.6353	1691.896	-0.0049	-2.9	4.79	47510.4	7.04	HUMAN	P06733	Alpha-enolase
2744	dirMS_041712_NAR_30mM_plus2.17667.18204.2	2	15.25	0	2.38E+06		(K)AILFVPR	(K)A I|L|F/V/P/R(R)		147.43	408.2604	815.514	-0.0003	-0.3	9.79	57660.2	6.38	HUMAN	Q9NQH7	Probable Xaa-Pro aminopeptidase 3
2745	dirMS_041712_NAR_40mM_plus2.11775.11816.3	3	15.25	1	2.80E+05		(R)IVAPGK(	(R)I V|A|P G K G I L A A/D/E S T/G S I/A K(R)		135.4	633.3568	1898.059	-0.0035	-1.8	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
2746	dirMS_041712_NAR_60mM_minus.8540.8625.3	3	15.24	0	2.74E+05		(R)LAQGHT	(R)L/A|Q G/H/T/T V/D/E/L A R(R)		107.93	470.9153	1410.734	-0.0022	-1.6	5.32	533778	5.74	HUMAN	Q15149	Plectin
2747	dirMS_041712_NAR_120mM_plus.18407.18464.3	3	15.24	1	6.09E+04	M75m	(R)RFDEILE	(R)R F D E\I\L\E|A|S/D G/I/m/V A R(G)	m:Oxidized methionine	149.78	613.3075	1821.916	15.9916	-1.8	4.32	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
2748	dirMS_041712_NAR_20mM_plus.12670.12670.2	2	15.24	0	1.21E+05		(K)GTIQVIT	(K)G T I/Q/V/I/T\Q/G T/S/L K(N)		160.13	673.3872	1345.769	-0.0014	-1.1	8.75	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
2749	dirMS_041712_NAR_30mM_plus2.6009.6009.2	2	15.24	0	9.97E+04		(R)QLAEED	(R)Q L/A/E/E/D/A A R(Q)		85.77	501.7464	1002.485	0.0005	0.5	4.14	533778	5.74	HUMAN	Q15149	Plectin
2750	dirMS_041712_NAR_50mM_plus2.16362.16499.3	3	15.24	0	1.45E+06		(K)IEVIKPG	(K)I/E|V|I/K/P G D L/G V D/L T S K(L)		154.62	561.9883	1683.953	-0.0024	-1.4	4.56	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
2751	dirMS_041712_NAR_50mM_plus2.5726.5726.3	3	15.24	1	1.05E+06		(K)TAGPIAS	(K)T A/G/P I/A S\A Q K Q P A G K(V)		91.9	475.5987	1424.786	-0.0041	-2.8	10	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
2752	dirMS_041712_NAR_50mM_plus2.9501.9501.3	3	15.24	1	3.39E+05		(R)AGTGVI	(R)A/G T/G/V/D N V/D/L/E/A A T R K(G)		117.4	539.6108	1616.824	-0.006	-3.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
2753	dirMS_041712_NAR_60mM_plus.11742.11742.2	2	15.24	0	1.31E+06		(R)FAQHGT	(R)F A/Q/H G\T|F E/Y\E/Y/S Q\R(W)		118.65	881.8928	1762.782	-0.0037	-2.1	5.4	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
2754	dirMS_041712_NAR_60mM_plus.12409.12534.3	3	15.24	1	3.85E+06		(K)LFNLSKE	(K)L/F|N L/S K/E D D/V/R(Q)		121.6	445.9046	1335.69	0.0089	6.7	4.56	25082	11.29	HUMAN	A2A3R5	40S ribosomal protein S6
2755	dirMS_041712_NAR_60mM_plus.12935.12982.3	3	15.24	0	1.26E+06		(K)VNGRPL	(K)V/N|G\R\P L E|M/I/E/P/R(T)		124.65	470.9225	1410.752	0.0008	0.5	6.11	16559.1	10.36	HUMAN	P62249	40S ribosomal protein S16
2756	dirMS_041712_NAR_60mM_plus.17087.17087.3	3	15.24	1	7.26E+06		(K)LKVPEW	(K)L/K/V/P E\W/V/D/T V K(L)		145.72	438.5872	1313.746	0.0007	0.5	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
2757	dirMS_041712_NAR_60mM_plus.9917.9918.3	3	15.24	1	1.03E+06		(R)SLNESKI	(R)S L|N E/S/K|I/E/I E|R(L)		109.93	439.9069	1317.701	0.0053	4	4.78	334221.3	6.44	HUMAN	P15924	Desmoplakin
2758	dirMS_041712_NAR_120mM_minus.14365.14529.3	3	15.23	1	1.43E+05	M313m	(R)RTVQSLI	(R)R T V Q\S\L/E|I|D|L/D/S m R(N)	m:Oxidized methionine	133.25	560.2849	1662.848	15.9922	-1.6	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2759	dirMS_041712_NAR_120mM_minus.5611.5769.3	3	15.23	0	1.21E+06		(R)AEAEAG	(R)A E|A|E|A/G S P R P D|P/R(E)		84.47	451.5563	1352.655	-0.001	-0.7	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
2760	dirMS_041712_NAR_30mM_minus2.15286.15286.2	2	15.23	0	4.79E+04		(K)LCDFGF/	(K)L/C|D/F G\F/A R(A)	C:Carbamidomethylation	135.8	493.2343	985.456	0.0053	5.4	5.84	143554.7	5.57	HUMAN	A8MU99	Serine/threonine-protein kinase 36
2761	dirMS_041712_NAR_30mM_plus2.9020.9020.2	2	15.23	0	5.79E+05		(R)LATNTS/	(R)L A|T/N T/S A/P D/L/K(N)		100.57	565.801	1130.605	-0.0105	-9.2	5.84	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
2762	dirMS_041712_NAR_40mM_plus2.19022.19110.3	3	15.23	1	3.19E+05		(R)GGPNIIT	(R)G G P|N|I|I|T L/A D I V/K/D/P V S R(T)		178.95	622.3522	1865.049	-0.007	-3.8	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
2763	dirMS_041712_NAR_60mM_plus.13790.14340.3	3	15.23	1	2.88E+07		(K)ASLENSI	(K)A/S|L/E/N S/L R E V E/A/R(Y)		129.92	491.928	1473.766	0.0039	2.6	4.79	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2764	dirMS_041712_NAR_60mM_plus.17760.17760.3	3	15.23	0	3.72E+05		(R)SLESLHS	(R)S L|E/S/L H S F V A A/A T K(E)		149.9	487.5963	1460.774	0	0	6.47	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
2765	dirMS_041712_NAR_60mM_minus.17101.17101.3	3	15.22	0	8.20E+04		(K)LLDSSTV	(K)L/L|D/S/S T/V T H L F K(I)		155.38	454.2519	1360.747	-0.0059	-4.4	6.74	25746.2	6.77	HUMAN	B4DXJ9	Proteasome (Prosome, macropain) subunit, alpha type, 6, isoform CRA_a
2766	dirMS_041712_NAR_120mM_plus.9709.9726.3	3	15.22	1	1.26E+06		(K)LEAEIAT	(K)L/E|A|E/I A T Y R/R(L)		104.37	407.8899	1221.659	-0.0035	-2.8	6.14	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2767	dirMS_041712_NAR_20mM_plus.15672.15672.3	3	15.22	0	7.37E+05		(K)VGINYQ	(K)V G I N Y Q|P P/T/V\V/P G G D L A K(V)		179.22	608.9991	1824.985	-0.0027	-1.5	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
2768	dirMS_041712_NAR_20mM_plus.16433.16706.2	2	15.22	0	5.45E+05		(K)LGGSAV	(K)L G G\S A/V|I|S L|E/G/K|P L(-)		185.73	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
2769	dirMS_041712_NAR_40mM_plus2.13987.13987.3	3	15.22	0	2.12E+05		(K)VALLLLD	(K)V A|L|L/L/L/D|Q/G A S/P H A A/A K(N)		148.2	558.9886	1674.954	-0.0025	-1.5	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
2770	dirMS_041712_NAR_50mM_plus2.6129.6129.3	3	15.22	0	1.25E+05		(R)SGSMDI	(R)S/G|S|M/D/P S/G A H P S V R(Q)		96.5	462.214	1384.627	0.0001	0	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
2771	dirMS_041712_NAR_60mM_plus.14508.14508.3	3	15.22	1	7.09E+05		(R)ELISNSSI	(R)E L|I/S/N/S/S/D A\L D K I R(Y)		132.23	520.952	1560.823	0.0187	12	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
2772	dirMS_041712_NAR_60mM_plus.17768.17768.3	3	15.22	1	1.13E+05		(K)WVAIQS	(K)W/V/A/I Q S V S A/W/P E K R(G)		150.05	552.9655	1656.886	-0.0037	-2.2	8.75	6412.4	9.52	HUMAN	J3KSS4	Cytosolic non-specific dipeptidase (Fragment)
2773	dirMS_041712_NAR_20mM_minus.11193.11429.2	2	15.21	0	1.17E+07	M148m	(R)DLTDYLr	(R)D L|T|D/Y/L/m/K(I)	m:Oxidized methionine	162.17	507.7443	998.486	15.995	0.1	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
2774	dirMS_041712_NAR_30mM_minus2.11048.11048.2	2	15.21	0	5.11E+05		(K)IVVVTA(	(K)I V|V/V/T\A G V/R(Q)		114.15	457.2948	913.583	-0.0006	-0.7	9.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
2775	dirMS_041712_NAR_50mM_minus2.12774.12774.3	3	15.21	1	1.29E+05		(R)TEMENE	(R)T/E|M E N E/F|V/L I K K(D)		140.62	494.2621	1480.772	0.0002	0.1	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
2776	dirMS_041712_NAR_50mM_minus2.7053.7053.3	3	15.21	1	2.04E+05		(K)GAVAED	(K)G A V|A|E D/G D/E L/R T E P E/A/K(K)		106.92	596.2904	1786.845	0.0113	6.3	4.08	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
2777	dirMS_041712_NAR_50mM_minus2.9684.9684.3	3	15.21	1	1.97E+05		(R)ALEEAM	(R)A L|E|E A/M E/Q K A E L E/R(L)		122.57	549.6072	1646.805	0.0016	1	4.33	227783.5	5.5	HUMAN	P35579	Myosin-9
2778	dirMS_041712_NAR_60mM_minus.11188.11189.3	3	15.21	1	8.90E+05	M232m	(R)MSmKE\	(R)M/S/m K E V D E Q|M|L/N|V|Q N K(N)	m:Oxidized methionine	122.73	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
2779	dirMS_041712_NAR_20mM_plus.8097.8114.2	2	15.21	0	8.65E+04		(R)AAPGAE	(R)A/A/P/G/A E/F A|P/N K(R)		125.65	536.7749	1072.542	0.0003	0.3	6.05	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
2780	dirMS_041712_NAR_30mM_plus2.11347.11364.2	2	15.21	0	6.30E+05		(R)MGESDI	(R)M/G|E|S/D/D/S I L/R(L)		113.68	561.7585	1122.51	0.0002	0.1	4.03	9225.3	9.16	HUMAN	P63220	40S ribosomal protein S21
2781	dirMS_041712_NAR_30mM_plus2.14333.14333.2	2	15.21	0	9.53E+05		(R)MGQM/	(R)M/G Q/M A|M|G/G A/M|G\I N N R(G)		127.35	769.8376	1538.67	-0.0015	-1	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
2782	dirMS_041712_NAR_60mM_plus.11262.11262.2	2	15.21	0	2.12E+06		(K)GIVEFAS	(K)G I|V/E/F/A S K P A A R(K)		116.18	623.3504	1245.695	-0.0015	-1.2	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
2783	dirMS_041712_NAR_60mM_plus.14804.14867.3	3	15.21	1	4.49E+05		(R)ELAVQI\	(R)E L/A/V/Q/I/Y/E E/A R K(F)		133.9	483.5949	1448.774	-0.0042	-2.9	4.79	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
2784	dirMS_041712_NAR_50mM_minus2.12131.12131.3	3	15.2	0	9.09E+03		(K)AASAGV	(K)A A|S/A/G V/P Y H/G E V/P V S L A R(A)		135.98	594.315	1780.934	-0.0036	-2	6.79	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
2785	dirMS_041712_NAR_50mM_minus2.8927.8927.3	3	15.2	0	2.36E+05		(R)VMLGET	(R)V M|L/G|E T N P A D/S K/P G T I R(G)		118.3	595.9744	1785.916	-0.0077	-4.3	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
2786	dirMS_041712_NAR_60mM_minus.12074.12130.3	3	15.2	1	3.97E+05		(K)QQEAAL	(K)Q Q/E/A/A/L/E/L E E/L\K|K(K)		127.52	510.2782	1528.822	-0.0017	-1.1	4.49	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
2787	dirMS_041712_NAR_20mM_plus.16625.16625.2	2	15.2	0	1.99E+05		(K)VQIAVA	(K)V Q|I|A/V/A/N A Q\E/L\L/Q/R(M)		186.25	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
2788	dirMS_041712_NAR_50mM_plus2.12219.12219.3	3	15.2	0	3.98E+05		(K)IVLEDGT	(K)I V|L/E/D G T/L/H V T E G S G R(Y)		132.23	561.6272	1682.871	-0.0037	-2.2	4.65	62748.9	5.95	HUMAN	Q16555	Dihydropyrimidinase-related protein 2
2789	dirMS_041712_NAR_60mM_plus.10750.11170.3	3	15.2	1	6.13E+06		(K)TAVCDIF	(K)T/A|V/C D/I/P P R G L K(M)	C:Carbamidomethylation	115.45	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
2790	dirMS_041712_NAR_120mM_minus.7446.7510.3	3	15.19	1	7.50E+05		(K)EAETRAI	(K)E/A|E/T/R A E/F/A/E/R(S)		94.98	436.8772	1308.618	-0.0008	-0.6	4.49	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
2791	dirMS_041712_NAR_30mM_minus2.15455.15565.2	2	15.19	0	3.22E+05		(R)AAPFSLE	(R)A A|P/F/S|L E/Y R(V)		138.3	527.2782	1053.536	0.0128	12.1	6.04	33115.9	5.54	HUMAN	Q15181	Inorganic pyrophosphatase
2792	dirMS_041712_NAR_50mM_minus2.16936.16936.3	3	15.19	1	9.17E+04		(K)AAILPTS	(K)A A/I/L/P T/S I/F L T N K K(G)		164.28	506.3077	1516.91	-0.0012	-0.8	10	61676.9	5.5	HUMAN	B4DV00	Protein arginine N-methyltransferase 5
2793	dirMS_041712_NAR_60mM_minus.19745.19893.3	3	15.19	1	1.81E+06		(K)EIIDLVLI	(K)E I/I/D/L/V/L/D/R I R(K)		179.88	452.2739	1354.805	0.0019	1.4	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
2794	dirMS_041712_NAR_30mM_plus2.12160.12160.2	2	15.19	0	4.46E+05		(R)GGAEGE	(R)G G\A|E/G E/L|Q/A L R(A)		116.58	550.7883	1100.57	-0.0001	-0.1	4.53	533778	5.74	HUMAN	Q15149	Plectin
2795	dirMS_041712_NAR_30mM_plus2.19785.19785.2	2	15.19	0	2.33E+05		(K)GFAFVQ	(K)G F\A|F/V|Q/Y|V/N E R(N)		157.57	665.3326	1329.659	-0.0007	-0.5	6	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
2796	dirMS_041712_NAR_30mM_plus2.19959.19959.2	2	15.19	0	5.04E+04		(K)TFESLVI	(K)T/F|E|S L/V D/F S K(A)		158.22	586.793	1172.583	-0.0047	-4	4.37	35407.1	6.73	HUMAN	E9PF18	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial
2797	dirMS_041712_NAR_60mM_plus.6934.6974.3	3	15.19	1	2.81E+05		(R)VISSIEQI	(R)V/I|S S I/E/Q/K T E/R(N)		94.73	430.5686	1289.706	-0.0147	-11.4	6.11	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
2798	dirMS_041712_NAR_50mM_minus2.16418.16418.3	3	15.18	0	1.24E+05		(R)IMEVID/	(R)I/M|E/V/I/D A I T/T T/A/Q S H/Q R(T)		161.6	638.6598	1913.975	-0.0101	-5.3	5.32	85815.7	7.35	HUMAN	P17858	6-phosphofructokinase, liver type
2799	dirMS_041712_NAR_50mM_minus2.17018.17038.3	3	15.18	0	1.55E+05		(R)LLEVLSG	(R)L L|E|V/L\S/G E I L/P K/P\T K(G)		165.35	546.3329	1636.988	-0.0042	-2.6	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
2800	dirMS_041712_NAR_50mM_minus2.7016.7166.3	3	15.18	1	7.15E+05		(K)GAVAED	(K)G A|V|A|E/D/G D E L R T E/P E/A K(K)		107.32	596.2904	1786.845	0.0113	6.3	4.08	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
2801	dirMS_041712_NAR_60mM_minus.13595.13626.3	3	15.18	0	2.18E+05		(K)FADEHV	(K)F/A|D E H\V|P G S/P F T V K(I)		135.83	510.9286	1530.759	0.0125	8.2	5.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
2802	dirMS_041712_NAR_60mM_minus.13829.14285.3	3	15.18	1	9.82E+06		(R)IQLVEEE	(R)I/Q\L|V/E E/E/L D/R A Q E/R(L)		138.48	576.6347	1727.892	-0.0027	-1.6	4.25	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
2803	dirMS_041712_NAR_60mM_minus.6491.6491.3	3	15.18	1	1.71E+05		(R)AQLGGF	(R)A Q|L|G G/P E A A/K S D E T A A K(-)		94.9	548.6116	1643.824	-0.0033	-2	4.68	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
2804	dirMS_041712_NAR_120mM_plus.14159.14159.4	4	15.18	1	5.85E+05		(R)LEAPELF	(R)L E|A/P E/L/P V/K V/N P/T K P R(R)		127.43	447.7616	1788.038	-0.0132	-7.4	8.59	10558	9.4	HUMAN	H0YE28	Protein C11orf31 (Fragment)
2805	dirMS_041712_NAR_120mM_plus.15296.15441.3	3	15.18	0	1.10E+06		(K)HLEINPI	(K)H/L|E I N\P D|H|P/I/V E T L R(Q)		133.9	594.9869	1782.95	-0.0036	-2	5.27	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
2806	dirMS_041712_NAR_20mM_plus.15105.15105.2	2	15.18	0	2.17E+05		(K)GLAITFV	(K)G L A\I|T|F/V|S/D E N D A K(I)		175.3	740.3693	1479.733	-0.0012	-0.8	4.03	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
2807	dirMS_041712_NAR_30mM_plus2.21121.21121.2	2	15.18	0	6.77E+05		(K)IPDWFLI	(K)I/P/D/W F L N R(Q)		165.77	530.785	1060.557	0.0053	5	5.84	9767.1	11.41	HUMAN	J3JS69	40S ribosomal protein S18
2808	dirMS_041712_NAR_30mM_minus2.17127.17127.2	2	15.17	0	4.44E+04		(K)LGINSLC	(K)L/G/I/N/S/L/Q E L/K(Q)		146.95	557.8242	1114.647	-0.0055	-5	6	25978.5	4.91	HUMAN	C9J502	Prostate leucine zipper variant 2
2809	dirMS_041712_NAR_30mM_minus2.19620.19620.2	2	15.17	0	4.38E+05		(R)ASLSLW	(R)A S/L/S\L/W/Q/A M E/K(G)		162.85	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
2810	dirMS_041712_NAR_40mM_minus2.12770.12835.3	3	15.17	0	1.42E+05		(K)IEVIKPG	(K)I/E|V|I/K/P/G D/L/G V D L T S K(L)		159.03	561.989	1683.953	-0.0003	-0.2	4.56	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
2811	dirMS_041712_NAR_50mM_minus2.10559.10561.3	3	15.17	1	2.88E+05		(K)NQVAM	(K)N Q|V|A/M/N/P T N/T V/F/D A K R(L)		128.55	602.6379	1805.896	0.0029	1.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
2812	dirMS_041712_NAR_50mM_minus2.13380.13380.3	3	15.17	0	3.49E+05		(R)EQTLSP1	(R)E Q/T L/S/P T/I/T/S/G L H N I A R(S)		143.7	613.3274	1837.977	-0.009	-4.9	6.85	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
2813	dirMS_041712_NAR_60mM_minus.10376.10376.3	3	15.17	1	6.05E+05	M88m	(K)DVDEAY	(K)D V|D/E|A Y\m N/K V E L E/S R(L)	m:Oxidized methionine	118.37	605.2791	1797.832	15.9904	-2.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
2814	dirMS_041712_NAR_120mM_plus.13278.13324.3	3	15.17	2	6.46E+05		(R)ELNITAA	(R)E L/N|I/T/A/A\K E I/E/V/G G G R K(A)		123.02	595.6661	1784.987	-0.0027	-1.5	6.33	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
2815	dirMS_041712_NAR_120mM_plus.17586.18122.3	3	15.17	1	2.34E+06		(R)RAPFDLI	(R)R A\P F\D|L|F E/N/R(K)		146.97	422.22	1264.643	0.0022	1.7	6.07	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
2816	dirMS_041712_NAR_30mM_plus2.20824.20913.2	2	15.17	0	3.07E+05		(K)LVLPSLI	(K)L V|L|P/S L/I/S S/R(I)		163.97	542.8382	1084.672	-0.0033	-3.1	9.75	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
2817	dirMS_041712_NAR_60mM_plus.12115.12115.2	2	15.17	1	1.52E+06		(R)DGKLVS	(R)D/G K/L|V/S\E S S D V/L/P K(-)		120.25	737.3869	1473.78	-0.013	-8.8	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2818	dirMS_041712_NAR_60mM_plus.12339.12339.3	3	15.17	1	4.98E+05		(R)TSDVGG	(R)T/S/D/V/G/G Y Y Y E/K I\E R(T)		121.18	560.6017	1679.791	-0.0006	-0.4	4.68	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
2819	dirMS_041712_NAR_120mM_minus.16063.16063.4	4	15.16	2	2.10E+05		(K)KQGGLC	(K)K Q G G L/G|P M N\I/P L|V S D/P K R(T)		141.62	477.5179	1907.053	-0.0034	-1.8	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
2820	dirMS_041712_NAR_30mM_minus2.14980.14980.2	2	15.16	0	5.54E+05	M316m	(R)ISEQFTA	(R)I/S\E/Q/F/T A/m F R(R)	m:Oxidized methionine	135.18	623.3014	1229.598	15.9972	1.8	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
2821	dirMS_041712_NAR_50mM_minus2.11493.11493.3	3	15.16	0	1.45E+05		(K)VSQPIE(	(K)V/S Q/P I|E G H A/A S F A/Q F K(M)		133.52	572.9609	1716.87	-0.0022	-1.3	6.72	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
2822	dirMS_041712_NAR_60mM_minus.10515.10515.3	3	15.16	1	1.64E+06		(K)TLQEVTI	(K)T L/Q/E V/T/E|M D/S V/K R(Y)		119.37	512.5957	1535.773	-0.0008	-0.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
2823	dirMS_041712_NAR_60mM_minus.13694.13694.3	3	15.16	1	2.69E+05		(K)SLLSNLD	(K)S L/L/S/N L\D E V/K K(E)		136	415.9055	1245.705	-0.0029	-2.4	5.79	96649	6.13	HUMAN	Q8WUM4	Programmed cell death 6-interacting protein
2824	dirMS_041712_NAR_30mM_plus2.11938.11973.2	2	15.16	0	6.57E+05		(K)LEAEIAT	(K)L/E|A|E|I\A|T Y R(R)		116.08	533.2814	1065.557	-0.002	-1.9	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2825	dirMS_041712_NAR_50mM_plus2.19780.19780.3	3	15.16	0	3.09E+05		(K)ILFIFIDSI	(K)I L|F|I/F I/D S D H T D N Q/R(I)		172.6	611.9758	1833.913	-0.0001	-0.1	4.41	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
2826	dirMS_041712_NAR_60mM_plus.16493.16946.3	3	15.16	0	1.18E+06		(K)TTISVAH	(K)T T|I/S/V/A/H/L/L A A/R(Q)		144.27	418.2478	1252.737	-0.0083	-6.7	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
2827	dirMS_041712_NAR_60mM_plus.5762.5762.3	3	15.16	1	8.61E+04	M117m	(R)ARQENG	(R)A R Q\E N G\m|P E/E/P A T T A R(G)	m:Oxidized methionine	88.33	591.9441	1757.824	15.9942	-0.4	4.79	64356.2	9.96	HUMAN	O96013	Serine/threonine-protein kinase PAK 4
2828	dirMS_041712_NAR_30mM_minus2.7408.7408.2	2	15.15	0	1.44E+05		(R)FGGSGS	(R)F/G/G\S/G/S Q/V/D/S A/R(M)		94.65	584.2729	1167.539	-0.0004	-0.3	5.84	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
2829	dirMS_041712_NAR_40mM_minus2.11961.11961.3	3	15.15	0	2.64E+05		(K)DAGEGL	(K)D A|G|E|G/L/L A V Q/I T D P E G K\P K(K)		153.95	646.6785	1938.018	0.0031	1.6	4.32	283472.4	5.71	HUMAN	P21333	Filamin-A

2830	dirMS_041712_NAR_50mM_minus2.7744.7765.3	3	15.15	0	2.44E+05		(R)LESGMC	(R)L/E|S G M Q/N/M/S I/H/T/K(T)		111.27	492.5712	1475.698	0.0009	0.6	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2831	dirMS_041712_NAR_60mM_minus.5713.5713.2	2	15.15	1	4.42E+06		(K)DSYVGD	(K)D S/Y/V/G/D/E A Q S/K/R(G)		87.58	677.8144	1354.623	-0.0018	-1.3	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
2832	dirMS_041712_NAR_120mM_plus.11645.11645.4	4	15.15	1	2.63E+05		(R)LQQLGE	(R)L Q\Q/L|G/E/A H/Q A E T E V L R R(E)		114.02	495.2678	1978.046	0.0029	1.5	5.5	97620.5	5.02	HUMAN	F5H4J1	Nuclear mitotic apparatus protein 1 (Fragment)
2833	dirMS_041712_NAR_30mM_plus2.17148.17290.2	2	15.15	0	3.36E+05		(K)TVFGVEI	(K)T V|F/G|V|E P|D L T R(E)		143.33	617.3263	1233.647	-0.0021	-1.7	4.37	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
2834	dirMS_041712_NAR_30mM_plus2.6622.6717.2	2	15.15	0	1.10E+06		(K)SLDEME	(K)S/L|D|E M/E/K(Q)		90	426.1971	851.381	0.0054	6.4	4.14	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
2835	dirMS_041712_NAR_50mM_plus2.14006.14006.3	3	15.15	1	6.07E+05		(K)GGELVY	(K)G G\E/L/V/Y/T/D S E A R D V/F E K(A)		141.53	638.9735	1914.908	-0.002	-1.1	4.18	533778	5.74	HUMAN	Q15149	Plectin
2836	dirMS_041712_NAR_50mM_plus2.19975.20249.3	3	15.15	0	2.96E+05		(R)DYLHLPI	(R)D Y L H L\P\P E\I|V|P/A T L R(R)		173.92	578.658	1733.959	0.001	0.6	5.32	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
2837	dirMS_041712_NAR_60mM_plus.17492.17492.3	3	15.15	1	3.74E+05		(R)KVPGVT	(R)K\V P G V\T A\I\E|L|D/E/D/T/G T F R(I)		148.18	650.0017	1948.002	-0.0117	-6	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
2838	dirMS_041712_NAR_120mM_minus.4243.4243.3	3	15.14	1	6.83E+05		(R)EPGPAG	(R)E P/G/P/A G R G D G/D S/G R(S)		70.47	443.2041	1327.599	-0.0008	-0.6	4.56	558007.1	5.44	HUMAN	P58107	Epiplakin
2839	dirMS_041712_NAR_50mM_minus2.14124.14124.3	3	15.14	0	3.40E+05		(K)SPAPPLL	(K)S/P/A/P/P L L H V/A A L G Q/K(Q)		148.45	500.2911	1498.874	-0.0153	-10.2	8.49	17549.1	10.39	HUMAN	E5RFJ3	DBIRD complex subunit KIAA1967 (Fragment)
2840	dirMS_041712_NAR_50mM_minus2.16703.16703.3	3	15.14	1	9.23E+04		(R)DSEQVA	(R)D/S/E/Q/V/A E/L K/Q E L A T L K(S)		163.05	601.3217	1801.954	-0.0036	-2	4.41	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
2841	dirMS_041712_NAR_50mM_minus2.8818.8839.3	3	15.14	1	2.50E+06	M227m	(R)mQKEIT	(R)m Q K E\I|T|A|L|A|P S T M K(I)	m:Oxidized methionine	118.07	522.2727	1548.812	15.9911	-2.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
2842	dirMS_041712_NAR_60mM_minus.13847.14329.3	3	15.14	1	9.82E+06		(R)IQLVEEE	(R)I/Q|L|V/E E/E L D/R A Q E/R(L)		138.48	576.6347	1727.892	-0.0027	-1.6	4.25	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
2843	dirMS_041712_NAR_60mM_minus.15008.15029.3	3	15.14	0	4.49E+06		(R)EHALLA	(R)E H A\L\L|A|Y/T/L/G V/K(Q)		144.57	438.9202	1314.742	0.0044	3.4	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
2844	dirMS_041712_NAR_20mM_plus.10634.10634.2	2	15.14	0	4.78E+04		(K)GILAADE	(K)G I|L|A|A|D E\S T\G S I/A/K(R)		145.93	666.8531	1332.7	-0.0016	-1.2	4.37	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
2845	dirMS_041712_NAR_20mM_plus.12947.12947.2	2	15.14	0	4.05E+05		(K)LSELEAA	(K)L/S|E|L/E A/A\L Q R(A)		161.95	565.3132	1129.621	-0.002	-1.8	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2846	dirMS_041712_NAR_50mM_plus2.11167.11167.3	3	15.14	0	3.91E+05		(K)LQAEAP	(K)L/Q/A E/A P/H I V V/G T P G R(V)		126.6	515.6223	1544.854	-0.002	-1.3	6.75	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
2847	dirMS_041712_NAR_120mM_minus.20018.20018.3	3	15.13	0	7.83E+04		(R)INLWHL	(R)I/N|L\W/H L/E/I T D R(S)		165.22	470.5897	1409.754	0.001	0.7	5.32	52204.6	5.82	HUMAN	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
2848	dirMS_041712_NAR_30mM_minus2.17811.17901.2	2	15.13	0	1.96E+05		(K)FFFDPSA	(K)F/F|F/D|P/S A/R(D)		151.65	493.7405	986.473	0.0007	0.7	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin
2849	dirMS_041712_NAR_30mM_minus2.18339.18573.2	2	15.13	0	4.14E+05		(R)ADLIAYL	(R)A/D|L|I|A/Y/L/K(K)		154.65	453.7668	906.529	-0.0032	-3.5	5.88	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
2850	dirMS_041712_NAR_50mM_minus2.15210.15210.3	3	15.13	0	4.10E+05		(K)AETLASS	(K)A E|T/L/A/S S/L Q E/D L/A H T R(N)		154.98	581.2998	1741.872	0.0133	7.7	4.65	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
2851	dirMS_041712_NAR_120mM_plus.8321.8337.3	3	15.13	1	9.59E+05		(R)VITEEEK	(R)V/I|T/E/E/E/K N F K(A)		97.13	412.8845	1236.647	-0.0081	-6.5	4.79	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
2852	dirMS_041712_NAR_20mM_plus.9468.9641.2	2	15.13	0	3.16E+05		(K)LVLVGD	(K)L/V|L|V/G/D/G G T G K(T)		137.4	508.292	1015.578	-0.0015	-1.5	5.84	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
2853	dirMS_041712_NAR_20mM_plus.9802.9802.2	2	15.13	0	1.46E+05		(K)YQAVTA	(K)Y Q|A|V/T/A T/L E/E K(R)		139.28	626.8223	1252.642	-0.0046	-3.7	4.53	23633.9	11.02	HUMAN	P40429	60S ribosomal protein L13a
2854	dirMS_041712_NAR_50mM_plus2.15515.15515.3	3	15.13	0	1.51E+06		(R)LASTLVH	(R)L/A|S T L V H L\G E Y/Q A|A\V/D G A R(K)		149.68	657.6802	1971.029	-0.0034	-1.7	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
2855	dirMS_041712_NAR_50mM_plus2.20652.20652.3	3	15.13	1	1.70E+05		(R)VNSKFD	(R)V N/S/K F D\T\I/Y\Q/I/L/L K(K)		177.62	561.3209	1681.952	-0.0042	-2.5	8.47	72626.7	9.13	HUMAN	Q14258	E3 ubiquitin/ISG15 ligase TRIM25
2856	dirMS_041712_NAR_60mM_plus.10013.10013.2	2	15.13	0	9.64E+05		(R)LESGMC	(R)L E|S G M\Q/N M S I/H/T|K(T)		110.1	738.3522	1475.698	-0.001	-0.7	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2857	dirMS_041712_NAR_120mM_minus.18191.18191.4	4	15.12	1	3.15E+05		(K)ILGSGIS	(K)I L G S G\I/S/S/S/S V/L/H G M V F K K(E)		154.12	487.5223	1947.073	-0.0058	-3	10	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
2858	dirMS_041712_NAR_120mM_minus.7300.7300.3	3	15.12	0	4.15E+05		(K)NNRPSE	(K)N/N|R P S E|G|P/L/Q/T/R(L)		94.1	456.9036	1368.698	-0.0016	-1.2	9.6	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
2859	dirMS_041712_NAR_30mM_minus2.15304.15609.2	2	15.12	0	3.50E+05		(R)IVFQEFR	(R)I/V|F/Q E/F/R(Q)		137.48	469.7582	938.509	-0.0003	-0.3	6	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
2860	dirMS_041712_NAR_50mM_minus2.11973.11973.3	3	15.12	1	3.56E+05		(K)AVLFCLS	(K)A/V|L F C/L/S/E D K/K(N)	C:Carbamidomethylation	136.05	437.2326	1309.682	0.0012	0.9	6.11	22956	8.8	HUMAN	E9PK25	Cofilin-1
2861	dirMS_041712_NAR_50mM_minus2.17426.17426.3	3	15.12	1	3.59E+05		(K)GYPPED	(K)G Y|P P E/D I/F N\L V G K K(V)		167.22	526.2832	1576.837	-0.0019	-1.2	6.07	40763.2	6.29	HUMAN	Q9NR45	Sialic acid synthase
2862	dirMS_041712_NAR_50mM_minus2.17921.17921.3	3	15.12	1	8.25E+05		(K)TFVNITP	(K)T F/V/N/I|T/P/A E V/G V L V G K D R(S)		171.32	639.0247	1915.065	-0.0052	-2.7	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
2863	dirMS_041712_NAR_60mM_minus.7132.7132.3	3	15.12	1	3.04E+05		(R)ELFESST	(R)E L|F/E/S/S T N N N K D/T K(Q)		98.72	542.9247	1626.761	-0.001	-0.6	4.68	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
2864	dirMS_041712_NAR_60mM_minus.9298.9298.3	3	15.12	1	2.37E+05		(R)QDSAAV	(R)Q D/S/A/A/V/G F/D Y K/E K(L)		111.87	486.5639	1457.691	-0.0136	-9.3	4.56	61756.2	5.24	HUMAN	Q14247	Src substrate cortactin
2865	dirMS_041712_NAR_120mM_plus.11651.11651.2	2	15.12	1	8.55E+05		(R)NLKASLE	(R)N/L|K/A/S/L E N S L R(E)		114.02	622.8511	1244.696	-0.0008	-0.6	8.75	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2866	dirMS_041712_NAR_20mM_plus.19128.19128.3	3	15.12	0	1.99E+05		(K)TLETQSA	(K)T L E\T Q S/A L G/P/A L Q/A A F K(L)		202.6	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
2867	dirMS_041712_NAR_50mM_plus2.10975.10975.3	3	15.12	0	1.94E+05		(K)ADDGRF	(K)A/D|D/G R P F/P Q V\I/K(S)		125.1	448.2419	1342.711	-0.0002	-0.2	6	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
2868	dirMS_041712_NAR_50mM_plus2.14296.14315.3	3	15.12	0	1.11E+06		(R)IVATKPL	(R)I/V|A/T K/P L/Y/V/A/L/A Q R(K)		143.7	514.9831	1542.937	-0.0019	-1.2	9.99	65918.2	9.74	HUMAN	E7EQV3	Polyadenylate-binding protein 1
2869	dirMS_041712_NAR_50mM_plus2.16908.17051.3	3	15.12	1	6.11E+05		(K)ISMPDID	(K)I/S\M/P|D I/D L/N L|K/G P K(V)		157.08	514.2847	1540.84	-0.0008	-0.5	5.96	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
2870	dirMS_041712_NAR_50mM_plus2.19871.20032.3	3	15.12	0	4.71E+05		(K)HSQFIGY	(K)H S Q F\I G|Y|P/I/T/L/Y L\E K(E)		173.82	603.6541	1808.958	-0.0104	-5.7	6.75	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
2871	dirMS_041712_NAR_60mM_plus.12326.12601.3	3	15.12	0	1.52E+06		(K)ADDGRF	(K)A/D|D/G R P/F|P Q V/I/K(S)		121.6	448.2414	1342.711	-0.0017	-1.3	6	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
2872	dirMS_041712_NAR_120mM_minus.14076.14076.2	2	15.11	1	4.39E+06		(K)FASFIDK	(K)F A|S/F|I/D K V/R(F)		130.18	541.7968	1082.599	-0.013	-12	8.75	19569.8	9.88	HUMAN	F8VRG4	Keratin, type II cytoskeletal 8 (Fragment)
2873	dirMS_041712_NAR_30mM_minus2.14298.14597.2	2	15.11	0	5.88E+06		(K)LLIEMEC	(K)L/L|I|E/M/E/Q/R(L)		133.73	516.281	1031.555	-0.0007	-0.6	4.53	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
2874	dirMS_041712_NAR_30mM_minus2.18046.18066.2	2	15.11	0	4.12E+05		(R)LLLNNDI	(R)L/L|L|N/N/D/N L L/R(E)		153.13	599.3487	1197.695	-0.0049	-4.1	5.84	19945.8	4.97	HUMAN	B4DG50	F-actin-capping protein subunit alpha-2
2875	dirMS_041712_NAR_30mM_plus2.12527.12527.2	2	15.11	0	2.66E+05		(R)ELAEDG	(R)E L|A|E/D G Y/S\G\V|E V R(V)		118.92	712.3382	1423.67	-0.0008	-0.6	4	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
2876	dirMS_041712_NAR_30mM_plus2.16992.16992.2	2	15.11	0	5.45E+05	M256m	(R)SLDmDS	(R)S/L/D m/D|S/I/I|A E/V\K(A)	m:Oxidized methionine	142.22	668.8384	1320.671	15.998	2.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
2877	dirMS_041712_NAR_30mM_plus2.21352.21375.2	2	15.11	0	2.35E+04		(R)GAFQNL	(R)G A F|Q/N/L/F/Q|S/V/R(E)		167.87	633.8315	1266.659	-0.0032	-2.5	9.75	68629.9	5.59	HUMAN	E7EVX6	Androgen receptor
2878	dirMS_041712_NAR_30mM_plus2.7713.8154.2	2	15.11	0	1.42E+06		(K)IAVAAQ	(K)I/A|V|A|A/Q/N/C Y K(V)	C:Carbamidomethylation	94.57	569.2905	1137.572	0.0016	1.4	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
2879	dirMS_041712_NAR_60mM_plus.20646.20646.3	3	15.11	1	7.14E+05		(R)LDLAGR	(R)L D|L/A G R D L T D/Y/L/M/K(I)		168.28	541.9516	1623.841	-0.0008	-0.5	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
2880	dirMS_041712_NAR_60mM_plus.5234.5234.3	3	15.11	0	2.64E+04		(R)TATEKP	(R)T A|T E/K/P G/P A E A A/R(Q)		84.77	433.5671	1298.67	0.0168	13	5.81	49823.3	9.39	HUMAN	B4DQQ4	NADPH:adrenodoxin oxidoreductase, mitochondrial
2881	dirMS_041712_NAR_120mM_minus.6752.7046.2	2	15.1	0	6.08E+06	M46m	(R)HQGVm	(R)H|Q|G V|m\V/G M/G Q|K(D)	m:Oxidized methionine	91.72	594.2863	1171.571	15.9943	-0.5	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
2882	dirMS_041712_NAR_40mM_minus2.11383.11646.3	3	15.1	0	8.05E+05		(R)TIQVENS	(R)T I|Q|V/E/N\S H L/I/L/T/G A/G A L N K(V)		151	660.3663	1979.092	-0.0077	-3.9	6.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
2883	dirMS_041712_NAR_40mM_minus2.8603.8603.3	3	15.1	0	2.87E+05		(R)SVIDPVF	(R)S V I|D|P/V/P A/P V G D S H V D G A A K(S)		132.52	644.3329	1930.987	-0.0027	-1.4	4.41	58326.8	5.7	HUMAN	Q13177	Serine/threonine-protein kinase PAK 2
2884	dirMS_041712_NAR_120mM_plus.8135.8135.3	3	15.1	0	7.47E+05		(K)LFNHAN	(K)L/F N/H A N/Q E V/Q/R(H)		96.6	452.5653	1355.681	-0.0001	-0.1	6.75	87537	9.67	HUMAN	Q9Y446	Plakophilin-3
2885	dirMS_041712_NAR_30mM_plus2.10614.10628.2	2	15.1	0	3.95E+05		(K)TGTVSLE	(K)T G|T|V/S/L/E/V/R(L)		109.33	481.2676	961.531	-0.0034	-3.5	5.66	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
2886	dirMS_041712_NAR_30mM_plus2.7652.8180.2	2	15.1	0	1.35E+07		(R)STFSTNY	(R)S T|F/S/T/N/Y/R(S)		94.53	488.2306	975.453	0.0009	0.9	8.46	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
2887	dirMS_041712_NAR_40mM_plus2.17814.17814.3	3	15.1	0	1.42E+05		(R)DIKPQN	(R)D I K P Q N\L\L|L/D/P D T A V L K(L)		170.92	631.6874	1893.069	-0.0215	-11.4	4.43	47257	9.38	HUMAN	P49841	Glycogen synthase kinase-3 beta
2888	dirMS_041712_NAR_50mM_plus2.16612.16736.3	3	15.1	0	5.93E+05		(K)AVDIPHI	(K)A/V|D/I/P H/M/D I E A L/K(K)		155.63	484.589	1451.756	-0.0038	-2.6	4.54	25002	10.06	HUMAN	P62906	60S ribosomal protein L10a
2889	dirMS_041712_NAR_60mM_plus.13118.13118.3	3	15.1	0	5.35E+04		(K)VNGRPL	(K)V/N/G R P L E M/I/E/P/R(T)		125.57	470.9225	1410.752	0.0008	0.5	6.11	16559.1	10.36	HUMAN	P62249	40S ribosomal protein S16
2890	dirMS_041712_NAR_60mM_plus.13606.14176.3	3	15.1	0	2.61E+07		(R)NLDIERF	(R)N/L|D|I/E R/P T Y/T/N L N/R(L)		129.02	573.6312	1718.882	-0.003	-1.7	6.07	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
2891	dirMS_041712_NAR_60mM_plus.14913.15180.3	3	15.1	1	5.39E+06		(R)GYSFTTT	(R)G Y|S|F/T T/T A E R E I V/R(D)		134.97	543.9389	1629.823	-0.021	-12.9	6.14	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
2892	dirMS_041712_NAR_60mM_plus.7178.7178.2	2	15.1	0	1.72E+06		(K)STTTGHI	(K)S T|T/T/G H L/I Y K(C)		95.58	560.8031	1120.6	-0.0008	-0.7	8.34	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
2893	dirMS_041712_NAR_120mM_minus.14478.14623.3	3	15.09	1	1.99E+06		(R)QLREYQ	(R)Q L/R E Y\Q/E/L/M N/V/K(L)		133.6	517.6038	1550.8	-0.0027	-1.7	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2894	dirMS_041712_NAR_30mM_minus2.9905.9928.2	2	15.09	0	8.17E+04		(R)LEDAAD	(R)L/E|D|A|A D/V/Y/R(G)		108.18	526.2618	1051.506	0.0109	10.3	4.03	102525.8	7.33	HUMAN	Q9BXJ9	N-alpha-acetyltransferase 15, NatA auxiliary subunit
2895	dirMS_041712_NAR_40mM_minus2.10357.10750.3	3	15.09	1	3.05E+06		(K)TITLEVEI	(K)T I|T|L/E/V/E/P S D T I E N V K A K(I)		145.98	663.0226	1987.059	-0.0061	-3.1	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
2896	dirMS_041712_NAR_50mM_minus2.10744.10744.3	3	15.09	0	2.68E+05		(K)VFEGNR	(K)V/F/E/G N R P T N S I\V/F/T K(L)		129.25	570.3032	1708.902	-0.0066	-3.9	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
2897	dirMS_041712_NAR_30mM_plus2.12002.12002.2	2	15.09	0	1.59E+05		(K)GYDVIA	(K)G Y D\V|I|A|Q/A Q/S G T G K(T)		115.98	697.848	1394.691	-0.0023	-1.7	5.83	16071.1	4.8	HUMAN	B4E102	Eukaryotic initiation factor 4A-I
2898	dirMS_041712_NAR_30mM_plus2.19060.19060.2	2	15.09	0	1.50E+05		(R)VYSLFLD	(R)V/Y/S L/F/L D/E S R(S)		153.13	614.8154	1228.621	0.0027	2.2	4.37	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
2899	dirMS_041712_NAR_30mM_plus2.8775.8934.2	2	15.09	0	2.43E+06		(R)VIGSGCI	(R)V/I|G/S/G C/N L/D S A/R(F)	C:Carbamidomethylation	99.68	624.802	1248.6	-0.0034	-2.7	5.81	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
2900	dirMS_041712_NAR_50mM_plus2.13203.13203.3	3	15.09	1	9.66E+05		(R)ELNITAA	(R)E L/N I/T A A K E\I/E|V/G G/G R(K)		137.7	552.9671	1656.892	-0.0048	-2.9	4.79	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
2901	dirMS_041712_NAR_50mM_plus2.17798.17852.3	3	15.09	0	4.45E+05	M64m	(R)GFGFITF	(R)G F|G\F|I|T/F T N/P E H A S V/A m R(A)	m:Oxidized methionine	161.67	666.658	1981.959	16.0006	2.8	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
2902	dirMS_041712_NAR_60mM_plus.9406.9447.3	3	15.09	1	1.94E+06		(K)VVWVEE	(K)V/V|W/V/E/E S D/K R(S)		107.43	416.221	1246.643	0.0058	4.7	4.68	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
2903	dirMS_041712_NAR_60mM_minus.12256.12282.3	3	15.08	1	7.93E+05		(K)AVIFCLS	(K)A V|I/F/C/L/S A D/K K(C)	C:Carbamidomethylation	127.92	417.9007	1251.677	0.011	8.8	8.64	15739.2	9.3	HUMAN	F6RFD5	Destrin
2904	dirMS_041712_NAR_60mM_minus.12541.12952.3	3	15.08	1	1.26E+06		(K)AVLFCLS	(K)A/V|L/F/C/L/S E D K/K(N)	C:Carbamidomethylation	131.25	437.2334	1309.682	0.0036	2.7	6.11	22956	8.8	HUMAN	E9PK25	Cofilin-1
2905	dirMS_041712_NAR_50mM_plus2.14794.14934.3	3	15.08	0	8.03E+05		(R)TIQVENS	(R)T I|Q|V/E N\S H L/I/L/T/G A/G A L N K(V)		146.07	660.3668	1979.092	-0.0062	-3.1	6.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
2906	dirMS_041712_NAR_60mM_plus.11245.11246.3	3	15.08	1	3.12E+05		(R)AGTGVD	(R)A/G/T|G/V/D N V D L E/A/A T R K(G)		116.3	539.6102	1616.824	-0.0078	-4.8	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
2907	dirMS_041712_NAR_60mM_plus.6488.6488.3	3	15.08	1	2.39E+05		(R)LTQEPES	(R)L/T|Q/E/P E S I R K(W)		92.45	400.8875	1200.658	-0.0103	-8.6	6.14	8409.9	4.52	HUMAN	H0Y9Q6	Clathrin light chain B (Fragment)
2908	dirMS_041712_NAR_20mM_minus.7205.7205.2	2	15.07	0	1.49E+04	M33m	(R)IDEmPE	(R)I/D|E m/P E/A A V K(S)	m:Oxidized methionine	120.27	559.7733	1102.545	15.9944	-0.4	4.14	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
2909	dirMS_041712_NAR_30mM_minus2.19507.19580.2	2	15.07	0	7.67E+06		(R)YLTVAA	(R)Y/L|T|V/A/A V/F R(G)		161.2	520.2998	1039.593	-0.0012	-1.1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
2910	dirMS_041712_NAR_40mM_minus2.13736.13826.3	3	15.07	1	3.98E+05		(R)VTFSGLF	(R)V T|F/S G L/R D T|V/T/P G E/L L/K(A)		164.73	611.6742	1833.012	-0.0036	-2	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
2911	dirMS_041712_NAR_50mM_minus2.10986.11110.3	3	15.07	1	5.59E+05		(K)QQEAAL	(K)Q\Q/E/A/A\L/E/L/E E L\K K(K)		131.1	510.2775	1528.822	-0.0038	-2.5	4.49	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
2912	dirMS_041712_NAR_50mM_minus2.11061.11258.3	3	15.07	0	1.44E+06		(R)NLDIERF	(R)N/L|D|I/E R/P T Y/T/N L N R(L)		131.95	573.6313	1718.882	-0.0027	-1.6	6.07	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
2913	dirMS_041712_NAR_50mM_minus2.16892.16892.3	3	15.07	1	2.84E+05		(R)SELELTL	(R)S/E|L/E/L/T L G K L E/Q V R(S)		163.78	538.9725	1614.906	-0.0032	-2	4.78	533778	5.74	HUMAN	Q15149	Plectin
2914	dirMS_041712_NAR_50mM_minus2.8695.8695.3	3	15.07	0	1.65E+05	M180m	(R)VVVLmG	(R)V/V|V|L m/G S/T S D/L G H C E K(I)	C:Carbamidomethylation m:Oxid	117.55	583.2829	1731.84	15.9937	-0.7	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
2915	dirMS_041712_NAR_30mM_plus2.11535.11535.2	2	15.07	0	5.15E+05		(R)SGEGEV	(R)S/G\E|G/E/V S G L\M/R(K)		114.07	561.2662	1121.526	-0.0004	-0.4	4.53	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
2916	dirMS_041712_NAR_30mM_plus2.14632.15016.2	2	15.07	0	3.35E+07		(K)WSLLQC	(K)W/S|L/L/Q/Q/Q/K(T)		130.53	515.7855	1030.568	-0.0043	-4.2	8.75	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
2917	dirMS_041712_NAR_50mM_plus2.13232.13232.3	3	15.07	0	2.15E+06		(R)SCTVNIN	(R)S C|T/V/N/I/M/F/G T/P Q E/H R(N)	C:Carbamidomethylation	138.4	592.9438	1776.816	0.0012	0.7	6.47	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
2918	dirMS_041712_NAR_60mM_plus.14463.14463.3	3	15.07	0	3.18E+06		(R)DLNYCF	(R)D L/N|Y/C/F/S G M S D H/R(Y)	C:Carbamidomethylation	132.38	534.5555	1601.647	0.0048	3	5.21	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
2919	dirMS_041712_NAR_60mM_plus.9853.9879.3	3	15.07	1	2.90E+05		(K)SEEQLKE	(K)S/E|E/Q/L/K E E/G I E/Y K(V)		109.28	527.9264	1581.764	0.0004	0.2	4.32	43928.7	6.58	HUMAN	B4DHG0	Dihydrolipoyl dehydrogenase, mitochondrial
2920	dirMS_041712_NAR_120mM_minus.7467.7591.3	3	15.06	1	1.42E+06		(R)RQLETL	(R)R Q\L E|T|L/G Q/E/K(L)		95.2	401.2208	1201.653	-0.0057	-4.7	6.14	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
2921	dirMS_041712_NAR_30mM_minus2.15769.15769.2	2	15.06	0	1.23E+05		(R)TINEVEN	(R)T I/N|E/V/E/N Q/I/L T R(D)		139.58	715.3834	1429.765	-0.005	-3.5	4.53	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
2922	dirMS_041712_NAR_50mM_minus2.15063.15063.3	3	15.06	0	4.19E+05		(K)IAILTCPF	(K)I A|I L T/C|P/F/E/P/P K P K(T)	C:Carbamidomethylation	153.57	537.6375	1610.898	0.0005	0.3	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
2923	dirMS_041712_NAR_20mM_plus.18567.18611.3	3	15.06	0	1.88E+04		(R)APVPAS	(R)A P\V\P\A S E\L\L|A|S/G/V/L/S R(A)		199.92	522.9655	1566.885	-0.003	-1.9	6.05	533778	5.74	HUMAN	Q15149	Plectin
2924	dirMS_041712_NAR_20mM_plus.8406.8406.2	2	15.06	0	1.04E+05	M607m M6	(R)mGLAm	(R)m G\L/A m|G/G G G\G A S F/D R(A)	m:Oxidized methionine	128.17	708.3061	1383.614	31.9905	0.5	5.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
2925	dirMS_041712_NAR_30mM_plus2.20116.20444.3	3	15.06	0	5.11E+05		(K)SYELPDC	(K)S Y\E|L/P D G Q|V|I/T I/G N E R(F)		159.87	597.6334	1790.892	-0.0063	-3.5	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
2926	dirMS_041712_NAR_30mM_plus2.5794.5794.2	2	15.06	0	2.62E+05		(K)TSEVNC	(K)T|S|E|V/N C/Y/R(C)	C:Carbamidomethylation	85.08	514.7261	1028.447	-0.0016	-1.6	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
2927	dirMS_041712_NAR_30mM_plus2.8660.8660.2	2	15.06	1	2.10E+05		(R)GVEEEEI	(R)G V/E/E/E\E/E D/G/E M/R E(-)		98.92	769.301	1537.596	-0.0011	-0.7	3.88	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F
2928	dirMS_041712_NAR_50mM_plus2.20077.20077.3	3	15.06	1	1.08E+05		(K)SVISGGL	(K)S V|I/S G G L/D/A L E F I G K K(T)		174.18	545.3096	1633.916	-0.0017	-1	5.79	22133.2	4.82	HUMAN	E5RGF9	Protein FAM114A2 (Fragment)
2929	dirMS_041712_NAR_50mM_plus2.7205.7205.3	3	15.06	1	1.94E+05		(R)DSFDGR	(R)D S|F/D/G R/G P/P G\P/E S Q S R(A)		103.85	563.592	1688.762	-0.0009	-0.5	4.56	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
2930	dirMS_041712_NAR_50mM_plus2.9830.9830.3	3	15.06	1	2.54E+05		(K)TTDMAF	(K)T/T/D M/A/P S K/E T E M A L A K(D)		119.22	575.2802	1723.824	0.0019	1.1	4.68	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
2931	dirMS_041712_NAR_60mM_plus.13065.13585.3	3	15.06	1	1.02E+06		(R)ISVYYNE	(R)I/S|V|Y/Y N/E A/T/G G K Y V/P R(A)		125.95	606.3113	1816.923	-0.0035	-1.9	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
2932	dirMS_041712_NAR_120mM_minus.8757.8757.3	3	15.05	0	5.76E+05		(R)THYSNIE	(R)T\H Y S N\I|E|A|N E/S/E E V/R(Q)		102.13	593.2723	1777.799	0.0036	2	4.48	21983.3	4.68	HUMAN	K7EIV0	Calpain small subunit 1
2933	dirMS_041712_NAR_30mM_minus2.17549.17549.2	2	15.05	0	4.37E+05		(R)EQLAIAE	(R)E Q|L/A/I/A E F A\R(S)		150.25	574.3084	1147.611	-0.0011	-0.9	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
2934	dirMS_041712_NAR_30mM_minus2.8132.8525.2	2	15.05	0	3.66E+06		(R)GTLDPV	(R)G T|L/D/P V/E/K(A)		100.18	429.7348	858.457	0.0056	6.5	4.37	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
2935	dirMS_041712_NAR_120mM_plus.6452.6635.3	3	15.05	1	1.74E+07		(R)TKTEISEI	(R)T\K\T E\I|S/E/M/N/R(N)		88.12	403.5365	1208.594	0.001	0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
2936	dirMS_041712_NAR_20mM_plus.6994.7014.2	2	15.05	0	2.19E+05		(R)LLEAAA	(R)L/L|E|A|A/A Q/S T K(G)		114.93	516.2866	1031.573	-0.0072	-7	6	533778	5.74	HUMAN	Q15149	Plectin
2937	dirMS_041712_NAR_40mM_plus2.17486.17486.3	3	15.05	1	3.17E+05		(K)TGISDVF	(K)T G I/S D\V/F A K/N D/L/A\V/V D/V R(I)		169.33	640.3451	1919.023	-0.0025	-1.3	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
2938	dirMS_041712_NAR_60mM_plus.12037.12098.3	3	15.05	1	7.57E+05		(R)ARQEEL	(R)A R Q\E E\L|Y|S/E/L/Q/A R(E)		120.1	531.6013	1592.803	-0.0134	-8.4	4.79	533778	5.74	HUMAN	Q15149	Plectin

2939	dirMS_041712_NAR_40mM_minus2.11002.11021.3	3	15.04	0	4.86E+05		(R)DAGEGL	(R)D A|G|E G/L/L A/V Q I/T D Q E/G\K\P K(R)		148.02	657.0157	1969.024	0.0089	4.5	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
2940	dirMS_041712_NAR_50mM_minus2.18368.18368.3	3	15.04	0	4.62E+05		(K)ALIEVLQ	(K)A L\I/E/V/L Q/P L I A/E H Q A R(R)		175.42	601.0139	1801.033	-0.0059	-3.3	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
2941	dirMS_041712_NAR_50mM_minus2.9195.9195.3	3	15.04	0	3.48E+05		(R)TIVITSHI	(R)T I|V|I/T S H/P G Q I V K(H)		120.98	464.9452	1392.821	0.0001	0.1	8.44	27999.4	5.61	HUMAN	B7Z5C0	DnaJ homolog subfamily A member 1
2942	dirMS_041712_NAR_20mM_plus.13905.13905.2	2	15.04	0	2.12E+05	M98m	(R)TLTIVDT	(R)T L|T/I/V/D\T G I G/m/T K(A)	m:Oxidized methionine	167.5	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
2943	dirMS_041712_NAR_50mM_plus2.14393.14574.3	3	15.04	1	1.20E+06		(K)ITDIIGKE	(K)I/T|D\I|I/G K E E G\I/G/P E N L R(G)		144.28	618.6652	1853.997	-0.0157	-8.5	4.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
2944	dirMS_041712_NAR_30mM_minus2.12953.13079.2	2	15.03	0	2.84E+05		(K)LSELEPG	(K)L S E|L|E|P/G T G D/L R(F)		124.53	643.8325	1286.659	-0.0009	-0.7	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
2945	dirMS_041712_NAR_60mM_minus.7674.7674.3	3	15.03	1	6.66E+05		(K)IVADKD	(K)I/V/A D K D|Y/S/V/T A N S K(I)		102.58	504.2624	1510.775	-0.0021	-1.4	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
2946	dirMS_041712_NAR_20mM_plus.12632.12632.2	2	15.03	0	9.34E+04	M91m	(R)AITGASL	(R)A I|T|G/A/S|L A D I m A K(R)	m:Oxidized methionine	159.93	639.3398	1261.682	15.9903	-3.6	5.88	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
2947	dirMS_041712_NAR_20mM_plus.13538.13538.2	2	15.03	0	1.60E+05	M98m	(R)TLTIVDT	(R)T L|T\I/V/D T G I/G\m/T K(A)	m:Oxidized methionine	165.8	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
2948	dirMS_041712_NAR_50mM_plus2.19863.19863.3	3	15.03	0	2.50E+05		(K)LFLFHTS	(K)L/F|L F H T S\L|P/I/A E|A/P G K(L)		172.83	580.9943	1740.968	0	0	6.75	108105.4	6.57	HUMAN	E7EP00	Protein transport protein Sec24C
2949	dirMS_041712_NAR_120mM_minus.9163.9163.2	2	15.02	0	4.74E+05		(K)HFVALS	(K)H/F|V|A\L/S T N T/T K(V)		103.53	609.8267	1218.648	-0.0016	-1.3	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
2950	dirMS_041712_NAR_30mM_minus2.12950.12950.2	2	15.02	0	2.77E+04		(K)LYLPVQ	(K)L Y|L|P V Q N K(A)		124.5	487.788	974.567	0.0018	1.8	8.59	22945.2	9.96	HUMAN	Q9Y6A4	UPF0468 protein C16orf80
2951	dirMS_041712_NAR_50mM_minus2.10818.10818.3	3	15.02	1	6.04E+05		(R)IAEFTTN	(R)I/A|E\F T T N L/T/E E E E K\S K(S)		130.4	623.6418	1868.912	-0.0015	-0.8	4.32	227783.5	5.5	HUMAN	P35579	Myosin-9
2952	dirMS_041712_NAR_50mM_minus2.13676.13676.3	3	15.02	0	7.43E+04		(K)MLDAE	(K)M\L/D/A E/D I V/N T A R/P D E/K(A)		146.2	606.2965	1816.875	0.0004	0.2	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
2953	dirMS_041712_NAR_50mM_minus2.15992.15992.3	3	15.02	0	2.36E+05		(K)AQDGS	(K)A/Q/D G S H P L/S/L Q D/L I E K(V)		159.08	584.3049	1750.897	0.0031	1.8	4.54	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
2954	dirMS_041712_NAR_60mM_minus.17913.18151.3	3	15.02	0	1.33E+06		(K)VSHLLGI	(K)V S H\L\L\G\I|N|V|T|D/F T R(G)		161.62	524.623	1571.854	0.0004	0.3	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
2955	dirMS_041712_NAR_20mM_plus.12513.12513.2	2	15.02	0	1.19E+05		(K)IISNASC	(K)I I/S/N|A S C T T/N C L A|P L A K(V)	C:Carbamidomethylation	159.55	917.4626	1833.92	-0.0018	-1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
2956	dirMS_041712_NAR_20mM_plus.13704.13764.2	2	15.02	0	2.08E+05		(K)APILIAT	(K)A P|I|L|I|A/T D/V A S R(G)		166.65	613.8559	1226.71	-0.0058	-4.7	5.88	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
2957	dirMS_041712_NAR_20mM_plus.18421.18555.2	2	15.02	0	1.78E+05		(R)NIPGITL	(R)N/I|P/G/I/T L L/N V/S K(L)		198.83	634.8801	1268.757	-0.0043	-3.4	8.75	37884.5	11.27	HUMAN	H3BM89	60S ribosomal protein L4
2958	dirMS_041712_NAR_30mM_plus2.10588.10588.2	2	15.02	0	3.47E+05		(K)VSYVQLI	(K)V/S|Y/V Q L/K(E)		108.8	418.7442	836.488	-0.0065	-7.8	8.56	334221.3	6.44	HUMAN	P15924	Desmoplakin
2959	dirMS_041712_NAR_30mM_plus2.13359.13359.2	2	15.02	0	5.70E+05		(K)CPFTGN	(K)C/P|F|T/G N V/S I/R(G)	C:Carbamidomethylation	122.88	575.7876	1150.567	0.0006	0.5	9.75	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
2960	dirMS_041712_NAR_30mM_plus2.22647.22659.3	3	15.02	0	5.00E+05		(R)ALTVPEL	(R)A L\T V/P E\L/T/Q Q V/F/D/A K(N)		175.77	553.9697	1659.895	-0.0007	-0.4	4.37	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
2961	dirMS_041712_NAR_30mM_plus2.7539.7559.2	2	15.02	0	8.08E+05		(R)LSVAAQ	(R)L/S|V/A|A/Q/E/A A/R(L)		93.83	508.2801	1015.553	-0.0002	-0.2	6	533778	5.74	HUMAN	Q15149	Plectin
2962	dirMS_041712_NAR_120mM_minus.14084.14374.3	3	15.01	1	1.40E+06		(R)RLEAAY	(R)R L E\A\A|Y|L/D|L/Q/R(I)		132.12	449.9126	1347.738	-0.0147	-10.9	6.07	15962.5	9.61	HUMAN	B4DT30	Tubulin-specific chaperone A
2963	dirMS_041712_NAR_20mM_minus.9696.9716.2	2	15.01	0	3.36E+05		(K)IGGIGTV	(K)I/G|G|I|G|T/V/P V G R(V)		147.47	513.3075	1025.61	-0.0025	-2.4	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
2964	dirMS_041712_NAR_30mM_minus2.15572.15572.2	2	15.01	0	1.45E+05		(K)AMTGV	(K)A M/T/G/V/E Q/W/P Y/R(A)		138.32	669.3172	1337.631	-0.0036	-2.7	6.04	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
2965	dirMS_041712_NAR_30mM_minus2.19359.19505.2	2	15.01	0	2.42E+05		(R)FEELNA	(R)F/E|E|L|N A/D/L/F/R(G)		160.88	627.3141	1253.616	0.0048	3.9	4.14	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
2966	dirMS_041712_NAR_40mM_minus2.12399.12399.3	3	15.01	0	1.70E+05		(R)GAPPSSI	(R)G A/P/P S S N I/E D/F H G L L/P K(G)		155.92	593.6401	1778.907	-0.0014	-0.8	5.32	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
2967	dirMS_041712_NAR_40mM_minus2.9212.9234.3	3	15.01	0	2.52E+05	M240m	(K)mLDAE	(K)m L|D|A/E/D/I/V/N T A R P D/E K(A)	m:Oxidized methionine	136.73	611.627	1816.875	15.9919	-1.6	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
2968	dirMS_041712_NAR_50mM_minus2.11664.11664.3	3	15.01	0	1.12E+05		(R)VTCPNH	(R)V/T/C/P N H|P D A\I L V/E D Y R(A)	C:Carbamidomethylation	134.77	633.641	1898.907	0.0019	1	4.54	25558.6	9.3	HUMAN	B1APE1	General transcription factor IIB (Fragment)
2969	dirMS_041712_NAR_50mM_minus2.14082.14082.3	3	15.01	0	3.40E+05		(K)SPAPPLL	(K)S/P/A|P/P L L H/V A A L/G Q K(Q)		148.45	500.2911	1498.874	-0.0153	-10.2	8.49	17549.1	10.39	HUMAN	E5RFJ3	DBIRD complex subunit KIAA1967 (Fragment)
2970	dirMS_041712_NAR_50mM_minus2.8922.8924.3	3	15.01	1	1.31E+05	M227m	(R)mQKEIT	(R)m Q K E I\T|A|L|A|P S T M/K(I)	m:Oxidized methionine	119.48	522.2727	1548.812	15.9911	-2.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
2971	dirMS_041712_NAR_120mM_plus.4103.4203.3	3	15.01	1	2.05E+06	M54m	(K)SLDEmE	(K)S/L|D/E/m/E/K Q/Q/R(E)	m:Oxidized methionine	70.2	427.2032	1263.6	15.9953	0.3	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
2972	dirMS_041712_NAR_20mM_plus.13157.13258.2	2	15.01	0	6.67E+05		(R)VLQALE	(R)V/L|Q|A/L E/G L/K(M)		164.38	485.8004	970.593	0.0004	0.4	5.97	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
2973	dirMS_041712_NAR_20mM_plus.18875.18875.2	2	15.01	0	2.32E+05		(R)IITLAGP	(R)I I|T L/A|G/P T N A I F K(A)		200.97	679.9039	1358.804	-0.0037	-2.7	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
2974	dirMS_041712_NAR_30mM_plus2.17947.18108.2	2	15.01	0	3.00E+05		(R)VNPALA	(R)V N|P/A/L|A/E L/N L R(S)		147.82	605.3509	1209.695	-0.0005	-0.4	5.97	20026.6	4.67	HUMAN	E9PIK5	Ribonuclease inhibitor (Fragment)
2975	dirMS_041712_NAR_40mM_plus2.18159.18409.3	3	15.01	1	1.59E+06		(R)GDLGIEI	(R)G D L|G|I\E/I/P A E K V F L A Q K(M)		173.97	610.0115	1828.022	-0.0015	-0.8	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
2976	dirMS_041712_NAR_50mM_plus2.13117.13117.3	3	15.01	0	7.93E+05		(R)VLHVSEI	(R)V L H V S E N\P\V|P/L T V R(V)		137.38	520.6339	1559.89	-0.0033	-2.1	6.72	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
2977	dirMS_041712_NAR_50mM_plus2.9307.9307.3	3	15.01	0	1.33E+05		(K)AEITLVA	(K)A E|I\T L/V/A T K/P E K(L)		116.23	433.922	1299.752	-0.0004	-0.3	6.18	98761.7	5.56	HUMAN	Q9UBF2	Coatomer subunit gamma-2
2978	dirMS_041712_NAR_60mM_plus.5212.5212.3	3	15.01	1	4.08E+05		(K)VSSAEG	(K)V/S|S A/E/G/A\A/K E/E P K(R)		85.05	434.8867	1302.654	-0.008	-6.2	4.79	4801.6	11.17	HUMAN	F2Z2W6	Non-histone chromosomal protein HMG-14
2979	dirMS_041712_NAR_20mM_minus.10877.10877.2	2	15	0	1.50E+06	M92m	(R)ImNTFS	(R)I m|N T/F/S V V/P/S/P K(V)	m:Oxidized methionine	157.1	668.3513	1319.703	15.9925	-1.8	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
2980	dirMS_041712_NAR_50mM_minus2.13359.13359.3	3	15	0	3.68E+05		(R)EQTLSP	(R)E Q|T/L/S/P T/I/T/S G L H N\I/A R(S)		143.63	613.3274	1837.977	-0.009	-4.9	6.85	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
2981	dirMS_041712_NAR_50mM_minus2.9055.9055.3	3	15	0	7.04E+04		(R)EANALA	(R)E A N|A/L/A/A G H/P A Q A V A/I N A R(L)		119.77	615.6611	1844.973	-0.0038	-2.1	6.85	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
2982	dirMS_041712_NAR_120mM_plus.16387.16387.4	4	15	1	1.30E+06		(R)YAEIVHL	(R)Y/A E/I V H L/T L/P/D/G/T K/R(S)		138.97	428.9885	1712.933	-0.0008	-0.5	6.75	21230	6.36	HUMAN	H0YC04	V-type proton ATPase subunit B, brain isoform (Fragment)
2983	dirMS_041712_NAR_120mM_plus.22933.22933.3	3	15	1	4.81E+05		(K)GLAPDLI	(K)G L|A/P/D/L/P E D L Y H L I K K(A)		174	608.0076	1822.011	-0.0027	-1.5	5.38	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
2984	dirMS_041712_NAR_50mM_plus2.9532.9532.3	3	15	0	5.99E+05		(K)GAVDG	(K)G A V/D G/G L/S/I/P H S T\K(R)		117.25	446.9057	1338.701	0.0013	1	6.74	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
2985	dirMS_041712_NAR_120mM_minus.9020.9020.2	2	14.99	0	5.98E+05		(K)HFVALS	(K)H/F|V|A/L S T N/T T K(V)		103.33	609.8267	1218.648	-0.0016	-1.3	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
2986	dirMS_041712_NAR_30mM_minus2.10859.10859.2	2	14.99	0	1.05E+06		(R)GYSFTT	(R)G Y|S|F/T/T T/A E R(E)		111.93	566.7699	1132.527	0.0056	4.9	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
2987	dirMS_041712_NAR_30mM_minus2.14619.15007.2	2	14.99	0	1.64E+07		(K)WSLLQC	(K)W/S|L/L/Q/Q/Q/K(T)		134.22	515.7847	1030.568	-0.0059	-5.7	8.75	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
2988	dirMS_041712_NAR_30mM_minus2.18847.18882.2	2	14.99	0	1.91E+05		(K)CFSVLG	(K)C|F|S|V/L/G F/C K(S)	C:Carbamidomethylation	157.42	559.2673	1117.517	0.0104	9.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
2989	dirMS_041712_NAR_40mM_minus2.14385.14413.3	3	14.99	1	2.00E+05		(R)GLLPGLL	(R)G L|L|P\G L L/P\A/P A/D K L T P K(G)		169.47	567.6813	1701.031	-0.0016	-0.9	8.59	153084.9	5.55	HUMAN	Q6P2E9	Enhancer of mRNA-decapping protein 4
2990	dirMS_041712_NAR_120mM_plus.20604.20624.4	4	14.99	1	2.15E+05		(K)AAIDWF	(K)A A|I/D/W/F D/G K E F H/G N I I/K(V)		161.23	491.0027	1960.992	-0.0026	-1.3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
2991	dirMS_041712_NAR_20mM_plus.15466.15542.2	2	14.99	0	2.37E+05		(K)TITLEVEI	(K)T I T\L/E|V|E|P S D T/I/E N V K(A)		179.03	894.4658	1787.927	-0.003	-1.7	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
2992	dirMS_041712_NAR_30mM_plus2.16622.16814.2	2	14.99	0	3.51E+05		(R)SIQADG	(R)S I|Q|A/D/G L/V/W/G S S K(L)		140.48	674.3475	1347.69	-0.0026	-1.9	5.55	24934.4	4.5	HUMAN	P24534	Elongation factor 1-beta
2993	dirMS_041712_NAR_30mM_plus2.9587.9587.2	2	14.99	0	2.50E+05		(K)NMGLY	(K)N/M|G|L/Y/G E/R(V)		104.62	470.2224	939.435	0.0022	2.4	6	43371.1	9.64	HUMAN	E7ERW2	Aspartate aminotransferase
2994	dirMS_041712_NAR_40mM_plus2.13738.13758.3	3	14.99	1	3.43E+05		(R)QVFGEA	(R)Q V F/G E/A T/K Q/P/G I/T F I/A A K(F)		147.45	636.0176	1906.043	-0.005	-2.6	8.59	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
2995	dirMS_041712_NAR_50mM_plus2.14421.14421.3	3	14.99	0	2.70E+06		(R)LSQYQE	(R)L/S|Q/Y Q E/P L H L P G V R(V)		144.57	546.2968	1636.881	-0.0047	-2.9	6.75	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
2996	dirMS_041712_NAR_50mM_plus2.15742.15743.3	3	14.99	1	6.78E+05		(K)GCLELIK	(K)G C|L/E/L I K E T G\V|P/I/A G R(H)	C:Carbamidomethylation	151.05	571.6495	1712.936	-0.0024	-1.4	6.14	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
2997	dirMS_041712_NAR_50mM_plus2.16579.16682.3	3	14.99	1	5.82E+05		(K)DANAKL	(K)D A/N|A K L\S E\L|E|A/A/L/Q R(A)		155.78	543.6256	1628.86	0.002	1.2	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
2998	dirMS_041712_NAR_60mM_plus.12164.12164.3	3	14.99	1	1.01E+06	M232m	(R)MSmKE	(R)M/S m K E\V D\E Q|M/L/N/V/Q/N K(N)	m:Oxidized methionine	120.57	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
2999	dirMS_041712_NAR_60mM_minus.7747.7857.3	3	14.98	1	4.17E+05		(K)KGTVEG	(K)K G T V E G\F\E|P/A/D/N K(C)		103.35	464.5665	1391.68	0.0048	3.5	4.68	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
3000	dirMS_041712_NAR_20mM_plus.8308.8308.2	2	14.98	0	9.05E+04		(K)GGEIQP	(K)G G\E|I|Q/P/V/S\V K(V)		127.42	507.2841	1013.563	-0.0017	-1.6	6	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
3001	dirMS_041712_NAR_30mM_plus2.19078.19078.2	2	14.98	0	1.48E+05		(R)VYSLFLD	(R)V/Y/S/L/F L/D E S R(S)		153.18	614.8154	1228.621	0.0027	2.2	4.37	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
3002	dirMS_041712_NAR_40mM_plus2.10241.10456.2	2	14.98	1	8.78E+05		(K)KITIADC	(K)K\I T\I|A|D\C\G\Q|L|E(-)	C:Carbamidomethylation	125.52	624.3146	1247.63	-0.0081	-6.5	4.75	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
3003	dirMS_041712_NAR_50mM_plus2.5143.5143.3	3	14.98	0	7.90E+04		(R)AEAEAG	(R)A E|A|E A/G S P R P D|P R(E)		85.77	451.5555	1352.655	-0.0034	-2.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
3004	dirMS_041712_NAR_60mM_plus.8513.8513.3	3	14.98	1	4.16E+05		(K)QGIETPE	(K)Q G/I/E/T|P E\D Q/N D/L R K(M)		102.63	548.2719	1642.803	-0.002	-1.2	4.32	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
3005	dirMS_041712_NAR_30mM_minus2.14735.14896.2	2	14.97	0	4.17E+05		(R)LWVDE	(R)L/W|V/D/E/A V/R(A)		134.55	494.2641	987.526	-0.0049	-4.9	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
3006	dirMS_041712_NAR_40mM_minus2.13115.13115.3	3	14.97	1	9.20E+04		(K)VLDSGA	(K)V L/D/S/G A/P I K/I/P V/G P E/T L G R(I)		160.87	640.3618	1919.096	-0.0252	-13.1	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
3007	dirMS_041712_NAR_50mM_minus2.7786.7786.3	3	14.97	0	2.44E+05		(R)LESGMC	(R)L E|S G|M Q/N|M/S I H T K(T)		111.27	492.5712	1475.698	0.0009	0.6	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
3008	dirMS_041712_NAR_60mM_minus.9565.9565.3	3	14.97	1	4.95E+05		(R)LQAEIE	(R)L/Q|A/E/I/E/G L K G Q R(A)		113.32	447.9164	1341.748	-0.0138	-10.3	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
3009	dirMS_041712_NAR_120mM_plus.8299.8300.3	3	14.97	2	1.65E+06		(K)KGAVAE	(K)K|G A|V/A E D G D/E/L R T E|P E|A\K(K)		97.05	638.9851	1914.94	0.0004	0.2	4.36	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
3010	dirMS_041712_NAR_120mM_plus.9219.9343.3	3	14.97	1	3.55E+06		(R)SRAEAE	(R)S R A E\A\E|S|M/Y/Q/I/K(Y)		102.38	471.5662	1412.684	0.0002	0.1	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
3011	dirMS_041712_NAR_30mM_plus2.22031.22031.2	2	14.97	0	2.62E+05		(K)LISLFQA	(K)L/I/S|L F Q A\M K(K)		171.07	525.8042	1050.602	-0.0005	-0.5	8.75	533778	5.74	HUMAN	Q15149	Plectin
3012	dirMS_041712_NAR_50mM_plus2.9541.9541.3	3	14.97	1	1.58E+05		(R)LGGSPF	(R)L/G|G/S/P F G/P A G T G K T E/S V\K(A)		117.22	563.9657	1689.881	0.0019	1.1	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
3013	dirMS_041712_NAR_60mM_plus.9142.9180.3	3	14.97	1	9.47E+05		(K)AQAEVE	(K)A Q|A|E/V/E/G L/G K G V A R(L)		105.8	462.2549	1384.754	-0.0042	-3	6.19	533778	5.74	HUMAN	Q15149	Plectin
3014	dirMS_041712_NAR_60mM_plus.9340.9340.3	3	14.97	1	2.84E+06		(R)AYQKQP	(R)A Y/Q|K Q|P T|I/F Q N K(K)		107.38	489.2643	1465.78	-0.0014	-1	9.7	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
3015	dirMS_041712_NAR_40mM_minus2.12688.12688.3	3	14.96	1	2.01E+05		(K)DVLFLK	(K)D V|L/F/L\K D C V/G P E V E K(A)	C:Carbamidomethylation	158.43	583.3021	1747.893	-0.0018	-1	4.32	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
3016	dirMS_041712_NAR_50mM_minus2.6924.7103.3	3	14.96	1	7.83E+05	M2747m	(K)TLQEVT	(K)T L|Q/E V/T E m/D/S V K/R(Y)	m:Oxidized methionine	106.27	517.9271	1535.773	15.9934	-1	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
3017	dirMS_041712_NAR_60mM_minus.10071.10279.3	3	14.96	0	5.90E+06		(R)GSAVHC	(R)G S/A/V/H/Q/L/S/E/E/L R(C)		117.4	442.5648	1325.681	-0.001	-0.7	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
3018	dirMS_041712_NAR_60mM_minus.9677.9677.3	3	14.96	0	3.48E+05		(R)QLSQAG	(R)Q L/S Q/A/G/S/F/S D|G T H/G G L R(Y)		113.6	573.2781	1717.825	-0.0055	-3.2	6.74	266161	5.68	HUMAN	E9PPU0	Epiplakin
3019	dirMS_041712_NAR_20mM_plus.9953.9953.2	2	14.96	0	1.64E+05		(K)YQAVTA	(K)Y/Q|A|V|T A T L E E K(R)		139.75	626.8223	1252.642	-0.0046	-3.7	4.53	23633.9	11.02	HUMAN	P40429	60S ribosomal protein L13a
3020	dirMS_041712_NAR_30mM_plus2.18765.18932.2	2	14.96	0	3.63E+05		(R)NLVCTD	(R)N L|V|C|T/D/L F T/R(G)	C:Carbamidomethylation	152.18	619.8128	1238.62	-0.0015	-1.2	5.84	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
3021	dirMS_041712_NAR_30mM_plus2.21961.21961.2	2	14.96	0	1.87E+05		(R)EGDVLT	(R)E G D\V/L/T|L/L/E S E R(E)		170.55	680.8538	1360.696	0.0049	3.6	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
3022	dirMS_041712_NAR_40mM_plus2.10726.10726.3	3	14.96	0	1.85E+05		(K)VGSLDN	(K)V/G|S L D/N V/G H L/P A G G A V K(I)		128.15	530.9567	1590.86	-0.0043	-2.7	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
3023	dirMS_041712_NAR_40mM_plus2.5875.5895.2	2	14.96	0	1.61E+05	M369m	(R)FGSGM	(R)F/G|S|G/M/N m/G R(I)	m:Oxidized methionine	92.73	486.7054	956.408	15.9958	1	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
3024	dirMS_041712_NAR_30mM_minus2.12358.12358.2	2	14.95	0	1.26E+05		(K)SIYYITG	(K)S I|Y/Y/I/T G/E/S/K(E)		121.13	580.7949	1160.583	-0.0009	-0.7	5.72	16789.1	8.77	HUMAN	H0Y5S7	Heat shock protein HSP 90-beta (Fragment)
3025	dirMS_041712_NAR_30mM_minus2.15726.16004.2	2	14.95	0	8.39E+05		(R)GGIVDE	(R)G G/I|V|D|E G/A\L L/R(A)		139.92	550.3083	1099.611	-0.0013	-1.2	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
3026	dirMS_041712_NAR_20mM_plus.15508.15508.3	3	14.95	0	1.97E+05		(K)TITLEVEI	(K)T I\T L E V E/P S/D/T/I/E N V K(A)		179.02	596.6463	1787.927	-0.003	-1.7	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
3027	dirMS_041712_NAR_30mM_plus2.20148.20148.2	2	14.95	0	1.34E+05		(K)NIEDVIA	(K)N I/E|D V/I/A Q G I|G/K(L)		160.27	628.8445	1256.685	-0.0028	-2.2	4.37	9098.8	4.38	HUMAN	H0YDD8	60S acidic ribosomal protein P2 (Fragment)
3028	dirMS_041712_NAR_50mM_plus2.17745.17915.3	3	14.95	0	5.68E+05		(K)TVSGVN	(K)T V|S/G V/N/G/P L/V/I/L/D H V K(V)		162.05	549.9834	1647.943	-0.0072	-4.4	6.41	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
3029	dirMS_041712_NAR_50mM_plus2.17749.17884.3	3	14.95	0	2.13E+06		(K)LILPHVD	(K)L/I|L/P H/V D I Q L/K(Y)		162.02	430.2706	1288.799	-0.0015	-1.2	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
3030	dirMS_041712_NAR_50mM_plus2.21192.21192.3	3	14.95	0	2.41E+06		(R)AGKPVI	(R)A G K\P V\I\C A\T Q/M|L/E S M/I/K(K)	C:Carbamidomethylation	180.53	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
3031	dirMS_041712_NAR_60mM_plus.8495.8495.3	3	14.95	0	5.94E+05		(K)GQVCV	(K)G Q|V|C V/M/I/H S/G S/R(G)	C:Carbamidomethylation	103.07	444.2219	1330.636	0.0157	11.8	9.75	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
3032	dirMS_041712_NAR_120mM_minus.4713.4885.3	3	14.94	0	1.09E+07	M46m M4	(R)HQGVm	(R)H Q\G\V\m|V/G/m/G Q/K(D)	m:Oxidized methionine	75.72	401.8604	1171.571	31.9956	4.8	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
3033	dirMS_041712_NAR_120mM_minus.6610.6610.2	2	14.94	1	1.91E+05		(K)SYKVSTS	(K)S Y/K/V/S/T/S\G P/R(A)		90.57	541.2833	1081.564	-0.0043	-4	9.99	19288.4	10.19	HUMAN	F8VQY3	Keratin, type II cytoskeletal 8 (Fragment)
3034	dirMS_041712_NAR_30mM_minus2.10107.10151.2	2	14.94	0	2.88E+06		(K)VIPELN	(K)V I|P/E L/N/G/K(L)		109.28	435.2563	869.509	-0.0038	-4.3	5.97	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
3035	dirMS_041712_NAR_30mM_minus2.17788.17788.2	2	14.94	0	1.59E+04		(R)SLAALS	(R)S L|A|A|L|S/Q I A|Y/Q R(N)		150.98	660.8642	1320.727	-0.0059	-4.5	8.46	64225	6.66	HUMAN	E7EX44	Caldesmon
3036	dirMS_041712_NAR_60mM_minus.9341.9378.3	3	14.94	0	1.14E+06		(R)QSVEND	(R)Q/S/V|E N D/I/H/G L/R(K)		112.07	423.218	1267.639	0.0005	0.4	5.32	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3037	dirMS_041712_NAR_20mM_plus.11476.11476.2	2	14.94	0	2.08E+05		(K)VGLQV	(K)V/G/L/Q/V V/A V K(A)		151.53	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
3038	dirMS_041712_NAR_20mM_plus.16626.16626.2	2	14.94	0	1.99E+05		(K)VQIAVA	(K)V Q|I/A V/A|N A/Q\E L|L Q R(M)		186.25	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
3039	dirMS_041712_NAR_20mM_plus.18713.18731.2	2	14.94	0	2.37E+05		(K)IYVDDGI	(K)I/Y|V/D/D G L|I|S L Q V K(Q)		200.67	731.9068	1462.815	-0.0088	-6	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
3040	dirMS_041712_NAR_40mM_plus2.16308.16308.2	2	14.94	0	1.50E+05		(R)YLTVAA	(R)Y/L|T\V/A/A/V/F/R(G)		162.03	520.2997	1039.593	-0.0014	-1.3	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3041	dirMS_041712_NAR_60mM_plus.20201.20202.3	3	14.94	1	3.02E+05		(K)IILDLISE	(K)I I|L/D|L/I/S E/S P I K/G R(A)		166.2	518.6452	1553.926	-0.0051	-3.3	6.07	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
3042	dirMS_041712_NAR_40mM_minus2.13543.13543.3	3	14.93	1	1.96E+05		(K)LGVQV	(K)L/G V/Q/V/V/I/T/D P E K L D Q I R(Q)		163.38	641.7007	1923.091	-0.0034	-1.8	4.56	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
3043	dirMS_041712_NAR_120mM_plus.13476.13476.3	3	14.93	1	2.61E+05		(R)AVVGV	(R)A V|V/G V/V/A G G G R I\D K P I L K(A)		124.08	583.6945	1749.074	-0.0056	-3.2	9.99	24115.6	11.59	HUMAN	E9PIZ3	60S ribosomal protein L8
3044	dirMS_041712_NAR_30mM_plus2.13663.13701.2	2	14.93	0	9.41E+04		(K)GLGLDE	(K)G L|G|L/D|E\S/G L/A/K(Q)		124.92	530.2889	1059.568	0.0025	2.3	4.37	50569.4	6.03	HUMAN	Q9Y265	RuvB-like 1
3045	dirMS_041712_NAR_30mM_plus2.16829.17007.2	2	14.93	0	4.15E+05		(K)FVADGI	(K)F/V|A|D/G I/F/K(A)		141.65	448.7485	896.488	0.0021	2.3	5.84	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
3046	dirMS_041712_NAR_30mM_minus2.18866.18866.2	2	14.92	0	1.91E+05		(K)CFSVLG	(K)C\F/S\V/L/G F/C K(S)	C:Carbamidomethylation	157.42	559.2673	1117.517	0.0104	9.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
3047	dirMS_041712_NAR_50mM_minus2.14601.14601.3	3	14.92	0	3.68E+05		(R)LASTLVH	(R)L/A/S T L V H L|G E Y/Q/A|A\V/D/G A R(K)		150.95	657.6803	1971.029	-0.0031	-1.6	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1

3048	dirMS_041712_NAR_60mM_minus.8214.8214.3	3	14.92	1	1.40E+05		(R)LSQIGVE	(R)L/S|Q/I/G V/E N T E E N R R(L)		106.05	548.9481	1644.83	-0.0002	-0.1	4.79	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
3049	dirMS_041712_NAR_60mM_minus.9884.9912.3	3	14.92	0	6.26E+05		(R)AHSSM	(R)A H\S S\M|V|G|V/N/L/P Q K(A)		114.95	456.576	1367.71	0.0035	2.5	8.8	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
3050	dirMS_041712_NAR_20mM_plus.14417.14417.2	2	14.92	0	1.59E+04		(K)TVFGVEI	(K)T V|F/G V/E P\D L/T R(E)		171.18	617.3237	1233.647	-0.0073	-5.9	4.37	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
3051	dirMS_041712_NAR_50mM_minus2.11597.11597.3	3	14.91	0	2.80E+05	M291m	(K)TGEEIFG	(K)T/G E/E/I/F/G T I G m R P N A K(N)	m:Oxidized methionine	134.18	579.6239	1720.869	15.9885	-3.7	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
3052	dirMS_041712_NAR_50mM_minus2.18184.18388.3	3	14.91	0	4.52E+06		(K)ALESPE	(K)A/L|E|S/P E R/P F\L\A I L|G G A K(V)		174.72	590.3356	1768.996	-0.0033	-1.9	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
3053	dirMS_041712_NAR_60mM_minus.18675.18797.3	3	14.91	0	2.97E+05		(K)LHDNLII	(K)L H D\N\L\I|I/S|D/L E/N T V/K(K)		165.95	575.3117	1723.922	-0.0019	-1.1	4.54	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
3054	dirMS_041712_NAR_120mM_plus.11184.11348.3	3	14.91	1	5.89E+05		(R)NREEEW	(R)N R E E\E\W|D|P/E/Y T/P K(S)		112.4	564.9219	1692.75	0.0011	0.7	4.25	108720.9	10.17	HUMAN	Q9Y2W1	Thyroid hormone receptor-associated protein 3
3055	dirMS_041712_NAR_120mM_plus.11589.11717.3	3	14.91	1	4.16E+06		(R)NLKASLE	(R)N L|K A S L|E/N/S|L/R(E)		114.02	415.5688	1244.696	-0.0039	-3.1	8.75	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3056	dirMS_041712_NAR_120mM_plus.8174.8174.2	2	14.91	0	5.56E+05		(K)HSGPNS	(K)H/S|G|P N S A D/S A N\D/G F V R(L)		96.55	815.8631	1630.72	-0.0015	-0.9	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
3057	dirMS_041712_NAR_20mM_plus.8299.8341.2	2	14.91	0	1.06E+05	M406m	(R)EYQELm	(R)E Y|Q/E/L/m/N V/K(L)	m:Oxidized methionine	127.52	585.2801	1153.556	15.9971	1.9	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
3058	dirMS_041712_NAR_30mM_plus2.20223.20223.2	2	14.91	0	1.79E+05		(R)FLGTEVL	(R)F/L/G/T/E/V L L/R(L)		160.75	524.3115	1047.62	-0.004	-3.8	6	103045.5	7.1	HUMAN	B9ZVT1	RNA-binding protein 12B
3059	dirMS_041712_NAR_30mM_plus2.9002.9002.2	2	14.91	0	2.40E+05		(R)SGQGAF	(R)S G|Q|G/A|F|G N/M/C R(G)	C:Carbamidomethylation	100.87	592.7504	1184.494	0	0	9.47	18988.7	11.2	HUMAN	H3BTP7	60S ribosomal protein L4 (Fragment)
3060	dirMS_041712_NAR_40mM_plus2.18369.18369.3	3	14.91	1	2.86E+05		(R)VAAKLE	(R)V A/A K L E V\A|P/I/S D I I A I K(S)		174.02	584.3591	1751.068	-0.005	-2.8	6.04	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
3061	dirMS_041712_NAR_50mM_plus2.10725.10725.3	3	14.91	1	8.49E+05		(R)DISTNK	(R)D I/S T N K V E Q|I|P Y/G E R(I)		124.08	583.6304	1748.881	-0.0047	-2.7	4.68	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
3062	dirMS_041712_NAR_20mM_minus.6166.6174.2	2	14.9	0	3.76E+06		(K)DSYVGD	(K)D S/Y|V|G/D E/A/Q/S K(R)		103.87	599.7642	1198.522	-0.0011	-0.9	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
3063	dirMS_041712_NAR_30mM_minus2.10495.10634.2	2	14.9	0	1.09E+06		(K)TIAPALV	(K)T I|A|P A L V/S K(K)		111.75	450.2803	899.556	-0.0027	-3	8.41	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
3064	dirMS_041712_NAR_40mM_minus2.11171.11171.3	3	14.9	0	8.43E+04		(K)MLDAE	(K)M/L/D/A E D/I V N/T A R P D/E|K(A)		148.55	606.297	1816.875	0.0019	1	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
3065	dirMS_041712_NAR_20mM_plus.17953.17953.2	2	14.9	0	1.97E+05		(K)GADFLV	(K)G A D F L|V|T E|V/E|N G G/S L G S K(K)		195.2	890.4414	1779.876	-0.0004	-0.2	4.14	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
3066	dirMS_041712_NAR_50mM_plus2.18319.18462.3	3	14.9	1	4.07E+05		(R)IAKEEIF	(R)I A K E E I|F|G|P V/Q/P L/F K(F)		164.98	572.6586	1715.973	-0.0118	-6.9	6.14	57661.7	6.36	HUMAN	P30837	Aldehyde dehydrogenase X, mitochondrial
3067	dirMS_041712_NAR_50mM_plus2.7315.7315.3	3	14.9	1	1.93E+05		(R)IVEQDTI	(R)I/V/E Q/D T M/P/P K G V/R(H)		104.88	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
3068	dirMS_041712_NAR_120mM_minus.8074.8096.4	4	14.89	2	6.38E+05		(R)ASVDTK	(R)A S\V D T K E/A E/G A/P/Q/V/E A G K/R(L)		98.37	486.5008	1942.983	-0.0015	-0.8	4.87	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
3069	dirMS_041712_NAR_120mM_minus.9989.10132.2	2	14.89	0	9.76E+05		(R)HVLVTL	(R)H|V|L|V/T L\G E|K(M)		109.08	498.298	995.588	0.0003	0.3	6.75	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
3070	dirMS_041712_NAR_30mM_minus2.16662.16662.2	2	14.89	0	1.61E+05		(R)NPSAAF	(R)N/P S/A A/F|F/C V A/R(L)	C:Carbamidomethylation	144.18	620.3013	1239.594	0.0014	1.1	9.75	18626.5	5.64	HUMAN	B8ZZK2	Gamma-glutamylcyclotransferase
3071	dirMS_041712_NAR_30mM_minus2.18825.18825.2	2	14.89	0	2.45E+05		(K)LLQDFF	(K)L/L|Q/D/F/F/N G R(D)		157.37	555.2906	1109.574	0.0001	0.1	5.84	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
3072	dirMS_041712_NAR_30mM_minus2.8947.9315.2	2	14.89	0	1.60E+07		(R)AQYDEL	(R)A/Q|Y/D/E/L/A/R(K)		104.02	483.2423	965.469	0.0086	8.9	4.37	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3073	dirMS_041712_NAR_50mM_minus2.13340.13573.3	3	14.89	0	3.52E+05		(R)AVAIDL	(R)A V|A\I/D L/P/G L G/H S K(E)		144.57	426.5785	1277.721	-0.0003	-0.2	6.79	19983.6	8.14	HUMAN	B4DQI4	Alpha/beta hydrolase domain-containing protein 14B
3074	dirMS_041712_NAR_60mM_minus.8646.9072.3	3	14.89	1	2.06E+06	M227m M	(R)mQKEIT	(R)m Q K E I T A|L|A|P/S/T m K(I)	m:Oxidized methionine	109.67	527.6044	1548.812	31.9862	-2.3	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
3075	dirMS_041712_NAR_60mM_minus.9430.9463.3	3	14.89	1	2.46E+05		(R)QERYEIE	(R)Q E/R Y\E\I|E|E/T/E T V/T K(S)		112.57	585.6185	1754.844	-0.0034	-1.9	4.32	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
3076	dirMS_041712_NAR_120mM_plus.16919.16920.3	3	14.89	1	1.40E+06		(K)RISEQFT	(K)R I S\E\Q|F|T|A/M/F/R(R)		141.67	462.5709	1385.699	-0.0013	-0.9	9.6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
3077	dirMS_041712_NAR_20mM_plus.14731.14731.2	2	14.89	0	6.83E+04		(R)IMNTFS	(R)I M/N T|F/S/V/V/P S P K(V)		173.27	660.3527	1319.703	-0.0047	-3.5	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
3078	dirMS_041712_NAR_20mM_plus.15612.15612.2	2	14.89	0	8.46E+04		(-)SDVLELT	(-)S D V/L/E/L|T/D/D N F E/S R(I)		179.27	820.3754	1639.745	-0.0011	-0.6	3.77	13747.3	6.8	HUMAN	H7BZJ3	Thioredoxin (Fragment)
3079	dirMS_041712_NAR_30mM_plus2.18779.19066.2	2	14.89	0	1.04E+06		(K)DAGTIA	(K)D A|G\T|I|A|G/L/N V L/R(I)		152.53	600.3411	1199.674	0.0007	0.6	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
3080	dirMS_041712_NAR_120mM_minus.5001.5010.3	3	14.88	1	5.75E+05		(R)AAEEED	(R)A/A|E/E/E D/E/A/D/P K/R(Q)		79.35	453.8716	1359.602	-0.002	-1.5	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
3081	dirMS_041712_NAR_40mM_minus2.11244.11244.3	3	14.88	0	4.48E+04		(R)EALAEA	(R)E A\L/A/E/A/A L E/S P R P A L V R(S)		149.25	598.3347	1792.992	-0.002	-1.1	4.79	22148.2	5.87	HUMAN	B3KY21	Na(+)/H(+) exchange regulatory cofactor NHE-RF1
3082	dirMS_041712_NAR_60mM_minus.10625.10625.3	3	14.88	0	2.54E+05		(R)GISEETT	(R)G I|S/E/E/T T/T G V H N L/Y K(M)		119.3	550.2838	1648.818	0.0192	11.6	5.4	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
3083	dirMS_041712_NAR_60mM_minus.12258.12258.3	3	14.88	0	2.05E+05		(K)LAQANG	(K)L/A\Q/A N/G W/G V/M\V/S H R(S)		128.17	509.2631	1525.769	0.0055	3.6	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
3084	dirMS_041712_NAR_20mM_plus.16648.16648.2	2	14.88	0	1.58E+05		(R)LLEAQIA	(R)L L/E A|Q\I|A/T G/G I|I/D\P K(E)		185.68	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
3085	dirMS_041712_NAR_20mM_plus.8278.8405.2	2	14.88	0	5.53E+05		(R)AVVIVDI	(R)A V|V|I|V|D/D/R(G)		127.7	443.7527	886.499	-0.0011	-1.3	4.21	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
3086	dirMS_041712_NAR_30mM_plus2.14467.14467.2	2	14.88	0	3.41E+05		(K)TLPQMF	(K)T L|P Q/M/F T/K(T)		129.05	483.2645	965.513	0.0093	9.6	8.41	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
3087	dirMS_041712_NAR_40mM_plus2.7947.8097.2	2	14.88	0	3.26E+05		(R)MGYMD	(R)M/G|Y|M D|P/R(E)		107.5	435.1865	869.364	0.0013	1.5	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
3088	dirMS_041712_NAR_50mM_plus2.15477.15477.3	3	14.88	1	8.15E+05		(K)EAFSLF	(K)E A/F|S/L/F/D K D G D G T I T T K(E)		149.52	615.6348	1844.891	-0.0014	-0.8	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
3089	dirMS_041712_NAR_50mM_plus2.18836.18836.3	3	14.88	1	4.36E+05		(K)AAIDWF	(K)A/A|I/D/W/F/D G K E/F S G N P I K(V)		167.18	632.3186	1894.933	0.0079	4.1	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
3090	dirMS_041712_NAR_50mM_plus2.22478.22478.3	3	14.88	1	1.26E+06		(R)GVMLA	(R)G V|M/L/A V/D A/V I A E L K K(Q)		195.7	519.6393	1556.908	-0.0047	-3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
3091	dirMS_041712_NAR_60mM_plus.11885.11885.3	3	14.88	0	8.64E+05		(R)NSNLVG	(R)N S/N|L/V/G A A/H E E/L Q Q S R(I)		119.28	584.9576	1752.862	-0.0041	-2.3	5.4	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
3092	dirMS_041712_NAR_120mM_minus.17125.17188.3	3	14.87	1	4.49E+05		(K)RISEQFT	(K)R I S\E\Q|F|T|A|M/F/R(R)		147.98	462.5714	1385.699	0.0002	0.2	9.6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
3093	dirMS_041712_NAR_30mM_minus2.14188.14230.2	2	14.87	0	4.17E+05		(K)MFLYAD	(K)M F|L|Y/A/D/N/E D R(A)		131.08	637.2806	1273.552	0.0022	1.7	4.03	24724.1	5.17	HUMAN	E7ETQ7	Vacuolar protein sorting-associated protein VTA1 homolog
3094	dirMS_041712_NAR_30mM_minus2.16935.16935.2	2	14.87	0	3.36E+05		(K)FANPFP	(K)F A|N|P/F/P A A V R(G)		146.37	545.2937	1089.584	-0.0039	-3.5	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
3095	dirMS_041712_NAR_30mM_minus2.17804.18048.2	2	14.87	0	3.35E+05		(K)EAFQLF	(K)E A|F/Q/L/F/D/R(T)		151.78	513.2571	1025.505	0.0019	1.8	4.37	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
3096	dirMS_041712_NAR_30mM_minus2.8569.8569.2	2	14.87	0	9.67E+04		(R)VGQDP	(R)V/G/Q/D/P/V L\R(Q)		101.38	442.2532	883.5	-0.0005	-0.5	5.81	14130.9	9.56	HUMAN	C9K0U8	Single-stranded DNA-binding protein (Fragment)
3097	dirMS_041712_NAR_50mM_minus2.13085.13085.3	3	14.87	0	3.53E+05		(R)ETNLDSI	(R)E T/N L/D/S L/P/L/V D/T H S K(R)		142.43	556.9529	1668.844	0.0002	0.1	4.53	53707.8	5.06	HUMAN	P08670	Vimentin
3098	dirMS_041712_NAR_60mM_minus.10038.10038.3	3	14.87	1	1.25E+05		(R)AGTGVD	(R)A G/T/G V/D/N V D L E/A/A T R\K(G)		115.55	539.6117	1616.824	-0.0033	-2	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
3099	dirMS_041712_NAR_60mM_minus.10682.10810.3	3	14.87	1	5.44E+05	M239m	(R)MSMKE	(R)M S|M K E V\D E\Q|m|L/N\V/Q N K(N)	m:Oxidized methionine	119.9	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3100	dirMS_041712_NAR_120mM_plus.9452.9594.3	3	14.87	1	6.52E+05		(R)GSNKLV	(R)G S N K L\V|I|E/E/A/E/R(S)		102.85	448.9084	1344.712	-0.0011	-0.8	4.79	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
3101	dirMS_041712_NAR_120mM_plus.9727.9727.2	2	14.87	0	8.09E+05		(R)FATHAA	(R)F A/T/H|A|A\A\L S V/R(N)		104.23	572.3112	1143.627	-0.0118	-10.3	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
3102	dirMS_041712_NAR_20mM_plus.12259.12366.2	2	14.87	0	2.65E+05		(K)LLQLVE	(K)L/L|Q|L|V/E D/R(G)		158.32	493.2863	985.568	-0.0023	-2.4	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
3103	dirMS_041712_NAR_30mM_plus2.13726.13809.2	2	14.87	0	1.74E+05		(K)FAFQAE	(K)F/A|F/Q|A/E/V N/R(M)		125.3	541.2764	1081.543	0.003	2.8	6	92752.5	4.76	HUMAN	P14625	Endoplasmin
3104	dirMS_041712_NAR_30mM_plus2.14285.14580.2	2	14.87	0	7.81E+05		(R)GLFDEY	(R)G L|F|D/E/Y/G/S K(K)		128.55	508.2403	1015.473	0.0002	0.2	4.37	92752.5	4.76	HUMAN	P14625	Endoplasmin
3105	dirMS_041712_NAR_30mM_plus2.19214.19570.2	2	14.87	0	8.31E+05		(R)DLTDYL	(R)D L|T/D/Y/L/M/K(I)		155.33	499.7467	998.486	-0.0002	-0.2	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
3106	dirMS_041712_NAR_50mM_plus2.8912.8912.3	3	14.87	0	1.99E+05		(K)VVQVSA	(K)V V/Q V/S/A G D/S/H T A A L/T D D G\R(V)		113.48	633.6509	1898.92	0.0179	9.4	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
3107	dirMS_041712_NAR_20mM_minus.14647.14647.2	2	14.86	0	2.10E+05		(K)LAVEAL	(K)L A|V/E A|L/S|S L D/G D/L A/G R(Y)		201.28	793.922	1586.838	-0.0017	-1.1	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
3108	dirMS_041712_NAR_50mM_minus2.13485.13485.3	3	14.86	0	2.98E+05		(K)VIQYLA	(K)V I|Q/Y L A/Y/V/A|S S/H K(S)		144.62	493.6043	1478.8	-0.0018	-1.2	8.48	227783.5	5.5	HUMAN	P35579	Myosin-9
3109	dirMS_041712_NAR_20mM_plus.18625.18782.2	2	14.86	0	2.00E+05		(R)VFIGNL	(R)V F|I|G|N/L N\T L/V V/K(K)		200.13	658.8999	1316.794	-0.0011	-0.9	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
3110	dirMS_041712_NAR_20mM_plus.9355.9355.2	2	14.86	0	1.86E+05		(K)SVTNED	(K)S V|T|N/E/D V|T Q E E/L/G G A/K(T)		136	838.9014	1676.797	-0.0018	-1.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
3111	dirMS_041712_NAR_30mM_plus2.13474.13474.2	2	14.86	0	1.03E+05		(R)TIYAGN	(R)T\I/Y/A|G N/A\L/C T V/K(C)	C:Carbamidomethylation	123.85	655.8414	1310.677	-0.0018	-1.4	8.26	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
3112	dirMS_041712_NAR_30mM_plus2.19307.19787.2	2	14.86	0	7.16E+05		(R)LDFNLIR	(R)L/D|F/N/L/I/R(V)		156.18	445.759	890.509	0.0013	1.5	5.84	18956.4	6.97	HUMAN	C9JLK0	Phosphoribosylaminoimidazolecarboxamide formyltransferase (Fragment)
3113	dirMS_041712_NAR_30mM_plus2.22589.22589.2	2	14.86	0	1.01E+06		(R)FLTWIL	(R)F/L|T|W I L/N/R(Y)		175.88	531.8078	1062.61	-0.0012	-1.1	9.75	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
3114	dirMS_041712_NAR_50mM_plus2.20623.20625.3	3	14.86	1	8.20E+05		(R)TLAEIAK	(R)T/L\A|E/I A/K A E L/D G T/I/L K(S)		176.45	562.6601	1685.968	-0.0026	-1.6	4.68	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
3115	dirMS_041712_NAR_30mM_minus2.10286.10617.2	2	14.85	0	2.26E+06		(R)LSIYEAR	(R)L/S/I/Y/E/A/R(C)		111.07	426.2334	851.462	-0.0026	-3.1	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
3116	dirMS_041712_NAR_50mM_minus2.12569.12569.3	3	14.85	0	3.06E+05		(K)AASDIA	(K)A/A/S D|I/A M T E/L/P P T H P I/R(L)		139.55	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
3117	dirMS_041712_NAR_50mM_minus2.15990.16128.3	3	14.85	0	5.46E+05		(K)GSDHSA	(K)G S D H S A S L\E|P|G E|L|A/E/L V R(S)		159.35	622.978	1866.919	0.0003	0.1	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
3118	dirMS_041712_NAR_50mM_minus2.17979.17999.3	3	14.85	1	1.70E+05		(K)AIDLFTD	(K)A I/D|L/F/T D|A/I/K L N P R(L)		171.33	529.6358	1586.89	0.0028	1.8	6	18141.9	4.7	HUMAN	F6VDH7	Hsc70-interacting protein (Fragment)
3119	dirMS_041712_NAR_60mM_minus.4991.4991.3	3	14.85	1	8.21E+04		(K)VSSAEG	(K)V/S/S/A E/G A A/K\E E P/K(R)		82.42	434.8904	1302.654	0.0031	2.3	4.79	4801.6	11.17	HUMAN	F2Z2W6	Non-histone chromosomal protein HMG-14
3120	dirMS_041712_NAR_120mM_plus.15280.15380.3	3	14.85	1	6.06E+05		(K)NREPVQ	(K)N R E P\V\Q|L|E|T/L/S I/R(G)		133.35	518.9599	1554.86	0.0053	3.4	6.14	8392.6	11.84	HUMAN	J3QLI9	Small nuclear ribonucleoprotein Sm D1
3121	dirMS_041712_NAR_20mM_plus.11969.12067.2	2	14.85	0	1.20E+05		(R)IYVVDV	(R)I/Y|V|V/D/V|G S E\P R(A)		156.17	617.3237	1233.647	-0.0073	-5.9	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
3122	dirMS_041712_NAR_20mM_plus.6014.6014.3	3	14.85	0	1.02E+06	M295m M	(R)mGQmA	(R)m G Q\m\A m\G\G\A/m/G/I/N N R(G)	m:Oxidized methionine	100.27	534.8861	1538.67	63.9743	-3.4	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
3123	dirMS_041712_NAR_30mM_plus2.11729.11903.2	2	14.85	0	1.54E+06		(K)FYEAFSK	(K)F/Y|E/A/F/S/K(N)		115.28	446.2164	891.425	0.0008	0.9	6	20127.1	9.4	HUMAN	H0Y598	Heat shock protein HSP 90-beta (Fragment)
3124	dirMS_041712_NAR_30mM_plus2.12270.12270.2	2	14.85	0	9.10E+05		(K)EVDEQM	(K)E V|D E/Q|M L\N V/Q/N K(N)		117.03	723.8478	1446.689	-0.001	-0.7	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3125	dirMS_041712_NAR_30mM_plus2.7300.7301.2	2	14.85	0	7.08E+04		(R)IVAECN	(R)I/V|A|E/C N/A V R(Q)	C:Carbamidomethylation	92.8	516.2677	1031.53	-0.0021	-2.1	6	89360.3	5.63	HUMAN	F8W845	Catenin alpha-1
3126	dirMS_041712_NAR_30mM_plus2.8539.8539.2	2	14.85	0	8.74E+05		(R)LGLGEG	(R)L/G/L/G E/G A/E E K(S)		98.95	501.7639	1002.51	0.0103	10.3	4.25	40096.8	9.24	HUMAN	C9JW69	Regulator of chromosome condensation (Fragment)
3127	dirMS_041712_NAR_40mM_plus2.13965.14010.3	3	14.85	0	2.17E+05		(K)VALLLLD	(K)V A|L/L|L/L/D Q/G A/S P H A A A K(N)		148.17	558.9886	1674.954	-0.0025	-1.5	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
3128	dirMS_041712_NAR_50mM_plus2.10702.10847.3	3	14.85	1	8.49E+05		(R)DISTNK	(R)D I/S T N K V/E/Q|I|P/Y/G E R(I)		124.08	583.6304	1748.881	-0.0047	-2.7	4.68	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
3129	dirMS_041712_NAR_60mM_plus.17897.17897.3	3	14.85	1	3.01E+05		(R)KGFSEG	(R)K G F S E G L\W|E|I/E/N N P\T V/K(A)		150.67	650.0017	1947.981	0.0095	4.9	4.79	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
3130	dirMS_041712_NAR_120mM_minus.13153.13432.4	4	14.84	2	3.61E+06		(R)AQKDEE	(R)A Q\K D E E|K M E\I|Q/E/I/Q/L/K(E)		128.07	490.7539	1960.006	-0.0118	-6	4.58	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
3131	dirMS_041712_NAR_120mM_minus.14840.14938.4	4	14.84	0	1.33E+06		(K)HLEINP	(K)H L\E\I\N/P D/H/P I/V/E/T L R(Q)		135.22	446.4924	1782.95	-0.0019	-1.1	5.27	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
3132	dirMS_041712_NAR_20mM_minus.14049.14049.2	2	14.84	0	6.94E+05		(K)SYELPD	(K)S Y E|L/P D/G Q V|I|T I/G N E R(F)		193.68	895.9481	1790.892	-0.003	-1.7	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
3133	dirMS_041712_NAR_30mM_minus2.15012.15261.2	2	14.84	0	3.89E+05		(R)IAAYLFK	(R)I/A|A/Y L/F/K(G)		135.42	413.2472	825.487	0.0002	0.3	8.59	15830.9	5.16	HUMAN	J3KRF5	Clathrin heavy chain 1 (Fragment)
3134	dirMS_041712_NAR_50mM_minus2.13987.13987.3	3	14.84	0	1.88E+04		(R)LTEDLEY	(R)L/T|E/D L E/Y/H E L L D R(A)		147.45	549.2731	1645.807	-0.002	-1.2	4.17	19946.4	5.79	HUMAN	H0YCV6	Oxysterol-binding protein 1 (Fragment)
3135	dirMS_041712_NAR_20mM_plus.18714.18781.2	2	14.84	0	1.68E+05		(R)IITLTGP	(R)I/I|T\L|T|G/P T N A I F K(A)		200.4	694.9091	1388.815	-0.0039	-2.8	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
3136	dirMS_041712_NAR_20mM_plus.7313.7313.2	2	14.84	0	3.27E+05	M281m	(R)AEAESm	(R)A E|A/E/S m Y Q/I/K(Y)	m:Oxidized methionine	118.63	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
3137	dirMS_041712_NAR_30mM_plus2.7623.7730.2	2	14.84	0	1.29E+06		(R)TVGIVGI	(R)T V|G|I|V/G N Q/P K(V)		94.25	506.7931	1012.579	0.0004	0.3	8.41	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
3138	dirMS_041712_NAR_40mM_plus2.14726.14796.3	3	14.84	1	1.18E+05		(K)VVEEAP	(K)V/V|E/E/A/P S I F L D/A E T R/R(A)		153.57	611.3255	1831.955	0.0071	3.9	4.41	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
3139	dirMS_041712_NAR_40mM_plus2.6994.6994.2	2	14.84	0	1.27E+05		(R)MGPVM	(R)M/G/P/V/M D/R(M)		100.62	403.1892	805.37	0.0016	2	5.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
3140	dirMS_041712_NAR_50mM_plus2.16969.16969.3	3	14.84	0	7.73E+05		(R)QYYTLL	(R)Q Y|Y T/L/L N Q/A/P/D\M L H R(K)		156.93	621.6447	1862.922	-0.0022	-1.2	6.74	4335.1	9.82	HUMAN	E5RH00	Ras GTPase-activating protein-binding protein 1
3141	dirMS_041712_NAR_50mM_minus2.15091.15091.3	3	14.83	1	2.94E+05		(K)VVEEAP	(K)V/V/E/E/A/P S I F L D A E T R R(A)		153.45	611.3243	1831.955	0.0035	1.9	4.41	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
3142	dirMS_041712_NAR_60mM_minus.13397.13585.3	3	14.83	1	1.40E+06		(R)QLREYQ	(R)Q L/R E Y\Q/E/L/M N/V/K(L)		135.27	517.6033	1550.8	-0.0042	-2.7	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
3143	dirMS_041712_NAR_60mM_minus.15457.15457.3	3	14.83	0	2.13E+05		(K)EGHVEV	(K)E/G H V E\V|V|S|E/L/L Q/R(E)		145.9	498.9349	1494.791	-0.0009	-0.6	4.75	48586.6	9.32	HUMAN	D6RCB2	Ankyrin-3
3144	dirMS_041712_NAR_60mM_minus.8171.8171.3	3	14.83	1	1.32E+05		(R)KQSTDE	(R)K\Q S T D\E\E/V/T/S L/A/K(S)		105.82	479.2451	1435.728	-0.0067	-4.7	4.68	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
3145	dirMS_041712_NAR_120mM_plus.15887.15907.4	4	14.83	0	6.37E+05		(R)GISTKPV	(R)G I S T K/P V Y I/P/E/V/E/L N H K(L)		136.73	481.7682	1924.054	-0.0029	-1.5	6.75	72626.7	9.13	HUMAN	Q14258	E3 ubiquitin/ISG15 ligase TRIM25
3146	dirMS_041712_NAR_120mM_plus.7400.7687.3	3	14.83	1	2.02E+06	M281m	(R)SRAEAE	(R)S R\A E\A\E|S/m/Y Q/I/K(Y)	m:Oxidized methionine	93.02	476.8977	1412.684	15.9947	-0.1	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
3147	dirMS_041712_NAR_30mM_plus2.13153.13189.2	2	14.83	0	7.55E+05		(R)GVVGPE	(R)G V|V|G/P E/L/Y G/R(L)		122.62	523.7794	1046.563	-0.0114	-10.9	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
3148	dirMS_041712_NAR_30mM_plus2.14644.14644.2	2	14.83	0	7.63E+05		(R)GVEICIA	(R)G V\E\I/C|I/A/T/P G R(L)	C:Carbamidomethylation	130.1	586.8051	1172.609	-0.0063	-5.4	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
3149	dirMS_041712_NAR_30mM_plus2.8337.8689.2	2	14.83	0	1.28E+07		(K)VIDDTNI	(K)V/I|D|D/T/N I/T/R(L)		99.22	523.7794	1046.548	0.0039	3.7	4.21	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3150	dirMS_041712_NAR_60mM_plus.12291.12346.3	3	14.83	1	1.09E+06		(R)VCEEIAI	(R)V/C|E E I A|I|I/P/S K K(L)	C:Carbamidomethylation	121.32	462.9253	1386.766	-0.0048	-3.4	6.11	21927.8	9.55	HUMAN	H0YK46	40S ribosomal protein S17 (Fragment)
3151	dirMS_041712_NAR_30mM_minus2.12540.12540.2	2	14.82	0	7.79E+05		(R)GVVGPE	(R)G V/V/G/P/E L/Y/G/R(L)		122.52	523.7834	1046.563	-0.0034	-3.2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
3152	dirMS_041712_NAR_30mM_minus2.12607.12708.2	2	14.82	1	3.06E+06		(K)KITIADC	(K)K\I\T I|A|D\C\G\Q|L|E(-)	C:Carbamidomethylation	123.18	624.3176	1247.63	-0.0021	-1.7	4.75	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
3153	dirMS_041712_NAR_40mM_minus2.14124.14137.3	3	14.82	0	6.82E+05		(R)IHFPLAT	(R)I H F\P L A\T|Y/A/P/V/I/S A E K(A)		167.8	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
3154	dirMS_041712_NAR_60mM_minus.11879.11879.2	2	14.82	1	3.16E+05		(K)TIDDLED	(K)T/I/D/D|L/E D K L/K(C)		126.35	595.3185	1189.631	-0.0013	-1.1	4.22	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
3155	dirMS_041712_NAR_30mM_plus2.16661.16936.2	2	14.82	0	2.37E+05		(R)EIGYPV	(R)E I|G Y/P/V/M I/K(A)		141.15	525.2819	1049.57	-0.0135	-12.8	6.1	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
3156	dirMS_041712_NAR_40mM_plus2.7903.7903.2	2	14.82	0	1.43E+05		(K)ASLENSL	(K)A/S|L/E/N S L R(E)		106.82	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18

3157	dirMS_041712_NAR_50mM_plus2.12261.12261.3	3	14.82	0	3.98E+05		(K)IVLEDGT	(K)I/V|L/E/D G T L|H V T E G S G R(Y)		132.23	561.6272	1682.871	-0.0037	-2.2	4.65	62748.9	5.95	HUMAN	Q16555	Dihydropyrimidinase-related protein 2
3158	dirMS_041712_NAR_50mM_plus2.13475.13475.3	3	14.82	0	2.57E+06		(K)AGVVGF	(K)A G/V/V/G/P/E/L H E Q L L S A E K(A)		138.58	592.986	1776.949	-0.0056	-3.1	4.75	533778	5.74	HUMAN	Q15149	Plectin
3159	dirMS_041712_NAR_30mM_minus2.16239.16708.2	2	14.81	0	7.48E+05		(K)FFVGGN	(K)F/F|V|G/G N/W/K(M)		143.3	477.745	954.483	-0.0005	-0.5	8.75	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
3160	dirMS_041712_NAR_50mM_minus2.6900.6900.3	3	14.81	0	5.92E+05		(R)EATNPP	(R)E A T N/P/P V/I Q/E E K/P K(K)		105.52	527.2846	1579.833	0.0066	4.2	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
3161	dirMS_041712_NAR_50mM_minus2.9355.9406.3	3	14.81	0	2.72E+05		(K)TGVAVN	(K)T/G\V|A/V/N/K/P A E F T V D/A/K(H)		122.03	549.6316	1646.875	0.0054	3.3	5.73	283472.4	5.71	HUMAN	P21333	Filamin-A
3162	dirMS_041712_NAR_60mM_minus.18440.18440.3	3	14.81	1	1.29E+05		(R)RFDEILE	(R)R F D\E\I\L\E\A|S/D/G|I|M/V/A R(G)		164.42	607.9739	1821.916	-0.0092	-5.1	4.32	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
3163	dirMS_041712_NAR_120mM_plus.12180.12222.4	4	14.81	1	2.72E+06		(K)TLTTVQ	(K)T L\T T V/Q/G I/A/D/D Y D K K/K(L)		117.32	449.7412	1795.944	-0.0006	-0.4	5.71	13778.5	7.96	HUMAN	K7EM18	Eukaryotic translation initiation factor 1
3164	dirMS_041712_NAR_30mM_plus2.20747.20747.2	2	14.81	0	2.72E+05		(K)GGIVGM	(K)G G I|V/G/M/T/L/P I A/R(D)		162.32	592.8453	1184.682	0.0013	1.1	9.75	27150.8	7.95	HUMAN	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2
3165	dirMS_041712_NAR_40mM_plus2.11950.12007.3	3	14.81	1	2.28E+05		(R)VVDALG	(R)V/V|D A/L/G/N A I/D/G K G P I G S K(T)		137.08	570.9838	1710.939	-0.0016	-1	5.93	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
3166	dirMS_041712_NAR_40mM_plus2.8169.8486.2	2	14.81	0	1.55E+06		(R)LASYLDF	(R)L/A|S|Y L/D/R(V)		109.68	419.2273	837.447	0.0008	1	5.83	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3167	dirMS_041712_NAR_50mM_plus2.12660.12660.3	3	14.81	1	3.83E+05		(K)LPGGELI	(K)L/P G G E L/N|P/G E/D/E V E/G L K/R(L)		134.28	636.9936	1908.966	0.0001	0.1	4.25	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
3168	dirMS_041712_NAR_50mM_plus2.15042.15042.3	3	14.81	0	4.96E+05		(K)TTISVAH	(K)T T|I/S V A/H/L/L A A/R(Q)		146.45	418.2499	1252.737	-0.002	-1.6	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
3169	dirMS_041712_NAR_40mM_minus2.14420.14420.3	3	14.8	0	2.72E+05		(R)DVCTELI	(R)D V|C/T/E L L/P L I K P Q G R(V)	C:Carbamidomethylation	168.95	580.3211	1738.952	-0.0033	-1.9	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
3170	dirMS_041712_NAR_50mM_minus2.16691.16814.3	3	14.8	1	1.60E+05		(K)NIPIPTLI	(K)N I/P I/P/T/L K D/F A/K(A)		163.38	452.9385	1356.789	0.0124	9.1	8.59	20960.6	7.05	HUMAN	H0YKU1	Tropomodulin-3 (Fragment)
3171	dirMS_041712_NAR_50mM_minus2.9045.9045.3	3	14.8	0	7.04E+04		(R)EANALA	(R)E A N/A/L/A/A G H/P A Q/A V A/I N A R(L)		119.77	615.6611	1844.973	-0.0038	-2.1	6.85	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
3172	dirMS_041712_NAR_60mM_minus.15007.15365.3	3	14.8	0	5.04E+06		(R)EHALLA	(R)E H\A\L\L|A|Y/T/L/G V/K(Q)		144.68	438.9202	1314.742	0.0044	3.4	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
3173	dirMS_041712_NAR_20mM_plus.16346.16346.2	2	14.8	0	1.40E+05		(R)QAQEYE	(R)Q A/Q E|Y/E/A/L/L N I K(V)		184.52	710.3754	1419.748	-0.0043	-3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3174	dirMS_041712_NAR_30mM_plus2.22091.22091.2	2	14.8	0	1.92E+05		(K)NSSYFVE	(K)N S/S Y/F/V|E W/I/P N/N V K(V)		171.77	848.9189	1696.833	-0.0024	-1.4	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
3175	dirMS_041712_NAR_30mM_minus2.10052.10072.2	2	14.79	0	1.12E+05		(K)CLDAVV	(K)C/L|D|A|V/V S T/R(H)	C:Carbamidomethylation	108.93	510.7635	1020.514	0.0055	5.4	5.84	50425	5.53	HUMAN	H0YH27	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
3176	dirMS_041712_NAR_30mM_minus2.9763.9763.2	2	14.79	0	6.20E+04		(R)ELSEQLC	(R)E L/S E Q/L/G/Q/A E/R(A)		107.38	630.312	1259.623	-0.0059	-4.7	4.25	266161	5.68	HUMAN	E9PPU0	Epiplakin
3177	dirMS_041712_NAR_60mM_minus.15439.15439.3	3	14.79	1	1.77E+05		(R)ASLISAV	(R)A/S/L/I/S/A V/S/D K L/R(W)		146.23	420.5811	1259.732	-0.003	-2.4	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
3178	dirMS_041712_NAR_30mM_plus2.10824.10824.2	2	14.79	0	5.58E+05		(R)LASFYER	(R)L/A|S|F/Y/E/R(A)		110.48	443.2301	885.447	0.0064	7.3	6	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
3179	dirMS_041712_NAR_30mM_plus2.11559.11559.2	2	14.79	0	1.26E+06		(R)GGGGNI	(R)G G/G G N|F|G|P G/P G S N/F R(G)		114.38	689.3175	1377.629	-0.0017	-1.2	9.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
3180	dirMS_041712_NAR_30mM_plus2.17754.17754.2	2	14.79	0	3.10E+05		(K)SLEDQV	(K)S L|E/D/Q/V/E M L R(T)		145.88	610.3003	1219.599	-0.0054	-4.4	4.14	61161.1	4.34	HUMAN	K7ELL7	Glucosidase 2 subunit beta
3181	dirMS_041712_NAR_40mM_plus2.14271.14271.3	3	14.79	1	7.99E+05		(R)IINEPTA	(R)I I|N E|P T A/A A I\A Y G L D K K(V)		149.77	596.6671	1787.99	-0.0034	-1.9	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
3182	dirMS_041712_NAR_120mM_minus.6097.6097.3	3	14.78	1	5.64E+05		(K)TCEESSF	(K)T/C/E/E/S/S/F C/K/R(Q)	C:Carbamidomethylation	86.8	435.1849	1303.541	-0.0004	-0.3	5.81	10576.1	11.44	HUMAN	E9PRF8	Neutral alpha-glucosidase AB
3183	dirMS_041712_NAR_60mM_minus.14088.14088.3	3	14.78	0	3.65E+05		(K)QLPLVKI	(K)Q L/P L/V/K/P Y L R(S)		138.22	409.59	1226.762	-0.0065	-5.3	9.99	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
3184	dirMS_041712_NAR_60mM_minus.4806.4806.3	3	14.78	1	7.13E+05	M137m	(R)mQNDT	(R)m Q|N/D T A/E/N E/T T E K/E|E K(S)	m:Oxidized methionine	79.37	638.2735	1896.813	15.9932	-0.9	4.14	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
3185	dirMS_041712_NAR_60mM_minus.9088.9088.2	2	14.78	0	9.67E+05		(K)QEYDES	(K)Q E|Y/D/E/S/G/P S I/V/H/R(K)		110.35	758.8539	1516.703	-0.0021	-1.4	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
3186	dirMS_041712_NAR_30mM_plus2.13638.13820.2	2	14.78	0	1.91E+06		(K)VLEGME	(K)V/L|E|G M/E V/V/R(K)		125.05	516.2816	1031.555	0.0005	0.5	4.53	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
3187	dirMS_041712_NAR_40mM_plus2.11313.11313.3	3	14.78	0	1.67E+05		(R)SVIDPVF	(R)S V/I/D/P\V/P A/P V G D S H V D G A A K(S)		132.95	644.3327	1930.987	-0.0033	-1.7	4.41	58326.8	5.7	HUMAN	Q13177	Serine/threonine-protein kinase PAK 2
3188	dirMS_041712_NAR_50mM_plus2.20884.20884.3	3	14.78	0	3.32E+06		(R)AGKPVI	(R)A G K\P V I C A|T/Q/M/L/E/S M/I/K(K)	C:Carbamidomethylation	179.12	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
3189	dirMS_041712_NAR_50mM_plus2.22294.22294.3	3	14.78	0	1.53E+06		(R)DALSDL	(R)D A/L/S D L A/L/H F L N K(M)		191.78	486.2644	1456.78	-0.0008	-0.6	5.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
3190	dirMS_041712_NAR_120mM_minus.21420.21434.3	3	14.77	0	8.12E+05		(R)LHFFMP	(R)L H F F M|P G\F|A|P\L/T S R(G)		182.17	540.9497	1620.835	-0.001	-0.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
3191	dirMS_041712_NAR_20mM_minus.7303.7316.2	2	14.77	0	1.32E+05	M374m	(R)mAPTPII	(R)m|A|P/T|P I/P T R(S)	m:Oxidized methionine	121.02	500.2679	983.534	15.9943	-0.7	9.5	76925.9	4.46	HUMAN	A8MV58	Drebrin
3192	dirMS_041712_NAR_40mM_minus2.15777.15829.3	3	14.77	0	7.17E+05		(K)GLAPDLI	(K)G L|A/P/D/L/P/E D L Y/H L I K(K)		184.48	565.3111	1693.916	0.0028	1.7	4.54	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
3193	dirMS_041712_NAR_50mM_minus2.10374.10374.3	3	14.77	0	1.46E+05		(K)VGSLDN	(K)V/G|S/L D N/V G H L/P A/G G A\V K(I)		126.9	530.9592	1590.86	0.0032	2	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
3194	dirMS_041712_NAR_50mM_minus2.14561.14623.3	3	14.77	1	6.71E+05		(K)VALNVS	(K)V/A|L|N|V/S/C A N L L D K D/I G S K(S)	C:Carbamidomethylation	151.22	639.6751	1917.011	-0.0002	-0.1	5.93	9239.5	7.98	HUMAN	E5RFT7	Copine-3 (Fragment)
3195	dirMS_041712_NAR_40mM_plus2.17503.17608.3	3	14.77	1	3.17E+05		(K)TGISDVF	(K)T G/I/S D V|F A/K N D|L/A|V/V D/V R(I)		169.33	640.3451	1919.023	-0.0025	-1.3	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
3196	dirMS_041712_NAR_50mM_plus2.14419.14492.3	3	14.77	1	1.75E+06		(K)LTEDKAI	(K)L/T|E D K A D V\Q/S|I/I|G/L Q R(F)		143.9	595.9941	1785.97	-0.0028	-1.5	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
3197	dirMS_041712_NAR_60mM_plus.7500.7500.3	3	14.77	1	5.05E+05		(K)SSGGREI	(K)S S|G G R E D\L|E/S\S/G L/Q|R(R)		97.3	526.5897	1577.751	0.0031	2	4.68	11625.5	8.01	HUMAN	B8ZZT7	Hematological and neurological-expressed 1 protein
3198	dirMS_041712_NAR_30mM_minus2.18136.18136.2	2	14.76	0	1.03E+05		(K)LLCGLLA	(K)L L|C|G/L L/A/E R(L)	C:Carbamidomethylation	152.35	522.7963	1044.587	-0.0017	-1.6	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
3199	dirMS_041712_NAR_40mM_minus2.14846.14846.3	3	14.76	1	1.64E+04		(R)GDLGIEI	(R)G D/L/G\I/E I/P A E K V F L A Q K(M)		172.22	610.0109	1828.022	-0.0033	-1.8	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
3200	dirMS_041712_NAR_40mM_minus2.9403.9404.3	3	14.76	0	1.42E+05		(K)QLTEED	(K)Q L/T E/E/D/G V/H/S V/I E E N\I K(C)		137.88	647.3235	1939.961	-0.0048	-2.5	4.25	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
3201	dirMS_041712_NAR_50mM_minus2.11448.11471.3	3	14.76	0	1.45E+05		(K)VSQPIEC	(K)V/S\Q/P I/E G H A/A/S F A Q/F/K(M)		133.52	572.9609	1716.87	-0.0022	-1.3	6.72	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
3202	dirMS_041712_NAR_120mM_plus.5479.5480.3	3	14.76	1	6.39E+05		(R)YYGGGS	(R)Y/Y|G/G G/S|E|G G R A P K(R)		81.9	433.5423	1298.612	0	0	8.5	64759.2	8.88	HUMAN	P14866	Heterogeneous nuclear ribonucleoprotein L
3203	dirMS_041712_NAR_50mM_plus2.12894.12894.3	3	14.76	1	3.37E+05		(R)ELAVQIY	(R)E L/A/V/Q/I/Y/E E A R K(F)		135.53	483.5916	1448.774	-0.0141	-9.7	4.79	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
3204	dirMS_041712_NAR_50mM_plus2.19278.19349.3	3	14.76	0	3.59E+05		(-)MKPLVV	(-)M K P L V V\F|V|L/G G/P G A G K(G)		169.73	523.9715	1569.919	-0.0186	-11.8	10	22450.2	5.44	HUMAN	P30085	UMP-CMP kinase
3205	dirMS_041712_NAR_60mM_plus.15641.15663.3	3	14.76	1	3.43E+06		(R)TEMENE	(R)T\E|M/E/N E/F/V/L I/K K(D)		138.23	494.2622	1480.772	0.0005	0.3	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
3206	dirMS_041712_NAR_20mM_minus.14688.14688.3	3	14.75	0	3.68E+05		(K)LAVEALS	(K)L A V\E A\L|S S/L D/G D/L/A/G R(Y)		201.3	529.6163	1586.838	-0.0041	-2.6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
3207	dirMS_041712_NAR_50mM_minus2.12962.12962.3	3	14.75	1	3.89E+05		(R)LSEDYG	(R)L/S/E/D/Y/G V L K T/D E G I A Y R(G)		141.73	643.6561	1928.96	-0.0063	-3.2	4.32	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
3208	dirMS_041712_NAR_50mM_minus2.15088.15107.3	3	14.75	1	2.54E+05		(K)LALDIEI	(K)L/A|L D/I E/I/A/T Y R/K(L)		154.13	469.2729	1405.805	-0.0008	-0.6	6.07	49564	5.84	HUMAN	E9PAX3	Glial fibrillary acidic protein
3209	dirMS_041712_NAR_50mM_minus2.15737.15737.3	3	14.75	1	4.93E+05		(K)QGGLGF	(K)Q G\G L/G/P M N I/P L V S D/P K R(T)		157.5	593.6566	1778.958	-0.0029	-1.6	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
3210	dirMS_041712_NAR_60mM_minus.11172.11400.3	3	14.75	1	5.95E+05	M136m	(K)VKEGmN	(K)V/K\E G m N\I|V|E A/M/E/R(F)	m:Oxidized methionine	122.87	507.9181	1505.745	15.9947	-0.1	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
3211	dirMS_041712_NAR_60mM_minus.12310.12310.3	3	14.75	1	4.35E+05		(R)INVYYNI	(R)I N/V|Y/Y\N E/A T/G G K Y/V P R(A)		127.72	615.3145	1843.934	-0.0048	-2.6	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
3212	dirMS_041712_NAR_20mM_plus.17079.17079.2	2	14.75	0	1.91E+05		(K)VQIAVA	(K)V Q I/A/V/A N/A/Q E/L\L/Q R(M)		188.3	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
3213	dirMS_041712_NAR_30mM_plus2.13495.13534.2	2	14.75	0	1.03E+05		(R)TIYAGN	(R)T/I|Y|A/G N|A|L/C T V K(C)	C:Carbamidomethylation	123.85	655.8414	1310.677	-0.0018	-1.4	8.26	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
3214	dirMS_041712_NAR_30mM_plus2.8714.8845.3	3	14.75	0	1.43E+06		(R)FGQGG	(R)F G\Q G G A G|P|V/G/G/Q/G P/R(G)		99.68	447.893	1341.666	-0.0014	-1	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
3215	dirMS_041712_NAR_40mM_plus2.17751.17751.3	3	14.75	0	3.79E+04		(R)AGLGSG	(R)A G L/G/S/G/L/S L/S/G L V/H P/E L S R(S)		170.98	617.3431	1850.013	0.0017	0.9	6.79	73325.2	9.19	HUMAN	F5H2A9	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial
3216	dirMS_041712_NAR_50mM_plus2.18656.19187.3	3	14.75	1	6.52E+06		(R)LDLAGR	(R)L/D|L|A/G R D L/T D/Y L/M/K(I)		167.65	541.9524	1623.841	0.0016	1	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
3217	dirMS_041712_NAR_60mM_plus.11480.11497.3	3	14.75	0	1.11E+06		(R)SIFQHIQ	(R)S I|F Q/H/I/Q S/A Q/S Q R(S)		117.93	510.6056	1529.782	0.0203	13.3	9.49	108720.9	10.17	HUMAN	Q9Y2W1	Thyroid hormone receptor-associated protein 3
3218	dirMS_041712_NAR_60mM_plus.15420.15420.3	3	14.75	1	3.85E+05		(R)SLIANLA	(R)S L/I/A/N/L/A A A\N C Y/K K(E)	C:Carbamidomethylation	137.43	512.9411	1536.82	-0.0115	-7.5	9.7	36978.6	6.33	HUMAN	B7Z800	Adenosine kinase
3219	dirMS_041712_NAR_60mM_plus.5566.5587.3	3	14.75	0	6.14E+05	M434m M4	(R)LESGmC	(R)L/E|S G m Q N m/S I/H/T/K(T)	m:Oxidized methionine	87.57	503.2333	1475.698	31.9872	-1.7	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
3220	dirMS_041712_NAR_30mM_minus2.16082.16082.2	2	14.74	0	2.79E+05		(R)GEVTAA	(R)G E|V/T/A/A/D L/F N S R(V)		141.65	640.3185	1279.628	0.002	1.6	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
3221	dirMS_041712_NAR_30mM_minus2.20017.20077.2	2	14.74	0	2.44E+04		(K)SLNILTA	(K)S L|N|I|L/T/A/F Q/K(K)		168.82	567.8283	1134.652	-0.0024	-2.1	8.47	18172.6	7.77	HUMAN	F8VY02	Endoplasmic reticulum resident protein 29
3222	dirMS_041712_NAR_50mM_minus2.10229.10329.3	3	14.74	0	1.46E+05		(K)VGSLDN	(K)V/G|S/L/D N/V G H\L/P A G G A V/K(I)		126.9	530.9592	1590.86	0.0032	2	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
3223	dirMS_041712_NAR_60mM_minus.11899.11899.2	2	14.74	1	3.16E+05		(K)TIDDLED	(K)T I|D|D/L E D K L/K(C)		126.35	595.3185	1189.631	-0.0013	-1.1	4.22	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
3224	dirMS_041712_NAR_120mM_plus.11653.11989.3	3	14.74	1	1.18E+06		(K)MKEIAE	(K)M/K E I A|E|A/Y/L/G/K(T)		114.3	418.2253	1252.661	0.0008	0.6	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
3225	dirMS_041712_NAR_120mM_plus.15275.15300.3	3	14.74	1	5.50E+05		(K)KKELEEI	(K)K\K E L\E E\I|V|Q/P I/I/S K(L)		133.28	551.998	1653.978	0.0009	0.5	6.23	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
3226	dirMS_041712_NAR_20mM_plus.10906.10906.2	2	14.74	0	2.19E+05	M33m	(K)VAGmD	(K)V A/G\m D|V|E/L/T V/E/E R(N)	m:Oxidized methionine	147.28	732.3555	1447.71	15.994	-0.6	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
3227	dirMS_041712_NAR_20mM_plus.11106.11106.2	2	14.74	0	9.73E+03		(R)TIYAGN	(R)T I|Y/A/G N/A\L C T V K(C)	C:Carbamidomethylation	148.83	655.8428	1310.677	0.001	0.8	8.26	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
3228	dirMS_041712_NAR_20mM_plus.18015.18015.2	2	14.74	0	1.71E+05		(R)SLVPAAI	(R)S L\V|P A/A/E|L L E S R(V)		195.18	642.8613	1284.716	-0.0005	-0.4	4.53	533778	5.74	HUMAN	Q15149	Plectin
3229	dirMS_041712_NAR_20mM_plus.7425.7472.2	2	14.74	0	2.40E+05		(K)VTLTSEE	(K)V/T|L/T|S/E E E A R(L)		119.92	567.7865	1134.564	0.002	1.8	4.25	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
3230	dirMS_041712_NAR_30mM_plus2.12710.12710.2	2	14.74	0	3.16E+05		(K)LVPVLSA	(K)L V/P/V/L S\A K(A)		119.62	413.7745	826.54	0.0021	2.5	8.75	37710.6	6.36	HUMAN	P37837	Transaldolase
3231	dirMS_041712_NAR_30mM_plus2.7070.7269.2	2	14.74	0	6.70E+05		(K)AQCPIVI	(K)A/Q|C|P/I V/E/R(L)	C:Carbamidomethylation	92.52	486.7542	972.493	0.008	8.2	6.05	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
3232	dirMS_041712_NAR_30mM_plus2.9521.9521.2	2	14.74	0	6.85E+05		(R)GGGQIII	(R)G G/G Q|I|I|P T A/R(R)		104.17	485.2772	969.548	-0.0005	-0.5	9.75	15036.9	7.16	HUMAN	K7EJ74	116 kDa U5 small nuclear ribonucleoprotein component (Fragment)
3233	dirMS_041712_NAR_40mM_plus2.7198.7480.2	2	14.74	0	3.09E+05		(K)VIDDTNI	(K)V/I|D|D|T/N I/T/R(L)		103.53	523.7788	1046.548	0.0027	2.5	4.21	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3234	dirMS_041712_NAR_50mM_plus2.21443.21443.3	3	14.74	1	1.51E+05		(K)ALFEEVF	(K)A L/F/E/E/V/P E L L T E A E K/K(E)		182.68	615.9987	1845.984	-0.0029	-1.6	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
3235	dirMS_041712_NAR_60mM_plus.15619.15619.2	2	14.74	1	4.11E+05		(R)TEMENE	(R)T/E|M|E/N E F V/L I/K K(D)		138.27	740.8875	1480.772	-0.0039	-2.6	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
3236	dirMS_041712_NAR_60mM_minus.13632.13633.3	3	14.73	1	1.80E+05		(K)QMADT	(K)Q/M/A/D/T G/K/L/N/T L/L Q R(A)		135.92	530.2846	1588.848	-0.0083	-5.2	8.75	91324.5	5.75	HUMAN	Q00839	Heterogeneous nuclear ribonucleoprotein U
3237	dirMS_041712_NAR_120mM_plus.10981.11111.3	3	14.73	1	5.81E+05		(K)VIADNV	(K)V/I/A/D/N V/K D W/S/K(V)		110.67	425.5621	1274.674	-0.0022	-1.7	5.93	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
3238	dirMS_041712_NAR_120mM_plus.14419.14917.4	4	14.73	1	2.10E+06		(K)GLDPAR	(K)G L\D\P A R V N V/P/V/I/G G H A G K(T)		130.67	439.9998	1756.982	-0.0043	-2.5	8.76	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
3239	dirMS_041712_NAR_20mM_plus.18857.18857.2	2	14.73	0	2.72E+05		(K)LAVEALS	(K)L A/V/E|A/L|S/S L/D G D/L A/G R(Y)		200.53	793.9214	1586.838	-0.0029	-1.8	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
3240	dirMS_041712_NAR_40mM_plus2.14948.14948.3	3	14.73	0	6.60E+04		(R)QAQEYE	(R)Q A Q E\Y\E/A|L|L N/I K(V)		154.73	473.9204	1419.748	-0.0012	-0.8	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3241	dirMS_041712_NAR_40mM_plus2.19355.19355.3	3	14.73	0	1.61E+06		(R)AGKPVI	(R)A G K\P V I\C A\T/Q/M/L/E S M I K(K)	C:Carbamidomethylation	180.63	626.3273	1876.969	-0.002	-1.1	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
3242	dirMS_041712_NAR_50mM_plus2.14176.14176.3	3	14.73	0	5.08E+05		(K)VTHAVV	(K)V T H A V V/T V|P A/Y/F/N/D/A Q/R(Q)		142.7	629.9955	1887.971	0.0008	0.4	6.71	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
3243	dirMS_041712_NAR_50mM_plus2.8776.8776.3	3	14.73	0	1.55E+06		(R)LESGMC	(R)L E/S G M Q/N M/S/I/H T K(T)		113.23	492.5704	1475.698	-0.0015	-1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
3244	dirMS_041712_NAR_60mM_plus.10282.10282.3	3	14.73	0	2.57E+05		(K)TVFAEHI	(K)T/V|F A E/H I/S D E C K(R)	C:Carbamidomethylation	111.73	479.2229	1435.652	0.0019	1.4	4.65	31471	10.11	HUMAN	B5MCW2	60S ribosomal protein L3 (Fragment)
3245	dirMS_041712_NAR_30mM_minus2.12624.13069.2	2	14.72	1	3.16E+06		(K)KITIADC	(K)K\I T I|A|D\C|G Q|L|E(-)	C:Carbamidomethylation	123.22	624.3176	1247.63	-0.0021	-1.7	4.75	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
3246	dirMS_041712_NAR_30mM_minus2.13603.13809.2	2	14.72	0	3.31E+05		(R)ISGLIYEE	(R)I/S|G|L|I|Y/E E/T R(G)		127.68	590.8127	1180.621	-0.0027	-2.3	4.53	11367.1	11.36	HUMAN	P62805	Histone H4
3247	dirMS_041712_NAR_60mM_minus.14177.14177.3	3	14.72	1	2.27E+05		(R)TFNTST	(R)T F/N/T/S T G G L/L/L/P S D/T K R(S)		138.82	603.3262	1807.955	0.0092	5.1	8.41	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
3248	dirMS_041712_NAR_120mM_plus.14840.14884.3	3	14.72	1	5.29E+05		(R)KLDELYC	(R)K L D E\L|Y/G/T/W/R(K)		131.2	427.5607	1280.663	0.0042	3.3	6.07	37884.5	11.27	HUMAN	H3BM89	60S ribosomal protein L4
3249	dirMS_041712_NAR_30mM_plus2.18570.18570.2	2	14.72	0	2.24E+05		(R)GNPTVE	(R)G N|P T/V|E V D L F/T S K(G)		150.92	703.8613	1406.716	-0.0009	-0.6	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
3250	dirMS_041712_NAR_30mM_plus2.19597.19597.2	2	14.72	0	3.99E+05		(K)LLQDFFI	(K)L/L|Q|D/F F N/G R(D)		156.8	555.2902	1109.574	-0.0007	-0.6	5.84	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
3251	dirMS_041712_NAR_40mM_plus2.14348.14436.3	3	14.72	1	1.80E+05		(K)IMASSPI	(K)I/M|A/S S/P D|M/D L/A T V S A L R K(M)		151.18	635.9975	1905.977	0.0007	0.4	5.96	36208.1	7.21	HUMAN	B4DMU0	Pyrroline-5-carboxylate reductase
3252	dirMS_041712_NAR_50mM_plus2.18170.18170.3	3	14.72	1	1.09E+05		(K)DLEIKIP	(K)D/L\E/I\K/I/P V V V R(L)		163.5	427.6021	1280.794	-0.0019	-1.5	6.07	44183.5	5.64	HUMAN	F5GXC8	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial
3253	dirMS_041712_NAR_60mM_plus.15308.15554.3	3	14.72	1	7.13E+06		(K)VKEGMI	(K)V K\E G M N\I|V|E/A/M/E/R(F)		137.73	502.5849	1505.745	-0.0049	-3.3	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
3254	dirMS_041712_NAR_60mM_plus.17677.17677.3	3	14.72	1	4.28E+05		(R)LMDLLG	(R)L/M|D\L/L/G E\G L K/R(S)		149.27	415.5712	1244.703	-0.0041	-3.3	6.07	52817.9	6.2	HUMAN	F5H3T8	Arginine--tRNA ligase, cytoplasmic
3255	dirMS_041712_NAR_50mM_minus2.13410.13410.3	3	14.71	0	1.48E+05		(R)IVATKPL	(R)I V/A T K/P L/Y V/A/L A/Q/R(K)		144.15	514.9821	1542.937	-0.0049	-3.2	9.99	65918.2	9.74	HUMAN	E7EQV3	Polyadenylate-binding protein 1
3256	dirMS_041712_NAR_60mM_minus.10704.10704.3	3	14.71	1	5.44E+05	M239m	(R)MSMKE	(R)M/S\M K E V D E Q|m|L/N/V/Q/N K(N)	m:Oxidized methionine	119.9	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3257	dirMS_041712_NAR_60mM_minus.18683.18683.3	3	14.71	0	2.97E+05		(K)LHDNLII	(K)L H D N L\I|I/S D/L/E N T V K(K)		165.95	575.3117	1723.922	-0.0019	-1.1	4.54	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
3258	dirMS_041712_NAR_120mM_plus.12297.12707.3	3	14.71	0	1.51E+06		(R)HVFGES	(R)H V\F G\E|S/D|E|L|I/G Q/K(V)		119.02	486.9124	1458.722	0.0003	0.2	4.65	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
3259	dirMS_041712_NAR_20mM_plus.6694.6694.2	2	14.71	0	2.51E+04		(R)AAPTAA	(R)A A/P/T/A/A/S/D/Q/P D S A A T T E K(A)		110.9	866.4036	1731.803	-0.0032	-1.9	4.03	22655.1	9.45	HUMAN	Q9BRP8	Partner of Y14 and mago
3260	dirMS_041712_NAR_30mM_plus2.18989.18989.2	2	14.71	0	2.07E+05		(K)YPQLLP	(K)Y/P|Q|L/L/P G I R(G)		153.25	528.814	1056.62	0.0007	0.6	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
3261	dirMS_041712_NAR_30mM_plus2.8362.8633.2	2	14.71	0	1.11E+06		(R)SLQSVAI	(R)S L|Q|S/V A/E/E R(A)		98.42	509.7627	1018.516	0.0018	1.7	4.53	20623.6	11.46	HUMAN	E7EQV9	Ribosomal protein L15 (Fragment)
3262	dirMS_041712_NAR_30mM_plus2.8560.8702.2	2	14.71	0	3.58E+05		(R)AVVGVV	(R)A V|V/G|V|V/A/G\G\G R(I)		99.07	471.2779	941.553	-0.0042	-4.4	9.79	24115.6	11.59	HUMAN	E9PIZ3	60S ribosomal protein L8
3263	dirMS_041712_NAR_40mM_plus2.20060.20060.3	3	14.71	1	1.43E+06		(R)ELAILLG	(R)E L/A I/L/L G/M L D/P/A E K D E K(G)		189.2	629.003	1884.999	-0.0042	-2.3	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
3264	dirMS_041712_NAR_20mM_plus.9051.9051.2	2	14.7	0	2.63E+05		(R)VLTVINC	(R)V L|T/V|I/N Q T Q K(E)		133.05	572.3399	1143.673	-0.0007	-0.6	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
3265	dirMS_041712_NAR_30mM_plus2.20035.20035.2	2	14.7	0	8.31E+04		(R)FEELTNL	(R)F/E|E/L/T/N L/I R(T)		158.62	567.8152	1134.615	0.0078	6.9	4.53	106155.7	5.45	HUMAN	B5ME19	Eukaryotic translation initiation factor 3 subunit C

3266	dirMS_041712_NAR_60mM_plus.16618.16618.3	3	14.7	1	5.49E+05		(K)AAVEWI	(K)A A|V/E/W/F D/G K D F Q G S K(L)		143.2	562.2762	1684.797	0.0175	10.4	4.56	65213.5	9.57	HUMAN	B0QYK0	Ewing sarcoma breakpoint region 1
3267	dirMS_041712_NAR_120mM_minus.7815.7905.3	3	14.69	1	5.78E+05		(R)LQSIGTE	(R)L/Q|S|I/G/T E/N T/E E N R R(F)		97.25	549.607	1646.809	-0.0028	-1.7	4.79	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
3268	dirMS_041712_NAR_120mM_minus.8411.8411.3	3	14.69	0	1.85E+05		(K)LFQECCI	(K)L/F/Q/E C/C/P/H/S T D R(V)	C:Carbamidomethylation	99.98	517.2227	1549.652	0.0013	0.9	5.32	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
3269	dirMS_041712_NAR_20mM_minus.14668.14668.2	2	14.69	0	2.10E+05		(K)LAVEALS	(K)L A|V E/A|L|S/S L/D\G D L A G R(Y)		201.28	793.922	1586.838	-0.0017	-1.1	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
3270	dirMS_041712_NAR_30mM_minus2.10487.10487.2	2	14.69	0	5.97E+05		(K)EAAENS	(K)E A|A/E/N S L V/A/Y/K(A)		110.83	597.8033	1194.6	-0.0008	-0.6	4.53	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
3271	dirMS_041712_NAR_40mM_minus2.10349.10764.3	3	14.69	1	3.05E+06		(K)TITLEVEI	(K)T I\T|L/E/V/E/P S D T I E N V K A K(I)		145.98	663.0226	1987.059	-0.0061	-3.1	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
3272	dirMS_041712_NAR_50mM_minus2.16186.16186.3	3	14.69	0	1.46E+05		(K)LDPHLVI	(K)L/D/P H/L V/L D/Q|L R(C)		160.2	440.2533	1318.748	-0.0024	-1.8	5.21	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
3273	dirMS_041712_NAR_120mM_plus.7403.7438.3	3	14.69	2	2.39E+05		(K)VVSETN	(K)V/V|S E/T N D T/K/V/L R/H(-)		92.38	499.9371	1497.802	-0.0052	-3.5	6.72	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
3274	dirMS_041712_NAR_30mM_plus2.12131.12131.2	2	14.69	0	1.34E+06		(K)GIYAVGI	(K)G I/Y|A/V|G D V/C G K(A)	C:Carbamidomethylation	117.58	569.7798	1138.556	-0.0038	-3.3	5.83	56826.6	9.16	HUMAN	P00390	Glutathione reductase, mitochondrial
3275	dirMS_041712_NAR_30mM_plus2.8771.8828.2	2	14.69	0	7.16E+04		(K)FGDSNT	(K)F/G|D|S|N T/V/M/R(F)		99.8	513.7373	1026.467	0	0	5.84	334221.3	6.44	HUMAN	P15924	Desmoplakin
3276	dirMS_041712_NAR_50mM_plus2.15011.15202.3	3	14.69	0	7.94E+05		(R)QIFHPE	(R)Q I/F H/P E Q/L/I/T G K(E)		147.53	470.9293	1410.774	-0.0006	-0.4	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
3277	dirMS_041712_NAR_60mM_plus.10819.11162.3	3	14.69	1	1.34E+06		(R)KAGNFY	(R)K\A G\N F\Y|V/P/A E/P/K(L)		115.4	440.9074	1320.695	0.013	9.8	8.5	24489.6	10.74	HUMAN	A8MUD9	60S ribosomal protein L7
3278	dirMS_041712_NAR_60mM_plus.16092.16234.3	3	14.69	1	6.29E+05		(R)IKIGDPL	(R)I K I G D/P\L|L/E/D/T/R(M)		141.63	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
3279	dirMS_041712_NAR_60mM_plus.16293.16293.3	3	14.69	0	6.39E+05		(R)ETHSAL	(R)E T H S\A\L/G|P\A/L/Q/A A/F K(L)		141.93	514.2744	1540.812	-0.0032	-2.1	6.85	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
3280	dirMS_041712_NAR_60mM_plus.18245.18245.3	3	14.69	1	9.27E+05		(K)EVNKFQ	(K)E V N K F Q M|A/Y/S/N/L/L/R(A)		152.8	571.6293	1712.879	-0.0055	-3.2	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
3281	dirMS_041712_NAR_50mM_minus2.14951.15090.3	3	14.68	1	2.09E+05		(K)VVEEAP	(K)V/V|E/E/A|P S I F L D/A E T R R(A)		153.72	611.3243	1831.955	0.0035	1.9	4.41	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
3282	dirMS_041712_NAR_120mM_plus.4205.4205.2	2	14.68	1	1.40E+06	M310m	(R)TKTEISE	(R)T/K|T|E|I|S E m N R(N)	m:Oxidized methionine	69.85	612.7976	1208.594	15.994	-0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
3283	dirMS_041712_NAR_120mM_plus.8497.8497.3	3	14.68	1	2.94E+05		(R)ASGNYA	(R)A/S|G/N/Y/A/T V I S H N P E T K K(T)		97.62	606.3102	1816.919	-0.0028	-1.5	8.55	24115.6	11.59	HUMAN	E9PIZ3	60S ribosomal protein L8
3284	dirMS_041712_NAR_30mM_plus2.8432.8632.2	2	14.68	0	9.63E+05		(K)LYEQLSC	(K)L/Y|E/Q/L/S/G/K(-)		99.03	469.2488	937.499	-0.0086	-9.2	6	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
3285	dirMS_041712_NAR_50mM_plus2.19650.19883.3	3	14.68	1	1.01E+06		(K)LKEAELL	(K)L K E A E L\L|E|P|L/M/P A I R(A)		172.58	574.9989	1722.982	-0.0001	-0.1	4.79	56164.6	6.01	HUMAN	E9PP73	Coatomer subunit beta (Fragment)
3286	dirMS_041712_NAR_60mM_plus.20561.20561.3	3	14.68	1	7.00E+05		(K)IKYPENF	(K)I/K Y P E N/F/F/L/L/R(G)		167.98	480.6056	1439.805	-0.0023	-1.6	8.59	33222.3	5.74	HUMAN	A6NNR3	Serine/threonine-protein phosphatase
3287	dirMS_041712_NAR_50mM_minus2.7699.7699.3	3	14.67	1	1.00E+05		(K)TAVCDIF	(K)T/A|V/C D I/P/P R G L K(M)	C:Carbamidomethylation	111.52	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
3288	dirMS_041712_NAR_20mM_plus.10550.10550.2	2	14.67	0	4.53E+04		(R)AQPSVS	(R)A Q|P S/V\S/L/G A A Y R(A)		145.72	610.3183	1219.643	-0.0136	-11.2	8.79	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
3289	dirMS_041712_NAR_20mM_plus.19015.19015.2	2	14.67	0	1.90E+05		(R)VCTLAII	(R)V C T\L|A|I|I|D P G D S D I I R(S)	C:Carbamidomethylation	202.68	879.4578	1757.91	-0.0019	-1.1	3.93	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
3290	dirMS_041712_NAR_30mM_plus2.18402.18441.2	2	14.67	0	7.81E+04		(R)VVNVSS	(R)V V|N\V|S/S I/M/S V/R(A)		149.77	595.8347	1190.656	0.006	5	9.72	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
3291	dirMS_041712_NAR_30mM_plus2.22052.22052.2	2	14.67	0	1.87E+05		(R)EGDVLT	(R)E G D\V/L/T/L/L|E/S E/R(E)		170.55	680.8538	1360.696	0.0049	3.6	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
3292	dirMS_041712_NAR_30mM_plus2.7468.7469.2	2	14.67	0	5.73E+05		(R)DGYQQI	(R)D G|Y|Q/Q/N/F/K(R)		93.6	500.2305	999.453	0.0007	0.7	5.83	70523.3	4.94	HUMAN	G3V153	Caprin-1
3293	dirMS_041712_NAR_60mM_plus.14679.14911.3	3	14.67	0	8.30E+05		(R)LYQQHC	(R)L/Y/Q Q H/G A G L/F/D/V T R(G)		134.47	535.6064	1604.818	-0.0133	-8.3	6.74	61760.3	6.01	HUMAN	O14773	Tripeptidyl-peptidase 1
3294	dirMS_041712_NAR_50mM_minus2.6185.6185.3	3	14.66	0	5.69E+04		(R)ASAAPK	(R)A S/A|A/P K/P E/P V/P/V Q K(V)		97.78	473.6033	1418.8	-0.0048	-3.4	8.64	23930.8	10.06	HUMAN	F5H0X8	PDZ and LIM domain protein 5
3295	dirMS_041712_NAR_50mM_minus2.8717.8717.3	3	14.66	1	8.70E+04		(R)LLDEEEA	(R)L/L|D/E E E A/T D N D L R A K(F)		117.43	577.9535	1731.84	0.0064	3.7	4.02	96649	6.13	HUMAN	Q8WUM4	Programmed cell death 6-interacting protein
3296	dirMS_041712_NAR_50mM_minus2.8947.8947.3	3	14.66	1	1.31E+05	M227m	(R)mQKEIT	(R)m Q K E I|T|A|L/A/P S/T M K(I)	m:Oxidized methionine	119.48	522.2727	1548.812	15.9911	-2.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
3297	dirMS_041712_NAR_60mM_minus.16933.16933.3	3	14.66	1	2.65E+05		(R)GQFSTD	(R)G Q|F/S T D/E L/V/A/E V E K R(N)		154	569.9569	1707.855	0.0013	0.8	4.41	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
3298	dirMS_041712_NAR_60mM_minus.9218.9218.3	3	14.66	0	2.84E+05		(K)ATAGDT	(K)A T|A/G D/T H\L/G G E D/F D/N R(L)		111.4	559.2488	1675.731	0.0012	0.7	4.22	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
3299	dirMS_041712_NAR_30mM_plus2.20365.20850.2	2	14.66	0	1.40E+06		(R)ILVATNL	(R)I/L|V|A|T/N L/F G R(G)		162.17	552.331	1103.657	-0.0024	-2.2	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
3300	dirMS_041712_NAR_50mM_plus2.11060.11060.3	3	14.66	1	2.67E+04		(R)SAAETV	(R)S A|A/E T V T K/G G I/M L/P/E/K(S)		125.88	544.624	1631.867	-0.0098	-6	5.86	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
3301	dirMS_041712_NAR_120mM_minus.11163.11404.3	3	14.65	0	4.42E+05		(K)SAKPTKI	(K)S A K|P T K P A A/S D|L|P\V|P A E G V R(N)		116.37	664.3662	1991.092	-0.008	-4	8.31	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
3302	dirMS_041712_NAR_30mM_minus2.11341.11603.2	2	14.65	0	1.18E+06		(K)LEAEIAT	(K)L/E|A|E|I A/T Y/R(R)		116.22	533.2797	1065.557	-0.0054	-5	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3303	dirMS_041712_NAR_30mM_minus2.12201.12201.2	2	14.65	0	3.38E+05		(K)ILYSQCG	(K)I L|Y|S/Q/C/G D V M\R(A)	C:Carbamidomethylation	119.22	671.3183	1341.629	0.0004	0.3	5.83	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
3304	dirMS_041712_NAR_40mM_minus2.9045.9045.3	3	14.65	1	9.47E+04		(K)LAEIGAF	(K)L/A|E|I/G|A/P I Q/G N R E E L V E R(L)		136.07	665.3586	1994.066	-0.0053	-2.6	4.49	38572.2	6.31	HUMAN	E9PJ04	Splicing factor 3B subunit 2 (Fragment)
3305	dirMS_041712_NAR_60mM_minus.11159.11215.3	3	14.65	1	2.07E+05		(K)FADLSE	(K)F A|D|L/S/E/A/A N R N N D A L/R(Q)		122.5	592.9581	1776.862	-0.0026	-1.5	4.56	49709.6	5.19	HUMAN	B0YJC4	Vimentin
3306	dirMS_041712_NAR_30mM_plus2.14645.14645.2	2	14.65	0	7.63E+05		(R)GVEICIA	(R)G V|E|I/C/I A/T/P G R(L)	C:Carbamidomethylation	130.1	586.8051	1172.609	-0.0063	-5.4	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
3307	dirMS_041712_NAR_40mM_plus2.10790.10790.3	3	14.65	0	6.60E+05		(R)LLEAQA	(R)L/L|E/A/Q/A/C/T/G G I I H P T T G Q K(L)	C:Carbamidomethylation	129.48	665.6807	1995.033	-0.0052	-2.6	6.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
3308	dirMS_041712_NAR_50mM_plus2.12001.12001.3	3	14.65	1	4.97E+05	M327m	(R)VAGGPC	(R)V/A/G G/P Q m I/Q|L/S L D G K/R(L)	m:Oxidized methionine	131.13	562.6377	1669.905	15.9931	-1	8.72	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
3309	dirMS_041712_NAR_50mM_plus2.19155.19155.3	3	14.65	0	4.98E+05		(R)GFGFITF	(R)G/F/G\F|I/T/F/T N/P E H A S V A M R(A)		168.98	661.3258	1981.959	0.004	2	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
3310	dirMS_041712_NAR_60mM_plus.15380.15443.3	3	14.65	1	4.00E+05		(R)SLIANLA	(R)S L|I/A/N L/A/A/A N/C Y K K(E)	C:Carbamidomethylation	137.37	512.9411	1536.82	-0.0115	-7.5	9.7	36978.6	6.33	HUMAN	B7Z800	Adenosine kinase
3311	dirMS_041712_NAR_60mM_plus.19565.19607.3	3	14.65	1	6.66E+05		(K)TVTAMD	(K)T V|T A/M/D/V/V/Y A L K/R(Q)		161	489.6071	1466.804	0.0032	2.2	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
3312	dirMS_041712_NAR_60mM_plus.9788.9788.3	3	14.65	1	1.29E+06		(K)EAALSTA	(K)E A A/L/S/T A/L/S E K/R(T)		109.78	425.898	1275.69	-0.0109	-8.5	6.24	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
3313	dirMS_041712_NAR_120mM_minus.6847.6981.2	2	14.64	1	2.88E+06		(R)TKTEISEI	(R)T/K|T|E|I|S/E M N/R(N)		92.53	604.8012	1208.594	0.0012	1	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
3314	dirMS_041712_NAR_20mM_minus.12323.12323.2	2	14.64	0	1.61E+05		(R)AAVIGPI	(R)A A/V|I/G/P D V F A K(L)		171.58	544.3103	1087.615	-0.0013	-1.2	5.88	266161	5.68	HUMAN	E9PPU0	Epiplakin
3315	dirMS_041712_NAR_30mM_minus2.17776.17974.2	2	14.64	0	3.94E+05		(K)GNFNYII	(K)G N|F/N/Y|I/E/F T/R(I)		151.3	630.8052	1260.601	0.0024	1.9	6	20513.6	4.62	HUMAN	J3QRS3	Myosin regulatory light chain 12A
3316	dirMS_041712_NAR_30mM_minus2.7769.7769.2	2	14.64	0	3.47E+05		(K)SLAAEEE	(K)S L|A/A|E/E|E A A R(Q)		96.33	523.7597	1046.511	0.0008	0.8	4.25	533778	5.74	HUMAN	Q15149	Plectin
3317	dirMS_041712_NAR_60mM_minus.12183.12183.3	3	14.64	0	3.77E+05		(K)VTNEFV	(K)V/T/N E/F V/H/I N/N L/K(L)		127.53	476.5974	1427.764	0.0135	9.5	6.72	18317.8	6.19	HUMAN	B7Z3E2	Serine/threonine-protein phosphatase 6 catalytic subunit
3318	dirMS_041712_NAR_20mM_plus.14297.14435.2	2	14.64	0	6.81E+05	M73m	(R)AVLVDLI	(R)A V|L|V|D|L|E|P G T\m D S V R(S)	m:Oxidized methionine	171.03	809.4082	1601.82	15.9888	-3.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
3319	dirMS_041712_NAR_30mM_plus2.19038.19038.2	2	14.64	0	1.51E+05		(R)VYSLFLD	(R)V/Y|S L/F/L D E S R(S)		153.08	614.8154	1228.621	0.0027	2.2	4.37	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
3320	dirMS_041712_NAR_30mM_plus2.5728.5770.2	2	14.64	0	2.46E+05		(R)QSSGAS	(R)Q S|S/G/A|S/S/S/S/F/S S S R(A)		84.3	681.3013	1361.593	0.0025	1.9	9.75	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
3321	dirMS_041712_NAR_50mM_plus2.20121.20121.3	3	14.64	0	2.56E+05		(R)LQSLPFA	(R)L/Q/S L/P F/A/L T H L N\L K(A)		173.95	532.3178	1594.931	0.0073	4.6	8.76	175851.7	5.01	HUMAN	Q14160	Protein scribble homolog
3322	dirMS_041712_NAR_60mM_plus.12410.12516.3	3	14.64	1	3.85E+06		(K)LFNLSKE	(K)L/F|N/L/S K/E D D/V/R(Q)		121.6	445.9046	1335.69	0.0089	6.7	4.56	25082	11.29	HUMAN	A2A3R5	40S ribosomal protein S6
3323	dirMS_041712_NAR_20mM_minus.10869.10869.2	2	14.63	0	1.46E+06	M92m	(R)ImNTFS	(R)I m/N T\F\S V/V|P/S P K(V)	m:Oxidized methionine	157.08	668.3513	1319.703	15.9925	-1.8	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
3324	dirMS_041712_NAR_30mM_minus2.8390.8390.2	2	14.63	0	5.11E+05		(K)SFQQSSI	(K)S F|Q Q/S/S L/S R(D)		100.55	520.2591	1039.517	-0.0058	-5.6	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
3325	dirMS_041712_NAR_50mM_minus2.10601.10601.3	3	14.63	0	1.70E+05		(R)LLELGPK	(R)L L|E|L|G P K/P E/V A Q Q\T R(K)		128.62	560.3182	1678.949	-0.0086	-5.1	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
3326	dirMS_041712_NAR_60mM_minus.9129.9166.3	3	14.63	1	1.02E+06		(R)ETAEAD	(R)E/T/A/E/A D/V|A S L N R R(I)		111.37	477.9107	1431.719	-0.0011	-0.8	4.68	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
3327	dirMS_041712_NAR_20mM_plus.17571.17571.2	2	14.63	0	3.20E+04		(K)LFVTND	(K)L F|V|T/N/D A/A T I L R(E)		192.63	667.3752	1333.747	-0.0043	-3.2	5.84	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
3328	dirMS_041712_NAR_30mM_plus2.9052.9596.2	2	14.63	0	7.51E+06		(R)AVVIVDI	(R)A V|V|I|V/D/D/R(G)		102.47	443.7534	886.499	0.0003	0.3	4.21	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
3329	dirMS_041712_NAR_40mM_plus2.16055.16055.3	3	14.63	0	3.19E+05		(K)VAIVKPC	(K)V/A|I/V K/P G V|P M E I V L N K(E)		161.2	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
3330	dirMS_041712_NAR_50mM_plus2.17899.17899.3	3	14.63	0	2.57E+05		(K)YAPLHL	(K)Y/A/P L/H/L/V/P L I E R(L)		162.08	474.2819	1420.831	0.0001	0	6.75	147553.6	6.73	HUMAN	E7EVF4	Cytoplasmic FMR1-interacting protein 2
3331	dirMS_041712_NAR_50mM_plus2.5216.5216.3	3	14.63	0	1.37E+06		(K)TATPQQ	(K)T/A|T/P Q Q/A Q E/V H E K(L)		86.38	489.5774	1466.723	-0.0057	-3.9	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
3332	dirMS_041712_NAR_60mM_plus.14361.14591.3	3	14.63	1	8.43E+06		(K)KVPQVS	(K)K\V P\Q\V S T|P/T|L|V/E V S R(N)		132.15	547.3173	1639.938	-0.0004	-0.2	8.75	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
3333	dirMS_041712_NAR_30mM_minus2.14918.15043.2	2	14.62	0	9.09E+05		(R)NFDEILR	(R)N/F|D/E/I/L/R(V)		135.07	453.7335	906.468	-0.0082	-9.1	4.37	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
3334	dirMS_041712_NAR_60mM_minus.17139.17139.3	3	14.62	1	7.39E+05		(K)QLDDLK	(K)Q/L/D D L/K/V/E L/S Q L R(V)		156.18	519.6267	1556.864	0.0013	0.8	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
3335	dirMS_041712_NAR_120mM_plus.20960.20960.3	3	14.62	2	1.39E+06		(R)TLAEIAK	(R)T L|A\E/I/A K V E L/D N\M/P L R G K(Q)		162.92	666.7047	1998.105	-0.0057	-2.8	5.85	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
3336	dirMS_041712_NAR_120mM_plus.7413.7454.3	3	14.62	1	1.14E+06		(R)EKVPGG	(R)E K V/P G G L|Q/G/S Q D/R(G)		92.32	457.5737	1370.702	0.0043	3.1	6.17	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
3337	dirMS_041712_NAR_120mM_plus.9842.9919.3	3	14.62	1	7.96E+05	M142m	(K)VKEGMI	(K)V K E G M N|I|V/E/A m/E R(F)	m:Oxidized methionine	104.72	507.918	1505.745	15.9944	-0.3	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
3338	dirMS_041712_NAR_30mM_plus2.18593.18678.2	2	14.62	0	2.03E+05		(K)SILFVPT	(K)S I|L/F|V|P/T S A P/R(G)		151.1	594.3409	1187.678	-0.0038	-3.2	9.47	92752.5	4.76	HUMAN	P14625	Endoplasmin
3339	dirMS_041712_NAR_40mM_plus2.18895.18895.3	3	14.62	1	3.85E+05		(R)TLAEIAK	(R)T L|A\E|I/A/K V E L/D/N M/P L R(G)		176.82	604.9967	1812.989	-0.0132	-7.3	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
3340	dirMS_041712_NAR_30mM_minus2.12954.13235.2	2	14.61	0	1.09E+06		(R)LTPEDF	(R)L/T|P/E/D/F A/R(A)		124.93	474.7377	948.479	-0.0104	-11	4.37	24724.1	5.17	HUMAN	E7ETQ7	Vacuolar protein sorting-associated protein VTA1 homolog
3341	dirMS_041712_NAR_30mM_minus2.19551.19551.2	2	14.61	0	4.63E+05		(R)ASLSLW	(R)A S/L|S|L/W/Q A/M E K(G)		162.7	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
3342	dirMS_041712_NAR_30mM_minus2.9480.9647.2	2	14.61	0	4.44E+05		(K)VCNPIIT	(K)V/C|N|P I|I/T K(L)	C:Carbamidomethylation	106.6	472.7669	944.523	0.0032	3.3	8.72	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
3343	dirMS_041712_NAR_60mM_minus.14891.14891.3	3	14.61	1	2.10E+05		(K)IDSRLEQ	(K)I/D S R L E Q|Y|T|S/A I E G T K(S)		142.88	604.3095	1810.918	-0.0042	-2.3	4.68	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
3344	dirMS_041712_NAR_50mM_plus2.11629.11839.3	3	14.61	1	1.78E+06		(K)TGQPMI	(K)T/G|Q|P M/I/N L Y/T/D R E T G K(L)		130.72	608.6361	1823.896	-0.0019	-1	5.73	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
3345	dirMS_041712_NAR_60mM_minus.16797.16813.3	3	14.6	1	2.46E+05		(R)KGFSEGI	(R)K G F S E G L\W|E|I|E/N/N P\T V K(A)		153.75	649.9986	1947.981	0.0002	0.1	4.79	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
3346	dirMS_041712_NAR_60mM_minus.9964.9985.3	3	14.6	0	1.56E+06		(R)EIVHIQA	(R)E/I\V\H\I Q A/G/Q|C/G N Q I/G A K(F)	C:Carbamidomethylation	115.57	608.3099	1822.923	-0.0077	-4.2	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3347	dirMS_041712_NAR_20mM_plus.16904.16904.2	2	14.6	0	3.11E+05		(K)VQIAVA	(K)V Q\I/A/V|A/N/A/Q E|L L Q/R(M)		187.77	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
3348	dirMS_041712_NAR_30mM_plus2.20743.20743.2	2	14.6	0	4.46E+05		(R)SLVPAAI	(R)S L|V/P A A E L L E/S R(V)		162.23	642.8602	1284.716	-0.0027	-2.1	4.53	533778	5.74	HUMAN	Q15149	Plectin
3349	dirMS_041712_NAR_30mM_plus2.21302.21302.2	2	14.6	0	2.83E+05		(R)GVVQEL	(R)G V\V/Q/E/L/Q Q\A|I/S K(L)		165.97	650.3632	1299.727	-0.0076	-5.8	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
3350	dirMS_041712_NAR_30mM_plus2.22193.22395.2	2	14.6	1	6.77E+05		(K)ATCKDL	(K)A T|C K D L\V|M|F|I(-)	C:Carbamidomethylation	172.75	599.3037	1197.601	-0.0005	-0.4	5.88	26705.5	7.89	HUMAN	P54819	Adenylate kinase 2, mitochondrial
3351	dirMS_041712_NAR_30mM_plus2.8261.8308.2	2	14.6	0	2.73E+05		(K)EIAENAL	(K)E I/A|E/N A/L/G K(H)		96.92	472.755	944.505	-0.002	-2.1	4.53	36982.9	6.37	HUMAN	P31942	Heterogeneous nuclear ribonucleoprotein H3
3352	dirMS_041712_NAR_50mM_plus2.18738.18738.3	3	14.6	1	4.36E+05		(K)AAIDWF	(K)A A|I/D|W/F/D G K E F S G N\P I K(V)		167.18	632.3186	1894.933	0.0079	4.1	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
3353	dirMS_041712_NAR_50mM_plus2.9938.9947.3	3	14.6	1	3.08E+05		(R)SATKVT	(R)S A|T K V|T A D|V|I/N/A/A E K(L)		119.68	506.6094	1517.817	-0.0033	-2.2	5.79	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
3354	dirMS_041712_NAR_20mM_plus.8104.8104.2	2	14.59	0	4.05E+05	M239m	(K)EVDEQn	(K)E V/D E Q m L\N|V/Q/N K(N)	m:Oxidized methionine	125.13	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3355	dirMS_041712_NAR_50mM_minus2.13285.13285.3	3	14.58	0	1.68E+05		(K)MLDAEI	(K)M/L/D/A/E/D/I V G T A R P D E K(A)		143.55	587.2894	1759.853	0.0006	0.3	4.1	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
3356	dirMS_041712_NAR_50mM_minus2.15931.15931.3	3	14.58	0	9.69E+04		(K)INLEAAE	(K)I N|L/E/A A E|L/G/E I S D I H/T K(L)		158.72	618.326	1852.965	-0.0016	-0.9	4.4	84268.2	6.32	HUMAN	Q9UHD2	Serine/threonine-protein kinase TBK1
3357	dirMS_041712_NAR_50mM_minus2.7200.7392.3	3	14.58	1	4.76E+06	M227m M	(R)mQKEIT	(R)m Q K E I T\A|L|A|P/S T m K(I)	m:Oxidized methionine	108.5	527.6049	1548.812	31.9877	-1.3	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
3358	dirMS_041712_NAR_60mM_minus.13284.13567.3	3	14.58	1	5.68E+05		(R)KLVIIEGI	(R)K\L V\I\I|E|G/D L/E/R(T)		135.13	428.9221	1284.752	-0.0004	-0.3	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
3359	dirMS_041712_NAR_20mM_plus.7410.7410.2	2	14.58	0	2.86E+05		(K)TGQAPC	(K)T G/Q|A|P/G Y S Y T/A/A N K(N)		119.52	714.8394	1428.675	-0.0039	-2.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
3360	dirMS_041712_NAR_60mM_plus.8343.8343.3	3	14.58	1	6.44E+05		(K)EPLYEKD	(K)E P L/Y\E K/D S/S/V/A A/R(F)		102.25	488.9148	1464.733	-0.0031	-2.1	4.68	26283.8	8.96	HUMAN	O43809	Cleavage and polyadenylation specificity factor subunit 5
3361	dirMS_041712_NAR_60mM_plus.8432.8432.3	3	14.58	1	1.94E+05		(R)TKSQGG	(R)T K\S Q G G E|P T/Y/N\V|A V/G R(A)		102.22	555.2829	1663.84	-0.0057	-3.4	8.26	9954.3	9.57	HUMAN	C9J0J7	Profilin-2
3362	dirMS_041712_NAR_120mM_minus.11364.11431.3	3	14.57	1	4.08E+05		(K)VIADNV	(K)V/I|A/D/N V/K/D W/S K(V)		116.48	425.5623	1274.674	-0.0016	-1.2	5.93	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
3363	dirMS_041712_NAR_50mM_minus2.7165.7165.3	3	14.57	0	3.33E+04		(K)IITGKPS	(K)I/I|T/G/K/P S G A I/S G V Q K(A)		107.57	485.9536	1455.853	-0.0067	-4.6	10	84268.2	6.32	HUMAN	Q9UHD2	Serine/threonine-protein kinase TBK1
3364	dirMS_041712_NAR_60mM_minus.12011.12011.3	3	14.57	1	2.51E+05		(R)GLAGLG	(R)G L|A G L/G D/V A E V R K(S)		127.02	428.9126	1284.727	-0.0038	-2.9	6.07	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
3365	dirMS_041712_NAR_30mM_plus2.18509.18509.2	2	14.57	0	1.54E+05		(R)AMLDQI	(R)A M|L|D/Q/L/M/G/T S/R(D)		150.35	611.8	1222.592	0.0009	0.7	5.88	5509.4	10.84	HUMAN	F8WB41	Putative RNA-binding protein Luc7-like 2
3366	dirMS_041712_NAR_30mM_plus2.9044.9074.2	2	14.57	0	1.78E+05		(R)LELQGPI	(R)L/E|L|Q/G/P/R(G)		100.93	406.7314	812.462	-0.007	-8.6	6	32503.1	5.29	HUMAN	H7BY16	Nucleolin (Fragment)
3367	dirMS_041712_NAR_120mM_minus.13892.13892.4	4	14.56	1	1.62E+06		(K)ASIHEA	(K)A/S|I/H/E A W T D/G K E/A M/L K(H)		129.97	447.476	1786.879	0.0029	1.6	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
3368	dirMS_041712_NAR_20mM_minus.14070.14070.3	3	14.56	0	6.38E+05		(K)SYELPDC	(K)S Y E\L|P\D G Q V/I|T/I/G N E R(F)		193.82	597.6345	1790.892	-0.003	-1.7	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
3369	dirMS_041712_NAR_40mM_minus2.14262.14262.3	3	14.56	0	1.90E+04		(R)VSAAVLI	(R)V/S/A/A\V/L/P L V/H/P L P E G L R(A)		167.98	590.0205	1768.048	-0.001	-0.6	6.72	63124.2	9.53	HUMAN	E7EVU5	Nuclear receptor corepressor 1 (Fragment)
3370	dirMS_041712_NAR_60mM_minus.10735.10735.3	3	14.56	0	5.06E+04		(R)AYADSY	(R)A Y|A/D/S/Y/Y Y/E D G G M K P R(V)		119.78	629.2712	1885.806	-0.0071	-3.8	4.56	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
3371	dirMS_041712_NAR_60mM_minus.10782.10782.3	3	14.56	0	5.06E+04		(R)AYADSY	(R)A Y|A/D/S Y/Y Y/E/D/G G M K P R(V)		119.78	629.2712	1885.806	-0.0071	-3.8	4.56	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
3372	dirMS_041712_NAR_120mM_plus.8348.8348.2	2	14.56	1	3.54E+05		(K)YEKDIAA	(K)Y|E/K/D/I A A Y R(A)		97.17	564.7869	1128.568	-0.0019	-1.7	6.07	25064.5	5.62	HUMAN	P09429	High mobility group protein B1
3373	dirMS_041712_NAR_20mM_plus.9447.9447.2	2	14.56	0	1.42E+05		(R)GTGIVSA	(R)G T G I/V|S A P V/P/K(K)		136.92	513.3057	1025.599	0.0052	5	8.75	21898	11.33	HUMAN	E9PM36	40S ribosomal protein S2
3374	dirMS_041712_NAR_30mM_plus2.13734.13824.2	2	14.56	0	6.83E+05		(K)TCTFILRI	(K)T/C|T/F/I/L/R(G)	C:Carbamidomethylation	125.53	455.7451	910.481	0.0014	1.6	9.41	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a

3375	dirMS_041712_NAR_30mM_plus2.17780.18166.2	2	14.56	0	2.92E+06		(R)GFSLEEL	(R)G F|S|L/E/E/L/R(V)		147.47	475.7563	950.494	0.0112	11.7	4.53	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
3376	dirMS_041712_NAR_30mM_plus2.18458.18458.2	2	14.56	0	2.36E+05		(K)GNFNYI	(K)G N|F|N/Y|I/E/F/T/R(I)		150.27	630.8035	1260.601	-0.001	-0.8	6	20513.6	4.62	HUMAN	J3QRS3	Myosin regulatory light chain 12A
3377	dirMS_041712_NAR_30mM_plus2.18515.18515.2	2	14.56	0	6.31E+04		(R)FAQPGS	(R)F A/Q|P/G S F E Y E Y A M R(W)		150.32	848.3763	1695.747	-0.0018	-1.1	4.53	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)
3378	dirMS_041712_NAR_30mM_minus2.13828.13828.2	2	14.55	0	2.26E+05		(K)TYSVEYL	(K)T/Y|S/V/E Y L/P K(V)		128.3	550.2855	1099.567	-0.0033	-3	5.66	258215.9	5.48	HUMAN	E7EN95	Filamin-B
3379	dirMS_041712_NAR_50mM_minus2.7424.7424.3	3	14.55	0	1.91E+04		(R)AVEVQG	(R)A V|E|V Q/G P S L/E S G D/H G K(I)		109.23	537.2631	1609.782	-0.0069	-4.3	4.65	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
3380	dirMS_041712_NAR_60mM_minus.14245.14479.3	3	14.55	1	1.30E+06		(R)MSMKE	(R)M/S\M K E V\D E\Q|M|L/N V/Q/N K(N)		140.47	641.9701	1923.897	-0.0015	-0.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3381	dirMS_041712_NAR_20mM_plus.13567.13567.2	2	14.55	0	1.45E+05	M273m	(K)mISDAIP	(K)m I/S/D A/I/P/E/L K(A)	m:Oxidized methionine	165.55	566.7967	1116.597	15.9892	-5	4.37	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
3382	dirMS_041712_NAR_30mM_plus2.11539.11578.2	2	14.55	0	1.45E+05		(K)MLVIEQ	(K)M/L|V|I/E/Q/C K(N)	C:Carbamidomethylation	113.97	510.764	1020.522	-0.0009	-0.9	5.75	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
3383	dirMS_041712_NAR_30mM_plus2.12967.13278.2	2	14.55	0	1.15E+06		(K)LVIITAG	(K)L/V|I|I/T/A/G A/R(Q)		122.35	457.2931	913.583	-0.004	-4.4	9.75	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
3384	dirMS_041712_NAR_30mM_plus2.14481.14752.2	2	14.55	0	6.95E+05		(R)SLSAIYL	(R)S L|S|A|I/Y/L E/K(L)		129.82	512.2888	1023.572	-0.0018	-1.7	5.72	533778	5.74	HUMAN	Q15149	Plectin
3385	dirMS_041712_NAR_30mM_plus2.14567.14735.2	2	14.55	0	2.53E+05		(R)SIGEYDV	(R)S I|G|E/Y/D|V L/R(G)		129.85	526.2726	1051.542	-0.0039	-3.7	4.37	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
3386	dirMS_041712_NAR_30mM_plus2.18527.18527.2	2	14.55	0	2.03E+05		(R)AVLNPL	(R)A V|L/N|P L/C Q V/D/Y R(A)	C:Carbamidomethylation	150.18	724.3703	1447.736	-0.0029	-2	5.88	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
3387	dirMS_041712_NAR_30mM_plus2.7432.7453.2	2	14.55	0	1.06E+06		(R)IADGYE	(R)I/A|D|G/Y/E/Q/A A/R(V)		93.37	547.2595	1093.527	-0.0155	-14.2	4.37	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
3388	dirMS_041712_NAR_40mM_plus2.16881.17057.3	3	14.55	1	3.08E+05		(R)LFVGNL	(R)L/F|V/G/N/L/P/T D I T E E D F K R(L)		166.38	665.3502	1994.023	0.0131	6.6	4.32	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
3389	dirMS_041712_NAR_60mM_plus.13187.13630.3	3	14.55	1	1.02E+06		(R)ISVYYNE	(R)I/S|V/Y/Y N E\A T/G G K Y V/P R(A)		125.95	606.3113	1816.923	-0.0035	-1.9	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
3390	dirMS_041712_NAR_60mM_plus.17557.17557.3	3	14.55	1	1.76E+05		(R)RTVQSL	(R)R T V Q S\L|E|I/D|L D S M/R(N)		148.8	554.954	1662.848	-0.0005	-0.3	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3391	dirMS_041712_NAR_120mM_minus.17743.17743.3	3	14.54	1	1.85E+05		(R)AGKLDP	(R)A G K/L D|P H/L/V L D Q L/R(C)		151.48	525.6385	1574.901	-0.0004	-0.2	6.79	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
3392	dirMS_041712_NAR_50mM_minus2.14877.14877.3	3	14.54	1	2.84E+05		(R)EAVTEIL	(R)E A\V/T/E I/L/G I/E P D R E K(G)		152.37	566.9683	1698.891	-0.0005	-0.3	4.25	25685.9	6.4	HUMAN	E9PGT1	Translin
3393	dirMS_041712_NAR_120mM_plus.14519.15064.3	3	14.54	1	3.52E+06		(R)KFLDGIY	(R)K\F\L\D\G\I|Y|V/S/E/K(G)		131.25	433.5709	1298.699	-0.0009	-0.7	6.07	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
3394	dirMS_041712_NAR_30mM_plus2.12376.12885.2	2	14.54	0	7.81E+05		(K)SIYYITG	(K)S I|Y|Y|I/T/G E/S K(E)		119.27	580.796	1160.583	0.0013	1.2	5.72	16789.1	8.77	HUMAN	H0Y5S7	Heat shock protein HSP 90-beta (Fragment)
3395	dirMS_041712_NAR_30mM_plus2.7580.7602.2	2	14.54	0	1.24E+05		(K)SAAMTL	(K)S A|A|M/T/L/N E/R(F)		93.52	496.7467	992.483	0.0032	3.2	5.72	83344.9	10.18	HUMAN	E9PK09	Bcl-2-associated transcription factor 1 (Fragment)
3396	dirMS_041712_NAR_50mM_plus2.10119.10236.3	3	14.54	0	6.15E+05		(K)VGQEIE	(K)V/G/Q/E/I E/V/R P G I V/S/K(D)		121.05	504.2907	1510.859	-0.0012	-0.8	6.11	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
3397	dirMS_041712_NAR_50mM_plus2.18520.18627.3	3	14.54	1	5.52E+05		(K)NAAGAL	(K)N A|A G/A/L/D L L/K E/L/K(N)		165.92	452.601	1355.789	-0.0008	-0.6	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
3398	dirMS_041712_NAR_60mM_plus.12059.12138.3	3	14.54	1	1.53E+06	M136m	(K)VKEGm	(K)V K E G m\N\I|V|E\A/M/E/R(F)	m:Oxidized methionine	120.35	507.9187	1505.745	15.9965	1	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
3399	dirMS_041712_NAR_60mM_plus.17939.17940.3	3	14.54	1	1.60E+05		(K)ILLAELE	(K)I/L|L/A E L/E Q L/K/G Q G K(S)		150.9	513.9717	1539.911	-0.0099	-6.4	6.14	49709.6	5.19	HUMAN	B0YJC4	Vimentin
3400	dirMS_041712_NAR_120mM_minus.11078.11140.3	3	14.53	1	7.77E+05		(R)RFDDAV	(R)R F D D\A|V|V|Q/S D/M/K(H)		115.05	470.8939	1410.668	-0.001	-0.7	4.43	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
3401	dirMS_041712_NAR_30mM_minus2.10978.10978.2	2	14.53	0	5.82E+05		(K)VAGQD	(K)V/A|G/Q/D/G S V/V/Q/F K(I)		113.8	617.824	1234.643	-0.0019	-1.5	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
3402	dirMS_041712_NAR_120mM_plus.10368.10662.3	3	14.53	1	3.83E+05		(K)KGENYV	(K)K\G E N Y\V|Y|I|N/E/A T/R(H)		108.4	519.5943	1556.77	-0.002	-1.3	6.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
3403	dirMS_041712_NAR_20mM_plus.18630.18630.2	2	14.53	0	2.78E+05		(K)LAVEALS	(K)L A/V/E A\L|S/S L/D/G D L A/G R(Y)		200.45	793.9214	1586.838	-0.0029	-1.8	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
3404	dirMS_041712_NAR_30mM_plus2.5791.5854.2	2	14.53	0	3.52E+05		(K)YAEAVTI	(K)Y/A|E|A/V/T/R(A)		84.63	405.2125	809.415	0.0025	3.1	6	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
3405	dirMS_041712_NAR_40mM_plus2.18220.18411.3	3	14.53	1	2.86E+05		(R)VAAKLE	(R)V A A K L E\V\A|P|I/S D/I I A I K(S)		174.02	584.3591	1751.068	-0.005	-2.8	6.04	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
3406	dirMS_041712_NAR_50mM_plus2.16005.16005.3	3	14.53	0	1.05E+06		(R)LSFQHD	(R)L/S/F Q H D|P E|T/S|V/L/V L R(K)		152.42	580.9801	1740.928	-0.0022	-1.2	5.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
3407	dirMS_041712_NAR_20mM_minus.12346.12346.2	2	14.52	0	7.12E+05	M185m	(K)LAVNm	(K)L A|V/N/m/V/P/F P R(L)	m:Oxidized methionine	172	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
3408	dirMS_041712_NAR_60mM_minus.7860.7943.3	3	14.52	1	5.22E+05		(K)IQDKEGI	(K)I Q\D/K E G/I|P/P D/Q Q R(L)		103.63	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
3409	dirMS_041712_NAR_20mM_plus.18720.18720.2	2	14.52	0	1.01E+05		(K)LTVYTTL	(K)L/T|V/Y/T/T/L I/D/V T K(G)		200.8	683.8948	1366.783	-0.0005	-0.4	5.83	42194.9	8.75	HUMAN	E7EMM4	Acid ceramidase
3410	dirMS_041712_NAR_30mM_plus2.20041.20041.2	2	14.52	0	6.71E+05		(K)SYELPD	(K)S Y E|L/P D/G Q/V I|T I|G N E/R(F)		159.7	895.9487	1790.892	-0.0018	-1	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
3411	dirMS_041712_NAR_30mM_plus2.6303.6303.2	2	14.52	0	2.56E+05		(K)SAVLQE	(K)S A/V/L|Q E A/R(I)		87.2	437.2414	873.479	-0.0033	-3.8	5.72	28218.2	9.35	HUMAN	F6X838	Coatomer subunit gamma-2
3412	dirMS_041712_NAR_60mM_plus.9432.9432.2	2	14.52	0	1.27E+06		(K)STAGDT	(K)S T/A/G D|T H L|G G E/D/F D|N/R(M)		107.4	846.3654	1691.726	-0.0021	-1.2	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
3413	dirMS_041712_NAR_30mM_minus2.12905.13137.2	2	14.51	0	7.12E+05		(R)VNFAMI	(R)V/N|F|A/M/N V/G\K(A)		124.37	490.2513	979.503	-0.0076	-7.8	8.72	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
3414	dirMS_041712_NAR_50mM_minus2.18357.18357.3	3	14.51	0	4.62E+05		(K)ALIEVLQ	(K)A L|I/E/V L Q/P L I/A E H Q A R(R)		175.42	601.0139	1801.033	-0.0059	-3.3	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
3415	dirMS_041712_NAR_120mM_plus.19580.19728.3	3	14.51	0	8.75E+05		(R)NSVSNF	(R)N/S|V/S N F/L/H/S L E/R(G)		156.15	468.2345	1402.707	-0.0184	-13.1	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
3416	dirMS_041712_NAR_30mM_plus2.12011.12011.2	2	14.51	0	6.83E+05		(K)CGDLVF	(K)C/G|D|L/V/F\A/K(M)	C:Carbamidomethylation	116.12	455.2298	909.45	0.0025	2.7	5.84	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
3417	dirMS_041712_NAR_30mM_plus2.12242.12391.2	2	14.51	0	8.43E+05		(K)GLLSAE	(K)G L|L|S/A/E/V A/R(L)		117.6	458.2693	915.526	0.0055	6	6	533778	5.74	HUMAN	Q15149	Plectin
3418	dirMS_041712_NAR_30mM_plus2.19225.19754.2	2	14.51	0	4.11E+06		(K)TLGILGL	(K)T/L|G|I|L/G/L/G R(I)		156.62	450.2857	899.567	-0.0032	-3.5	9.41	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
3419	dirMS_041712_NAR_30mM_plus2.6964.6964.2	2	14.51	0	1.34E+05		(K)YTQSNS	(K)Y/T|Q S|N/S V/C Y A K(N)	C:Carbamidomethylation	91.15	660.7963	1320.589	-0.0036	-2.7	8.5	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
3420	dirMS_041712_NAR_60mM_plus.7904.7938.3	3	14.51	1	1.08E+05		(K)ALAAGG	(K)A/L|A|A|G/G/Y/D V/E K N N S R(I)		99.43	522.2648	1564.771	0.0084	5.4	6.11	22579.8	10.91	HUMAN	P16401	Histone H1.5
3421	dirMS_041712_NAR_30mM_minus2.18575.18575.2	2	14.5	0	3.87E+05		(R)QAQEYE	(R)Q A/Q|E|Y/E A/L/L/N I K(V)		154.83	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3422	dirMS_041712_NAR_40mM_minus2.8727.8820.3	3	14.5	1	2.33E+05		(R)IVLAND	(R)I V|L/A/N/D P D/A D/R L A V/A E/K(Q)		134.3	603.9966	1809.97	0.0047	2.6	4.23	32837.5	6.16	HUMAN	B4E0G8	Phosphoglucomutase-2
3423	dirMS_041712_NAR_50mM_minus2.13258.13258.3	3	14.5	0	2.61E+05		(K)VTHAVV	(K)V T H A V\V T\V/P A|Y/F/N D/A Q R(Q)		143.18	629.9954	1887.971	0.0005	0.3	6.71	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
3424	dirMS_041712_NAR_50mM_minus2.7898.7898.3	3	14.5	1	1.50E+05		(K)TAVCDI	(K)T/A|V C D/I/P/P R G L K(M)	C:Carbamidomethylation	111.93	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
3425	dirMS_041712_NAR_60mM_minus.15988.16407.3	3	14.5	1	5.82E+05		(K)LKLSILY	(K)L K L S I\L|Y|P/A/T T G/R(N)		150.5	478.2883	1432.852	-0.0019	-1.3	9.99	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
3426	dirMS_041712_NAR_60mM_minus.16939.16939.3	3	14.5	1	2.24E+05		(R)KGFSEG	(R)K G F S E G L\W/E|I|E N N P\T V|K(A)		153.83	649.9986	1947.981	0.0002	0.1	4.79	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
3427	dirMS_041712_NAR_60mM_minus.18252.18252.3	3	14.5	1	1.37E+05		(R)SELELTL	(R)S E|L/E L/T L/G K L/E Q V/R(S)		163.05	538.9724	1614.906	-0.0035	-2.1	4.78	533778	5.74	HUMAN	Q15149	Plectin
3428	dirMS_041712_NAR_120mM_plus.11500.12033.3	3	14.5	1	2.54E+06		(R)FPGQLN	(R)F/P/G Q/L/N/A/D/L R K(L)		113.82	420.2353	1258.69	0.0011	0.9	8.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
3429	dirMS_041712_NAR_60mM_plus.9508.9683.3	3	14.5	1	1.92E+06		(K)LTRDET	(K)L T R D E T\N|Y|G|I/P Q/R(A)		107.8	521.6038	1562.792	0.0047	3	6.07	13083.6	6.26	HUMAN	D6R909	Guanine nucleotide-binding protein subunit beta-2-like 1
3430	dirMS_041712_NAR_20mM_minus.7047.7047.2	2	14.49	0	4.77E+05	M281m	(R)AEAESm	(R)A E|A/E/S m/Y Q I/K(Y)	m:Oxidized methionine	117.9	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
3431	dirMS_041712_NAR_30mM_minus2.18953.19212.2	2	14.49	0	9.54E+05		(K)MSIYQA	(K)M/S|I/Y/Q/A M W/K(G)		158.93	579.2789	1157.548	0.0023	2	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
3432	dirMS_041712_NAR_30mM_minus2.8479.8499.2	2	14.49	0	2.60E+05		(R)YLSEVAS	(R)Y/L|S|E/V A|S G D/N K(Q)		100.93	591.7852	1182.564	-0.0006	-0.5	4.37	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
3433	dirMS_041712_NAR_60mM_minus.14928.14944.3	3	14.49	0	2.96E+05		(K)WIGLDL	(K)W/I|G L D L/S/N/G K/P R(D)		143.43	452.5849	1355.743	-0.0029	-2.1	8.75	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
3434	dirMS_041712_NAR_120mM_plus.11449.11513.4	4	14.49	2	9.39E+05		(K)KTGQP	(K)K\T G Q|P\M|I/N L/Y/T D/R E T G K(L)		113.32	488.7518	1951.991	-0.0052	-2.7	8.5	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
3435	dirMS_041712_NAR_120mM_plus.23622.23915.3	3	14.49	0	8.56E+05		(R)LHFFMP	(R)L H\F\F\M|P G\F|A|P\L/T S R(G)		179.22	540.9492	1620.835	-0.0025	-1.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
3436	dirMS_041712_NAR_30mM_plus2.17265.17265.2	2	14.49	0	3.05E+05		(K)TVFGVE	(K)T V|F/G V|E P|D L T/R(E)		143.42	617.3263	1233.647	-0.0021	-1.7	4.37	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
3437	dirMS_041712_NAR_50mM_plus2.11330.11448.3	3	14.49	0	5.94E+05		(R)ITLRPDP	(R)I/T|L R P D|P\L/P E/R(S)		127.35	436.2535	1306.748	-0.0018	-1.4	6.07	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
3438	dirMS_041712_NAR_60mM_plus.11263.11263.2	2	14.49	0	2.12E+06		(K)GIVEFAS	(K)G I|V|E|F/A/S/K/P/A A R(K)		116.18	623.3504	1245.695	-0.0015	-1.2	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
3439	dirMS_041712_NAR_40mM_minus2.11472.11472.3	3	14.48	0	1.87E+05		(K)LVTSIGD	(K)L V/T/S|I/G D V V/N H/D P V V G D R(L)		150.45	631.3335	1891.987	-0.0013	-0.7	4.41	27786.2	5.93	HUMAN	H0Y4Z6	Phosphorylase (Fragment)
3440	dirMS_041712_NAR_20mM_plus.10549.10549.2	2	14.48	0	2.94E+04		(R)SSSVGSS	(R)S S S|V/G S|S/S S/Y|P I S/P A\V|S/R(T)		145.53	877.9279	1754.855	-0.007	-4	8.46	533778	5.74	HUMAN	Q15149	Plectin
3441	dirMS_041712_NAR_30mM_plus2.8328.8594.2	2	14.48	0	1.08E+06		(K)TAVCDI	(K)T A|V|C/D/I/P|P R(G)	C:Carbamidomethylation	99.48	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
3442	dirMS_041712_NAR_40mM_plus2.5714.5714.2	2	14.48	0	1.12E+05		(R)FSSSSGY	(R)F/S|S/S S/G/Y/G/G/G S S R(V)		90.98	618.2686	1235.529	0.0012	1	8.75	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
3443	dirMS_041712_NAR_50mM_plus2.16853.16853.3	3	14.48	1	4.74E+05		(K)VLDSGA	(K)V L/D|S/G A/P I/K I/P V G P E T L G R(I)		156.7	640.3623	1919.096	-0.0237	-12.3	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
3444	dirMS_041712_NAR_60mM_plus.12082.12176.3	3	14.48	1	1.99E+06		(R)MQKEIT	(R)M Q K E I T A|L/A/P/S T M/K(I)		120.7	516.9402	1548.812	-0.0064	-4.1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
3445	dirMS_041712_NAR_60mM_plus.7494.7535.3	3	14.48	1	3.06E+06		(K)QLELRQ	(K)Q/L/E/L/R Q/E E/E/R(R)		97.9	443.8995	1329.676	0.0082	6.2	4.49	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
3446	dirMS_041712_NAR_120mM_minus.13315.13315.4	4	14.47	1	9.47E+05		(K)SVHSSV	(K)S V H S S V/P|L/L/N S K D/P I D R(I)		127.18	466.7525	1863.992	-0.0041	-2.2	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
3447	dirMS_041712_NAR_30mM_minus2.14632.14651.2	2	14.47	0	1.01E+05		(R)LDIDSPP	(R)L/D|I|D|S|P/P I T A R(N)		133.55	599.3249	1197.647	-0.0049	-4.1	4.21	5755.5	5.75	HUMAN	H3BN34	Pyruvate kinase isozymes M1/M2 (Fragment)
3448	dirMS_041712_NAR_50mM_minus2.10283.10303.3	3	14.47	1	5.22E+05		(K)IAQLEE	(K)I/A|Q|L/E/E Q L/D N E T K/E R(Q)		127.12	605.9737	1815.908	-0.0018	-1	4.25	227783.5	5.5	HUMAN	P35579	Myosin-9
3449	dirMS_041712_NAR_60mM_minus.14525.14546.3	3	14.47	0	1.00E+06		(K)SLTNDW	(K)S L|T/N D/W/E/D H L/A/V K(H)		141.7	509.9191	1527.744	-0.0011	-0.7	4.53	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
3450	dirMS_041712_NAR_20mM_plus.17884.17884.2	2	14.47	0	1.27E+06		(R)YLTVAA	(R)Y/L/T/V/A A V F/R(G)		193.88	520.3009	1039.593	0.001	1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3451	dirMS_041712_NAR_30mM_plus2.10594.10627.2	2	14.47	0	3.95E+05		(K)TGTVSL	(K)T G|T|V/S/L/E/V/R(L)		109.33	481.2676	961.531	-0.0034	-3.5	5.66	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
3452	dirMS_041712_NAR_30mM_plus2.18231.18231.2	2	14.47	0	4.74E+05		(R)GYISPYF	(R)G Y|I|S|P Y F I N T S K(G)		149.62	695.3554	1389.705	-0.0014	-1	8.5	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
3453	dirMS_041712_NAR_30mM_plus2.21971.22380.2	2	14.47	0	2.46E+06		(R)VIFGLFG	(R)V/I|F/G/L/F/G/K(T)		172.28	440.7682	880.529	0	0	8.72	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
3454	dirMS_041712_NAR_30mM_plus2.7296.7314.2	2	14.47	0	7.19E+05		(K)STMQEL	(K)S T|M/Q|E|L/N/S R(L)		93.8	533.2595	1065.499	0.0124	11.6	5.72	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
3455	dirMS_041712_NAR_40mM_plus2.17588.17686.3	3	14.47	1	5.62E+05		(R)GLLPGL	(R)G L|L\P|G/L L/P\A/P A D K L T/P K(G)		170.58	567.6811	1701.031	-0.0022	-1.3	8.59	153084.9	5.55	HUMAN	Q6P2E9	Enhancer of mRNA-decapping protein 4
3456	dirMS_041712_NAR_50mM_plus2.17645.17645.3	3	14.47	1	2.09E+05		(R)EVQLEE	(R)E/V/Q/L/E/E L E A A R D L V S K(E)		160.73	610.3302	1828.965	0.011	6	4.25	45984.6	6.24	HUMAN	B4E1G6	Galactokinase
3457	dirMS_041712_NAR_50mM_plus2.7080.7080.3	3	14.47	1	3.75E+04		(R)ASVDTK	(R)A/S/V/D\T K E A\E G A/P Q V E\A G K(R)		103.02	596.2908	1786.882	-0.0239	-13.4	4.41	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
3458	dirMS_041712_NAR_50mM_plus2.8769.8769.3	3	14.47	1	2.21E+05		(K)TTSPPE	(K)T T|S/P P E V/S G Y S Y E K/T E/R(S)		113.33	644.3093	1930.903	0.0105	5.4	4.78	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
3459	dirMS_041712_NAR_60mM_plus.17185.17300.3	3	14.47	0	2.04E+05		(K)THLPGF	(K)T\H L\P G\F\V|E|Q/A E/A L/K(A)		147.35	513.9442	1539.817	0.0015	1	5.37	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
3460	dirMS_041712_NAR_120mM_minus.6799.7173.3	3	14.46	1	2.14E+07		(R)TKTEISE	(R)T\K\T E\I|S/E/M/N/R(N)		92.57	403.5363	1208.594	0.0004	0.3	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
3461	dirMS_041712_NAR_120mM_minus.8100.8100.3	3	14.46	2	1.87E+05		(R)ASVDTK	(R)A S V/D T\K/E A E G A/P Q/V/E/A G K R(L)		98.33	648.3315	1942.983	-0.0029	-1.5	4.87	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
3462	dirMS_041712_NAR_20mM_minus.13750.13750.2	2	14.46	0	3.99E+05		(K)LGGSAV	(K)L G\G S A|V/I/S L|E/G K|P L(-)		188.68	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
3463	dirMS_041712_NAR_30mM_minus2.16452.16452.2	2	14.46	0	2.53E+05		(R)ASLEAAI	(R)A S L\E/A|A/I/A/D A/E Q R(G)		143.58	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
3464	dirMS_041712_NAR_60mM_minus.10422.10422.3	3	14.46	1	2.88E+04		(K)SPFEVS	(K)S/P|F/E/V S V D K A/Q\G D/A S K(V)		117.73	555.6083	1664.813	-0.0023	-1.4	4.56	258215.9	5.48	HUMAN	E7EN95	Filamin-B
3465	dirMS_041712_NAR_30mM_plus2.14749.14811.2	2	14.46	0	7.63E+05		(K)FVMQEE	(K)F V|M|Q/E/E/F/S R(D)		130.1	586.778	1172.541	0.0083	7	4.53	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
3466	dirMS_041712_NAR_60mM_plus.13138.13138.3	3	14.46	1	7.13E+05		(R)INVYYN	(R)I/N/V/Y/Y N/E A T G G K Y/V P R(A)		126	615.3146	1843.934	-0.0045	-2.4	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
3467	dirMS_041712_NAR_60mM_plus.21561.21679.3	3	14.46	1	7.16E+05		(K)EIIDLVL	(K)E I/I/D/L/V/L D/R I R(K)		180.75	452.2733	1354.805	0.0001	0.1	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
3468	dirMS_041712_NAR_50mM_minus2.10539.10683.3	3	14.45	1	3.44E+05		(K)NQVAM	(K)N Q|V|A|M/N/P/T/N T/V F D A K R(L)		128.8	602.6379	1805.896	0.0029	1.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
3469	dirMS_041712_NAR_50mM_minus2.14498.14559.3	3	14.45	0	4.40E+05		(R)QVLIAS	(R)Q/V|L/I/A S/H|L/P S Y E L R(H)		150.95	542.6354	1625.901	-0.0093	-5.7	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
3470	dirMS_041712_NAR_50mM_minus2.14687.14687.3	3	14.45	0	6.40E+04		(K)VYTDVQ	(K)V Y|T/D/V/Q Q/V/A S S L T H P R(F)		151.52	600.976	1800.924	-0.0104	-5.8	6.71	74230.8	5.34	HUMAN	B1AH89	Tubulin tyrosine ligase-like family, member 12
3471	dirMS_041712_NAR_60mM_minus.7117.7117.3	3	14.45	1	3.04E+05		(R)ELFESST	(R)E L|F/E/S S T N N N K D/T K(Q)		98.72	542.9247	1626.761	-0.001	-0.6	4.68	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
3472	dirMS_041712_NAR_120mM_plus.15911.15911.4	4	14.45	1	8.06E+05		(K)THLPGF	(K)T H\L P G\F|V/E Q/A E/A L K A/K(G)		137.05	435.4926	1738.949	-0.0001	0	6.42	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
3473	dirMS_041712_NAR_20mM_plus.13896.13896.2	2	14.45	0	6.90E+04		(K)LLDLVQ	(K)L L|D|L\V|Q Q/S C N Y/K(Q)	C:Carbamidomethylation	167.73	740.8757	1480.746	-0.0023	-1.6	5.83	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
3474	dirMS_041712_NAR_20mM_plus.15021.15021.2	2	14.45	0	1.07E+05		(R)ILNVPQ	(R)I L/N|V/P Q/E L Y E/K(G)		174.67	673.3693	1345.736	-0.0049	-3.6	4.53	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
3475	dirMS_041712_NAR_50mM_plus2.6104.6104.3	3	14.45	0	1.85E+05		(R)ATAPQT	(R)A/T|A/P Q T Q/H/V/S P M R(Q)		96.3	475.2418	1423.711	-0.0002	-0.1	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
3476	dirMS_041712_NAR_20mM_minus.7854.7854.2	2	14.44	0	7.81E+04	M406m	(R)EYQELm	(R)E/Y/Q/E/L/m N V/K(L)	m:Oxidized methionine	128.13	585.2788	1153.556	15.9945	-0.3	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
3477	dirMS_041712_NAR_60mM_minus.10613.10613.3	3	14.44	0	1.44E+05	M271m	(R)DLNYCF	(R)D L|N/Y/C/F S G m S/D/H R(Y)	C:Carbamidomethylation m:Oxid	119.2	539.8863	1601.647	15.9972	1.4	5.21	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
3478	dirMS_041712_NAR_120mM_plus.4550.4660.3	3	14.44	0	8.70E+05		(R)YINTEH	(R)Y/I/N/T E/H/G G S Q A R(F)		74.22	444.8857	1332.629	0.0134	10.1	6.75	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
3479	dirMS_041712_NAR_120mM_plus.9978.10127.2	2	14.44	0	5.50E+05		(K)HLTDAY	(K)H|L|T D|A\Y|F/K(K)		105.57	497.7567	994.499	0.0069	6.9	6.74	25891.4	10.67	HUMAN	F8W181	60S ribosomal protein L6 (Fragment)
3480	dirMS_041712_NAR_30mM_plus2.10258.10558.2	2	14.44	0	1.57E+06		(K)VIPELN	(K)V I|P/E L/N/G/K(L)		108.53	435.2581	869.509	-0.0002	-0.2	5.97	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
3481	dirMS_041712_NAR_30mM_plus2.9400.9807.2	2	14.44	0	1.62E+06		(K)LIEVDDE	(K)L/I|E|V/D D/E/R(K)		105.03	494.7532	988.495	0.0046	4.6	3.91	10471.9	5.4	HUMAN	A2A3R7	40S ribosomal protein S6
3482	dirMS_041712_NAR_40mM_plus2.10941.10992.3	3	14.44	1	3.24E+05		(R)DVVICP	(R)D V|V|I/C/P D A S L E D A K K(E)	C:Carbamidomethylation	130.9	553.9465	1659.826	-0.0009	-0.5	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
3483	dirMS_041712_NAR_50mM_plus2.12618.12618.3	3	14.44	1	5.35E+05		(K)FSIEDLK	(K)F/S|I/E D/L/K/A Q P K(Q)		134.4	425.8966	1275.694	-0.0191	-15	6.07	13579.2	9.99	HUMAN	E9PPQ6	Thymocyte nuclear protein 1 (Fragment)

3484	dirMS_041712_NAR_120mM_minus.13316.13316.4	4	14.43	1	9.47E+05		(K)SVHSSVI	(K)S\V H S\S V/P L/L/N S K D/P I D R(I)		127.18	466.7525	1863.992	-0.0041	-2.2	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
3485	dirMS_041712_NAR_120mM_minus.8377.8394.3	3	14.43	0	1.85E+05		(K)LFQECCI	(K)L/F|Q/E/C C/P H S T D/R(V)	C:Carbamidomethylation	99.98	517.2227	1549.652	0.0013	0.9	5.32	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
3486	dirMS_041712_NAR_30mM_minus2.12471.12638.2	2	14.43	0	2.70E+05		(R)TLSGME	(R)T L|S|G/M/E/S/Y C V/R(A)	C:Carbamidomethylation	122.03	651.795	1302.582	0.001	0.8	5.66	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
3487	dirMS_041712_NAR_30mM_minus2.16157.16157.2	2	14.43	0	1.21E+05		(K)SSEELLS	(K)S S E/E/L|L|S/A/L Q/K(K)		141.47	602.816	1204.642	-0.0172	-14.3	4.53	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
3488	dirMS_041712_NAR_30mM_minus2.19598.19598.2	2	14.43	0	2.54E+05		(R)YLTVAA	(R)Y L/T|V/A A/V F/R(G)		162.82	520.2998	1039.593	-0.0012	-1.1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3489	dirMS_041712_NAR_40mM_minus2.14320.14410.3	3	14.43	0	2.72E+05		(R)DVCTELI	(R)D V|C|T/E L/L/P L I K/P Q/G R(V)	C:Carbamidomethylation	168.95	580.3211	1738.952	-0.0033	-1.9	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
3490	dirMS_041712_NAR_40mM_minus2.8129.8142.3	3	14.43	1	3.18E+05		(R)DGKLVS	(R)D/G K L V\S\E|S/S D|V/L/P K(-)		128.2	491.9311	1473.78	-0.0008	-0.5	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
3491	dirMS_041712_NAR_50mM_minus2.16531.16578.3	3	14.43	1	1.60E+05		(K)VVSSVL(	(K)V/V|S/S V L\Q/F G N I/S/F/K K(E)		162	551.6488	1652.937	-0.0052	-3.1	10	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
3492	dirMS_041712_NAR_50mM_minus2.19068.19068.3	3	14.43	1	1.34E+06		(R)KEGGLG	(R)K\E G G L G P L N|I|P/L/L A\D V T R(R)		187.5	621.6941	1863.07	-0.0021	-1.1	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
3493	dirMS_041712_NAR_20mM_plus.10450.10450.2	2	14.43	0	1.88E+05	M592m M!	(R)mGPAm	(R)m G/P A/m/G/P A/L G A G I E/R(M)	m:Oxidized methionine	144.65	730.3568	1427.713	31.993	2.1	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
3494	dirMS_041712_NAR_30mM_plus2.18567.18567.2	2	14.43	0	3.64E+05		(R)SSFYVN(	(R)S S F|Y/V/N G L/T\L/G G Q K(C)		150.97	735.8825	1470.759	-0.001	-0.7	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
3495	dirMS_041712_NAR_60mM_plus.6263.6263.3	3	14.43	1	3.09E+05		(R)GSCSTE\	(R)G/S|C|S/T E V E K E T Q E K(M)	C:Carbamidomethylation	91.08	537.9088	1611.717	-0.0048	-3	4.49	13871.4	9.22	HUMAN	O75348	V-type proton ATPase subunit G 1
3496	dirMS_041712_NAR_120mM_minus.10031.10155.3	3	14.42	0	5.96E+05		(R)HGESAV	(R)H G E\S\A\W|N|L/E/N/R(F)		109.4	438.2098	1312.603	0.012	9.1	5.4	28917.5	6.68	HUMAN	P18669	Phosphoglycerate mutase 1
3497	dirMS_041712_NAR_20mM_minus.12054.12401.3	3	14.42	0	2.99E+06	M313m	(R)TVQSLEI	(R)T\V\Q\S L\E|I/D/L/D/S m/R(N)	m:Oxidized methionine	170.78	508.2517	1506.747	15.9937	-0.8	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3498	dirMS_041712_NAR_50mM_minus2.15925.15925.3	3	14.42	0	3.64E+05		(K)LYGPTNI	(K)L Y|G/P/T N F S/P I/I N H V A R(F)		158.22	600.3221	1798.96	-0.0081	-4.5	8.75	60985.3	5.6	HUMAN	O75131	Copine-3
3499	dirMS_041712_NAR_60mM_minus.5572.5572.3	3	14.42	1	1.23E+04		(K)LAGESES	(K)L/A/G|E/S E/S N L R/K(A)		87.08	401.8822	1203.633	-0.0007	-0.6	6.14	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
3500	dirMS_041712_NAR_120mM_plus.11105.11105.3	3	14.42	0	1.04E+06		(K)NFYVEH	(K)N F/Y V/E/H/P E V A R(L)		111.43	454.2277	1360.664	0.0041	3	5.4	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
3501	dirMS_041712_NAR_30mM_plus2.19195.19641.2	2	14.42	0	1.20E+06		(R)LIDFLEC(	(R)L/I|D|F|L/E/C G/K(T)	C:Carbamidomethylation	155.15	547.7808	1094.555	-0.0007	-0.7	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
3502	dirMS_041712_NAR_30mM_plus2.5532.5590.2	2	14.42	0	2.38E+05	M154m M:	(R)mGYmD	(R)m/G/Y|m|D|P/R(E)	m:Oxidized methionine	83.4	451.1814	869.364	31.9911	1.4	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
3503	dirMS_041712_NAR_40mM_plus2.12152.12152.3	3	14.42	1	2.35E+05		(R)VVDALG	(R)V/V/D A/L/G N A/I D G K G P I G S K(T)		137.17	570.9838	1710.939	-0.0016	-1	5.93	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
3504	dirMS_041712_NAR_40mM_plus2.14370.14370.3	3	14.42	1	4.53E+05		(R)IINEPTA.	(R)I I|N/E/P T/A A A I A/Y G L D K/K(V)		150.6	596.6671	1787.99	-0.0034	-1.9	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
3505	dirMS_041712_NAR_60mM_plus.6445.6463.2	2	14.42	1	3.50E+05		(K)VQVEYK	(K)V/Q|V/E/Y K G E|T/K(S)		92.37	590.8148	1180.621	0.0015	1.3	6.11	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
3506	dirMS_041712_NAR_30mM_minus2.13245.13245.2	2	14.41	0	3.00E+05		(K)STYGWT	(K)S T|Y/G|W/T/A/N M E R(I)		125.7	658.2918	1315.574	0.0028	2.1	5.72	47825.1	5.07	HUMAN	Q58FG1	Putative heat shock protein HSP 90-alpha A4
3507	dirMS_041712_NAR_30mM_minus2.18823.18902.2	2	14.41	0	2.04E+05		(R)AIGIGAY	(R)A I|G|I|G/A/Y L V|R(L)		157.57	516.8122	1032.62	-0.0029	-2.8	8.79	9731	5.19	HUMAN	E9PEW7	Acetyl-CoA carboxylase 2
3508	dirMS_041712_NAR_50mM_minus2.12769.13106.3	3	14.41	0	4.17E+06	M84m	(K)YPIEHGI	(K)Y/P/I E H G I I|T/N/W|D/D m E K(I)	m:Oxidized methionine	141.65	659.6398	1960.911	15.9939	-0.5	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
3509	dirMS_041712_NAR_50mM_minus2.12837.12882.3	3	14.41	1	3.84E+05		(R)LSEDYG\	(R)L/S|E/D/Y G V/L K/T D E G/I A/Y R(G)		141.48	643.6561	1928.96	-0.0063	-3.2	4.32	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
3510	dirMS_041712_NAR_50mM_minus2.16836.16836.3	3	14.41	0	4.56E+05		(K)NILFVITI	(K)N I/L/F V/I/T K/P D V/Y/K(S)		164.1	517.2991	1549.899	-0.0161	-10.4	8.5	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
3511	dirMS_041712_NAR_50mM_minus2.18163.18171.3	3	14.41	0	2.31E+05		(K)ILFIFIDSI	(K)I/L\F|I/F I/D/S D H T D N/Q R(I)		172.78	611.9745	1833.913	-0.004	-2.2	4.41	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
3512	dirMS_041712_NAR_120mM_plus.6571.6571.3	3	14.41	1	1.74E+07		(R)TKTEISEI	(R)T K\T\E\I/S/E/M/N/R(N)		88.12	403.5365	1208.594	0.001	0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
3513	dirMS_041712_NAR_30mM_plus2.20716.20716.2	2	14.41	0	8.74E+05		(R)TVQSLEI	(R)T V|Q/S/L/E/I\D L D S M R(N)		162.18	753.8768	1506.747	-0.0005	-0.3	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3514	dirMS_041712_NAR_30mM_plus2.6410.6410.2	2	14.41	0	2.52E+05		(K)GEGQLG	(K)G E/G/Q|L/G/P A E R(A)		87.53	507.2537	1013.501	-0.0009	-0.9	4.53	96306.4	6.41	HUMAN	P13639	Elongation factor 2
3515	dirMS_041712_NAR_30mM_plus2.7553.7553.2	2	14.41	0	2.40E+05		(R)VLANPG	(R)V L|A/N|P/G N S Q V A R(V)		93.82	613.3361	1225.665	0.0002	0.1	9.72	16598.6	5.48	HUMAN	J3QR48	Importin subunit beta-1 (Fragment)
3516	dirMS_041712_NAR_40mM_plus2.10748.11012.3	3	14.41	0	9.41E+05		(R)LLEAQA(	(R)L/L|E|A/Q A/C/T G G I/I/H/P T T G Q K(L)	C:Carbamidomethylation	130.33	665.6807	1995.033	-0.0052	-2.6	6.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
3517	dirMS_041712_NAR_40mM_plus2.11309.11309.3	3	14.41	0	1.21E+05		(K)EAGELKI	(K)E A G E L/K P E E E I|T|V/G P V Q K(L)		132.8	651.6782	1953.017	0.0025	1.3	4.32	108281.4	5.72	HUMAN	P53618	Coatomer subunit beta
3518	dirMS_041712_NAR_40mM_plus2.11636.11636.3	3	14.41	1	2.52E+05		(R)IVAPGK(	(R)I/V|A|P G K G I L/A A D E S T G S I A K(R)		135.27	633.3568	1898.059	-0.0035	-1.8	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
3519	dirMS_041712_NAR_50mM_plus2.7506.7647.3	3	14.41	1	3.52E+05		(R)VVASDK	(R)V/V|A/S D K/E/T Y E/L R(Y)		105.87	470.5836	1409.727	0.0092	6.5	4.68	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
3520	dirMS_041712_NAR_60mM_plus.17857.17894.3	3	14.41	1	3.70E+05		(R)VVVDAL	(R)V/V|V/D/A/L/S G L K G D L A G/R(Y)		150.23	523.9678	1569.896	-0.007	-4.5	5.93	26949.2	7.99	HUMAN	C9JSQ1	Creatine kinase U-type, mitochondrial (Fragment)
3521	dirMS_041712_NAR_60mM_plus.20098.20118.3	3	14.41	1	3.34E+05		(K)GPVREG	(K)G P V R\E G D\V\L|T|L|L|E S E R(E)		165.02	590.6485	1769.939	-0.0083	-4.7	4.41	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
3522	dirMS_041712_NAR_40mM_minus2.14843.14843.3	3	14.4	1	1.22E+06	M116m	(R)ELAILLG	(R)E L/A I/L|L/G m L D/P A E K D/E K(G)	m:Oxidized methionine	171.37	634.338	1884.999	16.0008	3.1	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
3523	dirMS_041712_NAR_60mM_minus.7760.7838.3	3	14.4	1	4.17E+05		(K)KGTVEG	(K)K\G T V E G\F\E|P/A/D/N K(C)		103.35	464.5665	1391.68	0.0048	3.5	4.68	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
3524	dirMS_041712_NAR_120mM_plus.19049.19049.4	4	14.4	0	9.03E+05		(R)EVPIPEH	(R)E V/P I/P E/H|I/D|I/Y\H L T/R(E)		153.55	458.7454	1831.97	-0.0103	-5.6	5.28	27043.5	6.34	HUMAN	C9JHK9	ATP-binding cassette sub-family F member 2 (Fragment)
3525	dirMS_041712_NAR_120mM_plus.23106.23106.3	3	14.4	1	4.13E+05		(K)GLAPDLI	(K)G L\A|P/D L/P E D L Y H/L I K/K(A)		174.18	608.0076	1822.011	-0.0027	-1.5	5.38	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
3526	dirMS_041712_NAR_120mM_plus.7624.7624.2	2	14.4	1	1.19E+06		(R)AQYDEL	(R)A/Q|Y/D/E L/A/R K(N)		93.32	547.2874	1093.564	0.0039	3.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3527	dirMS_041712_NAR_120mM_plus.9979.10174.2	2	14.4	0	4.61E+05		(R)VHIEIGP	(R)V/H|I|E|I|G/P D|G R(V)		105.95	546.7931	1092.58	-0.0007	-0.6	5.32	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
3528	dirMS_041712_NAR_20mM_plus.18821.18821.2	2	14.4	0	2.84E+05		(K)LAVEALS	(K)L A V|E A\L|S/S/L|D/G D L A G R(Y)		200.5	793.9214	1586.838	-0.0029	-1.8	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
3529	dirMS_041712_NAR_30mM_plus2.10509.10547.2	2	14.4	0	3.85E+05		(R)DPYGFG	(R)D/P|Y|G|F G D/S R(D)		109.02	507.2274	1013.432	0.0152	15	4.21	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
3530	dirMS_041712_NAR_30mM_plus2.17911.18212.2	2	14.4	0	5.51E+05		(K)SFGLPSI(	(K)S F|G|L|P/S/I G R(L)		147.78	467.2628	933.515	0.0031	3.3	9.47	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
3531	dirMS_041712_NAR_40mM_plus2.12832.12832.3	3	14.4	1	4.30E+05		(R)VLELVSI	(R)V L|E/L/V|S I T A N K N T\C P G D R(S)	C:Carbamidomethylation	142.67	663.0201	1987.028	0.018	9.1	6.04	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
3532	dirMS_041712_NAR_40mM_plus2.7767.7767.2	2	14.4	0	8.63E+04		(R)FGQGG/	(R)F G Q|G/G/A/G/P V|G G Q G P R(G)		105.47	671.3368	1341.666	0.0005	0.4	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
3533	dirMS_041712_NAR_60mM_plus.16565.16565.3	3	14.4	1	3.69E+05		(-)MKLNISF	(-)M K/L N I S/F|P/A|T G C Q K(L)	C:Carbamidomethylation	142.85	532.2733	1594.808	-0.0026	-1.7	10	10471.9	5.4	HUMAN	A2A3R7	40S ribosomal protein S6
3534	dirMS_041712_NAR_120mM_minus.4529.4529.2	2	14.39	0	7.49E+05		(R)HSDGNL	(R)H/S|D G/N/L|C V|K(V)	C:Carbamidomethylation	73.97	515.2423	1029.478	-0.0009	-0.9	6.74	7781.8	6.82	HUMAN	E9PE20	Signal recognition particle 9 kDa protein
3535	dirMS_041712_NAR_50mM_minus2.19054.19060.3	3	14.39	1	1.34E+06		(R)KEGGLG	(R)K\E G G L G P\L|N\I|P/L/L/A D V T R(R)		187.5	621.6941	1863.07	-0.0021	-1.1	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
3536	dirMS_041712_NAR_20mM_plus.17725.17919.2	2	14.39	0	2.00E+05		(R)YISPDQL	(R)Y/I|S|P D Q L/A D/L Y K(S)		194.23	713.3667	1425.726	0.0001	0.1	4.21	47510.4	7.04	HUMAN	P06733	Alpha-enolase
3537	dirMS_041712_NAR_30mM_plus2.7924.7924.2	2	14.39	0	9.94E+05		(R)DYDDM!	(R)D Y|D|D M/S/P/R(R)		96.1	499.6972	998.388	-0.0013	-1.3	3.93	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
3538	dirMS_041712_NAR_50mM_plus2.18338.18563.3	3	14.39	1	3.49E+05		(R)GDSVIV\	(R)G D/S/V/I|V V/L/R N P L I/A/G K(-)		165.37	550.9999	1650.99	-0.005	-3	8.75	6144.3	10.23	HUMAN	K7EJB5	Small nuclear ribonucleoprotein Sm D2
3539	dirMS_041712_NAR_60mM_plus.10318.10362.3	3	14.39	0	1.35E+04		(K)AFFESHI	(K)A/F|F/E/S H/P A/P S A E/R(T)		113.22	482.5659	1445.681	0.0023	1.6	5.4	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
3540	dirMS_041712_NAR_60mM_plus.18613.18613.3	3	14.39	1	1.09E+05		(K)MFIGGL:	(K)M F/I/G G L/S/W D T T K K(D)		154.55	495.2592	1483.761	0.0017	1.1	8.35	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
3541	dirMS_041712_NAR_20mM_plus.15789.15789.3	3	14.38	0	1.53E+06	M73m	(R)AILVDLE	(R)A I|L|V D L E/P/G T m D S V R(S)	m:Oxidized methionine	179.32	544.6139	1615.836	15.9912	-2.3	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
3542	dirMS_041712_NAR_20mM_plus.18994.18994.3	3	14.38	0	1.11E+05		(R)VCTLAII(	(R)V C T L A I\I|D/P/G D S/D I I R(S)	C:Carbamidomethylation	202.28	586.641	1757.91	-0.0018	-1	3.93	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
3543	dirMS_041712_NAR_30mM_plus2.18606.18647.3	3	14.38	0	4.97E+05		(R)SSFYVN(	(R)S S\F Y V N/G\L/T/L/G/G Q K(C)		150.95	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
3544	dirMS_041712_NAR_30mM_plus2.22059.22059.2	2	14.38	0	1.78E+05		(K)NSSYFVE	(K)N S/S Y/F V/E/W/I|P N N/V K(V)		171.7	848.9189	1696.833	-0.0024	-1.4	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
3545	dirMS_041712_NAR_30mM_plus2.22345.22345.2	2	14.38	0	3.79E+05		(R)VGNLGL	(R)V/G N\L/G/L|A/T S/F F N E R(N)		172.8	762.8926	1524.781	-0.0026	-1.7	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
3546	dirMS_041712_NAR_50mM_minus2.10310.10310.3	3	14.37	0	1.46E+05		(K)VGSLDN	(K)V/G|S/L|D/N V/G H L/P A G G A V K(I)		126.9	530.9592	1590.86	0.0032	2	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
3547	dirMS_041712_NAR_50mM_minus2.7908.7994.3	3	14.37	1	3.94E+06	M239m	(R)MQKEIT	(R)M Q K E I T A|L|A|P/S/T m K(I)	m:Oxidized methionine	112.32	522.2727	1548.812	15.9911	-2.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
3548	dirMS_041712_NAR_60mM_minus.9933.9933.3	3	14.37	1	5.63E+05	M230m M:	(R)mSmKE\	(R)m S m K E V D E\Q|M|L/N/V\Q/N K(N)	m:Oxidized methionine	114.97	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3549	dirMS_041712_NAR_20mM_plus.18780.18780.2	2	14.37	0	2.25E+05		(K)TAVETA	(K)T A\V|E/T|A/V L|L L R(I)		200.22	593.3625	1185.72	-0.0024	-2	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
3550	dirMS_041712_NAR_20mM_plus.6410.6410.2	2	14.37	0	1.60E+05		(K)DSYVGD	(K)D S Y|V/G/D/E A Q S K(R)		107.17	599.7645	1198.522	-0.0005	-0.4	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
3551	dirMS_041712_NAR_30mM_plus2.11977.11977.2	2	14.37	0	4.31E+05		(K)AYGGAY	(K)A Y/G|G A/Y/D V\M S/S K(H)		115.77	624.7816	1248.556	-0.0006	-0.5	5.88	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
3552	dirMS_041712_NAR_50mM_plus2.16657.16657.3	3	14.37	0	1.44E+05		(R)DVQIGD	(R)D V|Q/I/G D I/V T V G E C R P L S K(T)	C:Carbamidomethylation	155.08	662.6825	1986.033	0.0005	0.2	4.56	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
3553	dirMS_041712_NAR_50mM_plus2.16971.16971.3	3	14.37	1	6.05E+05		(K)ISMPDIL	(K)I/S/M/P D/I D L N L K G P K(V)		157.1	514.2847	1540.84	-0.0008	-0.5	5.96	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
3554	dirMS_041712_NAR_30mM_minus2.5847.5847.2	2	14.36	0	5.74E+04		(R)LAEAEET	(R)L/A/E|A/E E/T/A R(T)		86.62	495.2478	989.49	-0.0015	-1.5	4.25	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
3555	dirMS_041712_NAR_40mM_minus2.12317.12489.3	3	14.36	1	2.92E+05		(K)DVAIKEF	(K)D V|A\I\K E/P\L\V/D/V\V D/P/K(Q)		156.1	546.3068	1636.916	-0.0098	-6	4.23	24376.8	6.08	HUMAN	E9PIX6	Protein arginine N-methyltransferase 1 (Fragment)
3556	dirMS_041712_NAR_50mM_minus2.12780.12780.3	3	14.36	1	3.77E+05		(K)NTVELL\	(K)N T|V/E/L/L/V E D K G N Q V Y R(C)		140.5	626.3309	1876.976	0.0018	1	4.68	258215.9	5.48	HUMAN	E7EN95	Filamin-B
3557	dirMS_041712_NAR_20mM_plus.15513.15691.3	3	14.36	0	2.11E+05		(R)GVVDSE	(R)G V\V D S E D/I/P/L N/L S/R(E)		179.38	505.2667	1513.786	-0.0001	-0.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
3558	dirMS_041712_NAR_20mM_plus.18626.18805.3	3	14.36	0	5.22E+05		(K)LAVEALS	(K)L A\V E A\L|S S L/D/G D/L/A/G R(Y)		200.47	529.6164	1586.838	-0.0038	-2.4	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
3559	dirMS_041712_NAR_20mM_plus.8912.9064.2	2	14.36	0	4.48E+05	M161m	(K)LLIEmEC	(K)L/L|I/E/m/E/Q/R(L)	m:Oxidized methionine	132.82	524.278	1031.555	15.9933	-1.5	4.53	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
3560	dirMS_041712_NAR_30mM_plus2.13235.13235.2	2	14.36	0	5.70E+05		(K)CPFTGN	(K)C/P|F|T/G N V/S I R(G)	C:Carbamidomethylation	122.88	575.7876	1150.567	0.0006	0.5	9.75	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
3561	dirMS_041712_NAR_30mM_plus2.19982.19982.2	2	14.36	0	2.64E+04		(R)ALMDSL	(R)A L|M/D/S/L/G/P E W R(L)		158.47	637.8131	1274.62	-0.0009	-0.7	4.37	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
3562	dirMS_041712_NAR_50mM_plus2.10809.10809.3	3	14.36	1	4.28E+05		(K)NQLTSN	(K)N Q|L/T/S N/P E N T V/F D A K R(L)		124.88	611.9758	1833.909	0.0039	2.1	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
3563	dirMS_041712_NAR_60mM_plus.17937.17937.3	3	14.36	1	1.75E+05		(K)FNADEF	(K)F N|A/D E F/E D M/V/A E K R(L)		150.68	567.5906	1700.758	-0.0012	-0.7	4.18	18819.6	10.31	HUMAN	F8W7C6	60S ribosomal protein L10
3564	dirMS_041712_NAR_120mM_minus.11732.11888.3	3	14.35	1	9.68E+05		(R)KFDQLL/	(R)K\F\D\Q\L|L|A E/E/K(A)		118.67	407.5551	1220.652	-0.0014	-1.1	4.68	232239.1	5.52	HUMAN	F2Z2U8	Myosin-14
3565	dirMS_041712_NAR_120mM_minus.4414.4676.3	3	14.35	0	3.14E+07	M46m M4!	(R)HQGVm	(R)H Q\G\V\m|V/G/m/G Q/K(D)	m:Oxidized methionine	74.18	401.8604	1171.571	31.9956	4.8	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
3566	dirMS_041712_NAR_20mM_minus.12303.12303.2	2	14.35	0	1.70E+05		(R)AAVIGPI	(R)A/A/V|I|G|P D/V F A K(L)		171.52	544.3103	1087.615	-0.0013	-1.2	5.88	266161	5.68	HUMAN	E9PPU0	Epiplakin
3567	dirMS_041712_NAR_30mM_minus2.11572.11741.2	2	14.35	0	5.18E+05		(R)DVCLYPI	(R)D V|C|L/Y/P/R(F)	C:Carbamidomethylation	117.17	461.7315	922.445	0.0106	11.5	5.83	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
3568	dirMS_041712_NAR_30mM_minus2.11672.11721.2	2	14.35	0	1.84E+05		(R)ENVNLA	(R)E N|V|N/L|A/Q/I/R(T)		117.28	528.7959	1056.58	0.0049	4.6	6.1	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
3569	dirMS_041712_NAR_30mM_minus2.17450.17671.2	2	14.35	0	4.37E+05		(R)EQLAIAE	(R)E Q|L|A|I/A/E/F A R(S)		150.25	574.3084	1147.611	-0.0011	-0.9	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
3570	dirMS_041712_NAR_60mM_minus.7977.7977.3	3	14.35	1	4.69E+05		(R)YLAEVA	(R)Y/L/A/E V A/T G E/K/R(A)		104.32	412.8902	1236.658	-0.0022	-1.8	6.14	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
3571	dirMS_041712_NAR_120mM_plus.12522.12715.3	3	14.35	0	6.26E+05		(K)HLSVND	(K)H L\S\V N\D|L/P/V/G/R(S)		119.52	402.8906	1206.659	-0.0017	-1.4	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
3572	dirMS_041712_NAR_20mM_plus.19365.19365.3	3	14.35	0	2.22E+05		(R)LAGTQP	(R)L A G T\Q/P L|E\V\L/E/A/V Q R(S)		204.52	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
3573	dirMS_041712_NAR_20mM_plus.8117.8117.2	2	14.35	0	6.42E+03		(K)TAVCDIF	(K)T A/V|C/D/I|P|P R(G)	C:Carbamidomethylation	127.22	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
3574	dirMS_041712_NAR_30mM_plus2.15883.16354.2	2	14.35	0	3.72E+06		(R)INEILSN/	(R)I/N|E|I|L|S/N A L/K(R)		138.07	557.8307	1114.647	0.0075	6.7	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
3575	dirMS_041712_NAR_40mM_plus2.18627.18627.3	3	14.35	1	3.56E+05		(R)TLAEIAK	(R)T L/A/E/I/A K V/E L D/N M/P L R(G)		176.47	604.9967	1812.989	-0.0132	-7.3	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
3576	dirMS_041712_NAR_40mM_plus2.6213.6213.2	2	14.35	1	2.84E+05		(R)YSGGNY	(R)Y/S|G/G/N Y R D N\Y|D|N(-)		95.58	719.2857	1437.567	-0.0024	-1.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
3577	dirMS_041712_NAR_50mM_plus2.10704.10704.3	3	14.35	0	4.20E+05		(K)TSEVDL/	(K)T/S|E|V D\L A K P L/V/K(F)		123.78	433.922	1299.752	-0.0004	-0.3	5.73	17178.3	5.63	HUMAN	C9IZF9	Programmed cell death 6-interacting protein (Fragment)
3578	dirMS_041712_NAR_60mM_plus.11280.11280.3	3	14.35	0	1.93E+06		(R)EIVHIQA	(R)E/I/V H I Q A G/Q/C/G/N Q I|G A/K(F)	C:Carbamidomethylation	116.42	608.311	1822.923	-0.0044	-2.4	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3579	dirMS_041712_NAR_60mM_plus.7456.7456.3	3	14.35	1	5.05E+05		(K)SSGGREI	(K)S/S/G G R E D L\E|S/S/G L Q|R(R)		97.3	526.5897	1577.751	0.0031	2	4.68	11625.5	8.01	HUMAN	B8ZZT7	Hematological and neurological-expressed 1 protein
3580	dirMS_041712_NAR_60mM_plus.8976.8976.2	2	14.35	0	1.94E+05		(R)VLIAAH(	(R)V/L|I|A|A/H G N S L/R(G)		105.23	575.8377	1150.669	-0.001	-0.9	9.73	28936.8	9.22	HUMAN	P15259	Phosphoglycerate mutase 2
3581	dirMS_041712_NAR_30mM_minus2.7571.7656.2	2	14.34	0	1.29E+06		(R)FVDPNT	(R)F/V|D|P/N/T Q E K(V)		95.88	539.2647	1077.521	0.001	0.9	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
3582	dirMS_041712_NAR_30mM_minus2.8079.8079.2	2	14.34	0	8.16E+04		(K)SLAAEEE	(K)S L|A/A/E/E E A/A/R(Q)		98.37	523.7597	1046.511	0.0008	0.8	4.25	533778	5.74	HUMAN	Q15149	Plectin
3583	dirMS_041712_NAR_40mM_minus2.8606.8607.3	3	14.34	0	2.85E+05		(R)SVIDPVF	(R)S V|I/D|P|V/P A/P V G D S H V D G A A K(S)		132.52	644.3329	1930.987	-0.0027	-1.4	4.41	58326.8	5.7	HUMAN	Q13177	Serine/threonine-protein kinase PAK 2
3584	dirMS_041712_NAR_60mM_minus.9321.9321.3	3	14.34	1	2.37E+05		(R)QDSAA\	(R)Q D/S A/A V/G/F D Y K E/K(L)		111.87	486.5639	1457.691	-0.0136	-9.3	4.56	61756.2	5.24	HUMAN	Q14247	Src substrate cortactin
3585	dirMS_041712_NAR_30mM_plus2.21241.21468.2	2	14.34	0	5.32E+05		(K)STLINTLI	(K)S/T|L|I/N/T L/F/K(S)		166.63	518.799	1036.604	-0.013	-12.5	8.47	18010.4	9.42	HUMAN	K7EIE4	Septin-9 (Fragment)
3586	dirMS_041712_NAR_30mM_plus2.6070.6088.2	2	14.34	0	2.40E+05		(R)IGDEDV(	(R)I/G|D|E/D/V/G/R(V)		86.23	430.7093	860.411	0.0005	0.6	4.03	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
3587	dirMS_041712_NAR_30mM_plus2.7054.7262.2	2	14.34	0	3.13E+06		(K)NAGFTP	(K)N A|G|F|T/P Q E/R(Q)		92.33	510.2497	1019.491	0.0016	1.6	6	29474.8	6.94	HUMAN	G3V3M6	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
3588	dirMS_041712_NAR_60mM_plus.15126.15289.3	3	14.34	1	8.60E+05		(R)MTGSEF	(R)M/T|G S E/F/D/F/E E M K R(K)		135.73	536.2355	1606.688	0.0043	2.7	4.41	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
3589	dirMS_041712_NAR_60mM_plus.6453.6453.3	3	14.34	1	1.35E+05		(R)SIPAGAE	(R)S I/P/A G A E/P G E K G S A R(K)		92.35	476.2505	1426.728	0.0085	5.9	5.87	18962.9	9.6	HUMAN	A6NGP5	Hematological and neurological-expressed 1-like protein
3590	dirMS_041712_NAR_30mM_minus2.16912.16912.2	2	14.33	0	4.99E+05		(K)NSLESY/	(K)N S|L|E/S Y/A/F/N M K(A)		146.6	652.3031	1303.599	0.0002	0.2	6	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
3591	dirMS_041712_NAR_60mM_minus.7902.8018.3	3	14.33	1	8.24E+05		(R)LREDEN.	(R)L R E D E N\A|E|P/V/G T T Y Q K(T)		104.68	617.3015	1849.893	-0.0027	-1.5	4.41	76925.9	4.46	HUMAN	A8MV58	Drebrin
3592	dirMS_041712_NAR_30mM_plus2.14774.14966.2	2	14.33	0	6.29E+05		(K)YDGIILP(	(K)Y/D|G\I|I/L/P|G/K(-)		130.85	488.28	975.551	0.0018	1.8	5.83	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11

3593	dirMS_041712_NAR_50mM_plus2.18670.18800.3	3	14.33	1	5.80E+05		(R)YLTAEET	(R)Y/L|T/A/E/E/T D K/I/I/N Y L R(E)		166.65	614.662	1841.964	0.0071	3.8	4.68	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
3594	dirMS_041712_NAR_50mM_plus2.6067.6146.3	3	14.33	0	1.85E+05		(R)ATAPQT	(R)A/T/A P/Q|T Q/H/V/S P M R(Q)		96.3	475.2418	1423.711	-0.0002	-0.1	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
3595	dirMS_041712_NAR_50mM_plus2.9308.9308.3	3	14.33	0	1.33E+05		(K)AEITLVA	(K)A E|I/T L/V/A T/K/P E K(L)		116.23	433.922	1299.752	-0.0004	-0.3	6.18	98761.7	5.56	HUMAN	Q9UBF2	Coatomer subunit gamma-2
3596	dirMS_041712_NAR_120mM_minus.10985.11425.4	4	14.32	0	1.57E+06		(K)SAKPTK	(K)S A K\P T K P A A/S\D\L\P\V|P/A/E/G V R(N)		116.33	498.5274	1991.092	-0.0042	-2.1	8.31	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
3597	dirMS_041712_NAR_120mM_minus.5446.5446.3	3	14.32	0	1.24E+05		(R)YIDTEH	(R)Y/I/D T E/H/G G S Q A R(F)		82.93	445.2092	1333.613	-0.0001	-0.1	5.32	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
3598	dirMS_041712_NAR_30mM_minus2.16333.16333.2	2	14.32	0	1.29E+05	M256m	(R)SLDmDS	(R)S L/D\m/D\S I/I A/E V K(A)	m:Oxidized methionine	142	668.8368	1320.671	15.9948	-0.1	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
3599	dirMS_041712_NAR_60mM_minus.14894.14894.3	3	14.32	0	4.07E+05		(K)WIGLDL	(K)W/I/G/L D/L S/N/G K/P R(D)		143.47	452.5849	1355.743	-0.0029	-2.1	8.75	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
3600	dirMS_041712_NAR_60mM_minus.16393.16393.3	3	14.32	0	2.04E+05		(R)HDPTSE	(R)H D P T S E\N|I|L Q/L V/K(A)		150.92	498.6051	1493.796	0.0049	3.3	5.32	13564.4	5.9	HUMAN	F8VZ98	Serine/threonine-protein kinase D1 (Fragment)
3601	dirMS_041712_NAR_120mM_plus.21623.21623.4	4	14.32	1	2.53E+05		(R)KVDIIAD	(R)K\V D\I I|A/D/A/A Y/S/I/F Q/K/P K(S)		166.88	477.5186	1907.064	-0.0111	-5.8	8.43	23634.7	4.93	HUMAN	B4DWC7	Hydroxysteroid dehydrogenase-like protein 2
3602	dirMS_041712_NAR_20mM_plus.12284.12568.2	2	14.32	0	1.98E+05		(R)GVEICIA	(R)G V|E|I/C I/A|T|P G R(L)	C:Carbamidomethylation	158.67	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
3603	dirMS_041712_NAR_30mM_plus2.10341.10520.2	2	14.32	0	9.85E+05		(R)FAQMLE	(R)F/A|Q|M/L/E/K(V)		108.48	433.7317	866.444	0.0121	13.9	6	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
3604	dirMS_041712_NAR_30mM_plus2.16785.16785.2	2	14.32	0	2.84E+05		(R)SIQADG	(R)S I|Q/A|D G L/V W/G/S S K(L)		140.7	674.3475	1347.69	-0.0026	-1.9	5.55	24934.4	4.5	HUMAN	P24534	Elongation factor 1-beta
3605	dirMS_041712_NAR_40mM_plus2.10247.10247.2	2	14.32	0	6.93E+04		(R)EYQELM	(R)E Y\Q/E|L/M/N/V K(L)		125.03	577.2823	1153.556	0.0015	1.3	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
3606	dirMS_041712_NAR_40mM_plus2.12281.12281.3	3	14.32	0	3.63E+04		(R)VLTEDE	(R)V/L|T\E/D E M G H/P E I/G D A I A R(L)		138.75	651.6493	1952.938	-0.0049	-2.5	4.17	40874	5.06	HUMAN	E9PCI9	Farnesyl pyrophosphate synthase
3607	dirMS_041712_NAR_40mM_plus2.14642.14642.3	3	14.32	0	5.34E+05		(K)IAILTCP	(K)I/A\I|L T/C/P F E/P P K P K(T)	C:Carbamidomethylation	153.53	537.6381	1610.898	0.0023	1.4	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
3608	dirMS_041712_NAR_50mM_minus2.19064.19064.3	3	14.31	1	1.34E+06		(R)KEGGLG	(R)K E G G L G\P L\N|I|P L/L A D V T R(R)		187.5	621.6941	1863.07	-0.0021	-1.1	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
3609	dirMS_041712_NAR_120mM_plus.5571.5571.3	3	14.31	1	7.62E+04		(R)YGEDNR	(R)Y/G|E/D N R G Y|G G S Q/G G G R(G)		82.97	543.9055	1629.7	0.0019	1.2	6.07	26157.9	4.57	HUMAN	K7EL85	TATA-binding protein-associated factor 2N (Fragment)
3610	dirMS_041712_NAR_20mM_plus.6932.6932.2	2	14.31	0	1.59E+05		(K)TTTAAA	(K)T T T A/A/A|V/A S/T/G\P/S S/R(S)		114.18	689.3492	1377.697	-0.0057	-4.2	9.41	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
3611	dirMS_041712_NAR_30mM_plus2.12023.12024.2	2	14.31	0	4.33E+05		(R)LYDVPA	(R)L/Y|D|V|P A N S M|R(L)		115.97	583.2879	1165.567	0.0015	1.3	5.83	16508.2	5.16	HUMAN	J3QSX4	Mitotic checkpoint protein BUB3
3612	dirMS_041712_NAR_30mM_plus2.7146.7304.2	2	14.31	0	1.70E+06		(K)TEISEM	(K)T E|I|S|E/M/N|R(N)		92.85	490.2294	979.451	0.0002	0.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
3613	dirMS_041712_NAR_30mM_plus2.9922.9922.2	2	14.31	0	1.65E+06		(K)GSFSDT	(K)G S/F/S/D/T/G L/G/D/G K(M)		106	570.7598	1140.517	-0.0044	-3.9	4.21	108720.9	10.17	HUMAN	Q9Y2W1	Thyroid hormone receptor-associated protein 3
3614	dirMS_041712_NAR_40mM_plus2.10695.10695.3	3	14.31	0	1.85E+05		(K)VGSLDN	(K)V/G/S|L/D N V G H L/P A G G A V K(I)		128.15	530.9567	1590.86	-0.0043	-2.7	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
3615	dirMS_041712_NAR_60mM_plus.11896.11953.3	3	14.31	1	8.29E+05		(R)QSVEAD	(R)Q/S/V/E/A/D/I/N G\L R R(V)		119.35	453.2446	1357.718	0.001	0.7	6.07	19213.2	4.66	HUMAN	K7EMD9	Keratin, type I cytoskeletal 13 (Fragment)
3616	dirMS_041712_NAR_30mM_minus2.13678.13678.2	2	14.3	0	2.27E+05		(K)LTVEEA	(K)L/T|V/E/E A/F K(A)		127.68	468.7559	936.504	0.0008	0.9	4.53	266161	5.68	HUMAN	E9PPU0	Epiplakin
3617	dirMS_041712_NAR_60mM_minus.11921.11921.3	3	14.3	1	3.03E+06	M72m	(R)TEmENE	(R)T E|m/E N E/F/V L/I/K K(D)	m:Oxidized methionine	126.87	499.5941	1480.772	15.9962	0.8	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
3618	dirMS_041712_NAR_20mM_plus.10530.10530.2	2	14.3	0	1.07E+05		(R)AVLLGP	(R)A V|L|L|G P P G A G K(G)		144.9	490.2992	979.593	-0.0024	-2.4	8.8	4460.2	8.14	HUMAN	F8VPP1	Adenylate kinase 2, mitochondrial
3619	dirMS_041712_NAR_20mM_plus.17804.17938.2	2	14.3	0	4.16E+05		(R)ILVATNL	(R)I/L|V|A/T/N L F/G R(G)		194.68	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
3620	dirMS_041712_NAR_20mM_plus.8088.8176.2	2	14.3	0	1.02E+05		(R)LLEAAS	(R)L/L|E|A/A/S V/S/S K(G)		125.87	502.7839	1004.562	-0.0017	-1.7	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
3621	dirMS_041712_NAR_30mM_plus2.12299.12299.2	2	14.3	0	7.33E+04		(R)AQIFAN	(R)A Q|I|F|A/N/T V D N/A R(I)		117.52	660.338	1319.67	-0.0015	-1.1	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3622	dirMS_041712_NAR_40mM_plus2.15016.15016.3	3	14.3	0	2.29E+05		(R)EVIDLLK	(R)E V/I/D/L/L/K P D Q V E G I Q K(S)		155.13	608.6749	1824.011	-0.0012	-0.6	4.32	156557.7	5.52	HUMAN	Q86UP2	Kinectin
3623	dirMS_041712_NAR_50mM_plus2.10124.10124.3	3	14.3	0	2.23E+05		(R)TITVALA	(R)T I|T V/A/L A D/G G R P D N T G R(G)		120.23	571.9661	1713.888	-0.0041	-2.4	5.63	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
3624	dirMS_041712_NAR_60mM_plus.7543.7543.2	2	14.3	1	7.47E+05		(R)VITEEEK	(R)V I|T/E/E/E/K N F K(A)		97.92	618.8282	1236.647	0.0021	1.7	4.79	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
3625	dirMS_041712_NAR_60mM_plus.9114.9304.3	3	14.3	0	2.11E+06		(K)NCPHIV	(K)N C|P H|I|V/V/G T/P G/R(I)	C:Carbamidomethylation	106.15	436.2272	1306.669	-0.0014	-1.1	9.75	28185.1	10.76	HUMAN	B4DIJ6	Spliceosome RNA helicase DDX39B
3626	dirMS_041712_NAR_120mM_minus.9835.9893.3	3	14.29	1	1.52E+06		(K)AADAEA	(K)A A D|A/E/A/E/V/A S L N R/R(I)		108.45	491.5865	1472.745	-0.0002	-0.2	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
3627	dirMS_041712_NAR_30mM_minus2.10330.10350.2	2	14.29	0	6.12E+05		(K)AVGQD	(K)A/V|G|Q/D/T L L/R(S)		110.63	486.7751	972.547	-0.0043	-4.5	5.88	72873.4	5.73	HUMAN	Q96S55	ATPase WRNIP1
3628	dirMS_041712_NAR_60mM_plus.6843.6887.2	2	14.29	1	5.64E+05		(R)LSVDYG	(R)L/S|V/D|Y|G K K(S)		94.35	455.257	909.504	0.0027	3	8.5	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
3629	dirMS_041712_NAR_120mM_minus.11469.11469.2	2	14.28	0	7.46E+05		(R)GSAVHC	(R)G S A/V/H|Q|L S/E/E\L R(C)		116.68	663.3434	1325.681	-0.0013	-1	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
3630	dirMS_041712_NAR_60mM_minus.17746.17746.3	3	14.28	1	4.16E+05	M148m	(R)LDLAGR	(R)L/D|L/A G R D L/T/D Y/L m K(I)	m:Oxidized methionine	159.32	547.2829	1623.841	15.9931	-1.1	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
3631	dirMS_041712_NAR_120mM_plus.19626.19640.3	3	14.28	1	4.65E+05		(K)NLRDID	(K)N L\R D I\D\E|V|S|S L/L R(T)		156.13	510.6138	1529.828	-0.0013	-0.9	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
3632	dirMS_041712_NAR_20mM_plus.17665.17665.3	3	14.28	0	1.23E+05		(K)LATQSN	(K)L A\T Q S N E\I T\I/P\V/T F E S R(A)		193.2	636.0003	1905.992	-0.0053	-2.8	4.53	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
3633	dirMS_041712_NAR_30mM_plus2.13463.13589.2	2	14.28	0	1.05E+06		(K)YGVSGY	(K)Y/G|V|S/G/Y/P/T L/K(I)		124.33	542.7882	1084.567	0.0018	1.6	8.5	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
3634	dirMS_041712_NAR_30mM_plus2.16197.16197.2	2	14.28	0	2.79E+05		(K)MDQAII	(K)M D/Q|A/I/I F/C R(T)	C:Carbamidomethylation	137.37	577.2809	1153.549	0.0053	4.6	5.59	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
3635	dirMS_041712_NAR_30mM_plus2.19722.19722.2	2	14.28	0	3.60E+05		(K)SNNVEM	(K)S N\N/V|E|M D W V/L K(H)		156.88	667.8205	1334.641	-0.0072	-5.4	4.37	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
3636	dirMS_041712_NAR_30mM_minus2.11717.11925.2	2	14.27	0	7.98E+05		(R)LPLETAY	(R)L/P|L|E|T A Y/R(R)		117.87	481.7625	962.531	-0.0128	-13.3	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
3637	dirMS_041712_NAR_30mM_minus2.17195.17195.2	2	14.27	0	1.03E+05		(R)NGGQIL	(R)N G G/Q|I/L I/A D/L/R(G)		147.92	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
3638	dirMS_041712_NAR_50mM_minus2.9763.9763.3	3	14.27	0	2.46E+05		(K)TSEVDL	(K)T/S|E V/D/L A K/P L V/K(F)		123.2	433.9205	1299.752	-0.0049	-3.8	5.73	17178.3	5.63	HUMAN	C9IZF9	Programmed cell death 6-interacting protein (Fragment)
3639	dirMS_041712_NAR_60mM_minus.17756.17756.3	3	14.27	1	2.33E+05		(R)LGLSTLG	(R)L/G/L/S\T L/G E/L/K Q N L S R(S)		159.42	543.6476	1628.933	-0.0047	-2.9	8.75	22294.4	5.26	HUMAN	O43399	Tumor protein D54
3640	dirMS_041712_NAR_120mM_plus.13268.13277.4	4	14.27	1	1.43E+06		(K)SVHSSV	(K)S V H S\S\V|P L/L/N S K/D/P I/D/R(I)		123.27	466.7533	1863.992	-0.0009	-0.5	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
3641	dirMS_041712_NAR_20mM_plus.16613.16613.2	2	14.27	0	1.91E+05		(K)VQIAVA	(K)V Q|I|A\V|A N/A/Q/E L/L Q R(M)		186.22	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
3642	dirMS_041712_NAR_30mM_plus2.20863.21330.2	2	14.27	0	4.30E+06		(K)FLPLFDR	(K)F/L|P|L F D/R(V)		165.65	454.2621	907.504	0.0133	14.7	5.84	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
3643	dirMS_041712_NAR_30mM_plus2.8349.8349.2	2	14.27	0	4.11E+05		(K)TAVCDI	(K)T A|V/C/D I|P\P R(G)	C:Carbamidomethylation	98	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
3644	dirMS_041712_NAR_50mM_plus2.16929.16929.3	3	14.27	1	6.11E+05		(K)ISMPDI	(K)I/S M/P/D I D|L N L\K/G P/K(V)		157.08	514.2847	1540.84	-0.0008	-0.5	5.96	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
3645	dirMS_041712_NAR_60mM_plus.14394.14394.3	3	14.27	0	2.46E+05		(R)VNAIEH	(R)V/N|A/I/E H/V/I I P R(I)		132	420.9182	1260.742	-0.0022	-1.8	6.72	21920.7	5.63	HUMAN	G3V2S6	V-type proton ATPase subunit D
3646	dirMS_041712_NAR_60mM_plus.20145.20183.3	3	14.27	0	4.68E+05		(R)DFLLKPE	(R)D F|L/L/K/P E L L/R(A)		165.73	415.2483	1243.741	-0.0105	-8.5	6.07	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
3647	dirMS_041712_NAR_60mM_plus.9541.9541.3	3	14.27	0	1.08E+06		(K)GHENVE	(K)G H E\N V\E\A\A|Q/A/E Y I E/K(F)		108.1	563.2692	1687.792	0.0008	0.5	4.48	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
3648	dirMS_041712_NAR_20mM_minus.11508.11553.2	2	14.26	0	1.03E+07	M148m	(R)DLTDYL	(R)D L|T|D|Y/L/m/K(I)	m:Oxidized methionine	162.28	507.7443	998.486	15.995	0.1	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
3649	dirMS_041712_NAR_30mM_minus2.11825.12161.2	2	14.26	0	5.97E+05		(R)SGYLLP	(R)S/G|Y|L|L|P D/T K(A)		118.77	497.265	993.525	-0.0024	-2.4	5.55	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
3650	dirMS_041712_NAR_60mM_minus.7285.7692.3	3	14.26	1	1.70E+06		(K)IQDKEG	(K)I Q/D K E G|I|P/P D/Q Q R(L)		99.7	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
3651	dirMS_041712_NAR_60mM_minus.8076.8094.3	3	14.26	1	1.61E+05		(K)DISTNY	(K)D I/S/T/N Y/Y/A/S/Q/K K(T)		105.07	473.231	1417.696	-0.0173	-12.2	8.43	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
3652	dirMS_041712_NAR_120mM_plus.6133.6300.3	3	14.26	0	7.89E+05		(K)QRPQAT	(K)Q/R/P Q\A|T/A/E/Q/I/R(L)		86.08	433.2367	1297.697	-0.0016	-1.2	9.6	113668.7	6.2	HUMAN	F8W726	Ubiquitin-associated protein 2-like
3653	dirMS_041712_NAR_20mM_plus.9055.9065.2	2	14.26	0	2.66E+05		(R)VLTVIN	(R)V L|T\V/I/N/Q/T Q|K(E)		133.07	572.3399	1143.673	-0.0007	-0.6	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
3654	dirMS_041712_NAR_20mM_plus.9333.9375.2	2	14.26	0	5.64E+05		(K)TIAPALV	(K)T I|A|P A L/V S K(K)		136.25	450.2814	899.556	-0.0005	-0.6	8.41	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
3655	dirMS_041712_NAR_40mM_plus2.13161.13300.3	3	14.26	0	1.97E+05		(R)DLSHIG	(R)D L S H I\G D\A\V|V|I/S/C/A K(D)	C:Carbamidomethylation	144.35	528.9395	1584.805	-0.0011	-0.7	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
3656	dirMS_041712_NAR_40mM_plus2.16019.16285.2	2	14.26	0	1.50E+05		(R)YLTVAA	(R)Y L|T|V/A/A V/F/R(G)		162.03	520.2997	1039.593	-0.0014	-1.3	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3657	dirMS_041712_NAR_60mM_plus.15998.15998.3	3	14.26	1	2.98E+05		(R)MSMKE	(R)M/S M K\E V D\E Q|M/L/N V Q N K(N)		139.27	641.9696	1923.897	-0.003	-1.6	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3658	dirMS_041712_NAR_120mM_minus.8475.8579.3	3	14.25	0	6.90E+05		(K)YKPESEE	(K)Y K|P E S E E|L/T/A/E/R(I)		100.73	484.5714	1451.701	-0.0016	-1.1	4.5	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
3659	dirMS_041712_NAR_20mM_minus.11736.11736.2	2	14.25	0	3.20E+05		(R)GALQNI	(R)G A L\Q|N|I|I\P A S/T G A A K(A)		165.35	706.3976	1411.79	-0.0024	-1.7	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
3660	dirMS_041712_NAR_50mM_minus2.10796.10819.3	3	14.25	1	6.04E+05		(R)IAEFTTN	(R)I/A|E/F/T/T|N L/T/E E E E K S K(S)		130.4	623.6418	1868.912	-0.0015	-0.8	4.32	227783.5	5.5	HUMAN	P35579	Myosin-9
3661	dirMS_041712_NAR_20mM_plus.13770.13952.2	2	14.25	0	2.82E+05		(R)INEILSN	(R)I/N|E|I|L/S N A L/K(R)		167.63	557.8267	1114.647	-0.0005	-0.5	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
3662	dirMS_041712_NAR_30mM_plus2.14308.14308.2	2	14.25	0	1.13E+04		(R)QLLEEEL	(R)Q L/L/E/E/E L/A R(L)		128.93	550.8009	1100.595	-0.0001	-0.1	4.25	533778	5.74	HUMAN	Q15149	Plectin
3663	dirMS_041712_NAR_30mM_plus2.16512.16512.2	2	14.25	0	3.03E+05		(K)LLDLVQ	(K)L L\D|L/V/Q/Q\S|C N Y K(Q)	C:Carbamidomethylation	139.13	740.8751	1480.746	-0.0035	-2.4	5.83	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
3664	dirMS_041712_NAR_30mM_plus2.21643.21643.2	2	14.25	0	3.07E+05		(R)FSWNV	(R)F S/W/N V W/P S S R(L)		169.08	633.3085	1265.606	0.0035	2.8	9.75	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
3665	dirMS_041712_NAR_40mM_plus2.15107.15500.3	3	14.25	0	9.12E+05		(R)DVQIGD	(R)D V\Q|I/G/D/I/V/T V/G E/C R P L S K(T)	C:Carbamidomethylation	157.25	662.6815	1986.033	-0.0025	-1.3	4.56	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
3666	dirMS_041712_NAR_50mM_plus2.15925.15925.3	3	14.25	1	1.41E+05		(K)VSEQGL	(K)V/S|E Q/G L I E I L K/K(V)		151.65	452.944	1356.81	0.0078	5.7	6.11	12899.6	6.59	HUMAN	K7EL31	Programmed cell death protein 5
3667	dirMS_041712_NAR_50mM_plus2.16450.16450.3	3	14.25	0	4.72E+05		(R)IETMLGI	(R)I/E\T M L G D|V A/V/A V/H|P K(D)		154.65	527.282	1579.851	-0.0198	-12.5	5.32	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
3668	dirMS_041712_NAR_60mM_plus.15419.15419.3	3	14.25	1	3.85E+05		(R)SLIANLA	(R)S L/I/A N/L/A A A/N C/Y K K(E)	C:Carbamidomethylation	137.43	512.9411	1536.82	-0.0115	-7.5	9.7	36978.6	6.33	HUMAN	B7Z800	Adenosine kinase
3669	dirMS_041712_NAR_60mM_plus.4797.4797.3	3	14.25	1	3.22E+05		(K)AGADEE	(K)A/G/A|D/E/E R A E/T A R(L)		79.42	425.868	1275.592	-0.0029	-2.3	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
3670	dirMS_041712_NAR_20mM_minus.14648.14648.2	2	14.24	0	2.02E+05		(K)TAVETA	(K)T A|V/E/T/A/V L\L L/R(I)		201.2	593.3613	1185.72	-0.0048	-4.1	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
3671	dirMS_041712_NAR_40mM_minus2.16101.16101.3	3	14.24	1	6.73E+05		(R)ELAILLG	(R)E L|A/I/L/L/G M/L/D/P A E K D E K(G)		189.58	629.0034	1884.999	-0.003	-1.6	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
3672	dirMS_041712_NAR_50mM_minus2.17031.17491.3	3	14.24	0	2.11E+07		(R)IHFPLAT	(R)I H\F\P L A\T\Y|A|P V/I/S A E K(A)		167.2	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
3673	dirMS_041712_NAR_50mM_minus2.7416.7416.3	3	14.24	0	6.77E+04		(K)STAGDT	(K)S/T|A/G D T H L/G G E D F D/N R(M)		108.82	564.5808	1691.726	0.0023	1.3	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
3674	dirMS_041712_NAR_120mM_plus.7912.8022.4	4	14.24	1	6.41E+05		(K)VLATVT	(K)V L\A T/V/T/K/P V G G D K/N/G G T R(V)		95.57	443.251	1769.987	-0.0047	-2.6	9.99	12738	10.72	HUMAN	F8VWR1	60S ribosomal protein L6 (Fragment)
3675	dirMS_041712_NAR_20mM_plus.12531.12607.3	3	14.24	0	3.48E+05		(K)IISNASC	(K)I I|S N\A\S C T T/N/C L/A/P L A K(V)	C:Carbamidomethylation	159.53	611.9768	1833.92	-0.0039	-2.1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
3676	dirMS_041712_NAR_20mM_plus.13791.13791.2	2	14.24	0	6.96E+04		(R)VEVTEF	(R)V/E|V/T E/F/E D/I K(S)		167.18	604.8056	1208.604	-0.0006	-0.5	4	30992.3	4.14	HUMAN	B2REB8	Protein SET
3677	dirMS_041712_NAR_20mM_plus.9068.9068.2	2	14.24	0	2.65E+05		(R)VLTVIN	(R)V L/T/V/I/N Q/T Q K(E)		133.08	572.3399	1143.673	-0.0007	-0.6	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
3678	dirMS_041712_NAR_50mM_plus2.17853.17855.3	3	14.24	0	2.58E+05		(R)IGRPSET	(R)I G R P S E T G\I|I G\I|I|D/P E C R(M)	C:Carbamidomethylation	161.9	661.6783	1983.033	-0.0124	-6.3	4.68	16255.6	5.76	HUMAN	F5GWI0	DNA damage-binding protein 1 (Fragment)
3679	dirMS_041712_NAR_60mM_plus.16676.16883.3	3	14.24	1	1.13E+06		(R)ELISNAS	(R)E L|I/S/N/A/S|D|A L D K I R(L)		144.67	515.6144	1544.828	0.0008	0.5	4.56	5582.4	4.81	HUMAN	F8W026	Endoplasmin (Fragment)
3680	dirMS_041712_NAR_60mM_plus.18889.18889.3	3	14.24	0	3.09E+05		(R)GGHVVE	(R)G G H V V E G L|A|G E/L E Q/L/R(A)		156.17	555.2949	1663.876	-0.0061	-3.6	4.75	106088.3	5.78	HUMAN	P10275	Androgen receptor
3681	dirMS_041712_NAR_60mM_plus.20611.20611.3	3	14.24	0	7.27E+05		(R)LGFHLP	(R)L/G\F H\L/P L E|V/A/Y/Q R(G)		168.62	514.9568	1542.843	0.0131	8.5	6.75	533778	5.74	HUMAN	Q15149	Plectin
3682	dirMS_041712_NAR_30mM_minus2.17509.17509.2	2	14.23	0	2.23E+05		(R)NGGQIL	(R)N G/G Q/I|L I/A D/L R(G)		149.25	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
3683	dirMS_041712_NAR_60mM_minus.6579.6579.3	3	14.23	0	5.72E+04		(K)ELVSDA	(K)E L/V/S\D/A/N Q|H/V/K(S)		95.22	413.8839	1239.633	0.0044	3.5	5.32	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
3684	dirMS_041712_NAR_20mM_plus.8012.8012.2	2	14.23	0	4.21E+05	M239m	(K)EVDEQ	(K)E V/D E Q/m L/N|V|Q\N/K(N)	m:Oxidized methionine	125.1	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3685	dirMS_041712_NAR_30mM_plus2.14793.14840.2	2	14.23	0	1.83E+05		(R)NWADV	(R)N/W|A|D|V/Q/S\Q L/R(H)		130.72	608.8101	1216.607	0.006	4.9	5.84	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
3686	dirMS_041712_NAR_40mM_plus2.10769.10909.3	3	14.23	0	9.41E+05		(R)LLEAQA	(R)L L|E|A/Q/A/C/T G G I/I H/P T T G Q K(L)	C:Carbamidomethylation	130.33	665.6807	1995.033	-0.0052	-2.6	6.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
3687	dirMS_041712_NAR_40mM_plus2.7869.7869.2	2	14.23	0	5.86E+05		(K)ASLENS	(K)A/S/L/E|N S L\R(E)		105.63	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3688	dirMS_041712_NAR_50mM_plus2.13465.13465.3	3	14.23	0	1.05E+06		(K)AASDIA	(K)A A\S D/I/A/M T/E/L/P P T H/P I R(L)		139.18	607.3177	1819.937	0.0015	0.8	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
3689	dirMS_041712_NAR_50mM_plus2.14623.14623.3	3	14.23	0	1.85E+05		(R)ISTLTIEE	(R)I/S/T/L/T/I E/E G/N L D I Q R P K(R)		144.78	643.0148	1927.05	-0.0196	-10.2	4.68	38649.2	6.88	HUMAN	Q12972	Nuclear inhibitor of protein phosphatase 1
3690	dirMS_041712_NAR_50mM_plus2.17919.18204.3	3	14.23	1	1.01E+06		(K)GPVREG	(K)G P V R E G D\V\L|T|L|L/E S E/R(E)		162.88	590.6519	1769.939	0.0019	1.1	4.41	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
3691	dirMS_041712_NAR_50mM_plus2.9860.9860.3	3	14.23	1	1.04E+06		(K)LKGEAT	(K)L K\G E A\T V|S/F/D D/P P S A K(A)		119.12	554.6155	1661.838	-0.0061	-3.7	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
3692	dirMS_041712_NAR_60mM_plus.6538.6538.3	3	14.23	1	6.89E+05		(R)NKQTYS	(R)N K Q T Y S|T E/P N/N L K(A)		92.93	512.9257	1536.765	-0.0027	-1.8	8.5	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
3693	dirMS_041712_NAR_120mM_minus.9915.9978.3	3	14.22	1	7.79E+05		(R)ETAEAD	(R)E/T/A/E/A D/V|A S L N R R(I)		108.67	477.9106	1431.719	-0.0014	-1	4.68	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
3694	dirMS_041712_NAR_30mM_minus2.14466.14684.2	2	14.22	0	5.00E+05		(R)TFEDFV	(R)T/F|E|D/F/V/R(I)		133.23	457.2246	913.441	0.0005	0.6	4.37	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
3695	dirMS_041712_NAR_30mM_minus2.7394.7394.2	2	14.22	0	2.50E+03		(R)TPEEYPE	(R)T/P|E|E Y/P E/S A K(V)		93.4	575.7705	1150.526	0.0075	6.5	4.25	21580.5	5.38	HUMAN	B4DGT0	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1
3696	dirMS_041712_NAR_30mM_minus2.8498.8542.2	2	14.22	0	6.85E+05		(R)QAEVEL	(R)Q/A\E/V/E/L/A/S/R(V)		100.67	501.7573	1002.521	-0.0141	-14.1	4.53	533778	5.74	HUMAN	Q15149	Plectin
3697	dirMS_041712_NAR_120mM_plus.7220.7332.3	3	14.22	1	7.86E+05		(R)KTGQAP	(R)K\T G Q A|P G\Y|S|Y\T/A A/N K(N)		91.62	519.5943	1556.77	-0.002	-1.3	9.53	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
3698	dirMS_041712_NAR_20mM_plus.17850.17850.2	2	14.22	0	1.59E+05		(R)TVQSLEI	(R)T V/Q|S/L/E|I D L D/S M R(N)		194.85	753.8776	1506.747	0.0011	0.7	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3699	dirMS_041712_NAR_30mM_plus2.14459.14660.2	2	14.22	0	5.85E+05		(K)IGLDFCK	(K)I/G|L/D|F/C/K(Y)	C:Carbamidomethylation	129.58	426.7164	852.428	-0.0029	-3.4	5.84	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
3700	dirMS_041712_NAR_40mM_plus2.20059.20059.3	3	14.22	1	5.88E+05		(K)EGGLGP	(K)E G G L/G/P/L/N/I/P L L A D V T R R(L)		189.8	631.0288	1891.076	-0.0041	-2.2	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
3701	dirMS_041712_NAR_50mM_plus2.14994.14994.3	3	14.22	1	1.14E+05		(R)LLDAQL	(R)L L|D/A/Q L/A T/G G L|V C P A R R(L)	C:Carbamidomethylation	147.2	604.3351	1810.996	-0.0049	-2.7	9.6	266161	5.68	HUMAN	E9PPU0	Epiplakin

3702	dirMS_041712_NAR_50mM_plus2.17527.17527.3	3	14.22	0	9.60E+05		(R)VLDPFTI	(R)V/L/D/P/F/T I/K P L D R(K)		160.52	471.9408	1413.81	-0.0022	-1.5	5.93	63448.4	7.29	HUMAN	B4E022	Transketolase
3703	dirMS_041712_NAR_30mM_minus2.17986.17986.2	2	14.21	0	2.20E+05		(K)EGMNIV	(K)E G M/N/I|V E A M E/R(F)		152.3	639.7955	1278.582	0.002	1.6	4.25	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
3704	dirMS_041712_NAR_50mM_minus2.12779.12779.3	3	14.21	1	3.77E+05		(K)NTVELL	(K)N T/V/E/L/L V E D/K G N Q V Y R(C)		140.5	626.3309	1876.976	0.0018	1	4.68	258215.9	5.48	HUMAN	E7EN95	Filamin-B
3705	dirMS_041712_NAR_50mM_minus2.5850.5850.3	3	14.21	0	1.31E+05		(R)AGAAG	(R)A G\A|A/G/G P E/E E A E/K P V K(T)		95.32	513.9233	1539.765	-0.0096	-6.2	4.49	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
3706	dirMS_041712_NAR_120mM_plus.11006.11006.4	4	14.21	0	8.17E+05		(R)GAIQFV	(R)G A|I\Q/F/V/T H/Y Q H/S S T Q R(R)		111.07	465.7339	1859.915	-0.0009	-0.5	8.76	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
3707	dirMS_041712_NAR_20mM_plus.12007.12024.2	2	14.21	0	6.74E+04		(K)VLIANN	(K)V L|I|A|N/N G I A/A/V K(C)		155.83	591.8632	1182.72	-0.0014	-1.2	8.72	269989.9	5.92	HUMAN	F8W8T8	Acetyl-CoA carboxylase 2
3708	dirMS_041712_NAR_30mM_plus2.10320.10320.2	2	14.21	0	5.06E+05		(K)EQVANS	(K)E Q/V/A/N/S/A F V E/R(C)		107.17	625.311	1249.617	-0.0024	-1.9	4.53	17664	8.77	HUMAN	H0Y6E4	Heat shock protein HSP 90-beta (Fragment)
3709	dirMS_041712_NAR_50mM_plus2.15516.15516.3	3	14.21	0	1.51E+06		(R)LASTLVH	(R)L A|S T L|V/H L\G E/Y Q A/A/V/D G A R(K)		149.68	657.6802	1971.029	-0.0034	-1.7	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
3710	dirMS_041712_NAR_50mM_plus2.6030.6030.3	3	14.21	0	8.84E+04		(R)ITPPAAK	(R)I T|P/P A A\K/P G S P Q A K(S)		95.85	454.9298	1362.774	0.0009	0.6	10	214357.5	7.19	HUMAN	P35658	Nuclear pore complex protein Nup214
3711	dirMS_041712_NAR_60mM_plus.12970.12992.3	3	14.21	1	4.93E+05		(K)FMLGK	(K)F/M/L/G/K/Q/E V/I/R(G)		124.43	407.5638	1220.682	-0.0051	-4.2	8.75	10155.5	5.89	HUMAN	A8MSS1	Peptidyl-prolyl cis-trans isomerase
3712	dirMS_041712_NAR_60mM_plus.6889.6957.3	3	14.21	1	5.25E+05		(K)LADLEQ	(K)L/A|D|L/E/Q/E/Q/S S K R(L)		94.5	468.5804	1403.713	0.0141	10.1	4.68	64248.4	9.08	HUMAN	Q9BW04	Specifically androgen-regulated gene protein
3713	dirMS_041712_NAR_30mM_minus2.13509.13654.2	2	14.2	0	6.19E+05		(K)TCTFILR	(K)T/C|T/F/I/L/R(G)	C:Carbamidomethylation	127.5	455.7458	910.481	0.0028	3.1	9.41	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
3714	dirMS_041712_NAR_30mM_minus2.13556.13556.2	2	14.2	0	1.78E+05	M357m	(R)FFmGN	(R)F/F|m|G N/Q V L/K(V)	m:Oxidized methionine	128.15	550.2855	1083.566	15.9982	3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
3715	dirMS_041712_NAR_30mM_minus2.18852.18852.2	2	14.2	0	5.41E+04		(R)CGGIQY	(R)C G G\I/Q|Y|L/Q|N A/I E S R(Q)	C:Carbamidomethylation	157.12	804.8951	1608.78	0.0031	1.9	6	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
3716	dirMS_041712_NAR_50mM_minus2.17698.17815.3	3	14.2	1	3.97E+05		(R)LKLPSIP	(R)L K L P S I|P\L|V|P V/S A Q K(R)		169.73	530.669	1589.999	-0.0064	-4.1	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
3717	dirMS_041712_NAR_60mM_minus.8998.8998.2	2	14.2	0	9.67E+05		(K)QEYDES	(K)Q E|Y/D/E/S/G|P S I/V H R(K)		110.35	758.8539	1516.703	-0.0021	-1.4	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
3718	dirMS_041712_NAR_30mM_plus2.6298.6298.2	2	14.2	0	3.31E+05	M369m	(R)FGSGMN	(R)F/G|S/G M N m/G R(I)	m:Oxidized methionine	87.53	486.7048	956.408	15.9946	-0.3	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
3719	dirMS_041712_NAR_30mM_plus2.8303.8679.2	2	14.2	0	1.26E+06		(R)TLLEGEE	(R)T L|L|E|G/E E/S/R(M)		98.95	517.2613	1033.516	-0.0007	-0.7	4.25	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
3720	dirMS_041712_NAR_40mM_plus2.11505.11505.3	3	14.2	0	5.67E+04		(R)LDDTVH	(R)L/D\D/T V/H V/V/I/A T/P G R(I)		134.08	498.2739	1492.812	-0.0047	-3.1	5.21	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
3721	dirMS_041712_NAR_50mM_plus2.12914.12914.3	3	14.2	1	3.26E+05		(R)ELAVQI	(R)E L/A/V/Q/I Y E/E A R K(F)		135.57	483.5916	1448.774	-0.0141	-9.7	4.79	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
3722	dirMS_041712_NAR_50mM_plus2.17612.17676.3	3	14.2	1	1.27E+06		(R)VTFSGL	(R)V/T|F/S/G L R D T\V|T/P G E L L K(A)		160.82	611.6724	1833.012	-0.009	-4.9	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
3723	dirMS_041712_NAR_120mM_minus.12496.13020.3	3	14.19	1	3.70E+06		(K)VKLEAEI	(K)V K L E A E|I|A/T/Y/R(R)		123.3	431.5783	1292.721	-0.0005	-0.4	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3724	dirMS_041712_NAR_20mM_minus.9272.9280.3	3	14.19	0	3.43E+05		(R)AQIFAN	(R)A Q\I\F A/N|T|V/D/N A/R(I)		142.32	440.5612	1319.67	-0.0012	-0.9	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3725	dirMS_041712_NAR_30mM_minus2.7300.7446.2	2	14.19	0	5.44E+06		(K)LLEGEES	(K)L/L|E|G E/E/S/R(I)		94.55	466.7386	932.468	0.0016	1.7	4.25	49709.6	5.19	HUMAN	B0YJC4	Vimentin
3726	dirMS_041712_NAR_50mM_minus2.11313.11313.3	3	14.19	1	2.04E+05		(K)MLVSGA	(K)M/L\V/S/G A G D I/K/L T/K(D)		132.4	444.9227	1332.756	-0.002	-1.5	8.35	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
3727	dirMS_041712_NAR_50mM_minus2.12907.12907.3	3	14.19	1	1.79E+05		(K)GGELVY	(K)G G\E|L/V/Y/T D/S E A R D/V F E K(A)		141.53	638.9739	1914.908	-0.0008	-0.4	4.18	533778	5.74	HUMAN	Q15149	Plectin
3728	dirMS_041712_NAR_60mM_minus.17438.17438.3	3	14.19	0	2.98E+05		(K)GSDHSA	(K)G S D H S A S L E|P G E|L A/E L V R(S)		156.93	622.9764	1866.919	-0.0045	-2.4	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
3729	dirMS_041712_NAR_30mM_plus2.20820.20820.2	2	14.19	0	2.76E+05		(R)ASLSLW	(R)A S/L/S/L|W Q A\M/E K(G)		163.05	632.3231	1263.64	-0.0013	-1	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
3730	dirMS_041712_NAR_50mM_plus2.16049.16131.3	3	14.19	1	5.32E+05		(K)YAVLYQ	(K)Y/A|V|L/Y Q/P L F D/K R(F)		152.5	504.9436	1512.821	-0.0047	-3.1	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
3731	dirMS_041712_NAR_50mM_plus2.16840.16840.3	3	14.19	1	2.93E+05	M148m	(R)LDLAGR	(R)L/D/L/A/G R D L/T D Y\L m K(I)	m:Oxidized methionine	156.47	547.2842	1623.841	15.997	1.3	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
3732	dirMS_041712_NAR_50mM_plus2.18987.18987.3	3	14.19	1	2.90E+05		(K)LALFQAI	(K)L/A|L/F/Q A I G K E V V D/R(A)		168.05	520.3019	1558.895	-0.004	-2.6	6.07	266161	5.68	HUMAN	E9PPU0	Epiplakin
3733	dirMS_041712_NAR_20mM_minus.11219.11464.2	2	14.18	0	1.17E+07	M148m	(R)DLTDYL	(R)D L|T|D/Y/L/m/K(I)	m:Oxidized methionine	162.17	507.7443	998.486	15.995	0.1	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
3734	dirMS_041712_NAR_20mM_minus.14469.14469.3	3	14.18	0	2.19E+05		(K)LAAELSA	(K)L A A E\L S A T\L|E/Q A/A/A/T A R(V)		198.9	562.9713	1686.902	-0.0027	-1.6	4.53	558007.1	5.44	HUMAN	P58107	Epiplakin
3735	dirMS_041712_NAR_50mM_minus2.16950.16950.3	3	14.18	1	2.20E+05		(K)SLLGKD	(K)S L|L/G/K D V L F/L K(D)		164.27	411.5911	1232.761	-0.0025	-2.1	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
3736	dirMS_041712_NAR_50mM_minus2.9075.9093.3	3	14.18	0	1.48E+05		(R)TITVALA	(R)T I|T/V/A|L A/D/G G R/P D N T G R(G)		120.08	571.9667	1713.888	-0.0023	-1.3	5.63	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
3737	dirMS_041712_NAR_60mM_minus.14433.14433.3	3	14.18	1	1.62E+05		(R)IQLVEEE	(R)I Q|L/V/E E E/L D R A Q E R(L)		139.57	576.6347	1727.892	-0.0027	-1.6	4.25	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
3738	dirMS_041712_NAR_20mM_plus.16240.16332.2	2	14.18	0	3.80E+05	M221m	(R)ALTVPEL	(R)A L|T|V|P E L T/Q Q/m F D\A K(N)	m:Oxidized methionine	184.3	854.4341	1691.867	15.9936	-0.7	4.37	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
3739	dirMS_041712_NAR_30mM_plus2.5774.5774.2	2	14.18	0	2.51E+05		(K)TSEVNC	(K)T|S|E|V/N C/Y R(C)	C:Carbamidomethylation	85.05	514.7261	1028.447	-0.0016	-1.6	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
3740	dirMS_041712_NAR_50mM_plus2.19152.19152.3	3	14.18	1	1.72E+06		(K)LIQLME	(K)L I|Q/L M/E/E I M A E K E/N K(T)		169.7	606.9845	1818.934	0.005	2.7	4.49	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
3741	dirMS_041712_NAR_50mM_plus2.6561.6561.3	3	14.18	0	6.49E+05	M434m	(R)LESGm	(R)L/E|S G/m Q N/M S I/H\T K(T)	m:Oxidized methionine	98.9	497.9026	1475.698	15.9951	0.1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
3742	dirMS_041712_NAR_60mM_plus.15213.15482.3	3	14.18	0	9.78E+05		(R)TVVTGIE	(R)T V|V/T|G I/E M/F/H K(S)		137	421.2292	1261.661	0.0121	9.6	6.41	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
3743	dirMS_041712_NAR_60mM_plus.17637.17637.3	3	14.18	1	4.81E+05		(R)LMDLLG	(R)L/M/D\L/L/G E\G L K/R(S)		149.12	415.5712	1244.703	-0.0041	-3.3	6.07	52817.9	6.2	HUMAN	F5H3T8	Arginine--tRNA ligase, cytoplasmic
3744	dirMS_041712_NAR_60mM_plus.7158.7158.2	2	14.18	0	1.72E+06		(K)STTTGHI	(K)S T/T/T/G H L I|Y/K(C)		95.58	560.8031	1120.6	-0.0008	-0.7	8.34	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
3745	dirMS_041712_NAR_30mM_minus2.13974.13974.2	2	14.17	0	3.15E+05		(R)LAGLFN	(R)L A|G\L/F N E/Q R(K)		129.43	524.2789	1047.558	-0.0076	-7.3	6	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
3746	dirMS_041712_NAR_40mM_minus2.11311.11370.3	3	14.17	0	1.95E+05		(K)LVTSIGD	(K)L V|T/S/I/G D V/V N H D/P V V G D R(L)		150.32	631.3335	1891.987	-0.0013	-0.7	4.41	27786.2	5.93	HUMAN	H0Y4Z6	Phosphorylase (Fragment)
3747	dirMS_041712_NAR_50mM_minus2.9405.9405.3	3	14.17	0	2.72E+05		(K)TGVAVN	(K)T\G/V|A V/N K/P A E\F T V D/A K(H)		122.03	549.6316	1646.875	0.0054	3.3	5.73	283472.4	5.71	HUMAN	P21333	Filamin-A
3748	dirMS_041712_NAR_60mM_minus.4809.4809.3	3	14.17	1	7.13E+05	M137m	(R)mQNDT	(R)m Q/N D/T A E N E T/T E/K E|E K(S)	m:Oxidized methionine	79.37	638.2735	1896.813	15.9932	-0.9	4.14	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
3749	dirMS_041712_NAR_60mM_minus.5863.5863.2	2	14.17	1	2.81E+06		(K)DSYVGD	(K)D S|Y|V/G D|E A/Q S K R(G)		88.47	677.8144	1354.623	-0.0018	-1.3	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
3750	dirMS_041712_NAR_30mM_plus2.12016.12115.2	2	14.17	0	6.51E+05		(K)SSLGPV	(K)S S|L/G|P V/G L/D K(M)		116.38	486.775	972.536	0.0067	6.9	5.55	47423	5.43	HUMAN	E7ERF2	T-complex protein 1 subunit alpha
3751	dirMS_041712_NAR_40mM_plus2.17048.17048.3	3	14.17	0	4.41E+05		(R)IHFPLAT	(R)I H/F P L A T Y/A/P V I/S A E K(A)		167.57	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
3752	dirMS_041712_NAR_40mM_plus2.9024.9024.3	3	14.17	0	5.80E+04		(R)AALAHS	(R)A A L A H S E E\V|T|A/S Q/V/A A T K(T)		115.18	595.3161	1783.919	0.0153	8.6	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
3753	dirMS_041712_NAR_60mM_plus.8369.8371.3	3	14.17	1	6.44E+05		(K)EPLYEK	(K)E P/L/Y/E/K/D S\S/V/A A/R(F)		102.25	488.9148	1464.733	-0.0031	-2.1	4.68	26283.8	8.96	HUMAN	O43809	Cleavage and polyadenylation specificity factor subunit 5
3754	dirMS_041712_NAR_120mM_minus.8483.8483.3	3	14.16	1	4.31E+05		(R)YLAEVA	(R)Y/L/A/E V A/T/G E/K/R(A)		100.85	412.8849	1236.658	-0.0181	-14.7	6.14	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
3755	dirMS_041712_NAR_30mM_minus2.15680.15680.2	2	14.16	0	9.77E+04		(R)GSTDNL	(R)G S T D/N/L|M/D/D I E/R(A)		138.77	683.3009	1365.595	-0.0006	-0.4	3.84	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
3756	dirMS_041712_NAR_30mM_minus2.8605.8704.2	2	14.16	0	8.94E+05		(K)VLTPTQ	(K)V L|T|P/T Q V K(N)		101.9	443.2733	885.54	-0.0011	-1.2	8.72	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
3757	dirMS_041712_NAR_40mM_minus2.11322.11322.3	3	14.16	0	2.05E+04		(K)VALLLLD	(K)V A/L L|L/L D\Q/G A S P|H A A/A K(N)		150	558.9882	1674.954	-0.0037	-2.2	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
3758	dirMS_041712_NAR_40mM_minus2.14260.14260.3	3	14.16	1	1.72E+05		(K)ITSDEPL	(K)I/T|S D E/P L T K D D I/P V F L R(H)		168.37	653.6833	1959.043	-0.008	-4.1	4.23	22313.1	4.9	HUMAN	B1AHE4	Ataxin 10 (Fragment)
3759	dirMS_041712_NAR_50mM_minus2.10500.10500.3	3	14.16	0	2.85E+05	M35m	(K)AASDIA	(K)A A|S D I/A m/T E/L|P/P T/H/P I R(L)	m:Oxidized methionine	127.88	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
3760	dirMS_041712_NAR_60mM_minus.17285.17448.3	3	14.16	0	3.22E+05		(K)GSDHSA	(K)G S D H\S A S L E|P G/E|L/A/E L V R(S)		156.83	622.9764	1866.919	-0.0045	-2.4	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
3761	dirMS_041712_NAR_60mM_minus.6811.7266.3	3	14.16	0	1.27E+06	M434m	(R)LESGm	(R)L/E|S/G m\Q/N M/S I/H/T K(T)	m:Oxidized methionine	97.23	497.9023	1475.698	15.9942	-0.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
3762	dirMS_041712_NAR_60mM_minus.9089.9089.2	2	14.16	0	9.67E+05		(K)QEYDES	(K)Q E|Y D/E/S/G P S/I V/H/R(K)		110.35	758.8539	1516.703	-0.0021	-1.4	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
3763	dirMS_041712_NAR_50mM_plus2.16314.16314.3	3	14.16	1	7.02E+05		(K)CEFQDA	(K)C E/F/Q D A|Y\V/L/L S E K K(I)	C:Carbamidomethylation	152.62	577.2866	1729.847	-0.0013	-0.8	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
3764	dirMS_041712_NAR_30mM_minus2.8001.8001.2	2	14.15	0	1.36E+05		(K)SLAAEEE	(K)S L|A|A/E/E E/A A/R(Q)		96.82	523.7597	1046.511	0.0008	0.8	4.25	533778	5.74	HUMAN	Q15149	Plectin
3765	dirMS_041712_NAR_50mM_minus2.15892.15892.3	3	14.15	0	9.69E+04		(K)INLEAAE	(K)I/N|L E/A A E L G E/I/S D I H/T K(L)		158.72	618.326	1852.965	-0.0016	-0.9	4.4	84268.2	6.32	HUMAN	Q9UHD2	Serine/threonine-protein kinase TBK1
3766	dirMS_041712_NAR_60mM_minus.12240.12240.3	3	14.15	0	2.05E+05		(K)LAQANG	(K)L A/Q|A N G W/G V/M V/S H/R(S)		128.17	509.2631	1525.769	0.0055	3.6	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
3767	dirMS_041712_NAR_120mM_plus.12619.13106.3	3	14.15	1	3.54E+06		(K)VKLEAEI	(K)V K L E\A\E|I|A/T/Y/R(R)		121.43	431.5774	1292.721	-0.0032	-2.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3768	dirMS_041712_NAR_30mM_plus2.9838.9838.2	2	14.15	0	2.05E+05		(K)LNCSPD	(K)L/N|C|S|P D/S F R(C)	C:Carbamidomethylation	104.85	548.2495	1095.489	0.003	2.7	5.84	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
3769	dirMS_041712_NAR_50mM_plus2.13165.13165.3	3	14.15	1	9.66E+05		(R)ELNITAA	(R)E L/N I/T\A/A K E/I/E/V/G G G R(K)		137.7	552.9671	1656.892	-0.0048	-2.9	4.79	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
3770	dirMS_041712_NAR_50mM_plus2.17479.17479.3	3	14.15	0	6.37E+05		(R)IMEVID	(R)I/M|E V/I D/A I/T T T A Q S H Q R(T)		160.35	638.6636	1913.975	0.0013	0.7	5.32	85815.7	7.35	HUMAN	P17858	6-phosphofructokinase, liver type
3771	dirMS_041712_NAR_50mM_plus2.19270.19270.3	3	14.15	1	4.32E+05		(R)LKVPPAI	(R)L K/V/P P A I\N Q/F/T Q A L D R(Q)		169.82	604.3351	1811.017	-0.0266	-14.7	8.75	30166.2	10.79	HUMAN	P62424	60S ribosomal protein L7a
3772	dirMS_041712_NAR_50mM_plus2.19657.19657.3	3	14.15	0	4.09E+04		(K)IFTPIVE	(K)I F/T/P I/V/E H L G L Q/I R(F)		173.07	545.9893	1635.958	-0.0047	-2.9	6.75	15289.3	10.14	HUMAN	F8WBJ6	RNA-binding protein PNO1
3773	dirMS_041712_NAR_50mM_plus2.19896.19896.3	3	14.15	1	8.17E+04		(R)ILTEAEI	(R)I/L|T E A/E I/D A/H L V A L A E R D(-)		172.9	660.3539	1979.044	0.0028	1.4	4.33	19157.6	5.18	HUMAN	B4DQR4	Proteasome subunit alpha type-6
3774	dirMS_041712_NAR_60mM_plus.11672.11672.3	3	14.15	1	2.93E+06		(K)KAEAGA	(K)K A E A G A G S\A/T/E/F/Q/F/R(G)		118.23	523.9277	1569.766	0.003	1.9	6.14	18897.4	10.15	HUMAN	P46783	40S ribosomal protein S10
3775	dirMS_041712_NAR_60mM_plus.9421.9421.3	3	14.15	1	4.42E+05		(K)CLDENL	(K)C/L|D|E/N L E/D A S Q C K K(L)	C:Carbamidomethylation	107.22	570.5876	1709.747	0.0013	0.8	4.32	14458.2	9.22	HUMAN	Q5JTJ3	Cytochrome c oxidase assembly factor 6 homolog
3776	dirMS_041712_NAR_20mM_minus.9727.9738.2	2	14.14	0	2.44E+05		(K)LVIITAG	(K)L V|I|I/T/A G/A R(Q)		147.62	457.2947	913.583	-0.0008	-0.9	9.75	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
3777	dirMS_041712_NAR_60mM_minus.15709.15849.3	3	14.14	1	3.91E+05		(K)KANLQI	(K)K A N L Q\I D\Q\I|N|T|D/L/N L E R(S)		148.05	666.6911	1998.061	-0.0027	-1.3	4.56	227783.5	5.5	HUMAN	P35579	Myosin-9
3778	dirMS_041712_NAR_60mM_minus.9149.9149.3	3	14.14	1	5.12E+04		(R)QLEEAEI	(R)Q L/E/E/A/E E E/A Q/R A N\A S R(R)		110.88	610.9566	1830.858	-0.0024	-1.3	4.33	227783.5	5.5	HUMAN	P35579	Myosin-9
3779	dirMS_041712_NAR_40mM_plus2.11789.11789.3	3	14.14	1	2.76E+05		(R)IVAPGK	(R)I V|A/P G\K G/I L A A D\E/S T G S I A K(R)		135.42	633.3568	1898.059	-0.0035	-1.8	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
3780	dirMS_041712_NAR_50mM_plus2.15958.15958.3	3	14.14	1	7.30E+05		(R)LKLPAV	(R)L K\L P A\V|V/T/A/D/L/R(L)		152.03	432.6039	1295.805	-0.0074	-5.7	8.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
3781	dirMS_041712_NAR_60mM_plus.13334.13562.3	3	14.14	1	5.66E+05		(R)ISVYYNE	(R)I/S|V/Y/Y N E/A/T G G K Y V P R(A)		128.32	606.3113	1816.923	-0.0035	-1.9	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
3782	dirMS_041712_NAR_60mM_plus.9405.9405.2	2	14.14	0	1.98E+06		(R)IGAEVY	(R)I/G|A|E V/Y/H N L/K(N)		107.55	572.3143	1143.616	0.0056	4.9	6.75	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
3783	dirMS_041712_NAR_50mM_minus2.17262.17431.3	3	14.13	0	2.00E+05		(R)DFLLKPE	(R)D F|L|L/K/P E L/L R(A)		167.07	415.255	1243.741	0.0096	7.7	6.07	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
3784	dirMS_041712_NAR_50mM_minus2.9377.9394.3	3	14.13	0	2.61E+05		(K)TGVAVN	(K)T/G\V|A|V/N K/P A E F/T V D/A K(H)		121.98	549.6316	1646.875	0.0054	3.3	5.73	283472.4	5.71	HUMAN	P21333	Filamin-A
3785	dirMS_041712_NAR_20mM_plus.12987.12987.2	2	14.13	0	1.49E+05		(R)LVVPAS	(R)L V|V|P A S Q C G S L I/G K(G)	C:Carbamidomethylation	161.83	714.8991	1428.788	0.003	2.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
3786	dirMS_041712_NAR_20mM_plus.16767.16767.2	2	14.13	0	4.11E+05		(K)LGGSAV	(K)L G G/S|A/V|I/S L/E\G\K|P L(-)		186.02	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
3787	dirMS_041712_NAR_40mM_plus2.13255.13255.3	3	14.13	1	2.42E+06		(K)VGEVIV	(K)V/G|E/V I V/T K D D A M L L/K(G)		145.27	544.307	1630.908	-0.002	-1.2	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
3788	dirMS_041712_NAR_50mM_plus2.14453.14538.3	3	14.13	1	1.66E+04		(K)NLKVTA	(K)N L K V T A\V/P/T/L L/K(Y)		143.12	432.9459	1296.825	-0.0018	-1.4	10	11462.8	5.18	HUMAN	I3L2R6	Thioredoxin domain-containing protein 17
3789	dirMS_041712_NAR_50mM_plus2.16274.16274.3	3	14.13	1	1.28E+05		(K)ILLAELE	(K)I/L/L/A|E L/E Q L K G Q G K(S)		153.83	513.9741	1539.911	-0.0027	-1.8	6.14	49709.6	5.19	HUMAN	B0YJC4	Vimentin
3790	dirMS_041712_NAR_50mM_plus2.21004.21345.3	3	14.13	0	8.90E+06		(R)LHFFMP	(R)L H\F\F\M\P/G\F|A|P\L/T S R(G)		181.53	540.9498	1620.835	-0.0007	-0.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
3791	dirMS_041712_NAR_50mM_plus2.6622.6622.3	3	14.13	1	1.11E+05		(R)ITGDPY	(R)I/T|G D/P/Y/K/V Q/Q A K(E)		99.47	449.9102	1347.727	-0.0106	-7.9	8.5	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
3792	dirMS_041712_NAR_60mM_plus.20121.20121.3	3	14.13	0	1.33E+06		(R)IHFPLAT	(R)I H F P L A\T Y/A/P/V I/S A E K(A)		165.92	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
3793	dirMS_041712_NAR_30mM_minus2.15942.15942.2	2	14.12	0	3.59E+05		(R)FGLNVS	(R)F/G|L/N/V/S S I S R(K)		140.05	540.2895	1079.584	-0.0127	-11.7	9.75	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
3794	dirMS_041712_NAR_40mM_minus2.11209.11209.3	3	14.12	1	1.92E+04	M250m	(R)DSDIIED	(R)D S/D|I/I/E D/V m V K/D L Q K(L)	m:Oxidized methionine	149.23	588.6311	1747.878	16.0005	3.2	4.04	55757.3	5.55	HUMAN	O94919	Endonuclease domain-containing 1 protein
3795	dirMS_041712_NAR_60mM_minus.14911.14911.3	3	14.12	1	3.69E+05		(R)IKIGDPL	(R)I K I G D\P\L|L/E/D/T R(M)		142.82	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
3796	dirMS_041712_NAR_120mM_plus.23964.24093.3	3	14.12	1	1.51E+05		(K)EIIDLVL	(K)E I/I/D/L/V/L D/R I/R(K)		180.03	452.2725	1354.805	-0.0023	-1.7	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
3797	dirMS_041712_NAR_30mM_plus2.11689.11689.2	2	14.12	0	5.34E+05		(K)VASGCLI	(K)V/A|S/G/C/L/D I/N S S V K(G)	C:Carbamidomethylation	114.8	675.3393	1349.673	-0.0016	-1.2	5.81	56837	7.19	HUMAN	E7ETT1	Propionyl-CoA carboxylase beta chain, mitochondrial
3798	dirMS_041712_NAR_30mM_plus2.14815.15006.2	2	14.12	0	2.30E+06		(K)DVNAAL	(K)D/V|N|A|A/I/A A I K(T)		130.12	493.2867	985.568	-0.0015	-1.6	5.84	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
3799	dirMS_041712_NAR_40mM_plus2.10721.10721.3	3	14.12	1	4.29E+05		(R)DGKLVS	(R)D G K\L/V S E|S/S/D V L/P K(-)		128.63	491.9315	1473.78	0.0004	0.3	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
3800	dirMS_041712_NAR_40mM_plus2.15936.15936.3	3	14.12	0	2.88E+05		(K)VAIVKP	(K)V A|I\V\K P G V/P/M|E/I V L N K(E)		160.9	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
3801	dirMS_041712_NAR_40mM_plus2.8276.8276.2	2	14.12	1	8.43E+04		(R)KQNDVF	(R)K Q N D/V/F/G E\A|E/Q(-)		109.62	632.7929	1264.58	-0.0019	-1.5	4.14	51209.4	5	HUMAN	P31150	Rab GDP dissociation inhibitor alpha
3802	dirMS_041712_NAR_50mM_plus2.17304.17304.3	3	14.12	1	4.93E+05		(K)LLVYEAL	(K)L/L|V/Y E A L/E Y A K/R(A)		159.23	489.9441	1467.821	-0.0028	-1.9	6.14	32535.6	9.19	HUMAN	B4DZW6	Regulator of microtubule dynamics protein 1
3803	dirMS_041712_NAR_50mM_plus2.7421.7421.3	3	14.12	2	2.21E+05		(K)KAVDED	(K)K/A V/D E D/P/E N/Q T/L R K(D)		105.35	548.2865	1642.84	0.0055	3.3	4.79	87525.2	4.91	HUMAN	B1AKU4	Kinesin-associated protein 3
3804	dirMS_041712_NAR_60mM_plus.5631.5631.3	3	14.12	0	1.11E+06		(K)TATPQQ	(K)T A|T/P Q Q A Q/E/V/H E K(L)		87.6	489.5727	1466.723	-0.0198	-13.5	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
3805	dirMS_041712_NAR_30mM_minus2.12659.12988.2	2	14.11	0	1.09E+06		(K)FSVSPV	(K)F/S|V/S|P\V/V/R(V)		123.77	445.759	890.509	0.0013	1.5	9.75	96306.4	6.41	HUMAN	P13639	Elongation factor 2
3806	dirMS_041712_NAR_30mM_minus2.14003.14187.2	2	14.11	0	4.29E+05		(R)VVFQEF	(R)V/V|F/Q/E|F/R(Q)		130.25	462.7452	924.494	-0.0107	-11.5	5.97	227783.5	5.5	HUMAN	P35579	Myosin-9
3807	dirMS_041712_NAR_50mM_minus2.17773.17773.3	3	14.11	1	1.01E+05		(K)ITQDIFQ	(K)I/T/Q/D/I/F/Q Q L L K/R(G)		169.85	501.6277	1502.869	-0.0004	-0.3	8.75	72796.9	6.75	HUMAN	A6NC17	Methionine--tRNA ligase, cytoplasmic
3808	dirMS_041712_NAR_120mM_plus.8323.8324.3	3	14.11	1	4.48E+05		(K)SSGGRE	(K)S/S G/G R E D\L|E|S/S/G L Q/R(R)		97.07	526.5882	1577.751	-0.0014	-0.9	4.68	11625.5	8.01	HUMAN	B8ZZT7	Hematological and neurological-expressed 1 protein
3809	dirMS_041712_NAR_120mM_plus.8610.8631.3	3	14.11	0	2.11E+06		(K)HTGPNS	(K)H T\G P N\S\P D T|A/N/D/G F/V/R(L)		98.97	562.26	1684.767	-0.0019	-1.2	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
3810	dirMS_041712_NAR_30mM_plus2.12482.12482.2	2	14.11	0	4.58E+05		(R)QGVDA	(R)Q G/V|D|A/D I|N G\L R(Q)		118.12	579.2997	1157.591	0.0012	1	4.21	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9

3811	dirMS_041712_NAR_30mM_plus2.6340.6695.2	2	14.11	0	1.66E+06		(K)LLEGEES	(K)L/L|E|G/E/E/S/R(I)		88.35	466.7379	932.468	0.0002	0.2	4.25	49709.6	5.19	HUMAN	B0YJC4	Vimentin
3812	dirMS_041712_NAR_30mM_plus2.7569.7578.2	2	14.11	0	5.36E+05		(K)IANPVE	(K)I/A|N|P/V/E/G S S G R(Q)		93.97	543.7824	1086.554	0.0037	3.4	6	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
3813	dirMS_041712_NAR_40mM_plus2.19385.19480.3	3	14.11	1	4.58E+05		(K)ALFEEVF	(K)A L|F|E/E V/P E L L T E A E K K(E)		181.77	615.9991	1845.984	-0.0017	-0.9	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
3814	dirMS_041712_NAR_50mM_plus2.17743.17784.3	3	14.11	0	6.69E+05		(K)ALVSHN	(K)A L V S H N G S\L\I|N|V|G S/L/L Q/R(A)		161.37	626.6872	1878.056	-0.0085	-4.5	9.8	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
3815	dirMS_041712_NAR_120mM_minus.7833.7865.3	3	14.1	1	5.78E+05		(R)LQSIGTE	(R)L/Q|S|I/G/T E/N T/E E N R R(F)		97.25	549.607	1646.809	-0.0028	-1.7	4.79	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
3816	dirMS_041712_NAR_20mM_minus.12285.12285.2	2	14.1	0	4.02E+05	M73m	(R)AVLVDLI	(R)A V L|V D\L/E|P G T\m D S V/R(S)	m:Oxidized methionine	172.08	809.4088	1601.82	15.99	-3	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
3817	dirMS_041712_NAR_30mM_minus2.17506.17506.2	2	14.1	0	4.67E+05		(K)LLCGLLA	(K)L L|C/G|L L/A E/R(L)	C:Carbamidomethylation	149.98	522.7963	1044.587	-0.0017	-1.6	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
3818	dirMS_041712_NAR_50mM_minus2.6103.6117.3	3	14.1	0	4.44E+05	M437m	(R)LESGMC	(R)L/E|S\G/M Q/N m S I/H/T K(T)	m:Oxidized methionine	97.77	497.9018	1475.698	15.9927	-1.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
3819	dirMS_041712_NAR_60mM_minus.11918.11918.3	3	14.1	0	1.45E+05		(R)DAYSGG	(R)D A/Y/S/G/G/A V/N/L Y/H V R(E)		126.78	507.9181	1521.745	-0.0047	-3.1	6.74	17952.8	6.73	HUMAN	E9PAV2	Proteasome subunit beta type-5
3820	dirMS_041712_NAR_60mM_minus.9652.9652.2	2	14.1	1	4.41E+05		(R)LQAEIE	(R)L Q|A E/I/E/G L/K/G Q R(A)		114.13	671.3768	1341.748	-0.0022	-1.6	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
3821	dirMS_041712_NAR_120mM_plus.14891.15228.2	2	14.1	0	3.44E+06		(R)DWSHY	(R)D/W/S/H/Y/F|K(I)		132.03	491.725	982.442	0.001	1	6.74	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3822	dirMS_041712_NAR_20mM_plus.19198.19198.2	2	14.1	0	1.33E+04		(K)EIIDLVL	(K)E I|I/D/L/V/L D R(I)		203.7	543.313	1085.62	-0.0014	-1.3	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
3823	dirMS_041712_NAR_20mM_plus.7617.7617.2	2	14.1	0	1.57E+05		(K)IAVAAQ	(K)I A/V|A/A|Q N/C/Y K(V)	C:Carbamidomethylation	122.43	569.2902	1137.572	0.001	0.9	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
3824	dirMS_041712_NAR_30mM_plus2.18718.18718.2	2	14.1	0	3.13E+05		(R)ESLEALL	(R)E S|L/E/A L/L/Q/R(A)		152	529.8026	1058.584	0.0139	13.1	4.53	107721.8	8.85	HUMAN	O94906	Pre-mRNA-processing factor 6
3825	dirMS_041712_NAR_30mM_plus2.19789.19789.2	2	14.1	0	1.30E+05		(R)NTWLY	(R)N T/W/L/Y Q A L/R(E)		157.12	582.8112	1164.616	-0.0009	-0.8	8.75	49457.5	6.47	HUMAN	P56545	C-terminal-binding protein 2
3826	dirMS_041712_NAR_50mM_plus2.4972.4980.3	3	14.1	1	1.04E+05		(K)VSSAEG	(K)V/S|S A E/G A/A K/E/E/P K(R)		83.1	434.8891	1302.654	-0.0008	-0.6	4.79	4801.6	11.17	HUMAN	F2Z2W6	Non-histone chromosomal protein HMG-14
3827	dirMS_041712_NAR_60mM_plus.20414.20414.3	3	14.1	1	4.21E+05		(K)NAAGAL	(K)N A|A\G A/L/D L L/K/E/L K(N)		166.93	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
3828	dirMS_041712_NAR_120mM_minus.9814.9840.3	3	14.09	1	2.01E+05		(R)SRSGEG	(R)S R S G E\G E|V|S/G L/M/R(K)		108.07	455.559	1364.659	0.0038	2.8	5.87	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
3829	dirMS_041712_NAR_20mM_minus.14639.14639.2	2	14.09	0	2.03E+05		(K)TAVETA	(K)T/A\V E/T/A/V/L|L\L R(I)		201.18	593.3613	1185.72	-0.0048	-4.1	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
3830	dirMS_041712_NAR_30mM_minus2.10764.10764.2	2	14.09	0	6.30E+05		(K)GFSLES	(K)G F/S/L/E/S C/R(S)	C:Carbamidomethylation	112.08	478.2237	955.43	0.0099	10.4	6	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
3831	dirMS_041712_NAR_30mM_minus2.18366.18366.2	2	14.09	0	2.28E+05		(K)YPQLLP	(K)Y/P/Q/L/L P/G I R(G)		154.92	528.816	1056.62	0.0047	4.4	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
3832	dirMS_041712_NAR_120mM_plus.19375.19453.3	3	14.09	1	6.90E+05		(K)YNQLLRI	(K)Y/N|Q/L/L/R I E E E/L G S/K(A)		155.23	564.6353	1691.896	-0.0049	-2.9	4.79	47510.4	7.04	HUMAN	P06733	Alpha-enolase
3833	dirMS_041712_NAR_120mM_plus.7391.7477.3	3	14.09	1	1.14E+06		(R)EKVPGG	(R)E K V|P G G\L|Q/G/S/Q D/R(G)		92.32	457.5737	1370.702	0.0043	3.1	6.17	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
3834	dirMS_041712_NAR_20mM_plus.13727.13727.2	2	14.09	0	1.07E+05		(R)LVVPAT	(R)L V|V|P A T Q/C G S/L\I G K(G)	C:Carbamidomethylation	166.98	721.9033	1442.804	-0.0042	-2.9	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
3835	dirMS_041712_NAR_20mM_plus.16243.16243.3	3	14.09	0	1.14E+06	M221m	(R)ALTVPEI	(R)A L\T\V|P E L/T/Q/Q m/F D/A K(N)	m:Oxidized methionine	184.33	569.9583	1691.867	15.9931	-1.1	4.37	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
3836	dirMS_041712_NAR_20mM_plus.16676.16676.3	3	14.09	0	2.39E+05		(K)VQIAVA	(K)V Q\I A V A N/A|Q/E/L/L/Q R(M)		186.48	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
3837	dirMS_041712_NAR_20mM_plus.16679.16679.2	2	14.09	0	1.48E+05		(R)LLEAQIA	(R)L L/E\A/Q I\A/T/G\G I I D|P K(E)		185.75	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
3838	dirMS_041712_NAR_20mM_plus.17812.17812.2	2	14.09	0	1.67E+05		(K)GADFLV	(K)G A D|F\L|V/T/E V/E/N G G S L G S K(K)		195	890.4414	1779.876	-0.0004	-0.2	4.14	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
3839	dirMS_041712_NAR_30mM_plus2.16760.16813.2	2	14.09	0	3.06E+05		(R)SIQADG	(R)S I|Q|A|D|G L/V/W/G S S K(L)		140.72	674.3475	1347.69	-0.0026	-1.9	5.55	24934.4	4.5	HUMAN	P24534	Elongation factor 1-beta
3840	dirMS_041712_NAR_40mM_plus2.6980.7125.2	2	14.09	0	2.31E+05		(K)NMMAA	(K)N/M|M|A|A|C D|P/R(H)	C:Carbamidomethylation	101.42	533.2182	1065.427	0.0017	1.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
3841	dirMS_041712_NAR_50mM_plus2.10892.10892.3	3	14.09	0	4.81E+05		(R)EALLSSA	(R)E A/L/L/S/S A|V D H G S D E V/K(F)		124.73	552.9403	1656.807	-0.0012	-0.7	4.31	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
3842	dirMS_041712_NAR_50mM_plus2.15407.15407.3	3	14.09	1	5.45E+05		(R)GDVVPK	(R)G D V|V|P K D V\N\A A/I A T/I K(T)		148.45	537.6393	1610.911	-0.0079	-4.9	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
3843	dirMS_041712_NAR_50mM_plus2.17509.17510.3	3	14.09	1	5.25E+05		(K)VKLAAV	(K)V K L A\A\V D A T\V|N/Q|V|L/A/S R(Y)		160.33	585.6736	1755.012	-0.0061	-3.5	8.72	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
3844	dirMS_041712_NAR_120mM_minus.9684.9684.3	3	14.08	0	4.38E+05		(K)QEYDES	(K)Q E|Y/D E S/G/P S/I/V/H R(K)		107.47	506.2424	1516.703	0.01	6.6	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
3845	dirMS_041712_NAR_30mM_minus2.11630.11700.2	2	14.08	0	2.14E+05		(R)GYFSEE	(R)G Y|F|S/E E/M N/R(V)		117.05	566.7446	1132.473	0.0091	8.1	4.53	533778	5.74	HUMAN	Q15149	Plectin
3846	dirMS_041712_NAR_60mM_minus.9383.9402.3	3	14.08	1	2.76E+05	M198m	(R)VFDKEG	(R)V/F|D K E G N G/T|V/m/G A E/I R(H)	m:Oxidized methionine	112.15	580.2853	1722.848	15.9934	-0.9	4.68	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
3847	dirMS_041712_NAR_20mM_plus.15487.15487.2	2	14.08	0	2.31E+05		(K)TITLEVE	(K)T I/T|L/E/V|E|P S D T I E N V K(A)		179.02	894.4658	1787.927	-0.003	-1.7	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
3848	dirMS_041712_NAR_20mM_plus.18972.18972.2	2	14.08	0	1.91E+05		(R)STGEAF	(R)S T G E A F|V|Q/F/A S Q E/I/A E|K(A)		202.2	921.4477	1841.892	-0.0035	-1.9	4.25	24249.1	6.99	HUMAN	D6RBM0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
3849	dirMS_041712_NAR_20mM_plus.19135.19135.3	3	14.08	0	1.98E+05		(R)LAGTQP	(R)L A G T Q/P L\E\V|L/E/A V/Q/R(S)		204	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
3850	dirMS_041712_NAR_40mM_plus2.20112.20112.3	3	14.08	1	5.30E+05		(K)EGGLGP	(K)E G G\L/G/P/L/N/I/P L\L A D/V T\R R(L)		189.92	631.0288	1891.076	-0.0041	-2.2	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
3851	dirMS_041712_NAR_50mM_plus2.17114.17343.3	3	14.08	1	1.19E+06		(K)DNNGVI	(K)D N|N/G/V/I/G L/L E/P M K K(S)		158.77	509.9448	1527.82	-0.0001	-0.1	6.07	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
3852	dirMS_041712_NAR_60mM_plus.17636.17681.3	3	14.08	1	2.35E+05		(R)KALDIAE	(R)K A L D\I A\E\N|E|M/P/G L M R(M)		149.22	563.2887	1687.851	0.001	0.6	4.68	48285.8	5.93	HUMAN	P23526	Adenosylhomocysteinase
3853	dirMS_041712_NAR_60mM_plus.9187.9187.3	3	14.08	1	2.08E+05		(K)YYDDTYI	(K)Y/Y/D/D T/Y/P/S V K E/Q/K(A)		105.92	545.9214	1635.754	-0.004	-2.5	4.56	18430.9	4.79	HUMAN	F8VS17	Coatomer subunit zeta-1
3854	dirMS_041712_NAR_20mM_minus.10729.10729.2	2	14.07	0	1.89E+05		(R)TTPSYV	(R)T T/P S Y/V|A F/T/D/T E R(L)		154.68	744.3547	1487.701	0.0009	0.6	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
3855	dirMS_041712_NAR_60mM_minus.12033.12113.3	3	14.07	1	2.54E+03		(R)VIDRELY	(R)V/I/D/R E\L\Y|Q/Q/L Q/R(G)		128.12	520.9529	1560.849	-0.0051	-3.3	6.04	533778	5.74	HUMAN	Q15149	Plectin
3856	dirMS_041712_NAR_20mM_plus.13955.13956.2	2	14.07	0	1.34E+05		(R)GGIVDE	(R)G G/I|V|D/E\G A/L L/R(A)		167.83	550.3066	1099.611	-0.0047	-4.3	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
3857	dirMS_041712_NAR_20mM_plus.15158.15158.2	2	14.07	0	5.88E+04		(R)EQLAIAE	(R)E Q|L/A/I/A/E/F A R(S)		176.1	574.312	1147.611	0.0061	5.3	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
3858	dirMS_041712_NAR_50mM_plus2.15927.15927.3	3	14.07	1	9.43E+04		(K)FAANINI	(K)F A|A N I/N K E S I\V/D/V/E/G V V R(K)		151.15	654.0215	1960.05	0.0001	0.1	4.68	20139.7	9.34	HUMAN	C9J7S3	Aspartate--tRNA ligase, cytoplasmic (Fragment)
3859	dirMS_041712_NAR_50mM_plus2.18207.18478.3	3	14.07	0	1.25E+06		(R)DFLLKPE	(R)D F|L/L/K/P/E L L R(A)		164.65	415.2519	1243.741	0.0003	0.2	6.07	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
3860	dirMS_041712_NAR_50mM_plus2.22256.22256.3	3	14.07	1	1.35E+06		(K)EGGLGP	(K)E G G L/G/P/L N/I/P L L A D V T R R(L)		191	631.029	1891.076	-0.0035	-1.9	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
3861	dirMS_041712_NAR_50mM_plus2.5995.5995.3	3	14.07	1	2.40E+04		(R)GTDDSP	(R)G T/D/D/S/P K D S Q/E/D\L/Q E R(H)		95.62	607.2766	1819.794	0.0212	11.6	3.96	23420.8	4.74	HUMAN	Q5H9L2	Transcription elongation factor A protein-like 5
3862	dirMS_041712_NAR_120mM_minus.11994.11994.3	3	14.06	0	3.85E+05		(R)HSSLAG	(R)H S\S L A G\C|Q/I|I/N Y R(T)	C:Carbamidomethylation	119.48	506.9192	1518.748	-0.0051	-3.4	8.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
3863	dirMS_041712_NAR_20mM_minus.11547.11547.2	2	14.06	0	1.40E+05	M98m	(R)TLTIVDT	(R)T L|T I/V/D T G I/G m T/K(A)	m:Oxidized methionine	163.17	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
3864	dirMS_041712_NAR_20mM_minus.12193.12193.2	2	14.06	0	1.08E+06	M313m	(R)TVQSLEI	(R)T V|Q|S L/E/I D L D S m R(N)	m:Oxidized methionine	170.78	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3865	dirMS_041712_NAR_50mM_minus2.13110.13110.3	3	14.06	0	3.56E+05		(R)ETNLDSI	(R)E T N L/D|S L/P/L V/D T/H S K(R)		142.45	556.9529	1668.844	0.0002	0.1	4.53	53707.8	5.06	HUMAN	P08670	Vimentin
3866	dirMS_041712_NAR_60mM_minus.4663.4663.3	3	14.06	1	6.72E+04		(R)AAEEED	(R)A/A/E/E E D/E/A D/P K R(Q)		77.55	453.872	1359.602	-0.0008	-0.6	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
3867	dirMS_041712_NAR_60mM_minus.9934.9934.3	3	14.06	1	5.63E+05	M230m M	(R)mSmKE	(R)m S\m K E V\D E/Q|M/L/N|V Q N K(N)	m:Oxidized methionine	114.97	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3868	dirMS_041712_NAR_120mM_plus.10062.10245.3	3	14.06	1	1.30E+07		(R)VKYETEL	(R)V/K Y\E T/E|L|A/M/R(Q)		107.35	413.8849	1239.64	0	0	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3869	dirMS_041712_NAR_120mM_plus.11130.11274.3	3	14.06	0	1.25E+06		(R)TICSHV	(R)T/I|C/S/H V Q N M I/K(G)	C:Carbamidomethylation	112.02	444.2263	1330.661	0.0037	2.8	8.44	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
3870	dirMS_041712_NAR_20mM_plus.12322.12547.2	2	14.06	0	1.78E+05		(K)TIIFVET	(K)T I|I/F V E/T/K(R)		158.87	475.7818	950.556	0.0006	0.6	5.66	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
3871	dirMS_041712_NAR_20mM_plus.13686.13686.2	2	14.06	0	3.11E+05		(R)VLQALE	(R)V L|Q/A/L E/G L\K(M)		165.42	485.8004	970.593	0.0004	0.4	5.97	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
3872	dirMS_041712_NAR_20mM_plus.18678.18678.2	2	14.06	0	1.61E+05		(R)IITLTGP	(R)I I|T/L/T/G/P T N A I F K(A)		200.33	694.9091	1388.815	-0.0039	-2.8	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
3873	dirMS_041712_NAR_30mM_plus2.10525.10541.2	2	14.06	0	9.14E+05		(R)LTVEEA	(R)L/T|V/E|E/A/V R(H)		109.33	458.7641	916.51	0.0111	12.1	4.53	862169.3	5.27	HUMAN	H3BPE1	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5
3874	dirMS_041712_NAR_30mM_plus2.13759.14035.2	2	14.06	0	1.84E+06		(R)LILIESR	(R)L/I|L|I/E/S/R(I)		125.87	422.2682	843.53	-0.0007	-0.8	6	17222	10.53	HUMAN	P62277	40S ribosomal protein S13
3875	dirMS_041712_NAR_30mM_plus2.14586.14586.2	2	14.06	0	2.53E+05		(R)SIGEYD	(R)S I|G E/Y D|V L R(G)		129.85	526.2726	1051.542	-0.0039	-3.7	4.37	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
3876	dirMS_041712_NAR_30mM_plus2.19949.20074.2	2	14.06	0	2.47E+05		(K)LALFQAI	(K)L/A|L|F/Q A I/G/K(E)		158.53	480.795	960.588	-0.005	-5.2	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
3877	dirMS_041712_NAR_30mM_plus2.21924.21962.2	2	14.06	0	1.55E+05		(K)ANFLQN	(K)A N|F|L|Q|N M/I E D/R(T)		170.25	675.8282	1350.647	0.0021	1.5	4.37	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
3878	dirMS_041712_NAR_30mM_plus2.8127.8127.2	2	14.06	0	1.36E+06		(K)QGGGG	(K)Q G\G/G G/G G G S/V|P G I E/R(M)		97.17	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
3879	dirMS_041712_NAR_50mM_plus2.17478.17478.3	3	14.06	0	6.20E+05		(R)IMEVID	(R)I/M|E|V/I/D A I/T T T A Q S H Q R(T)		160.32	638.6636	1913.975	0.0013	0.7	5.32	85815.7	7.35	HUMAN	P17858	6-phosphofructokinase, liver type
3880	dirMS_041712_NAR_50mM_plus2.19887.19887.3	3	14.06	0	2.50E+05		(K)LFLFHTS	(K)L F|L F H T S\L/P I/A/E/A/P/G K(L)		172.83	580.9943	1740.968	0	0	6.75	108105.4	6.57	HUMAN	E7EP00	Protein transport protein Sec24C
3881	dirMS_041712_NAR_30mM_minus2.11589.11589.2	2	14.05	0	5.18E+05		(R)DVCLYPI	(R)D V/C|L Y/P/R(F)	C:Carbamidomethylation	117.17	461.7315	922.445	0.0106	11.5	5.83	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
3882	dirMS_041712_NAR_50mM_minus2.12506.12506.3	3	14.05	1	1.67E+05		(K)IINADSE	(K)I/I/N\A/D S E D/P K Y I I N V K(Q)		139.08	611.3243	1831.98	-0.0217	-11.8	4.56	14693.3	4.69	HUMAN	C9JLS9	26S protease regulatory subunit 7 (Fragment)
3883	dirMS_041712_NAR_20mM_plus.14714.14714.2	2	14.05	0	1.98E+05	M179m M	(K)mFVLDE	(K)m F|V|L/D E A/D/E m L|S R(G)	m:Oxidized methionine	173.6	794.3555	1555.713	31.9906	0.5	3.91	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
3884	dirMS_041712_NAR_20mM_plus.16566.16566.2	2	14.05	0	1.38E+05		(K)TVDNFV	(K)T V|D N F|V/A L/A/T G E K(G)		185.88	682.8565	1364.706	0.0001	0.1	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
3885	dirMS_041712_NAR_30mM_plus2.13045.13105.2	2	14.05	0	2.47E+05		(K)IGGIGTV	(K)I/G|G\I|G/T/V|P V G R(V)		121.77	513.3084	1025.61	-0.0007	-0.7	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
3886	dirMS_041712_NAR_30mM_plus2.16064.16064.2	2	14.05	0	1.91E+06		(K)ICSWNV	(K)I/C|S/W/N V/D/G L\R(A)	C:Carbamidomethylation	137.87	610.3003	1219.589	0.0045	3.7	5.84	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
3887	dirMS_041712_NAR_30mM_plus2.21835.22044.2	2	14.05	0	3.21E+05		(R)SFITWLF	(R)S F|I|T|W|L/R(D)		170.53	461.7608	922.515	-0.0002	-0.2	9.47	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
3888	dirMS_041712_NAR_50mM_plus2.18059.18059.3	3	14.05	1	9.62E+04		(K)VVLDDK	(K)V/V|L/D/D K D Y F L F/R(D)		162.73	510.6044	1529.8	-0.0012	-0.8	4.43	5189.9	4.56	HUMAN	B8ZZ54	10 kDa heat shock protein, mitochondrial
3889	dirMS_041712_NAR_60mM_plus.20661.20661.3	3	14.05	0	1.68E+04		(K)HNQLPL	(K)H N Q L P L/V|I/E/F T/E Q T/A/P/K(I)		168.58	655.6825	1965.044	-0.0111	-5.6	5.4	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
3890	dirMS_041712_NAR_20mM_minus.12345.12345.2	2	14.04	0	7.22E+05	M185m	(K)LAVNm	(K)L/A|V N m/V/P F/P\R(L)	m:Oxidized methionine	171.98	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
3891	dirMS_041712_NAR_50mM_minus2.16041.16060.3	3	14.04	1	8.40E+04		(K)LQVDAL	(K)L/Q|V/D A L|I/D/T I/K K(S)		159.23	452.9385	1356.81	-0.0087	-6.4	5.96	234333.2	6.01	HUMAN	J3KNX9	Unconventional myosin-XVIIIa
3892	dirMS_041712_NAR_50mM_minus2.16637.16637.3	3	14.04	1	1.61E+05		(K)TVTAMD	(K)T V|T A/M D V/V/Y A L K R(Q)		162.78	489.6051	1466.804	-0.0028	-1.9	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
3893	dirMS_041712_NAR_20mM_plus.8851.8851.2	2	14.04	0	1.30E+05		(K)VLEEAN	(K)V/L|E/E/A\N Q/A\I/N/P K(L)		131.6	663.353	1325.706	-0.0072	-5.5	4.53	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
3894	dirMS_041712_NAR_50mM_plus2.11292.11292.3	3	14.04	1	2.98E+05		(R)ETGVDL	(R)E T/G V/D/L T K/D N M/A/L Q/R(V)		127.18	564.2856	1690.843	-0.0006	-0.4	4.56	73964.5	5.87	HUMAN	P38646	Stress-70 protein, mitochondrial
3895	dirMS_041712_NAR_50mM_plus2.15212.15212.3	3	14.04	1	5.13E+05		(K)TKDGQII	(K)T K D G Q I|L|P V/P N V V V/R(D)		148.45	545.6573	1634.959	-0.0015	-0.9	8.41	56825.2	9.49	HUMAN	Q9P258	Protein RCC2
3896	dirMS_041712_NAR_60mM_plus.11415.11415.3	3	14.04	1	4.52E+05		(K)TCVFEKE	(K)T C|V|F E/K E N D/P S V/M R(S)	C:Carbamidomethylation	117.33	571.2635	1711.778	-0.0019	-1.1	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
3897	dirMS_041712_NAR_60mM_plus.18515.18515.3	3	14.04	1	7.19E+05		(R)IRIDSLS	(R)I R I D S L\S A|Q|L|S Q/L Q/K(Q)		154.13	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
3898	dirMS_041712_NAR_120mM_minus.12022.12022.2	2	14.03	1	3.39E+05		(K)MKEIAE	(K)M K|E|I/A/E A/Y/L G K(T)		119.63	626.8305	1252.661	-0.0069	-5.5	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
3899	dirMS_041712_NAR_30mM_minus2.14674.14916.2	2	14.03	0	4.17E+05		(R)LWVDE	(R)L/W|V|D/E A V/R(A)		134.55	494.2641	987.526	-0.0049	-4.9	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
3900	dirMS_041712_NAR_40mM_minus2.9414.9414.3	3	14.03	0	9.99E+04		(K)AASDIA	(K)A A|S/D I|A/M T E/L/P/P T H P I R(L)		138.25	607.3174	1819.937	0.0006	0.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
3901	dirMS_041712_NAR_50mM_minus2.18366.18366.3	3	14.03	0	4.62E+05		(K)ALIEVLQ	(K)A L|I/E V/L Q/P L/I/A E H Q A R(R)		175.42	601.0139	1801.033	-0.0059	-3.3	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
3902	dirMS_041712_NAR_50mM_minus2.8737.8755.3	3	14.03	1	1.53E+05		(K)SPFEVSV	(K)S P|F/E|V S V D K/A Q G D/A S/K(V)		117.75	555.6099	1664.813	0.0025	1.5	4.56	258215.9	5.48	HUMAN	E7EN95	Filamin-B
3903	dirMS_041712_NAR_120mM_plus.13267.13424.4	4	14.03	1	1.43E+06		(K)SVHSSVI	(K)S V H\S S\V|P|L/L N S K/D/P I D/R(I)		123.27	466.7533	1863.992	-0.0009	-0.5	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
3904	dirMS_041712_NAR_20mM_plus.15629.15629.2	2	14.03	0	3.47E+05		(K)VGINYQ	(K)V G I/N Y\Q|P P T V\V|P/G G D L A/K(V)		179.05	912.9952	1824.985	-0.0023	-1.3	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
3905	dirMS_041712_NAR_20mM_plus.18965.18965.2	2	14.03	0	4.27E+04		(R)SIQLDGI	(R)S I/Q L/D/G L/V/W G\A/S K(L)		201.65	687.3716	1373.742	-0.0064	-4.7	5.55	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
3906	dirMS_041712_NAR_20mM_plus.7948.7948.2	2	14.03	0	4.82E+04		(K)YIDQEEL	(K)Y/I|D|Q E E L N K(T)		124.37	576.2845	1151.558	0.0038	3.3	4.14	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
3907	dirMS_041712_NAR_30mM_plus2.10626.10779.2	2	14.03	0	7.22E+05		(K)FLDQNL	(K)F/L|D|Q N/L/Q/K(Y)		109.55	503.271	1005.536	-0.0016	-1.6	5.84	334221.3	6.44	HUMAN	P15924	Desmoplakin
3908	dirMS_041712_NAR_30mM_plus2.18598.18598.2	2	14.03	0	1.48E+05		(R)TLTIVDT	(R)T L/T\I/V D/T/G/I G M T K(A)		151.4	675.3687	1349.735	-0.0044	-3.2	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
3909	dirMS_041712_NAR_30mM_plus2.20959.21193.2	2	14.03	0	3.92E+05		(K)TIFAYFT	(K)T/I|F|A/Y/F/T G S K(D)		165.37	567.7949	1134.583	-0.0005	-0.4	8.26	8599.5	5.51	HUMAN	I3L0K2	Thioredoxin domain-containing protein 17
3910	dirMS_041712_NAR_60mM_plus.12320.12380.3	3	14.03	1	3.98E+05		(R)TSDVGG	(R)T/S|D|V/G/G Y/Y/Y E K I|E R(T)		121.38	560.6017	1679.791	-0.0006	-0.4	4.68	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
3911	dirMS_041712_NAR_60mM_plus.12479.12479.3	3	14.03	1	3.27E+06		(K)VKLEAEI	(K)V K L E A E|I/A/T/Y/R(R)		122.93	431.5782	1292.721	-0.0008	-0.6	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
3912	dirMS_041712_NAR_50mM_minus2.12417.12417.3	3	14.02	1	8.29E+04		(K)QLQALS	(K)Q L/Q/A/L/S S E L/A/Q A R D E/T K(K)		138.55	629.9954	1887.977	-0.0054	-2.9	4.68	71218.8	6.3	HUMAN	A7YIJ8	Radixin
3913	dirMS_041712_NAR_50mM_minus2.7686.7686.3	3	14.02	0	2.46E+05		(R)AALAHS	(R)A A L A H S E E\V|T/A|S Q/V A/A\T/K(T)		110.93	595.3104	1783.919	-0.0018	-1	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
3914	dirMS_041712_NAR_60mM_minus.17284.17284.3	3	14.02	0	3.14E+05		(K)GSDHSA	(K)G S D H\S A S\L/E|P/G E/L/A\E L\V R(S)		156.82	622.9764	1866.919	-0.0045	-2.4	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
3915	dirMS_041712_NAR_120mM_plus.8150.8150.2	2	14.02	0	4.29E+05		(K)AGEVFI	(K)A/G\E|V/F I/H|K(D)		96.3	450.7531	900.494	0.0051	5.7	6.79	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
3916	dirMS_041712_NAR_20mM_plus.18712.18712.2	2	14.02	0	2.34E+05		(K)IYVDDGI	(K)I/Y|V|D D/G\L I/S L/Q V K(Q)		200.65	731.9068	1462.815	-0.0088	-6	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
3917	dirMS_041712_NAR_30mM_plus2.11688.11688.2	2	14.02	0	5.34E+05		(K)VASGCLI	(K)V/A|S/G/C L/D I/N S S V K(G)	C:Carbamidomethylation	114.8	675.3393	1349.673	-0.0016	-1.2	5.81	56837	7.19	HUMAN	E7ETT1	Propionyl-CoA carboxylase beta chain, mitochondrial
3918	dirMS_041712_NAR_60mM_plus.14788.14949.3	3	14.02	1	1.28E+06		(R)KFLDGIY	(R)K\F\L D\G\I|Y|V/S/E/K(G)		134.67	433.5671	1298.699	-0.0123	-9.5	6.07	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
3919	dirMS_041712_NAR_120mM_minus.8180.8180.3	3	14.01	2	1.08E+06		(K)KGAVAE	(K)K|G/A\V/A/E D G D/E/L R T\E\P E\A|K(K)		99.27	638.9836	1914.94	-0.0041	-2.1	4.36	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)

3920	dirMS_041712_NAR_30mM_minus2.11130.11130.2	2	14.01	0	6.40E+05		(K)VAGQD(	(K)V/A|G|Q/D/G S V V/Q/F K(I)		114.03	617.824	1234.643	-0.0019	-1.5	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
3921	dirMS_041712_NAR_30mM_minus2.18285.18285.2	2	14.01	0	1.57E+05		(K)FGAYIVI	(K)F G/A|Y/I/V/D/G L R(Q)		153.6	555.7984	1110.594	-0.0047	-4.2	5.83	269989.9	5.92	HUMAN	F8W8T8	Acetyl-CoA carboxylase 2
3922	dirMS_041712_NAR_50mM_minus2.12487.12487.3	3	14.01	0	1.87E+05		(R)VLVVHD	(R)V/L/V/V/H D/G F E G L/A K(G)		139.63	461.9238	1383.763	-0.0062	-4.5	5.32	18719.9	6.91	HUMAN	F8VP00	6-phosphofructokinase, muscle type (Fragment)
3923	dirMS_041712_NAR_60mM_minus.10374.10374.3	3	14.01	0	5.97E+05		(K)AQVARP	(K)A/Q|V/A/R P G G D T I/F/G K(I)		117.88	472.9235	1416.759	-0.0034	-2.4	8.79	7323.5	9.4	HUMAN	D6RC06	Histidine triad nucleotide-binding protein 1
3924	dirMS_041712_NAR_60mM_minus.14868.14868.3	3	14.01	1	2.72E+05		(R)KLQEEEI	(R)K L Q E E E\L\L/A/T|Q/V/D|M R(A)		142.8	601.6438	1802.932	-0.0148	-8.2	4.41	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
3925	dirMS_041712_NAR_20mM_plus.12477.12477.2	2	14.01	0	1.88E+05		(R)GVEICIA	(R)G V\E/I|C I/A T/P G R(L)	C:Carbamidomethylation	158.73	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
3926	dirMS_041712_NAR_30mM_plus2.12059.12138.2	2	14.01	0	3.47E+05		(R)DVCLYPI	(R)D V|C/L/Y/P/R(F)	C:Carbamidomethylation	116.58	461.7327	922.445	0.013	14.1	5.83	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
3927	dirMS_041712_NAR_30mM_plus2.19499.19499.2	2	14.01	0	2.88E+04		(R)FLLADNI	(R)F L|L|A/D/N\L Y C/K(A)	C:Carbamidomethylation	155.03	628.8226	1256.634	0.0036	2.8	5.83	22400.1	6.19	HUMAN	F5H2A7	Prefoldin subunit 3
3928	dirMS_041712_NAR_30mM_plus2.20437.20437.2	2	14.01	0	3.07E+05		(R)FEELNAI	(R)F/E|E|L/N A/D L/F R(G)		161.07	627.3106	1253.616	-0.0022	-1.7	4.14	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
3929	dirMS_041712_NAR_50mM_plus2.9135.9156.3	3	14.01	1	3.70E+05		(R)IITEGFE/	(R)I|I|T|E/G F/E/A/A K E K(A)		115.27	445.9079	1335.716	-0.0063	-4.7	4.79	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
3930	dirMS_041712_NAR_20mM_minus.7839.7872.2	2	14	0	1.69E+05		(K)SVEAAA	(K)S V|E|A/A/A/E/L S A/K(D)		128.45	538.2838	1075.563	-0.0027	-2.5	4.53	12131.5	11.14	HUMAN	F5GXR3	Parathymosin
3931	dirMS_041712_NAR_30mM_minus2.12205.12205.2	2	14	0	1.31E+05		(R)TLSGME	(R)T L|S G M/E/S/Y C V R(A)	C:Carbamidomethylation	119.47	651.795	1302.582	0.001	0.8	5.66	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
3932	dirMS_041712_NAR_30mM_minus2.19028.19114.2	2	14	0	2.61E+05		(K)SYELPD(	(K)S Y E|L|P D G Q/V|I/T\I/G N E R(F)		158.88	895.9492	1790.892	-0.0008	-0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
3933	dirMS_041712_NAR_60mM_minus.8097.8097.3	3	14	1	4.11E+05		(R)YLAEVA'	(R)Y L/A E\V/A/T G E/K/R(A)		104.48	412.8902	1236.658	-0.0022	-1.8	6.14	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
3934	dirMS_041712_NAR_120mM_plus.15261.15478.4	4	14	0	2.28E+06		(K)HLEINPI	(K)H L\E\I\N|P D H/P I V/E T L/R(Q)		133.9	446.4951	1782.95	0.0089	5	5.27	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
3935	dirMS_041712_NAR_20mM_plus.11309.11309.3	3	14	0	1.13E+05		(R)GCITIIG(	(R)G C\I T\I I/G G G D T/A/T/C C A K(W)	C:Carbamidomethylation	150.28	585.5999	1754.787	-0.0019	-1.1	5.84	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
3936	dirMS_041712_NAR_20mM_plus.17612.17612.2	2	14	0	1.07E+05	M90m	(R)LFVGNLI	(R)L F V G N/L|P/P D\I T/E E E m R(K)	m:Oxidized methionine	192.97	938.4602	1859.921	15.9923	-1.4	4	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
3937	dirMS_041712_NAR_30mM_plus2.11588.11588.2	2	14	0	3.91E+06		(K)SCNCLLI	(K)S/C|N C L/L|L/K(V)	C:Carbamidomethylation	114.55	504.2556	1007.501	0.0027	2.7	8.47	47510.4	7.04	HUMAN	P06733	Alpha-enolase
3938	dirMS_041712_NAR_30mM_plus2.14019.14019.2	2	14	0	2.47E+05		(K)SSGGFV'	(K)S S|G/G F|V/W/A/C/K(N)	C:Carbamidomethylation	126.2	549.7552	1098.504	-0.0006	-0.5	8.47	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
3939	dirMS_041712_NAR_30mM_plus2.16688.16827.2	2	14	0	3.46E+05		(R)SIQADG	(R)S I/Q|A/D|G L/V|W G S S K(L)		140.6	674.3475	1347.69	-0.0026	-1.9	5.55	24934.4	4.5	HUMAN	P24534	Elongation factor 1-beta
3940	dirMS_041712_NAR_30mM_plus2.7618.7640.2	2	14	0	1.73E+06		(R)MGPVM	(R)M/G|P|V/M D/R(M)		94.18	403.1894	805.37	0.002	2.5	5.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
3941	dirMS_041712_NAR_40mM_plus2.14581.14581.3	3	14	0	4.84E+05		(K)IAILTCPI	(K)I A|I L/T/C P F E/P/P K P K(T)	C:Carbamidomethylation	153.47	537.6381	1610.898	0.0023	1.4	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
3942	dirMS_041712_NAR_60mM_plus.16901.16901.3	3	14	0	8.89E+05		(K)TTISVAH	(K)T/T|I/S V A H L\L/A A/R(Q)		144.63	418.2478	1252.737	-0.0083	-6.7	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
3943	dirMS_041712_NAR_30mM_minus2.12393.12807.2	2	13.99	0	5.64E+05		(K)GDYPLE/	(K)G D/Y|P/L/E/A V/R(M)		122.22	510.2598	1019.516	-0.0033	-3.2	4.37	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
3944	dirMS_041712_NAR_30mM_minus2.15615.15615.2	2	13.99	0	1.51E+05		(K)AMTGVI	(K)A M|T|G V/E Q/W P Y/R(A)		138.37	669.3172	1337.631	-0.0036	-2.7	6.04	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
3945	dirMS_041712_NAR_50mM_minus2.11474.11474.3	3	13.99	1	2.41E+04		(R)ESDVPLI	(R)E/S D V/P/L K\T/E E F E V T K(T)		133.62	584.3049	1750.874	0.0256	14.6	4.25	18909	6.21	HUMAN	Q969H8	UPF0556 protein C19orf10
3946	dirMS_041712_NAR_50mM_minus2.13446.13446.3	3	13.99	1	5.31E+05		(K)LTEDKAI	(K)L/T/E D K A D V Q/S\I/I|G/L Q R(F)		144.8	595.9939	1785.97	-0.0034	-1.9	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
3947	dirMS_041712_NAR_60mM_minus.9631.9758.3	3	13.99	1	5.37E+05		(R)IITEGFE/	(R)I/I|T E/G F/E A A/K E K(A)		113.88	445.91	1335.716	0	0	4.79	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
3948	dirMS_041712_NAR_120mM_plus.8693.8738.2	2	13.99	0	8.36E+05		(K)HFVALS'	(K)H/F|V/A/L|S T/N/T/T K(V)		99.1	609.8311	1218.648	0.0072	5.9	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
3949	dirMS_041712_NAR_30mM_plus2.17274.17774.2	2	13.99	0	7.74E+05		(K)LMFEELI	(K)L/M|F/E/E/L/R(N)		145.37	469.2488	937.481	0.0092	9.8	4.53	19338.9	5.33	HUMAN	E7EQS9	tRNA-splicing ligase RtcB homolog
3950	dirMS_041712_NAR_40mM_plus2.15431.15431.3	3	13.99	0	2.03E+05		(K)GVTIIGP	(K)G V T/I/I/G/P A/T/V G G I K/P G C F K(I)	C:Carbamidomethylation	156.62	624.683	1872.041	-0.0067	-3.6	10	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
3951	dirMS_041712_NAR_50mM_plus2.19032.19154.3	3	13.99	1	1.72E+06		(K)LIQLMEI	(K)L/I|Q|L/M E E I/M/A/E K E/N K(T)		169.7	606.9845	1818.934	0.005	2.7	4.49	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
3952	dirMS_041712_NAR_60mM_plus.17883.17909.3	3	13.99	1	2.50E+05		(R)GQFSTD	(R)G Q|F/S/T D E L/V/A/E V/E/K R(N)		150.63	569.9588	1707.855	0.007	4.1	4.41	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
3953	dirMS_041712_NAR_120mM_minus.12144.12144.3	3	13.98	1	3.21E+05		(K)TLTTVQ(	(K)T L|T/T V/Q/G I/A D D Y D K K/K(L)		120.02	599.3185	1795.944	-0.0027	-1.5	5.71	13778.5	7.96	HUMAN	K7EM18	Eukaryotic translation initiation factor 1
3954	dirMS_041712_NAR_30mM_minus2.13638.13673.2	2	13.98	0	6.95E+05		(R)LPLQDV'	(R)L/P|L/Q/D V/Y/K(I)		128	488.273	975.551	-0.0122	-12.5	5.83	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
3955	dirMS_041712_NAR_20mM_plus.10185.10185.2	2	13.98	0	2.01E+05		(K)LSDGVA'	(K)L/S/D/G V A V|L K(V)		143.02	451.2712	901.535	-0.0002	-0.2	5.84	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
3956	dirMS_041712_NAR_20mM_plus.18846.18846.2	2	13.98	0	1.81E+05		(K)TAVETA'	(K)T A\V/E/T A/V L|L L/R(I)		200.4	593.3625	1185.72	-0.0024	-2	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
3957	dirMS_041712_NAR_30mM_plus2.6032.6032.2	2	13.98	0	1.69E+05		(R)SQESGY'	(R)S Q|E|S/G/Y/Y D/R(M)		85.9	552.7331	1104.459	-0.0003	-0.3	4.37	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
3958	dirMS_041712_NAR_30mM_plus2.6607.6888.2	2	13.98	0	1.10E+06		(K)SLDEME	(K)S/L|D|E M/E/K(Q)		90	426.1971	851.381	0.0054	6.4	4.14	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
3959	dirMS_041712_NAR_30mM_plus2.9392.9392.2	2	13.98	0	6.90E+05		(K)SVEAAA	(K)S V|E/A/A/A/E/L/S A K(D)		103.03	538.2855	1075.563	0.0007	0.7	4.53	12131.5	11.14	HUMAN	F5GXR3	Parathymosin
3960	dirMS_041712_NAR_50mM_plus2.21495.21495.3	3	13.98	0	8.95E+04		(K)GAEILEV	(K)G A|E/I/L/E/V L/H S L P A\V/R(Q)		183.4	535.3092	1603.917	-0.0036	-2.2	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
3961	dirMS_041712_NAR_60mM_plus.11782.11801.3	3	13.98	1	1.10E+06		(K)QSSSSRI	(K)Q/S/S S/S R D D N M/F/Q I/G/K(M)		119.07	567.2609	1699.77	-0.0023	-1.3	5.96	14395.1	9.6	HUMAN	P53999	Activated RNA polymerase II transcriptional coactivator p15
3962	dirMS_041712_NAR_60mM_plus.9382.9382.2	2	13.98	0	1.98E+06		(R)IGAEVYI	(R)I/G|A/E/V/Y/H N\L\K(N)		107.55	572.3143	1143.616	0.0056	4.9	6.75	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
3963	dirMS_041712_NAR_120mM_minus.11726.11726.3	3	13.97	2	3.38E+05		(R)SGKYDLI	(R)S G K Y/D L D/F K/S|P D D|P S R(Y)		117.87	609.6226	1826.855	-0.0023	-1.3	4.58	47510.4	7.04	HUMAN	P06733	Alpha-enolase
3964	dirMS_041712_NAR_30mM_minus2.14319.14319.2	2	13.97	0	7.55E+04		(R)TPYGASI	(R)T/P|Y/G/A|S I F\Q S K(E)		131.18	599.8093	1198.61	0.0011	0.9	8.26	44815.8	6.62	HUMAN	B3KQ29	Transducin-like enhancer protein 4
3965	dirMS_041712_NAR_30mM_minus2.14339.14339.2	2	13.97	0	1.70E+05		(K)IVVLLQR	(K)I/V|V/L L/Q/R(L)		131.83	420.7871	840.567	0.0004	0.4	9.75	28772.3	6.28	HUMAN	A6NJG9	Proteasome activator complex subunit 1
3966	dirMS_041712_NAR_30mM_minus2.16427.16427.2	2	13.97	0	5.06E+05	M185m	(K)LAVNm\	(K)L/A/V/N/m/V P F P R(L)	m:Oxidized methionine	142.53	580.3178	1143.634	15.994	-0.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
3967	dirMS_041712_NAR_30mM_minus2.8899.8899.2	2	13.97	0	4.88E+05		(K)SDPVVS'	(K)S D/P V/V/S Y/R(E)		102.7	461.7315	922.463	-0.0071	-7.7	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
3968	dirMS_041712_NAR_60mM_minus.15161.15206.3	3	13.97	1	3.39E+05		(K)AKLEQLI	(K)A K L E Q\L|F|Q/D E V/A/K(A)		144.37	506.9421	1518.816	-0.0045	-3	4.68	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
3969	dirMS_041712_NAR_60mM_minus.15721.15721.3	3	13.97	1	1.58E+06		(R)KDDPVT	(R)K D D\P V\T\N L/N N/A|F E V/A E K(Y)		147.43	635.317	1903.94	-0.0032	-1.7	4.32	21601.4	6.27	HUMAN	K7EJH8	Alpha-actinin-4 (Fragment)
3970	dirMS_041712_NAR_60mM_minus.17275.17275.3	3	13.97	0	9.52E+04		(R)GFGHIG	(R)G F G H I G I\A\V|P D/V Y S A/C K(R)	C:Carbamidomethylation	156.02	597.6347	1790.889	0.0001	0.1	6.74	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
3971	dirMS_041712_NAR_60mM_minus.18816.18816.3	3	13.97	0	2.56E+05		(K)LHDNLII	(K)L H\D/N L\I|I/S|D L E N T V K(K)		166.17	575.3117	1723.922	-0.0019	-1.1	4.54	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
3972	dirMS_041712_NAR_120mM_plus.9455.9455.3	3	13.97	0	3.32E+05		(K)QEYDES(	(K)Q E Y|D E/S/G/P/S/I/V H/R(K)		102.88	506.2393	1516.703	0.0007	0.5	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
3973	dirMS_041712_NAR_120mM_plus.9745.9839.3	3	13.97	0	9.06E+05		(R)HGESAV	(R)H G\E S\A\W|N|L/E/N R(F)		104.47	438.2077	1312.603	0.0057	4.3	5.4	28917.5	6.68	HUMAN	P18669	Phosphoglycerate mutase 1
3974	dirMS_041712_NAR_20mM_plus.16208.16208.3	3	13.97	0	1.32E+05		(R)LLDAQL/	(R)L/L D/A Q\L A/T/G G|I/V/D/P R(L)		183.53	513.6218	1538.854	-0.0028	-1.8	4.21	533778	5.74	HUMAN	Q15149	Plectin
3975	dirMS_041712_NAR_20mM_plus.18100.18115.2	2	13.97	0	1.72E+05		(K)DAGVIA(	(K)D A\G|V|I/A/G L/N/V L/R(I)		196.72	599.3505	1197.695	-0.0013	-1.1	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
3976	dirMS_041712_NAR_30mM_plus2.17966.17966.2	2	13.97	0	2.91E+05		(R)VNPALA	(R)V N|P A|L|A E/L N L R(S)		147.78	605.3509	1209.695	-0.0005	-0.4	5.97	20026.6	4.67	HUMAN	E9PIK5	Ribonuclease inhibitor (Fragment)
3977	dirMS_041712_NAR_30mM_plus2.20672.20672.2	2	13.97	0	2.60E+05		(R)ASLSLW	(R)A S|L/S\L/W/Q/A M E K(G)		162.9	632.3231	1263.64	-0.0013	-1	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
3978	dirMS_041712_NAR_30mM_plus2.22008.22008.2	2	13.97	0	1.96E+05		(R)LVFGFLI	(R)L V/F/G/F L N\G/R(A)		170.8	511.7906	1022.578	-0.0043	-4.2	9.75	10585.9	6.9	HUMAN	G3V2H3	Purine nucleoside phosphorylase (Fragment)
3979	dirMS_041712_NAR_40mM_plus2.12257.12257.3	3	13.97	0	2.19E+05		(K)AASDIAI	(K)A A/S/D\I/A M T/E L/P/P T H P I R(L)		139.18	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
3980	dirMS_041712_NAR_50mM_plus2.14642.14642.3	3	13.97	1	5.92E+05		(R)ELVFKEI	(R)E L|V/F/K E D G Q E/Y/A Q V I/K(M)		144.98	632.6588	1895.975	-0.0131	-6.9	4.41	14568.9	5.17	HUMAN	A6NJH9	Eukaryotic translation initiation factor 1A, Y-chromosomal
3981	dirMS_041712_NAR_60mM_plus.13736.13904.3	3	13.97	1	1.40E+06		(R)EMDRET	(R)E|M/D R E T\L|I/D/V/A/R(T)		128.93	483.2457	1447.721	0.0016	1.1	4.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
3982	dirMS_041712_NAR_60mM_plus.17942.17942.3	3	13.97	1	3.58E+05		(K)CEFQDA	(K)C E|F\Q/D A/Y/V L/L S E/K/K(I)	C:Carbamidomethylation	150.55	577.288	1729.847	0.0029	1.7	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
3983	dirMS_041712_NAR_40mM_minus2.8086.8086.2	2	13.96	0	7.00E+04		(R)IVLQIDN	(R)I V|L/Q/I/D N A R(L)		128.1	521.3059	1041.605	-0.0006	-0.6	5.84	20842.9	5.32	HUMAN	C9JM50	Keratin, type I cytoskeletal 19 (Fragment)
3984	dirMS_041712_NAR_50mM_minus2.7924.7924.3	3	13.96	1	1.81E+05		(R)IITEGFE/	(R)I/I/T E/G F E A A/K E K(A)		112.27	445.912	1335.716	0.006	4.5	4.79	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
3985	dirMS_041712_NAR_120mM_plus.4136.4136.3	3	13.96	1	1.59E+07	M310m	(R)TKTEISEI	(R)T\K|T E\I|S/E/m N/R(N)	m:Oxidized methionine	69.77	408.8687	1208.594	15.9976	2.2	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
3986	dirMS_041712_NAR_120mM_plus.8674.8674.2	2	13.96	0	8.21E+05		(K)HFVALS'	(K)H/F|V|A L/S/T N/T T K(V)		99.08	609.8311	1218.648	0.0072	5.9	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
3987	dirMS_041712_NAR_20mM_plus.13705.13705.2	2	13.96	0	2.22E+05	M98m	(R)TLTIVDT	(R)T L\T\I/V|D/T G/I/G m T K(A)	m:Oxidized methionine	166.8	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
3988	dirMS_041712_NAR_20mM_plus.18118.18266.2	2	13.96	0	1.13E+05		(K)LVLPSLIS	(K)L V|L|P/S/L I/S S R(I)		196.6	542.8388	1084.672	-0.0021	-2	9.75	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
3989	dirMS_041712_NAR_20mM_plus.18792.18792.2	2	13.96	0	2.87E+05		(K)LAVEALS	(K)L A V\E/A|L/S/S/L D/G D L A G R(Y)		200.48	793.9214	1586.838	-0.0029	-1.8	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
3990	dirMS_041712_NAR_30mM_plus2.18403.18403.2	2	13.96	0	2.19E+05		(K)GVEGLII	(K)G V|E G L|I|D I/E/N/P\N R(V)		149.47	713.3669	1425.733	-0.0067	-4.7	4.14	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
3991	dirMS_041712_NAR_50mM_plus2.16910.16910.3	3	13.96	1	9.13E+05		(K)LFTAESL	(K)L/F|T/A E S L/I/G L K N P|E K(S)		157.53	553.9791	1659.932	-0.0089	-5.3	6.14	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
3992	dirMS_041712_NAR_60mM_plus.11301.11301.3	3	13.96	0	1.93E+06		(R)EIVHIQA	(R)E/I V H I Q A G/Q/C/G N Q I|G A K(F)	C:Carbamidomethylation	116.42	608.311	1822.923	-0.0044	-2.4	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3993	dirMS_041712_NAR_60mM_plus.11320.11320.3	3	13.96	0	1.93E+06		(R)EIVHIQA	(R)E/I V H I Q A/G/Q/C/G/N Q I G A K(F)	C:Carbamidomethylation	116.42	608.311	1822.923	-0.0044	-2.4	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
3994	dirMS_041712_NAR_60mM_plus.16411.16569.3	3	13.96	1	6.93E+05		(K)AAVEWI	(K)A/A/V|E/W/F/D/G K D F Q G S K(L)		142.92	562.2762	1684.797	0.0175	10.4	4.56	65213.5	9.57	HUMAN	B0QYK0	Ewing sarcoma breakpoint region 1
3995	dirMS_041712_NAR_60mM_plus.16699.16763.3	3	13.96	1	3.08E+05		(K)ARLEIEP	(K)A R L E\I\E|P|E/W A/Y/G K(K)		144.35	521.2734	1561.801	0.0047	3	4.79	25233.4	9.34	HUMAN	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3
3996	dirMS_041712_NAR_60mM_plus.17169.17169.3	3	13.96	1	1.45E+04		(R)LLDAQL/	(R)L/L|D A/Q/L/A T G G L V C P A R R(L)	C:Carbamidomethylation	148.03	604.3409	1810.996	0.0125	6.9	9.6	266161	5.68	HUMAN	E9PPU0	Epiplakin
3997	dirMS_041712_NAR_60mM_plus.17680.17680.3	3	13.96	1	4.10E+05		(K)ISDSEGF	(K)I/S/D/S/E/G F/K/A N L S L L R(R)		149.75	550.632	1649.886	-0.0043	-2.6	6.07	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
3998	dirMS_041712_NAR_120mM_minus.5466.5466.2	2	13.95	0	1.59E+05	M161m	(R)mQHLIA	(R)m Q|H/L I|A R(E)	m:Oxidized methionine	83.22	442.7426	868.482	15.9958	1	9.52	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
3999	dirMS_041712_NAR_40mM_minus2.15537.15580.3	3	13.95	1	7.01E+05		(K)LLPLVSD	(K)L L|P/L/V/S D/E/V/F I R D/V A K(V)		180.3	605.3511	1814.042	-0.0035	-1.9	4.56	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
4000	dirMS_041712_NAR_50mM_minus2.11386.11386.3	3	13.95	1	1.33E+05		(K)DVDEAY	(K)D V|D/E A/Y M/N K V/E L E S R(L)		133.2	599.9481	1797.832	-0.0026	-1.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
4001	dirMS_041712_NAR_60mM_minus.14890.14890.3	3	13.95	0	3.37E+05		(R)AVAIDLI	(R)A V|A\I/D L/P G L G H S K(E)		142.65	426.578	1277.721	-0.0018	-1.4	6.79	19983.6	8.14	HUMAN	B4DQI4	Alpha/beta hydrolase domain-containing protein 14B
4002	dirMS_041712_NAR_60mM_minus.6264.6264.3	3	13.95	1	1.15E+05		(K)DSYVGD	(K)D S/Y/V|G D E A|Q S K R(G)		93.23	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
4003	dirMS_041712_NAR_20mM_plus.13709.13709.3	3	13.95	0	1.00E+05		(K)IFVGNVS	(K)I F V G\N V|S\A A/C/T/S/Q/E L R(S)	C:Carbamidomethylation	166.63	584.6279	1751.874	-0.0053	-3.1	6	37433.2	9.17	HUMAN	B0LM41	Protein RBM14-RBM4
4004	dirMS_041712_NAR_20mM_plus.17517.17517.2	2	13.95	0	1.61E+05	M74m	(R)mIAGQV	(R)m I|A|G Q\V|L/D I N L A A E\P K(V)	m:Oxidized methionine	192.85	849.9568	1682.915	15.9918	-1.9	4.37	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
4005	dirMS_041712_NAR_30mM_plus2.16200.16482.2	2	13.95	0	5.66E+05		(R)YIEIFR(S	(R)Y/I|E/I/F/R(S)		138.45	420.7344	840.461	0.0001	0.1	6	36982.9	6.37	HUMAN	P31942	Heterogeneous nuclear ribonucleoprotein H3
4006	dirMS_041712_NAR_30mM_plus2.8895.8895.2	2	13.95	0	3.86E+05		(R)CSEQVQ	(R)C S|E/Q\V/Q/D|F|T\K(C)	C:Carbamidomethylation	100.43	621.2771	1241.547	0.0002	0.2	4.37	13533.5	9.82	HUMAN	H7C3D8	COX assembly mitochondrial protein homolog (Fragment)
4007	dirMS_041712_NAR_120mM_minus.6940.6940.2	2	13.94	1	2.88E+06		(R)TKTEISEI	(R)T K|T/E/I/S E/M N R(N)		92.53	604.8012	1208.594	0.0012	1	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
4008	dirMS_041712_NAR_30mM_minus2.16227.16227.2	2	13.94	0	1.63E+05		(K)SSEELLS/	(K)S S E/E|L|L|S A L Q/K(K)		141.32	602.816	1204.642	-0.0172	-14.3	4.53	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
4009	dirMS_041712_NAR_30mM_minus2.8588.8588.2	2	13.94	0	9.67E+04		(R)VGQDP\	(R)V/G/Q/D|P V/L/R(Q)		101.38	442.2532	883.5	-0.0005	-0.5	5.81	14130.9	9.56	HUMAN	C9K0U8	Single-stranded DNA-binding protein (Fragment)
4010	dirMS_041712_NAR_50mM_minus2.9347.9389.3	3	13.94	0	2.64E+05	M167m	(R)ImLFTNI	(R)I/m|L|F/T N E D N/P H/G N D S A K(A)	m:Oxidized methionine	121.37	640.2914	1902.865	15.9946	-0.2	4.54	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
4011	dirMS_041712_NAR_60mM_minus.15456.15579.3	3	13.94	1	4.69E+05		(K)YQLDKD	(K)Y/Q|L D/K/D/G V V/L/F/K(K)		146.33	475.5992	1424.778	0.0047	3.3	5.96	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
4012	dirMS_041712_NAR_60mM_minus.18540.18540.3	3	13.94	1	1.69E+05		(K)VVLDDK	(K)V/V/L/D/D K D/Y F L F R(D)		165.1	510.6099	1529.8	0.0153	10	4.43	5189.9	4.56	HUMAN	B8ZZ54	10 kDa heat shock protein, mitochondrial
4013	dirMS_041712_NAR_20mM_plus.17706.17805.2	2	13.94	0	4.14E+05		(R)ILVATNL	(R)I/L|V|A/T N/L/F/G R(G)		194.48	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
4014	dirMS_041712_NAR_20mM_plus.8387.8387.2	2	13.94	0	8.56E+04		(R)LAPEYE/	(R)L A|P/E/Y E/A/A A T R(L)		127.75	596.3035	1191.6	-0.0007	-0.6	4.53	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
4015	dirMS_041712_NAR_30mM_plus2.12095.12161.2	2	13.94	0	1.13E+05		(K)VWNLAI	(K)V/W|N|L/A/N C K(L)	C:Carbamidomethylation	116.4	502.7542	1004.498	0.0029	2.9	8.72	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
4016	dirMS_041712_NAR_30mM_plus2.19888.19888.2	2	13.94	0	2.26E+05		(K)GFAFVQ	(K)G F|A|F/V|Q/Y V/N E R(N)		157.63	665.3326	1329.659	-0.0007	-0.5	6	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
4017	dirMS_041712_NAR_50mM_plus2.13442.13442.3	3	13.94	0	9.05E+05		(R)TVVTGIE	(R)T V|V/T/G I/E M F H K(S)		138.55	421.225	1261.661	-0.0005	-0.4	6.41	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
4018	dirMS_041712_NAR_60mM_plus.7339.7418.3	3	13.94	0	5.01E+05		(R)SSGHSSS	(R)S S G H S S S E|L|S|P/D A V E K(A)		96.95	539.584	1616.74	-0.0024	-1.5	4.65	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
4019	dirMS_041712_NAR_60mM_plus.8497.8497.3	3	13.94	0	5.94E+05		(K)GQVCVN	(K)G Q|V/C V/M I/H|S G S R(G)	C:Carbamidomethylation	103.07	444.2219	1330.636	0.0157	11.8	9.75	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
4020	dirMS_041712_NAR_60mM_plus.9332.9332.3	3	13.94	0	4.66E+05	M89m	(K)VYNYNH	(K)V/Y/N Y/N/H L m/P T R(Y)	m:Oxidized methionine	106.8	475.2309	1407.684	15.9944	-0.4	8.57	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
4021	dirMS_041712_NAR_30mM_minus2.5793.6230.2	2	13.93	0	8.35E+05		(K)YAEAVTI	(K)Y/A|E|A|V/T/R(A)		86.87	405.2098	809.415	-0.0029	-3.5	6	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
4022	dirMS_041712_NAR_50mM_minus2.12792.12792.3	3	13.93	1	3.26E+06		(R)TEMENE	(R)T\E|M E N E F/V/L I/K K(D)		141.72	494.2621	1480.772	0.0002	0.1	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
4023	dirMS_041712_NAR_60mM_minus.15558.15578.3	3	13.93	0	3.57E+05		(K)THLPGF'	(K)T\H\L\P G\F\V|E|Q/A E A L/K(A)		146.42	513.947	1539.817	0.0099	6.4	5.37	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
4024	dirMS_041712_NAR_60mM_minus.17185.17680.3	3	13.93	1	1.28E+07	M148m	(R)LDLAGR	(R)L/D|L|A/G R D L/T/D/Y L/m K(I)	m:Oxidized methionine	157.95	547.2829	1623.841	15.9931	-1.1	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
4025	dirMS_041712_NAR_40mM_plus2.10715.10715.3	3	13.93	0	1.85E+05		(K)VGSLDN	(K)V/G|S/L D/N V/G\H L/P A G G A V/K(I)		128.15	530.9567	1590.86	-0.0043	-2.7	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
4026	dirMS_041712_NAR_50mM_plus2.9602.9602.3	3	13.93	1	3.39E+05		(R)AGTGVD	(R)A/G/T/G/V/D/N V/D L E A/A T R\K(G)		117.4	539.6108	1616.824	-0.006	-3.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
4027	dirMS_041712_NAR_60mM_plus.10817.10817.2	2	13.93	1	9.74E+05		(R)VKYETEI	(R)V/K/Y/E T E L/A/M R(Q)		113.65	620.326	1239.64	0.0045	3.7	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4028	dirMS_041712_NAR_60mM_plus.4780.4780.3	3	13.93	1	1.77E+06		(R)AAEEED	(R)A A\E/E/E/D E/A D/P K/R(Q)		80	453.872	1359.602	-0.0008	-0.6	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin

4029	dirMS_041712_NAR_30mM_minus2.15470.15470.2	2	13.92	0	3.81E+05		(R)AAPFSLE	(R)A A/P/F/S/L E/Y/R(V)		138.3	527.2782	1053.536	0.0128	12.1	6.04	33115.9	5.54	HUMAN	Q15181	Inorganic pyrophosphatase
4030	dirMS_041712_NAR_30mM_minus2.18311.18534.2	2	13.92	0	2.28E+05		(K)YPQLLP(	(K)Y/P|Q/L|L/P G I R(G)		154.92	528.816	1056.62	0.0047	4.4	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
4031	dirMS_041712_NAR_30mM_minus2.18572.18572.2	2	13.92	0	3.09E+05		(K)YPQLLP(	(K)Y/P/Q/L|L/P G I/R(G)		155.32	528.816	1056.62	0.0047	4.4	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
4032	dirMS_041712_NAR_30mM_minus2.5205.5407.2	2	13.92	0	7.07E+05		(R)TDTGEP	(R)T/D|T|G|E P M/G R(G)		82.22	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
4033	dirMS_041712_NAR_40mM_minus2.14853.14853.3	3	13.92	1	1.13E+06	M116m	(R)ELAILLG	(R)E L A|I/L L/G m L D/P A E K D E K(G)	m:Oxidized methionine	171.42	634.338	1884.999	16.0008	3.1	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
4034	dirMS_041712_NAR_60mM_minus.14281.14281.3	3	13.92	0	4.62E+05		(R)SDSFENI	(R)S D|S/F/E N/P V/L/Q Q H F/R(N)		139.27	568.6086	1703.814	-0.0024	-1.4	5.3	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
4035	dirMS_041712_NAR_20mM_plus.7638.7837.2	2	13.92	0	6.94E+05		(K)VIDDTNI	(K)V/I|D|D/T N I/T/R(L)		123.18	523.7766	1046.548	-0.0017	-1.7	4.21	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4036	dirMS_041712_NAR_50mM_plus2.20866.20866.3	3	13.92	1	7.61E+04		(K)TSAQVV	(K)T S|A Q/V/V/L D G L V D K I G D/V/K(C)		178.37	619.6814	1857.033	-0.0031	-1.7	4.43	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
4037	dirMS_041712_NAR_60mM_plus.7240.7411.2	2	13.92	1	1.58E+06		(R)AAPGAE	(R)A/A/P/G A|E|F/A\P N K/R(R)		96.2	614.8248	1228.643	-0.001	-0.8	8.79	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
4038	dirMS_041712_NAR_60mM_plus.9429.9429.2	2	13.92	0	1.98E+06		(R)IGAEVYI	(R)I/G\A/E/V|Y/H/N L K(N)		107.55	572.3143	1143.616	0.0056	4.9	6.75	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
4039	dirMS_041712_NAR_30mM_minus2.11407.11407.2	2	13.91	0	1.21E+05	M39m	(K)mFLYAD	(K)m F|L/Y/A/D/N E D/R(A)	m:Oxidized methionine	115.58	645.2795	1273.552	16	3.9	4.03	24724.1	5.17	HUMAN	E7ETQ7	Vacuolar protein sorting-associated protein VTA1 homolog
4040	dirMS_041712_NAR_30mM_minus2.12151.12180.2	2	13.91	0	3.38E+05		(K)ILYSQCG	(K)I L|Y/S/Q/C G D V M/R(A)	C:Carbamidomethylation	119.22	671.3183	1341.629	0.0004	0.3	5.83	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
4041	dirMS_041712_NAR_30mM_minus2.14104.14455.2	2	13.91	0	1.06E+06		(R)FLDPNTI	(R)F/L|D|P/N T L E/R(L)		131.2	552.7932	1104.568	0.0107	9.7	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
4042	dirMS_041712_NAR_50mM_minus2.8660.8660.3	3	13.91	0	1.65E+05	M180m	(R)VVVLm(	(R)V V|V/L/m/G S T S D L G H/C E K(I)	C:Carbamidomethylation m:Oxid	117.55	583.2829	1731.84	15.9937	-0.7	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
4043	dirMS_041712_NAR_60mM_minus.11568.11568.3	3	13.91	1	2.94E+05		(R)VFDKEG	(R)V F/D K E G|N G T|V|M/G A/E I R(H)		124.35	574.9539	1722.848	-0.0008	-0.5	4.68	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
4044	dirMS_041712_NAR_120mM_plus.10177.10435.3	3	13.91	1	1.33E+06		(R)YLAEFAT	(R)Y/L|A E/F/A/T/G N D R K(E)		107.65	462.2337	1384.686	0.001	0.7	6.07	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
4045	dirMS_041712_NAR_120mM_plus.10839.10881.3	3	13.91	1	4.58E+05		(R)RFDDAV	(R)R\F D D\A\V|V|Q/S D/M/K(H)		110.08	470.8945	1410.668	0.0008	0.5	4.43	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
4046	dirMS_041712_NAR_120mM_plus.8455.8476.4	4	13.91	0	3.85E+05		(K)LLETTDR	(K)L/L/E/T/T/D R P D G H Q/N N L/R(S)		97.58	470.4895	1878.942	-0.0055	-2.9	5.38	82375.7	4.6	HUMAN	B7ZAV6	Importin subunit beta-1
4047	dirMS_041712_NAR_120mM_plus.8614.8786.3	3	13.91	0	1.32E+06		(R)RPELEDS	(R)R P\E|L|E|D/S/T/L/R(Y)		98.35	405.8796	1215.633	-0.0085	-7	4.68	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
4048	dirMS_041712_NAR_20mM_plus.16643.16643.3	3	13.91	0	2.14E+05		(K)VQIAVA	(K)V Q\I A V\A N\A|Q/E/L/L/Q R(M)		186.3	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
4049	dirMS_041712_NAR_20mM_plus.18407.18407.2	2	13.91	0	1.95E+05		(R)AAVEEG	(R)A A V E\E/G/I|V|L\G|G G C A L/L R(C)	C:Carbamidomethylation	197.9	842.9549	1684.905	-0.0025	-1.5	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
4050	dirMS_041712_NAR_30mM_plus2.7258.7258.2	2	13.91	0	6.90E+04		(R)SQLQISN	(R)S Q|L|Q|I/S|N/N R(T)		92.6	530.2783	1059.554	-0.0048	-4.6	9.47	334221.3	6.44	HUMAN	P15924	Desmoplakin
4051	dirMS_041712_NAR_40mM_plus2.13445.13465.3	3	13.91	1	3.11E+05		(K)VIDPATA	(K)V/I|D|P A/T A/T\S V D L R D/I/K(I)		145.75	571.9836	1713.938	-0.0019	-1.1	4.43	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
4052	dirMS_041712_NAR_50mM_plus2.16374.16374.3	3	13.91	0	2.89E+05		(K)ACQSIYF	(K)A C|Q/S\I/Y/P L/H D/V F V R(K)	C:Carbamidomethylation	154.4	568.9562	1704.853	0.0014	0.8	6.79	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
4053	dirMS_041712_NAR_20mM_minus.13276.13276.2	2	13.9	0	2.34E+05		(R)GVVDSE	(R)G V/V D S\E/D/I|P L N|L/S R(E)		183.02	757.3944	1513.786	-0.0041	-2.7	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
4054	dirMS_041712_NAR_30mM_minus2.10239.10413.2	2	13.9	0	1.06E+06		(K)DVGSLA	(K)D V|G\S|L/A|S V Q|R(Y)		109.78	516.281	1031.548	0.0067	6.5	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin
4055	dirMS_041712_NAR_30mM_minus2.15664.15664.2	2	13.9	0	2.70E+04	M1342m	(R)ASLSLW	(R)A S/L|S|L\W Q A/m/E K(G)	m:Oxidized methionine	138.55	640.3185	1263.64	15.9895	-4.2	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
4056	dirMS_041712_NAR_30mM_minus2.8013.8131.2	2	13.9	0	2.96E+05		(R)FLNAEN.	(R)F/L|N|A|E N/A|Q K(F)		98.62	517.7675	1034.526	0.0012	1.1	6	20592.3	9.75	HUMAN	B3KUP2	RAN binding protein 1, isoform CRA_f
4057	dirMS_041712_NAR_50mM_minus2.15448.15448.3	3	13.9	1	1.73E+05		(K)DVLFLKI	(K)D V/L|F/L K D C V/G P\E V/E K(A)	C:Carbamidomethylation	156.42	583.3014	1747.893	-0.0039	-2.2	4.32	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
4058	dirMS_041712_NAR_60mM_minus.9590.9671.3	3	13.9	1	2.76E+06	M239m	(R)MQKEIT	(R)M Q/K E I T A|L|A/P/S T m K(I)	m:Oxidized methionine	114.28	522.2733	1548.812	15.9929	-1.3	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
4059	dirMS_041712_NAR_120mM_plus.11648.11659.3	3	13.9	0	5.02E+05		(R)HSSLAG(	(R)H S\S L\A G\C|Q|I|I/N Y R(T)	C:Carbamidomethylation	114.17	506.9192	1518.748	-0.0051	-3.4	8.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
4060	dirMS_041712_NAR_30mM_plus2.16699.16699.2	2	13.9	0	9.86E+05		(R)AALQELI	(R)A A/L/Q/E L/L/S K(G)		139.35	486.7894	972.572	-0.0009	-0.9	6.05	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
4061	dirMS_041712_NAR_30mM_plus2.18556.18556.2	2	13.9	0	3.64E+05		(R)SSFYVN(	(R)S S/F\Y/V|N|G L T\L G/G Q/K(C)		150.97	735.8825	1470.759	-0.001	-0.7	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
4062	dirMS_041712_NAR_30mM_plus2.21112.21112.2	2	13.9	0	6.77E+05		(K)IPDWFLI	(K)I/P/D/W/F L/N R(Q)		165.77	530.785	1060.557	0.0053	5	5.84	9767.1	11.41	HUMAN	J3JS69	40S ribosomal protein S18
4063	dirMS_041712_NAR_30mM_plus2.6226.6226.2	2	13.9	0	5.49E+05		(K)IVEMSTS	(K)I/V|E/M/S T/S K(T)		87.1	447.7285	894.46	-0.0104	-11.6	6	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
4064	dirMS_041712_NAR_30mM_plus2.9082.9082.2	2	13.9	0	2.75E+05	M406m	(R)EYQELm	(R)E Y/Q/E/L/m/N V/K(L)	m:Oxidized methionine	101.23	585.2792	1153.556	15.9953	0.4	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
4065	dirMS_041712_NAR_40mM_plus2.7594.7594.2	2	13.9	0	6.02E+05		(K)ASLENSI	(K)A/S/L/E/N S L R(E)		105.33	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4066	dirMS_041712_NAR_50mM_plus2.10708.10708.3	3	13.9	0	4.45E+05		(K)MIVDPV	(K)M I|V/D/P/V E/P H/G E M K(F)		123.4	494.5783	1481.713	0.0076	5.2	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
4067	dirMS_041712_NAR_50mM_plus2.11679.11679.3	3	13.9	0	3.41E+05		(K)SNMGH	(K)S N/M G H P E/P A/S/G/L A A/L A K(V)		128.55	550.9462	1650.827	-0.0028	-1.7	6.47	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
4068	dirMS_041712_NAR_50mM_plus2.16381.16394.3	3	13.9	0	1.45E+06		(K)IEVIKPG	(K)I/E|V/I/K/P G D L/G V D L T S K(L)		154.62	561.9883	1683.953	-0.0024	-1.4	4.56	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
4069	dirMS_041712_NAR_60mM_plus.12847.12910.3	3	13.9	0	3.95E+06		(R)ITLRPDP	(R)I/T|L R P D|P\L/P E/R(S)		123.53	436.2506	1306.748	-0.0105	-8	6.07	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
4070	dirMS_041712_NAR_60mM_plus.5129.5129.3	3	13.9	0	2.14E+04		(K)EILEGPS	(K)E I|L E G/P S P/E W/E T K(A)		85.37	505.5852	1514.737	0.0037	2.5	4.09	89503.2	9.38	HUMAN	Q9HBT7	Zinc finger protein 287
4071	dirMS_041712_NAR_60mM_minus.11151.11151.2	2	13.89	1	2.01E+05		(R)DGKLVS	(R)D G K/L|V|S E S S D/V L\P K(-)		122.23	737.3855	1473.78	-0.0158	-10.7	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
4072	dirMS_041712_NAR_20mM_plus.15084.15126.2	2	13.89	0	2.17E+05		(K)GLAITFV	(K)G L A\I|T|F/V|S/D E N D A K(I)		175.3	740.3693	1479.733	-0.0012	-0.8	4.03	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
4073	dirMS_041712_NAR_20mM_plus.8860.9097.2	2	13.89	0	1.23E+06	M239m	(K)EITALAP	(K)E I|T|A|L|A|P S T m K(I)	m:Oxidized methionine	132.6	589.309	1161.618	15.9923	-2.2	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
4074	dirMS_041712_NAR_40mM_plus2.19346.19346.3	3	13.89	0	1.61E+06		(R)AGKPVI(	(R)A G K P V\I\C A\T Q|M/L/E S M I K(K)	C:Carbamidomethylation	180.63	626.3273	1876.969	-0.002	-1.1	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
4075	dirMS_041712_NAR_60mM_plus.12728.12729.3	3	13.89	1	1.27E+06		(R)MLFKDI	(R)M/L|F K/D D Y|P/S S/P P K(C)		123.65	508.9175	1524.74	-0.0023	-1.5	5.71	20685.4	9.18	HUMAN	B0QYN7	SUMO-conjugating enzyme UBC9
4076	dirMS_041712_NAR_60mM_plus.7458.7458.3	3	13.89	1	9.72E+05		(K)GGETIK(	(K)G G|E|T/I/K Q L/Q/E R(A)		97.52	420.23	1258.675	0.0005	0.4	6.14	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
4077	dirMS_041712_NAR_30mM_minus2.13393.13571.2	2	13.88	0	5.79E+05		(R)TIAQDY(	(R)T I|A|Q/D/Y/G\V/L K(A)		126.9	554.3051	1107.604	-0.0015	-1.4	5.5	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
4078	dirMS_041712_NAR_30mM_minus2.14353.14353.2	2	13.88	0	1.99E+05		(R)ELAFQIS	(R)E L/A/F/Q/I/S/K(E)		131.7	468.2614	935.52	-0.0041	-4.4	6.1	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
4079	dirMS_041712_NAR_30mM_minus2.6957.7297.2	2	13.88	0	9.72E+05		(K)IVEMSTS	(K)I/V|E/M/S/T/S/K(T)		93.58	447.7317	894.46	-0.004	-4.4	6	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
4080	dirMS_041712_NAR_50mM_minus2.12368.12368.3	3	13.88	0	2.32E+05		(K)AASDIAI	(K)A A/S D\I|A/M/T/E L/P P T H P I R(L)		138.97	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
4081	dirMS_041712_NAR_120mM_plus.7142.7206.3	3	13.88	1	1.11E+06		(R)SDYDGI(	(R)S/D|Y/D/G I/G S R/G D R(S)		91.03	433.1967	1297.577	-0.0012	-0.9	4.43	15031.5	6.72	HUMAN	B4DLA0	ATP-dependent RNA helicase DDX3X
4082	dirMS_041712_NAR_20mM_plus.12395.12395.2	2	13.88	0	1.87E+05		(R)GVEICIA	(R)G V|E/I/C/I/A\T/P G R(L)	C:Carbamidomethylation	158.58	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
4083	dirMS_041712_NAR_20mM_plus.13430.13683.2	2	13.88	0	2.13E+05	M98m	(R)TLTIVDT	(R)T L|T\I|V/D|T G I|G m T K(A)	m:Oxidized methionine	166.47	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
4084	dirMS_041712_NAR_20mM_plus.17966.17966.2	2	13.88	0	1.95E+05		(K)GADFLV	(K)G A D/F L|V|T\E/V|E N G G S L/G S\K(K)		195.22	890.4414	1779.876	-0.0004	-0.2	4.14	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
4085	dirMS_041712_NAR_40mM_plus2.11210.11210.3	3	13.88	0	1.02E+05		(R)VLVASS\	(R)V/L|V/A/S/S V V A G E S Q K/P E L K(A)		132.05	614.3443	1841.038	-0.0195	-10.6	6.11	61441.6	5.93	HUMAN	G8JLE9	Fragile X mental retardation protein 1
4086	dirMS_041712_NAR_50mM_plus2.15329.15329.3	3	13.88	0	9.75E+05		(R)QVLIASH	(R)Q V\L/I/A/S H/L/P S Y E L/R(H)		149.48	542.6394	1625.901	0.0027	1.6	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
4087	dirMS_041712_NAR_60mM_plus.7404.7404.3	3	13.88	0	4.28E+05		(K)ITPAHD(	(K)I/T/P A H D Q/N D/Y/E V/G Q R(H)		96.47	581.6074	1742.809	-0.0016	-0.9	4.54	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
4088	dirMS_041712_NAR_60mM_plus.8216.8216.3	3	13.88	1	8.11E+05		(R)FEPYANI	(R)F E|P/Y/A N/P T K R(Y)		101.27	408.2176	1222.622	0.0167	13.7	8.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
4089	dirMS_041712_NAR_20mM_minus.10614.10680.2	2	13.87	0	2.00E+05		(R)TTPSYVA	(R)T/T|P S Y/V/A|F T D/T E R(L)		154.63	744.3547	1487.701	0.0009	0.6	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
4090	dirMS_041712_NAR_40mM_minus2.16109.16109.3	3	13.87	1	6.62E+05		(R)ELAILLG	(R)E L/A/I/L/L\G M/L D/P A E K D E K(G)		189.6	629.0034	1884.999	-0.003	-1.6	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
4091	dirMS_041712_NAR_50mM_minus2.14733.14733.3	3	13.87	1	1.82E+05		(K)ELKIDIIP	(K)E L K I D I\I|P/N/P Q E R(T)		151.52	522.2945	1564.869	-0.0004	-0.2	4.68	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
4092	dirMS_041712_NAR_60mM_minus.9322.9322.3	3	13.87	1	2.37E+05		(R)QDSAAV	(R)Q D S A/A/V/G/F D/Y K E K(L)		111.87	486.5639	1457.691	-0.0136	-9.3	4.56	61756.2	5.24	HUMAN	Q14247	Src substrate cortactin
4093	dirMS_041712_NAR_20mM_plus.16231.16231.3	3	13.87	0	1.32E+05		(R)LLDAQL/	(R)L L D/A\Q L A T G/G|I/V/D/P R(L)		183.53	513.6218	1538.854	-0.0028	-1.8	4.21	533778	5.74	HUMAN	Q15149	Plectin
4094	dirMS_041712_NAR_20mM_plus.17964.17964.2	2	13.87	0	1.96E+05		(K)VANVSL	(K)V A/N/V|S/L/L/A/L Y K(G)		195.33	595.8558	1190.714	-0.01	-8.4	8.56	15978.4	10.84	HUMAN	P62266	40S ribosomal protein S23
4095	dirMS_041712_NAR_30mM_plus2.8419.8419.2	2	13.87	0	1.01E+06		(R)ALANSL/	(R)A L|A/N/S/L A/C Q G/K(Y)	C:Carbamidomethylation	97.78	566.7922	1132.578	-0.0008	-0.7	8.8	13951.6	9.48	HUMAN	H3BR68	Fructose-bisphosphate aldolase A (Fragment)
4096	dirMS_041712_NAR_30mM_plus2.9055.9055.2	2	13.87	0	5.15E+05		(R)LATNTS/	(R)L/A|T N/T/S A P D L/K(N)		100.7	565.801	1130.605	-0.0105	-9.2	5.84	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
4097	dirMS_041712_NAR_40mM_plus2.14922.14922.3	3	13.87	0	3.03E+05		(R)IEGDMI\	(R)I/E|G D M I V C/A A/Y/A H E L/P K(Y)	C:Carbamidomethylation	153.93	639.6498	1916.925	0.0104	5.4	4.65	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
4098	dirMS_041712_NAR_50mM_plus2.6147.6147.3	3	13.87	0	1.25E+05		(R)SGSMDI	(R)S/G|S M/D/P/S/G A H P S V R(Q)		96.5	462.214	1384.627	0.0001	0	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
4099	dirMS_041712_NAR_20mM_minus.10086.10086.2	2	13.86	0	1.24E+05		(R)YALYDA	(R)Y A|L|Y/D A T Y E T K(E)		150.82	669.3156	1337.626	-0.0021	-1.5	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
4100	dirMS_041712_NAR_50mM_minus2.14942.15170.3	3	13.86	0	4.69E+05		(K)IAILTCPI	(K)I/A|I|L/T/C/P F E/P P K/P K(T)	C:Carbamidomethylation	153.5	537.6375	1610.898	0.0005	0.3	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
4101	dirMS_041712_NAR_120mM_plus.13623.13926.3	3	13.86	0	1.60E+06		(R)NLDIERI	(R)N/L|D|I/E R/P T Y/T/N L N R(L)		125.65	573.6317	1718.882	-0.0015	-0.9	6.07	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
4102	dirMS_041712_NAR_20mM_plus.12993.12993.2	2	13.86	0	2.33E+04		(K)AVDSLVI	(K)A V/D/S/L/V/P I G R(G)		162.43	513.8007	1026.594	-0.0001	-0.1	5.88	48851.3	9.2	HUMAN	K7EK63	ATP synthase subunit alpha, mitochondrial
4103	dirMS_041712_NAR_20mM_plus.13796.13796.2	2	13.86	0	4.19E+04		(K)IVLTNPV	(K)I V|L T|N/P V C T E V G E/K(I)	C:Carbamidomethylation	167.07	779.9082	1558.815	-0.0054	-3.5	4.53	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
4104	dirMS_041712_NAR_20mM_plus.15836.15836.2	2	13.86	0	7.36E+05	M73m	(R)AILVDLE	(R)A I L/V/D L|E|P G T m D\S V R(S)	m:Oxidized methionine	179.55	816.4181	1615.836	15.9929	-1.2	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
4105	dirMS_041712_NAR_30mM_plus2.19241.19241.2	2	13.86	0	1.73E+05		(K)YPQLLP(	(K)Y/P/Q/L/L/P G I R(G)		153.33	528.814	1056.62	0.0007	0.6	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
4106	dirMS_041712_NAR_30mM_plus2.20483.20483.2	2	13.86	0	1.76E+05		(K)GSFSEQ(	(K)G S/F/S|E/Q/G I/N E/F\L/R(E)		161.02	742.362	1483.718	-0.0009	-0.6	4.53	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
4107	dirMS_041712_NAR_40mM_plus2.17987.17987.3	3	13.86	0	2.83E+05		(K)LLYDLAI	(K)L L|Y/D/L A D Q/L/H A A V\G A S R(A)		171.38	604.9967	1812.96	0.0153	8.4	5.21	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
4108	dirMS_041712_NAR_50mM_plus2.5148.5154.3	3	13.86	0	7.90E+04		(R)AEAEAG	(R)A E|A|E/A/G S P R/P D|P/R(E)		85.77	451.5555	1352.655	-0.0034	-2.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
4109	dirMS_041712_NAR_60mM_plus.10963.10963.3	3	13.86	1	2.14E+06		(R)KLDPGSI	(R)K\L D P G S|E E|T/Q|T/L/V R(E)		114.92	524.9456	1572.823	-0.0005	-0.3	4.68	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
4110	dirMS_041712_NAR_20mM_minus.10994.11296.2	2	13.85	0	3.73E+06	M148m	(R)DLTDYLr	(R)D L|T|D|Y/L/m/K(I)	m:Oxidized methionine	161.35	507.7443	998.486	15.995	0.1	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
4111	dirMS_041712_NAR_20mM_minus.14722.14890.2	2	13.85	0	3.01E+06		(K)EIIDLVLI	(K)E I|I/D/L/V/L/D/R(I)		203.67	543.3133	1085.62	-0.0008	-0.7	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
4112	dirMS_041712_NAR_40mM_minus2.8291.8291.3	3	13.85	0	2.03E+05	M35m	(K)AASDIAr	(K)A A|S D I/A m T E L/P P T/H P I R(L)	m:Oxidized methionine	128.85	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
4113	dirMS_041712_NAR_50mM_minus2.7412.7412.3	3	13.85	0	1.42E+04		(K)QEYDES(	(K)Q E/Y/D E/S G/P/S I/V H/R(K)		109.17	506.2404	1516.703	0.004	2.6	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
4114	dirMS_041712_NAR_60mM_minus.14870.14870.3	3	13.85	1	3.80E+05		(R)IKIGDPL	(R)I K/I G D/P\L/L/E/D/T R(M)		142.73	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
4115	dirMS_041712_NAR_60mM_minus.6327.6327.3	3	13.85	1	3.26E+04		(K)LEEAEKA	(K)L E/E A E/K/A/A/D E/S E R(G)		93.93	492.8981	1476.681	-0.0015	-1	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
4116	dirMS_041712_NAR_60mM_minus.9099.9193.3	3	13.85	1	1.02E+06		(R)ETAEAD'	(R)E/T/A/E/A D/V/A/S L N R R(I)		111.37	477.9107	1431.719	-0.0011	-0.8	4.68	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
4117	dirMS_041712_NAR_120mM_plus.20351.20351.3	3	13.85	0	3.29E+05		(R)INLWHL	(R)I/N/L/W/H/L E I T D/R(S)		159.47	470.5889	1409.754	-0.0014	-1	5.32	52204.6	5.82	HUMAN	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
4118	dirMS_041712_NAR_20mM_plus.14017.14017.2	2	13.85	0	9.86E+04	M313m	(R)TVQSLEI	(R)T V/Q/S/L/E|I D L D S m R(N)	m:Oxidized methionine	168.37	761.8738	1506.747	15.9935	-0.9	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4119	dirMS_041712_NAR_20mM_plus.17169.17190.2	2	13.85	0	9.08E+05		(R)VLITTDL	(R)V/L|I/T/T/D L L/A/R(G)		190.55	557.8442	1114.683	-0.0019	-1.7	5.81	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
4120	dirMS_041712_NAR_50mM_plus2.16977.16977.3	3	13.85	1	4.54E+05		(K)VLDSGA	(K)V/L|D/S G A/P I\K I/P V G P/E/T L G R(I)		156.95	640.3623	1919.096	-0.0237	-12.3	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
4121	dirMS_041712_NAR_50mM_plus2.21413.21413.3	3	13.85	0	4.74E+06		(R)LHFFMP	(R)L H F\F\M\P G\F|A|P\L T S R(G)		182.07	540.9498	1620.835	-0.0007	-0.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
4122	dirMS_041712_NAR_60mM_plus.9175.9311.3	3	13.85	1	1.59E+06		(R)SRAEAES	(R)S R A E\A\E|S|M/Y/Q/I/K(Y)		105.9	471.5691	1412.684	0.0089	6.3	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
4123	dirMS_041712_NAR_30mM_minus2.16116.16116.2	2	13.84	1	1.52E+05		(R)FVLSQAI	(R)F V|L|S/Q A K/D E\L(-)		141.4	575.3113	1149.615	0.0003	0.3	4.37	41053.3	5.58	HUMAN	Q86UY0	TXNDC5 protein
4124	dirMS_041712_NAR_40mM_minus2.14882.14911.3	3	13.84	1	5.46E+05		(R)GDLGIEI	(R)G D/L\G|I|E/I/P A E K V F L A Q K(M)		173.02	610.0109	1828.022	-0.0033	-1.8	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
4125	dirMS_041712_NAR_60mM_minus.8224.8224.3	3	13.84	0	1.91E+05		(R)QYDISDI	(R)Q Y/D/I/S D/P Q/R/P R(L)		105.63	458.8971	1374.676	0.0007	0.5	5.96	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
4126	dirMS_041712_NAR_30mM_plus2.13565.13688.2	2	13.84	0	2.41E+06		(K)LIGEYGL	(K)L/I|G/E/Y/G L/R(N)		124.88	460.7596	920.52	-0.0081	-8.8	6	9591.1	10.94	HUMAN	A8MXK4	40S ribosomal protein S9
4127	dirMS_041712_NAR_50mM_plus2.9827.9827.3	3	13.84	1	2.02E+05		(R)AESGPD	(R)A E|S G/P D L R\Y E V/T|S/G G G/G T S R(M)		119.13	665.9843	1995.937	0.0017	0.9	4.68	334221.3	6.44	HUMAN	P15924	Desmoplakin
4128	dirMS_041712_NAR_60mM_plus.6958.6958.3	3	13.84	1	1.77E+05		(K)VQVYQE	(K)V/Q|V/Y Q E/P N/R E/T/R(V)		94.82	506.9252	1518.766	-0.0049	-3.2	6.11	35946.5	9.41	HUMAN	B7ZKZ1	Phosphoribosyl pyrophosphate synthase-associated protein 2
4129	dirMS_041712_NAR_50mM_minus2.12544.12690.3	3	13.83	0	4.05E+05		(R)SLATTRI	(R)S L|A|T|T/R P T V/N A D D|L L/K(V)		140.2	572.3135	1714.933	-0.0074	-4.3	5.68	49182.3	7.8	HUMAN	Q9UN37	Vacuolar protein sorting-associated protein 4A
4130	dirMS_041712_NAR_50mM_minus2.15135.15135.3	3	13.83	0	2.95E+05		(R)DGLAFN	(R)D G L A/F/N/A/L/I H R(H)		155.02	409.5594	1226.664	-0.0004	-0.3	6.74	146974	5.55	HUMAN	C9JRP8	Spectrin beta chain, non-erythrocytic 4
4131	dirMS_041712_NAR_120mM_plus.6459.6621.2	2	13.83	0	4.57E+05		(K)HQPTAII	(K)H/Q|P T A I\I|A/K(T)		87.75	489.7897	978.573	-0.001	-1	8.76	63448.4	7.29	HUMAN	B4E022	Transketolase
4132	dirMS_041712_NAR_30mM_plus2.12982.13118.2	2	13.83	0	6.50E+05		(K)GDYPLE/	(K)G D|Y/P/L/E/A V/R(M)		121.92	510.2633	1019.516	0.0037	3.6	4.37	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
4133	dirMS_041712_NAR_50mM_plus2.10328.10328.3	3	13.83	1	2.19E+05		(R)TGLIKGS	(R)T|G\L|I K/G S G T A/E V/E/L K(K)		121.85	501.6143	1502.842	-0.0141	-9.4	5.81	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
4134	dirMS_041712_NAR_50mM_plus2.10640.10640.3	3	13.83	0	3.46E+05		(R)AIGSASE	(R)A I|G/S A/S E G A Q S S L Q E V Y/H K(S)		123.47	654.657	1961.956	0.0001	0.1	5.4	20148.5	4.65	HUMAN	B4E2V4	Proteasome (Prosome, macropain) subunit, alpha type, 5, isoform CRA_c
4135	dirMS_041712_NAR_50mM_plus2.7973.8205.3	3	13.83	0	2.70E+05		(K)STAGDT	(K)S T|A/G D/T/H/L/G G E D F D/N R(M)		109.7	564.5793	1691.726	-0.0022	-1.3	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
4136	dirMS_041712_NAR_60mM_plus.14411.14447.3	3	13.83	1	1.86E+03		(R)TVENIKI	(R)T/V|E/N I/K/D/P\L F/R(F)		133.2	444.5813	1331.732	-0.0024	-1.8	5.74	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
4137	dirMS_041712_NAR_120mM_minus.13523.13544.3	3	13.82	0	5.03E+05		(K)YNPTWI	(K)Y N|P/T/W/H/C I V G R(N)	C:Carbamidomethylation	128.4	468.2346	1402.669	0.0208	14.8	8.75	10536.9	6.9	HUMAN	P63167	Dynein light chain 1, cytoplasmic

4138	dirMS_041712_NAR_20mM_minus.12055.12055.2	2	13.82	0	1.19E+06	M256m	(R)SLDmDS	(R)S L|D/m\D/S/I I|A E\V/K(A)	m:Oxidized methionine	170.22	668.8364	1320.671	15.994	-0.7	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
4139	dirMS_041712_NAR_30mM_minus2.19457.19457.2	2	13.82	0	1.03E+06		(R)LFDQAF	(R)L/F/D/Q/A/F G L|P R(L)		162.27	582.315	1163.621	0.002	1.7	5.84	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
4140	dirMS_041712_NAR_30mM_minus2.19543.19543.2	2	13.82	0	2.75E+05		(R)ILVATNL	(R)I/L|V|A/T N L/F G R(G)		162.1	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
4141	dirMS_041712_NAR_50mM_minus2.10748.10748.3	3	13.82	0	1.78E+05		(R)LLELGPK	(R)L/L\E L/G P K/P E V|A Q Q T R(K)		129.08	560.3182	1678.949	-0.0086	-5.1	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
4142	dirMS_041712_NAR_50mM_minus2.11342.11342.3	3	13.82	1	5.02E+05		(K)ILIANTG	(K)I/L|I/A N/T/G M D T D/K I/K(I)		133.4	511.6179	1532.835	0.0039	2.5	5.96	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
4143	dirMS_041712_NAR_120mM_plus.14793.14954.3	3	13.82	0	1.55E+06		(-)MVNHFI	(-)M/V/N H/F/I/A E/F K(R)		131.67	412.5446	1235.624	-0.0049	-4	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
4144	dirMS_041712_NAR_20mM_plus.16787.16787.2	2	13.82	0	3.08E+05		(K)VQIAVA	(K)V Q|I/A|V|A/N A/Q E L/L Q R(M)		187.02	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
4145	dirMS_041712_NAR_30mM_plus2.12359.12861.2	2	13.82	0	7.56E+05		(R)LLVVTDI	(R)L/L|V|V/T D|P/R(A)		119.23	456.779	912.551	-0.0006	-0.6	5.84	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
4146	dirMS_041712_NAR_30mM_plus2.18887.18887.2	2	13.82	0	1.87E+05		(K)LNLGTV	(K)L N|L/G/T V/G F/Y R(T)		152.8	570.3123	1139.621	-0.0034	-3	8.75	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
4147	dirMS_041712_NAR_40mM_plus2.9052.9238.2	2	13.82	0	5.38E+05		(R)GGNFGF	(R)G G\N|F|G/F/G D/S/R(G)		116.43	507.2256	1013.444	0.0004	0.4	5.84	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
4148	dirMS_041712_NAR_50mM_plus2.11496.11496.3	3	13.82	1	2.80E+06	M72m	(R)TEmENE	(R)T/E/m E N\E\F V/L I/K K(D)	m:Oxidized methionine	127.98	499.5943	1480.772	15.9968	1.2	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
4149	dirMS_041712_NAR_50mM_plus2.12313.12451.3	3	13.82	1	7.86E+05		(K)IEVEKPF	(K)I/E|V E/K/P F A I A K E(-)		133.12	458.5944	1373.767	0.0012	0.8	5.01	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
4150	dirMS_041712_NAR_50mM_plus2.5862.5862.3	3	13.82	1	1.71E+05		(R)ATEGM	(R)A T|E/G/M/V/V/A/D/K N C S K(I)	C:Carbamidomethylation	94.28	503.9061	1509.704	0.0002	0.1	6.11	15607.8	9.99	HUMAN	B4E0P1	Proteasome (Prosome, macropain) subunit, beta type, 7, isoform CRA_b
4151	dirMS_041712_NAR_60mM_plus.9245.9245.3	3	13.82	1	3.38E+05		(K)YIDENQI	(K)Y/I/D\E/N Q D R Y I/K(K)		106.53	486.2401	1456.707	-0.0009	-0.6	4.56	6412.4	9.52	HUMAN	J3KSS4	Cytosolic non-specific dipeptidase (Fragment)
4152	dirMS_041712_NAR_30mM_minus2.20190.20272.2	2	13.81	0	6.55E+05		(K)IGFPWSI	(K)I/G/F|P/W/S\E I R(N)		171.88	552.7932	1104.584	-0.0045	-4.1	6	71218.8	6.3	HUMAN	A7YIJ8	Radixin
4153	dirMS_041712_NAR_30mM_minus2.7344.7382.2	2	13.81	0	5.46E+05		(R)DATME	(R)D A|T|M/E/V/Q/R(G)		94.87	475.2269	949.441	0.0058	6.1	4.37	558007.1	5.44	HUMAN	P58107	Epiplakin
4154	dirMS_041712_NAR_40mM_minus2.9385.9445.3	3	13.81	0	2.76E+05		(K)AGVVGF	(K)A/G|V\V|G|P E L/H/E Q L L S A E/K(A)		138.13	592.9867	1776.949	-0.0035	-2	4.75	533778	5.74	HUMAN	Q15149	Plectin
4155	dirMS_041712_NAR_50mM_minus2.11264.11264.3	3	13.81	1	1.86E+05		(R)DNKQA	(R)D N K Q A\G\V/F/E/P T I V K(V)		132.05	515.9485	1545.827	0.0038	2.5	6.07	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
4156	dirMS_041712_NAR_50mM_minus2.14145.14145.3	3	13.81	1	1.56E+05		(K)KGVNLP	(K)K G V N L P G\A\A|V/D|L/P A V/S E K(D)		148.73	588.9987	1764.985	-0.0039	-2.2	6.07	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
4157	dirMS_041712_NAR_60mM_minus.12602.12764.3	3	13.81	1	1.12E+06		(K)AVLFCLS	(K)A V/L|F/C/L/S E D/K K(N)	C:Carbamidomethylation	131.03	437.2334	1309.682	0.0036	2.7	6.11	22956	8.8	HUMAN	E9PK25	Cofilin-1
4158	dirMS_041712_NAR_120mM_plus.9704.9704.2	2	13.81	0	8.09E+05		(R)FATHAA	(R)F A/T/H/A|A\A L S V|R(N)		104.23	572.3112	1143.627	-0.0118	-10.3	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
4159	dirMS_041712_NAR_20mM_plus.11926.11926.2	2	13.81	0	7.68E+04		(K)ILQDGG	(K)I/L|Q/D/G G L Q V/V E K(Q)		155.55	649.8662	1298.731	-0.0063	-4.9	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
4160	dirMS_041712_NAR_30mM_plus2.16130.16130.2	2	13.81	0	2.79E+05		(K)MDQAII	(K)M/D Q|A|I/I/F/C/R(T)	C:Carbamidomethylation	137.37	577.2809	1153.549	0.0053	4.6	5.59	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
4161	dirMS_041712_NAR_40mM_plus2.13263.13421.3	3	13.81	0	6.01E+05		(R)QVSASE	(R)Q/V S A/S E L/H/T S G\I/L/G/P E T L R(D)		145.08	665.6807	1995.051	-0.023	-11.5	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
4162	dirMS_041712_NAR_50mM_plus2.9720.9720.3	3	13.81	1	3.83E+05		(K)LTSDDVI	(K)L/T/S D D/V K/E/Q I Y K(L)		118.77	480.2521	1438.742	-0.0007	-0.5	4.56	12573.5	10.39	HUMAN	E9PS50	40S ribosomal protein S13 (Fragment)
4163	dirMS_041712_NAR_60mM_plus.12448.12627.3	3	13.81	0	1.52E+06		(K)ADDGRI	(K)A/D|D/G R/P F/P Q V/I\K(S)		121.6	448.2414	1342.711	-0.0017	-1.3	6	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
4164	dirMS_041712_NAR_30mM_minus2.17126.17126.2	2	13.8	0	4.44E+04		(K)LGINSLC	(K)L G|I|N/S/L/Q E\L K(Q)		146.95	557.8242	1114.647	-0.0055	-5	6	25978.5	4.91	HUMAN	C9J502	Prostate leucine zipper variant 2
4165	dirMS_041712_NAR_30mM_minus2.9063.9084.2	2	13.8	0	8.36E+05		(R)ALANSL	(R)A L|A/N/S/L\A/C/Q/G K(Y)	C:Carbamidomethylation	103.73	566.7927	1132.578	0.0002	0.2	8.8	13951.6	9.48	HUMAN	H3BR68	Fructose-bisphosphate aldolase A (Fragment)
4166	dirMS_041712_NAR_50mM_minus2.13554.13554.3	3	13.8	0	3.38E+05		(K)MLDAED	(K)M/L/D/A E/D I/V N T A R\P D E K(A)		145.72	606.2965	1816.875	0.0004	0.2	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
4167	dirMS_041712_NAR_50mM_minus2.14706.14706.3	3	13.8	1	4.18E+05		(K)GCLELIK	(K)G C/L E L I/K E/T G/V/P I/A G/R(H)	C:Carbamidomethylation	151.82	571.6494	1712.936	-0.0027	-1.6	6.14	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
4168	dirMS_041712_NAR_50mM_minus2.16456.16456.3	3	13.8	1	1.60E+05		(K)VVSSVL	(K)V V|S S/V L/Q/F/G N I S F K K(E)		162	551.6488	1652.937	-0.0052	-3.1	10	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
4169	dirMS_041712_NAR_60mM_minus.15834.15834.3	3	13.8	1	3.14E+05		(R)IDTRNEI	(R)I D|T R N E L/E|S/Y/A Y S L/K(N)		148.13	601.3049	1801.897	0.0035	1.9	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
4170	dirMS_041712_NAR_20mM_plus.17996.17996.2	2	13.8	0	1.36E+05		(R)LFDQAF	(R)L F|D Q/A/F/G/L/P R(L)		195.52	582.3166	1163.621	0.0052	4.4	5.84	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
4171	dirMS_041712_NAR_30mM_plus2.13844.13879.2	2	13.8	0	6.93E+04		(R)LNLNNT	(R)L/N|L|N|N T/V|L/S K(R)		127.2	558.323	1115.642	-0.0032	-2.8	8.75	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
4172	dirMS_041712_NAR_30mM_plus2.16608.16608.2	2	13.8	0	3.86E+04		(K)LGEWV	(K)L/G/E/W/V/G L C K(I)	C:Carbamidomethylation	140.05	531.2766	1061.545	0.0011	1	6	14914.1	6.84	HUMAN	P25398	40S ribosomal protein S12
4173	dirMS_041712_NAR_30mM_plus2.16644.16644.2	2	13.8	0	3.08E+05		(R)SIQADG	(R)S I|Q/A|D/G L V/W G S/S K(L)		140.3	674.3475	1347.69	-0.0026	-1.9	5.55	24934.4	4.5	HUMAN	P24534	Elongation factor 1-beta
4174	dirMS_041712_NAR_40mM_plus2.13621.13621.3	3	13.8	1	1.31E+04		(K)DMELPT	(K)D M/E/L/P T E K E V A L/V K(D)		146.4	534.6192	1601.845	-0.0024	-1.5	4.41	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
4175	dirMS_041712_NAR_40mM_plus2.19985.19985.3	3	13.8	1	1.56E+06		(R)ELAILLG	(R)E L/A I/L/L G/M/L D/P A E\K D/E K(G)		189.1	629.003	1884.999	-0.0042	-2.3	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
4176	dirMS_041712_NAR_50mM_plus2.10121.10121.3	3	13.8	0	4.13E+05		(R)MVQVH	(R)M V/Q|V/H/E/L|G C E G I/S K(S)	C:Carbamidomethylation	120.23	529.5984	1586.767	0.0141	8.9	5.38	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
4177	dirMS_041712_NAR_60mM_plus.13794.13930.3	3	13.8	0	7.04E+05		(K)VLSLNFS	(K)V/L|S L/N/F/S\E/C H T K(I)	C:Carbamidomethylation	129.08	478.9108	1434.705	0.0133	9.3	6.72	16092.9	6.43	HUMAN	D6RAC7	Ras GTPase-activating protein-binding protein 2 (Fragment)
4178	dirMS_041712_NAR_60mM_plus.18330.18330.3	3	13.8	1	2.93E+05		(K)LLQDFF	(K)L L|Q/D/F/F N G R D L N K(S)		152.73	527.2793	1579.823	0.0006	0.4	5.96	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
4179	dirMS_041712_NAR_120mM_minus.14882.14882.3	3	13.79	1	2.69E+05		(K)KKELEE	(K)K K E L E E\I|V|Q/P I I/S K(L)		135.13	551.9968	1653.978	-0.0027	-1.6	6.23	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
4180	dirMS_041712_NAR_20mM_minus.9217.9217.2	2	13.79	0	1.90E+05	M239m	(K)EITALAP	(K)E I|T|A|L|A|P S T m K(I)	m:Oxidized methionine	141.92	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
4181	dirMS_041712_NAR_30mM_minus2.13925.14079.2	2	13.79	0	5.48E+05		(R)DVQEIFI	(R)D V|Q|E\I/F/R(L)		129.28	453.7335	906.468	-0.0082	-9.1	4.37	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
4182	dirMS_041712_NAR_20mM_plus.17622.17645.3	3	13.79	0	1.23E+05		(K)LATQSN	(K)L A T Q S N E\I/T\I/P/V/T/F/E S R(A)		193.2	636.0003	1905.992	-0.0053	-2.8	4.53	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
4183	dirMS_041712_NAR_20mM_plus.17655.17655.2	2	13.79	0	8.14E+04		(R)TTLLPGL	(R)T T/L|L|P G L L K(T)		193.85	478.3131	955.619	0.0003	0.3	8.41	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
4184	dirMS_041712_NAR_30mM_plus2.17876.18106.2	2	13.79	0	4.74E+05		(K)LLLWSQ	(K)L/L|L|W/S Q/R(M)		147.83	458.2693	915.541	-0.0097	-10.6	9.75	22576.6	9.45	HUMAN	E9PKG0	Plectin (Fragment)
4185	dirMS_041712_NAR_30mM_plus2.18587.18692.2	2	13.79	0	1.13E+06		(K)AAIDWF	(K)A A|I|D|W/F/D/G K(E)		151.52	511.7539	1022.494	0.0064	6.2	4.21	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
4186	dirMS_041712_NAR_30mM_plus2.19869.19917.2	2	13.79	0	2.00E+05		(R)IIPGFM	(R)I/I|P G/F M/C Q G G D/F T/R(H)	C:Carbamidomethylation	157.72	799.8749	1598.745	-0.0029	-1.8	5.84	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
4187	dirMS_041712_NAR_40mM_plus2.10338.10338.2	2	13.79	0	9.40E+04		(K)IGGIGTV	(K)I/G/G\I/G/T/V|P V G R(V)		125.75	513.3081	1025.61	-0.0013	-1.2	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
4188	dirMS_041712_NAR_50mM_plus2.14696.14696.3	3	13.79	0	2.11E+06		(R)QVSASE	(R)Q V/S A/S E L H T S G I L/G P E T L/R(D)		144.9	665.6855	1995.051	-0.0086	-4.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
4189	dirMS_041712_NAR_50mM_plus2.15882.15882.3	3	13.79	1	3.70E+06		(K)ISDSEGF	(K)I/S|D/S/E/G F/K A N/L S/L L R(R)		151.2	550.6331	1649.886	-0.001	-0.6	6.07	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
4190	dirMS_041712_NAR_50mM_plus2.16705.16943.3	3	13.79	0	1.57E+06		(K)GSDHSA	(K)G S D H S A\S L\E|P/G E/L/A/E L V/R(S)		156.28	622.9846	1866.919	0.0201	10.7	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
4191	dirMS_041712_NAR_120mM_minus.19660.19660.3	3	13.78	0	7.14E+05		(R)NSVSNF	(R)N|S|V/S N F L/H/S L E R(G)		162.22	468.2346	1402.707	-0.0181	-12.9	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
4192	dirMS_041712_NAR_30mM_minus2.12998.12998.2	2	13.78	0	2.66E+05		(K)AFCGFEI	(K)A/F/C|G F/E D/P R(T)	C:Carbamidomethylation	124.05	549.7307	1098.467	-0.0132	-12	4.37	533778	5.74	HUMAN	Q15149	Plectin
4193	dirMS_041712_NAR_30mM_minus2.15571.15571.2	2	13.78	0	9.61E+04		(K)TLAAEM	(K)T\L|A|A/E/M/Q/E L R(V)		137.87	581.3003	1161.593	0.0001	0.1	4.53	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
4194	dirMS_041712_NAR_30mM_minus2.5081.5081.2	2	13.78	0	4.08E+05		(R)TDTGEP	(R)T|D|T/G E P/M/G R(G)		81.3	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
4195	dirMS_041712_NAR_40mM_minus2.14086.14086.3	3	13.78	0	3.46E+05		(R)LLEVLSG	(R)L/L|E V/L S/G E I L/P K P/T K(G)		166.62	546.333	1636.988	-0.0039	-2.4	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
4196	dirMS_041712_NAR_50mM_minus2.10415.10415.3	3	13.78	0	2.83E+05	M35m	(K)AASDIA	(K)A A/S D|I/A m/T E/L/P P T H P I R(L)	m:Oxidized methionine	127.63	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
4197	dirMS_041712_NAR_50mM_minus2.12503.12503.3	3	13.78	1	3.24E+05		(K)LYEQILA	(K)L/Y/E Q I\L|A|E/N E K L K(A)		139.15	530.9592	1590.874	-0.0107	-6.7	4.79	22046.7	5.8	HUMAN	H0YIM2	Protein phosphatase 1 regulatory subunit 12A (Fragment)
4198	dirMS_041712_NAR_50mM_minus2.12781.12781.3	3	13.78	1	3.77E+05		(K)NTVELL	(K)N/T|V/E/L L V/E D K G N Q V Y R(C)		140.5	626.3309	1876.976	0.0018	1	4.68	258215.9	5.48	HUMAN	E7EN95	Filamin-B
4199	dirMS_041712_NAR_60mM_minus.11025.11025.3	3	13.78	1	1.61E+05		(K)LLEDKN	(K)L/L|E D/K N|G E V Q N L A/V K(C)		121.37	557.3065	1669.912	-0.007	-4.2	4.68	6116.1	5.2	HUMAN	F5H6I6	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
4200	dirMS_041712_NAR_120mM_plus.12204.12580.4	4	13.78	2	2.74E+06		(K)IGRIEDV	(K)I G R I E D\V|T|P I/P S/D/S T R/R(K)		118.42	478.7604	1912.025	-0.0049	-2.6	6.12	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
4201	dirMS_041712_NAR_120mM_plus.4082.4293.3	3	13.78	1	1.73E+07	M310m	(R)TKTEISE	(R)T\K\T E\I|S/E/m/N/R(N)	m:Oxidized methionine	69.83	408.8687	1208.594	15.9976	2.2	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
4202	dirMS_041712_NAR_20mM_plus.10650.10650.3	3	13.78	0	7.11E+04	M175m	(R)LEQGQA	(R)L E Q G Q A\I/D/D|L/m|P A Q K(-)	m:Oxidized methionine	146.07	558.2795	1656.826	15.9978	1.7	4.03	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
4203	dirMS_041712_NAR_20mM_plus.16981.16981.2	2	13.78	0	2.55E+05		(K)VQIAVA	(K)V Q|I/A|V/A N A/Q E L L/Q R(M)		188.03	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
4204	dirMS_041712_NAR_20mM_plus.8773.8773.2	2	13.78	0	6.19E+04		(K)EQVANS	(K)E Q/V/A/N/S/A F V E/R(C)		130.78	625.3102	1249.617	-0.004	-3.2	4.53	17664	8.77	HUMAN	H0Y6E4	Heat shock protein HSP 90-beta (Fragment)
4205	dirMS_041712_NAR_50mM_plus2.10618.10618.3	3	13.78	0	3.46E+05		(R)AIGSASE	(R)A I/G S/A/S|E G A Q S S L Q E V Y H K(S)		123.47	654.657	1961.956	0.0001	0.1	5.4	20148.5	4.65	HUMAN	B4E2V4	Proteasome (Prosome, macropain) subunit, alpha type, 5, isoform CRA_c
4206	dirMS_041712_NAR_50mM_plus2.9305.9305.3	3	13.78	1	1.01E+06		(K)TAVCDIF	(K)T/A|V/C/D|I/P P/R G L K(M)	C:Carbamidomethylation	116.55	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
4207	dirMS_041712_NAR_20mM_minus.12182.12182.2	2	13.77	0	1.06E+06	M313m	(R)TVQSLEI	(R)T V|Q\S/L/E/I D L D/S m R(N)	m:Oxidized methionine	170.72	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4208	dirMS_041712_NAR_40mM_minus2.5905.5905.2	2	13.77	0	1.29E+06		(K)AGFAGD	(K)A G/F/A/G/D/D A P R(A)		98.13	488.7279	976.448	0.0002	0.2	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
4209	dirMS_041712_NAR_50mM_minus2.15255.15378.3	3	13.77	0	5.45E+05		(R)DGLAFN	(R)D G L|A/F/N A/L/I/H/R(H)		155.45	409.5594	1226.664	-0.0004	-0.3	6.74	146974	5.55	HUMAN	C9JRP8	Spectrin beta chain, non-erythrocytic 4
4210	dirMS_041712_NAR_120mM_plus.8436.8588.3	3	13.77	1	5.21E+06	M174m	(R)VKYETEL	(R)V/K Y E T\E|L/A/m/R(Q)	m:Oxidized methionine	97.8	419.2172	1239.64	15.9969	1.6	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4211	dirMS_041712_NAR_30mM_plus2.12841.12841.2	2	13.77	0	1.77E+05		(K)YFDSGD	(K)Y/F|D/S G/D/Y N M A\K(A)		120.37	655.7724	1310.536	0.0017	1.3	4.21	15633.5	7.82	HUMAN	A6NMQ3	Alpha-endosulfine
4212	dirMS_041712_NAR_30mM_plus2.15852.15979.2	2	13.77	0	5.70E+05		(K)LLYNNV	(K)L L|Y|N/N/V/S N F/G/R(L)		136.3	648.8354	1296.67	-0.006	-4.6	8.75	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
4213	dirMS_041712_NAR_30mM_plus2.8966.8966.2	2	13.77	0	2.25E+05		(R)TVIDYN	(R)T V|I|D/Y N G E R(T)		100.52	533.7622	1066.516	0.0008	0.7	4.37	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
4214	dirMS_041712_NAR_40mM_plus2.15059.15059.3	3	13.77	0	2.29E+05		(R)EVIDLLK	(R)E V|I/D L/L/K P D Q V E G I Q K(S)		155.13	608.6749	1824.011	-0.0012	-0.6	4.32	156557.7	5.52	HUMAN	Q86UP2	Kinectin
4215	dirMS_041712_NAR_50mM_plus2.12385.12385.3	3	13.77	1	1.70E+06		(R)SGKAPIL	(R)S G K A P I\L\I|A|T/D/V A S R(G)		133.47	500.2911	1498.859	0	0	8.46	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
4216	dirMS_041712_NAR_50mM_plus2.14213.14213.3	3	13.77	1	6.66E+05		(R)MSMKE	(R)M/S M K E V D\E\Q|M\L/N/V Q/N K(N)		142.87	641.9706	1923.897	0	0	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
4217	dirMS_041712_NAR_50mM_plus2.19524.19544.3	3	13.77	1	1.14E+06		(R)GDLGIEI	(R)G D|L/G|I\E/I/P A E K V F L A Q K(M)		171.68	610.0104	1828.022	-0.0048	-2.6	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
4218	dirMS_041712_NAR_60mM_plus.6727.6727.2	2	13.77	1	4.77E+05		(K)GPSSVEI	(K)G/P|S|S/V/E/D I K/A/K(M)		93.85	565.8054	1130.605	-0.0017	-1.5	6.07	32745.6	4.64	HUMAN	P06748	Nucleophosmin
4219	dirMS_041712_NAR_60mM_plus.9726.9826.3	3	13.77	1	1.31E+06		(K)LAELKQ	(K)L/A|E/L|K/Q/E/C L\A R(G)	C:Carbamidomethylation	109.57	444.2368	1330.715	-0.0189	-14.2	6.14	6106	9.22	HUMAN	F8VS12	SAP domain-containing ribonucleoprotein
4220	dirMS_041712_NAR_120mM_minus.12101.12101.4	4	13.76	2	2.92E+05		(R)ILELDQF	(R)I L/E/L/D Q/F/K/G Q/Q G Q K R(F)		120.05	447.7491	1787.976	-0.0017	-0.9	8.59	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
4221	dirMS_041712_NAR_20mM_minus.13342.13477.2	2	13.76	0	6.91E+05		(K)DAGTIA	(K)D A\G\T|I|A/G/L/N V L/R(I)		184.93	600.3403	1199.674	-0.0009	-0.8	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
4222	dirMS_041712_NAR_30mM_minus2.20197.20235.2	2	13.76	0	6.55E+05		(K)IGFPWSI	(K)I/G/F|P/W/S E/I R(N)		171.88	552.7932	1104.584	-0.0045	-4.1	6	71218.8	6.3	HUMAN	A7YIJ8	Radixin
4223	dirMS_041712_NAR_50mM_minus2.11119.11259.3	3	13.76	1	4.95E+05	M327m	(R)VAGGPC	(R)V/A|G/G/P Q m/I/Q|L/S L D/G K R(L)	m:Oxidized methionine	131.88	562.6354	1669.905	15.9862	-5.1	8.72	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
4224	dirMS_041712_NAR_50mM_minus2.11372.11511.3	3	13.76	0	1.45E+05		(K)VSQPIEC	(K)V/S/Q/P I E/G H/A/A S F A Q F K(M)		133.52	572.9609	1716.87	-0.0022	-1.3	6.72	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
4225	dirMS_041712_NAR_50mM_minus2.13569.13723.3	3	13.76	1	5.31E+05		(K)LTEDKAI	(K)L/T|E D/K A D V\Q|S/I/I/G L Q R(F)		144.8	595.9939	1785.97	-0.0034	-1.9	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
4226	dirMS_041712_NAR_50mM_minus2.15928.16015.3	3	13.76	0	2.60E+05		(R)GFGHIG	(R)G F G H I G I\A\V|P/D/V/Y/S A C K(R)	C:Carbamidomethylation	159	597.6337	1790.889	-0.0029	-1.6	6.74	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
4227	dirMS_041712_NAR_60mM_minus.19279.19279.3	3	13.76	0	1.04E+06		(R)SLHDAL	(R)S L H/D A L\C|V|L/A Q T V K(D)	C:Carbamidomethylation	171.22	518.9484	1554.831	-0.0002	-0.1	6.46	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
4228	dirMS_041712_NAR_20mM_plus.19051.19051.2	2	13.76	0	5.75E+04		(K)ILTFDQL	(K)I/L/T|F/D Q L A L D S\P K(G)		202.35	730.9063	1460.8	0.0058	4	4.21	14643	11.93	HUMAN	F8VUA6	60S ribosomal protein L18 (Fragment)
4229	dirMS_041712_NAR_30mM_plus2.19215.19215.2	2	13.76	0	9.99E+05		(R)SSIAGLL	(R)S/S|I|A/G L/L/L K(A)		154.92	451.2894	901.572	-0.0002	-0.2	8.47	533778	5.74	HUMAN	Q15149	Plectin
4230	dirMS_041712_NAR_30mM_plus2.19679.19679.2	2	13.76	0	2.35E+05		(K)APDFVF	(K)A/P/D/F|V/F/Y|A P R(L)		156.72	591.8008	1182.594	0.0001	0.1	5.88	71218.8	6.3	HUMAN	A7YIJ8	Radixin
4231	dirMS_041712_NAR_30mM_plus2.21854.21854.2	2	13.76	0	8.60E+04		(K)GLVQAL	(K)G L V\Q/A/L|G/L|S N/F\N S R(Q)		169.63	738.3989	1475.796	-0.006	-4.1	9.75	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
4232	dirMS_041712_NAR_50mM_plus2.14537.14537.3	3	13.76	1	5.76E+05		(R)SEGVVA	(R)S E/G V\V/A/V L L T K K(S)		144.37	415.2585	1243.762	-0.0011	-0.9	8.31	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
4233	dirMS_041712_NAR_60mM_plus.15074.15137.3	3	13.76	0	7.31E+05		(K)IVLDNSV	(K)I/V|L/D N S V/F/S E/H/R(N)		135.72	472.5788	1415.728	-0.0059	-4.2	5.32	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
4234	dirMS_041712_NAR_60mM_plus.17704.17764.3	3	13.76	1	2.85E+05		(K)IIVDELK	(K)I/I|V/D E L/K/Q E V/I/S T S S K(A)		149.28	597.0009	1788.995	-0.0072	-4	4.68	30149.5	5.96	HUMAN	D6RAC2	Guanine nucleotide-binding protein subunit beta-2-like 1
4235	dirMS_041712_NAR_30mM_minus2.16922.16922.2	2	13.75	0	1.24E+05		(R)ASLEAAI	(R)A S L|E/A A|I/A D A/E/Q R(G)		145.22	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
4236	dirMS_041712_NAR_40mM_minus2.11043.11128.3	3	13.75	0	4.70E+05		(R)DAGEGL	(R)D A|G|E/G/L/L A V Q I T/D/Q E G/K\P K(R)		148.08	657.0157	1969.024	0.0089	4.5	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
4237	dirMS_041712_NAR_50mM_minus2.14977.14977.3	3	13.75	0	4.42E+05		(R)LQQELD	(R)L Q|Q/E L D D L/T/V D L D/H Q\R(Q)		153.05	646.6559	1937.956	-0.0032	-1.6	4.03	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
4238	dirMS_041712_NAR_60mM_minus.9414.9414.3	3	13.75	0	1.04E+05	M409m	(K)VLAmSG	(K)V/L|A\m S G D/P/N Y/L H/R(M)	m:Oxidized methionine	112.23	496.9147	1472.732	15.9981	2.1	6.71	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
4239	dirMS_041712_NAR_20mM_plus.12492.12492.3	3	13.75	0	3.48E+05		(K)IISNASC	(K)I I\S N\A\S/C T T N/C L/A/P L A K(V)	C:Carbamidomethylation	159.53	611.9768	1833.92	-0.0039	-2.1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
4240	dirMS_041712_NAR_30mM_plus2.17209.17209.2	2	13.75	0	4.62E+05	M256m	(R)SLDmDS	(R)S L/D m D\S I|I A E\V K(A)	m:Oxidized methionine	142.6	668.8384	1320.671	15.998	2.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
4241	dirMS_041712_NAR_30mM_plus2.7359.7359.2	2	13.75	1	2.13E+05		(R)YSGGNY	(R)Y/S/G G N Y R/D N Y|D|N(-)		93.03	719.2864	1437.567	-0.001	-0.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
4242	dirMS_041712_NAR_30mM_plus2.7523.7542.2	2	13.75	0	6.70E+05		(K)LLADQA	(K)L/L|A|D/Q|A E/A/R(R)		93.78	493.7641	986.527	-0.0056	-5.7	4.37	23361.4	11.6	HUMAN	J3KTE4	Ribosomal protein L19
4243	dirMS_041712_NAR_40mM_plus2.13228.13228.3	3	13.75	1	1.17E+05		(R)ETFEKTF	(R)E T|F/E\K T P\V/E V/P/V/G G F K(G)		144.53	588.6444	1763.921	-0.0028	-1.6	4.79	533778	5.74	HUMAN	Q15149	Plectin
4244	dirMS_041712_NAR_50mM_plus2.18401.18401.3	3	13.75	1	3.90E+05		(R)IAKEEIF	(R)I A K E E I/F/G/P/V/Q P L F/K(F)		164.9	572.6586	1715.973	-0.0118	-6.9	6.14	57661.7	6.36	HUMAN	P30837	Aldehyde dehydrogenase X, mitochondrial
4245	dirMS_041712_NAR_50mM_plus2.22162.22162.3	3	13.75	1	5.40E+05		(R)ELAILLG	(R)E L|A/I/L L/G/M L/D/P A E K D E K(G)		190.32	629.004	1884.999	-0.0012	-0.7	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
4246	dirMS_041712_NAR_120mM_minus.10477.10477.3	3	13.74	1	1.88E+05		(K)VEYSEEE	(K)V/E/Y/S E/E E L K T H I/S K(G)		111.32	564.6199	1691.849	-0.0035	-2.1	4.91	65375.7	6.12	HUMAN	B1AHC8	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)

4247	dirMS_041712_NAR_20mM_minus.13391.13391.2	2	13.74	0	6.80E+05		(K)DAGTIA(	(K)D A G\T|I|A/G L N/V L R(I)		184.9	600.3403	1199.674	-0.0009	-0.8	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
4248	dirMS_041712_NAR_20mM_minus.14375.14375.2	2	13.74	0	2.36E+05		(K)DAGVIA(	(K)D A G V|I|A/G L N V L/R(I)		198.13	599.3503	1197.695	-0.0017	-1.4	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
4249	dirMS_041712_NAR_20mM_minus.9666.9747.2	2	13.74	0	2.44E+05		(K)LVIITAG	(K)L/V|I|I/T|A/G A R(Q)		147.62	457.2947	913.583	-0.0008	-0.9	9.75	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
4250	dirMS_041712_NAR_30mM_minus2.12724.12724.2	2	13.74	0	2.31E+05		(R)DTYVSSI	(R)D T/Y|V|S/S F P/R(A)		122.43	536.2608	1071.511	0.0038	3.5	5.83	34425.5	9.08	HUMAN	P23193	Transcription elongation factor A protein 1
4251	dirMS_041712_NAR_30mM_minus2.16153.16153.2	2	13.74	0	3.19E+05	M185m	(K)LAVNm\	(K)L A|V|N|m/V/P F P R(L)	m:Oxidized methionine	142.33	580.3178	1143.634	15.994	-0.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
4252	dirMS_041712_NAR_50mM_minus2.16931.16931.3	3	13.74	0	2.37E+05		(R)LGIEGLS	(R)L/G/I/E/G L S L/H N V/L K(L)		164.22	464.9452	1392.821	0.0001	0.1	6.75	177928	5.42	HUMAN	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1
4253	dirMS_041712_NAR_60mM_minus.8283.8283.3	3	13.74	1	1.04E+04		(R)SSPVPP\	(R)S S|P V/P/P V P E/R\R(G)		106.18	407.5617	1220.675	-0.004	-3.3	9.32	96735.1	9.2	HUMAN	J3KPS2	Protein FAM83H (Fragment)
4254	dirMS_041712_NAR_20mM_plus.14316.14316.3	3	13.74	0	8.76E+05	M73m	(R)AVLVDLI	(R)A V\L|V D L E/P G T m/D S V R(S)	m:Oxidized methionine	171.03	539.9421	1601.82	15.9914	-2.2	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
4255	dirMS_041712_NAR_30mM_plus2.16977.17513.2	2	13.74	0	1.53E+06		(K)NLYIISVI	(K)N/L|Y|I/I/S V/K(G)		143.67	475.2893	949.572	-0.0004	-0.4	8.59	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
4256	dirMS_041712_NAR_30mM_plus2.6259.6405.2	2	13.74	0	3.31E+05	M367m	(R)FGSGmI	(R)F/G|S|G/m N/M/G R(I)	m:Oxidized methionine	87.53	486.7048	956.408	15.9946	-0.3	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
4257	dirMS_041712_NAR_50mM_plus2.11576.11844.3	3	13.74	1	3.79E+05		(K)IGRIEDV	(K)I G R I E D V|T|P\I|P S/D/S T R(R)		130.28	585.9784	1755.924	-0.0029	-1.7	4.56	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
4258	dirMS_041712_NAR_50mM_plus2.16727.16727.3	3	13.74	0	4.75E+05		(K)SPVTTLL	(K)S/P/V T T L/L E C M H/K(L)	C:Carbamidomethylation	155.32	472.5735	1415.702	0.0038	2.7	6.47	142137.5	9.17	HUMAN	E7ENU4	Double-stranded RNA-specific adenosine deaminase
4259	dirMS_041712_NAR_60mM_plus.17916.17916.3	3	13.74	1	1.75E+05		(K)FNADEF	(K)F/N/A D E F/E D/M/V/A E K R(L)		150.68	567.5906	1700.758	-0.0012	-0.7	4.18	18819.6	10.31	HUMAN	F8W7C6	60S ribosomal protein L10
4260	dirMS_041712_NAR_60mM_plus.8342.8342.3	3	13.74	1	6.44E+05		(K)EPLYEKD	(K)E P L/Y|E K D/S|S/V/A A R(F)		102.25	488.9148	1464.733	-0.0031	-2.1	4.68	26283.8	8.96	HUMAN	O43809	Cleavage and polyadenylation specificity factor subunit 5
4261	dirMS_041712_NAR_30mM_minus2.19101.19101.2	2	13.73	0	2.61E+05		(K)SYELPDC	(K)S Y E|L|P D G Q/V I T I\G/N E R(F)		158.88	895.9492	1790.892	-0.0008	-0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
4262	dirMS_041712_NAR_40mM_minus2.12008.12008.3	3	13.73	0	2.78E+05		(K)DAGEGL	(K)D A|G E|G/L/L A V/Q I T D/P E G K/P K(K)		154.02	646.6785	1938.018	0.0031	1.6	4.32	283472.4	5.71	HUMAN	P21333	Filamin-A
4263	dirMS_041712_NAR_50mM_minus2.12227.12350.3	3	13.73	1	2.81E+06		(R)GYSFTT1	(R)G Y|S|F/T T/T A E/R E I V/R(D)		138.1	543.9458	1629.823	-0.0003	-0.2	6.14	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
4264	dirMS_041712_NAR_50mM_minus2.8739.8739.3	3	13.73	1	9.59E+04		(K)ALDLDSS	(K)A L|D|L/D/S S C K E/A A D G Y Q R(C)	C:Carbamidomethylation	117.47	633.6221	1898.855	-0.0031	-1.7	4.23	60404.6	6.4	HUMAN	F5H0T1	Stress-induced-phosphoprotein 1
4265	dirMS_041712_NAR_60mM_minus.6746.6746.3	3	13.73	0	4.43E+04	M437m	(R)LESGMC	(R)L E|S G/M Q N m/S I H/T/K(T)	m:Oxidized methionine	96.18	497.9023	1475.698	15.9942	-0.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
4266	dirMS_041712_NAR_60mM_minus.9416.9416.3	3	13.73	0	1.04E+05	M409m	(K)VLAmSG	(K)V L|A/m/S/G D|P\N Y/L|H R(M)	m:Oxidized methionine	112.23	496.9147	1472.732	15.9981	2.1	6.71	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
4267	dirMS_041712_NAR_20mM_plus.16519.16519.2	2	13.73	0	1.71E+05		(R)LLEAQIA	(R)L L E A/Q I/A/T|G G\I I D/P K(E)		185.37	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
4268	dirMS_041712_NAR_30mM_plus2.19576.19804.2	2	13.73	0	4.94E+05		(K)NLIDAG\	(K)N L|I|D|A|G V|D/A L R(V)		156.75	578.8183	1156.632	-0.0027	-2.4	4.21	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
4269	dirMS_041712_NAR_50mM_plus2.10118.10118.3	3	13.73	0	7.46E+05		(R)GISEETT	(R)G I|S E/E/T T/T G V H N L Y/K(M)		120.05	550.2759	1648.818	-0.0045	-2.8	5.4	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
4270	dirMS_041712_NAR_50mM_plus2.6458.6479.3	3	13.73	1	1.97E+05		(K)IVSGKDY	(K)I/V|S G K/D Y/N/V/T/A N S K(L)		98.92	499.2611	1495.775	-0.0064	-4.2	8.5	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
4271	dirMS_041712_NAR_120mM_minus.10510.10912.2	2	13.72	1	3.38E+06		(R)VKYETEL	(R)V/K|Y|E/T E/L/A/M/R(Q)		113.43	620.3232	1239.64	-0.0011	-0.9	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4272	dirMS_041712_NAR_120mM_minus.17504.17521.4	4	13.72	1	5.43E+05		(R)GFGHIG	(R)G F G H I G I A\V/P D V/Y/S A C K R(F)	C:Carbamidomethylation	150.4	487.502	1946.991	-0.0044	-2.2	8.6	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
4273	dirMS_041712_NAR_20mM_minus.10395.10395.2	2	13.72	0	4.57E+04	M145m	(R)VVLFEm	(R)V V|L/F/E m E/A R(K)	m:Oxidized methionine	152.52	555.2868	1093.571	15.9953	0.3	4.53	27142.4	5.34	HUMAN	E5RG68	Copine-3 (Fragment)
4274	dirMS_041712_NAR_50mM_minus2.12905.12905.3	3	13.72	1	1.79E+05		(K)GGELVY	(K)G G\E/L|V|Y/T D S E A R D V F E K(A)		141.53	638.9739	1914.908	-0.0008	-0.4	4.18	533778	5.74	HUMAN	Q15149	Plectin
4275	dirMS_041712_NAR_50mM_minus2.13402.13548.3	3	13.72	1	5.31E+05		(K)LTEDKAI	(K)L/T|E D K A D\V\Q S|I|I/G L Q/R(F)		144.8	595.9939	1785.97	-0.0034	-1.9	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
4276	dirMS_041712_NAR_50mM_minus2.7891.7891.3	3	13.72	1	1.10E+05		(K)VLLQSKI	(K)V L|L/Q/S K D Q|I/T A/G N A A R(K)		111.77	562.3158	1684.934	-0.0012	-0.7	8.72	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
4277	dirMS_041712_NAR_60mM_minus.6480.6480.3	3	13.72	1	8.87E+04		(K)SESPKEP	(K)S E/S/P/K E/P E/Q/L/R(K)		94.9	433.8887	1299.654	-0.0024	-1.8	4.78	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
4278	dirMS_041712_NAR_60mM_minus.9411.9424.3	3	13.72	0	2.36E+05		(K)GISVHIS	(K)G I|S/V/H I/S N A E/P K(H)		112.42	417.9007	1251.669	0.0184	14.7	6.75	33803.8	6.12	HUMAN	B1AKP7	TAR DNA binding protein
4279	dirMS_041712_NAR_120mM_plus.20222.20433.3	3	13.72	1	3.71E+06		(K)AAIDWF	(K)A A|I/D|W/F/D/G K E/F H G N I\I K(V)		158.78	654.3334	1960.992	-0.0059	-3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
4280	dirMS_041712_NAR_30mM_plus2.18778.18778.2	2	13.72	0	3.32E+05		(R)ESLEALL	(R)E S/L/E/A L/L/Q/R(A)		152.07	529.8026	1058.584	0.0139	13.1	4.53	107721.8	8.85	HUMAN	O94906	Pre-mRNA-processing factor 6
4281	dirMS_041712_NAR_40mM_plus2.11333.11333.3	3	13.72	0	3.11E+04		(K)LQALAN	(K)L Q|A|L/A N E Q/A\A A A/H E L E/K(M)		132.83	602.981	1806.935	-0.006	-3.3	4.75	156557.7	5.52	HUMAN	Q86UP2	Kinectin
4282	dirMS_041712_NAR_50mM_plus2.17780.17780.3	3	13.72	1	6.96E+05		(K)SLLGKD\	(K)S L|L G K/D V L F/L/K(D)		161.7	411.5915	1232.761	-0.0013	-1.1	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
4283	dirMS_041712_NAR_120mM_minus.6624.6687.2	2	13.71	1	4.24E+06		(K)IREEYPD	(K)I/R|E E|Y|P D|R(I)		90.72	539.2683	1077.532	-0.003	-2.8	4.68	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
4284	dirMS_041712_NAR_30mM_minus2.14041.14328.2	2	13.71	0	6.95E+05		(K)ALEIIPR(	(K)A/L|E|I\I/P/R(Q)		130.62	406.2554	811.504	-0.0001	-0.1	6.05	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
4285	dirMS_041712_NAR_50mM_minus2.16381.16381.3	3	13.71	0	1.72E+05		(R)GGYVLH	(R)G G Y/V/L/H I G T I/Y/G D/L K(V)		161.75	535.9583	1605.863	-0.0032	-2	6.74	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
4286	dirMS_041712_NAR_120mM_plus.10184.10354.3	3	13.71	0	1.24E+06		(R)ILRPWQ	(R)I/L/R P W|Q|S S E|T/R(S)		106.65	458.2486	1372.733	-0.0019	-1.4	9.6	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
4287	dirMS_041712_NAR_120mM_plus.10464.10591.3	3	13.71	1	3.83E+05		(K)KGENYV	(K)K\G E/N Y V|Y|I/N/E/A T R(H)		108.4	519.5943	1556.77	-0.002	-1.3	6.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
4288	dirMS_041712_NAR_120mM_plus.18636.18636.4	4	13.71	1	4.62E+05		(R)SKDVVE	(R)S K D V V\E|P/L L R P Q W Y V/R(C)		150.48	497.0291	1985.097	-0.0021	-1.1	8.31	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
4289	dirMS_041712_NAR_20mM_plus.12254.12363.2	2	13.71	0	2.36E+05		(K)DLAGSII	(K)D L|A|G S I/I/G/K(G)		158.22	437.2558	873.504	0.0003	0.4	5.84	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
4290	dirMS_041712_NAR_20mM_plus.16771.16771.2	2	13.71	0	3.05E+05		(K)VQIAVA	(K)V Q|I|A\V/A N A Q/E/L L/Q R(M)		186.97	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
4291	dirMS_041712_NAR_30mM_plus2.21851.21851.2	2	13.71	0	3.21E+05		(R)SFITWLF	(R)S F/I|T/W L R(D)		170.53	461.7608	922.515	-0.0002	-0.2	9.47	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
4292	dirMS_041712_NAR_40mM_plus2.13861.13861.3	3	13.71	0	2.23E+05		(K)VALLLLD	(K)V A\L\L|L/L/D Q G/A/S/P H A A A K(N)		148.13	558.9886	1674.954	-0.0025	-1.5	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
4293	dirMS_041712_NAR_50mM_plus2.15354.15354.3	3	13.71	1	7.54E+05		(K)EAFSLFD	(K)E A/F|S/L/F/D K D G D/G T/I T T K(E)		149.33	615.6348	1844.891	-0.0014	-0.8	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
4294	dirMS_041712_NAR_50mM_plus2.7352.7352.3	3	13.71	0	8.75E+04		(R)EGATVY.	(R)E G A/T V/Y A/T G T H/A Q V\E D/G R(L)		104.62	621.2948	1861.868	0.0024	1.3	4.65	36208.1	7.21	HUMAN	B4DMU0	Pyrroline-5-carboxylate reductase
4295	dirMS_041712_NAR_60mM_plus.8473.8473.2	2	13.71	0	4.27E+05		(R)FACHSA:	(R)F/A|C/H/S A/S/L T\V R(N)	C:Carbamidomethylation	102.73	624.8118	1248.615	0.001	0.8	9.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
4296	dirMS_041712_NAR_40mM_minus2.14606.14606.3	3	13.7	1	1.43E+05		(K)GTVPDD	(K)G T|V/P/D D A V E A L A D S L G K K(E)		170.32	595.9791	1785.923	-0.0001	-0.1	4.23	81397.3	4.99	HUMAN	B7Z468	Calpastatin
4297	dirMS_041712_NAR_40mM_minus2.14958.14958.3	3	13.7	0	1.07E+05		(R)EAVELPI	(R)E A V/E/L/P L/T/H F E L Y K(Q)		173.08	563.6324	1688.889	-0.0068	-4	4.75	47479.5	5.09	HUMAN	P43686	26S protease regulatory subunit 6B
4298	dirMS_041712_NAR_60mM_minus.15724.15724.3	3	13.7	1	4.02E+05		(R)AEGAIA(	(R)A E|G A/I/A G F R D/P F S G K(Q)		147.97	508.2601	1522.765	0.0009	0.6	6.12	266161	5.68	HUMAN	E9PPU0	Epiplakin
4299	dirMS_041712_NAR_60mM_minus.5040.5050.3	3	13.7	1	2.11E+05		(R)MQNDT	(R)M/Q|N/D/T A E/N E/T T E/K/E E K(S)		82.83	632.9407	1896.813	-0.0052	-2.7	4.14	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
4300	dirMS_041712_NAR_30mM_plus2.21242.21242.2	2	13.7	0	1.88E+05		(R)QTLMW	(R)Q T/L/M/W/S/A T/W/P K(E)		165.95	674.8389	1348.672	-0.0013	-1	8.75	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
4301	dirMS_041712_NAR_50mM_plus2.18799.18799.3	3	13.7	0	4.20E+05		(R)AGLGSG	(R)A G L/G|S/G L/S L/S G L/V/H P E\L S R(S)		167.15	617.3412	1850.013	-0.004	-2.2	6.79	73325.2	9.19	HUMAN	F5H2A9	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial
4302	dirMS_041712_NAR_120mM_minus.19451.19486.3	3	13.69	1	1.83E+04		(K)RSIQFVI	(K)R S I Q\F\V/D\W|C/P T G F K(V)	C:Carbamidomethylation	161.3	580.9561	1740.853	0.0011	0.6	8.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
4303	dirMS_041712_NAR_20mM_minus.14643.14643.2	2	13.69	0	2.10E+05		(K)LAVEALS	(K)L A V E/A\L/S S/L/D\G D L A|G R(Y)		201.28	793.922	1586.838	-0.0017	-1.1	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
4304	dirMS_041712_NAR_30mM_minus2.14874.14874.2	2	13.69	0	4.25E+05		(R)LCFEGLF	(R)L/C|F|E G L/R(S)	C:Carbamidomethylation	134.25	447.7317	894.45	0.0059	6.6	6	533778	5.74	HUMAN	Q15149	Plectin
4305	dirMS_041712_NAR_50mM_minus2.13670.13822.3	3	13.69	0	1.70E+06		(R)VAPDEH	(R)V A|P D E H P I L\L/T/E A/P L N/P K(I)		146.33	652.0252	1954.064	-0.0034	-1.7	4.65	42344.8	5.39	HUMAN	Q562R1	Beta-actin-like protein 2
4306	dirMS_041712_NAR_50mM_minus2.14171.14171.3	3	13.69	0	1.50E+05		(K)SIEIPRP\	(K)S I|E\I/P R\P V D G V/E V|P/G C G K(I)	C:Carbamidomethylation	148.28	636.9917	1908.985	-0.0242	-12.7	4.68	34243.5	4.88	HUMAN	K7ENG2	Splicing factor U2AF 65 kDa subunit
4307	dirMS_041712_NAR_30mM_plus2.6385.6779.2	2	13.69	0	1.71E+06		(R)MGANN	(R)M/G|A|N/N/L/E/R(M)		89.4	452.7228	904.431	0.0078	8.6	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
4308	dirMS_041712_NAR_40mM_plus2.8043.8168.2	2	13.69	0	2.13E+05		(R)AVVIVDI	(R)A V|V|I/V/D/D/R(G)		108.22	443.7528	886.499	-0.0009	-1.1	4.21	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
4309	dirMS_041712_NAR_50mM_plus2.20346.20346.3	3	13.69	1	3.35E+06		(R)TLAEIAK	(R)T L/A/E I/A K V E L/D N M/P L R(G)		174.87	604.9965	1812.989	-0.0138	-7.6	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
4310	dirMS_041712_NAR_50mM_plus2.9821.9867.3	3	13.69	1	1.86E+05	M244m	(K)ILIANTG	(K)I/L|I/A/N T G m D T D/K I/K(I)	m:Oxidized methionine	118.97	516.9418	1532.835	15.9756	-12.5	5.96	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
4311	dirMS_041712_NAR_30mM_minus2.13899.13899.2	2	13.68	0	1.66E+05		(K)NVIGLQI	(K)N V|I|G/L Q/M|G T N\R(G)		129.38	601.8183	1202.631	-0.0017	-1.4	9.75	22562.2	8.8	HUMAN	P37802	Transgelin-2
4312	dirMS_041712_NAR_30mM_minus2.15417.15458.2	2	13.68	0	5.21E+05		(R)YPVNSV	(R)Y/P|V|N/S V N I/L/K(A)		137.12	573.8282	1146.652	-0.0026	-2.3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
4313	dirMS_041712_NAR_120mM_plus.20387.20387.3	3	13.68	0	3.09E+05		(R)INLWHL	(R)I/N\L/W|H L E I/T D R(S)		159.53	470.5889	1409.754	-0.0014	-1	5.32	52204.6	5.82	HUMAN	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
4314	dirMS_041712_NAR_20mM_plus.17672.17872.2	2	13.68	0	2.00E+05		(R)YISPDQL	(R)Y I|S|P/D Q L/A\D L Y\K(S)		194.23	713.3667	1425.726	0.0001	0.1	4.21	47510.4	7.04	HUMAN	P06733	Alpha-enolase
4315	dirMS_041712_NAR_30mM_plus2.10624.10839.2	2	13.68	0	1.47E+06		(K)FYEQFSI	(K)F/Y|E/Q/F/S/K(N)		109.57	474.7276	948.446	0.0018	1.9	6	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
4316	dirMS_041712_NAR_30mM_plus2.16841.16991.2	2	13.68	0	4.42E+05		(R)DFFLAN.	(R)D F|F|L A/N/A/S/R(A)		141.87	520.7632	1040.516	0.0032	3	5.84	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
4317	dirMS_041712_NAR_40mM_plus2.7960.7960.2	2	13.68	0	3.26E+05		(R)MGYMD	(R)M/G\Y|M/D|P/R(E)		107.5	435.1865	869.364	0.0013	1.5	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
4318	dirMS_041712_NAR_50mM_plus2.18016.18016.3	3	13.68	1	1.54E+06		(R)ELIKVLEI	(R)E L\I K V\L E E A/N/Q/A/I/N|P K(L)		163.3	603.6741	1809.012	-0.0039	-2.2	4.79	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
4319	dirMS_041712_NAR_50mM_plus2.18300.18300.3	3	13.68	0	2.22E+05		(R)IDILDSA	(R)I/D/I|L/D/S A L L R P G/R(I)		164.5	480.2828	1438.838	-0.0038	-2.6	5.96	44954.5	8.44	HUMAN	A8K3Z3	26S protease regulatory subunit 8
4320	dirMS_041712_NAR_50mM_plus2.19030.19030.3	3	13.68	0	5.50E+05		(R)GFGFITF	(R)G F/G/F/I/T/F T/N/P E H A S V A M R(A)		168.75	661.3258	1981.959	0.004	2	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
4321	dirMS_041712_NAR_120mM_minus.11345.11480.3	3	13.67	0	2.31E+05		(R)GFCLPPI	(R)G F/C L/P/P/H C S/R(G)	C:Carbamidomethylation	116.42	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
4322	dirMS_041712_NAR_120mM_minus.12569.12569.3	3	13.67	1	2.56E+05		(K)ARLENEI	(K)A R L E N E/I/A/T Y R(N)		122.33	445.9006	1335.701	-0.0143	-10.7	6.19	51115.6	4.9	HUMAN	O76014	Keratin, type I cuticular Ha7
4323	dirMS_041712_NAR_120mM_minus.12598.13043.3	3	13.67	1	3.62E+06		(K)VKLEAEI	(K)V K\L E\A\E|I|A/T/Y/R(R)		123.37	431.5783	1292.721	-0.0005	-0.4	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4324	dirMS_041712_NAR_40mM_minus2.15041.15042.3	3	13.67	0	2.40E+06		(K)ALESPEF	(K)A/L|E/S/P E R P F\L/A I L/G G A K(V)		174.68	590.3353	1768.996	-0.0042	-2.4	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
4325	dirMS_041712_NAR_50mM_minus2.13195.13195.3	3	13.67	0	2.72E+04		(R)IYDAQN	(R)I/Y/D A Q N/E L/S A A T H/L/T S/K(L)		141.85	621.3116	1861.929	-0.0088	-4.7	5.32	15355.1	5.12	HUMAN	C9JAB0	DCC-interacting protein 13-alpha (Fragment)
4326	dirMS_041712_NAR_50mM_minus2.14483.14580.3	3	13.67	0	4.40E+05		(R)QVLIASI	(R)Q V|L/I/A/S/H L/P S Y E/L R(H)		150.95	542.6354	1625.901	-0.0093	-5.7	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
4327	dirMS_041712_NAR_50mM_minus2.15500.15500.3	3	13.67	0	7.78E+04		(R)DLTPEHI	(R)D L/T/P E/H L/P/L L/R(N)		155.98	435.2497	1303.737	-0.0023	-1.8	5.32	38779.2	5.93	HUMAN	Q96C86	m7GpppX diphosphatase
4328	dirMS_041712_NAR_50mM_minus2.17037.17037.3	3	13.67	1	5.94E+04		(R)EFTRLEI(	(R)E F T R L E I/C/N|L/T/P D A L K(S)	C:Carbamidomethylation	164.93	640.6675	1919.989	-0.0016	-0.8	4.68	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
4329	dirMS_041712_NAR_60mM_minus.17095.17118.3	3	13.67	1	1.90E+05		(K)LLQDFFI	(K)L/L|Q/D/F F N G R D L/N/K(S)		155.28	527.277	1579.823	-0.0063	-4	5.96	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
4330	dirMS_041712_NAR_60mM_minus.7085.7293.3	3	13.67	0	2.51E+06	M434m	(R)LESGmC	(R)L/E|S G m Q/N/M/S I/H/T/K(T)	m:Oxidized methionine	98.97	497.9023	1475.698	15.9942	-0.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
4331	dirMS_041712_NAR_30mM_plus2.12778.12988.2	2	13.67	0	5.63E+05		(R)CNNVLY	(R)C/N|N|V|L/Y/I/R(G)	C:Carbamidomethylation	120.8	526.2726	1051.535	0.0026	2.5	8.75	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F
4332	dirMS_041712_NAR_30mM_plus2.13832.13865.2	2	13.67	0	4.18E+04		(R)LNLNNT	(R)L/N|L|N|N T/V/L\S K(R)		127.13	558.323	1115.642	-0.0032	-2.8	8.75	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
4333	dirMS_041712_NAR_30mM_plus2.19806.19806.2	2	13.67	0	2.35E+05		(K)GFAFVQ	(K)G F|A|F|V/Q/Y\V N E R(N)		157.57	665.3326	1329.659	-0.0007	-0.5	6	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
4334	dirMS_041712_NAR_30mM_plus2.20439.20439.2	2	13.67	0	6.53E+04		(K)SYELPDC	(K)S Y\E|L|P D G Q V I/T/I G N E\R(F)		160.92	895.9487	1790.892	-0.0018	-1	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
4335	dirMS_041712_NAR_40mM_plus2.11297.11297.3	3	13.67	0	2.83E+04		(K)AGVSISV	(K)A G V|S/I/S V V/H G N L S E E A A K(Q)		132.63	589.9796	1767.924	0.0007	0.4	5.4	50949.8	9.28	HUMAN	P36551	Coproporphyrinogen-III oxidase, mitochondrial
4336	dirMS_041712_NAR_40mM_plus2.12885.12885.3	3	13.67	0	4.88E+03		(R)EQTLSP1	(R)E Q\T/L/S/P T I T/S G L H N\I A R(S)		142.85	613.3236	1837.977	-0.0204	-11.1	6.85	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
4337	dirMS_041712_NAR_60mM_plus.11651.11671.3	3	13.67	1	2.93E+06		(K)KAEAGA	(K)K\A E A G\A G\S\A|T|E/F/Q/F/R(G)		118.23	523.9277	1569.766	0.003	1.9	6.14	18897.4	10.15	HUMAN	P46783	40S ribosomal protein S10
4338	dirMS_041712_NAR_30mM_minus2.13569.13569.2	2	13.66	0	5.78E+05		(K)TCTFILR(	(K)T/C|T/F/I/L R(G)	C:Carbamidomethylation	127.4	455.7458	910.481	0.0028	3.1	9.41	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
4339	dirMS_041712_NAR_30mM_minus2.7774.7774.2	2	13.66	0	1.29E+05		(K)VTQVDC	(K)V T/Q/V/D/G N/S P V/R(F)		96.45	586.3085	1171.607	0.0031	2.7	5.81	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
4340	dirMS_041712_NAR_120mM_plus.20727.20727.4	4	13.66	2	3.87E+05		(R)TLAEIAK	(R)T\L|A E/I/A K V/E L D N M/P L R G K(Q)		161.73	500.2814	1998.105	-0.0015	-0.7	5.85	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
4341	dirMS_041712_NAR_20mM_plus.10468.10468.2	2	13.66	0	1.10E+05	M267m	(R)LITLEEEr	(R)L/I|T\L/E/E E m/T K(Y)	m:Oxidized methionine	145.17	611.8175	1206.629	15.9991	3.4	4.25	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
4342	dirMS_041712_NAR_20mM_plus.11344.11344.2	2	13.66	0	1.74E+05		(K)VGLQVV	(K)V/G/L Q V/V/A V K(A)		150.73	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
4343	dirMS_041712_NAR_20mM_plus.13960.13960.2	2	13.66	0	6.90E+04		(K)IEVLEEEI	(K)I E|V|L/E E/E L/R(L)		168.03	565.3132	1129.61	0.0092	8.1	4.09	334221.3	6.44	HUMAN	P15924	Desmoplakin
4344	dirMS_041712_NAR_20mM_plus.8296.8320.2	2	13.66	0	9.05E+04		(K)GGEIQP'	(K)G G\E|I|Q/P V\S/V|K(V)		127.42	507.2841	1013.563	-0.0017	-1.6	6	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
4345	dirMS_041712_NAR_30mM_plus2.16703.16703.2	2	13.66	0	4.62E+05		(K)GCSFLPI	(K)G C\S\F/L|P D/P Y Q K(Q)	C:Carbamidomethylation	140.67	656.306	1311.604	0.0009	0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
4346	dirMS_041712_NAR_30mM_plus2.17856.17895.2	2	13.66	0	1.40E+05		(R)NELSGA	(R)N E|L|S|G/A/L/T/G L T R(V)		146.73	616.3341	1231.664	-0.0032	-2.6	6	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
4347	dirMS_041712_NAR_30mM_plus2.19323.19323.2	2	13.66	0	2.98E+05		(K)TVDNFV	(K)T V|D|N F/V/A/L A T G E K(G)		155	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
4348	dirMS_041712_NAR_30mM_plus2.22077.22077.2	2	13.66	0	1.51E+05		(K)GLSSLLC	(K)G L|S/S/L/L C N F/T/K(S)	C:Carbamidomethylation	171.68	620.3199	1239.64	-0.0077	-6.2	8.75	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
4349	dirMS_041712_NAR_30mM_plus2.8912.8912.2	2	13.66	0	1.86E+05		(R)QPLGAT	(R)Q P/L|G/A/T S G A/S L/K(T)		100.28	565.3227	1129.621	0.017	15	8.75	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
4350	dirMS_041712_NAR_40mM_plus2.14071.14071.3	3	13.66	0	1.11E+05		(R)LVLEVA(	(R)L V|L/E/V A/Q/H L G E S T V R(T)		149.15	550.9762	1650.917	-0.0033	-2	5.4	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
4351	dirMS_041712_NAR_40mM_plus2.17731.17731.3	3	13.66	1	1.96E+05		(R)LKLPSIPI	(R)L K L P S I\P L/V|P V/S A Q K(R)		170.73	530.671	1589.999	-0.0004	-0.3	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
4352	dirMS_041712_NAR_50mM_plus2.16556.16557.3	3	13.66	1	3.33E+05		(K)LLTGELL	(K)L L|T/G E L/L/P T D/G M I R/K(H)		155.22	552.9815	1656.935	-0.0054	-3.2	6.07	73070	7.16	HUMAN	Q75MJ1	ATP-binding cassette sub-family F member 2
4353	dirMS_041712_NAR_60mM_plus.10544.10650.3	3	13.66	1	1.05E+06		(K)MADEAI	(K)M/A|D/E/A I\L Q E R E/R(G)		113	487.578	1460.716	0.0032	2.2	4.41	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
4354	dirMS_041712_NAR_30mM_minus2.12445.12445.2	2	13.65	0	4.97E+05		(K)GDYPLE.	(K)G D/Y|P/L/E/A V R(M)		122.13	510.2598	1019.516	-0.0033	-3.2	4.37	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
4355	dirMS_041712_NAR_30mM_minus2.15557.15557.2	2	13.65	0	1.82E+05		(K)EILFYDR	(K)E I|L/F/Y D/R(I)		137.7	478.2479	955.488	0.0002	0.2	4.37	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b

4356	dirMS_041712_NAR_40mM_minus2.12653.12727.3	3	13.65	1	2.01E+05		(K)DVLFLKI	(K)D V|L|F/L/K/D C V/G P E V E K(A)	C:Carbamidomethylation	158.43	583.3021	1747.893	-0.0018	-1	4.32	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
4357	dirMS_041712_NAR_50mM_minus2.6779.6779.3	3	13.65	1	2.52E+05		(R)ASVDTK	(R)A S V/D T K E A E/G A|P Q/V E A/G K(R)		104.8	596.2904	1786.882	-0.0251	-14	4.41	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
4358	dirMS_041712_NAR_60mM_minus.17199.17199.3	3	13.65	1	3.11E+05		(K)DANAKL	(K)D A|N A K L\S E\L/E|A/A/L/Q R(A)		156.03	543.6239	1628.86	-0.0031	-1.9	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
4359	dirMS_041712_NAR_120mM_plus.13958.13958.3	3	13.65	2	7.22E+04		(K)AFAAQE	(K)A/F|A|A/Q E D L E K T K E E/L K(T)		126.38	617.3224	1849.954	-0.0015	-0.8	4.58	71218.8	6.3	HUMAN	A7YIJ8	Radixin
4360	dirMS_041712_NAR_20mM_plus.17838.17871.2	2	13.65	0	1.98E+05		(R)SLVPAAI	(R)S L|V|P/A/A E L/L E/S R(V)		194.77	642.8613	1284.716	-0.0005	-0.4	4.53	533778	5.74	HUMAN	Q15149	Plectin
4361	dirMS_041712_NAR_20mM_plus.7325.7325.2	2	13.65	0	2.82E+05		(K)TGQAPC	(K)T G Q|A|P G Y|S Y/T A\A N K(N)		119.5	714.8394	1428.675	-0.0039	-2.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
4362	dirMS_041712_NAR_50mM_plus2.14065.14065.3	3	13.65	0	1.72E+06	M457m	(R)mGPLGL	(R)m|G/P/L/G L D H/M/A\S S I E/R(M)	m:Oxidized methionine	142.67	543.9304	1613.777	15.9992	2.6	5.3	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
4363	dirMS_041712_NAR_60mM_plus.11432.11626.3	3	13.65	1	1.47E+06		(R)GASKEIL	(R)G A/S K E I\L\S/E/V/E/R(N)		117.95	439.9069	1317.701	0.0053	4	4.79	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
4364	dirMS_041712_NAR_120mM_minus.8247.8247.3	3	13.64	1	5.91E+05		(K)SSGGREI	(K)S/S/G G R E D L E|S|S/G/L Q\R(R)		99.45	526.5882	1577.751	-0.0014	-0.9	4.68	11625.5	8.01	HUMAN	B8ZZT7	Hematological and neurological-expressed 1 protein
4365	dirMS_041712_NAR_30mM_minus2.7129.7129.2	2	13.64	0	3.86E+05		(K)QQTLEA	(K)Q\Q/T|L/E/A/E E/A K(R)		93.4	573.7846	1146.564	-0.0018	-1.6	4.25	76925.9	4.46	HUMAN	A8MV58	Drebrin
4366	dirMS_041712_NAR_50mM_minus2.17232.17445.3	3	13.64	0	1.05E+06	M195m	(R)LHFFmP	(R)L H F\F m|P G|F|A/P L T S R(G)	m:Oxidized methionine	167.33	546.2872	1620.835	16.0115	10.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
4367	dirMS_041712_NAR_60mM_minus.13930.13930.3	3	13.64	1	2.82E+05		(R)SLIANLA	(R)S L/I/A/N L|A A/A/N C Y K K(E)	C:Carbamidomethylation	137.85	512.9419	1536.82	-0.0091	-5.9	9.7	36978.6	6.33	HUMAN	B7Z800	Adenosine kinase
4368	dirMS_041712_NAR_120mM_plus.20207.20432.3	3	13.64	1	3.71E+06		(K)AAIDWF	(K)A/A|I/D|W/F D/G K E F H\G N I I/K(V)		158.78	654.3334	1960.992	-0.0059	-3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
4369	dirMS_041712_NAR_30mM_plus2.12962.13402.2	2	13.64	1	5.17E+06		(K)KITIADC	(K)K\I T\I|A|D\C\G\Q|L|E(-)	C:Carbamidomethylation	122.8	624.3183	1247.63	-0.0007	-0.6	4.75	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
4370	dirMS_041712_NAR_30mM_plus2.14483.14723.2	2	13.64	0	6.60E+05		(R)DLAPIGI	(R)D/L|A|P/I/G I/R(V)		129.75	427.7575	854.509	-0.0017	-2	5.84	27150.8	7.95	HUMAN	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2
4371	dirMS_041712_NAR_30mM_plus2.18933.18933.2	2	13.64	0	5.13E+04		(R)MGPGIC	(R)M/G/P G\I/G/A I L E R(S)		152.52	557.3091	1113.609	0.0024	2.2	5.75	14175.1	9.89	HUMAN	H0YKS1	Myelin expression factor 2 (Fragment)
4372	dirMS_041712_NAR_30mM_plus2.22414.22414.2	2	13.64	0	2.83E+05		(K)CMPTFC	(K)C M/P/T F Q F/F K(K)	C:Carbamidomethylation	172.85	603.2777	1205.548	-0.0001	-0.1	8.75	9680	5.77	HUMAN	B1ALW1	Thioredoxin
4373	dirMS_041712_NAR_30mM_plus2.6031.6047.2	2	13.64	0	1.59E+05		(R)LQDTSS\	(R)L/Q|D|T/S S/Y/A K(I)		85.92	506.7507	1012.495	-0.0004	-0.4	5.83	334221.3	6.44	HUMAN	P15924	Desmoplakin
4374	dirMS_041712_NAR_60mM_plus.6752.6752.3	3	13.64	1	3.47E+05		(K)TQMTSA	(K)T Q|M/T/S A V R/E/P K(L)		93.58	416.5533	1247.641	0.0041	3.3	8.41	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
4375	dirMS_041712_NAR_60mM_plus.8930.9162.3	3	13.64	0	1.59E+06		(K)EFHLNES	(K)E F H L N\E/S/G/D/P/S/S K(S)		105.52	482.8882	1446.65	0.0005	0.3	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
4376	dirMS_041712_NAR_60mM_plus.9422.9422.3	3	13.64	1	4.42E+05		(K)CLDENLI	(K)C L|D/E/N L/E D A/S Q/C K K(L)	C:Carbamidomethylation	107.22	570.5876	1709.747	0.0013	0.8	4.32	14458.2	9.22	HUMAN	Q5JTJ3	Cytochrome c oxidase assembly factor 6 homolog
4377	dirMS_041712_NAR_120mM_minus.14124.14350.3	3	13.63	2	1.13E+06		(K)VLAGDK	(K)V/L|A|G/D/K/N F I T A E E/L R/R(E)		131.63	611.338	1832.003	-0.003	-1.7	6.15	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
4378	dirMS_041712_NAR_30mM_minus2.5060.5060.2	2	13.63	0	3.65E+05		(R)TDTGEP	(R)T D|T/G/E P M G/R(G)		81.17	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
4379	dirMS_041712_NAR_30mM_minus2.8427.8427.2	2	13.63	0	1.09E+05		(K)CAMTAL	(K)C/A|M/T A/L/S S K(L)	C:Carbamidomethylation	100.45	484.7299	968.454	-0.0014	-1.5	8.75	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
4380	dirMS_041712_NAR_40mM_minus2.11267.11627.3	3	13.63	0	8.05E+05		(R)TIQVENS	(R)T I|Q|V/E/N\S H L\I/L/T/G A G A L N K(V)		151	660.3663	1979.092	-0.0077	-3.9	6.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
4381	dirMS_041712_NAR_60mM_minus.13658.13658.3	3	13.63	0	2.50E+05		(K)VSHVST(	(K)V S H V\S T G G G\A|S|L/E/L L/E/G K(V)		136.38	580.9746	1740.913	-0.0034	-2	5.4	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
4382	dirMS_041712_NAR_60mM_minus.7841.8056.3	3	13.63	1	5.85E+05		(K)IQDKEGI	(K)I Q\D K E G|I|P|P D/Q Q R(L)		103.83	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
4383	dirMS_041712_NAR_120mM_plus.8432.8432.3	3	13.63	1	1.83E+05		(K)ALSRQEI	(K)A L/S R Q E|M/Q|E/V/Q S S R(S)		97.45	550.2746	1648.807	0.0021	1.3	6.19	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
4384	dirMS_041712_NAR_30mM_plus2.14360.14360.2	2	13.63	0	5.73E+05		(K)CCSGAII'	(K)C/C|S/G A/I I/V/L T/K(S)	C:Carbamidomethylation	128.2	611.3189	1221.633	-0.0025	-2	8.75	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
4385	dirMS_041712_NAR_40mM_plus2.6280.6387.2	2	13.63	0	2.04E+05		(K)TEISEMN	(K)T/E|I|S/E M/N/R(N)		96.33	490.2292	979.451	-0.0002	-0.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
4386	dirMS_041712_NAR_50mM_plus2.12325.12325.3	3	13.63	1	4.91E+05		(K)ILDSVGII	(K)I/L|D/S V/G I E/A D D D R\L N K(V)		132.85	591.6385	1772.902	-0.0015	-0.9	4.04	11664.7	4.42	HUMAN	P05387	60S acidic ribosomal protein P2
4387	dirMS_041712_NAR_50mM_plus2.7568.7773.3	3	13.63	0	1.97E+06		(K)EAPPME	(K)E A\P/P/M/E/K/P E V V/K(T)		106.32	451.9073	1353.708	-0.0009	-0.7	4.79	14798.1	10.35	HUMAN	K7EJ78	40S ribosomal protein S15 (Fragment)
4388	dirMS_041712_NAR_60mM_plus.10343.10901.3	3	13.63	1	2.26E+06		(K)TAVCDIF	(K)T/A|V/C D/I/P/P R G L K(M)	C:Carbamidomethylation	115.63	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
4389	dirMS_041712_NAR_120mM_minus.13512.13512.3	3	13.62	2	9.83E+05		(R)AQKDEE	(R)A Q|K/D E/E/K\M|E I/Q\E/I Q L K(E)		128.13	654.0058	1960.006	-0.0027	-1.4	4.58	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
4390	dirMS_041712_NAR_30mM_minus2.6822.6822.2	2	13.62	0	1.51E+04		(K)AMEAV/	(K)A M|E A|V/A|A Q G/K(A)		91.35	488.2495	975.493	-0.0011	-1.1	6.05	28936.8	9.22	HUMAN	P15259	Phosphoglycerate mutase 2
4391	dirMS_041712_NAR_40mM_minus2.12130.12130.3	3	13.62	0	3.21E+05		(K)IAILTCPI	(K)I A/I L/T/C|P E E/P P K/P K(T)	C:Carbamidomethylation	155.3	537.6382	1610.898	0.0026	1.6	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
4392	dirMS_041712_NAR_50mM_minus2.10228.10228.3	3	13.62	0	1.39E+05		(K)VGSLDN	(K)V/G|S/L/D N V/G H L/P A G G A V K(I)		126.85	530.9592	1590.86	0.0032	2	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
4393	dirMS_041712_NAR_60mM_minus.15466.15466.3	3	13.62	1	2.23E+05		(R)GPIKFN\	(R)G P/I/K F N V|W/D/T A/G Q E\K(F)		146.48	563.9575	1689.86	-0.0015	-0.9	6.07	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
4394	dirMS_041712_NAR_20mM_plus.10938.11020.2	2	13.62	0	1.17E+05		(K)EITALAP	(K)E I|T|A|L|A P S/T M K(I)		148.15	581.3129	1161.618	0.0001	0.1	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
4395	dirMS_041712_NAR_20mM_plus.13288.13408.2	2	13.62	0	4.79E+05	M148m	(R)DLTDYLr	(R)D L|T/D/Y/L/m/K(I)	m:Oxidized methionine	164.72	507.7439	998.486	15.9942	-0.7	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
4396	dirMS_041712_NAR_20mM_plus.7792.7792.3	3	13.62	0	1.06E+05		(K)AQAAAF	(K)A Q A\A A/P\A S V|P A/Q A/P K(R)		123.6	459.9204	1377.748	-0.0018	-1.3	8.8	17808.8	11.77	HUMAN	P47914	60S ribosomal protein L29
4397	dirMS_041712_NAR_30mM_plus2.6333.6333.2	2	13.62	0	4.73E+04	M924m	(K)FGDSNT	(K)F/G\D/S/N T/V/m R(F)	m:Oxidized methionine	87.4	521.7347	1026.467	15.9948	-0.1	5.84	334221.3	6.44	HUMAN	P15924	Desmoplakin
4398	dirMS_041712_NAR_40mM_plus2.14863.14863.3	3	13.62	1	2.18E+04		(K)VTADVII	(K)V/T|A/D|V/I/N A/A E/K L Q V V G R(A)		154.18	595.0062	1783.007	-0.0032	-1.8	6.04	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
4399	dirMS_041712_NAR_40mM_plus2.17403.17403.3	3	13.62	1	2.00E+05		(R)GDSVIV\	(R)G D/S V/I/V V/L R N P L/I A G K(-)		168.75	551.0007	1650.99	-0.0026	-1.6	8.75	6144.3	10.23	HUMAN	K7EJB5	Small nuclear ribonucleoprotein Sm D2
4400	dirMS_041712_NAR_50mM_plus2.20514.20514.3	3	13.62	1	1.87E+04		(K)SSVLENF	(K)S S|V|L/E N/F\V/G R D/F L P\R(G)		176.38	579.3128	1735.913	0.0113	6.5	5.79	73288.1	8.96	HUMAN	E5RHK8	Dynamin-3
4401	dirMS_041712_NAR_50mM_plus2.21533.21533.3	3	13.62	0	8.95E+04		(K)GAEILEV	(K)G A|E|I/L E V/L H/S L/P A V R(Q)		183.4	535.3092	1603.917	-0.0036	-2.2	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
4402	dirMS_041712_NAR_60mM_plus.12081.12218.3	3	13.62	1	1.99E+06		(R)MQKEIT	(R)M Q\K E I T/A|L|A/P/S T M K(I)		120.7	516.9402	1548.812	-0.0064	-4.1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
4403	dirMS_041712_NAR_20mM_minus.11276.11276.2	2	13.61	0	7.93E+04	M148m	(R)DLTDYLr	(R)D L|T/D Y L/m K(I)	m:Oxidized methionine	160.1	507.7443	998.486	15.995	0.1	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
4404	dirMS_041712_NAR_20mM_minus.13773.13847.2	2	13.61	0	2.58E+05		(R)IVLLDSS	(R)I/V|L|L/D S S/L\E/Y/K(K)		189.27	640.3594	1279.714	-0.0029	-2.2	4.37	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
4405	dirMS_041712_NAR_30mM_minus2.18093.18114.2	2	13.61	0	2.92E+05		(K)LLCGLLA	(K)L L|C/G L/L/A E/R(L)	C:Carbamidomethylation	152.05	522.7963	1044.587	-0.0017	-1.6	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
4406	dirMS_041712_NAR_40mM_minus2.16016.16016.3	3	13.61	0	1.60E+06	M166m	(K)VLDFEHI	(K)V/L/D/F E H F L/P m L/Q/T V/A K(N)	m:Oxidized methionine	187.72	635.3376	1888.004	15.9945	-0.2	5.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
4407	dirMS_041712_NAR_50mM_minus2.12480.12504.3	3	13.61	1	3.32E+05		(K)LYEQILA	(K)L/Y|E/Q I/L|A|E N E K L K(A)		139.12	530.9592	1590.874	-0.0107	-6.7	4.79	22046.7	5.8	HUMAN	H0YIM2	Protein phosphatase 1 regulatory subunit 12A (Fragment)
4408	dirMS_041712_NAR_50mM_minus2.16668.16668.3	3	13.61	1	2.61E+05		(R)SELELTL	(R)S E|L E/L T/L G K/L E Q V R(S)		163.6	538.9725	1614.906	-0.0032	-2	4.78	533778	5.74	HUMAN	Q15149	Plectin
4409	dirMS_041712_NAR_50mM_minus2.8826.8826.3	3	13.61	1	2.18E+05		(K)VCGDSD	(K)V/C|G D S D K G F V/V/I/N Q/K(G)	C:Carbamidomethylation	118.03	555.9474	1665.826	0.0012	0.7	5.93	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
4410	dirMS_041712_NAR_60mM_minus.7822.7822.3	3	13.61	0	1.10E+05		(K)LFQECCI	(K)L/F/Q/E C C/P/H S T D/R(V)	C:Carbamidomethylation	103.25	517.2229	1549.652	0.0019	1.2	5.32	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
4411	dirMS_041712_NAR_120mM_plus.13271.13335.4	4	13.61	2	1.88E+06		(R)ELNITAA	(R)E L/N I/T/A/A K E I/E V/G G G R K(A)		123.02	447.0018	1784.987	-0.0011	-0.6	6.33	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
4412	dirMS_041712_NAR_20mM_plus.14461.14461.2	2	13.61	0	1.33E+05		(R)FIDTTLA	(R)F I|D T T/L/A/I T S R(F)		171.52	619.3413	1237.679	-0.0034	-2.7	5.84	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
4413	dirMS_041712_NAR_20mM_plus.18644.18644.3	3	13.61	0	5.11E+05		(K)LAVEALS	(K)L A V E\A\L S/S L/D/G D/L/A G R(Y)		200.45	529.6164	1586.838	-0.0038	-2.4	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
4414	dirMS_041712_NAR_40mM_plus2.12300.12300.2	2	13.61	0	3.90E+04		(R)YIELLTR(	(R)Y I/E/L/L/T R(S)		138.3	454.2649	907.525	-0.0022	-2.4	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
4415	dirMS_041712_NAR_40mM_plus2.5408.5408.2	2	13.61	0	4.44E+04		(R)SQESGY'	(R)S Q|E|S|G|Y/Y D R(M)		88.63	552.733	1104.459	-0.0005	-0.5	4.37	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
4416	dirMS_041712_NAR_50mM_plus2.13703.13703.3	3	13.61	0	3.05E+05		(K)ASLASLP	(K)A S L A/S L/P/P L/H V A K(L)		140.47	435.2622	1303.773	-0.0012	-0.9	8.8	141626	5.5	HUMAN	A8MY36	Dynactin subunit 1
4417	dirMS_041712_NAR_60mM_plus.12103.12146.3	3	13.61	1	3.93E+05		(K)FADLSE/	(K)F/A|D|L|S/E/A A N R N N D/A L R(Q)		120.47	592.9581	1776.862	-0.0026	-1.5	4.56	49709.6	5.19	HUMAN	B0YJC4	Vimentin
4418	dirMS_041712_NAR_60mM_minus.11524.11524.3	3	13.6	1	2.94E+05		(R)VFDKEG	(R)V/F/D K E G\N G T|V/M/G/A E I R(H)		124.35	574.9539	1722.848	-0.0008	-0.5	4.68	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
4419	dirMS_041712_NAR_60mM_minus.12121.12641.3	3	13.6	0	2.01E+07		(R)NLDIERF	(R)N/L/D|I/E R/P T Y/T/N L N R(L)		129.65	573.6304	1718.882	-0.0054	-3.1	6.07	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
4420	dirMS_041712_NAR_120mM_plus.8766.8766.3	3	13.6	0	3.36E+05		(R)FACHSA	(R)F/A/C/H S|A/S/L/T\V/R(N)	C:Carbamidomethylation	99.38	416.8772	1248.615	0.0017	1.3	9.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
4421	dirMS_041712_NAR_20mM_plus.7459.7482.2	2	13.6	0	2.44E+05		(R)TVGIVGI	(R)T/V|G|I|V/G N Q P/K(V)		119.85	506.7922	1012.579	-0.0014	-1.4	8.41	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
4422	dirMS_041712_NAR_30mM_plus2.16002.16002.2	2	13.6	0	4.81E+05		(R)MGPNIY	(R)M G/P/N|I/Y E L/R(T)		136.78	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
4423	dirMS_041712_NAR_30mM_plus2.9769.9769.2	2	13.6	0	1.36E+06		(R)QLSSGV:	(R)Q/L|S/S/G/V/S E/I R(H)		104.9	538.2855	1075.574	-0.0105	-9.8	6	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
4424	dirMS_041712_NAR_40mM_plus2.12876.12899.3	3	13.6	0	3.13E+05		(K)VVEIAPA	(K)V V|E|I/A/P A A/H L/D/P Q L R(T)		142.63	543.6417	1628.912	-0.0013	-0.8	5.32	58266.4	9.46	HUMAN	B4DN00	Pyruvate carboxylase, mitochondrial
4425	dirMS_041712_NAR_50mM_plus2.20893.20893.3	3	13.6	1	7.61E+04		(K)TSAQVV	(K)T S/A/Q|V/V/L D G\L V D K I G D V K(C)		178.37	619.6814	1857.033	-0.0031	-1.7	4.43	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
4426	dirMS_041712_NAR_50mM_plus2.7792.7792.3	3	13.6	0	2.10E+05		(R)DGQVIN	(R)D G Q|V/I/N E T S Q/H/H D D L|E(-)		106.82	612.9457	1836.8	0.0231	12.6	4.28	53707.8	5.06	HUMAN	P08670	Vimentin
4427	dirMS_041712_NAR_120mM_minus.7359.7509.2	2	13.59	1	1.94E+06		(R)LSVDYGI	(R)L/S|V/D|Y/G K K(S)		94.83	455.2555	909.504	-0.0003	-0.3	8.5	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
4428	dirMS_041712_NAR_20mM_minus.14719.14719.2	2	13.59	0	9.82E+05		(K)EIIDLVLI	(K)E I/I/D/L/V/L D/R(I)		202.93	543.3133	1085.62	-0.0008	-0.7	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
4429	dirMS_041712_NAR_30mM_minus2.10723.10791.2	2	13.59	0	6.30E+05		(K)GFSLESC	(K)G F|S|L/E/S C/R(S)	C:Carbamidomethylation	112.08	478.2237	955.43	0.0099	10.4	6	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
4430	dirMS_041712_NAR_30mM_minus2.12009.12075.2	2	13.59	0	2.55E+05		(K)YFDSGD	(K)Y/F|D|S/G D/Y N/M A K(A)		118.87	655.7712	1310.536	-0.0007	-0.5	4.21	15633.5	7.82	HUMAN	A6NMQ3	Alpha-endosulfine
4431	dirMS_041712_NAR_30mM_minus2.16654.16806.3	3	13.59	0	7.83E+05		(R)ASLEAAI	(R)A S\L E A\A|I/A/D/A/E/Q R(G)		144.25	448.8965	1344.675	-0.0004	-0.3	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
4432	dirMS_041712_NAR_30mM_minus2.17182.17182.2	2	13.59	0	2.69E+05		(R)LLNTFLE	(R)L/L|N|T/F L E R(L)		146.93	503.2871	1005.573	-0.0058	-5.8	6	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
4433	dirMS_041712_NAR_30mM_minus2.19559.19616.2	2	13.59	0	4.72E+05		(R)ASLSLW	(R)A S/L/S/L/W/Q/A/M E/K(G)		162.75	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
4434	dirMS_041712_NAR_20mM_plus.15338.15338.2	2	13.59	0	1.68E+04	M73m	(R)AILVDLE	(R)A I/L\V|D\L/E/P G T m D S V R(S)	m:Oxidized methionine	177.98	816.4181	1615.836	15.9929	-1.2	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
4435	dirMS_041712_NAR_20mM_minus.10747.10747.2	2	13.58	0	4.12E+05		(K)DVNAAI.	(K)D V|N|A/A I/A A\I K(T)		155.97	493.287	985.568	-0.0009	-1	5.84	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
4436	dirMS_041712_NAR_20mM_minus.11554.11554.2	2	13.58	0	1.40E+05	M98m	(R)TLTIVDT	(R)T L/T|I/V/D/T/G I G m\T K(A)	m:Oxidized methionine	163.17	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
4437	dirMS_041712_NAR_60mM_minus.11505.11507.3	3	13.58	1	1.31E+05		(R)LSFDKD/	(R)L/S|F D K/D/A|M/V A R(A)		124.22	418.2174	1252.635	0.0022	1.8	5.96	35556.4	9.3	HUMAN	F2Z393	Transaldolase
4438	dirMS_041712_NAR_20mM_plus.8107.8107.2	2	13.58	0	2.09E+05		(R)FGQGG/	(R)F G Q/G/G/A|G/P V G G Q G P R(G)		125.22	671.3361	1341.666	-0.0009	-0.7	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
4439	dirMS_041712_NAR_20mM_plus.8872.9144.2	2	13.58	0	1.23E+06	M239m	(K)EITALAP	(K)E I|T|A|L|A|P/S T m K(I)	m:Oxidized methionine	132.6	589.309	1161.618	15.9923	-2.2	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
4440	dirMS_041712_NAR_30mM_plus2.11961.11961.2	2	13.58	0	1.36E+05		(R)YITQSGI	(R)Y I|T/Q/S\G D Y Q L R(T)		115.88	672.3314	1343.659	-0.0035	-2.6	5.83	5236	9.87	HUMAN	K7EK69	AP-1 complex subunit mu-2 (Fragment)
4441	dirMS_041712_NAR_30mM_plus2.13993.14309.2	2	13.58	0	1.22E+06		(R)SVPTWL	(R)S V|P/T|W/L/K(L)		126.78	415.7394	830.477	-0.0055	-6.7	8.47	12573.5	10.39	HUMAN	E9PS50	40S ribosomal protein S13 (Fragment)
4442	dirMS_041712_NAR_30mM_plus2.14416.14573.2	2	13.58	0	5.64E+05		(R)IILLAEGI	(R)I/I|L|L/A E/G R(L)		129.25	442.7821	884.556	0.0005	0.6	6	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
4443	dirMS_041712_NAR_30mM_plus2.19971.19992.2	2	13.58	0	8.31E+04		(R)FEELTNL	(R)F E|E|L|T|N/L I/R(T)		158.62	567.8152	1134.615	0.0078	6.9	4.53	106155.7	5.45	HUMAN	B5ME19	Eukaryotic translation initiation factor 3 subunit C
4444	dirMS_041712_NAR_40mM_plus2.16185.16185.3	3	13.58	1	1.95E+05		(K)LGVQVV	(K)L G V/Q/V/V/I/T D/P E K L D Q I R(Q)		161.77	641.701	1923.091	-0.0025	-1.3	4.56	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
4445	dirMS_041712_NAR_40mM_plus2.18673.18673.3	3	13.58	0	4.72E+04		(R)NEVSFVI	(R)N/E/V/S F V/I/H N L P V L A K(M)		175.93	560.6533	1679.948	-0.0026	-1.5	6.75	35663.7	5.91	HUMAN	B4DWK0	Selenide, water dikinase 1
4446	dirMS_041712_NAR_50mM_plus2.11459.11459.3	3	13.58	0	3.42E+05		(K)YTVQDE	(K)Y/T/V/Q/D E S H S E\W/V S C V R(F)	C:Carbamidomethylation	127.98	661.2946	1981.871	-0.0016	-0.8	4.65	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
4447	dirMS_041712_NAR_50mM_plus2.12384.12426.3	3	13.58	1	1.70E+06		(R)SGKAPIL	(R)S G K A\P I\L|I|A/T/D/V/A/S R(G)		133.47	500.2911	1498.859	0	0	8.46	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
4448	dirMS_041712_NAR_50mM_plus2.6484.6484.3	3	13.58	1	5.14E+04		(R)AGGEEL	(R)A/G/G E/E/L D/E/G V A K D N/A K(I)		99	534.9257	1602.761	0.002	1.2	4.18	89879.1	4.58	HUMAN	Q32MZ4	Leucine-rich repeat flightless-interacting protein 1
4449	dirMS_041712_NAR_40mM_minus2.12584.12584.3	3	13.57	1	5.98E+05		(R)VCENIPI	(R)V/C|E N I/P I\V L/C G N K V D\I/K(D)	C:Carbamidomethylation	157.7	657.6842	1971.04	-0.0021	-1.1	6.04	14844.8	5.89	HUMAN	B4DV51	GTP-binding nuclear protein Ran
4450	dirMS_041712_NAR_40mM_minus2.14258.14258.3	3	13.57	1	2.95E+05		(K)VIAATNI	(K)V I|A A/T N R V D|I L D/P A/L L R(S)		167.82	617.3653	1850.086	-0.0045	-2.4	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
4451	dirMS_041712_NAR_120mM_plus.23917.23917.3	3	13.57	1	3.42E+05	M145m	(R)GVmLA\	(R)G V/m/L/A V/D A V|I A E L K K(Q)	m:Oxidized methionine	179.77	524.9713	1556.908	15.9913	-2.3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
4452	dirMS_041712_NAR_120mM_plus.8479.8479.3	3	13.57	1	2.94E+05		(R)ASGNYA	(R)A/S|G/N/Y/A T/V I S H N P E T K K(T)		97.62	606.3102	1816.919	-0.0028	-1.5	8.55	24115.6	11.59	HUMAN	E9PIZ3	60S ribosomal protein L8
4453	dirMS_041712_NAR_20mM_plus.7693.7693.2	2	13.57	0	1.57E+05		(K)IAVAAQ	(K)I/A|V/A/A/Q N C Y K(V)	C:Carbamidomethylation	122.43	569.2902	1137.572	0.001	0.9	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
4454	dirMS_041712_NAR_30mM_plus2.19403.19403.2	2	13.57	0	2.93E+05		(K)TVDNFV	(K)T V|D/N F/V/A/L A T G E/K(G)		155.2	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
4455	dirMS_041712_NAR_40mM_plus2.18254.18254.3	3	13.57	1	2.86E+05		(R)VAAKLE'	(R)V/A A K L E V\A|P\I/S D I I A I K(S)		174.02	584.3591	1751.068	-0.005	-2.8	6.04	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
4456	dirMS_041712_NAR_60mM_plus.15393.15393.3	3	13.57	1	5.97E+05		(R)FVNVVP	(R)F/V|N\V|V/P T F G K K(K)		137.58	412.5761	1235.715	-0.0009	-0.7	10	10904.6	11.56	HUMAN	E9PR30	40S ribosomal protein S30
4457	dirMS_041712_NAR_40mM_minus2.14622.14622.3	3	13.56	1	1.39E+05		(K)GTVPDD	(K)G T/V/P/D D A V/E A L/A D/S L G K K(E)		170.35	595.9791	1785.923	-0.0001	-0.1	4.23	81397.3	4.99	HUMAN	B7Z468	Calpastatin
4458	dirMS_041712_NAR_50mM_minus2.12756.12756.3	3	13.56	1	3.86E+05		(K)NTVELL\	(K)N T|V/E/L/L/V E D K G N/Q V Y/R(C)		140.47	626.3309	1876.976	0.0018	1	4.68	258215.9	5.48	HUMAN	E7EN95	Filamin-B
4459	dirMS_041712_NAR_50mM_plus2.15946.16012.3	3	13.56	1	3.45E+05		(K)QLDDLK'	(K)Q L/D D/L K/V/E/L/S Q L R(V)		159.03	519.6261	1556.864	-0.0005	-0.3	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
4460	dirMS_041712_NAR_60mM_minus.14159.14159.3	3	13.56	0	3.03E+05		(K)YGYTHLS	(K)Y/G\Y/T/H/L/S/T G/D/L L/R(S)		138.93	499.2614	1495.754	0.0157	10.5	6.74	21748.6	8.92	HUMAN	P00568	Adenylate kinase isoenzyme 1
4461	dirMS_041712_NAR_120mM_plus.15269.15269.4	4	13.56	0	2.28E+06		(K)HLEINPI	(K)H L\E\I N/P D H/P/I/V/E T L R(Q)		133.9	446.4951	1782.95	0.0089	5	5.27	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
4462	dirMS_041712_NAR_20mM_plus.8086.8086.2	2	13.56	0	2.12E+05		(R)FGQGG/	(R)F/G|Q|G|G A\G/P V|G G/Q G P R(G)		125.2	671.3361	1341.666	-0.0009	-0.7	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
4463	dirMS_041712_NAR_30mM_plus2.10324.10324.2	2	13.56	0	2.86E+05		(R)LNQDQI	(R)L/N|Q|D Q L/D/A/V/S K(Y)		107.42	615.819	1230.632	-0.0017	-1.4	4.21	20235.4	6.77	HUMAN	E9PLA9	Caprin-1 (Fragment)
4464	dirMS_041712_NAR_30mM_plus2.6388.6654.2	2	13.56	0	3.84E+05		(R)SPDNPN	(R)S/P|D|N|P/M/N Q R(A)		88.78	529.7357	1058.468	-0.0042	-4	5.55	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124

4465	dirMS_041712_NAR_40mM_plus2.10694.10714.3	3	13.56	0	1.85E+05		(K)VGSLDN	(K)V G|S/L/D/N V G H/L/P A G G A V K(I)		128.15	530.9567	1590.86	-0.0043	-2.7	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
4466	dirMS_041712_NAR_40mM_plus2.12538.12538.3	3	13.56	0	3.87E+05		(K)AASDIAI	(K)A A/S D I A/M/T E/L/P P/T H P I R(L)		139.97	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
4467	dirMS_041712_NAR_50mM_plus2.12511.12511.3	3	13.56	1	3.06E+05		(R)SGVGLS	(R)S G V/G/L/S/S/Y L/S T E K D A S\P K(T)		133.63	609.3102	1825.918	-0.0018	-1	5.79	64248.4	9.08	HUMAN	Q9BW04	Specifically androgen-regulated gene protein
4468	dirMS_041712_NAR_50mM_plus2.13321.13322.3	3	13.56	1	4.37E+05		(K)QLQALS	(K)Q L/Q/A/L/S\S E L A/Q A R D E/T/K(K)		138.2	629.9955	1887.977	-0.0051	-2.7	4.68	71218.8	6.3	HUMAN	A7YIJ8	Radixin
4469	dirMS_041712_NAR_50mM_plus2.21762.21762.3	3	13.56	0	3.03E+05		(K)AYNMVI	(K)A Y/N/M/V D I I/H/S V V D/E/R(E)		185.65	587.6346	1760.864	0.0257	14.6	4.54	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
4470	dirMS_041712_NAR_50mM_plus2.6093.6429.3	3	13.56	0	5.83E+05	M70m	(K)EAPPmE	(K)E A|P/P/m E K/P E V/V/K(T)	m:Oxidized methionine	96.68	457.2387	1353.708	15.9933	-1.2	4.79	14798.1	10.35	HUMAN	K7EJ78	40S ribosomal protein S15 (Fragment)
4471	dirMS_041712_NAR_60mM_plus.14386.14386.3	3	13.56	1	8.33E+05		(R)TIRYPDP	(R)T/I/R Y P D/P/L/I K(V)		131.87	405.9078	1215.71	-0.0007	-0.6	8.25	29825.4	10.37	HUMAN	P62701	40S ribosomal protein S4, X isoform
4472	dirMS_041712_NAR_60mM_plus.7688.7786.3	3	13.56	1	1.31E+06		(K)KGTVEG	(K)K G T V\E\G\F|E|P/A/D/N K(C)		98.42	464.5649	1391.68	0	0	4.68	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
4473	dirMS_041712_NAR_60mM_plus.8416.8437.3	3	13.56	1	2.08E+06		(K)EAIEGTY	(K)E A|I/E/G T Y/I/D/K K(C)		102.38	422.8929	1266.658	0.0065	5.2	4.68	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
4474	dirMS_041712_NAR_30mM_minus2.8415.8668.2	2	13.55	0	2.91E+06		(R)IMDQTL	(R)I/M|D/Q/T/L/K(A)		101.18	424.7339	848.455	0.0059	7	5.84	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
4475	dirMS_041712_NAR_120mM_plus.9659.9722.3	3	13.55	1	1.50E+06		(R)SRNTDE	(R)S R N T D|E|M|V|E/L/R(I)		104.13	450.556	1349.648	0.0057	4.2	4.68	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
4476	dirMS_041712_NAR_60mM_plus.13865.13865.3	3	13.55	1	4.89E+05		(K)VKTDTV	(K)V K T D\T V|L|I/L/C R(K)	C:Carbamidomethylation	129.2	439.9237	1317.756	0.0007	0.5	8.72	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
4477	dirMS_041712_NAR_30mM_minus2.10189.10225.2	2	13.54	0	3.91E+05		(K)ATAVVD	(K)A/T|A|V|V/D G A\F K(E)		109.9	489.7645	978.525	-0.0037	-3.8	5.88	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
4478	dirMS_041712_NAR_30mM_minus2.5796.5796.2	2	13.54	0	6.55E+04		(K)TSETLSC	(K)T S|E|T/L/S Q A G Q/K(A)		85.58	575.2877	1149.575	-0.0065	-5.6	5.66	25978.5	4.91	HUMAN	C9J502	Prostate leucine zipper variant 2
4479	dirMS_041712_NAR_50mM_minus2.16579.16579.3	3	13.54	1	1.60E+05		(K)VVSSVL(	(K)V/V/S S V L Q/F/G N I/S/F K K(E)		162	551.6488	1652.937	-0.0052	-3.1	10	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
4480	dirMS_041712_NAR_120mM_plus.15972.15972.3	3	13.54	1	8.08E+04		(K)THLPGF	(K)T\H|L|P G F\V/E\Q/A|E A L K A K(G)		137.02	580.3208	1738.949	-0.0008	-0.5	6.42	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
4481	dirMS_041712_NAR_20mM_plus.12638.12638.2	2	13.54	0	1.19E+05		(K)IISNASC	(K)I I|S N|A|S C T T N C L|A|P L A/K(V)	C:Carbamidomethylation	159.55	917.4626	1833.92	-0.0018	-1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
4482	dirMS_041712_NAR_20mM_plus.16523.16523.3	3	13.54	0	2.04E+05		(K)TVTNAV	(K)T V T N A V V T V/P/A/Y/F/N D S Q R(Q)		184.62	661.3368	1981.998	-0.0019	-1	5.5	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
4483	dirMS_041712_NAR_30mM_plus2.14391.14857.2	2	13.54	0	7.11E+06		(R)NLLSVA	(R)N/L|L|S/V/A/Y|K(N)		129.83	454.2621	907.525	-0.0078	-8.6	8.59	18789.1	6.77	HUMAN	A2IDB2	14-3-3 protein eta (Fragment)
4484	dirMS_041712_NAR_30mM_plus2.19426.19426.2	2	13.54	0	2.87E+05		(K)TVDNFV	(K)T V|D N/F/V/A L/A T/G E K(G)		155.25	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
4485	dirMS_041712_NAR_30mM_plus2.21982.21982.2	2	13.54	0	1.87E+05		(R)EGDVLT	(R)E G D|V/L|T/L|L/E/S E\R(E)		170.55	680.8538	1360.696	0.0049	3.6	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
4486	dirMS_041712_NAR_30mM_plus2.22093.22093.2	2	13.54	0	5.37E+03		(R)DLLFQAI	(R)D L|L/F|Q/A/L/G R(T)		171.48	516.7959	1032.584	0.0009	0.8	5.84	66742	6.4	HUMAN	Q9NSD9	Phenylalanine--tRNA ligase beta subunit
4487	dirMS_041712_NAR_30mM_plus2.7106.7106.2	2	13.54	0	1.37E+05		(R)TTTGSYI	(R)T T|T/G/S/Y I A N/R(V)		91.82	542.274	1083.543	-0.0022	-2	8.41	10799.8	5.07	HUMAN	I3L3X7	Proteasome subunit beta type-6 (Fragment)
4488	dirMS_041712_NAR_50mM_plus2.12866.12866.3	3	13.54	0	5.97E+05		(R)FDAERP	(R)F/D|A/E R P V\D C S V/I V/V N K(Q)	C:Carbamidomethylation	135.82	616.6476	1847.932	-0.0038	-2	4.56	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
4489	dirMS_041712_NAR_50mM_plus2.18202.18202.3	3	13.54	1	1.60E+06		(R)ELIKVLEI	(R)E L|I K V L\E E A\N/Q/A|I/N/P K(L)		163.67	603.6741	1809.012	-0.0039	-2.2	4.79	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
4490	dirMS_041712_NAR_60mM_plus.13043.13043.3	3	13.54	1	3.99E+05		(K)LAEQAE	(K)L/A|E/Q/A E/R Y D D M A A A M K(A)		124.77	604.9452	1812.825	-0.0044	-2.5	4.32	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
4491	dirMS_041712_NAR_60mM_plus.19380.19404.3	3	13.54	1	6.47E+05		(R)TRIEGLL	(R)T R I E G L|L|A/A/F/P/K(L)		159.78	439.262	1315.773	-0.0018	-1.4	8.41	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
4492	dirMS_041712_NAR_60mM_plus.20627.20627.3	3	13.54	1	2.87E+05		(K)ITQDIFQ	(K)I/T/Q/D/I F/Q Q L L K/R(G)		168.08	501.626	1502.869	-0.0055	-3.7	8.75	72796.9	6.75	HUMAN	A6NC17	Methionine--tRNA ligase, cytoplasmic
4493	dirMS_041712_NAR_60mM_plus.9141.9141.3	3	13.54	1	2.99E+05		(R)FVKQDC	(R)F/V/K Q D|Q|V/C/I A R(L)	C:Carbamidomethylation	106	455.2428	1363.715	-0.0012	-0.9	8.75	53458.1	5.47	HUMAN	H3BR35	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A (Fragment)
4494	dirMS_041712_NAR_60mM_plus.9963.9998.3	3	13.54	1	7.09E+05		(K)ATFIKVP	(K)A T|F/I/K/V/P Q/N Q N G K(S)		110.03	482.2682	1444.791	-0.0006	-0.4	10	32503.1	5.29	HUMAN	H7BY16	Nucleolin (Fragment)
4495	dirMS_041712_NAR_30mM_minus2.17108.17122.2	2	13.53	0	8.20E+04		(K)FAEAFE	(K)F A|E|A/F/E|A/I/P R(A)		146.93	575.7971	1150.589	-0.0022	-1.9	4.53	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
4496	dirMS_041712_NAR_40mM_minus2.9912.9912.3	3	13.53	0	6.21E+04		(R)VVIIGAG	(R)V V\I/I/G A G K/P A A\V V/L/Q T K(G)		139.62	555.3529	1664.047	-0.0028	-1.7	10	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
4497	dirMS_041712_NAR_50mM_minus2.12250.12250.3	3	13.53	1	1.37E+05		(R)VFDKDG	(R)V F/D K D G N G\Y|I|S/A/A/E L R(H)		137.82	585.6286	1754.871	0.0005	0.3	4.56	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
4498	dirMS_041712_NAR_120mM_plus.9120.9120.3	3	13.53	1	3.33E+05		(R)SSGGSYI	(R)S S|G G/S/Y R D S Y D S/Y/A/T H N E(-)		101.37	665.9373	1995.795	0.0022	1.1	4.81	18647.7	9.51	HUMAN	Q14011	Cold-inducible RNA-binding protein
4499	dirMS_041712_NAR_20mM_plus.13659.13659.2	2	13.53	0	1.80E+05	M98m	(R)TLTIVDT	(R)T L|T|I/V|D T G I G m T/K(A)	m:Oxidized methionine	166.4	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
4500	dirMS_041712_NAR_30mM_plus2.14061.14336.2	2	13.53	0	7.39E+05		(K)ALEIIPR(	(K)A L|E|I\I/P/R(Q)		127.17	406.255	811.504	-0.0009	-1.1	6.05	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
4501	dirMS_041712_NAR_30mM_plus2.16177.16177.2	2	13.53	0	2.79E+05		(K)MDQAII	(K)M/D/Q|A/I/I/F C R(T)	C:Carbamidomethylation	137.37	577.2809	1153.549	0.0053	4.6	5.59	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
4502	dirMS_041712_NAR_30mM_plus2.17376.17376.2	2	13.53	0	7.45E+05		(R)IMNTFS	(R)I M|N/T/F/S/V V P S/P K(V)		144.9	660.3537	1319.703	-0.0027	-2	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
4503	dirMS_041712_NAR_40mM_plus2.15040.15040.3	3	13.53	1	1.82E+05		(R)EGIVTAT	(R)E G I/V/T/A T E Q E V K E D I A K(L)		155.1	620.6583	1859.96	0.0007	0.4	4.25	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
4504	dirMS_041712_NAR_50mM_plus2.10751.10971.3	3	13.53	1	2.59E+06		(R)VCEEIAII	(R)V/C|E E\I\A\I|I P S K K(L)	C:Carbamidomethylation	125.03	462.9247	1386.766	-0.0066	-4.7	6.11	21927.8	9.55	HUMAN	H0YK46	40S ribosomal protein S17 (Fragment)
4505	dirMS_041712_NAR_50mM_plus2.12021.12021.3	3	13.53	0	4.17E+05		(K)QADLYIS	(K)Q/A/D/L/Y/I/S E G/L H P/R(I)		131.4	500.2606	1498.765	0.0024	1.6	5.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
4506	dirMS_041712_NAR_50mM_plus2.14902.14902.3	3	13.53	1	1.13E+06		(R)VEKIPGC	(R)V/E K I|P G G\I|I/E/D/S C/V\L R(G)	C:Carbamidomethylation	146.32	595.6548	1784.958	-0.0076	-4.3	4.68	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
4507	dirMS_041712_NAR_50mM_plus2.6731.6731.3	3	13.53	0	1.60E+05		(K)IGEEEIQ	(K)I/G/E/E E/I/Q K P/E E K(V)		100.35	476.9126	1428.722	0.0016	1.1	4.32	81733.5	5.24	HUMAN	E9PAW1	Splicing factor 3A subunit 1
4508	dirMS_041712_NAR_60mM_plus.11291.11291.2	2	13.53	0	6.36E+05		(K)NFYVEH	(K)N F|Y|V/E/H/P E V/A R(L)		116.55	680.8363	1360.664	0.0009	0.7	5.4	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
4509	dirMS_041712_NAR_60mM_plus.12009.12154.3	3	13.53	1	7.31E+06		(R)DGKLVS	(R)D G K L\V\S\E|S/S/D/V L/P/K(-)		120.27	491.928	1473.78	-0.0101	-6.8	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
4510	dirMS_041712_NAR_60mM_plus.8553.8553.3	3	13.53	1	4.16E+05		(K)QGIETPE	(K)Q G I/E/T/P E/D Q/N D L R K(M)		102.63	548.2719	1642.803	-0.002	-1.2	4.32	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
4511	dirMS_041712_NAR_120mM_minus.11453.11487.3	3	13.52	1	1.32E+06	M406m	(R)QLREYQ	(R)Q L R E Y\Q|E|L m/N V/K(L)	m:Oxidized methionine	116.77	522.9361	1550.8	15.9942	-0.5	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
4512	dirMS_041712_NAR_30mM_minus2.11887.12011.2	2	13.52	0	3.33E+05		(R)FGISSVP	(R)F/G|I/S/S V/P T/K(G)		118.22	468.2614	935.52	-0.0041	-4.4	8.75	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
4513	dirMS_041712_NAR_40mM_minus2.5919.5919.2	2	13.52	0	1.33E+06		(K)AGFAGD	(K)A G/F|A/G/D/D A\P R(A)		98.17	488.7279	976.448	0.0002	0.2	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
4514	dirMS_041712_NAR_40mM_minus2.9405.9405.3	3	13.52	0	1.42E+05		(K)QLTEED(	(K)Q L/T/E/E/D G V/H S V I E E N I K(C)		137.88	647.3235	1939.961	-0.0048	-2.5	4.25	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
4515	dirMS_041712_NAR_50mM_minus2.10348.10348.3	3	13.52	0	1.46E+05		(K)VGSLDN	(K)V/G|S L/D N V/G H L/P A G G A V K(I)		126.9	530.9592	1590.86	0.0032	2	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
4516	dirMS_041712_NAR_60mM_minus.12140.12140.3	3	13.52	1	3.77E+05		(K)AAAGKA	(K)A/A|A G K/A\E L/E|L E/L/G R(I)		127.53	476.5974	1427.785	-0.0076	-5.3	4.79	533778	5.74	HUMAN	Q15149	Plectin
4517	dirMS_041712_NAR_120mM_plus.15209.15225.4	4	13.52	1	1.03E+06		(K)DHASIQI	(K)D H A S I\Q/M/N/V/A E/V/D K/V T G R(F)		133.17	493.25	1969.976	0.0022	1.1	5.38	9225.3	9.16	HUMAN	P63220	40S ribosomal protein S21
4518	dirMS_041712_NAR_120mM_plus.22512.22512.4	4	13.52	1	5.59E+05		(K)SKGLAPI	(K)S K G\L A\P D\L|P E D/L Y H L I K(K)		171.52	478.0137	1909.043	-0.01	-5.2	5.36	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
4519	dirMS_041712_NAR_20mM_plus.17053.17053.2	2	13.52	0	1.36E+05		(K)FATEAAI	(K)F A/T/E/A|A/I/T I L R(I)		188.82	603.3442	1205.689	-0.0077	-6.4	6	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
4520	dirMS_041712_NAR_20mM_plus.17670.17670.2	2	13.52	0	8.56E+04		(R)GDGPICI	(R)G/D/G P I|C\L/V/L/A|P T R(E)	C:Carbamidomethylation	193.13	684.8681	1368.73	-0.0015	-1.1	5.84	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
4521	dirMS_041712_NAR_20mM_plus.9587.9587.2	2	13.52	0	8.24E+04	M2819m	(K)GLPSPYI	(K)G L/P/S/P/Y N/m S S A P G S R(S)	m:Oxidized methionine	137.4	768.8596	1520.716	15.9957	0.5	8.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
4522	dirMS_041712_NAR_30mM_plus2.13221.13221.2	2	13.52	0	2.78E+05		(R)GGAEQF	(R)G G A\E|Q|F/M/E\E/T E R(S)		122.33	692.2951	1383.584	-0.0016	-1.2	4.09	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
4523	dirMS_041712_NAR_40mM_plus2.19951.19951.3	3	13.52	0	4.60E+05	M166m	(K)VLDFEHI	(K)V/L/D F E H F/L/P m/L Q T\V A K(N)	m:Oxidized methionine	187.63	635.3379	1888.004	15.9954	0.3	5.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
4524	dirMS_041712_NAR_50mM_plus2.10106.10106.3	3	13.52	1	5.94E+04		(K)ITIKNDP	(K)I T/I/K/N D/P S L/P E/P K(C)		120.53	484.6079	1451.81	-0.0013	-0.9	6.07	20203.8	9.79	HUMAN	B4DG16	Asparagine--tRNA ligase, cytoplasmic
4525	dirMS_041712_NAR_50mM_plus2.19261.19261.3	3	13.52	0	4.30E+05		(R)GFGFITF	(R)G F|G F/I|T/F/T N P E H A S V A M R(A)		169.17	661.3258	1981.959	0.004	2	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
4526	dirMS_041712_NAR_50mM_plus2.9470.9470.3	3	13.52	0	7.71E+05		(R)DNIQGI	(R)D N|I\Q G I|T/K/P A I R(R)		117.22	442.5902	1325.754	0.0025	1.9	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
4527	dirMS_041712_NAR_60mM_plus.13701.13742.3	3	13.52	1	4.08E+05		(K)SGYLAGI	(K)S/G|Y|L|A G D K/L|L/P Q R(V)		128.58	473.2654	1417.78	0.0019	1.3	8.31	67933	6.08	HUMAN	P26038	Moesin
4528	dirMS_041712_NAR_120mM_minus.12085.12085.3	3	13.51	0	2.17E+05		(R)QADFEA	(R)Q/A D F E/A/H N I/L/R(E)		119.82	438.5572	1313.66	-0.0026	-2	5.32	66612.6	7.28	HUMAN	F8W720	GMP synthase [glutamine-hydrolyzing]
4529	dirMS_041712_NAR_30mM_minus2.18951.19015.2	2	13.51	0	6.16E+05		(K)LALFQAI	(K)L/A|L/F/Q A/I/G/K(E)		158.7	480.7964	960.588	-0.0022	-2.2	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
4530	dirMS_041712_NAR_30mM_minus2.9028.9045.2	2	13.51	0	4.00E+05		(K)DVDEAY	(K)D V|D|E|A|Y M/N K(V)		103.58	542.736	1084.462	0.0032	2.9	4.03	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
4531	dirMS_041712_NAR_40mM_minus2.10799.10799.3	3	13.51	0	1.24E+05	M56m	(K)VAIVKP(	(K)V/A|I|V|K/P G\V/P m E I V L N K(E)	m:Oxidized methionine	146.9	575.0112	1707.024	15.9953	0.2	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
4532	dirMS_041712_NAR_40mM_minus2.14153.14153.3	3	13.51	0	1.71E+05		(K)LQAVEV	(K)L Q|A V/E V/V/I/T H L A P G/T K(H)		167.22	559.3273	1675.974	-0.0068	-4	6.75	16120	9.05	HUMAN	Q9Y2V2	Calcium-regulated heat stable protein 1
4533	dirMS_041712_NAR_40mM_minus2.7678.7678.3	3	13.51	0	6.54E+04		(K)EVVKPV	(K)E V V K\P V/P|I/T S/P A V/S K(V)		123.68	517.6416	1550.915	-0.005	-3.2	8.69	65142.1	9.24	HUMAN	Q96HC4	PDZ and LIM domain protein 5
4534	dirMS_041712_NAR_50mM_minus2.14675.14675.3	3	13.51	0	1.16E+04		(K)GILADEI	(K)G I/L/A/D/E D S S R P V W L K(A)		150.35	562.6354	1685.886	0.0059	3.5	4.56	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
4535	dirMS_041712_NAR_50mM_minus2.18500.18500.3	3	13.51	1	1.47E+06		(R)VISGVLC	(R)V I|S/G\V/L/Q L G N I/V F K K(E)		177	539.0018	1614.994	-0.0033	-2	10	227783.5	5.5	HUMAN	P35579	Myosin-9
4536	dirMS_041712_NAR_50mM_minus2.9346.9346.3	3	13.51	1	1.36E+05		(R)QEEELQ	(R)Q/E/E/E/L/Q A/K/D E E L L/K(V)		121.4	567.9554	1701.854	-0.0025	-1.5	4.14	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
4537	dirMS_041712_NAR_20mM_plus.14684.14684.2	2	13.51	0	1.99E+05		(K)VSTLPAI	(K)V/S|T L|P A I/T/L K(L)		172.6	521.8283	1042.651	-0.0013	-1.3	8.72	20599.3	9.19	HUMAN	H7C1V0	Cathepsin D light chain (Fragment)
4538	dirMS_041712_NAR_20mM_plus.15772.15772.2	2	13.51	0	4.76E+05		(R)GVVDSE	(R)G V V/D S E/D|I/P/L N L S\R(E)		179.47	757.3956	1513.786	-0.0017	-1.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
4539	dirMS_041712_NAR_30mM_plus2.19520.19520.2	2	13.51	0	9.95E+03		(R)FLLADNI	(R)F L|L/A/D N/L/Y/C/K(A)	C:Carbamidomethylation	155.87	628.8226	1256.634	0.0036	2.8	5.83	22400.1	6.19	HUMAN	F5H2A7	Prefoldin subunit 3
4540	dirMS_041712_NAR_30mM_plus2.5731.5814.2	2	13.51	0	4.13E+05		(K)GSSNSY	(K)G/S|S/N/S/Y/A|I/K(K)		84.45	463.7311	926.458	-0.0029	-3.1	8.59	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
4541	dirMS_041712_NAR_40mM_plus2.17059.17059.3	3	13.51	0	6.64E+04		(R)IHFPLAT	(R)I H F\P L A\T/Y|A/P V/I S A E K(A)		166.77	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
4542	dirMS_041712_NAR_40mM_plus2.17958.17958.3	3	13.51	1	7.73E+04	M116m	(R)ELAILLG	(R)E L\A/I/L/L/G/m L D/P A E K\D/E K(G)	m:Oxidized methionine	171.67	634.3333	1884.999	15.9867	-4.3	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
4543	dirMS_041712_NAR_50mM_plus2.10082.10125.3	3	13.51	0	2.23E+05		(R)TITVALA	(R)T I|T|V/A/L A D/G/G R P D/N T G R(G)		120.23	571.9661	1713.888	-0.0041	-2.4	5.63	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
4544	dirMS_041712_NAR_50mM_plus2.13259.13259.3	3	13.51	0	3.85E+05		(K)VQASLA	(K)V Q|A/S/L A/A N T F T I/T G H A/E T K(Q)		137.68	654.0087	1960.013	-0.0019	-1	6.72	11802.2	5.6	HUMAN	D6RDG3	Transcription factor BTF3 (Fragment)
4545	dirMS_041712_NAR_60mM_plus.12427.12474.3	3	13.51	0	1.52E+06		(K)ADDGRF	(K)A/D|D/G/R P F/P Q\V/I/K(S)		121.6	448.2414	1342.711	-0.0017	-1.3	6	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
4546	dirMS_041712_NAR_20mM_minus.13287.13287.3	3	13.5	0	2.65E+05		(K)VGINYQ	(K)V G I N Y Q P P T V/V/P G G D L A K(V)		183.15	608.9971	1824.985	-0.0087	-4.8	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
4547	dirMS_041712_NAR_40mM_minus2.14425.14425.3	3	13.5	1	1.33E+05		(R)LKLPSIPI	(R)L K L P S I/P L/V|P V S A Q K(R)		169.38	530.6703	1589.999	-0.0025	-1.6	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
4548	dirMS_041712_NAR_50mM_minus2.10264.10264.3	3	13.5	0	2.72E+05		(R)TFIAIKPI	(R)T/F|I/A/I K/P D/G V Q R(G)		126.83	448.923	1344.763	-0.009	-6.7	8.41	6640.6	8.25	HUMAN	C9K028	Nucleoside diphosphate kinase A (Fragment)
4549	dirMS_041712_NAR_50mM_minus2.8023.8023.3	3	13.5	1	1.15E+05		(K)TAVCDIF	(K)T/A/V/C D/I/P P R/G L K(M)	C:Carbamidomethylation	112.25	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
4550	dirMS_041712_NAR_30mM_plus2.6658.6658.2	2	13.5	0	2.92E+05		(R)EAGEQG	(R)E A/G E/Q/G D/I E/P R(R)		89.77	600.7772	1200.549	-0.002	-1.7	4	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
4551	dirMS_041712_NAR_30mM_plus2.9686.9686.2	2	13.5	0	3.55E+05		(R)TSLGPN(	(R)T S/L/G/P N G L D/K(M)		104.43	501.2717	1001.526	0.0099	9.9	5.5	55804.4	5.33	HUMAN	B7ZAR1	T-complex protein 1 subunit epsilon
4552	dirMS_041712_NAR_40mM_plus2.10066.10066.2	2	13.5	0	1.20E+05		(R)YSGSYNI	(R)Y/S/G S|Y/N\D|Y L R(A)		123.83	619.2788	1237.548	0.0019	1.6	5.83	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
4553	dirMS_041712_NAR_50mM_plus2.15039.15080.3	3	13.5	1	4.04E+05		(K)LIVAYVD	(K)L/I|V/A/Y V D D L D R/R(G)		147.27	483.2728	1447.79	0.0135	9.3	4.43	124127.1	8.81	HUMAN	O14776	Transcription elongation regulator 1
4554	dirMS_041712_NAR_60mM_plus.14989.15165.3	3	13.5	0	7.90E+05		(R)SCTVNIN	(R)S C/T/V/N/I/M|F/G T P Q E/H R(N)	C:Carbamidomethylation	135.17	592.9433	1776.816	-0.0003	-0.1	6.47	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
4555	dirMS_041712_NAR_120mM_minus.13806.14169.3	3	13.49	1	4.47E+06		(K)ASLENSI	(K)A/S|L/E/N S L/R E V/E/A R(Y)		130.5	491.9266	1473.766	-0.0003	-0.2	4.79	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4556	dirMS_041712_NAR_30mM_minus2.11646.11899.3	3	13.49	0	3.96E+06		(R)AQIFAN	(R)A Q\I\F A N/T|V/D/N A/R(I)		117.57	440.5617	1319.67	0.0003	0.2	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4557	dirMS_041712_NAR_30mM_minus2.18397.18742.2	2	13.49	0	2.30E+05		(K)AVVMDI	(K)A V|V|M|D|L L/R(Q)		155.32	458.7685	916.528	0.0013	1.4	5.88	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
4558	dirMS_041712_NAR_60mM_minus.16960.16960.3	3	13.49	1	2.51E+05		(K)MFGIDR	(K)M/F/G/I D R D A I A Q/A V R(G)		154.6	521.6047	1562.811	-0.0112	-7.2	5.71	63448.4	7.29	HUMAN	B4E022	Transketolase
4559	dirMS_041712_NAR_120mM_plus.10588.10588.3	3	13.49	1	7.58E+05		(K)IKGEHP(	(K)I/K/G E H/P/G L/S I|G\D/V A K(K)		108.45	507.6167	1520.843	-0.0076	-5	6.75	24408.7	5.92	HUMAN	B2RPK0	Putative high mobility group protein B1-like 1
4560	dirMS_041712_NAR_120mM_plus.7396.7396.3	3	13.49	0	1.08E+05		(K)CIGKPG(	(K)C I/G K/P G G/S L/D N/S E/Q K(C)	C:Carbamidomethylation	92.13	530.5901	1589.759	-0.003	-1.9	6.07	9122.2	9.22	HUMAN	K7EIT2	Mitochondrial import inner membrane translocase subunit Tim13
4561	dirMS_041712_NAR_20mM_plus.14746.14766.2	2	13.49	0	1.98E+05	M179m M:	(K)mFVLDE	(K)m F|V|L/D|E A/D/E/m\L S R(G)	m:Oxidized methionine	173.6	794.3555	1555.713	31.9906	0.5	3.91	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
4562	dirMS_041712_NAR_40mM_plus2.5424.5441.2	2	13.49	0	2.45E+05	M300m	(K)NMmAA	(K)N/M|m|A|A/C/D|P R(H)	C:Carbamidomethylation m:Oxid	89.2	541.2145	1065.427	15.9943	-0.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
4563	dirMS_041712_NAR_40mM_plus2.7573.7573.2	2	13.49	0	5.87E+05		(K)ASLENSI	(K)A/S|L/E/N/S L/R(E)		105.32	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4564	dirMS_041712_NAR_50mM_plus2.10954.10954.3	3	13.49	0	2.31E+05		(K)TKPYIQV	(K)T/K/P Y\I Q/V D|I/G/G G Q T K(T)		125.32	535.6231	1604.864	-0.0095	-5.9	8.17	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
4565	dirMS_041712_NAR_50mM_plus2.15969.15969.3	3	13.49	1	7.39E+04		(K)LGINSLC	(K)L/G/I/N/S/L Q E L K Q N I A K(G)		151.78	556.9915	1668.964	-0.0043	-2.6	8.59	25978.5	4.91	HUMAN	C9J502	Prostate leucine zipper variant 2
4566	dirMS_041712_NAR_50mM_plus2.16304.16445.3	3	13.49	1	4.23E+05		(K)DVLFLKI	(K)D V|L\F|L K/D C V/G P/E V E/K(A)	C:Carbamidomethylation	154.42	583.3027	1747.893	0	0	4.32	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
4567	dirMS_041712_NAR_30mM_minus2.13180.13180.2	2	13.48	0	2.99E+04		(K)IALLEEA	(K)I/A|L|L/E E/A K(K)		125.27	443.7658	886.524	-0.0001	-0.1	4.53	71218.8	6.3	HUMAN	A7YIJ8	Radixin
4568	dirMS_041712_NAR_30mM_minus2.19132.19132.2	2	13.48	0	4.66E+04		(R)YLTVAA	(R)Y/L|T/V/A A\V F R(G)		159.13	520.2998	1039.593	-0.0012	-1.1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
4569	dirMS_041712_NAR_30mM_minus2.6881.6924.2	2	13.48	0	1.89E+05		(K)DYNVTA	(K)D Y|N|V/T/A/N S K(L)		92	506.2404	1011.474	-0.0006	-0.6	5.83	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
4570	dirMS_041712_NAR_50mM_minus2.16447.16447.3	3	13.48	1	1.04E+06		(R)VTFSGLF	(R)V/T|F|S/G L R D T V T/P G E L L K(A)		162.47	611.672	1833.012	-0.0102	-5.6	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
4571	dirMS_041712_NAR_60mM_minus.10169.10169.3	3	13.48	1	1.75E+05	M88m	(K)DVDEAY	(K)D V|D|E/A Y m N K V E L/E/S/R(L)	m:Oxidized methionine	117.05	605.2791	1797.832	15.9904	-2.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
4572	dirMS_041712_NAR_60mM_minus.18659.18659.3	3	13.48	0	2.93E+05		(K)TFLVWV	(K)T F/L/V/W V/N E/E D H L R(V)		165.78	553.2818	1657.833	-0.0024	-1.5	4.65	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
4573	dirMS_041712_NAR_60mM_minus.6251.6251.3	3	13.48	1	1.15E+05		(K)DSYVGD	(K)D S\Y|V/G D/E/A/Q S K/R(G)		93.23	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle

4574	dirMS_041712_NAR_120mM_plus.8175.8218.3	3	13.48	1	7.73E+05		(R)SQYEQL	(R)S Q|Y/E Q L/A/E/Q N R\K(D)		96.67	498.5821	1493.734	-0.0025	-1.7	5.86	59054.3	5.14	HUMAN	P13645	Keratin, type I cytoskeletal 10
4575	dirMS_041712_NAR_40mM_plus2.18131.18131.3	3	13.48	0	9.77E+04	M159m	(R)SVAAIH	(R)S V|A/A I H P S L E\I/P m/L I/P K(E)	m:Oxidized methionine	172.8	611.3472	1816.04	15.9869	-4.4	6.47	31606.3	6.72	HUMAN	B4E329	Phosphoribosyl pyrophosphate synthase-associated protein 2
4576	dirMS_041712_NAR_50mM_plus2.19263.19263.3	3	13.48	0	3.59E+05		(-)MKPLVV	(-)M K P L V V/F V|L/G/G/P G A G K(G)		169.73	523.9715	1569.919	-0.0186	-11.8	10	22450.2	5.44	HUMAN	P30085	UMP-CMP kinase
4577	dirMS_041712_NAR_50mM_plus2.9093.9093.3	3	13.48	1	2.45E+05		(K)LLDGPS	(K)L L/D/G P S T E K/D/L D E K(K)		115.15	520.5958	1559.78	-0.0071	-4.5	4.11	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
4578	dirMS_041712_NAR_30mM_minus2.12056.12584.2	2	13.47	0	1.76E+06		(R)LQAEIE	(R)L/Q|A\E/I/E/G L/K(G)		121.93	500.7842	1000.567	-0.0062	-6.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
4579	dirMS_041712_NAR_50mM_minus2.12866.12867.3	3	13.47	0	1.53E+05		(K)ASLASLP	(K)A S|L|A/S/L/P/P\L H V A K(L)		141.37	435.2622	1303.773	-0.0012	-0.9	8.8	141626	5.5	HUMAN	A8MY36	Dynactin subunit 1
4580	dirMS_041712_NAR_20mM_plus.15582.15652.2	2	13.47	0	3.47E+05		(K)VGINYQ	(K)V G I N/Y|Q|P P T V|V|P G G D L/A K(V)		179.05	912.9952	1824.985	-0.0023	-1.3	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
4581	dirMS_041712_NAR_30mM_plus2.10660.10807.2	2	13.47	0	4.56E+05		(K)CIAMC	(K)C|I|A|M/C/M D/R(Y)	C:Carbamidomethylation	109.65	528.7093	1056.409	0.002	1.9	5.84	9122.2	9.22	HUMAN	K7EIT2	Mitochondrial import inner membrane translocase subunit Tim13
4582	dirMS_041712_NAR_30mM_plus2.12672.12672.2	2	13.47	0	1.61E+05		(R)ELAEDG	(R)E L|A/E D/G Y/S/G V/E V R(V)		118.68	712.3382	1423.67	-0.0008	-0.6	4	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
4583	dirMS_041712_NAR_30mM_plus2.13736.13736.2	2	13.47	0	1.10E+06		(R)ANTFVA	(R)A N|T/F/V/A E L K(G)		124.65	496.774	992.541	-0.0004	-0.4	6.05	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
4584	dirMS_041712_NAR_30mM_plus2.16181.16181.2	2	13.47	0	6.33E+05		(R)GLCAIA	(R)G L/C\A/I|A Q A/E/S L R(Y)	C:Carbamidomethylation	138.37	644.8372	1288.668	-0.0007	-0.5	6	18529.2	9.98	HUMAN	E9PL45	40S ribosomal protein S3
4585	dirMS_041712_NAR_40mM_plus2.13942.13943.3	3	13.47	0	2.92E+05		(R)LASTLV	(R)L/A\S/T/L V H L G E Y/Q A|A|V D/G A R(K)		148.43	657.6841	1971.029	0.0083	4.2	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
4586	dirMS_041712_NAR_40mM_plus2.19575.19642.3	3	13.47	0	1.06E+06		(R)GLAPVQ	(R)G L|A|P/V Q A Y L/H/I P D/I I/K(V)		183.65	583.3378	1748.011	-0.0117	-6.7	6.74	58266.4	9.46	HUMAN	B4DN00	Pyruvate carboxylase, mitochondrial
4587	dirMS_041712_NAR_50mM_plus2.16149.16149.3	3	13.47	1	1.29E+06		(K)GADFLV	(K)G A/D\F L|V|T E/V E N G G S L G S K K(G)		152.28	636.6618	1907.971	-0.0001	0	4.68	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
4588	dirMS_041712_NAR_60mM_plus.12753.12753.3	3	13.47	1	1.03E+06		(R)DLDRIA	(R)D L/D R I A|G Q|V/A A A N K(K)		123.8	481.263	1441.776	-0.0013	-0.9	5.96	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
4589	dirMS_041712_NAR_60mM_plus.5732.5732.3	3	13.47	0	1.87E+05		(R)STFETE	(R)S T/F/E/T E/H/A/G Q R(D)		88.4	421.5294	1262.576	-0.0024	-1.9	5.38	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
4590	dirMS_041712_NAR_60mM_plus.6917.7075.3	3	13.47	0	1.22E+06	M437m	(R)LESGM	(R)L/E|S G M Q N m/S I/H/T/K(T)	m:Oxidized methionine	95.27	497.903	1475.698	15.9963	1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
4591	dirMS_041712_NAR_120mM_minus.12146.12274.4	4	13.46	2	4.00E+05		(K)KGTVEG	(K)K\G T V\E\G\F\E|P/A D N K/C L L/R(A)	C:Carbamidomethylation	120.57	484.251	1933.98	0.0021	1.1	6.18	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
4592	dirMS_041712_NAR_30mM_minus2.10329.10367.2	2	13.46	0	6.38E+05		(K)AVGQD	(K)A/V|G/Q/D/T L/L/R(S)		110.68	486.7751	972.547	-0.0043	-4.5	5.88	72873.4	5.73	HUMAN	Q96S55	ATPase WRNIP1
4593	dirMS_041712_NAR_50mM_minus2.18212.18285.3	3	13.46	1	1.04E+06		(R)KAIIIFVP	(R)K A I I\I\F|V|P V P Q L K(S)		173.77	489.3206	1465.95	-0.0032	-2.2	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
4594	dirMS_041712_NAR_20mM_plus.18710.18768.3	3	13.46	0	5.22E+05		(K)LAVEAL	(K)L A\V E A\L\S\S L/D/G D/L/A/G R(Y)		200.47	529.6164	1586.838	-0.0038	-2.4	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
4595	dirMS_041712_NAR_20mM_plus.6950.6950.2	2	13.46	0	9.56E+04		(K)AAAAAA	(K)A A|A|A|A|A/A\L Q A K(S)		114.28	478.7792	956.552	-0.0012	-1.3	8.8	37884.5	11.27	HUMAN	H3BM89	60S ribosomal protein L4
4596	dirMS_041712_NAR_30mM_plus2.10913.10913.2	2	13.46	0	5.70E+05		(K)EAAENS	(K)E A|A E/N/S L/V/A/Y|K(A)		110.22	597.8036	1194.6	-0.0002	-0.1	4.53	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
4597	dirMS_041712_NAR_30mM_plus2.11318.11318.2	2	13.46	0	9.73E+04		(R)VEFMD	(R)V/E|F/M\D/D/T S/R(S)		112.67	550.2401	1099.473	0.0005	0.4	4.03	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
4598	dirMS_041712_NAR_30mM_plus2.17759.17759.2	2	13.46	0	1.40E+05		(R)NELSGA	(R)N E|L|S G/A|L/T/G L T/R(V)		146.73	616.3341	1231.664	-0.0032	-2.6	6	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
4599	dirMS_041712_NAR_30mM_plus2.18552.18552.2	2	13.46	0	1.54E+05		(R)AMLDQ	(R)A/M|L/D/Q L/M/G/T S/R(D)		150.35	611.8	1222.592	0.0009	0.7	5.88	5509.4	10.84	HUMAN	F8WB41	Putative RNA-binding protein Luc7-like 2
4600	dirMS_041712_NAR_30mM_plus2.9861.9941.2	2	13.46	0	3.98E+05		(R)VPLSAY	(R)V/P|L|S/A Y E/R(V)		105.42	467.7537	934.499	0.0009	0.9	5.97	300351.7	12.1	HUMAN	Q9UQ35	Serine/arginine repetitive matrix protein 2
4601	dirMS_041712_NAR_40mM_plus2.18491.18503.3	3	13.46	0	5.33E+05		(R)DYLHLP	(R)D Y L H\L\P P\E\I|V|P/A T L/R(R)		175.73	578.6565	1733.959	-0.0035	-2	5.32	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
4602	dirMS_041712_NAR_40mM_plus2.18796.18796.3	3	13.46	0	7.21E+05		(R)DYLHLP	(R)D Y L H L\P P E\I\V/P/A/T L R(R)		176.53	578.6565	1733.959	-0.0035	-2	5.32	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
4603	dirMS_041712_NAR_50mM_plus2.10247.10247.3	3	13.46	1	1.76E+05		(R)QELILSN	(R)Q E/L\I/L/S N S E/D K/S/I R(V)		121.43	544.624	1631.86	-0.0024	-1.5	4.68	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
4604	dirMS_041712_NAR_50mM_plus2.19031.19031.3	3	13.46	0	5.50E+05		(R)GFGFIT	(R)G F\G|F|I/T/F T N P E/H/A S V A M R(A)		168.75	661.3258	1981.959	0.004	2	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
4605	dirMS_041712_NAR_50mM_plus2.21788.21788.3	3	13.46	0	3.29E+05		(K)AYNMV	(K)A/Y/N|M\V/D I/I H S V V D/E R(E)		185.73	587.6346	1760.864	0.0257	14.6	4.54	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
4606	dirMS_041712_NAR_60mM_plus.12391.12391.3	3	13.46	0	1.77E+06		(K)RPGAAL	(K)R P G\A A\L D|P/G C V L\A K(M)	C:Carbamidomethylation	121.05	475.5976	1424.768	0.0104	7.3	8.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
4607	dirMS_041712_NAR_60mM_plus.20481.20481.3	3	13.46	1	4.21E+05		(K)NAAGAL	(K)N A|A/G A L D/L/L K E/L K(N)		166.93	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
4608	dirMS_041712_NAR_50mM_minus2.17264.17276.3	3	13.45	1	2.93E+04		(K)IILDLIS	(K)I/I|L/D/L I/S/E S/P I K G R(A)		166.75	518.6444	1553.926	-0.0075	-4.8	6.07	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
4609	dirMS_041712_NAR_50mM_minus2.17497.17497.3	3	13.45	1	2.94E+05		(K)GYPPED	(K)G Y/P/P E D I F/N L V G K/K(V)		167.38	526.2832	1576.837	-0.0019	-1.2	6.07	40763.2	6.29	HUMAN	Q9NR45	Sialic acid synthase
4610	dirMS_041712_NAR_60mM_minus.12136.12153.3	3	13.45	0	7.93E+05	M1m	(-)mVNHFI	(-)m V/N H/F/I/A E/F/K(R)	m:Oxidized methionine	127.92	417.8768	1235.624	15.9917	-2.6	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
4611	dirMS_041712_NAR_60mM_minus.18638.18638.3	3	13.45	0	2.91E+05		(K)TFLVWV	(K)T F/L/V/W/V/N E E D H L R(V)		165.78	553.2818	1657.833	-0.0024	-1.5	4.65	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
4612	dirMS_041712_NAR_60mM_minus.8456.8457.3	3	13.45	0	1.53E+05		(K)ISSDLDG	(K)I/S/S/D/L/D G H/P V/P K(Q)		107.3	422.2222	1264.653	-0.0011	-0.9	5.21	63448.4	7.29	HUMAN	B4E022	Transketolase
4613	dirMS_041712_NAR_60mM_minus.9399.9544.3	3	13.45	1	8.61E+05	M142m	(K)VKEGM	(K)V K E G M N\I|V/E/A/m E R(F)	m:Oxidized methionine	112.42	507.9181	1505.745	15.9947	-0.1	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
4614	dirMS_041712_NAR_30mM_plus2.13364.13364.2	2	13.45	0	2.13E+05		(R)QQGLA	(R)Q Q/G L/A/S/Y D/Y V R(R)		122.92	650.3201	1299.633	0.0001	0.1	5.83	533778	5.74	HUMAN	Q15149	Plectin
4615	dirMS_041712_NAR_40mM_plus2.17173.17173.3	3	13.45	0	7.36E+05		(R)IHFPLAT	(R)I H F P L A T Y|A/P V I S/A E K(A)		168.3	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
4616	dirMS_041712_NAR_50mM_plus2.13556.13556.3	3	13.45	1	3.68E+05		(R)SLIANLA	(R)S L|I/A/N L|A A/A/N C Y K K(E)	C:Carbamidomethylation	139	512.9444	1536.82	-0.0016	-1.1	9.7	36978.6	6.33	HUMAN	B7Z800	Adenosine kinase
4617	dirMS_041712_NAR_50mM_plus2.22117.22117.3	3	13.45	1	2.51E+05		(R)KEGGLG	(R)K E G G L G P L N\I|P L/L A/D V T R(R)		189.68	621.6925	1863.07	-0.0069	-3.7	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
4618	dirMS_041712_NAR_50mM_plus2.8186.8186.3	3	13.45	1	3.71E+05		(R)VLVNDA	(R)V/L|V/N D/A Q K V/T\E G Q Q E R(L)		109.88	605.3151	1813.94	-0.0095	-5.2	4.68	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
4619	dirMS_041712_NAR_30mM_minus2.7661.7661.2	2	13.44	0	2.31E+05		(R)QDVDN	(R)Q D/V/D/N A/S L/A/R(L)		96.17	544.7694	1088.533	-0.0016	-1.4	4.21	49709.6	5.19	HUMAN	B0YJC4	Vimentin
4620	dirMS_041712_NAR_40mM_minus2.9930.9930.3	3	13.44	0	1.70E+04		(R)VVIIGA	(R)V V|I|I/G A G K/P A A V V L Q T K(G)		139.7	555.3529	1664.047	-0.0028	-1.7	10	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
4621	dirMS_041712_NAR_50mM_minus2.17180.17514.3	3	13.44	1	4.37E+05		(K)GYPPED	(K)G Y|P/P E D I F/N/L/V/G K K(V)		166.97	526.2832	1576.837	-0.0019	-1.2	6.07	40763.2	6.29	HUMAN	Q9NR45	Sialic acid synthase
4622	dirMS_041712_NAR_50mM_minus2.7868.7890.3	3	13.44	1	1.26E+05		(K)LLDGPS	(K)L/L|D|G/P S T E/K D L D/E/K(K)		112	520.5968	1559.78	-0.0041	-2.6	4.11	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
4623	dirMS_041712_NAR_20mM_plus.14673.14673.3	3	13.44	0	1.12E+05		(R)LQEAGI	(R)L Q E A G I|L|S/A/E E L Q/R(L)		172.33	519.6131	1556.828	-0.0031	-2	4.25	533778	5.74	HUMAN	Q15149	Plectin
4624	dirMS_041712_NAR_20mM_plus.16758.16758.3	3	13.44	0	2.96E+05		(K)VQIAVA	(K)V Q\I A V\A\N A/Q/E|L/L/Q R(M)		186.87	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
4625	dirMS_041712_NAR_20mM_plus.17596.17596.2	2	13.44	0	1.61E+05	M74m	(R)mIAGQ	(R)m I|A\G Q/V|L/D I\N L/A\A E/P K(V)	m:Oxidized methionine	192.85	849.9568	1682.915	15.9918	-1.9	4.37	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
4626	dirMS_041712_NAR_30mM_plus2.10090.10490.2	2	13.44	0	7.47E+05		(R)LGAPAL	(R)L/G|A|P/A/L/T S R(Q)		107.25	443.2607	885.515	-0.0011	-1.3	9.75	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
4627	dirMS_041712_NAR_30mM_plus2.12403.12403.2	2	13.44	0	5.80E+05		(R)YSGSYN	(R)Y/S|G S Y/N D/Y/L/R(A)		118.28	619.2776	1237.548	-0.0005	-0.4	5.83	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
4628	dirMS_041712_NAR_30mM_plus2.12719.12823.2	2	13.44	0	2.74E+05		(K)YFDSGD	(K)Y/F|D|S/G/D/Y/N M A K(A)		119.78	655.7724	1310.536	0.0017	1.3	4.21	15633.5	7.82	HUMAN	A6NMQ3	Alpha-endosulfine
4629	dirMS_041712_NAR_30mM_plus2.13013.13013.2	2	13.44	0	5.45E+05		(R)CNNVLY	(R)C N|N/V/L/Y I/R(G)	C:Carbamidomethylation	120.83	526.2726	1051.535	0.0026	2.5	8.75	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F
4630	dirMS_041712_NAR_30mM_plus2.7147.7284.2	2	13.44	0	1.70E+06		(K)TEISEM	(K)T\E|I|S/E/M/N R(N)		92.85	490.2294	979.451	0.0002	0.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
4631	dirMS_041712_NAR_50mM_plus2.16976.16976.3	3	13.44	1	4.54E+05		(K)VLDSGA	(K)V L/D|S/G A/P I/K/I/P V/G P E T\L G R(I)		156.95	640.3623	1919.096	-0.0237	-12.3	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
4632	dirMS_041712_NAR_50mM_plus2.19137.19137.3	3	13.44	0	4.79E+05		(R)CRPDQL	(R)C R P D Q L T/G|L/S/L/L|P\L S E K(A)	C:Carbamidomethylation	168.18	643.0148	1927.032	-0.0019	-1	6.07	533778	5.74	HUMAN	Q15149	Plectin
4633	dirMS_041712_NAR_50mM_plus2.22198.22198.3	3	13.44	1	5.40E+05		(R)ELAILLG	(R)E L/A I/L/L G M/L/D/P A E K D E K(G)		190.32	629.004	1884.999	-0.0012	-0.7	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
4634	dirMS_041712_NAR_50mM_plus2.6150.6150.3	3	13.44	1	1.12E+05		(R)VVSSIE	(R)V/V/S\S/I E Q K T E G A E K(K)		96.75	502.2651	1504.785	-0.0046	-3	4.79	8491.4	6.28	HUMAN	E5RIR4	14-3-3 protein zeta/delta (Fragment)
4635	dirMS_041712_NAR_60mM_plus.12071.12071.2	2	13.44	1	1.52E+06		(R)DGKLVS	(R)D/G K L|V|S E S S D/V/L|P K(-)		120.25	737.3869	1473.78	-0.013	-8.8	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
4636	dirMS_041712_NAR_60mM_plus.6306.6306.3	3	13.44	1	2.17E+05		(K)QMNDE	(K)Q M N D/E/K/T A/A/D/Y/K(I)		91.65	471.8823	1413.632	0.0009	0.6	4.56	9786.1	5.52	HUMAN	E9PS38	Protein NEDD8-MDP1
4637	dirMS_041712_NAR_120mM_minus.17543.17543.3	3	13.43	1	5.17E+05		(R)KVNNA	(R)K V N\N A D D\F|P/N L F R(Q)		150.13	517.2634	1549.776	-0.0001	-0.1	5.96	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
4638	dirMS_041712_NAR_20mM_minus.13153.13153.2	2	13.43	0	4.63E+05		(K)TITLEVE	(K)T I T L/E/V/E|P S/D T I/E/N V K(A)		183.05	894.4654	1787.927	-0.0038	-2.1	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
4639	dirMS_041712_NAR_40mM_minus2.11214.11214.3	3	13.43	1	1.21E+05		(K)VIDPAT	(K)V I|D/P/A/T A T S V/D L R/D/I K(I)		149.38	571.9828	1713.938	-0.0043	-2.5	4.43	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
4640	dirMS_041712_NAR_40mM_minus2.12193.12193.3	3	13.43	0	4.30E+05		(K)IAILTCP	(K)I A/I/L/T C/P F E/P P K P K(T)	C:Carbamidomethylation	155.62	537.6382	1610.898	0.0026	1.6	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
4641	dirMS_041712_NAR_50mM_minus2.7167.7167.3	3	13.43	1	2.39E+04		(K)GAVAED	(K)G A V|A/E D G D E L R T E P E/A K(K)		107.67	596.2904	1786.845	0.0113	6.3	4.08	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
4642	dirMS_041712_NAR_50mM_minus2.9552.9552.3	3	13.43	1	2.33E+06		(R)MQKEIT	(R)M Q K E I T/A|L/A|P S T M K(I)		123.35	516.9426	1548.812	0.0008	0.5	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
4643	dirMS_041712_NAR_120mM_plus.8110.8151.2	2	13.43	0	6.21E+05		(R)YAHVVL	(R)Y/A|H|V/V L/R(K)		96.72	429.2529	857.499	-0.0007	-0.8	8.75	17718.4	10.99	HUMAN	P62269	40S ribosomal protein S18
4644	dirMS_041712_NAR_20mM_plus.14277.14277.2	2	13.43	0	3.41E+04		(R)IALTDN	(R)I/A|L/T/D N\A\L I A R(S)		170.65	585.8432	1170.684	-0.005	-4.2	5.84	24489.6	10.74	HUMAN	A8MUD9	60S ribosomal protein L7
4645	dirMS_041712_NAR_20mM_plus.18839.18839.2	2	13.43	0	2.79E+05		(K)LAVEAL	(K)L A/V E/A/L|S/S/L D|G\D L/A/G R(Y)		200.52	793.9214	1586.838	-0.0029	-1.8	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
4646	dirMS_041712_NAR_30mM_plus2.15227.15691.2	2	13.43	0	1.64E+06		(R)YIELLTR	(R)Y/I|E|L/L|T/R(S)		132.8	454.2621	907.525	-0.0078	-8.6	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
4647	dirMS_041712_NAR_30mM_plus2.19088.19153.2	2	13.43	0	2.78E+05		(R)LTAEDL	(R)L/T|A/E/D/L|F E/A R(I)		153.22	582.796	1164.59	-0.0048	-4.1	4.14	533778	5.74	HUMAN	Q15149	Plectin
4648	dirMS_041712_NAR_40mM_plus2.17443.17443.3	3	13.43	0	4.17E+05		(R)DVCTEL	(R)D V/C|T E L/L/P L/I/K/P Q G R(V)	C:Carbamidomethylation	169.57	580.3213	1738.952	-0.0027	-1.5	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
4649	dirMS_041712_NAR_60mM_plus.11043.11043.3	3	13.43	1	1.97E+06		(R)KLDPGS	(R)K L D|P G S/E|E/T/Q/T/L V R(E)		115.02	524.9456	1572.823	-0.0005	-0.3	4.68	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
4650	dirMS_041712_NAR_60mM_plus.13947.14370.3	3	13.43	0	1.99E+06		(K)GIHPTII	(K)G I H\P T\I|I|S/E/S F Q K(A)		130.72	486.2646	1456.78	-0.0002	-0.1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
4651	dirMS_041712_NAR_20mM_minus.9779.9779.2	2	13.42	0	3.36E+05		(K)IGGIGTV	(K)I/G/G\I/G\T/V/P V G R(V)		147.47	513.3075	1025.61	-0.0025	-2.4	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
4652	dirMS_041712_NAR_30mM_minus2.14988.15196.2	2	13.42	0	5.95E+05		(K)LYANM	(K)L/Y|A|N/M/F E/R(L)		135.42	522.2529	1043.498	0.0006	0.6	6	9740.1	10.08	HUMAN	H0YFG2	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed (Fragment)
4653	dirMS_041712_NAR_60mM_minus.11061.11061.3	3	13.42	1	3.17E+06		(R)DGKLVS	(R)D G K L V S E/S/S/D/V/L/P K(-)		122.2	491.927	1473.78	-0.0131	-8.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
4654	dirMS_041712_NAR_120mM_plus.17880.17880.4	4	13.42	0	3.77E+05		(R)HLLQAP	(R)H L L Q\A|P V/D/D\A Q/E/I L/H/S R(F)		146.78	486.2589	1942.014	-0.0003	-0.2	5.21	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
4655	dirMS_041712_NAR_30mM_plus2.13914.14015.2	2	13.42	0	4.51E+05		(K)LVPVGY	(K)L V|P|V/G/Y G I/R(K)		126.23	487.2951	973.583	0	0	8.75	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
4656	dirMS_041712_NAR_30mM_plus2.18449.18669.2	2	13.42	0	8.06E+05		(K)QLLLQL	(K)Q L|L|L|Q/L|N Q/Q R(T)		150.85	627.3688	1253.732	-0.0021	-1.7	9.75	67181.8	5.96	HUMAN	Q96JB3	Hypermethylated in cancer 2 protein
4657	dirMS_041712_NAR_30mM_plus2.18501.18501.2	2	13.42	0	6.99E+05		(K)EGMNIV	(K)E G M/N/I|V E/A M E R(F)		150.78	639.7958	1278.582	0.0026	2.1	4.25	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
4658	dirMS_041712_NAR_30mM_plus2.20957.20957.2	2	13.42	0	2.33E+05		(K)VFSIGPV	(K)V/F|S\I/G/P V F/R(A)		164.52	511.2941	1021.583	-0.002	-2	9.72	57534.6	6.11	HUMAN	P14868	Aspartate--tRNA ligase, cytoplasmic
4659	dirMS_041712_NAR_30mM_plus2.7005.7166.2	2	13.42	0	2.52E+05		(R)FVDPNT	(R)F V|D|P N/T Q E K(V)		91.67	539.2643	1077.521	0.0002	0.2	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
4660	dirMS_041712_NAR_40mM_plus2.13508.13569.3	3	13.42	0	2.43E+05		(K)SIEIPRP	(K)S I|E|I/P R P V D G V/E|V/P G C G K(I)	C:Carbamidomethylation	145.88	637.0002	1908.985	0.0013	0.7	4.68	34243.5	4.88	HUMAN	K7ENG2	Splicing factor U2AF 65 kDa subunit
4661	dirMS_041712_NAR_50mM_plus2.10848.10893.3	3	13.42	0	4.89E+05		(R)EALLSSA	(R)E A|L/L/S/S A\V|D|H G S D E/V/K(F)		124.7	552.9403	1656.807	-0.0012	-0.7	4.31	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
4662	dirMS_041712_NAR_50mM_plus2.12198.12218.3	3	13.42	0	3.98E+05		(K)IVLEDGT	(K)I/V|L/E/D G T L/H V/T/E G S G R(Y)		132.23	561.6272	1682.871	-0.0037	-2.2	4.65	62748.9	5.95	HUMAN	Q16555	Dihydropyrimidinase-related protein 2
4663	dirMS_041712_NAR_60mM_plus.6875.6905.3	3	13.42	1	2.99E+06		(R)LQSIGTE	(R)L/Q|S|I/G/T E/N T/E E N R/R(F)		94.57	549.6075	1646.809	-0.0013	-0.8	4.79	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
4664	dirMS_041712_NAR_120mM_minus.6881.7172.3	3	13.41	1	2.14E+07		(R)TKTEISE	(R)T K\T E\I|S|E/M/N/R(N)		92.57	403.5363	1208.594	0.0004	0.3	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
4665	dirMS_041712_NAR_30mM_minus2.7452.7513.2	2	13.41	0	5.81E+05		(K)AVELAA	(K)A V|E|L/A|A/N T/K(G)		95.82	458.753	916.51	-0.0111	-12.1	6.05	63448.4	7.29	HUMAN	B4E022	Transketolase
4666	dirMS_041712_NAR_50mM_minus2.15971.15971.3	3	13.41	0	2.36E+05		(K)AQDGS	(K)A Q|D/G S H/P L S L/Q D L I E K(V)		159.08	584.3049	1750.897	0.0031	1.8	4.54	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
4667	dirMS_041712_NAR_120mM_plus.9734.9736.4	4	13.41	0	2.37E+05	M275m	(K)SGVYQH	(K)S/G|V/Y Q/H V/T G E M m/G G H/A I R(I)	m:Oxidized methionine	104.28	487.2313	1929.906	15.9976	1.4	6.66	38790.8	5.88	HUMAN	P07858	Cathepsin B
4668	dirMS_041712_NAR_30mM_plus2.13915.14152.2	2	13.41	0	1.45E+06		(R)DVQEIF	(R)D V|Q|E I/F/R(L)		126.7	453.7343	906.468	-0.0066	-7.3	4.37	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
4669	dirMS_041712_NAR_50mM_plus2.16472.16472.3	3	13.41	1	4.23E+05		(K)DVLFLK	(K)D V|L/F/L K D/C V/G P E V E K(A)	C:Carbamidomethylation	154.42	583.3027	1747.893	0	0	4.32	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
4670	dirMS_041712_NAR_120mM_minus.8622.8808.3	3	13.4	1	7.08E+06	M174m	(R)VKYETEL	(R)V/K\Y E T E|L/A/m/R(Q)	m:Oxidized methionine	101.98	419.2167	1239.64	15.9954	0.4	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4671	dirMS_041712_NAR_30mM_minus2.17485.17485.2	2	13.4	0	2.29E+05		(R)NGGQIL	(R)N G|G|Q/I|L I/A/D/L R(G)		149.22	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
4672	dirMS_041712_NAR_50mM_minus2.14076.14098.3	3	13.4	1	3.57E+05		(K)VIDPAT	(K)V/I|D|P A/T A T|S V D L R D I K(I)		148.1	571.9822	1713.938	-0.0061	-3.6	4.43	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
4673	dirMS_041712_NAR_50mM_minus2.14312.14312.3	3	13.4	0	4.31E+05		(R)QIFHPE	(R)Q I/F H P/E Q/L I/T/G/K(E)		149.72	470.9286	1410.774	-0.0027	-1.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
4674	dirMS_041712_NAR_120mM_plus.24456.24636.4	4	13.4	1	1.18E+06		(R)GHYTIG	(R)G H\Y\T I\G\K E\I\I\D\L|V/L/D/R(I)		184.3	461.2589	1842.012	0.0018	1	5.38	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
4675	dirMS_041712_NAR_30mM_plus2.10528.10528.2	2	13.4	0	3.54E+05		(R)DPYGFG	(R)D/P|Y|G|F\G\D/S/R(D)		108.9	507.2274	1013.432	0.0152	15	4.21	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
4676	dirMS_041712_NAR_30mM_plus2.4879.4879.2	2	13.4	0	5.87E+05	M571m	(R)mGANS	(R)m/G/A|N/S L/E R(M)	m:Oxidized methionine	76.8	447.2119	877.42	15.9969	2.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
4677	dirMS_041712_NAR_40mM_plus2.19959.19959.3	3	13.4	0	4.60E+05	M166m	(K)VLDFEH	(K)V L/D F E H F L|P/m/L Q T V A K(N)	m:Oxidized methionine	187.63	635.3379	1888.004	15.9954	0.3	5.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
4678	dirMS_041712_NAR_50mM_plus2.18756.18968.3	3	13.4	1	4.36E+05		(K)AAIDW	(K)A/A|I/D/W|F D G K E F S G N/P I K(V)		167.18	632.3186	1894.933	0.0079	4.1	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
4679	dirMS_041712_NAR_50mM_plus2.6133.6133.3	3	13.4	1	6.55E+04		(R)NTDVA	(R)N T|D|V|A/Q S P E A/P K/Q E A P A K(K)		96.33	627.6463	1880.935	-0.0105	-5.6	4.68	152868.9	8.79	HUMAN	Q9P2E9	Ribosome-binding protein 1
4680	dirMS_041712_NAR_50mM_plus2.7141.7141.3	3	13.4	0	9.72E+04		(K)VLATVT	(K)V L|A/T V T K/P V G/G D/K(N)		103.27	428.9213	1284.752	-0.0028	-2.2	8.56	12738	10.72	HUMAN	F8VWR1	60S ribosomal protein L6 (Fragment)
4681	dirMS_041712_NAR_20mM_minus.9576.9580.2	2	13.39	0	3.70E+05		(R)LQAEIE	(R)L/Q|A|E|I E/G L/K(G)		145.97	500.7862	1000.567	-0.0022	-2.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
4682	dirMS_041712_NAR_30mM_minus2.10458.10458.2	2	13.39	0	8.52E+05		(K)YETELA	(K)Y/E|T/E L A M/R(Q)		111.27	506.7468	1012.477	0.0095	9.4	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18

4683	dirMS_041712_NAR_30mM_minus2.19751.19812.2	2	13.39	0	1.11E+06		(K)FLPLFDR	(K)F/L|P/L F D/R(V)		164.83	454.2604	907.504	0.0099	10.9	5.84	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
4684	dirMS_041712_NAR_50mM_minus2.10059.10059.3	3	13.39	0	5.64E+05	M147m	(K)LQmEAP	(K)L\Q|m|E\A P/H\I|I|V G/T P G R(V)	m:Oxidized methionine	125.58	545.6267	1618.873	15.9922	-1.7	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
4685	dirMS_041712_NAR_120mM_plus.8401.8401.3	3	13.39	0	3.40E+05		(K)YKPESEE	(K)Y K P E S E E|L/T/A/E/R(I)		97.4	484.5712	1451.701	-0.0022	-1.5	4.5	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
4686	dirMS_041712_NAR_20mM_plus.11556.11556.2	2	13.39	0	1.72E+05		(K)VGLQVV	(K)V/G/L\Q\V\V A V\K(A)		151.75	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
4687	dirMS_041712_NAR_20mM_plus.12394.12394.2	2	13.39	0	1.87E+05		(R)GVEICIA	(R)G V E|I/C/I A/T/P G R(L)	C:Carbamidomethylation	158.58	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
4688	dirMS_041712_NAR_20mM_plus.15936.15936.2	2	13.39	0	3.24E+05	M81m	(K)SFYPEEV	(K)S F/Y/P\E E V/S S m V L T K(M)	m:Oxidized methionine	180.88	816.8988	1616.788	16.0027	4.8	4.53	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
4689	dirMS_041712_NAR_20mM_plus.19049.19049.3	3	13.39	0	2.07E+05		(K)TLETQS	(K)T L\E T Q S A L|G/P/A L Q|A/A F K(L)		202.57	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
4690	dirMS_041712_NAR_20mM_plus.8616.8803.2	2	13.39	0	2.49E+05		(R)VPPPPPI	(R)V/P|P|P/P P I A R(A)		130.63	472.2851	943.572	-0.0094	-10	9.72	32085.2	8.93	HUMAN	B4DY08	Heterogeneous nuclear ribonucleoproteins C1/C2
4691	dirMS_041712_NAR_30mM_plus2.7310.7353.2	2	13.39	0	3.37E+05		(K)DYAESV	(K)D Y|A|E/S/V/G R(K)		93.07	448.71	896.411	0.0019	2.1	4.37	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
4692	dirMS_041712_NAR_40mM_plus2.17470.17470.3	3	13.39	0	1.58E+05		(R)VYAILTH	(R)V Y/A I/L T/H G I|F S G P\A I S R(I)		169.33	601.3376	1801.996	0.0023	1.3	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
4693	dirMS_041712_NAR_50mM_plus2.9936.9956.3	3	13.39	1	3.03E+05		(K)VCGDSD	(K)V/C|G D/S D K G/F|V/V I N Q K(G)	C:Carbamidomethylation	119.55	555.947	1665.826	0	0	5.93	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
4694	dirMS_041712_NAR_60mM_plus.15252.15309.3	3	13.39	1	8.29E+04		(R)KEFSPF	(R)K\E F/S\P\F|G T/I/T S/A/K(V)		137.1	471.585	1412.742	-0.0016	-1.1	8.59	65918.2	9.74	HUMAN	E7EQV3	Polyadenylate-binding protein 1
4695	dirMS_041712_NAR_50mM_minus2.11845.11845.3	3	13.38	1	6.27E+06		(K)KVPQVS	(K)K\V P Q\V\S T/P T|L/V|E V/S R(N)		136.32	547.3172	1639.938	-0.0007	-0.4	8.75	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
4696	dirMS_041712_NAR_50mM_minus2.15910.15910.3	3	13.38	1	8.21E+04		(K)DANAKL	(K)D A N\A K L S E\L|E/A/A L/Q R(A)		158.97	543.6248	1628.86	-0.0004	-0.2	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
4697	dirMS_041712_NAR_120mM_plus.21328.21447.3	3	13.38	1	3.11E+05		(R)KVESLW	(R)K V E S L\W|P/I/F/R(I)		165.75	425.5799	1274.726	-0.0004	-0.3	8.75	14138.1	9.89	HUMAN	C9JNV2	Protein BUD31 homolog
4698	dirMS_041712_NAR_120mM_plus.9076.9365.2	2	13.38	0	4.16E+06		(K)HVVFIA	(K)H|V|V|F I|A Q/R(R)		101.58	485.2849	969.563	-0.0003	-0.3	9.75	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
4699	dirMS_041712_NAR_30mM_plus2.16261.16261.2	2	13.38	0	1.38E+06		(R)GGIVDE	(R)G G I|V/D/E G A/L L R(A)		138.9	550.3082	1099.611	-0.0015	-1.3	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
4700	dirMS_041712_NAR_40mM_plus2.17466.17466.3	3	13.38	1	3.17E+05		(K)TGISDV	(K)T G\I|S/D/V\F A K N D\L/A/V V D V/R(I)		169.33	640.3451	1919.023	-0.0025	-1.3	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
4701	dirMS_041712_NAR_60mM_plus.16770.16770.3	3	13.38	0	2.63E+05		(R)YQEALH	(R)Y Q|E/A L/H|L/G S Q/L L R(E)		144.15	509.946	1527.828	-0.0044	-2.9	6.75	47748.2	6.08	HUMAN	O00231	26S proteasome non-ATPase regulatory subunit 11
4702	dirMS_041712_NAR_120mM_minus.11368.11481.3	3	13.37	0	2.31E+05		(R)GFCLPP	(R)G F|C L/P/P/H/C S/R(G)	C:Carbamidomethylation	116.42	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
4703	dirMS_041712_NAR_20mM_minus.14886.14888.2	2	13.37	0	2.08E+06		(K)EIIDLVL	(K)E I|I/D/L|V/L D/R(I)		204	543.3133	1085.62	-0.0008	-0.7	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
4704	dirMS_041712_NAR_30mM_minus2.16345.16345.2	2	13.37	0	1.94E+05		(K)ACGNFG	(K)A C/G/N/F|G I P C E L R(V)	C:Carbamidomethylation	142.53	697.3207	1393.635	-0.001	-0.7	6.05	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
4705	dirMS_041712_NAR_30mM_minus2.19443.19443.2	2	13.37	0	2.19E+05		(R)ILVATNL	(R)I L|V/A|T/N L/F G R(G)		161.95	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
4706	dirMS_041712_NAR_40mM_minus2.5909.5909.2	2	13.37	0	1.30E+06		(K)AGFAGD	(K)A G/F|A/G D D/A/P R(A)		98.15	488.7279	976.448	0.0002	0.2	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
4707	dirMS_041712_NAR_50mM_minus2.12648.12673.3	3	13.37	1	3.98E+05		(K)NTVELL	(K)N T|V|E/L/L V E/D K/G N Q V Y R(C)		140.43	626.3309	1876.976	0.0018	1	4.68	258215.9	5.48	HUMAN	E7EN95	Filamin-B
4708	dirMS_041712_NAR_50mM_minus2.13092.13092.3	3	13.37	1	2.73E+04		(K)VVSSSIV	(K)V V|S\S S I V D K/Y I G E/S A R(L)		142.6	570.6413	1709.907	0.0025	1.5	6.04	29938.9	6.07	HUMAN	H0YJC0	26S protease regulatory subunit 10B (Fragment)
4709	dirMS_041712_NAR_50mM_minus2.13319.13319.3	3	13.37	0	3.99E+05		(R)EQTLSP	(R)E Q T/L/S/P T/I/T/S G L H N\I A R(S)		143.55	613.3274	1837.977	-0.009	-4.9	6.85	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
4710	dirMS_041712_NAR_50mM_minus2.9744.9744.3	3	13.37	0	2.51E+05		(K)TSEVDL	(K)T/S/E V D/L A/K/P L/V/K(F)		123.18	433.9205	1299.752	-0.0049	-3.8	5.73	17178.3	5.63	HUMAN	C9IZF9	Programmed cell death 6-interacting protein (Fragment)
4711	dirMS_041712_NAR_60mM_minus.12120.12120.3	3	13.37	1	2.15E+05		(K)YADEEIP	(K)Y/A|D/E E I/P R S P F K(V)		127.3	484.5732	1451.717	-0.0115	-7.9	4.68	258215.9	5.48	HUMAN	E7EN95	Filamin-B
4712	dirMS_041712_NAR_60mM_minus.6159.6166.3	3	13.37	1	2.64E+05		(K)LEEAEK	(K)L/E|E A E/K/A A/D/E S E/R(G)		92.57	492.8981	1476.681	-0.0015	-1	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
4713	dirMS_041712_NAR_20mM_plus.11000.11000.2	2	13.37	0	1.17E+05		(K)EITALAP	(K)E I/T|A/L|A P S T M K(I)		148.15	581.3129	1161.618	0.0001	0.1	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
4714	dirMS_041712_NAR_50mM_plus2.11427.11427.3	3	13.37	1	3.29E+05		(K)VAVVAG	(K)V/A|V|V/A/G Y G D V G/K G C A Q A L R(G)	C:Carbamidomethylation	127.85	630.9984	1890.985	-0.0048	-2.5	8.56	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
4715	dirMS_041712_NAR_50mM_plus2.15125.15125.3	3	13.37	1	4.23E+05		(R)LSQELEY	(R)L/S|Q/E/L E/Y L T E D V K R(L)		147.3	574.9669	1722.891	-0.0047	-2.7	4.41	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
4716	dirMS_041712_NAR_60mM_plus.11861.12249.3	3	13.37	1	7.49E+06		(R)FPGQLN	(R)F/P/G Q|L|N/A/D/L R K(L)		119.62	420.23	1258.69	-0.0148	-11.8	8.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
4717	dirMS_041712_NAR_60mM_plus.11870.11870.3	3	13.37	1	7.13E+05	M239m	(R)MSMKE	(R)M/S M K E V D E Q/m|L/N/V\Q/N\K(N)	m:Oxidized methionine	119.38	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
4718	dirMS_041712_NAR_120mM_minus.10924.11026.3	3	13.36	1	6.07E+05		(R)FYKNEG	(R)F Y/K N E G/G/T/W/S/V/E\K(V)		113.78	515.5834	1544.738	-0.0023	-1.5	6.14	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
4719	dirMS_041712_NAR_20mM_minus.13741.13741.2	2	13.36	0	3.90E+05		(K)LGGSAV	(K)L G G S\A V\I|S L E/G K|P L(-)		188.65	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
4720	dirMS_041712_NAR_30mM_minus2.14083.14329.2	2	13.36	0	5.90E+05		(R)SEQFINL	(R)S E|Q|F|I/N/L/R(E)		130.73	503.7677	1006.532	-0.0035	-3.5	5.72	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
4721	dirMS_041712_NAR_30mM_minus2.15799.15799.2	2	13.36	0	2.84E+05		(K)EGALDL	(K)E G\A|L/D/L/S G L R(A)		139.08	515.7847	1030.553	0.0094	9.1	4.37	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
4722	dirMS_041712_NAR_30mM_minus2.16076.16076.2	2	13.36	0	1.21E+05		(K)SSEELLS	(K)S S|E E|L|L|S A L\Q/K(K)		141.47	602.816	1204.642	-0.0172	-14.3	4.53	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
4723	dirMS_041712_NAR_40mM_minus2.8165.8165.3	3	13.36	0	2.24E+05	M35m	(K)AASDIA	(K)A A|S D I A/m T E L/P/P T H P/I R(L)	m:Oxidized methionine	128.48	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
4724	dirMS_041712_NAR_60mM_minus.13418.13418.3	3	13.36	1	4.64E+05		(K)TKEVYEL	(K)T K/E V\Y E|L|L D/S/P G K(V)		134.5	493.5966	1478.774	0.0015	1	4.68	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
4725	dirMS_041712_NAR_60mM_minus.9769.9865.3	3	13.36	1	8.70E+05		(R)VKYETEL	(R)V/K Y E\T\E|L/A/M/R(Q)		114.7	413.8839	1239.64	-0.003	-2.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4726	dirMS_041712_NAR_120mM_plus.8149.8149.2	2	13.36	0	4.29E+05		(K)AGEVFI	(K)A/G E|V/F/I/H/K(D)		96.3	450.7531	900.494	0.0051	5.7	6.79	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
4727	dirMS_041712_NAR_40mM_plus2.17766.17767.3	3	13.36	1	1.96E+05		(R)LKLPSIP	(R)L K\L|P S I|P\L|V|P V S A Q K(R)		170.73	530.671	1589.999	-0.0004	-0.3	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
4728	dirMS_041712_NAR_50mM_plus2.10069.10069.3	3	13.36	1	2.46E+06		(K)ATAVVD	(K)A T/A/V/V/D G A F/K E V K(L)		120.07	445.5822	1334.731	0.0006	0.5	6.11	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
4729	dirMS_041712_NAR_50mM_plus2.14758.14967.3	3	13.36	1	1.17E+04		(K)YMACCL	(K)Y/M|A/C/C L L Y R G D\V V/P/K(E)	C:Carbamidomethylation	144.47	615.6348	1844.886	0.0043	2.3	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
4730	dirMS_041712_NAR_50mM_plus2.5685.5685.3	3	13.36	1	1.06E+06		(K)TAGPIA	(K)T A/G\P I/A/S A Q\K Q P A G K(V)		91.9	475.5987	1424.786	-0.0041	-2.8	10	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
4731	dirMS_041712_NAR_60mM_plus.12928.13025.3	3	13.36	0	6.26E+05		(K)VFEGNR	(K)V/F|E/G N R P T N S I V/F/T/K(L)		124.57	570.3039	1708.902	-0.0045	-2.7	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
4732	dirMS_041712_NAR_60mM_plus.17830.17888.3	3	13.36	1	8.12E+05		(R)LKLPAV	(R)L K L P A\V|V|T/A/D/L/R(L)		150.67	432.6056	1295.805	-0.0023	-1.8	8.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
4733	dirMS_041712_NAR_20mM_minus.13070.13070.2	2	13.35	0	1.79E+05		(K)LLCGLLA	(K)L L|C/G/L/L A E/R(L)	C:Carbamidomethylation	181.28	522.7982	1044.587	0.0021	2	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
4734	dirMS_041712_NAR_20mM_minus.8618.8711.2	2	13.35	0	1.86E+05		(K)LVLVGD	(K)L V|L|V/G D/G G/T G K(T)		136.13	508.2919	1015.578	-0.0017	-1.7	5.84	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
4735	dirMS_041712_NAR_30mM_minus2.10129.10205.2	2	13.35	0	7.62E+05	M161m	(K)LLIEmEC	(K)L/L|I/E/m E/Q/R(L)	m:Oxidized methionine	109.23	524.2789	1031.555	15.9951	0.2	4.53	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
4736	dirMS_041712_NAR_30mM_minus2.13432.13667.2	2	13.35	0	4.74E+05		(K)NLVTED	(K)N L|V|T|E D/V M/R(M)		126.98	538.7747	1076.541	0.0017	1.5	4.37	12797.5	10.58	HUMAN	K7EIL4	Glucose-6-phosphate isomerase (Fragment)
4737	dirMS_041712_NAR_30mM_minus2.17903.18390.2	2	13.35	0	1.62E+06		(R)GLFIIDG	(R)G L|F|I I D/G K(G)		153.33	431.7497	862.503	-0.0112	-12.9	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
4738	dirMS_041712_NAR_40mM_minus2.14721.14721.3	3	13.35	1	1.38E+05		(R)EQIPAG	(R)E/Q\I/P A G T L L/L A V E D P E K R(V)		170.83	660.3663	1979.081	0.0036	1.8	4.41	19773.1	4.48	HUMAN	B4DEU5	L-fucose kinase
4739	dirMS_041712_NAR_50mM_minus2.9237.9239.3	3	13.35	1	2.01E+05		(K)GITEQQ	(K)G I|T E Q/Q/K/E G L E I/V/K(M)		120.58	524.6237	1571.864	-0.0074	-4.7	4.79	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
4740	dirMS_041712_NAR_50mM_minus2.9460.9460.3	3	13.35	0	1.88E+04		(K)ADHTLS	(K)A D H T L S S L/E|P/A/Y S A K(W)		122.27	530.5989	1589.781	0.0016	1	5.32	43384.7	7.78	HUMAN	B7Z9G5	BRO1 domain-containing protein BROX
4741	dirMS_041712_NAR_60mM_minus.13131.13151.3	3	13.35	1	1.52E+05		(R)VLITEN	(R)V/L|I|T E N D/V/K/E G L Q R(S)		132.97	538.6313	1613.886	-0.0064	-3.9	4.68	72873.4	5.73	HUMAN	Q96S55	ATPase WRNIP1
4742	dirMS_041712_NAR_60mM_minus.9469.9469.3	3	13.35	1	6.72E+05		(K)TFDQLT	(K)T F|D Q L/T/P D/E S K E R(L)		113.37	522.5846	1565.744	-0.0049	-3.2	4.32	17272.1	6.63	HUMAN	E9PJD5	Reticulocalbin-1
4743	dirMS_041712_NAR_120mM_plus.11218.11218.3	3	13.35	0	5.10E+05		(R)SIFQHIQ	(R)S I|F Q/H/I Q S A Q S Q R(S)		112.47	510.5986	1529.782	-0.0007	-0.4	9.49	108720.9	10.17	HUMAN	Q9Y2W1	Thyroid hormone receptor-associated protein 3
4744	dirMS_041712_NAR_20mM_plus.16397.16415.3	3	13.35	0	1.35E+05		(R)QAQEYE	(R)Q A\Q E\Y\E/A|L/L N I K(V)		184.45	473.9191	1419.748	-0.0051	-3.6	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4745	dirMS_041712_NAR_20mM_plus.7308.7308.2	2	13.35	0	2.85E+04		(R)VLEEGS	(R)V/L|E\E G S V E A/R(T)		118.03	544.7829	1088.558	0.0003	0.3	4.25	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
4746	dirMS_041712_NAR_30mM_plus2.18151.18151.2	2	13.35	0	2.14E+05		(R)QITLND	(R)Q I/T\L|N/D\L/P V G R(S)		147.93	613.3465	1225.69	-0.0042	-3.4	5.84	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
4747	dirMS_041712_NAR_30mM_plus2.20688.20688.2	2	13.35	0	8.74E+05		(R)TVQSLE	(R)T V/Q/S L/E|I D L/D S M R(N)		162.18	753.8768	1506.747	-0.0005	-0.3	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4748	dirMS_041712_NAR_30mM_plus2.21395.21395.2	2	13.35	0	3.37E+04		(R)GAFQNL	(R)G A/F/Q|N/L/F Q S/V R(E)		168.02	633.8315	1266.659	-0.0032	-2.5	9.75	68629.9	5.59	HUMAN	E7EVX6	Androgen receptor
4749	dirMS_041712_NAR_30mM_plus2.22014.22014.2	2	13.35	0	1.55E+05		(K)ANFLQN	(K)A N/F/L/Q/N/M I E/D/R(T)		170.25	675.8282	1350.647	0.0021	1.5	4.37	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
4750	dirMS_041712_NAR_30mM_plus2.23516.23516.2	2	13.35	0	1.80E+05		(R)IAIYELLF	(R)I/A|I/Y/E L/L F/K(E)		190.25	555.3331	1109.661	-0.0016	-1.4	6	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
4751	dirMS_041712_NAR_40mM_plus2.9068.9068.2	2	13.35	0	4.81E+05		(R)GGNFGF	(R)G G/N F/G F|G D/S/R(G)		116.33	507.2256	1013.444	0.0004	0.4	5.84	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
4752	dirMS_041712_NAR_50mM_plus2.14800.14800.3	3	13.35	0	6.51E+05		(K)SPAPPLL	(K)S/P|A|P/P L L H V/A A L G Q K(Q)		145.78	500.2911	1498.874	-0.0153	-10.2	8.49	17549.1	10.39	HUMAN	E5RFJ3	DBIRD complex subunit KIAA1967 (Fragment)
4753	dirMS_041712_NAR_60mM_plus.10377.10458.3	3	13.35	1	1.61E+06		(R)TNAENE	(R)T/N|A/E N E F V/T I/K\K(D)		112.27	465.2512	1393.732	0.0069	4.9	5.81	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
4754	dirMS_041712_NAR_60mM_plus.16336.16487.3	3	13.35	0	6.18E+05		(K)MTHLPE	(K)M T H\L P E\L/D|T/L/S/S E/R(A)		142.28	543.6023	1628.795	-0.0025	-1.5	4.65	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
4755	dirMS_041712_NAR_60mM_plus.20601.20726.3	3	13.35	0	7.27E+05		(R)LGFHLP	(R)L G F H L\P L/E|V/A/Y/Q/R(G)		168.62	514.9568	1542.843	0.0131	8.5	6.75	533778	5.74	HUMAN	Q15149	Plectin
4756	dirMS_041712_NAR_120mM_minus.13976.13976.4	4	13.34	1	1.60E+06		(K)ASIHEA	(K)A/S|I/H/E A W/T D/G K/E A M L K(H)		129.98	447.476	1786.879	0.0029	1.6	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
4757	dirMS_041712_NAR_30mM_minus2.10243.10642.2	2	13.34	0	2.07E+06		(R)QTVAV	(R)Q T|V/A/V/G V/I/K(A)		110.7	457.7858	914.567	-0.0026	-2.9	8.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
4758	dirMS_041712_NAR_50mM_minus2.10400.10400.3	3	13.34	0	2.78E+05	M35m	(K)AASDIA	(K)A A/S D\I/A/m T E L/P/P T H/P I R(L)	m:Oxidized methionine	127.6	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
4759	dirMS_041712_NAR_50mM_minus2.11268.11269.3	3	13.34	0	1.66E+04		(R)VVVLM	(R)V/V|V|L/M/G S T/S D L G H C E K(I)	C:Carbamidomethylation	132.28	577.9535	1731.84	0.0055	3.2	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
4760	dirMS_041712_NAR_50mM_minus2.11764.11764.3	3	13.34	1	4.83E+05		(K)KVPQVS	(K)K\V P Q V S/T/P T|L/V/E/V S R(N)		135.22	547.3172	1639.938	-0.0007	-0.4	8.75	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
4761	dirMS_041712_NAR_50mM_minus2.7935.7935.3	3	13.34	0	8.88E+04		(K)TAVEHA	(K)T/A/V E/H A/T/D E D I/L A K(G)		112.23	504.9229	1512.754	0.0001	0.1	4.31	288852.1	5.33	HUMAN	E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein
4762	dirMS_041712_NAR_60mM_minus.15391.15519.3	3	13.34	0	4.11E+05		(K)EGHVEV	(K)E/G H V E\V\V|S/E/L/L Q/R(E)		146.25	498.9349	1494.791	-0.0009	-0.6	4.75	48586.6	9.32	HUMAN	D6RCB2	Ankyrin-3
4763	dirMS_041712_NAR_120mM_plus.6241.6385.3	3	13.34	1	5.04E+05		(R)ARSDEG	(R)A R S D E\G\Q|L|S|P/A T R(G)		86.7	463.2395	1387.692	0.0115	8.3	6.12	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
4764	dirMS_041712_NAR_30mM_plus2.6362.6363.2	2	13.34	0	2.46E+05		(K)SGYLSSE	(K)S/G|Y|L|S/S E/R(L)		87.22	449.7152	898.427	-0.0034	-3.7	5.72	65692.2	5.7	HUMAN	E7EQR4	Ezrin
4765	dirMS_041712_NAR_40mM_plus2.19762.19762.3	3	13.34	1	4.44E+05		(R)ILDDDT	(R)I L|D/D D T I/I/T T L E N L K R(E)		185.12	625.0111	1873.028	-0.0089	-4.8	4.23	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
4766	dirMS_041712_NAR_50mM_plus2.10974.11014.3	3	13.34	1	4.55E+05		(R)AIPNNQ	(R)A I|P/N N Q/V/L/G\K I/E R(A)		125.48	484.6151	1451.833	-0.0021	-1.5	8.79	16368.4	9.95	HUMAN	O60869	Endothelial differentiation-related factor 1
4767	dirMS_041712_NAR_50mM_plus2.11818.11818.3	3	13.34	1	1.75E+06		(K)TGQPM	(K)T G\Q|P/M/I N L Y T D R E T G K(L)		130.72	608.6361	1823.896	-0.0019	-1	5.73	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
4768	dirMS_041712_NAR_120mM_minus.7431.7431.3	3	13.33	0	1.20E+05		(R)NIDEHA	(R)N I/D E/H/A/N/E D V E/R(M)		94.67	480.884	1440.635	0.0025	1.7	4.17	22768.7	8.94	HUMAN	P61026	Ras-related protein Rab-10
4769	dirMS_041712_NAR_50mM_minus2.12147.12147.3	3	13.33	0	9.09E+03		(K)AASAGV	(K)A A|S\A/G\V/P Y H G E/V/P V S L A R(A)		135.98	594.315	1780.934	-0.0036	-2	6.79	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
4770	dirMS_041712_NAR_50mM_minus2.14372.14372.3	3	13.33	1	1.09E+06		(K)EAFSLF	(K)E A/F/S L/F/D\K D G D G T I T T/K(E)		149.93	615.6336	1844.891	-0.005	-2.7	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
4771	dirMS_041712_NAR_50mM_minus2.15740.15740.3	3	13.33	0	1.29E+05		(K)FTISDHP	(K)F/T|I/S/D H|P Q\P I D/P L L K(N)		157.77	574.3122	1720.927	-0.0048	-2.8	5.21	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
4772	dirMS_041712_NAR_60mM_minus.14207.14207.3	3	13.33	1	2.27E+05		(R)TFNTST	(R)T F|N/T S\T G G L/L/L|P S D T K R(S)		138.82	603.3262	1807.955	0.0092	5.1	8.41	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
4773	dirMS_041712_NAR_120mM_plus.15951.15951.3	3	13.33	1	8.08E+04		(K)THLPGF	(K)T\H/L|P G F\V|E\Q/A/E A/L K/A K(G)		137.02	580.3208	1738.949	-0.0008	-0.5	6.42	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
4774	dirMS_041712_NAR_120mM_plus.18256.18316.4	4	13.33	1	1.06E+06		(K)EMVELP	(K)E M V|E/L/P L R H/P A L/F/K(A)		149.07	420.7376	1679.93	-0.0016	-0.9	6.86	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
4775	dirMS_041712_NAR_120mM_plus.21172.21172.4	4	13.33	1	1.17E+06		(R)DYLHLP	(R)D Y L H L\P/P/E I/V/P A T L R R(S)		164.15	473.2689	1890.06	-0.0058	-3.1	6.75	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
4776	dirMS_041712_NAR_30mM_plus2.10174.10174.2	2	13.33	0	2.33E+05		(K)TAVCDI	(K)T/A|V|C D/I/P|P R(G)	C:Carbamidomethylation	105.85	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
4777	dirMS_041712_NAR_30mM_plus2.18561.18561.2	2	13.33	0	6.99E+05		(K)EGMNIV	(K)E G M/N/I|V E/A/M E/R(F)		150.78	639.7958	1278.582	0.0026	2.1	4.25	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
4778	dirMS_041712_NAR_30mM_plus2.8955.9005.2	2	13.33	0	3.45E+05		(K)GGEIQP	(K)G G\E|I|Q|P V/S V/K(V)		100.77	507.2843	1013.563	-0.0013	-1.2	6	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
4779	dirMS_041712_NAR_40mM_plus2.13883.13883.3	3	13.33	0	2.23E+05		(K)VALLLLD	(K)V A L|L/L/L D Q/G A S P H A A A K(N)		148.13	558.9886	1674.954	-0.0025	-1.5	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
4780	dirMS_041712_NAR_40mM_plus2.17566.17587.3	3	13.33	1	5.62E+05		(R)GLLPGL	(R)G L|L\P\G L/L/P\A/P A D K L T/P K(G)		170.58	567.6811	1701.031	-0.0022	-1.3	8.59	153084.9	5.55	HUMAN	Q6P2E9	Enhancer of mRNA-decapping protein 4
4781	dirMS_041712_NAR_120mM_minus.15258.15258.3	3	13.32	2	9.57E+05		(R)ALKDEE	(R)A L/K D E E/K/M/E|L/Q|E I\Q/L/K(E)		137.72	649.0139	1945.031	-0.0039	-2	4.58	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
4782	dirMS_041712_NAR_30mM_minus2.14024.14024.2	2	13.32	0	2.71E+05		(R)IYVVDV	(R)I Y|V|V|D V/G S E/P R(A)		129.55	617.3267	1233.647	-0.0013	-1	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
4783	dirMS_041712_NAR_30mM_minus2.6776.6776.2	2	13.32	0	2.56E+05		(R)IGDEDV	(R)I/G|D E D/V/G/R(V)		91.67	430.7116	860.411	0.0051	5.9	4.03	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
4784	dirMS_041712_NAR_60mM_minus.11395.11395.3	3	13.32	1	8.92E+05	M232m	(R)MSmKE	(R)M/S/m K E V D E/Q|M/L/N\V/Q N K(N)	m:Oxidized methionine	122.82	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
4785	dirMS_041712_NAR_60mM_minus.4992.4992.3	3	13.32	1	1.11E+05		(K)DSYVGD	(K)D S/Y/V/G/D E/A Q S K R(G)		82.27	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
4786	dirMS_041712_NAR_120mM_plus.9666.9720.4	4	13.32	2	3.92E+06		(R)VLTVIN	(R)V/L T/V/I/N Q T Q K/E/N L R K(F)		104.23	446.7653	1784.039	0.0005	0.3	9.99	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
4787	dirMS_041712_NAR_20mM_plus.10922.10922.2	2	13.32	0	2.62E+04		(K)ALIAAQ	(K)A L I/A/A/Q|Y S|G A Q/V R(V)		147.72	674.3695	1347.738	-0.0062	-4.6	8.79	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
4788	dirMS_041712_NAR_20mM_plus.13278.13278.2	2	13.32	0	9.69E+04		(R)AELIVQ	(R)A E|L\I/V|Q/P/E L K(Y)		164.3	570.3361	1139.667	-0.0021	-1.9	4.53	334221.3	6.44	HUMAN	P15924	Desmoplakin
4789	dirMS_041712_NAR_30mM_plus2.22642.22642.3	3	13.32	0	5.00E+05		(R)ALTVPE	(R)A L T\V/P E L/T Q Q/V/F D A K(N)		175.77	553.9697	1659.895	-0.0007	-0.4	4.37	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
4790	dirMS_041712_NAR_40mM_plus2.8979.8979.2	2	13.32	0	1.19E+05		(R)GYSFTT	(R)G Y|S\F/T T/T A E/R(E)		114.9	566.7672	1132.527	0.0002	0.2	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
4791	dirMS_041712_NAR_50mM_plus2.9965.9965.3	3	13.32	0	1.16E+06		(K)INEKPQ	(K)I/N/E/K/P Q V|I/A/D/Y E S G R(A)		119.77	573.6314	1718.871	0.0089	5.2	4.68	16368.4	9.95	HUMAN	O60869	Endothelial differentiation-related factor 1

4792	dirMS_041712_NAR_60mM_plus.19303.19303.3	3	13.32	1	1.96E+05		(R)AGEAGK	(R)A G/E\A|G K L E E\V\M/Q/E/L/R(A)		159.22	553.9525	1659.837	0.0059	3.6	4.49	54918.3	5.61	HUMAN	Q9BR76	Coronin-1B
4793	dirMS_041712_NAR_60mM_plus.7536.7672.3	3	13.32	0	1.38E+06	M80m	(R)TICSHVC	(R)T/I|C/S/H/V/Q N m I K(G)	C:Carbamidomethylation m:Oxid	97.92	449.5594	1330.661	16.003	6	8.44	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
4794	dirMS_041712_NAR_20mM_minus.12556.12556.3	3	13.31	0	5.42E+05	M73m	(R)AVLVDLI	(R)A V\L/V D\L/E|P G T\m D S/V R(S)	m:Oxidized methionine	173.05	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
4795	dirMS_041712_NAR_20mM_minus.14710.14710.2	2	13.31	0	1.74E+05		(K)TAVETA'	(K)T A|V/E/T/A V L|L L R(I)		201.37	593.3613	1185.72	-0.0048	-4.1	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
4796	dirMS_041712_NAR_30mM_minus2.10714.11210.2	2	13.31	0	9.63E+05		(K)SSFLVDC	(K)S S|F|L|V/D/C/S K(A)	C:Carbamidomethylation	113.15	521.7502	1042.487	0.0058	5.5	5.55	258215.9	5.48	HUMAN	E7EN95	Filamin-B
4797	dirMS_041712_NAR_30mM_minus2.16078.16078.2	2	13.31	0	2.17E+04		(K)VNYILES	(K)V N/Y I/L E/S/R(A)		140.85	497.265	993.536	-0.0136	-13.7	5.97	26855.2	9.54	HUMAN	B7Z5E5	Target of rapamycin complex 2 subunit MAPKAP1
4798	dirMS_041712_NAR_20mM_plus.18879.18879.2	2	13.31	0	9.89E+04		(K)LTVYTTL	(K)L T\V|Y/T T L/I D V T/K(G)		200.9	683.8948	1366.783	-0.0005	-0.4	5.83	42194.9	8.75	HUMAN	E7EMM4	Acid ceramidase
4799	dirMS_041712_NAR_50mM_plus2.15410.15410.3	3	13.31	0	1.43E+06		(R)LASTLVH	(R)L A|S T L V|H L G E Y Q A/A/V D G A R(K)		149.62	657.6802	1971.029	-0.0034	-1.7	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
4800	dirMS_041712_NAR_50mM_plus2.5316.5316.3	3	13.31	0	3.81E+05	M116m	(R)ATAPQT	(R)A/T/A/P Q/T Q/H V S/P m R(Q)	m:Oxidized methionine	87.6	480.5727	1423.711	15.9925	-1.7	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
4801	dirMS_041712_NAR_50mM_plus2.7488.7488.3	3	13.31	1	3.52E+05		(R)VVASDK	(R)V/V/A/S D K E/T Y E L/R(Y)		105.87	470.5836	1409.727	0.0092	6.5	4.68	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
4802	dirMS_041712_NAR_60mM_plus.18287.18287.3	3	13.31	1	9.14E+05		(K)EVNKFQ	(K)E V/N K F Q M A/Y/S N/L L R(A)		152.85	571.6293	1712.879	-0.0055	-3.2	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
4803	dirMS_041712_NAR_30mM_minus2.19195.19195.2	2	13.3	0	1.03E+05		(K)TVALWD	(K)T/V/A\L|W/D/L R(N)		159.23	487.2765	973.547	-0.0008	-0.8	5.5	19598	4.45	HUMAN	B4DRT0	Histone-binding protein RBBP4
4804	dirMS_041712_NAR_50mM_minus2.12500.13012.3	3	13.3	1	7.56E+06		(R)IQLVEEE	(R)I/Q|L|V/E E E L D R A Q E/R(L)		140.42	576.6348	1727.892	-0.0024	-1.4	4.25	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
4805	dirMS_041712_NAR_60mM_minus.14322.14460.3	3	13.3	1	3.35E+05		(K)KSDIDEI'	(K)K S D I\D E\I|V\L|V/G/G S T R(I)		139.68	530.2846	1588.854	-0.0148	-9.3	4.56	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
4806	dirMS_041712_NAR_60mM_minus.16973.16993.3	3	13.3	1	2.04E+06		(K)LLQDFFN	(K)L/L|Q/D/F/F/N/G K E L N K(S)		155.22	522.6138	1565.832	-0.0054	-3.4	6.07	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
4807	dirMS_041712_NAR_60mM_minus.5365.5365.3	3	13.3	0	2.19E+04		(R)ESPGAA	(R)E S/P G A/A A T/S/S S G P Q A Q Q H/R(G)		85.48	622.9613	1866.869	0.0005	0.2	6.85	74981.5	9.96	HUMAN	Q7L2J0	7SK snRNA methylphosphate capping enzyme
4808	dirMS_041712_NAR_120mM_plus.23757.23757.4	4	13.3	2	2.20E+05		(R)RGVMLA	(R)R G V\M|L|A V/D A V/I A E L K K(Q)		179.67	429.0075	1713.009	-0.001	-0.6	8.59	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
4809	dirMS_041712_NAR_30mM_plus2.11785.11785.2	2	13.3	0	5.40E+05		(K)VASGCLI	(K)V/A|S/G/C/L|D I/N S S V K(G)	C:Carbamidomethylation	114.82	675.3393	1349.673	-0.0016	-1.2	5.81	56837	7.19	HUMAN	E7ETT1	Propionyl-CoA carboxylase beta chain, mitochondrial
4810	dirMS_041712_NAR_30mM_plus2.20771.20771.2	2	13.3	0	3.91E+05		(R)SLVPAAI	(R)S L\V|P A/A/E\L/L E S R(V)		162.33	642.8602	1284.716	-0.0027	-2.1	4.53	533778	5.74	HUMAN	Q15149	Plectin
4811	dirMS_041712_NAR_30mM_plus2.7560.7577.2	2	13.3	0	7.76E+05		(K)CCTESLV	(K)C|C|T|E/S/L/V/N R(R)	C:Carbamidomethylation	93.95	569.7533	1138.498	0.0014	1.2	6	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
4812	dirMS_041712_NAR_40mM_plus2.10416.10416.2	2	13.3	0	9.40E+04		(K)IGGIGTV	(K)I/G|G|I/G T V/P V/G R(V)		125.75	513.3081	1025.61	-0.0013	-1.2	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
4813	dirMS_041712_NAR_40mM_plus2.9428.9428.2	2	13.3	0	9.68E+04		(R)ISVYYNE	(R)I/S/V/Y/Y N\E A T G G K(Y)		118.55	651.3206	1301.637	-0.0033	-2.5	6	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
4814	dirMS_041712_NAR_60mM_plus.5300.5310.3	3	13.3	1	1.42E+05	M117m	(K)EmQLRC	(K)E m/Q/L/R/Q/E/E/E/R(R)	m:Oxidized methionine	85.4	455.2157	1347.632	16.0004	4	4.49	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
4815	dirMS_041712_NAR_30mM_minus2.16330.16330.2	2	13.29	0	1.45E+05		(R)SLVSGLI	(R)S L|V/S\G/L I/R(L)		142.08	422.7649	844.525	-0.0026	-3	9.47	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
4816	dirMS_041712_NAR_40mM_minus2.9624.9624.2	2	13.29	0	1.24E+06		(R)VAPEEH	(R)V A/P E E/H|P V L/L T E A P L/N/P K(A)		139.8	977.5343	1954.064	-0.0031	-1.6	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
4817	dirMS_041712_NAR_50mM_minus2.14940.14940.3	3	13.29	0	4.19E+05		(K)IAILTCPF	(K)I/A|I/L T/C/P F E P P K P K(T)	C:Carbamidomethylation	153.32	537.6375	1610.898	0.0005	0.3	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
4818	dirMS_041712_NAR_60mM_minus.14259.14259.3	3	13.29	1	8.82E+05		(R)MSMKE'	(R)M/S M K E V D E Q|M|L/N V Q/N K(N)		140.17	641.9701	1923.897	-0.0015	-0.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
4819	dirMS_041712_NAR_120mM_plus.11424.11506.4	4	13.29	2	2.22E+06		(K)QAGPAS	(K)Q A/G P A/S\V/P/L R T E E E F K/K(F)		113.4	472.5046	1886.997	-0.0005	-0.3	6.23	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
4820	dirMS_041712_NAR_20mM_plus.15480.15480.2	2	13.29	0	4.07E+05		(R)GVVDSE	(R)G V V|D/S\E|D\I|P L\N/L/S R(E)		179.15	757.3956	1513.786	-0.0017	-1.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
4821	dirMS_041712_NAR_30mM_plus2.13529.13529.2	2	13.29	0	1.10E+06		(R)ANTFVA	(R)A N/T|F/V/A E/L/K(G)		124.65	496.774	992.541	-0.0004	-0.4	6.05	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
4822	dirMS_041712_NAR_30mM_plus2.18971.19221.2	2	13.29	0	2.07E+05		(K)YPQLLP(	(K)Y/P|Q/L|L/P G I/R(G)		153.25	528.814	1056.62	0.0007	0.6	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
4823	dirMS_041712_NAR_30mM_plus2.22113.22113.2	2	13.29	0	2.01E+05		(K)NSSYFVE	(K)N S S/Y F\V/E/W/I/P N N V K(V)		171.82	848.9189	1696.833	-0.0024	-1.4	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
4824	dirMS_041712_NAR_50mM_plus2.11426.11426.3	3	13.29	1	3.29E+05		(K)VAVVAG	(K)V A|V|V|A|G/Y G D V G K G C A Q A L R(G)	C:Carbamidomethylation	127.85	630.9984	1890.985	-0.0048	-2.5	8.56	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
4825	dirMS_041712_NAR_50mM_plus2.5256.5256.3	3	13.29	0	1.37E+06		(K)TATPQQ	(K)T A|T/P Q Q/A Q E V/H E K(L)		86.38	489.5774	1466.723	-0.0057	-3.9	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
4826	dirMS_041712_NAR_60mM_plus.20624.20647.3	3	13.29	0	7.27E+05		(R)LGFHLPI	(R)L G F H L\P L|E|V/A/Y/Q/R(G)		168.62	514.9568	1542.843	0.0131	8.5	6.75	533778	5.74	HUMAN	Q15149	Plectin
4827	dirMS_041712_NAR_40mM_minus2.6164.6234.2	2	13.28	0	9.42E+05		(R)STFSTNY	(R)S T|F|S/T/N/Y R(S)		101.98	488.2302	975.453	0.0001	0.1	8.46	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4828	dirMS_041712_NAR_60mM_minus.10872.11021.3	3	13.28	1	4.59E+05		(K)GSITISAE	(K)G S|I|T/I/S A E E/I K D/N R(V)		121.13	511.6045	1532.792	0.0075	4.9	4.68	27142.4	5.34	HUMAN	E5RG68	Copine-3 (Fragment)
4829	dirMS_041712_NAR_120mM_plus.18392.18392.4	4	13.28	0	4.29E+05		(R)QALHSLI	(R)Q A L H S L/E L H Y Q/A/F/L/R(D)		149.4	457.2493	1825.971	0.0046	2.5	6.92	533778	5.74	HUMAN	Q15149	Plectin
4830	dirMS_041712_NAR_20mM_plus.16939.16939.3	3	13.28	0	3.07E+05		(K)VQIAVA	(K)V Q I A V/A\N A|Q/E|L|L Q R(M)		187.85	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
4831	dirMS_041712_NAR_30mM_plus2.18927.18927.2	2	13.28	0	1.87E+05		(K)LNLGTV(	(K)L/N|L|G T/V/G F Y R(T)		152.8	570.3123	1139.621	-0.0034	-3	8.75	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
4832	dirMS_041712_NAR_30mM_plus2.20780.20780.3	3	13.28	0	1.06E+06		(R)TVQSLEI	(R)T V Q\S L E|I/D|L/D S M R(N)		162.32	502.9201	1506.747	-0.0011	-0.7	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4833	dirMS_041712_NAR_30mM_plus2.6709.6709.2	2	13.28	0	5.75E+04		(K)TVGVEP.	(K)T/V|G|V\E/P A/A D G K(G)		89.45	522.2782	1043.537	0.0124	11.8	4.37	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
4834	dirMS_041712_NAR_40mM_plus2.6857.6857.2	2	13.28	0	5.56E+03		(R)LSVAAQ	(R)L/S|V/A|A/Q/E A A R(L)		100.35	508.2775	1015.553	-0.0054	-5.3	6	533778	5.74	HUMAN	Q15149	Plectin
4835	dirMS_041712_NAR_50mM_plus2.10871.10871.3	3	13.28	0	4.89E+05		(R)EALLSSA	(R)E A/L/L/S/S A|V D H G S D E V K(F)		124.7	552.9403	1656.807	-0.0012	-0.7	4.31	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
4836	dirMS_041712_NAR_60mM_plus.14426.14426.2	2	13.28	1	8.40E+05		(K)KVPQVS	(K)K|V/P Q V/S T/P T\L V E V S R(N)		132.12	820.4708	1639.938	-0.0034	-2.1	8.75	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
4837	dirMS_041712_NAR_60mM_plus.15564.15589.3	3	13.28	1	2.59E+05		(K)ALELDSN	(K)A L|E|L/D/S/N N E/K G L/F R(R)		138.02	535.9438	1605.823	-0.0063	-3.9	4.68	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
4838	dirMS_041712_NAR_60mM_plus.7690.7704.3	3	13.28	0	9.11E+05		(K)LFQECCI	(K)L/F|Q/E C/C/P H S T D R(V)	C:Carbamidomethylation	98.37	517.2234	1549.652	0.0034	2.2	5.32	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
4839	dirMS_041712_NAR_20mM_minus.6903.6903.2	2	13.27	0	1.34E+05	M453m	(K)ImATPE(	(K)I m|A|T/P E Q V|G K(M)	m:Oxidized methionine	115.42	545.2807	1073.566	15.9882	-6.2	6	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
4840	dirMS_041712_NAR_30mM_minus2.9963.10045.2	2	13.27	0	8.46E+05		(K)IAGPGL(	(K)I/A|G|P/G L G S G V/R(A)		108.65	492.2788	983.563	-0.0129	-13.1	9.75	258215.9	5.48	HUMAN	E7EN95	Filamin-B
4841	dirMS_041712_NAR_20mM_plus.18759.18759.2	2	13.27	0	2.00E+05		(R)VFIGNLN	(R)V/F|I|G N/L N T L V/V/K(K)		200.13	658.8999	1316.794	-0.0011	-0.9	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
4842	dirMS_041712_NAR_20mM_plus.6401.6405.2	2	13.27	0	1.60E+05		(K)DSYVGD	(K)D S/Y|V|G D/E/A Q/S/K(R)		107.17	599.7645	1198.522	-0.0005	-0.4	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
4843	dirMS_041712_NAR_30mM_plus2.11426.11426.2	2	13.27	0	4.41E+05		(R)FASGGC	(R)F A|S/G/G C D N L/I/K(L)	C:Carbamidomethylation	113.55	591.286	1181.562	0.0028	2.4	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
4844	dirMS_041712_NAR_30mM_plus2.22327.22327.2	2	13.27	0	3.79E+05		(R)VGNLGL	(R)V G N|L/G\L|A\T/S F F\N/E R(N)		172.8	762.8926	1524.781	-0.0026	-1.7	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
4845	dirMS_041712_NAR_40mM_plus2.19242.19279.3	3	13.27	1	4.28E+05		(K)LLPLVSD	(K)L L\P/L/V/S D E/V/F I/R D/V/A K(V)		180.72	605.3503	1814.042	-0.0059	-3.2	4.56	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
4846	dirMS_041712_NAR_50mM_plus2.12640.12640.3	3	13.27	0	5.15E+05		(R)IMDPNI'	(R)I/M/D/P N/I V/G S E H/Y D/V A R(G)		134.6	605.9694	1815.869	0.0242	13.3	4.54	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
4847	dirMS_041712_NAR_50mM_plus2.16580.16580.3	3	13.27	1	2.04E+05		(R)LDDFFK'	(R)L/D/D/F F K/V T G S L S S A K(R)		155.03	538.95	1614.837	-0.0019	-1.2	5.96	42934.5	9.09	HUMAN	P39748	Flap endonuclease 1
4848	dirMS_041712_NAR_50mM_plus2.18216.18216.2	2	13.27	0	5.20E+05		(R)IHFPLAT	(R)I/H|F|P L/A/T\Y A P V I/S A/E K(A)		164.6	878.9842	1756.963	-0.0021	-1.2	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
4849	dirMS_041712_NAR_60mM_plus.5211.5211.3	3	13.27	1	4.08E+05		(K)VSSAEG/	(K)V/S/S/A/E G A\A K E E P K(R)		85.05	434.8867	1302.654	-0.008	-6.2	4.79	4801.6	11.17	HUMAN	F2Z2W6	Non-histone chromosomal protein HMG-14
4850	dirMS_041712_NAR_30mM_minus2.9347.9357.2	2	13.26	0	1.01E+06		(K)QADVNI	(K)Q/A|D\V/N/L|V/N/A K(L)		105.43	536.2917	1071.579	-0.0032	-3	5.84	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
4851	dirMS_041712_NAR_40mM_minus2.11805.11887.3	3	13.26	0	1.02E+04		(K)LVEALCA	(K)L/V|E/A/L|C A/E H Q I N L I K(V)	C:Carbamidomethylation	152.93	584.3199	1750.952	-0.0069	-3.9	5.4	14914.1	6.84	HUMAN	P25398	40S ribosomal protein S12
4852	dirMS_041712_NAR_50mM_minus2.13286.13286.3	3	13.26	1	2.02E+05	M17m	(K)GAEEmE	(K)G A|E/E/m/E T\V I P V D V M R R(A)	m:Oxidized methionine	143.75	616.6435	1831.904	16.0119	9.2	4.41	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
4853	dirMS_041712_NAR_20mM_plus.15773.15773.2	2	13.26	0	4.76E+05		(R)GVVDSE	(R)G V V\D|S E/D/I|P L/N L S R(E)		179.47	757.3956	1513.786	-0.0017	-1.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
4854	dirMS_041712_NAR_30mM_plus2.12569.12569.2	2	13.26	0	1.85E+05		(R)ELAEDG'	(R)E L/A/E/D/G Y/S G V E/V R(V)		118.53	712.3382	1423.67	-0.0008	-0.6	4	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
4855	dirMS_041712_NAR_30mM_plus2.20691.20691.2	2	13.26	0	2.60E+05		(R)ASLSLW	(R)A S/L/S/L/W/Q\A\M/E K(G)		162.9	632.3231	1263.64	-0.0013	-1	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
4856	dirMS_041712_NAR_50mM_plus2.20018.20018.3	3	13.26	1	1.05E+04		(K)QNDQV!	(K)Q N D\Q/V/S F/A/S L V|E E L K/K(V)		172.43	612.3205	1834.955	-0.0076	-4.1	4.68	69285	5.2	HUMAN	G3V4Y7	Kinectin
4857	dirMS_041712_NAR_50mM_plus2.8931.8931.3	3	13.26	1	2.37E+04		(R)GGSDDS	(R)G G S/D/D|S/S K/D/P I D\V N\Y E K(L)		114.08	609.2765	1825.809	0.0063	3.5	4.03	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
4858	dirMS_041712_NAR_120mM_minus.14167.14167.3	3	13.25	1	6.63E+04		(K)ASLENSL	(K)A/S|L/E/N S L R E V E A\R(Y)		131.78	491.9266	1473.766	-0.0003	-0.2	4.79	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4859	dirMS_041712_NAR_20mM_minus.14111.14111.2	2	13.25	0	1.31E+06		(K)SYELPD(	(K)S Y E|L/P D G Q V I|T I/G N E R(F)		194.08	895.9481	1790.892	-0.003	-1.7	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
4860	dirMS_041712_NAR_60mM_minus.10301.10542.3	3	13.25	1	6.05E+05	M88m	(K)DVDEAY	(K)D V|D/E/A/Y m N K V E/L E/S R(L)	m:Oxidized methionine	118.37	605.2791	1797.832	15.9904	-2.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
4861	dirMS_041712_NAR_120mM_plus.13399.13399.4	4	13.25	1	1.43E+06		(K)SVHSSVI	(K)S V H S S V|P/L/L N S K D/P I D R(I)		123.27	466.7533	1863.992	-0.0009	-0.5	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
4862	dirMS_041712_NAR_20mM_plus.10909.10909.3	3	13.25	0	1.01E+05		(K)ALIAAQ'	(K)A L\I A A Q|Y/S/G/A/Q V R(V)		147.88	449.9174	1347.738	-0.0003	-0.2	8.79	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
4863	dirMS_041712_NAR_20mM_plus.18264.18264.2	2	13.25	0	1.68E+05		(K)DAGVIA(	(K)D A G\V|I/A/G L\N/V L R(I)		196.73	599.3505	1197.695	-0.0013	-1.1	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
4864	dirMS_041712_NAR_20mM_plus.19226.19226.2	2	13.25	0	1.30E+05		(R)EGDVLT	(R)E G D\V/L|T/L/L E S E R(E)		203.6	680.8536	1360.696	0.0045	3.3	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
4865	dirMS_041712_NAR_30mM_plus2.12816.12816.2	2	13.25	0	3.70E+05		(R)ELAEDG'	(R)E L|A\E|D G\Y S|G V/E/V R(V)		120.6	712.3382	1423.67	-0.0008	-0.6	4	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
4866	dirMS_041712_NAR_30mM_plus2.20994.21014.2	2	13.25	0	2.61E+05		(K)TIFAYFT(	(K)T I|F|A/Y F T G/S K(D)		164.7	567.7949	1134.583	-0.0005	-0.4	8.26	8599.5	5.51	HUMAN	I3L0K2	Thioredoxin domain-containing protein 17
4867	dirMS_041712_NAR_30mM_plus2.7004.7004.2	2	13.25	0	1.34E+05		(K)YTQSNS'	(K)Y T/Q/S/N S/V/C Y/A/K(N)	C:Carbamidomethylation	91.15	660.7963	1320.589	-0.0036	-2.7	8.5	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
4868	dirMS_041712_NAR_30mM_plus2.9306.9306.2	2	13.25	0	2.98E+05		(K)SVEAAA	(K)S V|E/A/A A E L S/A/K(D)		103.27	538.2855	1075.563	0.0007	0.7	4.53	12131.5	11.14	HUMAN	F5GXR3	Parathymosin
4869	dirMS_041712_NAR_40mM_plus2.14030.14030.3	3	13.25	1	8.78E+04		(R)STGLELE	(R)S T|G L/E L E T/P S L V/P V K\K(N)		148.73	566.6552	1697.968	-0.0173	-10.2	5.86	34828	9.96	HUMAN	F5H5K4	Serine/threonine-protein phosphatase 1 regulatory subunit 10
4870	dirMS_041712_NAR_50mM_plus2.18645.18645.3	3	13.25	1	5.52E+05		(K)NAAGAL	(K)N A|A|G A/L/D L/L K E L K(N)		165.92	452.601	1355.789	-0.0008	-0.6	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
4871	dirMS_041712_NAR_60mM_plus.15661.15682.3	3	13.25	1	2.49E+05		(R)TEMENE	(R)T E|M E N E/F/V/L I/K/K(D)		138.75	494.2622	1480.772	0.0005	0.3	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
4872	dirMS_041712_NAR_60mM_plus.8014.8246.3	3	13.25	1	6.20E+05		(R)LSQIGVE	(R)L/S|Q|I/G V E/N T E E N R R(L)		101.08	548.9468	1644.83	-0.0041	-2.5	4.79	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
4873	dirMS_041712_NAR_60mM_plus.8380.8383.3	3	13.25	1	2.51E+05		(R)TERFGQ	(R)T E R F G Q\G G\A|G|P/V\G/G Q G P R(G)		101.95	576.6232	1727.857	-0.0022	-1.2	9.26	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
4874	dirMS_041712_NAR_120mM_minus.14880.14880.3	3	13.24	0	3.67E+05		(K)HLEINPD	(K)H L|E I N/P D\H|P/I V E T\L R(Q)		135.25	594.9872	1782.95	-0.0027	-1.5	5.27	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
4875	dirMS_041712_NAR_120mM_minus.15278.15427.3	3	13.24	2	9.57E+05		(R)ALKDEEI	(R)A L|K|D E/E/K M E/L/Q|E|I Q L/K(E)		137.72	649.0139	1945.031	-0.0039	-2	4.58	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
4876	dirMS_041712_NAR_120mM_minus.8498.8498.3	3	13.24	1	4.31E+05		(R)YLAEVA'	(R)Y/L/A E V A/T G E/K R(A)		100.85	412.8849	1236.658	-0.0181	-14.7	6.14	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
4877	dirMS_041712_NAR_50mM_minus2.11680.11680.3	3	13.24	0	3.27E+04	M425m M4	(R)VFITDDF	(R)V/F/I/T/D D/F H D m m/P K(Y)	m:Oxidized methionine	134.58	543.2416	1595.723	31.987	-1.7	4.41	92752.5	4.76	HUMAN	P14625	Endoplasmin
4878	dirMS_041712_NAR_50mM_minus2.15082.15082.3	3	13.24	1	1.11E+06		(R)DVDFELI	(R)D V|D F/E/L/I K V E G K(V)		154	464.5852	1391.742	-0.0006	-0.4	4.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
4879	dirMS_041712_NAR_50mM_minus2.19058.19066.3	3	13.24	1	1.34E+06		(R)KEGGLG	(R)K E G G L G P L N\I|P/L|L/A D V T R(R)		187.5	621.6941	1863.07	-0.0021	-1.1	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
4880	dirMS_041712_NAR_60mM_minus.18486.18486.3	3	13.24	1	1.29E+05		(R)RFDEILE	(R)R F D E\I\L\E|A/S D/G\I/M V A R(G)		164.42	607.9739	1821.916	-0.0092	-5.1	4.32	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
4881	dirMS_041712_NAR_60mM_minus.6653.6653.3	3	13.24	0	4.07E+04		(K)VDCTAH	(K)V D/C T A/H S D V/C/S/A/Q G V R(G)	C:Carbamidomethylation	95.73	587.9248	1761.764	-0.0044	-2.5	5.21	41053.3	5.58	HUMAN	Q86UY0	TXNDC5 protein
4882	dirMS_041712_NAR_120mM_plus.8301.8319.2	2	13.24	1	1.05E+06		(R)KVIDDTI	(R)K|V|I|D|D/T N\I/T/R(L)		97.03	587.8203	1174.643	-0.0093	-7.9	5.96	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4883	dirMS_041712_NAR_20mM_plus.12304.12304.2	2	13.24	0	1.37E+05		(R)GVEICIA	(R)G V/E\I/C/I/A/T|P G R(L)	C:Carbamidomethylation	158.27	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
4884	dirMS_041712_NAR_20mM_plus.17702.17702.2	2	13.24	0	1.91E+05		(R)YISPDQL	(R)Y I|S/P D Q/L A D/L Y/K(S)		194.18	713.3667	1425.726	0.0001	0.1	4.21	47510.4	7.04	HUMAN	P06733	Alpha-enolase
4885	dirMS_041712_NAR_20mM_plus.18101.18101.2	2	13.24	0	1.13E+05		(K)LVLPSLI!	(K)L/V|L/P S L I|S S/R(I)		196.6	542.8388	1084.672	-0.0021	-2	9.75	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
4886	dirMS_041712_NAR_30mM_plus2.15236.15236.2	2	13.24	0	1.49E+05		(K)AFQNVF	(K)A F|Q|N|V|F A/P/R(N)		132.4	525.2819	1049.553	0.0038	3.7	9.79	60786.2	8.94	HUMAN	B4DYH8	N-acetylglucosamine-6-sulfatase
4887	dirMS_041712_NAR_30mM_plus2.15486.15486.2	2	13.24	0	4.18E+05		(R)MAGAIA	(R)M/A/G\A/I/A/Q/G L I R(A)		133.57	550.816	1100.624	0.0002	0.2	9.5	4449.1	11.42	HUMAN	F8WEI0	Pyrroline-5-carboxylate reductase 3
4888	dirMS_041712_NAR_30mM_plus2.20136.20136.2	2	13.24	0	1.49E+05		(K)TVALWD	(K)T V/A|L/W/D L/R(N)		159.03	487.2769	973.547	0	0	5.5	19598	4.45	HUMAN	B4DRT0	Histone-binding protein RBBP4
4889	dirMS_041712_NAR_50mM_plus2.18201.18201.3	3	13.24	1	1.60E+06		(R)ELIKVLEI	(R)E L I K V L\E E A/N/Q/A\I/N/P K(L)		163.67	603.6741	1809.012	-0.0039	-2.2	4.79	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
4890	dirMS_041712_NAR_60mM_plus.9413.9434.3	3	13.24	1	6.18E+05		(R)LTYEIED	(R)L/T|Y/E/I/E D E K R(R)		107.38	432.5543	1295.648	0.0006	0.4	4.41	334221.3	6.44	HUMAN	P15924	Desmoplakin
4891	dirMS_041712_NAR_30mM_minus2.17041.17205.2	2	13.23	0	3.12E+05		(R)LLNTFLE	(R)L/L|N/T/F\L/E|R(L)		146.72	503.2871	1005.573	-0.0058	-5.8	6	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
4892	dirMS_041712_NAR_30mM_minus2.7280.7280.2	2	13.23	0	2.62E+05		(K)DAQGQI	(K)D A|Q/G Q|P\G L E R(A)		93.63	535.762	1070.523	-0.0058	-5.4	4.37	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
4893	dirMS_041712_NAR_50mM_minus2.12623.12623.3	3	13.23	0	1.09E+06	M114m M:	(R)AGKPVI(	(R)A G K|P V\I/C\A\T/Q/m|L E/S m I K(K)	C:Carbamidomethylation m:Oxid	139.87	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
4894	dirMS_041712_NAR_50mM_minus2.14137.14137.3	3	13.23	1	1.67E+06		(R)ELISNAS	(R)E L|I/S N/A S/D\A L D K I R(L)		148.03	515.6179	1544.828	0.0113	7.3	4.56	5582.4	4.81	HUMAN	F8W026	Endoplasmin (Fragment)
4895	dirMS_041712_NAR_50mM_minus2.8677.8677.3	3	13.23	0	1.65E+05	M180m	(R)VVVLm(	(R)V V/V/L/m/G S/T S D L G H C E K(I)	C:Carbamidomethylation m:Oxid	117.55	583.2829	1731.84	15.9937	-0.7	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
4896	dirMS_041712_NAR_60mM_minus.10600.10600.3	3	13.23	0	2.57E+05		(R)SVIHSLA	(R)S V/I H/S L/A|S V/E A Q K(S)		119.02	456.9195	1368.748	-0.0042	-3.1	6.47	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
4897	dirMS_041712_NAR_60mM_minus.15359.15359.2	2	13.23	0	3.82E+05		(R)EHALLA'	(R)E H/A|L|L/A/Y/T L G\V K(Q)		144.73	657.873	1314.742	-0.0029	-2.2	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
4898	dirMS_041712_NAR_60mM_minus.16755.16755.3	3	13.23	1	4.77E+04		(K)ALQFLEE	(K)A L|Q/F/L E E\V/K/V S/R(E)		152.85	473.6009	1418.8	-0.012	-8.5	6.19	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
4899	dirMS_041712_NAR_20mM_plus.13821.13821.2	2	13.23	0	2.90E+04		(K)TGAAPII	(K)T G|A|A/P I I/D V V R(S)		167.35	556.3256	1111.647	-0.0031	-2.8	5.5	10240.9	10.46	HUMAN	E9PJD9	60S ribosomal protein L27a
4900	dirMS_041712_NAR_20mM_plus.19063.19063.2	2	13.23	0	5.75E+04		(K)ILTFDQL	(K)I L/T\F/D Q\L|A\L D S\P K(G)		202.35	730.9063	1460.8	0.0058	4	4.21	14643	11.93	HUMAN	F8VUA6	60S ribosomal protein L18 (Fragment)

4901	dirMS_041712_NAR_30mM_plus2.13660.13682.2	2	13.23	0	5.27E+05		(K)VSIYEA	(K)V/S|I/Y/E/A M/R(R)		124.8	484.7469	968.487	-0.0005	-0.5	5.97	533778	5.74	HUMAN	Q15149	Plectin
4902	dirMS_041712_NAR_30mM_plus2.21891.21891.2	2	13.23	0	8.17E+04		(K)GLVQAL	(K)G L V/Q/A|L/G/L/S N F/N S R(Q)		169.73	738.3989	1475.796	-0.006	-4.1	9.75	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
4903	dirMS_041712_NAR_30mM_plus2.7180.7267.2	2	13.23	0	1.70E+06		(K)TEISEM	(K)T|E|I|S/E/M N R(N)		92.85	490.2294	979.451	0.0002	0.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
4904	dirMS_041712_NAR_50mM_plus2.15777.15792.3	3	13.23	0	1.18E+05		(K)GQYFGE	(K)G Q|Y/F/G E L/A/L/V/T N K P R(A)		151.15	564.9788	1692.907	0.0151	8.9	8.59	10305.6	6.94	HUMAN	H7C330	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
4905	dirMS_041712_NAR_60mM_plus.6353.6353.3	3	13.23	0	9.24E+04		(R)HNGAA	(R)H N\G A\A\E|P/E|P E A/E\T A R(G)		91.8	526.9106	1578.714	0.003	1.9	4.48	87537	9.67	HUMAN	Q9Y446	Plakophilin-3
4906	dirMS_041712_NAR_60mM_plus.9945.9981.3	3	13.23	1	4.99E+05		(R)GSNMD	(R)G S/N|M/D/F/R E/P T E E E/R(A)		109.93	566.2455	1696.723	-0.0012	-0.7	4.25	27441.6	6.68	HUMAN	Q15056	Eukaryotic translation initiation factor 4H
4907	dirMS_041712_NAR_20mM_minus.10770.10770.2	2	13.22	0	4.20E+05		(K)DVNAAI	(K)D V|N/A/A I/A/A I/K(T)		155.98	493.287	985.568	-0.0009	-1	5.84	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
4908	dirMS_041712_NAR_20mM_minus.9753.9753.2	2	13.22	0	1.57E+05		(K)LSELEPG	(K)L S/E|L|E|P G T G\D L R(F)		147.78	643.8318	1286.659	-0.0023	-1.8	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
4909	dirMS_041712_NAR_40mM_minus2.10982.10982.3	3	13.22	0	4.88E+05		(R)DAGEGL	(R)D A|G\E/G L/L A V Q I T D Q E/G K/P K(R)		147.97	657.0157	1969.024	0.0089	4.5	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
4910	dirMS_041712_NAR_40mM_minus2.12011.12011.3	3	13.22	1	5.22E+03		(R)IINEPTA	(R)I I/N E/P/T A A A I/A/Y G L D K R(E)		153.6	606.0008	1815.996	-0.0085	-4.7	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
4911	dirMS_041712_NAR_50mM_minus2.13264.13264.3	3	13.22	0	1.69E+05		(K)MLDAE	(K)M/L|D/A\E D I V/G T A R P D E K(A)		143.52	587.2894	1759.853	0.0006	0.3	4.1	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
4912	dirMS_041712_NAR_50mM_minus2.15951.15951.3	3	13.22	1	8.21E+04		(K)DANAKL	(K)D A/N A K L S E\L|E|A/A/L/Q R(A)		158.97	543.6248	1628.86	-0.0004	-0.2	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
4913	dirMS_041712_NAR_50mM_minus2.8454.8454.3	3	13.22	1	1.45E+05		(K)LTSDDV	(K)L/T/S/D/D/V K/E Q I Y/K(L)		115.95	480.252	1438.742	-0.001	-0.7	4.56	12573.5	10.39	HUMAN	E9PS50	40S ribosomal protein S13 (Fragment)
4914	dirMS_041712_NAR_20mM_plus.17537.17537.2	2	13.22	0	1.61E+05	M74m	(R)mIAGQ	(R)m I\A|G Q|V|L D I N L A A E|P K(V)	m:Oxidized methionine	192.85	849.9568	1682.915	15.9918	-1.9	4.37	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
4915	dirMS_041712_NAR_30mM_plus2.16803.16803.2	2	13.22	0	4.21E+05		(K)GCSFLP	(K)G C\S/F/L|P D/P Y Q K(Q)	C:Carbamidomethylation	140.9	656.306	1311.604	0.0009	0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
4916	dirMS_041712_NAR_30mM_plus2.21621.21660.2	2	13.22	0	3.17E+05		(R)FSWNV	(R)F/S/W|N|V W|P S S R(L)		169.12	633.3085	1265.606	0.0035	2.8	9.75	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
4917	dirMS_041712_NAR_30mM_plus2.22244.22282.2	2	13.22	0	1.08E+06		(K)IGFPWS	(K)I/G/F|P/W/S E I R(N)		173.1	552.8032	1104.584	0.0155	14	6	71218.8	6.3	HUMAN	A7YIJ8	Radixin
4918	dirMS_041712_NAR_30mM_plus2.5795.6002.2	2	13.22	0	6.94E+05		(R)EMEEQ	(R)E M|E/E/Q/M/R(R)		85.55	476.6984	952.386	0.0032	3.4	4.25	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
4919	dirMS_041712_NAR_50mM_plus2.14314.14314.3	3	13.22	1	8.83E+05		(K)ATLPSP	(K)A T|L/P/S/P D K L P G F K(M)		143.57	457.5906	1370.768	-0.0106	-7.7	8.64	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
4920	dirMS_041712_NAR_120mM_minus.11517.11578.4	4	13.21	0	1.81E+05		(R)TGVELG	(R)T G V/E/L/G K/P T H/F T V N A K(A)		117.05	425.4844	1698.917	-0.0016	-0.9	8.29	283472.4	5.71	HUMAN	P21333	Filamin-A
4921	dirMS_041712_NAR_30mM_minus2.10395.10640.2	2	13.21	0	8.52E+05		(K)YETELA	(K)Y/E|T|E L/A/M/R(Q)		111.27	506.7468	1012.477	0.0095	9.4	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4922	dirMS_041712_NAR_30mM_minus2.19111.19111.2	2	13.21	0	1.94E+05		(K)MAILQI	(K)M/A/I|L Q I M K(E)		158.5	474.2745	947.542	0.0001	0.1	8.5	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
4923	dirMS_041712_NAR_50mM_minus2.14712.14712.3	3	13.21	1	2.98E+05		(R)EAVTEIL	(R)E A V/T/E/I L/G I E/P D R E K(G)		152.25	566.9683	1698.891	-0.0005	-0.3	4.25	25685.9	6.4	HUMAN	E9PGT1	Translin
4924	dirMS_041712_NAR_50mM_minus2.14903.14904.3	3	13.21	1	1.69E+05		(R)ALASQL	(R)A L|A|S/Q L/Q D S L K D/L K(A)		152.8	510.6213	1529.853	-0.004	-2.6	6	124367.7	5.51	HUMAN	P18206	Vinculin
4925	dirMS_041712_NAR_50mM_minus2.17774.17774.3	3	13.21	1	2.31E+05		(K)LALFQAI	(K)L/A L/F Q A I/G/K/E V/V D R(A)		170.53	520.3043	1558.895	0.0032	2	6.07	266161	5.68	HUMAN	E9PPU0	Epiplakin
4926	dirMS_041712_NAR_60mM_minus.6677.6677.3	3	13.21	1	7.84E+04		(R)VVSSIE	(R)V/V|S S I/E Q K T E G A E K(K)		96.13	502.2642	1504.785	-0.0073	-4.8	4.79	8491.4	6.28	HUMAN	E5RIR4	14-3-3 protein zeta/delta (Fragment)
4927	dirMS_041712_NAR_20mM_plus.10506.10506.3	3	13.21	0	2.60E+05		(R)AQIFAN	(R)A Q\I F A N T/V/D/N A/R(I)		145.25	440.5608	1319.67	-0.0024	-1.8	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4928	dirMS_041712_NAR_20mM_plus.18103.18116.3	3	13.21	0	1.36E+05		(R)AILVDLE	(R)A I\L\V D L E/P/G T/M D S V/R(S)		196.55	539.2833	1615.836	-0.0006	-0.4	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
4929	dirMS_041712_NAR_30mM_plus2.12039.12039.2	2	13.21	0	1.99E+05		(R)VFNETPI	(R)V F/N E|T/P I N/P R(K)		116.15	593.8147	1186.622	0.0006	0.5	5.97	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
4930	dirMS_041712_NAR_30mM_plus2.19411.19411.2	2	13.21	0	1.85E+04		(K)MNEFLE	(K)M/N/E/F/L/E/N F/E K(N)		155.87	650.7974	1300.588	-0.0003	-0.2	4.25	28580.2	9.35	HUMAN	Q9UFN0	Protein NipSnap homolog 3A
4931	dirMS_041712_NAR_30mM_plus2.19620.19761.2	2	13.21	0	3.95E+05		(K)SNNVE	(K)S N|N|V|E/M\D W V/L K(H)		156.78	667.8205	1334.641	-0.0072	-5.4	4.37	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
4932	dirMS_041712_NAR_30mM_plus2.19740.19740.2	2	13.21	0	3.55E+05		(K)SNNVE	(K)S N|N|V|E M D\W V/L|K(H)		156.9	667.8205	1334.641	-0.0072	-5.4	4.37	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
4933	dirMS_041712_NAR_40mM_plus2.16346.16408.3	3	13.21	1	3.74E+05		(R)CITDPQ	(R)C\I|T/D/P Q T G\L C/L L/P/L K E K(K)	C:Carbamidomethylation	163.12	662.6815	1986.04	-0.0099	-5	6.07	533778	5.74	HUMAN	Q15149	Plectin
4934	dirMS_041712_NAR_30mM_minus2.15534.15534.2	2	13.2	0	3.29E+04		(K)FLMAN	(K)F/L|M|A/N G/Q L V\K(M)		138.07	560.8108	1120.618	-0.004	-3.6	8.75	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
4935	dirMS_041712_NAR_40mM_minus2.12956.12956.3	3	13.2	0	1.54E+05		(K)GVTIIGP	(K)G V T|I/I/G/P A T/V/G G I K P G C F\K(I)	C:Carbamidomethylation	159.62	624.6828	1872.041	-0.0073	-3.9	10	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
4936	dirMS_041712_NAR_50mM_minus2.14899.14946.3	3	13.2	1	2.76E+05		(K)NIYVLQ	(K)N I|Y|V|L Q/E L D/N P G A K R(I)		152.62	577.3116	1729.923	-0.0029	-1.7	6.07	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
4937	dirMS_041712_NAR_120mM_plus.21575.21575.4	4	13.2	2	4.41E+05	M145m	(R)RGVmL	(R)R\G V\m\L A|V/D/A V/I A E L K/K(Q)	m:Oxidized methionine	166.23	433.0059	1713.009	15.9926	-1.3	8.59	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
4938	dirMS_041712_NAR_20mM_plus.17770.18014.2	2	13.2	0	2.21E+05		(R)SLVPAA	(R)S L|V|P A A/E L|L/E S R(V)		194.8	642.8613	1284.716	-0.0005	-0.4	4.53	533778	5.74	HUMAN	Q15149	Plectin
4939	dirMS_041712_NAR_30mM_plus2.14612.14756.2	2	13.2	0	5.66E+05		(K)IAWALS	(K)I/A|W|A/L/S/R(K)		129.9	408.7395	816.473	-0.0009	-1.1	9.75	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
4940	dirMS_041712_NAR_30mM_plus2.16024.16024.2	2	13.2	0	1.46E+06		(R)MGAG	(R)M/G|A|G\M|G F/G L E R(M)		137.42	563.2636	1125.518	0.002	1.7	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
4941	dirMS_041712_NAR_30mM_plus2.21420.21550.2	2	13.2	0	3.50E+05		(K)FDGILG	(K)F D/G|I|L|G M/A Y P R(I)		167.42	620.3199	1239.619	0.0135	10.9	5.83	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
4942	dirMS_041712_NAR_60mM_plus.18638.18638.3	3	13.2	1	6.36E+05		(R)IRIDSLS	(R)I R I D S L\S\A\Q|L/S Q/L Q K(Q)		154.55	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
4943	dirMS_041712_NAR_60mM_plus.19846.19854.3	3	13.2	1	1.10E+06		(K)SLLGKD	(K)S/L|L/G K D V/L\F/L/K(D)		163.93	411.5915	1232.761	-0.0013	-1.1	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
4944	dirMS_041712_NAR_60mM_plus.20129.20287.3	3	13.2	0	4.68E+05		(R)DFLLKP	(R)D F|L/L/K/P E L L/R(A)		165.73	415.2483	1243.741	-0.0105	-8.5	6.07	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
4945	dirMS_041712_NAR_120mM_minus.9752.9776.3	3	13.19	1	4.02E+05		(K)YAGKDG	(K)Y/A|G K/D G Y N|Y/T/L/S K(T)		107.67	493.9089	1479.711	0.0007	0.5	8.38	11854.4	6.57	HUMAN	P31949	Protein S100-A11
4946	dirMS_041712_NAR_30mM_minus2.16074.16074.2	2	13.19	0	2.24E+04		(K)SEGGFI	(K)S E|G G/F/I/W A/C K(N)	C:Carbamidomethylation	141.03	577.7702	1154.53	0.0032	2.8	5.72	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
4947	dirMS_041712_NAR_30mM_minus2.8517.8726.2	2	13.19	0	1.64E+07		(R)QLETLG	(R)Q\L|E/T/L/G Q/E/K(L)		101.52	523.2783	1045.552	-0.0031	-3	4.53	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
4948	dirMS_041712_NAR_40mM_minus2.12585.12585.3	3	13.19	1	5.98E+05		(R)VCENIP	(R)V/C|E N|I/P I V L C G N K V D|I K(D)	C:Carbamidomethylation	157.7	657.6842	1971.04	-0.0021	-1.1	6.04	14844.8	5.89	HUMAN	B4DV51	GTP-binding nuclear protein Ran
4949	dirMS_041712_NAR_50mM_minus2.8778.8778.3	3	13.19	1	1.53E+05		(K)SPFEVS	(K)S/P|F E V S V D/K|A Q/G D\A/S K(V)		117.75	555.6099	1664.813	0.0025	1.5	4.56	258215.9	5.48	HUMAN	E7EN95	Filamin-B
4950	dirMS_041712_NAR_60mM_minus.6578.6578.3	3	13.19	0	9.81E+04		(K)CIGKPG	(K)C I/G K/P G/G S L/D N/S E Q/K(C)	C:Carbamidomethylation	95.25	530.5892	1589.759	-0.0057	-3.6	6.07	9122.2	9.22	HUMAN	K7EIT2	Mitochondrial import inner membrane translocase subunit Tim13
4951	dirMS_041712_NAR_120mM_plus.16832.16949.4	4	13.19	0	1.91E+06		(K)HLEINP	(K)H L\E\I\N|P D H\S\I\I/E/T L/R(Q)		141.77	447.491	1786.945	-0.0025	-1.4	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
4952	dirMS_041712_NAR_20mM_plus.10651.10651.2	2	13.19	0	6.78E+04		(K)VLQLYP	(K)V/L|Q/L|Y/P N N/K(A)		145.98	544.8057	1088.61	-0.0057	-5.3	8.56	9740.1	10.08	HUMAN	H0YFG2	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed (Fragment)
4953	dirMS_041712_NAR_20mM_plus.13539.13539.2	2	13.19	0	1.58E+05	M98m	(R)TLTIVDT	(R)T L|T I|V/D T/G\I G m/T K(A)	m:Oxidized methionine	165.82	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
4954	dirMS_041712_NAR_20mM_plus.18394.18394.2	2	13.19	0	1.95E+05		(R)AAVEEG	(R)A A V E E|G/I|V\L\G/G/G C A\L L/R(C)	C:Carbamidomethylation	197.9	842.9549	1684.905	-0.0025	-1.5	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
4955	dirMS_041712_NAR_30mM_plus2.15880.15880.2	2	13.19	0	3.21E+05		(R)YSVDIPL	(R)Y/S|V/D/I/P/L D K(T)		136.13	525.2819	1049.551	0.0052	4.9	4.21	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
4956	dirMS_041712_NAR_30mM_plus2.21832.21832.2	2	13.19	0	8.73E+04		(K)GLVQAL	(K)G L V Q/A L|G/L/S/N F N S R(Q)		169.57	738.3989	1475.796	-0.006	-4.1	9.75	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
4957	dirMS_041712_NAR_30mM_plus2.7528.7562.2	2	13.19	0	7.19E+05		(K)AQYEDI	(K)A Q|Y|E/D/I/A/Q/K(S)		93.8	533.2595	1065.521	-0.0094	-8.8	4.37	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
4958	dirMS_041712_NAR_50mM_plus2.11463.11463.3	3	13.19	0	4.76E+05		(R)LLELGP	(R)L L/E/L/G/P K/P E V A Q Q T R(K)		128.13	560.3195	1678.949	-0.0047	-2.8	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
4959	dirMS_041712_NAR_50mM_plus2.12912.12931.3	3	13.19	1	3.89E+05		(K)LAEIGA	(K)L/A/E|I/G A/P I/Q G/N R E E L V E R(L)		135.98	665.3593	1994.066	-0.0032	-1.6	4.49	38572.2	6.31	HUMAN	E9PJ04	Splicing factor 3B subunit 2 (Fragment)
4960	dirMS_041712_NAR_50mM_plus2.17282.17282.3	3	13.19	0	7.92E+05		(K)VLISSLQ	(K)V/L|I/S/S L/Q D C L H G I E S K(S)	C:Carbamidomethylation	159.25	600.3189	1798.937	0.0054	3	5.32	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
4961	dirMS_041712_NAR_50mM_plus2.22253.22253.3	3	13.19	1	1.35E+06		(K)EGGLGP	(K)E/G G L/G/P/L/N I P L L A D V T R R(L)		191	631.029	1891.076	-0.0035	-1.9	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
4962	dirMS_041712_NAR_50mM_plus2.9164.9323.3	3	13.19	1	1.16E+06		(K)TAVCDI	(K)T/A|V|C/D/I/P P R G L K(M)	C:Carbamidomethylation	116.32	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
4963	dirMS_041712_NAR_30mM_minus2.16718.16718.3	3	13.18	0	7.00E+05		(R)ASLEAA	(R)A S L E A A\I|A/D/A/E/Q R(G)		144.35	448.8965	1344.675	-0.0004	-0.3	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
4964	dirMS_041712_NAR_30mM_minus2.6240.6240.2	2	13.18	0	5.09E+04		(R)SAENPP	(R)S A/E N|P/P S/G S V|R(K)		87.98	550.7684	1100.533	-0.0036	-3.2	5.72	32364.3	9.76	HUMAN	Q15014	Mortality factor 4-like protein 2
4965	dirMS_041712_NAR_40mM_minus2.6003.6003.2	2	13.18	0	1.06E+06		(K)AGFAG	(K)A/G/F/A/G|D D/A/P R(A)		98.45	488.7279	976.448	0.0002	0.2	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
4966	dirMS_041712_NAR_50mM_minus2.10801.10801.3	3	13.18	1	2.51E+05		(K)NQVAM	(K)N Q/V/A\M/N/P T N/T V/F/D A K/R(L)		129.32	602.6379	1805.896	0.0029	1.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
4967	dirMS_041712_NAR_50mM_minus2.12335.12392.3	3	13.18	0	2.81E+05		(K)QLTEED	(K)Q L/T/E/E/D/G V H/S V/I E E N I K(C)		138.65	647.3249	1939.961	-0.0006	-0.3	4.25	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
4968	dirMS_041712_NAR_50mM_minus2.7108.7125.3	3	13.18	1	6.97E+04	M1489m	(R)ALEEAm	(R)A/L|E/E/A/m E Q K/A E/L E R(L)	m:Oxidized methionine	107.35	554.9379	1646.805	15.9937	-0.7	4.33	227783.5	5.5	HUMAN	P35579	Myosin-9
4969	dirMS_041712_NAR_50mM_minus2.9051.9051.3	3	13.18	1	1.29E+05	M88m	(K)DVDEAY	(K)D V/D\E A Y/m N K V/E/L/E/S/R(L)	m:Oxidized methionine	119.57	605.2817	1797.832	15.9982	1.8	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
4970	dirMS_041712_NAR_60mM_minus.18580.18580.3	3	13.18	0	2.58E+05		(R)DFLLKP	(R)D F|L L/K/P E L L/R(A)		165.43	415.25	1243.741	-0.0054	-4.4	6.07	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
4971	dirMS_041712_NAR_60mM_minus.9697.9697.3	3	13.18	0	3.48E+05		(R)QLSQAG	(R)Q L/S/Q/A/G/S/F S D/G T H G G L R(Y)		113.6	573.2781	1717.825	-0.0055	-3.2	6.74	266161	5.68	HUMAN	E9PPU0	Epiplakin
4972	dirMS_041712_NAR_20mM_plus.12785.12785.2	2	13.18	0	2.85E+04	M92m	(R)ImNTFS	(R)I/m|N\T/F S V V/P S/P K(V)	m:Oxidized methionine	160.95	668.3516	1319.703	15.9931	-1.3	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
4973	dirMS_041712_NAR_20mM_plus.8082.8082.2	2	13.18	0	4.16E+05	M239m	(K)EVDEQ	(K)E V/D/E/Q/m L/N V/Q/N/K(N)	m:Oxidized methionine	125.1	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
4974	dirMS_041712_NAR_40mM_plus2.10095.10095.2	2	13.18	0	1.20E+05		(R)YSGSYN	(R)Y/S/G S Y/N D/Y/L/R(A)		123.83	619.2788	1237.548	0.0019	1.6	5.83	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
4975	dirMS_041712_NAR_50mM_plus2.11401.11479.3	3	13.18	0	3.26E+05		(K)VFEGNR	(K)V/F|E/G N R P T N S I V F/T/K(L)		127.97	570.3045	1708.902	-0.0027	-1.6	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
4976	dirMS_041712_NAR_50mM_plus2.20122.20122.3	3	13.18	0	2.56E+05		(R)LQSLPF	(R)L Q S\L/P F/A/L/T/H L N L K(A)		173.95	532.3178	1594.931	0.0073	4.6	8.76	175851.7	5.01	HUMAN	Q14160	Protein scribble homolog
4977	dirMS_041712_NAR_50mM_plus2.8975.9008.3	3	13.18	1	3.16E+05		(K)VLLQSK	(K)V/L|L|Q/S/K D Q I/T A/G N A A R(K)		114.58	562.315	1684.934	-0.0036	-2.1	8.72	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
4978	dirMS_041712_NAR_20mM_minus.13125.13125.2	2	13.17	0	4.63E+05		(K)TITLEVE	(K)T I/T L/E/V/E/P S D T I E N V K(A)		183.05	894.4654	1787.927	-0.0038	-2.1	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
4979	dirMS_041712_NAR_40mM_minus2.13930.13930.3	3	13.17	0	5.98E+04		(R)LLAEIGA	(R)L L/A/E/I/G\A V\T L V S A P R P D|S R(H)		165.87	655.7064	1965.113	-0.0081	-4.1	6.07	27279.2	9.51	HUMAN	A9C4B9	tRNA splicing endonuclease 34 homolog (S. cerevisiae) (Fragment)
4980	dirMS_041712_NAR_60mM_minus.11735.11735.3	3	13.17	1	4.61E+05	M232m	(R)MSmKE	(R)M S m K E V\D\E\Q|M/L/N/V/Q/N K(N)	m:Oxidized methionine	125.58	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
4981	dirMS_041712_NAR_20mM_plus.15460.15581.2	2	13.17	0	3.47E+05		(K)VGINYQ	(K)V G I N Y|Q|P/P T V/V|P G G D L A K(V)		179.05	912.9952	1824.985	-0.0023	-1.3	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
4982	dirMS_041712_NAR_20mM_plus.17873.17873.2	2	13.17	0	1.62E+05		(R)TVQSLE	(R)T V\Q/S\L|E/I D L/D/S M R(N)		194.9	753.8776	1506.747	0.0011	0.7	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4983	dirMS_041712_NAR_20mM_plus.8348.8348.2	2	13.17	0	1.32E+04		(R)LAAVDV	(R)L A|A V/D V/S A R(A)		127.57	451.2557	901.51	-0.006	-6.7	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin
4984	dirMS_041712_NAR_30mM_plus2.18063.18063.2	2	13.17	0	2.28E+05		(R)QITLND	(R)Q I/T L|N/D/L/P V G R(S)		147.85	613.3465	1225.69	-0.0042	-3.4	5.84	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
4985	dirMS_041712_NAR_40mM_plus2.11228.11228.3	3	13.17	0	1.02E+05		(R)VLVASS	(R)V/L|V/A/S S/V V A G E/S Q K P E L K(A)		132.1	614.3443	1841.038	-0.0195	-10.6	6.11	61441.6	5.93	HUMAN	G8JLE9	Fragile X mental retardation protein 1
4986	dirMS_041712_NAR_50mM_plus2.9520.9520.3	3	13.17	1	1.58E+05		(R)LGGSPF	(R)L/G/G/S|P F/G/P\A G T G K T E S V K(A)		117.22	563.9657	1689.881	0.0019	1.1	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
4987	dirMS_041712_NAR_60mM_plus.11741.11741.3	3	13.17	0	4.34E+06		(K)TGNLGN	(K)T/G|N|L/G N V/V/H I E R(F)		119.1	436.9042	1308.702	-0.0038	-2.9	6.41	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
4988	dirMS_041712_NAR_120mM_minus.10524.10524.3	3	13.16	1	1.73E+06		(R)VKYETE	(R)V K Y E T\E|L/A M/R(Q)		111.65	413.885	1239.64	0.0003	0.2	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4989	dirMS_041712_NAR_40mM_minus2.6706.6706.2	2	13.16	0	4.17E+05		(R)LASYLD	(R)L/A|S|Y L D R(V)		108.32	419.2267	837.447	-0.0004	-0.4	5.83	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
4990	dirMS_041712_NAR_60mM_minus.17034.17034.3	3	13.16	1	2.71E+05	M182m	(R)GmLRE	(R)G m/L/R E D/A\V|L/E/Y L/K(I)	m:Oxidized methionine	154.97	518.2737	1536.809	15.9975	1.7	4.68	67933	6.08	HUMAN	P26038	Moesin
4991	dirMS_041712_NAR_30mM_plus2.13619.13843.2	2	13.16	0	3.70E+06		(K)DVNAA	(K)D V|N|A|A|I/A/T I K(T)		125.07	508.2931	1015.578	0.0007	0.7	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
4992	dirMS_041712_NAR_50mM_plus2.11674.11674.3	3	13.16	1	1.31E+05		(K)IGRIEDV	(K)I/G R I E D V T|P/I|P S D/S T R(R)		128.73	585.9784	1755.924	-0.0029	-1.7	4.56	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
4993	dirMS_041712_NAR_50mM_plus2.15523.15635.3	3	13.16	1	2.34E+05		(R)AEGAIA	(R)A/E|G A/I/A/G F R D/P F S G/K(Q)		150.1	508.2614	1522.765	0.0048	3.1	6.12	266161	5.68	HUMAN	E9PPU0	Epiplakin
4994	dirMS_041712_NAR_120mM_minus.10682.10682.3	3	13.15	0	7.82E+05		(R)GFCLPP	(R)G F/C|L/P/P H/C S R(G)	C:Carbamidomethylation	113.4	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
4995	dirMS_041712_NAR_30mM_minus2.15744.15841.2	2	13.15	0	4.68E+04		(R)INEILSN	(R)I/N|E|I|L/S N A L K(R)		139.15	557.8242	1114.647	-0.0055	-5	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
4996	dirMS_041712_NAR_120mM_plus.6665.6688.2	2	13.15	0	3.07E+05		(R)SHEGET	(R)S/H|E|G E/T\A|Y I/R(V)		88.3	581.7777	1162.549	-0.0006	-0.5	5.38	16510	11.51	HUMAN	J3KSR8	Serine/arginine-rich-splicing factor 1 (Fragment)
4997	dirMS_041712_NAR_20mM_plus.6880.6880.2	2	13.15	0	4.06E+05	M132m	(R)DmVGIA	(R)D m|V|G\I/A Q/T G S G K(T)	m:Oxidized methionine	112.88	590.2864	1163.573	15.993	-1.6	5.84	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
4998	dirMS_041712_NAR_30mM_plus2.13935.13935.2	2	13.15	0	1.87E+05		(K)NFGIGQ	(K)N F|G|I/G Q D I Q/P K(R)		126.08	608.8192	1216.632	-0.0009	-0.8	5.84	30166.2	10.79	HUMAN	P62424	60S ribosomal protein L7a
4999	dirMS_041712_NAR_50mM_plus2.9809.9809.3	3	13.15	1	2.54E+05		(K)TTDMA	(K)T/T/D/M/A/P S K/E T E M A L A K(D)		119.22	575.2802	1723.824	0.0019	1.1	4.68	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
5000	dirMS_041712_NAR_60mM_plus.10226.10226.2	2	13.15	0	2.03E+06		(K)GIVEFS	(K)G I/V/E|F S G K/P A A/R(K)		111.3	616.3425	1231.679	-0.0016	-1.3	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
5001	dirMS_041712_NAR_60mM_plus.10733.11022.3	3	13.15	1	2.15E+06		(R)KLDPGS	(R)K\L D\P G S|E\E|T/Q/T/L/V/R(E)		114.92	524.9456	1572.823	-0.0005	-0.3	4.68	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
5002	dirMS_041712_NAR_60mM_plus.16809.17174.3	3	13.15	1	2.15E+05		(K)YMACCL	(K)Y/M|A/C/C/L L Y R G D|V V/P K(E)	C:Carbamidomethylation	145.85	615.6325	1844.886	-0.0026	-1.4	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
5003	dirMS_041712_NAR_50mM_minus2.15655.15655.3	3	13.14	1	2.43E+05		(K)DVLFLK	(K)D V|L/F/L K D C V/G P E V E/K(A)	C:Carbamidomethylation	156.48	583.3014	1747.893	-0.0039	-2.2	4.32	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
5004	dirMS_041712_NAR_60mM_minus.16850.16953.3	3	13.14	1	3.95E+05		(R)ARFEEL	(R)A R F E E\L|N|A|D/L/F R(G)		153.98	494.2594	1480.754	0.0093	6.3	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
5005	dirMS_041712_NAR_20mM_plus.7622.7622.2	2	13.14	0	1.57E+05		(K)IAVAAQ	(K)I/A|V/A/A Q/N/C/Y K(V)	C:Carbamidomethylation	122.43	569.2902	1137.572	0.001	0.9	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
5006	dirMS_041712_NAR_30mM_plus2.10028.10043.2	2	13.14	0	2.67E+05		(R)IGLIQG	(R)I/G|L|I/Q/G N R(V)		105.97	435.7618	870.516	0.0007	0.9	9.75	18719.9	6.91	HUMAN	F8VP00	6-phosphofructokinase, muscle type (Fragment)
5007	dirMS_041712_NAR_30mM_plus2.10802.10867.2	2	13.14	0	2.91E+05		(R)MVEGY	(R)M/V|E|G Y/Q/G L/R(C)		110.07	526.7621	1052.519	-0.0024	-2.3	5.75	22576.6	9.45	HUMAN	E9PKG0	Plectin (Fragment)
5008	dirMS_041712_NAR_30mM_plus2.13535.13535.2	2	13.14	0	1.03E+05		(R)TIYAGN	(R)T I|Y|A|G N\A/L C/T V K(C)	C:Carbamidomethylation	123.85	655.8414	1310.677	-0.0018	-1.4	8.26	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
5009	dirMS_041712_NAR_30mM_plus2.17604.17711.2	2	13.14	0	4.94E+05		(R)LSYTQLL	(R)L/S|Y/T/Q/L L/R(R)		145.92	497.2902	993.573	0.0004	0.4	8.75	533778	5.74	HUMAN	Q15149	Plectin

5010	dirMS_041712_NAR_40mM_plus2.17449.17449.3	3	13.14	0	1.56E+05		(R)VYAILTH	(R)V/Y|A|I/L T H G I/F S/G P A I S R(I)		169.32	601.3376	1801.996	0.0023	1.3	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
5011	dirMS_041712_NAR_50mM_plus2.18673.19211.3	3	13.14	1	6.52E+06		(R)LDLAGR	(R)L/D|L|A/G R/D L T D/Y L/M K(I)		167.65	541.9524	1623.841	0.0016	1	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
5012	dirMS_041712_NAR_50mM_plus2.7826.7826.3	3	13.14	1	3.33E+04	M250m	(K)TTDmA	(K)T T|D/m/A/P S K E T E M A/L A K(D)	m:Oxidized methionine	108.25	580.6104	1723.824	15.9925	-1.4	4.68	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
5013	dirMS_041712_NAR_30mM_minus2.15870.15870.2	2	13.13	0	2.33E+04		(K)MLLYTE	(K)M/L|L|Y/T E V T R(Y)		139.67	563.2971	1125.597	-0.0103	-9.2	5.75	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
5014	dirMS_041712_NAR_40mM_minus2.8859.8859.3	3	13.13	1	2.33E+05		(R)IVLAND	(R)I V|L/A N/D P D A D R L A/V A E K(Q)		134.3	603.9966	1809.97	0.0047	2.6	4.23	32837.5	6.16	HUMAN	B4E0G8	Phosphoglucomutase-2
5015	dirMS_041712_NAR_50mM_minus2.16704.16704.3	3	13.13	1	1.57E+05		(K)NIPIPTL	(K)N I P I/P/T/L K D/F A/K(A)		163.35	452.9385	1356.789	0.0124	9.1	8.59	20960.6	7.05	HUMAN	H0YKU1	Tropomodulin-3 (Fragment)
5016	dirMS_041712_NAR_120mM_plus.13753.13753.2	2	13.13	1	5.06E+06		(K)FASFIDK	(K)F/A|S|F I/D K V/R(F)		125.95	541.8027	1082.599	-0.0012	-1.1	8.75	19569.8	9.88	HUMAN	F8VRG4	Keratin, type II cytoskeletal 8 (Fragment)
5017	dirMS_041712_NAR_120mM_plus.17019.17019.4	4	13.13	1	5.53E+05		(R)ELDTVTL	(R)E L D T\V/T/L/E D I/K E H V/K(Q)		142.12	442.9894	1768.933	0.003	1.7	4.5	61090.6	8.58	HUMAN	O43242	26S proteasome non-ATPase regulatory subunit 3
5018	dirMS_041712_NAR_20mM_plus.12591.12591.2	2	13.13	0	9.34E+04	M91m	(R)AITGASL	(R)A I/T/G/A S/L/A/D I m A K(R)	m:Oxidized methionine	159.93	639.3398	1261.682	15.9903	-3.6	5.88	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
5019	dirMS_041712_NAR_20mM_plus.14844.14844.2	2	13.13	0	1.13E+05		(K)LLGELL	(K)L L/G E|L/L Q/D N A/K(L)		173.7	607.3421	1213.679	-0.0018	-1.4	4.37	35556.4	9.3	HUMAN	F2Z393	Transaldolase
5020	dirMS_041712_NAR_30mM_plus2.11920.11920.2	2	13.13	0	1.79E+05		(R)LSALLQ	(R)L/S/A\L/L/Q E/T K(E)		115.55	501.7877	1002.583	-0.0149	-14.8	6	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
5021	dirMS_041712_NAR_30mM_plus2.15858.16035.2	2	13.13	0	3.25E+05		(R)YSVDIPL	(R)Y/S|V/D|I/P\L/D K(T)		136.15	525.2819	1049.551	0.0052	4.9	4.21	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
5022	dirMS_041712_NAR_40mM_plus2.11550.11550.2	2	13.13	0	5.28E+04		(R)TFEDFV	(R)T F/E/D/F V/R(I)		134.22	457.2245	913.441	0.0003	0.3	4.37	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
5023	dirMS_041712_NAR_50mM_plus2.10372.10373.3	3	13.13	0	4.48E+05		(R)AASIFG	(R)A/A|S|I/F/G G A K/P V/D T A A R(E)		122.1	511.2769	1531.823	-0.0066	-4.3	8.79	64861.3	5.86	HUMAN	B4DS13	Eukaryotic translation initiation factor 4B
5024	dirMS_041712_NAR_50mM_plus2.21377.21377.3	3	13.13	1	2.03E+05		(R)TEGLSV	(R)T E|G\L/S V/L/S\Q A M/A V I K E K(I)		182.72	602.0007	1803.988	-0.0009	-0.5	5.81	31604.9	6.88	HUMAN	G3V4T5	Eukaryotic translation initiation factor 2 subunit 1 (Fragment)
5025	dirMS_041712_NAR_60mM_plus.7138.7138.2	2	13.13	0	1.72E+06		(K)STTTGH	(K)S/T|T/T/G H L\I|Y/K(C)		95.58	560.8031	1120.6	-0.0008	-0.7	8.34	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
5026	dirMS_041712_NAR_120mM_minus.10503.10503.3	3	13.12	1	2.17E+05	M86m	(K)mKEIAE	(K)m K E\I\A/E/A/Y/L/G/K(T)	m:Oxidized methionine	111.63	423.557	1252.661	15.9959	0.7	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
5027	dirMS_041712_NAR_120mM_minus.13857.13857.3	3	13.12	1	1.94E+05		(R)IAWDDE	(R)I/A/W/D/D/E E/T R D G F R(L)		129.68	537.2494	1609.724	0.0095	5.9	4.11	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
5028	dirMS_041712_NAR_50mM_minus2.15907.15907.3	3	13.12	0	3.64E+05		(K)LYGPTN	(K)L Y|G/P T N/F/S/P\I I N H V A R(F)		158.22	600.3221	1798.96	-0.0081	-4.5	8.75	60985.3	5.6	HUMAN	O75131	Copine-3
5029	dirMS_041712_NAR_50mM_minus2.16469.16469.3	3	13.12	0	1.77E+05		(R)GGYVLH	(R)G G/Y|V/L/H/I/G T I Y/G D/L K(V)		161.78	535.9583	1605.863	-0.0032	-2	6.74	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
5030	dirMS_041712_NAR_50mM_minus2.16617.16617.3	3	13.12	1	9.23E+04		(R)DSEQVA	(R)D S/E/Q/V/A E|L K Q E L A T L/K(S)		163.05	601.3217	1801.954	-0.0036	-2	4.41	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
5031	dirMS_041712_NAR_50mM_minus2.17857.17857.3	3	13.12	0	3.01E+05		(K)HNQLPL	(K)H N Q L P L\V|I|E/F/T/E Q T/A P K(I)		170.03	655.6843	1965.044	-0.0057	-2.9	5.4	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
5032	dirMS_041712_NAR_120mM_plus.12902.13175.3	3	13.12	0	9.51E+05		(K)HYGPGV	(K)H Y\G P G\W|V|S/M/A/N/A G K(D)		121.57	492.2383	1474.69	0.0108	7.3	8.6	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
5033	dirMS_041712_NAR_120mM_plus.19503.19514.4	4	13.12	0	4.61E+05		(K)AHLLAD	(K)A H\L\L\A/D M A H\I S G\L|V/A/A/K(V)		155.57	430.2407	1717.942	-0.0008	-0.5	6.96	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
5034	dirMS_041712_NAR_20mM_plus.17306.17306.2	2	13.12	0	5.76E+05		(K)VLTPELY	(K)V L|T|P E L Y A/E/L/R(A)		189.78	652.3664	1303.726	-0.0001	-0.1	4.53	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
5035	dirMS_041712_NAR_30mM_plus2.17819.17821.2	2	13.12	0	9.29E+05		(R)SMVEDI	(R)S M|V|E/D I/T/G L R(L)		146.58	560.7925	1120.567	0.011	9.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
5036	dirMS_041712_NAR_30mM_plus2.22231.22231.2	2	13.12	0	3.69E+05		(R)VGNLGL	(R)V G/N L/G\L/A/T S/F/F N E R(N)		172.78	762.8926	1524.781	-0.0026	-1.7	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
5037	dirMS_041712_NAR_40mM_plus2.6668.6744.2	2	13.12	0	5.39E+05		(R)FFSDCK	(R)F/F|S/D|C/K(I)	C:Carbamidomethylation	99.92	402.1734	803.339	0.0003	0.3	5.84	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
5038	dirMS_041712_NAR_40mM_plus2.8867.8867.2	2	13.12	0	1.06E+05		(K)TEWLD	(K)T|E|W L/D G/K(H)		114.47	424.7133	848.415	0.0045	5.3	4.37	18393.6	9.55	HUMAN	A2BFH1	Peptidyl-prolyl cis-trans isomerase A-like 4G
5039	dirMS_041712_NAR_60mM_plus.5735.5757.3	3	13.12	0	1.46E+05	M116m	(R)ATAPQT	(R)A T|A/P/Q/T Q/H V/S P m R(Q)	m:Oxidized methionine	88.28	480.5724	1423.711	15.9916	-2.3	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
5040	dirMS_041712_NAR_20mM_minus.13842.13842.2	2	13.11	0	2.40E+05		(R)IVLLDSS	(R)I/V|L/L/D S S L\E Y K(K)		189.37	640.3594	1279.714	-0.0029	-2.2	4.37	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
5041	dirMS_041712_NAR_30mM_minus2.10454.10454.2	2	13.11	0	9.33E+05		(K)GSDFDC	(K)G S\D/F/D/C E L/R(L)	C:Carbamidomethylation	111.28	549.7307	1098.452	0.0021	1.9	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
5042	dirMS_041712_NAR_30mM_minus2.11562.11606.2	2	13.11	0	3.67E+05		(K)EIAEAYL	(K)E I|A/E/A Y/L/G/K(T)		115.85	497.265	993.525	-0.0024	-2.4	4.53	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
5043	dirMS_041712_NAR_30mM_minus2.14926.15013.2	2	13.11	0	2.48E+05		(R)SLLLSVN	(R)S L|L|L|S/V/N A/R(G)		134.95	486.7933	972.584	-0.0043	-4.5	9.47	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
5044	dirMS_041712_NAR_30mM_minus2.15199.15199.2	2	13.11	0	7.18E+05	M2249m	(K)MSIYQA	(K)M S|I/Y/Q/A/m W K(G)	m:Oxidized methionine	135.72	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
5045	dirMS_041712_NAR_30mM_minus2.9689.9689.2	2	13.11	0	4.78E+05		(R)TSLGPN	(R)T S|L/G/P\N G L D K(M)		106.28	501.2667	1001.526	-0.0001	-0.1	5.5	55804.4	5.33	HUMAN	B7ZAR1	T-complex protein 1 subunit epsilon
5046	dirMS_041712_NAR_40mM_minus2.11798.11798.3	3	13.11	0	2.24E+05		(R)LASTLV	(R)L/A|S T L/V/H L/G E Y/Q A/A/V D G A R(K)		153.02	657.6842	1971.029	0.0086	4.4	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
5047	dirMS_041712_NAR_60mM_minus.10828.10828.3	3	13.11	1	5.44E+05	M239m	(R)MSMKE	(R)M/S\M K E\V\D\E/Q/m\L/N V\Q\N/K(N)	m:Oxidized methionine	119.9	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
5048	dirMS_041712_NAR_120mM_plus.11198.11370.3	3	13.11	1	5.79E+05		(R)YYTVFD	(R)Y/Y|T/V/F D/R D N N R(V)		112.43	488.2287	1462.671	0.0006	0.4	5.96	20599.3	9.19	HUMAN	H7C1V0	Cathepsin D light chain (Fragment)
5049	dirMS_041712_NAR_30mM_plus2.14411.14411.2	2	13.11	0	2.63E+05		(R)ELLELAS	(R)E L|L/E L/A/S/R(M)		128.5	465.7671	930.525	0.0015	1.6	4.53	109301.2	7.85	HUMAN	H0Y394	Vigilin (Fragment)
5050	dirMS_041712_NAR_30mM_plus2.18935.18935.2	2	13.11	0	3.42E+05		(R)LTAEDL	(R)L/T/A/E/D\L/F/E\A R(I)		153.03	582.796	1164.59	-0.0048	-4.1	4.14	533778	5.74	HUMAN	Q15149	Plectin
5051	dirMS_041712_NAR_50mM_plus2.14722.14738.3	3	13.11	1	3.32E+05		(R)ALSNLE	(R)A L|S/N|L/E/S I/P G G Y N A L R R(M)		145.45	610.9972	1830.982	-0.005	-2.7	8.79	16443.8	5	HUMAN	H0YDS0	Ubiquilin-1 (Fragment)
5052	dirMS_041712_NAR_50mM_plus2.17119.17390.3	3	13.11	1	5.39E+05		(R)LGLSTL	(R)L/G\L|S/T/L/G E L K/Q N L S/R(S)		158.65	543.648	1628.933	-0.0035	-2.2	8.75	22294.4	5.26	HUMAN	O43399	Tumor protein D54
5053	dirMS_041712_NAR_50mM_plus2.17821.17821.3	3	13.11	0	2.13E+06		(K)LILPHVD	(K)L I/L/P H/V/D I|Q L K(Y)		162.02	430.2706	1288.799	-0.0015	-1.2	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
5054	dirMS_041712_NAR_50mM_plus2.20178.20178.3	3	13.11	0	5.36E+05		(R)QARPTY	(R)Q/A/R P T Y|A|T/A/M/L/Q/S L L K(-)		174.55	597.9962	1791.979	-0.0045	-2.5	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
5055	dirMS_041712_NAR_60mM_plus.9552.9552.3	3	13.11	0	1.08E+06		(K)GHENVE	(K)G H\E N V\E\A\A|Q/A/E Y/I/E K(F)		108.1	563.2692	1687.792	0.0008	0.5	4.48	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
5056	dirMS_041712_NAR_30mM_minus2.16938.16955.2	2	13.1	0	5.12E+05		(K)NSLESY	(K)N S|L|E|S/Y/A|F N M K(A)		146.62	652.3031	1303.599	0.0002	0.2	6	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
5057	dirMS_041712_NAR_30mM_minus2.6585.6585.2	2	13.1	0	2.34E+05		(R)QQYESV	(R)Q Q|Y/E/S/V/A A|K(N)		89.95	512.2534	1023.511	-0.011	-10.8	6	49709.6	5.19	HUMAN	B0YJC4	Vimentin
5058	dirMS_041712_NAR_30mM_minus2.9375.9395.2	2	13.1	0	3.01E+05		(K)LYSESLA	(K)L/Y|S/E S/L A/R(Y)		105.42	469.7484	938.494	-0.0046	-5	6	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
5059	dirMS_041712_NAR_20mM_plus.14327.14327.2	2	13.1	0	8.76E+04		(K)GVVDSD	(K)G V|V/D S D D L|P L N/V/S R(E)		170.28	743.3789	1485.754	-0.0038	-2.6	3.93	92752.5	4.76	HUMAN	P14625	Endoplasmin
5060	dirMS_041712_NAR_20mM_plus.17131.17131.3	3	13.1	0	1.44E+05		(R)AVLVDL	(R)A V L V D L E/P/G T M D S V/R(S)		189.48	534.6105	1601.82	-0.0034	-2.1	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
5061	dirMS_041712_NAR_30mM_plus2.18332.18332.2	2	13.1	0	2.25E+05		(K)GVEGLI	(K)G V|E\G\L/I|D I E|N/P\N R(V)		149.43	713.3669	1425.733	-0.0067	-4.7	4.14	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
5062	dirMS_041712_NAR_30mM_plus2.9123.9558.2	2	13.1	0	6.73E+05		(K)ATFDAIS	(K)A/T|F/D A/I/S/K(T)		102.87	426.7266	852.446	-0.0002	-0.3	5.88	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
5063	dirMS_041712_NAR_40mM_plus2.12941.12941.3	3	13.1	1	9.72E+05		(K)TITLEVE	(K)T I|T L/E/V E/P S D T I E N V K A K(I)		143.43	663.0201	1987.059	-0.0136	-6.9	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
5064	dirMS_041712_NAR_50mM_plus2.14290.14290.3	3	13.1	0	7.47E+05		(R)LQAYHT	(R)L Q|A Y H T Q T/T|P/L I/E/Y Y/R(K)		143.55	666.341	1997.013	-0.0043	-2.1	6.75	21283.1	6.45	HUMAN	F8VY04	Adenylate kinase 2, mitochondrial
5065	dirMS_041712_NAR_60mM_minus.8404.8404.3	3	13.09	1	6.45E+04		(K)QGIETP	(K)Q G\I\E/T/P E D/Q/N/D L R/K(M)		106.97	548.2737	1642.803	0.0034	2.1	4.32	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
5066	dirMS_041712_NAR_120mM_plus.11204.11375.3	3	13.09	0	6.41E+05		(R)SIFQHIQ	(R)S I/F Q/H/I/Q/S A Q S Q R(S)		112.73	510.5986	1529.782	-0.0007	-0.4	9.49	108720.9	10.17	HUMAN	Q9Y2W1	Thyroid hormone receptor-associated protein 3
5067	dirMS_041712_NAR_20mM_plus.18596.18596.3	3	13.09	0	4.71E+05		(K)LAVEAL	(K)L A V E A\L S S/L/D/G D|L/A G R(Y)		200.38	529.6164	1586.838	-0.0038	-2.4	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
5068	dirMS_041712_NAR_30mM_plus2.10022.10522.2	2	13.09	0	4.46E+06		(K)VCADLI	(K)V/C|A|D L/I/R(G)	C:Carbamidomethylation	107.62	423.7294	846.45	0.0013	1.6	5.81	6885.1	10.56	HUMAN	E5RJX2	40S ribosomal protein S20
5069	dirMS_041712_NAR_30mM_plus2.17162.17162.2	2	13.09	0	5.03E+05	M256m	(R)SLDmDS	(R)S L/D\m D/S I/I|A/E/V/K(A)	m:Oxidized methionine	142.52	668.8384	1320.671	15.998	2.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
5070	dirMS_041712_NAR_30mM_plus2.9820.9836.2	2	13.09	0	3.31E+05		(R)DLMAC	(R)D/L|M|A|C|A/Q T/G S G K(T)	C:Carbamidomethylation	104.87	619.7793	1238.55	0.0009	0.8	5.84	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
5071	dirMS_041712_NAR_40mM_plus2.10654.10654.3	3	13.09	0	1.77E+05		(K)MAPVPL	(K)M A/P V/P/L D D/S N R P A S L T K(D)		128.32	604.6467	1811.932	-0.0065	-3.6	5.71	53030.7	11.3	HUMAN	E9PJA7	Bcl-2-associated transcription factor 1
5072	dirMS_041712_NAR_40mM_plus2.6131.6131.2	2	13.09	0	5.66E+04		(R)QAFPNT	(R)Q A|F|P/N/T/N R(W)		94.88	474.2383	947.469	0	0	9.75	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
5073	dirMS_041712_NAR_50mM_plus2.15983.16026.3	3	13.09	1	1.07E+06		(R)EIISFGS	(R)E I|I/S/F/G S/G Y/G G N S L L G K K(C)		152.03	609.6588	1826.965	-0.0028	-1.6	8.59	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
5074	dirMS_041712_NAR_50mM_plus2.21454.21454.3	3	13.09	1	3.90E+05	M145m	(R)GVmLA	(R)G V/m\L/A V|D A V/I A E L K K(Q)	m:Oxidized methionine	182.6	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
5075	dirMS_041712_NAR_60mM_plus.11554.11700.3	3	13.09	1	7.92E+05		(K)TAVCDI	(K)T/A|V/C D I/P/P R G L K(M)	C:Carbamidomethylation	119.07	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
5076	dirMS_041712_NAR_60mM_plus.19793.19793.3	3	13.09	0	7.84E+03		(K)SFLIWV	(K)S F/L|I/W/V N/E E D/H T R(V)		162.93	549.2699	1645.797	-0.0017	-1.1	4.65	29478.9	6.26	HUMAN	E9PCP8	Creatine kinase U-type, mitochondrial
5077	dirMS_041712_NAR_30mM_minus2.10627.10659.2	2	13.08	0	1.07E+05		(K)FMGTEL	(K)F/M|G/T/E L/N/G K(T)		111.75	498.7451	996.482	0.001	1	6	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
5078	dirMS_041712_NAR_50mM_minus2.14209.14230.3	3	13.08	1	2.89E+05	M93m	(K)SELVAm	(K)S E|L|V/A/m/L E/E E E L/R K(A)	m:Oxidized methionine	148.75	564.6215	1675.857	15.9928	-1.2	4.32	18679.2	5.61	HUMAN	B4DWW1	ADP-ribosylation factor-like protein 1
5079	dirMS_041712_NAR_50mM_minus2.16343.16343.3	3	13.08	0	1.75E+05	M1m	(-)mKPLVV	(-)m K P\L\V V\F\V|L/G/G P G\A G K(G)	m:Oxidized methionine	161.27	529.3077	1569.919	15.99	-3.1	10	22450.2	5.44	HUMAN	P30085	UMP-CMP kinase
5080	dirMS_041712_NAR_60mM_minus.10705.10705.3	3	13.08	1	5.44E+05	M239m	(R)MSMKE	(R)M S/M K E V\D E/Q m|L N/V/Q/N K(N)	m:Oxidized methionine	119.9	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
5081	dirMS_041712_NAR_20mM_plus.14467.14467.2	2	13.08	0	1.59E+04		(K)TVFGVE	(K)T V|F/G V/E P\D/L T R(E)		171.18	617.3237	1233.647	-0.0073	-5.9	4.37	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
5082	dirMS_041712_NAR_20mM_plus.19017.19017.2	2	13.08	0	1.05E+05		(K)DTSYLF	(K)D T S\Y/L/F/I/T/G P D V V K(S)		201.92	777.9049	1554.805	-0.0025	-1.6	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
5083	dirMS_041712_NAR_20mM_plus.9378.9378.2	2	13.08	0	6.69E+04		(K)TGQEIP	(K)T/G/Q/E|I/P V/N V/R(F)		135.92	556.8027	1112.606	-0.0077	-6.9	5.66	28051.5	4.98	HUMAN	J3QKT2	Cytosolic non-specific dipeptidase (Fragment)
5084	dirMS_041712_NAR_30mM_plus2.5709.5709.2	2	13.08	0	2.46E+05		(R)QSSGAS	(R)Q S|S G A|S/S/S S/F/S S S R(A)		84.3	681.3013	1361.593	0.0025	1.9	9.75	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
5085	dirMS_041712_NAR_40mM_plus2.13433.13433.3	3	13.08	0	2.64E+05		(K)NLPPSG	(K)N L|P\P S\G A V P V T G/I/P P H V V K(V)		145.08	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
5086	dirMS_041712_NAR_50mM_plus2.20898.20898.3	3	13.08	0	3.55E+06		(R)AGKPVI	(R)A G K\P V\I C A|T/Q|M|L/E/S M I K(K)	C:Carbamidomethylation	179.2	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
5087	dirMS_041712_NAR_60mM_plus.15488.15559.3	3	13.08	1	8.07E+05		(R)QATKD	(R)Q A T K D A G T|I|A|G/L/N V L/R(I)		137.93	543.3085	1627.913	-0.0016	-1	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
5088	dirMS_041712_NAR_30mM_minus2.14382.14624.2	2	13.07	0	3.02E+05		(R)IILLAEG	(R)I/I|L|L/A/E/G/R(L)		132.58	442.7816	884.556	-0.0005	-0.5	6	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
5089	dirMS_041712_NAR_30mM_minus2.20075.20075.2	2	13.07	0	8.03E+04		(K)SLNILTA	(K)S L/N|I|L/T A|F Q K(K)		169.83	567.8283	1134.652	-0.0024	-2.1	8.47	18172.6	7.77	HUMAN	F8VY02	Endoplasmic reticulum resident protein 29
5090	dirMS_041712_NAR_50mM_minus2.10328.10328.3	3	13.07	0	1.46E+05		(K)VGSLDN	(K)V/G/S L D N V/G H/L/P A G G A V K(I)		126.9	530.9592	1590.86	0.0032	2	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
5091	dirMS_041712_NAR_50mM_minus2.15440.15440.3	3	13.07	0	3.28E+05		(R)LSFQHD	(R)L/S/F Q H D\P E\T|S V/L V/L R(K)		156.07	580.9793	1740.928	-0.0046	-2.6	5.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
5092	dirMS_041712_NAR_60mM_minus.13904.13904.3	3	13.07	0	4.24E+05		(K)DCGATV	(K)D C/G A T W|V/V L/G/H S E/R(R)	C:Carbamidomethylation	137.97	529.5838	1586.738	-0.0012	-0.7	5.32	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
5093	dirMS_041712_NAR_60mM_minus.8305.8310.3	3	13.07	1	1.25E+06	M2747m	(K)TLQEVT	(K)T L|Q/E V/T E/m/D/S V K R(Y)	m:Oxidized methionine	106.78	517.927	1535.773	15.9931	-1.2	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
5094	dirMS_041712_NAR_20mM_plus.16650.16650.2	2	13.07	0	2.56E+04		(R)LIDFLEC	(R)L/I/D\F/L/E C G K(T)	C:Carbamidomethylation	185.57	547.7827	1094.555	0.0031	2.8	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
5095	dirMS_041712_NAR_20mM_plus.17750.17967.2	2	13.07	0	2.19E+05		(R)SLVPAA	(R)S L/V|P/A/A E/L/L\E S R(V)		194.75	642.8613	1284.716	-0.0005	-0.4	4.53	533778	5.74	HUMAN	Q15149	Plectin
5096	dirMS_041712_NAR_20mM_plus.18230.18230.2	2	13.07	0	1.00E+05		(R)AILVDLE	(R)A I L|V/D\L|E|P G T M/D S V/R(S)		196.67	808.419	1615.836	-0.0053	-3.3	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
5097	dirMS_041712_NAR_20mM_plus.18676.18676.2	2	13.07	0	2.80E+05		(K)TAVETA	(K)T A\V|E|T/A/V/L|L L R(I)		199.97	593.3625	1185.72	-0.0024	-2	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
5098	dirMS_041712_NAR_30mM_plus2.13131.13131.2	2	13.07	0	4.67E+05		(R)AFLIEEQ	(R)A F/L|I/E/E Q K(I)		122.38	489.2625	977.53	-0.0125	-12.8	4.53	13520.9	11.92	HUMAN	P49207	60S ribosomal protein L34
5099	dirMS_041712_NAR_30mM_plus2.18720.18720.2	2	13.07	0	1.16E+05		(K)GLIPWE	(K)G L|I|P/W/E Q A A R(L)		152.62	570.8113	1140.616	-0.0007	-0.6	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
5100	dirMS_041712_NAR_30mM_plus2.18954.18954.2	2	13.07	0	5.13E+04		(R)MGPGI	(R)M/G|P G I|G A/I L E R(S)		152.52	557.3091	1113.609	0.0024	2.2	5.75	14175.1	9.89	HUMAN	H0YKS1	Myelin expression factor 2 (Fragment)
5101	dirMS_041712_NAR_30mM_plus2.19301.19301.2	2	13.07	0	2.93E+05		(K)TVDNFV	(K)T\V|D N F|V/A/L A T/G E K(G)		154.93	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
5102	dirMS_041712_NAR_30mM_plus2.21401.21423.2	2	13.07	0	1.58E+05		(R)VFIGNL	(R)V F|I|G N L/N T L V/V|K(K)		167.38	658.8983	1316.794	-0.0043	-3.3	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
5103	dirMS_041712_NAR_30mM_plus2.6072.6092.3	3	13.07	0	1.68E+05		(R)NQGGY	(R)N Q\G G Y G G S S/S/S/S/S/Y/G/S G R(R)		86.23	565.5708	1694.7	-0.0022	-1.3	8.59	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
5104	dirMS_041712_NAR_40mM_plus2.16038.16038.3	3	13.07	0	3.15E+05		(K)VAIVKP	(K)V/A/I V K P G V|P M E\I V L N K(E)		161.13	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
5105	dirMS_041712_NAR_40mM_plus2.16085.16085.3	3	13.07	1	1.88E+05		(K)LGVQVV	(K)L/G V/Q|V/V I T/D/P E K L D Q I/R(Q)		161.47	641.701	1923.091	-0.0025	-1.3	4.56	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
5106	dirMS_041712_NAR_50mM_plus2.18074.18074.3	3	13.07	1	1.61E+06		(R)ELIKVLE	(R)E L\I K V L E E\A/N Q|A|I/N|P K(L)		163.43	603.6741	1809.012	-0.0039	-2.2	4.79	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
5107	dirMS_041712_NAR_50mM_plus2.8642.8642.3	3	13.07	1	1.01E+05		(K)TAVCDI	(K)T/A|V/C D I/P P R G L/K(M)	C:Carbamidomethylation	112.57	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
5108	dirMS_041712_NAR_30mM_minus2.15174.15469.2	2	13.06	0	4.43E+05		(R)GLVGEII	(R)G L|V/G/E I/I/K(R)		136.28	414.7625	828.519	-0.0012	-1.5	6	6640.6	8.25	HUMAN	C9K028	Nucleoside diphosphate kinase A (Fragment)
5109	dirMS_041712_NAR_60mM_minus.17611.17611.3	3	13.06	0	1.17E+05		(R)GGHVV	(R)G G H V V E G L|A\G/E|L/E/Q L R(A)		158.32	555.2959	1663.876	-0.0031	-1.8	4.75	106088.3	5.78	HUMAN	P10275	Androgen receptor
5110	dirMS_041712_NAR_60mM_minus.8731.8731.3	3	13.06	1	2.84E+05		(R)LGTPELS	(R)L/G|T/P/E/L S/T A E/R K(E)		108.45	434.572	1301.706	-0.0045	-3.5	6.14	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
5111	dirMS_041712_NAR_120mM_plus.15176.15276.3	3	13.06	1	5.50E+05	M276m	(R)RFDAm	(R)R F D A|m|P/F/T L/R(A)	m:Oxidized methionine	132.72	423.8875	1253.646	16.002	5.6	9.6	42088	5.39	HUMAN	F8VTY8	Proliferation-associated protein 2G4
5112	dirMS_041712_NAR_20mM_plus.17694.17694.2	2	13.06	0	2.22E+05		(K)LLYAFAE	(K)L L/Y/A|F A E\A T V P K(V)		192.97	661.8712	1322.736	-0.0003	-0.3	6	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
5113	dirMS_041712_NAR_30mM_plus2.6865.6988.2	2	13.06	0	2.30E+06		(R)MGANS	(R)M/G|A|N|S L/E/R(M)		90.92	439.2141	877.42	0.0013	1.5	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
5114	dirMS_041712_NAR_50mM_plus2.17363.17512.3	3	13.06	1	7.36E+05		(K)SELVAM	(K)S E|L|V/A/M/L E E/E E L R K(A)		159.72	559.2899	1675.857	-0.002	-1.2	4.32	18679.2	5.61	HUMAN	B4DWW1	ADP-ribosylation factor-like protein 1
5115	dirMS_041712_NAR_60mM_plus.11927.11927.3	3	13.06	1	6.23E+05		(K)SVSDYD	(K)S V|S D/Y/D G K L S N F K(T)		119.6	487.2426	1459.706	0.0069	4.7	5.68	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
5116	dirMS_041712_NAR_60mM_plus.7606.7842.3	3	13.06	1	1.31E+06		(K)KGTVEG	(K)K\G T V\E G\F|E|P/A D/N K(C)		98.42	464.5649	1391.68	0	0	4.68	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
5117	dirMS_041712_NAR_30mM_minus2.11237.11237.2	2	13.05	0	1.32E+05		(R)AMGEQ	(R)A/M|G/E/Q A/V/A L A/R(A)		114.68	558.7916	1116.583	-0.0071	-6.3	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
5118	dirMS_041712_NAR_30mM_minus2.17374.17374.2	2	13.05	0	2.59E+05		(R)NGGQIL	(R)N G|G Q|I/L I|A/D/L R(G)		148.65	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog

5119	dirMS_041712_NAR_30mM_minus2.6192.6192.2	2	13.05	0	2.84E+05		(K)TSEVNC	(K)T/S/E|V|N C Y R(C)	C:Carbamidomethylation	88	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
5120	dirMS_041712_NAR_40mM_minus2.14866.14873.3	3	13.05	1	5.46E+05		(R)GDLGIEI	(R)G D L G/I/E/I/P A/E K/V F L A/Q K(M)		173.02	610.0109	1828.022	-0.0033	-1.8	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
5121	dirMS_041712_NAR_60mM_minus.6557.6576.3	3	13.05	1	2.18E+05		(R)KTGQAP	(R)K\T G Q A|P/G\Y|S|Y\T A/A N K(N)		95.27	519.5963	1556.77	0.004	2.6	9.53	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
5122	dirMS_041712_NAR_120mM_plus.5595.5595.3	3	13.05	1	4.53E+05		(K)AQQELE	(K)A Q|Q/E/L/E E Q T R/R(A)		81.9	463.2395	1387.692	0.0115	8.3	4.79	67933	6.08	HUMAN	P26038	Moesin
5123	dirMS_041712_NAR_20mM_plus.10949.10949.3	3	13.05	0	1.01E+05		(K)ALIAAQ	(K)A L\I A|A Q Y/S/G A/Q V R(V)		147.88	449.9174	1347.738	-0.0003	-0.2	8.79	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
5124	dirMS_041712_NAR_20mM_plus.15489.15489.2	2	13.05	0	5.10E+04		(R)AITIAGV	(R)A I T\I/A/G\V|P Q S V T/E C V K(Q)	C:Carbamidomethylation	178.55	836.9443	1672.894	-0.0125	-7.5	6.05	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
5125	dirMS_041712_NAR_20mM_plus.9585.9585.2	2	13.05	0	5.40E+05		(R)ISVYYNE	(R)I/S\V|Y/Y/N E A T G G K(Y)		138.23	651.3211	1301.637	-0.0023	-1.8	6	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
5126	dirMS_041712_NAR_30mM_plus2.18041.18041.2	2	13.05	0	2.31E+05		(R)QITLNDI	(R)Q I|T L|N D L/P V\G R(S)		147.83	613.3465	1225.69	-0.0042	-3.4	5.84	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
5127	dirMS_041712_NAR_30mM_plus2.6090.6116.2	2	13.05	0	1.91E+05		(R)GCLDEE	(R)G/C|L|D/E/E/T S/R(A)	C:Carbamidomethylation	86.25	533.7267	1066.447	-0.0008	-0.8	4.14	533778	5.74	HUMAN	Q15149	Plectin
5128	dirMS_041712_NAR_50mM_plus2.17208.17208.3	3	13.05	0	2.70E+05		(K)VVDELN	(K)V/V/D/E/L N L L/H T E\L A/K(Q)		158.33	531.9659	1593.885	-0.0015	-0.9	4.65	16381.6	5.83	HUMAN	F8VWV2	DCC-interacting protein 13-beta (Fragment)
5129	dirMS_041712_NAR_50mM_plus2.19655.19655.3	3	13.05	1	1.38E+05		(R)VAAKLE	(R)V A A K L\E\V\A|P I/S/D I I/A I K(S)		171.43	584.3568	1751.068	-0.0119	-6.8	6.04	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
5130	dirMS_041712_NAR_50mM_plus2.7564.7627.3	3	13.05	1	2.75E+05		(K)MQASIE	(K)M/Q|A/S I/E K G G S L/P|K(V)		105.85	449.2397	1345.714	-0.0099	-7.3	8.35	32745.6	4.64	HUMAN	P06748	Nucleophosmin
5131	dirMS_041712_NAR_60mM_plus.8376.8376.3	3	13.05	0	6.61E+05	M148m	(R)AHSSm	(R)A H\S S\m\V|G/V/N L/P/Q K(A)	m:Oxidized methionine	102.07	461.9069	1367.71	15.9962	0.9	8.8	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
5132	dirMS_041712_NAR_50mM_minus2.11701.11726.3	3	13.04	0	2.08E+05	M221m	(K)mLDAED	(K)m L|D/A/E D I/V/G T A R P D/E K(A)	m:Oxidized methionine	134.85	592.6214	1759.853	15.9966	0.9	4.1	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
5133	dirMS_041712_NAR_50mM_minus2.12754.12773.3	3	13.04	1	1.29E+05		(R)TEMENE	(R)T|E\M E/N E|F/V/L I/K K(D)		140.62	494.2621	1480.772	0.0002	0.1	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
5134	dirMS_041712_NAR_120mM_plus.14420.14555.4	4	13.04	1	1.05E+06		(K)GLDPAR	(K)G L\D\P A R V N V/P V/I/G G H A G K(T)		129.83	439.9998	1756.982	-0.0043	-2.5	8.76	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
5135	dirMS_041712_NAR_30mM_plus2.10173.10575.2	2	13.04	0	2.33E+05		(K)TAVCDIF	(K)T A|V|C/D/I|P|P R(G)	C:Carbamidomethylation	105.85	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
5136	dirMS_041712_NAR_30mM_plus2.15981.15981.2	2	13.04	0	4.68E+05		(R)MGPNIY	(R)M/G|P N/I/Y/E/L/R(T)		136.68	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
5137	dirMS_041712_NAR_50mM_plus2.12596.12596.3	3	13.04	1	3.83E+05		(K)LPGGELI	(K)L/P|G G E L N P G E/D E/V/E/G\L K R(L)		134.28	636.9936	1908.966	0.0001	0.1	4.25	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
5138	dirMS_041712_NAR_50mM_plus2.20061.20136.3	3	13.04	1	1.08E+05		(K)SVISGGL	(K)S V|I/S/G\G L D A L/E F I/G K/K(T)		174.18	545.3096	1633.916	-0.0017	-1	5.79	22133.2	4.82	HUMAN	E5RGF9	Protein FAM114A2 (Fragment)
5139	dirMS_041712_NAR_50mM_plus2.9949.9949.3	3	13.04	0	3.50E+05		(K)VAKPVV	(K)V A\K P V\V\E|M/D/G D/E M T R(I)		119.73	559.6043	1676.798	0.0001	0.1	4.32	35557.8	9.19	HUMAN	H0YL11	Isocitrate dehydrogenase [NADP], mitochondrial
5140	dirMS_041712_NAR_60mM_plus.12359.12457.3	3	13.04	1	5.45E+05		(K)FVMQEE	(K)F/V|M/Q/E E/F S R D/G K(A)		121.7	491.5693	1472.684	0.0095	6.5	4.68	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
5141	dirMS_041712_NAR_60mM_plus.17856.17856.3	3	13.04	1	2.77E+05		(R)LIDFLES	(R)L/I|D/F/L E S/G/K T N L R(R)		150.53	502.6147	1505.832	-0.0027	-1.8	6.07	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
5142	dirMS_041712_NAR_60mM_plus.7133.7145.3	3	13.04	1	1.14E+05		(K)SETELKD	(K)S E|T E L/K/D/T Y/A R(W)		95.65	438.2182	1312.638	0.0021	1.6	4.68	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
5143	dirMS_041712_NAR_30mM_minus2.9310.9310.2	2	13.03	0	3.53E+05		(K)CAADLG	(K)C/A|A|D|L/G L N/K(G)	C:Carbamidomethylation	104.88	481.2466	961.477	0.0088	9.1	5.84	13915.8	6.43	HUMAN	P49773	Histidine triad nucleotide-binding protein 1
5144	dirMS_041712_NAR_40mM_minus2.13932.13932.3	3	13.03	1	2.77E+04		(R)LQISTPD	(R)L Q|I/S T/P D/I K D N I V/A Q L\K(Q)		166.05	632.6978	1896.08	-0.0012	-0.6	5.96	42442.7	4.65	HUMAN	F5GWX8	Interferon regulatory factor 6
5145	dirMS_041712_NAR_50mM_minus2.16038.16038.3	3	13.03	1	3.45E+05		(K)QLDDLK	(K)Q L|D D/L/K/V E/L/S Q L R(V)		159.03	519.6261	1556.864	-0.0005	-0.3	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
5146	dirMS_041712_NAR_30mM_plus2.11658.11658.2	2	13.03	0	5.70E+05		(R)AMGEQ	(R)A M|G\E/Q/A V/A L\A/R(A)		114.4	558.7944	1116.583	-0.0015	-1.3	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
5147	dirMS_041712_NAR_30mM_plus2.22004.22028.2	2	13.03	0	1.87E+05		(R)EGDVLT	(R)E G D\V|L|T|L/L/E/S E R(E)		170.55	680.8538	1360.696	0.0049	3.6	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
5148	dirMS_041712_NAR_30mM_plus2.8664.8681.2	2	13.03	0	3.15E+05		(K)TAEFQV	(K)T/A|E/F/Q/V A/R(T)		99.3	461.2413	921.479	-0.0035	-3.8	5.66	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
5149	dirMS_041712_NAR_40mM_plus2.13932.13932.3	3	13.03	1	2.11E+04		(K)VGLQVV	(K)V G L|Q/V/V A V K/A P/G F G D/N/R(K)		148.4	576.3214	1726.96	-0.0102	-5.9	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
5150	dirMS_041712_NAR_40mM_plus2.17837.17837.3	3	13.03	0	1.42E+05		(R)DIKPQN	(R)D I\K P Q N\L|L|L/D/P D T A V L/K(L)		170.92	631.6874	1893.069	-0.0215	-11.4	4.43	47257	9.38	HUMAN	P49841	Glycogen synthase kinase-3 beta
5151	dirMS_041712_NAR_40mM_plus2.18977.18977.3	3	13.03	1	2.88E+05		(R)GGPNIIT	(R)G G P\N I/I/T L/A D I V/K D/P V S R(T)		178.85	622.3522	1865.049	-0.007	-3.8	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
5152	dirMS_041712_NAR_60mM_plus.9036.9036.3	3	13.03	0	5.09E+05		(R)LAQGHT	(R)L/A Q/G H T/T V/D E L A R(R)		104.88	470.9225	1410.734	0.0194	13.7	5.32	533778	5.74	HUMAN	Q15149	Plectin
5153	dirMS_041712_NAR_120mM_minus.10954.11006.3	3	13.02	1	1.13E+06		(K)KGENYV	(K)K\G E N Y V|Y|I|N/E/A T R(H)		113.53	519.5935	1556.77	-0.0044	-2.8	6.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
5154	dirMS_041712_NAR_30mM_minus2.14165.14165.2	2	13.02	0	4.12E+05		(K)MFLYAD	(K)M/F|L|Y/A D N E D/R(A)		131.07	637.2806	1273.552	0.0022	1.7	4.03	24724.1	5.17	HUMAN	E7ETQ7	Vacuolar protein sorting-associated protein VTA1 homolog
5155	dirMS_041712_NAR_50mM_minus2.15652.15652.3	3	13.02	1	4.93E+05		(K)QGGLGF	(K)Q G G L/G/P M\N I/P/L V/S D/P K R(T)		157.5	593.6566	1778.958	-0.0029	-1.6	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
5156	dirMS_041712_NAR_50mM_minus2.7927.7927.3	3	13.02	0	8.88E+04		(K)TAVEHA	(K)T A|V E/H A T/D/E D I/L A/K(G)		112.23	504.9229	1512.754	0.0001	0.1	4.31	288852.1	5.33	HUMAN	E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein
5157	dirMS_041712_NAR_120mM_plus.18649.19135.4	4	13.02	1	2.66E+06		(K)FQIPPN	(K)F Q\I|P/P N/A E L K/Y E L H/L K(S)		151.82	485.7703	1940.064	-0.0046	-2.4	6.75	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
5158	dirMS_041712_NAR_120mM_plus.4164.4223.2	2	13.02	1	1.45E+06	M310m	(R)TKTEISE	(R)T/K|T|E/I|S E m N R(N)	m:Oxidized methionine	69.8	612.7976	1208.594	15.994	-0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
5159	dirMS_041712_NAR_20mM_plus.9445.9445.2	2	13.02	0	1.86E+05		(K)SVTNED	(K)S V/T/N E\D/V/T Q/E E L/G G A\K(T)		136	838.9014	1676.797	-0.0018	-1.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
5160	dirMS_041712_NAR_30mM_plus2.12274.12563.2	2	13.02	0	9.65E+05		(K)VLQLYPI	(K)V L|Q|L|Y|P/N N K(A)		117.97	544.8062	1088.61	-0.0047	-4.4	8.56	9740.1	10.08	HUMAN	H0YFG2	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed (Fragment)
5161	dirMS_041712_NAR_30mM_plus2.14598.14874.2	2	13.02	0	8.51E+05		(R)ISPLQFR	(R)I/S|P/L/Q F/R(-)		129.97	430.7564	860.499	0.0067	7.7	9.75	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
5162	dirMS_041712_NAR_30mM_plus2.17276.17276.2	2	13.02	0	3.86E+05		(R)IMNTFS	(R)I/M|N T|F/S V\V P S P K(V)		144.5	660.3537	1319.703	-0.0027	-2	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
5163	dirMS_041712_NAR_30mM_plus2.21786.21786.2	2	13.02	0	2.29E+05		(R)TTNFAG	(R)T T/N F/A/G I L/S Q|G L R(I)		169.4	689.3749	1377.748	-0.006	-4.3	9.41	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
5164	dirMS_041712_NAR_50mM_plus2.15126.15126.3	3	13.02	1	4.23E+05		(R)LSQELEY	(R)L/S|Q/E/L E Y L/T E D V K/R(L)		147.3	574.9669	1722.891	-0.0047	-2.7	4.41	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
5165	dirMS_041712_NAR_50mM_plus2.18989.18989.3	3	13.02	1	4.36E+05		(K)AAIDWF	(K)A/A I/D\W/F/D G K/E F S G N P I K(V)		167.18	632.3186	1894.933	0.0079	4.1	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
5166	dirMS_041712_NAR_60mM_plus.10451.10753.3	3	13.02	1	1.05E+06		(K)MADEAI	(K)M/A|D|E/A I L Q E R E/R(G)		113	487.578	1460.716	0.0032	2.2	4.41	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
5167	dirMS_041712_NAR_120mM_minus.11341.11341.3	3	13.01	0	4.42E+05		(K)SAKPTKI	(K)S A K/P T K/P A A S D\L|P V|P A E G V R(N)		116.37	664.3662	1991.092	-0.008	-4	8.31	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
5168	dirMS_041712_NAR_120mM_minus.8099.8099.3	3	13.01	1	2.84E+05		(R)SQYEQL	(R)S Q|Y/E Q/L A/E Q N R K(D)		98.28	498.5798	1493.734	-0.0094	-6.3	5.86	59054.3	5.14	HUMAN	P13645	Keratin, type I cytoskeletal 10
5169	dirMS_041712_NAR_30mM_minus2.17967.18213.2	2	13.01	0	1.62E+06		(R)GLFIIDG	(R)G L|F|I I D/G K(G)		153.33	431.7497	862.503	-0.0112	-12.9	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
5170	dirMS_041712_NAR_50mM_minus2.15214.15214.3	3	13.01	1	2.52E+05		(K)LALDIEI	(K)L/A|L D I/E/I/A/T Y R/K(L)		154.37	469.2729	1405.805	-0.0008	-0.6	6.07	49564	5.84	HUMAN	E9PAX3	Glial fibrillary acidic protein
5171	dirMS_041712_NAR_60mM_minus.15854.15854.3	3	13.01	1	3.20E+05		(R)IDTRNEI	(R)I D/T R N E\L|E/S Y/A Y S L K(N)		148.2	601.3049	1801.897	0.0035	1.9	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
5172	dirMS_041712_NAR_30mM_plus2.13699.13715.2	2	13.01	0	3.81E+05		(R)QLQNIIC	(R)Q L|Q|N|I|I/Q/A T S R(E)		125.07	636.3523	1271.707	-0.0093	-7.3	9.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
5173	dirMS_041712_NAR_30mM_plus2.19619.19697.2	2	13.01	0	2.31E+05		(K)LLQDFFI	(K)L/L|Q/D F/F/N G R(D)		156.9	555.2902	1109.574	-0.0007	-0.6	5.84	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
5174	dirMS_041712_NAR_30mM_plus2.22246.22246.2	2	13.01	0	2.13E+05		(K)NSSYFVE	(K)N S\S Y F|V\E W I|P N N V K(V)		171.88	848.9189	1696.833	-0.0024	-1.4	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
5175	dirMS_041712_NAR_30mM_plus2.7642.7666.2	2	13.01	0	1.47E+06		(K)ISTISSVR	(K)I/S|T/I/S S V/R(N)		94.05	431.7495	862.499	-0.0075	-8.7	9.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
5176	dirMS_041712_NAR_50mM_plus2.21475.21475.3	3	13.01	0	3.39E+06		(R)LHFFMP	(R)L H F\F\M P G\F|A/P|L/T S R(G)		182.25	540.9498	1620.835	-0.0007	-0.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
5177	dirMS_041712_NAR_50mM_plus2.7209.7209.3	3	13.01	0	1.11E+05		(K)TNPPLIC	(K)T N|P/P/L I Q E K/P A/K(T)		104	445.9257	1335.763	-0.0005	-0.4	8.26	102841.5	6.73	HUMAN	D3DQV9	Eukaryotic translation initiation factor 4 gamma 2 (Fragment)
5178	dirMS_041712_NAR_30mM_minus2.10612.10761.2	2	13	0	1.97E+06		(R)APIIAVT	(R)A/P|I|I|A/V T R(N)		111.93	420.769	840.53	0.0006	0.7	9.79	53557.7	6.39	HUMAN	H3BTN5	Pyruvate kinase (Fragment)
5179	dirMS_041712_NAR_50mM_minus2.16392.16434.3	3	13	1	6.81E+04		(R)CITDPQ	(R)C I|T/D/P Q|T G\L C L/L/P L K E K(K)	C:Carbamidomethylation	161.65	662.6828	1986.04	-0.006	-3	6.07	533778	5.74	HUMAN	Q15149	Plectin
5180	dirMS_041712_NAR_20mM_plus.11620.11620.2	2	13	0	9.38E+04		(R)AQAALA	(R)A Q A\A\L/A/V/N/I/S A/A/R(G)		153.22	628.3565	1255.712	-0.006	-4.8	9.79	58479.6	6.23	HUMAN	P40227	T-complex protein 1 subunit zeta
5181	dirMS_041712_NAR_20mM_plus.12565.12586.2	2	13	0	2.52E+05		(K)DVNAAI	(K)D V|N|A/A/I/A A I K(T)		159.55	493.2863	985.568	-0.0023	-2.4	5.84	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
5182	dirMS_041712_NAR_30mM_plus2.18884.18884.2	2	13	0	5.13E+04		(R)MGPGIC	(R)M/G/P G\I|G/A/I L E R(S)		152.52	557.3091	1113.609	0.0024	2.2	5.75	14175.1	9.89	HUMAN	H0YKS1	Myelin expression factor 2 (Fragment)
5183	dirMS_041712_NAR_30mM_plus2.20459.20459.2	2	13	0	1.80E+05		(K)GSFSEQ	(K)G S F|S E/Q|G I|N E/F L R(E)		161	742.362	1483.718	-0.0009	-0.6	4.53	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
5184	dirMS_041712_NAR_30mM_plus2.21828.21828.2	2	13	0	2.02E+05		(K)ALELNM	(K)A/L|E\L N/M L S L/K(G)		169.75	566.3204	1131.644	-0.0107	-9.4	6.05	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
5185	dirMS_041712_NAR_50mM_plus2.15417.15417.3	3	13	1	4.03E+05		(R)LAAELNI	(R)L/A/A E/L N K F/M L/E K(V)		149.05	469.5948	1406.771	-0.0014	-1	6.14	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
5186	dirMS_041712_NAR_50mM_plus2.9605.9606.3	3	13	0	7.67E+05		(K)YIQQTKI	(K)Y I/Q/Q|T/K/P L/T L E/R(T)		117.07	497.2822	1489.837	-0.0053	-3.5	8.59	26283.8	8.96	HUMAN	O43809	Cleavage and polyadenylation specificity factor subunit 5
5187	dirMS_041712_NAR_20mM_minus.9739.9739.2	2	12.99	0	2.50E+05	M33m	(K)VAGmD	(K)V/A|G/m D/V/E L/T V E E R(N)	m:Oxidized methionine	147.53	732.355	1447.71	15.993	-1.3	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
5188	dirMS_041712_NAR_30mM_minus2.13940.13940.2	2	12.99	0	1.66E+05		(K)NVIGLQI	(K)N V|I|G\L/Q/M G T N R(G)		129.38	601.8183	1202.631	-0.0017	-1.4	9.75	22562.2	8.8	HUMAN	P37802	Transgelin-2
5189	dirMS_041712_NAR_30mM_minus2.19006.19155.2	2	12.99	0	2.61E+05		(K)SYELPDC	(K)S Y/E|L|P D G Q/V/I/T/I/G N E R(F)		158.88	895.9492	1790.892	-0.0008	-0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
5190	dirMS_041712_NAR_40mM_minus2.14533.14533.3	3	12.99	1	1.17E+06	M116m	(R)ELAILLG	(R)E L/A/I/L/L G/m L D P A E K D/E K(G)	m:Oxidized methionine	171.02	634.338	1884.999	16.0008	3.1	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
5191	dirMS_041712_NAR_50mM_minus2.8526.8526.3	3	12.99	1	2.43E+05		(R)AGTGVD	(R)A G/T/G/V/D/N V D/L/E/A A T R\K(G)		116.55	539.6119	1616.824	-0.0027	-1.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
5192	dirMS_041712_NAR_60mM_minus.10103.10103.3	3	12.99	1	6.76E+04		(K)ALDLDS	(K)A L/D|L D/S S C K E A/A/D G Y Q R(C)	C:Carbamidomethylation	115.93	633.6235	1898.855	0.0011	0.6	4.23	60404.6	6.4	HUMAN	F5H0T1	Stress-induced-phosphoprotein 1
5193	dirMS_041712_NAR_60mM_minus.11929.11929.3	3	12.99	0	1.77E+05	M271m	(R)DLSYCLS	(R)D L|S/Y/C/L/S G m Y D H R(Y)	C:Carbamidomethylation m:Oxid	126.72	544.8984	1616.683	15.9975	1.6	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
5194	dirMS_041712_NAR_60mM_minus.16369.16369.3	3	12.99	0	2.27E+05		(R)HDPTSEI	(R)H D\P T S E N\I/L Q L/V/K(A)		150.78	498.6051	1493.796	0.0049	3.3	5.32	13564.4	5.9	HUMAN	F8VZ98	Serine/threonine-protein kinase D1 (Fragment)
5195	dirMS_041712_NAR_120mM_plus.14914.14914.3	3	12.99	0	1.55E+06		(-)MVNHFI	(-)M/V|N/H/F I A E/F K(R)		131.67	412.5446	1235.624	-0.0049	-4	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
5196	dirMS_041712_NAR_50mM_plus2.17785.17892.3	3	12.99	0	5.68E+05		(K)TVSGVN	(K)T V|S/G V N G/P L/V/I/L/D H V K(V)		162.05	549.9834	1647.943	-0.0072	-4.4	6.41	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
5197	dirMS_041712_NAR_50mM_plus2.6719.6732.3	3	12.99	0	1.60E+05		(K)IGEEEIQ	(K)I/G|E/E/E/I/Q K P E E K(V)		100.35	476.9126	1428.722	0.0016	1.1	4.32	81733.5	5.24	HUMAN	E9PAW1	Splicing factor 3A subunit 1
5198	dirMS_041712_NAR_60mM_plus.11188.11212.3	3	12.99	0	4.60E+06		(R)DNIQGI	(R)D N|I|Q/G\I/T K/P A I/R(R)		116.45	442.588	1325.754	-0.0041	-3.1	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
5199	dirMS_041712_NAR_60mM_plus.9830.9830.3	3	12.99	1	1.29E+06		(K)EAALSTA	(K)E A A/L/S/T/A L/S E K R(T)		109.78	425.898	1275.69	-0.0109	-8.5	6.24	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
5200	dirMS_041712_NAR_120mM_minus.13562.13562.3	3	12.98	0	7.83E+04		(K)LSLGTYA	(K)L S/L/G/T|Y/A S/L/H G R(I)		128.13	425.5623	1274.685	-0.0128	-10.1	8.75	67446.5	5.63	HUMAN	F8VQE1	LIM domain and actin-binding protein 1
5201	dirMS_041712_NAR_120mM_minus.17608.17608.4	4	12.98	1	5.36E+05		(R)GFGHIG	(R)G F G H I G I A\V|P/D/V Y/S A C/K R(F)	C:Carbamidomethylation	150.42	487.502	1946.991	-0.0044	-2.2	8.6	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
5202	dirMS_041712_NAR_20mM_minus.13338.13338.2	2	12.98	0	5.67E+05		(K)DAGTIA	(K)D A G T|I/A/G/L N V L R(I)		184.72	600.3403	1199.674	-0.0009	-0.8	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
5203	dirMS_041712_NAR_30mM_minus2.12447.12549.2	2	12.98	0	2.62E+05		(K)STLTDSL	(K)S T|L/T|D S/L/V/C/K(A)	C:Carbamidomethylation	121.85	562.2838	1123.566	-0.006	-5.4	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
5204	dirMS_041712_NAR_30mM_minus2.18305.18305.2	2	12.98	0	4.10E+05		(R)QAQEYE	(R)Q A/Q\E/Y/E/A L/L N/I/K(V)		154.6	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5205	dirMS_041712_NAR_50mM_minus2.12630.13026.3	3	12.98	1	1.49E+06	M320m	(K)YmACCL	(K)Y/m|A/C/C L L Y R G D\V\V/P K(E)	C:Carbamidomethylation m:Oxid	141.15	620.9644	1844.886	15.9931	-1	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
5206	dirMS_041712_NAR_50mM_minus2.14691.14691.3	3	12.98	1	9.01E+05		(R)IINEPTA	(R)I I|N/E/P T A A A/I A Y/G L D K R(E)		152.55	606.0022	1815.996	-0.0043	-2.4	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
5207	dirMS_041712_NAR_50mM_minus2.4947.4947.3	3	12.98	1	4.33E+05		(R)AAEDDE	(R)A/A|E/D D E D/D/D V/D T K K(Q)		82.37	522.5522	1565.645	-0.0029	-1.8	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
5208	dirMS_041712_NAR_60mM_minus.15158.15158.2	2	12.98	0	4.20E+05		(R)EHALLA	(R)E H|A|L/L|A Y T L G V K(Q)		144.65	657.873	1314.742	-0.0029	-2.2	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
5209	dirMS_041712_NAR_20mM_plus.10758.11241.2	2	12.98	0	2.76E+06		(K)DVNAAI	(K)D V|N|A|A|I/A T I/K(T)		149.97	508.292	1015.578	-0.0015	-1.5	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
5210	dirMS_041712_NAR_20mM_plus.17530.17530.3	3	12.98	0	6.52E+04		(K)ITNLTQC	(K)I T N L/T Q/Q|L/E/Q/A/S I V K(K)		192.92	562.6523	1685.943	-0.0009	-0.5	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
5211	dirMS_041712_NAR_30mM_plus2.11587.11886.2	2	12.98	0	4.44E+06		(K)SCNCLLL	(K)S/C|N/C L/L/L|K(V)	C:Carbamidomethylation	114.7	504.2556	1007.501	0.0027	2.7	8.47	47510.4	7.04	HUMAN	P06733	Alpha-enolase
5212	dirMS_041712_NAR_30mM_plus2.21156.21156.2	2	12.98	0	3.35E+05		(R)GVVQEL	(R)G V|V/Q|E/L Q Q A I/S K(L)		165.75	650.3632	1299.727	-0.0076	-5.8	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
5213	dirMS_041712_NAR_30mM_plus2.5468.5468.3	3	12.98	0	6.70E+04		(R)GGSGGS	(R)G G\S G G S Y G\G G G S/G G G Y/G/G/G S G S R(G)		82.82	597.9128	1791.728	-0.0039	-2.2	8.59	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
5214	dirMS_041712_NAR_40mM_plus2.12845.12845.3	3	12.98	0	7.57E+04		(R)GVVGG	(R)G V/V\G|G V/T G I I/T K/P V E G A/K(K)		142.2	561.3291	1681.985	-0.012	-7.1	8.59	424721.6	6.38	HUMAN	Q709C8	Vacuolar protein sorting-associated protein 13C
5215	dirMS_041712_NAR_40mM_plus2.19122.19285.3	3	12.98	0	3.19E+05		(K)AIEPPPL	(K)A I|E|P/P/P L D A V I/E A E/H T L R(E)		179.85	657.6841	1971.055	-0.0168	-8.5	4.4	142268.2	6.41	HUMAN	Q08211	ATP-dependent RNA helicase A
5216	dirMS_041712_NAR_30mM_minus2.6545.6545.2	2	12.97	0	2.34E+05		(R)QQYESV	(R)Q Q|Y/E S V/A/A\K(N)		89.95	512.2534	1023.511	-0.011	-10.8	6	49709.6	5.19	HUMAN	B0YJC4	Vimentin
5217	dirMS_041712_NAR_30mM_minus2.7470.7470.2	2	12.97	0	5.49E+04		(R)GAEQLA	(R)G A|E|Q/L\A/E/G G R(M)		95.05	494.2466	987.485	0.0005	0.5	4.53	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b
5218	dirMS_041712_NAR_40mM_minus2.12599.12599.3	3	12.97	1	5.98E+05		(R)VCENIPI	(R)V/C|E/N I/P I V L C G N K V D\I K(D)	C:Carbamidomethylation	157.7	657.6842	1971.04	-0.0021	-1.1	6.04	14844.8	5.89	HUMAN	B4DV51	GTP-binding nuclear protein Ran
5219	dirMS_041712_NAR_40mM_minus2.14294.14294.3	3	12.97	1	1.61E+05		(K)TGISDVF	(K)T G\I/S D V F A K N D L/A|V V/D/V R(I)		168.48	640.3454	1919.023	-0.0016	-0.8	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
5220	dirMS_041712_NAR_40mM_minus2.15439.15439.3	3	12.97	1	2.95E+05		(R)GGPNIIT	(R)G G/P N/I/I/T L/A D I/V K D/P V S R(T)		178.48	622.3523	1865.049	-0.0067	-3.6	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
5221	dirMS_041712_NAR_60mM_minus.18619.18619.3	3	12.97	0	2.89E+05		(K)TFLVWV	(K)T F|L\V/W V/N/E/E D/H/L R(V)		165.77	553.2818	1657.833	-0.0024	-1.5	4.65	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
5222	dirMS_041712_NAR_60mM_minus.19992.19992.3	3	12.97	1	7.92E+05		(R)LIALLEVI	(R)L I|A\L/L/E/V L S Q K R(M)		182.05	461.6287	1382.873	-0.0014	-1	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
5223	dirMS_041712_NAR_60mM_minus.9371.9371.3	3	12.97	1	1.18E+05		(R)SYLTPVF	(R)S Y|L/T/P V R D E E S E S Q R(K)		112.02	599.2883	1795.846	0.0047	2.6	4.41	76931.3	5.22	HUMAN	F8VZN8	Protein phosphatase 1 regulatory subunit 12A (Fragment)
5224	dirMS_041712_NAR_120mM_plus.8777.8777.3	3	12.97	0	2.74E+06		(K)HTGPNS	(K)H T G P/N\S\P D|T A/N/D G F\V R(L)		99.25	562.26	1684.767	-0.0019	-1.2	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
5225	dirMS_041712_NAR_30mM_plus2.12926.12926.2	2	12.97	0	3.70E+05		(R)ELAEDG	(R)E L/A/E/D G/Y/S/G V/E V R(V)		120.6	712.3382	1423.67	-0.0008	-0.6	4	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
5226	dirMS_041712_NAR_30mM_plus2.17893.17916.2	2	12.97	0	2.19E+05		(R)ILNVPQI	(R)I L|N|V|P Q/E L Y E K(G)		146.72	673.3645	1345.736	-0.0145	-10.8	4.53	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
5227	dirMS_041712_NAR_40mM_plus2.19237.19237.3	3	12.97	0	1.61E+06		(R)AGKPVI	(R)A G K|P V I C A\T/Q/M/L/E S M I/K(K)	C:Carbamidomethylation	180.63	626.3273	1876.969	-0.002	-1.1	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)

5228	dirMS_041712_NAR_40mM_plus2.20068.20068.3	3	12.97	1	5.88E+05		(K)EGGLGP	(K)E G G L/G/P L/N/I P L L A D V T R R(L)		189.8	631.0288	1891.076	-0.0041	-2.2	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
5229	dirMS_041712_NAR_40mM_plus2.7045.7429.2	2	12.97	0	2.91E+06		(R)STFSTNY	(R)S T|F/S/T/N/Y R(S)		101.98	488.2297	975.453	-0.0009	-0.9	8.46	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5230	dirMS_041712_NAR_50mM_plus2.6374.6398.3	3	12.97	0	6.38E+05	M437m	(R)LESGMC	(R)L/E|S G M Q/N m/S I/H/T K(T)	m:Oxidized methionine	98.88	497.9026	1475.698	15.9951	0.1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
5231	dirMS_041712_NAR_60mM_plus.12184.12184.3	3	12.97	1	1.01E+06	M232m	(R)MSmKE	(R)M/S/m K E V D E\Q\M/L/N V Q/N K(N)	m:Oxidized methionine	120.57	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
5232	dirMS_041712_NAR_60mM_plus.6433.6433.2	2	12.97	0	1.74E+05		(R)DAVTYT	(R)D A\V|T/Y/T E H A K(R)		92.18	567.775	1134.543	0.0001	0.1	5.32	11367.1	11.36	HUMAN	P62805	Histone H4
5233	dirMS_041712_NAR_30mM_minus2.14084.14084.2	2	12.96	0	2.19E+05		(R)GANDFN	(R)G A/N/D/F/M/C D E M/E R(S)	C:Carbamidomethylation	130.03	737.7725	1474.54	-0.0018	-1.2	3.91	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
5234	dirMS_041712_NAR_30mM_minus2.18872.18872.2	2	12.96	0	1.32E+04		(R)NTWLYC	(R)N T/W|L/Y/Q/A L/R(E)		157.48	582.8109	1164.616	-0.0015	-1.3	8.75	49457.5	6.47	HUMAN	P56545	C-terminal-binding protein 2
5235	dirMS_041712_NAR_40mM_minus2.8143.8143.3	3	12.96	1	3.18E+05		(R)DGKLVS	(R)D G K L\V\S E/S/S D V L/P K(-)		128.2	491.9311	1473.78	-0.0008	-0.5	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
5236	dirMS_041712_NAR_50mM_minus2.15108.15108.3	3	12.96	1	2.85E+05		(K)VVEEAP	(K)V V|E/E A/P S I F L D A E T R/R(A)		153.48	611.3243	1831.955	0.0035	1.9	4.41	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
5237	dirMS_041712_NAR_120mM_plus.13319.13352.3	3	12.96	0	6.88E+05		(K)HIMGQN	(K)H I\M\G Q\N\V|A/D/Y M/R(Y)		123.07	478.8925	1434.662	0.0013	0.9	6.74	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
5238	dirMS_041712_NAR_120mM_plus.18691.19093.4	4	12.96	1	2.39E+06		(K)FQIPPN	(K)F Q|I/P/P/N/A E/L K Y E L H L K(S)		151.9	485.7703	1940.064	-0.0046	-2.4	6.75	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
5239	dirMS_041712_NAR_20mM_plus.8356.8356.2	2	12.96	0	4.09E+04	M105m	(K)mADEA	(K)m A\D E\A\V|C V|G P A|P T S K(S)	C:Carbamidomethylation m:Oxid	127.8	774.8589	1532.708	16.0022	4.7	4.37	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
5240	dirMS_041712_NAR_30mM_plus2.4498.4498.2	2	12.96	0	3.33E+05	M131m	(K)AmPATS	(K)A m|P/A T S A E G R(Q)	m:Oxidized methionine	73.1	503.7289	990.467	15.9832	-11.6	6.05	16817.7	6.72	HUMAN	H0YC17	TNFAIP3-interacting protein 1 (Fragment)
5241	dirMS_041712_NAR_30mM_plus2.5484.5547.2	2	12.96	0	5.72E+05		(R)GGAGV	(R)G G|A|G|V|G/S M/T/K(I)		83.05	432.7161	864.424	0.0005	0.6	8.75	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
5242	dirMS_041712_NAR_30mM_plus2.9560.9560.2	2	12.96	0	4.96E+05		(K)TAVCDIF	(K)T/A|V|C/D/I/P|P R(G)	C:Carbamidomethylation	105.07	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
5243	dirMS_041712_NAR_40mM_plus2.18461.18477.3	3	12.96	0	1.98E+06		(K)ALESPER	(K)A/L\E|S/P E R P/F L A I L/G/G A K(V)		175.55	590.3359	1768.996	-0.0024	-1.4	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
5244	dirMS_041712_NAR_40mM_plus2.8996.8996.3	3	12.96	0	4.93E+04		(K)VVQVSA	(K)V V|Q/V/S A G D S H T A/A L T D D G R(V)		115.07	633.6448	1898.92	-0.0004	-0.2	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
5245	dirMS_041712_NAR_50mM_plus2.15503.15503.3	3	12.96	1	7.67E+05		(K)VQGGAL	(K)V/Q|G/G A/L E D S Q L V/A G V A F K K(T)		150.35	639.6848	1917.044	-0.0042	-2.2	6.04	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
5246	dirMS_041712_NAR_50mM_plus2.9324.9324.3	3	12.96	1	1.02E+06		(K)TAVCDIF	(K)T A|V/C/D/I/P P R G L K(M)	C:Carbamidomethylation	116.6	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
5247	dirMS_041712_NAR_60mM_plus.13021.13064.3	3	12.96	1	2.54E+05		(R)VVGAM	(R)V/V|G A/M Q/L/Y/S V D/R K(V)		124.97	489.2643	1465.783	-0.0048	-3.3	8.56	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
5248	dirMS_041712_NAR_60mM_plus.16385.16403.3	3	12.96	1	5.36E+05		(R)VTPTRT	(R)V/T|P T R T E I/I/I/L/A T R(T)		142.83	528.653	1583.948	-0.0035	-2.2	9.57	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
5249	dirMS_041712_NAR_60mM_plus.16642.16642.3	3	12.96	1	6.93E+05		(R)STNKGT.	(R)S T N K G T A\Y\T/F/F/T\P G N L K(Q)		144.48	616.3117	1846.933	-0.0128	-7	9.7	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
5250	dirMS_041712_NAR_60mM_plus.6403.6422.3	3	12.96	1	4.82E+05		(K)TIAPQN	(K)T/I|A|P/Q N A P R D E/S R(G)		92.2	485.5816	1454.735	-0.0044	-3	5.73	53030.7	11.3	HUMAN	E9PJA7	Bcl-2-associated transcription factor 1
5251	dirMS_041712_NAR_60mM_plus.6930.6947.3	3	12.96	1	3.73E+05		(K)DGGFCE	(K)D/G|G|F/C/E/V/C K K(L)	C:Carbamidomethylation	94.72	400.5114	1199.518	0.0013	1.1	6.07	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
5252	dirMS_041712_NAR_120mM_minus.21430.21430.3	3	12.95	0	8.12E+05		(R)LHFFMP	(R)L H F F M|P G\F\A/P|L/T S R(G)		182.17	540.9497	1620.835	-0.001	-0.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
5253	dirMS_041712_NAR_20mM_minus.7646.7646.2	2	12.95	0	7.13E+05	M239m	(K)EVDEQm	(K)E V/D\E Q m L/N|V|Q/N/K(N)	m:Oxidized methionine	125.03	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
5254	dirMS_041712_NAR_30mM_minus2.10784.11213.2	2	12.95	0	2.51E+06		(R)TSASIILR	(R)T/S|A/S/I/I/L/R(G)		112.08	430.7619	860.52	-0.0035	-4	9.41	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
5255	dirMS_041712_NAR_30mM_minus2.15806.15806.2	2	12.95	0	1.25E+05		(R)TINEVEN	(R)T I/N E|V|E/N\Q I/L/T R(D)		139.6	715.3834	1429.765	-0.005	-3.5	4.53	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
5256	dirMS_041712_NAR_30mM_minus2.9632.9632.2	2	12.95	0	9.57E+05		(K)EAESSPF	(K)E A|E/S/S/P F V/E/R(L)		107.35	575.7705	1150.537	-0.0038	-3.3	4.25	92752.5	4.76	HUMAN	P14625	Endoplasmin
5257	dirMS_041712_NAR_50mM_minus2.7420.7420.3	3	12.95	1	8.03E+04		(R)VAVEAK	(R)V A|V E A K N\P A D/L/P/K(L)		109.27	451.2571	1351.758	-0.0012	-0.9	6.04	96306.4	6.41	HUMAN	P13639	Elongation factor 2
5258	dirMS_041712_NAR_50mM_minus2.9713.9713.3	3	12.95	1	7.87E+04		(R)SVLGEAI	(R)S V|L/G E/A D/Q K G S L V A/P D R(L)		123.27	581.2998	1741.908	-0.0231	-13.2	4.56	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
5259	dirMS_041712_NAR_20mM_plus.15171.15171.2	2	12.95	0	3.01E+05		(K)LLCGLLA	(K)L/L/C/G L/L A E R(L)	C:Carbamidomethylation	176.75	522.7971	1044.587	-0.0001	-0.1	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
5260	dirMS_041712_NAR_20mM_plus.18995.18995.2	2	12.95	0	1.82E+05		(R)VCTLAII	(R)V C/T\L/A|I|I/D\P G D S D I I R(S)	C:Carbamidomethylation	202.65	879.4578	1757.91	-0.0019	-1.1	3.93	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
5261	dirMS_041712_NAR_20mM_plus.7066.7066.2	2	12.95	0	4.35E+05		(R)IQEAGTI	(R)I/Q|E/A/G T E V V K(A)		115.37	537.2946	1073.584	-0.0018	-1.7	4.53	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
5262	dirMS_041712_NAR_30mM_plus2.12605.12605.2	2	12.95	0	5.61E+05		(K)NAGVEG	(K)N A|G\V/E/G S L I V/E K(I)		118.43	608.3313	1215.658	-0.0026	-2.2	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
5263	dirMS_041712_NAR_30mM_plus2.18907.19033.3	3	12.95	0	1.36E+05		(K)DAGTIA	(K)D A\G\T I/A/G L/N V/L/R(I)		152.62	400.563	1199.674	0.0002	0.2	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
5264	dirMS_041712_NAR_30mM_plus2.5531.5531.2	2	12.95	0	2.56E+05		(R)TGPPMC	(R)T/G|P/P M G S R(F)		82.32	401.6975	802.388	0.0001	0.2	9.41	27441.6	6.68	HUMAN	Q15056	Eukaryotic translation initiation factor 4H
5265	dirMS_041712_NAR_50mM_plus2.17302.17302.3	3	12.95	0	3.07E+05		(R)DLKPSNI	(R)D L K P S N\L\L/I/N T/T C D/L K(I)	C:Carbamidomethylation	158.4	615.664	1844.979	-0.0012	-0.6	5.96	30925	5.63	HUMAN	B3KR49	Mitogen-activated protein kinase 3
5266	dirMS_041712_NAR_60mM_plus.5645.5645.3	3	12.95	1	3.86E+04		(R)TLEEKEC	(R)T/L|E/E/K/E Q E E A R(L)		87.77	454.555	1361.654	-0.0039	-2.8	4.32	95923.1	9.67	HUMAN	Q9BUQ8	Probable ATP-dependent RNA helicase DDX23
5267	dirMS_041712_NAR_120mM_minus.15023.15067.4	4	12.94	1	3.11E+05		(R)EALLSSA	(R)E\A L/L/S S/A/V/D/H\G S D E V K/F R(Q)		135.92	490.7539	1959.977	0.0167	8.5	4.75	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
5268	dirMS_041712_NAR_30mM_minus2.13872.14047.2	2	12.94	0	3.82E+05		(R)LAGLFNI	(R)L/A|G L/F/N/E/Q/R(K)		129.28	524.2789	1047.558	-0.0076	-7.3	6	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
5269	dirMS_041712_NAR_30mM_minus2.14843.14843.2	2	12.94	0	1.40E+05		(R)WALSQS	(R)W A|L|S/Q/S N|P S A L/R(E)		134.55	665.3481	1329.691	-0.0021	-1.5	9.75	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
5270	dirMS_041712_NAR_30mM_minus2.14882.14950.2	2	12.94	0	2.44E+05		(K)IDIIPNP	(K)I D|I|I|P/N P Q E/R(T)		134.87	597.8249	1194.648	-0.0052	-4.3	4.37	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
5271	dirMS_041712_NAR_40mM_minus2.12223.12223.3	3	12.94	0	4.74E+05		(K)IAILTCPF	(K)I/A|I/L T/C/P F E/P P K P K(T)	C:Carbamidomethylation	155.73	537.6382	1610.898	0.0026	1.6	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
5272	dirMS_041712_NAR_60mM_minus.15488.15602.3	3	12.94	1	1.72E+05		(R)GRLPLLA	(R)G R\L\P\L|L|A/V/C D/Y K(Q)	C:Carbamidomethylation	146.87	468.9273	1404.767	0.0006	0.4	8.59	533778	5.74	HUMAN	Q15149	Plectin
5273	dirMS_041712_NAR_120mM_plus.10149.10695.3	3	12.94	0	1.61E+06		(R)GFCLPPI	(R)G F|C L/P/P/H C S/R(G)	C:Carbamidomethylation	108.33	410.8593	1230.551	0.0127	10.3	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
5274	dirMS_041712_NAR_120mM_plus.18142.18168.3	3	12.94	1	1.16E+06		(R)RAPFDLI	(R)R\A\P F\D|L|F E/N/R(K)		147.75	422.22	1264.643	0.0022	1.7	6.07	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
5275	dirMS_041712_NAR_120mM_plus.4312.4401.3	3	12.94	1	3.08E+05		(K)AGADEE	(K)A/G|A/D/E/E R A E/T/A/R(L)		71.55	425.869	1275.592	0.0001	0.1	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
5276	dirMS_041712_NAR_40mM_plus2.12295.12397.3	3	12.94	0	3.16E+05		(K)AASDIAN	(K)A A\S D|I/A/M/T E L/P P T H P I R(L)		139.5	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
5277	dirMS_041712_NAR_40mM_plus2.14012.14012.3	3	12.94	1	8.78E+04		(R)STGLELE	(R)S T|G L/E L E/T/P S L V/P V K/K(N)		148.73	566.6552	1697.968	-0.0173	-10.2	5.86	34828	9.96	HUMAN	F5H5K4	Serine/threonine-protein phosphatase 1 regulatory subunit 10
5278	dirMS_041712_NAR_40mM_plus2.7182.7366.2	2	12.94	0	2.20E+05		(R)AQYDEL	(R)A Q|Y/D/E/L/A/R(K)		102.77	483.2372	965.469	-0.0016	-1.6	4.37	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5279	dirMS_041712_NAR_40mM_plus2.7774.7774.2	2	12.94	0	1.91E+04		(R)SEGFDT	(R)S E|G|F/D/T Y R(C)		105.63	487.7152	974.421	0.0017	1.8	4.37	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
5280	dirMS_041712_NAR_50mM_plus2.6151.6151.3	3	12.94	1	1.12E+05		(R)VVSSIEC	(R)V/V|S/S/I E Q K T E G A E K(K)		96.75	502.2651	1504.785	-0.0046	-3	4.79	8491.4	6.28	HUMAN	E5RIR4	14-3-3 protein zeta/delta (Fragment)
5281	dirMS_041712_NAR_60mM_plus.15605.15605.2	2	12.94	1	4.11E+05		(R)TEMENE	(R)T E|M|E/N/E F V/L I|K K(D)		138.27	740.8875	1480.772	-0.0039	-2.6	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
5282	dirMS_041712_NAR_60mM_plus.7480.7480.3	3	12.94	1	9.89E+05		(K)GGETIK	(K)G G E/T I/K/Q/L/Q E R(A)		97.62	420.23	1258.675	0.0005	0.4	6.14	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
5283	dirMS_041712_NAR_120mM_minus.11674.11674.4	4	12.93	2	9.96E+05		(R)SGKYDLI	(R)S G\K Y D\L\D\F/K/S P D D/P/S R(Y)		117.92	457.4692	1826.855	-0.0006	-0.3	4.58	47510.4	7.04	HUMAN	P06733	Alpha-enolase
5284	dirMS_041712_NAR_60mM_minus.10563.10563.3	3	12.93	1	1.64E+06		(K)TLQEVTI	(K)T L/Q E/V/T/E/M D S/V K R(Y)		119.37	512.5957	1535.773	-0.0008	-0.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
5285	dirMS_041712_NAR_120mM_plus.4337.4341.3	3	12.93	1	3.08E+05		(K)AGADEE	(K)A/G|A/D/E/E|R A E T A R(L)		71.55	425.869	1275.592	0.0001	0.1	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
5286	dirMS_041712_NAR_20mM_plus.17235.17235.2	2	12.93	0	8.90E+04		(R)AVLVDLI	(R)A/V L\V|D|L|E/P G T\M D S V R(S)		189.62	801.414	1601.82	0.0004	0.2	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
5287	dirMS_041712_NAR_20mM_plus.6988.6988.2	2	12.93	0	2.19E+05		(R)LLEAAA	(R)L L|E|A A/A/Q/S T K(G)		114.93	516.2866	1031.573	-0.0072	-7	6	533778	5.74	HUMAN	Q15149	Plectin
5288	dirMS_041712_NAR_30mM_plus2.10610.10790.2	2	12.93	0	2.02E+06		(R)GLDISN	(R)G L|D|I/S/N V/K(H)		109.57	423.244	845.473	0.008	9.5	5.84	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
5289	dirMS_041712_NAR_30mM_plus2.11683.11683.2	2	12.93	0	6.20E+05		(R)AMGEQ	(R)A M/G E/Q/A/V|A L A/R(A)		114.52	558.7944	1116.583	-0.0015	-1.3	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
5290	dirMS_041712_NAR_30mM_plus2.9667.9667.2	2	12.93	0	1.58E+05		(R)ASAVSEI	(R)A S|A|V|S/E L\S P R(E)		105.27	508.7716	1016.537	-0.0012	-1.2	6.05	108720.9	10.17	HUMAN	Q9Y2W1	Thyroid hormone receptor-associated protein 3
5291	dirMS_041712_NAR_50mM_plus2.14908.14908.3	3	12.93	0	5.02E+05		(K)TTISVAH	(K)T T|I/S/V A/H/L\L/A A/R(Q)		146.45	418.2499	1252.737	-0.002	-1.6	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
5292	dirMS_041712_NAR_60mM_plus.9461.9461.2	2	12.93	0	4.97E+05		(K)SYCAEIA	(K)S Y/C|A/E I/A H\N V|S/S/K(N)	C:Carbamidomethylation	107.47	733.3425	1465.674	0.0037	2.5	6.47	15730.4	11.67	HUMAN	D3YTB1	60S ribosomal protein L32 (Fragment)
5293	dirMS_041712_NAR_120mM_minus.9128.9128.3	3	12.92	0	1.73E+05		(K)VSYGIGI	(K)V/S|Y/G/I/G D E E H D Q E G/R(V)		104.22	564.2496	1690.73	0.0039	2.3	4.17	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
5294	dirMS_041712_NAR_20mM_minus.13561.13561.2	2	12.92	0	3.53E+05		(K)DAGTIA	(K)D A/G T|I/A/G\L N V L R(I)		185.43	600.3403	1199.674	-0.0009	-0.8	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
5295	dirMS_041712_NAR_20mM_minus.8897.8897.2	2	12.92	0	1.37E+05		(R)LEQYTS	(R)L E/Q Y/T S A I/E/G T/K(S)		137.98	670.3403	1339.674	-0.0007	-0.5	4.53	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
5296	dirMS_041712_NAR_30mM_minus2.18845.18845.2	2	12.92	0	9.16E+04		(R)NYLSIFR	(R)N/Y|L|S I/F R(K)		157.13	456.7503	912.494	-0.0005	-0.5	8.75	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
5297	dirMS_041712_NAR_50mM_minus2.12443.12443.3	3	12.92	1	2.16E+05	M4131m	(K)ISmPEVI	(K)I/S m/P/E V/D/L/N L K/G P K(M)	m:Oxidized methionine	139.38	519.6148	1540.84	15.9895	-3.5	6.07	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
5298	dirMS_041712_NAR_120mM_plus.18482.18943.4	4	12.92	1	2.62E+06		(K)FQIPPN	(K)F Q\I|P/P|N/A E/L K/Y E L H L K(S)		151.22	485.7703	1940.064	-0.0046	-2.4	6.75	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
5299	dirMS_041712_NAR_120mM_plus.8541.8541.3	3	12.92	0	1.86E+06		(K)HTGPNS	(K)H T G\P N\S P D T/A/N/D|G F/V R(L)		98.87	562.26	1684.767	-0.0019	-1.2	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
5300	dirMS_041712_NAR_20mM_plus.8115.8115.2	2	12.92	0	8.65E+04		(R)AAPGAE	(R)A A|P/G/A/E F/A P N K(R)		125.65	536.7749	1072.542	0.0003	0.3	6.05	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
5301	dirMS_041712_NAR_30mM_plus2.6020.6020.2	2	12.92	0	1.82E+05		(R)DSEIMQ	(R)D S|E|I/M/Q/Q/K(Q)		86	489.7318	978.456	0.0003	0.3	4.37	5215.9	10.07	HUMAN	B5MCG1	Small EDRK-rich factor 2
5302	dirMS_041712_NAR_50mM_plus2.14724.14724.3	3	12.92	0	7.40E+05		(K)LTLLHYD	(K)L/T L L H/Y D|P V V/K(Q)		144.95	433.2551	1297.751	-0.0007	-0.5	6.74	7676.1	11.12	HUMAN	O75394	39S ribosomal protein L33, mitochondrial
5303	dirMS_041712_NAR_50mM_plus2.16352.16393.3	3	12.92	0	3.08E+05		(R)VSLDVN	(R)V/S|L/D V N H F/A/P D E L T V K(T)		154.13	595.312	1783.922	-0.001	-0.6	4.54	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
5304	dirMS_041712_NAR_60mM_plus.11383.11383.3	3	12.92	0	3.70E+05		(R)SLGTAD	(R)S L/G T A/D/V/H F E\R(K)		116.88	411.2075	1231.607	0.0014	1.1	5.3	27557.2	11.05	HUMAN	E9PB61	THO complex subunit 4
5305	dirMS_041712_NAR_60mM_plus.12960.12960.3	3	12.92	0	1.26E+06		(K)VNGRPL	(K)V/N|G R|P L E M\I\E/P R(T)		124.65	470.9225	1410.752	0.0008	0.5	6.11	16559.1	10.36	HUMAN	P62249	40S ribosomal protein S16
5306	dirMS_041712_NAR_60mM_plus.7224.7224.3	3	12.92	1	4.31E+05		(K)VVSETN	(K)V V/S E/T/N\D T/K V L/R(H)		95.93	454.2511	1360.743	-0.0043	-3.2	6.04	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
5307	dirMS_041712_NAR_20mM_minus.12267.12267.3	3	12.91	0	5.12E+05	M73m	(R)AVLVDLI	(R)A V L V/D L\E/P/G T m/D S V R(S)	m:Oxidized methionine	172.05	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
5308	dirMS_041712_NAR_20mM_minus.13117.13117.2	2	12.91	0	4.63E+05		(K)TITLEVEI	(K)T I/T\L E/V|E/P/S D T I/E/N V K(A)		183.05	894.4654	1787.927	-0.0038	-2.1	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
5309	dirMS_041712_NAR_30mM_minus2.10516.10516.2	2	12.91	0	1.47E+06		(R)GLTSVIN	(R)G L/T|S/V/I/N Q K(L)		111.3	480.2794	959.552	-0.0005	-0.5	8.75	36923.1	5.71	HUMAN	P07195	L-lactate dehydrogenase B chain
5310	dirMS_041712_NAR_30mM_minus2.13523.13523.2	2	12.91	0	5.19E+05		(R)YALYDA	(R)Y A|L/Y/D/A\T Y E/T K(E)		126.48	669.3172	1337.626	0.0011	0.9	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
5311	dirMS_041712_NAR_30mM_minus2.20456.20456.2	2	12.91	0	4.58E+05		(R)FLTWILN	(R)F/L|T|W I/L N/R(Y)		175.92	531.8089	1062.61	0.001	1	9.75	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
5312	dirMS_041712_NAR_40mM_minus2.11778.11942.3	3	12.91	1	5.04E+05		(K)VALNVS	(K)V/A|L/N/V/S C A N L L D K D/I/G S K(S)	C:Carbamidomethylation	153.28	639.6749	1917.011	-0.0008	-0.4	5.93	9239.5	7.98	HUMAN	E5RFT7	Copine-3 (Fragment)
5313	dirMS_041712_NAR_50mM_minus2.16187.16187.3	3	12.91	0	1.46E+05		(K)LDPHLVI	(K)L D/P/H|L\V\L/D Q L R(C)		160.2	440.2533	1318.748	-0.0024	-1.8	5.21	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
5314	dirMS_041712_NAR_120mM_plus.20065.20065.4	4	12.91	2	2.03E+05		(K)QLKLDP	(K)Q L K L D/P S|I/F/E/S L Q K E/R(V)		158.5	483.519	1931.06	-0.0055	-2.8	6.18	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
5315	dirMS_041712_NAR_20mM_plus.15796.15796.3	3	12.91	0	5.41E+05		(K)VGINYQ	(K)V G I N Y Q|P P/T V V/P G G D L A K(V)		179.43	608.9991	1824.985	-0.0027	-1.5	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
5316	dirMS_041712_NAR_20mM_plus.18572.18572.2	2	12.91	0	1.96E+05		(R)VFIGNLN	(R)V/F|I/G/N\L N T L V V/K(K)		200.12	658.8999	1316.794	-0.0011	-0.9	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
5317	dirMS_041712_NAR_20mM_plus.18698.18854.2	2	12.91	0	2.32E+05		(R)IITLAGP	(R)I I|T|L/A|G/P T N A I F K(A)		200.97	679.9039	1358.804	-0.0037	-2.7	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
5318	dirMS_041712_NAR_20mM_plus.19018.19018.2	2	12.91	0	5.75E+04		(K)ILTFDQL	(K)I L/T/F D Q/L A/L/D/S P K(G)		202.35	730.9063	1460.8	0.0058	4	4.21	14643	11.93	HUMAN	F8VUA6	60S ribosomal protein L18 (Fragment)
5319	dirMS_041712_NAR_30mM_plus2.12118.12118.2	2	12.91	0	3.47E+05		(R)DVCLYPI	(R)D V|C/L/Y/P R(F)	C:Carbamidomethylation	116.58	461.7327	922.445	0.013	14.1	5.83	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
5320	dirMS_041712_NAR_30mM_plus2.20706.20706.2	2	12.91	0	2.60E+05		(R)ASLSLW	(R)A S/L/S L/W/Q/A/M/E K(G)		162.9	632.3231	1263.64	-0.0013	-1	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
5321	dirMS_041712_NAR_40mM_plus2.10702.10702.3	3	12.91	1	4.10E+05		(R)DGKLVS	(R)D G K L V\S E|S/S D|V L/P/K(-)		128.58	491.9315	1473.78	0.0004	0.3	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
5322	dirMS_041712_NAR_50mM_plus2.7372.7393.3	3	12.91	1	1.63E+05		(R)TESTPIT	(R)T E|S/T/P I/T/A V\K Q/P E K(V)		104.68	510.2769	1528.822	-0.0056	-3.6	5.81	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
5323	dirMS_041712_NAR_60mM_plus.12530.12831.3	3	12.91	0	8.61E+04		(R)LFGGNF.	(R)L/F/G G N F/A/H/Q/A S V A/R(V)		120.92	492.2556	1474.755	-0.0027	-1.8	9.75	61760.3	6.01	HUMAN	O14773	Tripeptidyl-peptidase 1
5324	dirMS_041712_NAR_60mM_plus.12877.12997.3	3	12.91	0	1.96E+06		(K)SQIHDIV	(K)S Q I H D\I\V|L|V/G/G S T/R(I)		124.55	494.6067	1481.807	-0.0015	-1	6.46	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
5325	dirMS_041712_NAR_20mM_minus.13381.13381.2	2	12.9	0	6.66E+05		(K)DAGTIA	(K)D A G T|I/A/G L N V/L R(I)		184.88	600.3403	1199.674	-0.0009	-0.8	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
5326	dirMS_041712_NAR_30mM_minus2.10684.10857.2	2	12.9	0	6.01E+05	M23m	(K)LYLADPr	(K)L/Y|L|A/D/P m/K(A)	m:Oxidized methionine	112.18	483.7524	950.502	15.996	1.1	5.83	7781.8	6.82	HUMAN	E9PE20	Signal recognition particle 9 kDa protein
5327	dirMS_041712_NAR_40mM_minus2.14513.14867.3	3	12.9	1	1.50E+06	M116m	(R)ELAILLG	(R)E L\A|I/L|L/G m L D/P A E K D/E K(G)	m:Oxidized methionine	171.22	634.338	1884.999	16.0008	3.1	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
5328	dirMS_041712_NAR_50mM_minus2.16077.16077.3	3	12.9	1	1.46E+05		(K)ISMPDID	(K)I/S/M/P D I D L/N L K G P K(V)		159.93	514.2852	1540.84	0.0007	0.5	5.96	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
5329	dirMS_041712_NAR_50mM_minus2.16410.16410.3	3	12.9	1	8.40E+05		(R)VTFSGLF	(R)V/T/F/S/G L\R D/T V T/P G E L L K(A)		162.35	611.672	1833.012	-0.0102	-5.6	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
5330	dirMS_041712_NAR_50mM_minus2.4945.4945.3	3	12.9	1	4.33E+05		(R)AAEDDE	(R)A/A/E/D/D E D/D D/V D T K K(Q)		82.37	522.5522	1565.645	-0.0029	-1.8	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
5331	dirMS_041712_NAR_60mM_minus.12119.12119.3	3	12.9	1	2.15E+05		(K)YADEEIP	(K)Y/A/D E E/I/P R S P F/K(V)		127.3	484.5732	1451.717	-0.0115	-7.9	4.68	258215.9	5.48	HUMAN	E7EN95	Filamin-B
5332	dirMS_041712_NAR_120mM_plus.5547.5547.3	3	12.9	1	3.76E+05		(K)TCEESSF	(K)T|C/E/E/S S F/C K/R(Q)	C:Carbamidomethylation	82.18	435.1877	1303.541	0.008	6.1	5.81	10576.1	11.44	HUMAN	E9PRF8	Neutral alpha-glucosidase AB
5333	dirMS_041712_NAR_30mM_plus2.17185.17185.2	2	12.9	0	4.83E+05	M256m	(R)SLDmDS	(R)S L/D\m/D|S I/I|A/E|V K(A)	m:Oxidized methionine	142.55	668.8384	1320.671	15.998	2.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
5334	dirMS_041712_NAR_30mM_plus2.7259.7259.2	2	12.9	0	6.90E+04		(R)SQLQISN	(R)S Q|L|Q|I/S\N N\R(T)		92.6	530.2783	1059.554	-0.0048	-4.6	9.47	334221.3	6.44	HUMAN	P15924	Desmoplakin
5335	dirMS_041712_NAR_30mM_plus2.7702.7745.2	2	12.9	0	9.74E+06		(R)QLETLG	(R)Q L|E/T/L/G Q/E/K(L)		94.33	523.2797	1045.552	-0.0003	-0.3	4.53	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
5336	dirMS_041712_NAR_60mM_plus.10189.10189.3	3	12.9	1	5.14E+05		(R)RQQEQ	(R)R/Q\Q/E\Q|Q/V/P I/L/E K(F)		111.28	499.2786	1495.823	-0.0015	-1	6.14	276046.1	6.01	HUMAN	P49327	Fatty acid synthase

5337	dirMS_041712_NAR_60mM_plus.12408.12644.3	3	12.9	1	3.85E+06		(K)LFNLSKE	(K)L/F/N/L/S K/E D D/V/R(Q)		121.6	445.9046	1335.69	0.0089	6.7	4.56	25082	11.29	HUMAN	A2A3R5	40S ribosomal protein S6
5338	dirMS_041712_NAR_60mM_plus.16280.16362.3	3	12.9	1	1.84E+05		(K)KAPDFV	(K)K\A P D\F\V|F/Y/A/P R(L)		141.8	437.5685	1310.689	0.0018	1.3	8.59	71218.8	6.3	HUMAN	A7YIJ8	Radixin
5339	dirMS_041712_NAR_120mM_minus.5002.5002.3	3	12.89	1	5.75E+05		(R)AAEEED	(R)A/A/E E E/D E/A/D/P K R(Q)		79.35	453.8716	1359.602	-0.002	-1.5	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
5340	dirMS_041712_NAR_20mM_minus.10390.10390.2	2	12.89	0	1.44E+05		(R)IYVVDV	(R)I Y|V|V/D/V/G/S E/P R(A)		152.93	617.3216	1233.647	-0.0115	-9.3	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
5341	dirMS_041712_NAR_30mM_minus2.14902.15324.2	2	12.89	0	1.56E+06		(R)QITVND	(R)Q I|T/V/N D/L/P V G/R(S)		135.22	606.3404	1211.674	-0.0007	-0.6	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
5342	dirMS_041712_NAR_50mM_minus2.13010.13010.3	3	12.89	0	3.33E+05		(R)ETNLDS	(R)E T/N L/D/S L/P L\V D T H S K(R)		142.35	556.9529	1668.844	0.0002	0.1	4.53	53707.8	5.06	HUMAN	P08670	Vimentin
5343	dirMS_041712_NAR_60mM_minus.15179.15179.2	2	12.89	0	4.20E+05		(R)EHALLA	(R)E/H|A\L/L|A/Y T L/G V K(Q)		144.65	657.873	1314.742	-0.0029	-2.2	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
5344	dirMS_041712_NAR_20mM_plus.15974.15974.2	2	12.89	0	2.84E+05	M81m	(K)SFYPEEV	(K)S F|Y|P E E V S S m V L/T K(M)	m:Oxidized methionine	181.2	816.8988	1616.788	16.0027	4.8	4.53	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
5345	dirMS_041712_NAR_30mM_plus2.13210.13443.2	2	12.89	0	1.01E+06		(K)LYDIDV	(K)L/Y|D/I D/V/A/K(V)		123	468.7614	936.504	0.0118	12.7	4.21	22029.9	10.62	HUMAN	A8MUS3	60S ribosomal protein L23a
5346	dirMS_041712_NAR_50mM_plus2.17272.17299.3	3	12.89	0	6.18E+05		(K)VLISSLQ	(K)V L|I/S/S/L/Q D C L/H/G I/E S K(S)	C:Carbamidomethylation	159.32	600.3189	1798.937	0.0054	3	5.32	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
5347	dirMS_041712_NAR_50mM_plus2.21497.21497.3	3	12.89	1	1.97E+05		(R)LIALLEV	(R)L/I|A L/L E/V/L/S Q K R(M)		183.25	461.6293	1382.873	0.0004	0.3	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
5348	dirMS_041712_NAR_50mM_plus2.8350.8350.3	3	12.89	1	3.49E+05		(R)VAVEAK	(R)V/A/V E/A K/N P A/D L/P/K(L)		110.53	451.2563	1351.758	-0.0036	-2.7	6.04	96306.4	6.41	HUMAN	P13639	Elongation factor 2
5349	dirMS_041712_NAR_60mM_plus.13667.13715.3	3	12.89	1	5.96E+05		(R)FKIPGSP	(R)F K/I/P G S|P|P/E/S M G R(G)		128.43	468.2401	1402.715	-0.009	-6.4	8.75	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
5350	dirMS_041712_NAR_60mM_plus.7108.7139.3	3	12.89	1	4.52E+05		(K)AADIDQ	(K)A/A|D|I/D/Q/E V K E/R(A)		95.48	425.2176	1273.638	0	0	4.32	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
5351	dirMS_041712_NAR_20mM_minus.14681.14681.3	3	12.88	0	3.68E+05		(K)LAVEAL	(K)L A\V\E A\L\S\S/L/D/G D/L/A G R(Y)		201.3	529.6163	1586.838	-0.0041	-2.6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
5352	dirMS_041712_NAR_30mM_minus2.16892.16892.2	2	12.88	0	3.21E+05		(K)FANPFP	(K)F A|N|P/F/P/A A V R(G)		146.33	545.2937	1089.584	-0.0039	-3.5	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
5353	dirMS_041712_NAR_60mM_minus.18361.18361.3	3	12.88	1	4.80E+05		(K)TQLNLL	(K)T Q/L/N/L/L/L/D/K L R(S)		163.37	442.9403	1326.81	-0.004	-3	8.41	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
5354	dirMS_041712_NAR_20mM_plus.10509.10509.2	2	12.88	0	6.67E+04	S50s	(R)LLDEEIs	(R)L/L|D/E E I s|R(V)	s:N-acetylglucosamine (S)	145.4	589.309	974.515	203.0954	13.6	4.14	37784.1	8.78	HUMAN	Q96PU8	Protein quaking
5355	dirMS_041712_NAR_20mM_plus.11502.11503.2	2	12.88	0	1.17E+06		(K)DVNAAI	(K)D V|N/A|A/I/A T I K(T)		151.15	508.292	1015.578	-0.0015	-1.5	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
5356	dirMS_041712_NAR_20mM_plus.19255.19255.2	2	12.88	0	1.70E+04		(R)ALIAGG	(R)A L/I|A/G/G G|A/P E I E\L A L R(L)		203.82	775.9467	1550.89	-0.0039	-2.5	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
5357	dirMS_041712_NAR_20mM_plus.7710.7710.2	2	12.88	0	4.28E+04		(K)AVTEQG	(K)A V/T E\Q|G/A E L/S N E E R(N)		122.93	766.8616	1532.719	-0.0028	-1.8	4.09	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
5358	dirMS_041712_NAR_30mM_plus2.10423.10423.2	2	12.88	0	5.36E+04		(K)TAVCDI	(K)T A|V|C|D I/P|P R(G)	C:Carbamidomethylation	108.98	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
5359	dirMS_041712_NAR_30mM_plus2.11978.11978.2	2	12.88	0	4.31E+05		(K)AYGGAY	(K)A/Y|G G A/Y D V/M/S S K(H)		115.77	624.7816	1248.556	-0.0006	-0.5	5.88	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
5360	dirMS_041712_NAR_50mM_plus2.8298.8298.3	3	12.88	0	9.05E+04		(K)QQSIAG	(K)Q Q/S/I/A/G S A\D/S/K/P I D V S R(L)		110.42	586.971	1758.898	0.0004	0.2	5.96	34637.3	8.91	HUMAN	Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1
5361	dirMS_041712_NAR_60mM_plus.6776.6776.3	3	12.88	1	3.47E+05		(K)TQMTS	(K)T\Q|M/T/S/A V R E/P K(L)		93.58	416.5533	1247.641	0.0041	3.3	8.41	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
5362	dirMS_041712_NAR_20mM_minus.10794.10794.2	2	12.87	0	6.56E+04		(K)VNQIGS	(K)V N/Q I|G/S/V|T E S I Q A C K(L)	C:Carbamidomethylation	155.45	817.4099	1633.821	-0.0089	-5.4	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
5363	dirMS_041712_NAR_30mM_minus2.16099.16099.2	2	12.87	1	1.48E+05		(R)FVLSQA	(R)F V|L/S Q A\K D E\L(-)		141.37	575.3113	1149.615	0.0003	0.3	4.37	41053.3	5.58	HUMAN	Q86UY0	TXNDC5 protein
5364	dirMS_041712_NAR_30mM_minus2.7392.7393.2	2	12.87	0	2.50E+03		(R)TPEEYP	(R)T/P|E|E|Y/P/E S A K(V)		93.4	575.7705	1150.526	0.0075	6.5	4.25	21580.5	5.38	HUMAN	B4DGT0	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1
5365	dirMS_041712_NAR_40mM_minus2.12604.12604.3	3	12.87	1	5.98E+05		(R)VCENIP	(R)V/C|E/N\I/P I V\L/C G N K V D\I K(D)	C:Carbamidomethylation	157.7	657.6842	1971.04	-0.0021	-1.1	6.04	14844.8	5.89	HUMAN	B4DV51	GTP-binding nuclear protein Ran
5366	dirMS_041712_NAR_40mM_minus2.7988.7988.3	3	12.87	0	1.24E+05	M147m	(K)LQmEA	(K)L Q/m/E A/P/H/I/I/V/G T/P G R(V)	m:Oxidized methionine	127.3	545.627	1618.873	15.9931	-1.1	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
5367	dirMS_041712_NAR_50mM_minus2.13284.13284.3	3	12.87	0	1.68E+05		(K)MLDAE	(K)M L|D A\E D/I/V/G T A R P D/E K(A)		143.55	587.2894	1759.853	0.0006	0.3	4.1	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
5368	dirMS_041712_NAR_50mM_minus2.14792.14792.3	3	12.87	0	4.06E+05		(K)YPIEHGI	(K)Y P/I E H G I I/T/N/W/D D|M E K(I)		152.47	654.3084	1960.911	-0.0003	-0.1	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
5369	dirMS_041712_NAR_60mM_minus.11501.11501.3	3	12.87	1	2.76E+06		(R)MQKEIT	(R)M Q K/E I\T A|L|A/P S T M K(I)		123.4	516.9421	1548.812	-0.0007	-0.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
5370	dirMS_041712_NAR_20mM_plus.11124.11124.2	2	12.87	0	1.26E+05		(K)TIVFVET	(K)T I|V|F/V E/T K(R)		148.35	468.7674	936.54	-0.0125	-13.4	5.66	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
5371	dirMS_041712_NAR_20mM_plus.14572.14572.2	2	12.87	0	2.36E+05		(K)VSTLPA	(K)V/S/T/L/P A I T L K(L)		172.35	521.8283	1042.651	-0.0013	-1.3	8.72	20599.3	9.19	HUMAN	H7C1V0	Cathepsin D light chain (Fragment)
5372	dirMS_041712_NAR_20mM_plus.14767.14787.2	2	12.87	0	6.83E+04		(R)IMNTFS	(R)I M|N|T/F/S/V/V/P S P K(V)		173.27	660.3527	1319.703	-0.0047	-3.5	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
5373	dirMS_041712_NAR_30mM_plus2.22891.22993.2	2	12.87	0	1.70E+06		(R)NLPFDF	(R)N/L|P|F|D F T/W K(M)		180.48	584.2953	1167.583	0	0	5.84	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
5374	dirMS_041712_NAR_40mM_plus2.6380.6380.2	2	12.87	0	8.35E+04		(R)VTDALN	(R)V/T|D A L N A/T R(A)		96.72	480.7594	960.511	0.0006	0.7	5.81	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
5375	dirMS_041712_NAR_50mM_plus2.16489.16489.3	3	12.87	0	5.57E+05		(R)QVVQGI	(R)Q V/V/Q/G L L S E/T/Y L E A\H/R(I)		154.53	614.9984	1842.971	0.0098	5.3	5.4	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
5376	dirMS_041712_NAR_30mM_minus2.14663.14789.2	2	12.86	0	3.15E+05		(K)FVMQE	(K)F/V|M/Q/E/E F S R(D)		133.63	586.7762	1172.541	0.0047	4	4.53	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
5377	dirMS_041712_NAR_30mM_minus2.18300.18300.2	2	12.86	0	2.25E+05		(K)ALQFLE	(K)A L|Q|F\L/E E V K(V)		153.85	538.7985	1076.599	-0.0089	-8.3	4.53	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
5378	dirMS_041712_NAR_40mM_minus2.15019.15019.3	3	12.86	1	7.94E+04		(R)VLEALLP	(R)V L/E/A L L/P L K G L E E R(V)		173.35	527.317	1579.942	-0.0053	-3.4	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
5379	dirMS_041712_NAR_50mM_minus2.14900.14900.3	3	12.86	1	2.76E+05		(K)NIYVLQ	(K)N/I/Y/V L Q E/L D/N/P G A K R(I)		152.62	577.3116	1729.923	-0.0029	-1.7	6.07	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
5380	dirMS_041712_NAR_60mM_minus.6907.6907.3	3	12.86	1	6.14E+04		(R)DSGRGD	(R)D S\G R\G D S V|S\D/S/G S D A/L R(S)		97.03	560.916	1680.742	-0.0085	-5.1	4.14	50974.6	5.31	HUMAN	B5ME91	Programmed cell death protein 4
5381	dirMS_041712_NAR_120mM_plus.8191.8191.3	3	12.86	1	2.71E+06		(R)AAPGAE	(R)A A/P/G A E/F A P N/K R(R)		96.73	410.2196	1228.643	0.001	0.8	8.79	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
5382	dirMS_041712_NAR_20mM_plus.10454.10454.2	2	12.86	0	1.10E+05	M267m	(R)LITLEEE	(R)L I|T|L|E|E E m T K(Y)	m:Oxidized methionine	145.17	611.8175	1206.629	15.9991	3.4	4.25	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
5383	dirMS_041712_NAR_20mM_plus.12279.12279.2	2	12.86	0	1.17E+05		(K)VNQIGS	(K)V/N|Q|I|G S/V/T E/S I Q/A C K(L)	C:Carbamidomethylation	157.67	817.4114	1633.821	-0.0059	-3.6	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
5384	dirMS_041712_NAR_20mM_plus.13914.13914.2	2	12.86	0	6.90E+04		(K)LLDLVQ	(K)L L\D\L\V/Q/Q/S/C N Y K(Q)	C:Carbamidomethylation	167.73	740.8757	1480.746	-0.0023	-1.6	5.83	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
5385	dirMS_041712_NAR_20mM_plus.15503.15607.2	2	12.86	0	3.47E+05		(K)VGINYQ	(K)V G I/N|Y/Q|P/P T V V|P G G D L A K(V)		179.05	912.9952	1824.985	-0.0023	-1.3	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
5386	dirMS_041712_NAR_20mM_plus.18964.18964.2	2	12.86	0	5.05E+04		(R)NLTALG	(R)N L/T|A\L/G L N L/V\A/S G G/T A K(A)		201.52	800.4534	1599.906	-0.0069	-4.3	8.75	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
5387	dirMS_041712_NAR_30mM_plus2.10820.10993.2	2	12.86	0	1.03E+06		(R)LSIYEAR	(R)L S|I/Y/E/A/R(C)		110.4	426.2291	851.462	-0.0112	-13.2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
5388	dirMS_041712_NAR_30mM_plus2.17139.17139.2	2	12.86	0	5.18E+05	M256m	(R)SLDmDS	(R)S L/D|m D S I/I A E/V K(A)	m:Oxidized methionine	142.48	668.8384	1320.671	15.998	2.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
5389	dirMS_041712_NAR_30mM_plus2.6198.6233.2	2	12.86	0	3.58E+05		(K)ESPQEIA	(K)E S/P/Q/E/I/A/R(K)		86.92	465.2373	929.469	-0.0014	-1.5	4.53	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
5390	dirMS_041712_NAR_40mM_plus2.13073.13192.3	3	12.86	0	3.31E+05		(K)LQMEA	(K)L/Q\M E/A/P/H/I|I V/G T P G R(V)		144.07	540.2954	1618.873	-0.0017	-1.1	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
5391	dirMS_041712_NAR_40mM_plus2.5866.5866.2	2	12.86	0	1.61E+05	M369m	(R)FGSGM	(R)F/G|S/G M/N m G R(I)	m:Oxidized methionine	92.73	486.7054	956.408	15.9958	1	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
5392	dirMS_041712_NAR_60mM_plus.17811.17832.3	3	12.86	1	2.77E+05		(R)LIDFLES	(R)L/I/D/F L/E/S G K T N L R(R)		150.53	502.6147	1505.832	-0.0027	-1.8	6.07	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
5393	dirMS_041712_NAR_30mM_minus2.14853.14943.2	2	12.85	0	4.34E+05		(R)LCFEGL	(R)L/C|F/E|G L/R(S)	C:Carbamidomethylation	134.23	447.7317	894.45	0.0059	6.6	6	533778	5.74	HUMAN	Q15149	Plectin
5394	dirMS_041712_NAR_30mM_minus2.16268.16268.2	2	12.85	0	7.58E+04		(K)YMACCL	(K)Y M/A/C/C L/L/Y/R(G)	C:Carbamidomethylation	141.37	625.2802	1249.553	0.0005	0.4	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
5395	dirMS_041712_NAR_60mM_minus.13505.13505.3	3	12.85	1	1.01E+05		(K)SIYGERF	(K)S I|Y/G E R F P D/E/N/F K(L)		135.35	534.591	1601.759	-0.001	-0.6	4.68	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
5396	dirMS_041712_NAR_60mM_minus.15119.15557.3	3	12.85	1	1.58E+06		(R)TIPWLE	(R)T I|P/W/L/E/D R V P Q K(T)		145.48	494.6084	1481.811	-0.0004	-0.3	5.74	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
5397	dirMS_041712_NAR_60mM_minus.17015.17015.3	3	12.85	0	1.13E+05		(R)FHQLDI	(R)F H\Q L D\I/D|D|L/Q/S I/R(A)		154.95	533.9428	1599.813	0.0013	0.8	4.41	24897.7	9.84	HUMAN	A8MTM1	Carbonyl reductase [NADPH] 1
5398	dirMS_041712_NAR_60mM_minus.17436.17436.3	3	12.85	0	3.06E+05		(K)GSDHSA	(K)G S D H S A S L\E|P G/E/L/A\E L V R(S)		156.9	622.9764	1866.919	-0.0045	-2.4	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
5399	dirMS_041712_NAR_60mM_minus.9327.9357.3	3	12.85	0	1.14E+06		(R)QSVEND	(R)Q S/V/E N D/I/H/G L/R(K)		112.07	423.218	1267.639	0.0005	0.4	5.32	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5400	dirMS_041712_NAR_20mM_plus.12678.12678.2	2	12.85	0	1.02E+05		(R)LAVEAL	(R)L/A|V E/A/L V R(T)		160.5	435.7739	870.541	-0.0002	-0.2	6	65558.6	9.87	HUMAN	G3V1S7	Hyaluronan synthase 1
5401	dirMS_041712_NAR_20mM_plus.9143.9143.2	2	12.85	0	6.95E+05	M239m	(K)EITALAP	(K)E I|T/A/L/A/P S T m K(I)	m:Oxidized methionine	133.05	589.309	1161.618	15.9923	-2.2	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
5402	dirMS_041712_NAR_30mM_plus2.7609.7610.2	2	12.85	0	1.05E+06		(K)AAIAQL	(K)A A|I|A/Q/L/N G K(E)		94.28	443.2607	885.515	-0.0011	-1.3	8.8	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
5403	dirMS_041712_NAR_30mM_plus2.8518.8645.2	2	12.85	0	4.63E+05		(R)AVNYFS	(R)A V|N/Y/F/S/K(V)		98.88	414.7159	828.425	-0.0005	-0.6	8.63	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
5404	dirMS_041712_NAR_50mM_plus2.19517.19517.3	3	12.85	0	7.75E+05		(R)DFNHIN	(R)D F/N H I N\V|E/L/S L L G K(K)		170.17	533.6223	1598.854	-0.0013	-0.8	5.32	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
5405	dirMS_041712_NAR_60mM_plus.14811.14811.3	3	12.85	1	9.63E+04		(R)KFLDGIY	(R)K\F L D G\I/Y/V/S E K(G)		133.93	433.5671	1298.699	-0.0123	-9.5	6.07	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
5406	dirMS_041712_NAR_40mM_minus2.13956.13956.3	3	12.84	0	5.98E+04		(R)LLAEIGA	(R)L L/A|E|I|G A/V T L V S A P R P D S R(H)		165.87	655.7064	1965.113	-0.0081	-4.1	6.07	27279.2	9.51	HUMAN	A9C4B9	tRNA splicing endonuclease 34 homolog (S. cerevisiae) (Fragment)
5407	dirMS_041712_NAR_50mM_minus2.7716.7716.3	3	12.84	1	4.75E+04		(K)TTSPPE	(K)T T|S/P/P E V S G Y S/Y E K/T E/R(S)		110.92	644.3067	1930.903	0.0027	1.4	4.78	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
5408	dirMS_041712_NAR_60mM_minus.13439.13439.3	3	12.84	1	4.53E+05		(K)TKEVYE	(K)T/K E V\Y E|L|L/D/S/P G K(V)		134.53	493.5966	1478.774	0.0015	1	4.68	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
5409	dirMS_041712_NAR_120mM_plus.10288.10288.3	3	12.84	0	1.14E+06		(R)ILRPWQ	(R)I/L/R/P W Q|S S E T/R(S)		106.78	458.2486	1372.733	-0.0019	-1.4	9.6	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
5410	dirMS_041712_NAR_120mM_plus.9640.9640.3	3	12.84	1	1.40E+05		(R)RLDECE	(R)R L D E C\E/E|A/F Q G T/K(V)	C:Carbamidomethylation	104.07	528.2449	1582.717	0.0036	2.2	4.41	22568.6	6.35	HUMAN	B3KQ25	Proteasome activator complex subunit 3
5411	dirMS_041712_NAR_20mM_plus.8594.8594.2	2	12.84	0	1.56E+05		(K)TAVCDI	(K)T/A/V|C/D I/P|P R(G)	C:Carbamidomethylation	129.47	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
5412	dirMS_041712_NAR_30mM_plus2.11919.11919.2	2	12.84	0	2.07E+05		(R)GLLGDA	(R)G L\L/G D/A|P N D/P R(G)		115.62	562.7857	1124.57	-0.0053	-4.7	4.21	63055.8	6.41	HUMAN	E7EWR4	Cleavage stimulation factor subunit 2
5413	dirMS_041712_NAR_30mM_plus2.14312.14513.2	2	12.84	0	4.27E+05		(R)ELAFQIS	(R)E L|A/F/Q/I/S/K(E)		128.55	468.2629	935.52	-0.0011	-1.2	6.1	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
5414	dirMS_041712_NAR_30mM_plus2.16702.16840.2	2	12.84	0	4.75E+05		(K)GCSFLP	(K)G C|S|F/L|P D/P Y\Q/K(Q)	C:Carbamidomethylation	140.72	656.306	1311.604	0.0009	0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
5415	dirMS_041712_NAR_30mM_plus2.8892.9033.2	2	12.84	0	9.55E+05		(R)SPPPGM	(R)S P|P|P/G M/G L N Q N R(G)		100.62	634.3137	1267.621	-0.0011	-0.8	9.47	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
5416	dirMS_041712_NAR_40mM_plus2.12420.12420.3	3	12.84	0	3.25E+05		(K)AASDIA	(K)A A|S D I|A M/T E L/P P T/H P I R(L)		139.55	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
5417	dirMS_041712_NAR_50mM_plus2.13441.13441.3	3	12.84	1	2.13E+06	M357m	(R)ALAEIAK	(R)A L|A|E/I/A/K A\E\L D/D/T P m R(G)	m:Oxidized methionine	139.13	587.3005	1743.895	15.9924	-1.4	4.32	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
5418	dirMS_041712_NAR_50mM_plus2.15609.15609.3	3	12.84	1	3.02E+05		(R)AEGAIA	(R)A E|G A/I/A/G F R D/P F S G K(Q)		150.27	508.2614	1522.765	0.0048	3.1	6.12	266161	5.68	HUMAN	E9PPU0	Epiplakin
5419	dirMS_041712_NAR_50mM_plus2.22194.22220.3	3	12.84	1	1.35E+06		(K)EGGLGP	(K)E G G\L/G|P/L N I/P L\L A D/V T R R(L)		191	631.029	1891.076	-0.0035	-1.9	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
5420	dirMS_041712_NAR_60mM_plus.18805.18805.3	3	12.84	1	7.20E+05		(R)NILGGT	(R)N I/L/G G\T V/F R E P I I/C/K(N)	C:Carbamidomethylation	156.6	572.9812	1716.947	-0.0175	-10.2	8.75	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
5421	dirMS_041712_NAR_30mM_minus2.10023.10044.2	2	12.83	0	1.30E+06		(R)ANFENL	(R)A N|F/E N L/A/K(E)		109	453.7335	906.468	-0.0082	-9.1	6.05	35720	5.34	HUMAN	B4E358	Src substrate cortactin
5422	dirMS_041712_NAR_30mM_minus2.12574.12657.2	2	12.83	0	2.70E+05		(R)TLSGME	(R)T L|S|G\M|E/S/Y C V/R(A)	C:Carbamidomethylation	122.03	651.795	1302.582	0.001	0.8	5.66	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
5423	dirMS_041712_NAR_60mM_minus.16101.16159.3	3	12.83	1	3.83E+05		(K)NIYVLQ	(K)N I|Y/V/L Q/E/L D N/P G A K/R(I)		150.42	577.3128	1729.923	0.0007	0.4	6.07	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
5424	dirMS_041712_NAR_60mM_minus.16118.16428.3	3	12.83	1	4.97E+05		(K)NIYVLQ	(K)N I|Y/V/L Q/E L/D/N/P G A K R(I)		150.78	577.3128	1729.923	0.0007	0.4	6.07	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
5425	dirMS_041712_NAR_120mM_plus.5485.5485.3	3	12.83	1	4.01E+05		(K)CDSSPD	(K)C D/S/S|P D S/A/E D/V R K(V)	C:Carbamidomethylation	81.9	489.2122	1465.622	-0.0003	-0.2	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
5426	dirMS_041712_NAR_120mM_plus.6366.6366.2	2	12.83	1	3.44E+05		(K)DSYVGD	(K)D/S Y|V/G/D E A/Q S K R(G)		86.3	677.815	1354.623	-0.0006	-0.5	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
5427	dirMS_041712_NAR_20mM_plus.10089.10089.2	2	12.83	0	2.75E+05		(K)LVSESSD	(K)L V/S E/S/S D/V/L/P K(-)		141.1	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
5428	dirMS_041712_NAR_30mM_plus2.17631.17631.2	2	12.83	0	3.10E+05		(K)SLEDQV	(K)S L/E|D Q/V/E/M L R(T)		145.7	610.3003	1219.599	-0.0054	-4.4	4.14	61161.1	4.34	HUMAN	K7ELL7	Glucosidase 2 subunit beta
5429	dirMS_041712_NAR_30mM_plus2.6849.6849.2	2	12.83	0	2.27E+05		(R)NMGYV	(R)N/M|G/Y/V/Q|Q R(R)		90.27	498.2399	995.473	-0.0002	-0.2	8.75	28637.7	6.66	HUMAN	B4DDM6	Mitotic checkpoint protein BUB3
5430	dirMS_041712_NAR_40mM_plus2.13180.13180.3	3	12.83	0	1.97E+05		(R)DLSHIG	(R)D L S H I G D A\V|V/I/S C/A K(D)	C:Carbamidomethylation	144.35	528.9395	1584.805	-0.0011	-0.7	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
5431	dirMS_041712_NAR_40mM_plus2.13426.13486.3	3	12.83	1	3.11E+05		(K)VIDPAT	(K)V/I|D|P A/T A T S V D L R D/I K(I)		145.75	571.9836	1713.938	-0.0019	-1.1	4.43	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
5432	dirMS_041712_NAR_50mM_plus2.14253.14293.3	3	12.83	0	2.31E+06		(K)QIGNVA	(K)Q I/G N V A/A|L/P/G I/V/H R(S)		143.27	482.2828	1444.838	-0.0045	-3.1	9.75	19338.9	5.33	HUMAN	E7EQS9	tRNA-splicing ligase RtcB homolog
5433	dirMS_041712_NAR_50mM_plus2.18506.18506.3	3	12.83	0	4.12E+05		(R)VYAILTH	(R)V Y/A|I/L T H G I/F\S G P A I/S R(I)		165.83	601.3347	1801.996	-0.0064	-3.5	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
5434	dirMS_041712_NAR_50mM_plus2.19322.19322.3	3	12.83	1	4.32E+05		(R)LKVPPAI	(R)L/K V|P/P A I/N Q F/T/Q A L D R(Q)		169.82	604.3351	1811.017	-0.0266	-14.7	8.75	30166.2	10.79	HUMAN	P62424	60S ribosomal protein L7a
5435	dirMS_041712_NAR_50mM_plus2.19784.19784.3	3	12.83	1	1.78E+05		(R)TSLLTLE	(R)T S|L/L/T L E/D V\K Q E/L I/K(L)		172.23	577.3359	1729.995	-0.0014	-0.8	4.68	156316.8	8.61	HUMAN	Q7Z478	ATP-dependent RNA helicase DHX29
5436	dirMS_041712_NAR_60mM_plus.15503.15503.3	3	12.83	0	3.46E+05		(K)DCGATV	(K)D C|G A/T W V/V/L/G H S E R(R)	C:Carbamidomethylation	137.57	529.5842	1586.738	0	0	5.32	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
5437	dirMS_041712_NAR_60mM_plus.17955.17955.3	3	12.83	0	2.48E+05		(R)FHQLDI	(R)F H Q L D\I D/D/L/Q/S\I R(A)		151.47	533.9414	1599.813	-0.0029	-1.8	4.41	24897.7	9.84	HUMAN	A8MTM1	Carbonyl reductase [NADPH] 1
5438	dirMS_041712_NAR_120mM_minus.11952.11952.3	3	12.82	2	2.05E+05		(R)YESLTDF	(R)Y/E|S L T/D/P S K L/D/S G K E L K(I)		119.27	637.325	1909.975	-0.0149	-7.8	4.78	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
5439	dirMS_041712_NAR_20mM_minus.12169.12169.2	2	12.82	0	5.04E+05	M185m	(K)LAVNm	(K)L A/V|N\m/V/P F P R(L)	m:Oxidized methionine	171.05	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
5440	dirMS_041712_NAR_30mM_minus2.9490.9493.2	2	12.82	0	4.94E+05		(K)ELSEALT	(K)E L/S/E A/L/T/R(H)		106.03	459.7452	918.489	-0.006	-6.5	4.53	83905.8	6.62	HUMAN	P41250	Glycine--tRNA ligase
5441	dirMS_041712_NAR_50mM_minus2.16817.16817.3	3	12.82	0	1.15E+05		(K)TVSGVN	(K)T V/S G V N/G|P L V/I L/D/H V K(V)		164.88	549.9835	1647.943	-0.0069	-4.2	6.41	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
5442	dirMS_041712_NAR_50mM_minus2.7889.8035.3	3	12.82	1	3.94E+06	M239m	(R)MQKEIT	(R)M Q K E I T A\L|A|P/S T m K(I)	m:Oxidized methionine	112.32	522.2727	1548.812	15.9911	-2.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
5443	dirMS_041712_NAR_60mM_minus.14470.14470.3	3	12.82	1	1.03E+05		(R)IQLVEEE	(R)I Q|L/V/E E E/L D/R A Q E R(L)		139.7	576.6347	1727.892	-0.0027	-1.6	4.25	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
5444	dirMS_041712_NAR_60mM_minus.16999.16999.3	3	12.82	0	1.13E+05		(R)FHQLDI	(R)F H Q\L D\I\D D|L/Q/S I/R(A)		154.95	533.9428	1599.813	0.0013	0.8	4.41	24897.7	9.84	HUMAN	A8MTM1	Carbonyl reductase [NADPH] 1
5445	dirMS_041712_NAR_60mM_minus.17253.17357.3	3	12.82	0	3.22E+05		(K)GSDHSA	(K)G S D H S A S\L E|P/G E|L A E/L V/R(S)		156.83	622.9764	1866.919	-0.0045	-2.4	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)

5446	dirMS_041712_NAR_20mM_plus.14015.14436.3	3	12.82	0	3.57E+06	M313m	(R)TVQSLEI	(R)T V\Q\S L\E\I/D/L/D/S m/R(N)	m:Oxidized methionine	170.13	508.2519	1506.747	15.9943	-0.4	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5447	dirMS_041712_NAR_30mM_plus2.21480.21480.3	3	12.82	0	5.51E+05		(R)VNQAIW	(R)V N\Q A\I W\L|L/C/T G A R(E)	C:Carbamidomethylation	166.88	501.2717	1501.794	0.0062	4.1	9.72	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
5448	dirMS_041712_NAR_30mM_plus2.8652.8678.2	2	12.82	0	1.11E+06		(R)TLLEGEE	(R)T L|L|E/G/E E/S\R(M)		99.18	517.2613	1033.516	-0.0007	-0.7	4.25	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
5449	dirMS_041712_NAR_40mM_plus2.19099.19099.3	3	12.82	1	3.19E+05		(R)GGPNIIT	(R)G G\P\N\I/I/T L A/D I V K D/P V S R(T)		178.95	622.3522	1865.049	-0.007	-3.8	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
5450	dirMS_041712_NAR_40mM_plus2.6670.6680.2	2	12.82	0	5.32E+05		(R)FFSDCK(	(R)F/F|S/D|C K(I)	C:Carbamidomethylation	99.9	402.1734	803.339	0.0003	0.3	5.84	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
5451	dirMS_041712_NAR_50mM_plus2.14357.14377.3	3	12.82	0	4.02E+06		(R)VAPDEH	(R)V A|P D E H\P I L/L|T/E A/P L N/P K(I)		143.75	652.0254	1954.064	-0.0028	-1.4	4.65	42344.8	5.39	HUMAN	Q562R1	Beta-actin-like protein 2
5452	dirMS_041712_NAR_50mM_plus2.17773.17773.3	3	12.82	1	3.77E+05		(K)IEEIKDFI	(K)I/E|E/I K D/F L/L T A R(R)		161.72	483.2728	1447.815	-0.0117	-8.1	4.68	2559	9.99	HUMAN	J3KSP2	60S ribosomal protein L38 (Fragment)
5453	dirMS_041712_NAR_50mM_plus2.8957.8974.3	3	12.82	1	1.62E+05		(R)LGAAPE	(R)L/G|A\A/P/E E E S A Y/V/A G E K R(Q)		114.3	592.9628	1776.876	-0.0024	-1.4	4.5	30276.7	5	HUMAN	F2Z2K0	NSFL1 cofactor p47
5454	dirMS_041712_NAR_20mM_minus.12084.12084.2	2	12.81	0	8.92E+05	M313m	(R)TVQSLEI	(R)T V/Q|S L/E\I\D L\D S m R(N)	m:Oxidized methionine	170.45	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5455	dirMS_041712_NAR_20mM_minus.13273.13273.2	2	12.81	0	1.13E+06	M73m	(R)AILVDLE	(R)A/I L\V/D|L/E|P G T m D/S V R(S)	m:Oxidized methionine	182.78	816.4184	1615.836	15.9935	-0.8	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
5456	dirMS_041712_NAR_30mM_minus2.17432.17692.2	2	12.81	0	4.37E+05		(R)EQLAIAE	(R)E Q|L|A|I/A/E/F A/R(S)		150.25	574.3084	1147.611	-0.0011	-0.9	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
5457	dirMS_041712_NAR_50mM_minus2.11352.11387.3	3	12.81	1	9.59E+04		(R)LLIVSTTI	(R)L L|I|V/S T T/P Y S E K D/T K(Q)		133.12	565.6428	1694.921	-0.0072	-4.3	6.07	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
5458	dirMS_041712_NAR_60mM_minus.15517.15517.3	3	12.81	1	2.23E+05		(R)GPIKFN\	(R)G P I K F N V|W|D T A/G Q E/K(F)		146.48	563.9575	1689.86	-0.0015	-0.9	6.07	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
5459	dirMS_041712_NAR_60mM_minus.9971.9971.3	3	12.81	1	1.21E+05		(K)IFQKGES	(K)I/F\Q K G E S|P\V/D/Y D/G G R(T)		115.3	556.6051	1667.802	-0.0016	-1	4.56	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
5460	dirMS_041712_NAR_20mM_plus.7462.7462.2	2	12.81	0	1.21E+05		(K)AQYEDI/	(K)A Q|Y/E/D/I A/N R(S)		120.45	540.2601	1079.512	0.0013	1.2	4.37	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
5461	dirMS_041712_NAR_30mM_plus2.14368.14500.2	2	12.81	0	2.87E+05		(R)ELLELAS	(R)E L|L/E\L/A/S/R(M)		128.55	465.7671	930.525	0.0015	1.6	4.53	109301.2	7.85	HUMAN	H0Y394	Vigilin (Fragment)
5462	dirMS_041712_NAR_30mM_plus2.20096.20096.2	2	12.81	0	1.52E+05		(K)TVALWD	(K)T V/A|L/W D/L/R(N)		159.02	487.2769	973.547	0	0	5.5	19598	4.45	HUMAN	B4DRT0	Histone-binding protein RBBP4
5463	dirMS_041712_NAR_30mM_plus2.22897.22941.2	2	12.81	0	1.70E+06		(R)NLPFDFT	(R)N L|P|F/D F T W K(M)		180.48	584.2953	1167.583	0	0	5.84	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
5464	dirMS_041712_NAR_30mM_plus2.8260.8490.2	2	12.81	0	6.56E+05		(R)FAQIVQ	(R)F/A|Q|I/V/Q/K(G)		97.57	417.2466	833.488	-0.002	-2.4	8.75	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
5465	dirMS_041712_NAR_50mM_plus2.14198.14198.3	3	12.81	1	1.01E+06		(K)ALQQGL	(K)A L/Q\Q/G L\V/G L E L/K E/K(L)		142.27	509.3022	1525.895	-0.0028	-1.8	6.18	266161	5.68	HUMAN	E9PPU0	Epiplakin
5466	dirMS_041712_NAR_120mM_minus.20273.20273.3	3	12.8	0	2.30E+05		(K)KPGGFD	(K)K\P G G F D I|S L/F Y/R(D)		166.55	467.2504	1399.737	-0.0002	-0.2	8.59	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
5467	dirMS_041712_NAR_30mM_minus2.10138.10276.2	2	12.8	0	1.64E+06		(K)TEWLDG	(K)T|E|W/L/D/G K(H)		109.63	424.7117	848.415	0.0013	1.5	4.37	18393.6	9.55	HUMAN	A2BFH1	Peptidyl-prolyl cis-trans isomerase A-like 4G
5468	dirMS_041712_NAR_30mM_minus2.12484.12783.2	2	12.8	0	5.07E+05		(R)GQVVSL	(R)G Q|V|V|S/L/I/R(M)		122.25	436.2706	871.536	-0.0021	-2.4	9.75	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
5469	dirMS_041712_NAR_50mM_minus2.12168.12168.3	3	12.8	0	1.95E+05		(K)FADEHV	(K)F/A/D E/H\V|P/G S P F\T V K(I)		137.67	510.9256	1530.759	0.0035	2.3	5.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
5470	dirMS_041712_NAR_120mM_plus.4557.4671.3	3	12.8	0	8.70E+05		(R)YINTEHG	(R)Y/I|N/T E/H/G G S Q\A R(F)		74.22	444.8857	1332.629	0.0134	10.1	6.75	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
5471	dirMS_041712_NAR_20mM_plus.15738.15738.2	2	12.8	0	2.19E+05		(K)TITLEVEI	(K)T I|T\L/E|V|E/P S D T I E N V K(A)		179.1	894.4658	1787.927	-0.003	-1.7	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
5472	dirMS_041712_NAR_20mM_plus.16762.16762.2	2	12.8	0	1.25E+05		(R)LLEAQIA	(R)L L E A Q I/A|T G/G I\I\D/P K(E)		185.92	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
5473	dirMS_041712_NAR_20mM_plus.18732.18732.2	2	12.8	0	2.32E+05		(R)IITLAGPT	(R)I I/T\L/A|G|P T N A/I F/K(A)		200.97	679.9039	1358.804	-0.0037	-2.7	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
5474	dirMS_041712_NAR_30mM_plus2.10069.10069.2	2	12.8	0	2.05E+05		(K)LVIEEAE	(K)L/V|I/E/E A E/R(S)		106.72	479.7648	958.52	0.0019	2	4.25	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
5475	dirMS_041712_NAR_30mM_plus2.17521.17736.2	2	12.8	0	4.78E+05		(R)AIGNIEL	(R)A I|G/N|I|E/L|G I/R(S)		145.28	528.3113	1055.621	-0.0054	-5.2	6.05	75482.2	6.34	HUMAN	D6RA32	Microtubule-associated protein 1B (Fragment)
5476	dirMS_041712_NAR_30mM_plus2.9976.9976.2	2	12.8	0	2.33E+05		(K)TAVCDIF	(K)T A|V|C D/I/P|P R(G)	C:Carbamidomethylation	105.85	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
5477	dirMS_041712_NAR_40mM_plus2.19962.19977.3	3	12.8	1	1.54E+06		(R)ELAILLG	(R)E L/A/I/L|L G M L/D/P A E/K D E K(G)		189.08	629.003	1884.999	-0.0042	-2.3	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
5478	dirMS_041712_NAR_50mM_plus2.17140.17287.3	3	12.8	1	1.72E+05		(K)LLVYEAL	(K)L/L|V/Y/E A L E/Y/A K R(A)		160	489.9441	1467.821	-0.0028	-1.9	6.14	32535.6	9.19	HUMAN	B4DZW6	Regulator of microtubule dynamics protein 1
5479	dirMS_041712_NAR_60mM_plus.10564.10939.3	3	12.8	0	3.72E+06		(R)AHSSM\	(R)A H\S S\M\V|G\V/N|L/P Q/K(A)		114.23	456.5782	1367.71	0.0101	7.3	8.8	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
5480	dirMS_041712_NAR_60mM_plus.5694.5694.3	3	12.8	1	1.91E+05		(R)SGGGYG	(R)S/G/G/G/Y/G/G D R S S G G G Y S/G D\R(S)		88.07	583.5777	1748.722	-0.0033	-1.9	5.68	21563.9	10.01	HUMAN	K7EKB2	TATA-binding protein-associated factor 2N (Fragment)
5481	dirMS_041712_NAR_30mM_minus2.11344.11421.2	2	12.79	0	2.19E+05		(K)ATAVMF	(K)A T|A|V|M|P D/G Q F/K(D)		115.47	582.7922	1164.572	0.0054	4.6	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
5482	dirMS_041712_NAR_30mM_minus2.16314.16314.2	2	12.79	0	1.34E+05	M256m	(R)SLDmDS	(R)S L|D\m D S/I/I|A E/V K(A)	m:Oxidized methionine	141.95	668.8368	1320.671	15.9948	-0.1	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
5483	dirMS_041712_NAR_30mM_minus2.5301.5301.2	2	12.79	0	5.80E+05		(R)TDTGEP	(R)T/D|T/G/E\P M G R(G)		82.53	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
5484	dirMS_041712_NAR_50mM_minus2.9391.9391.3	3	12.79	0	6.84E+04		(R)AASIFGC	(R)A A/S/I/F/G G A K/P V D T A A R(E)		121.62	511.2773	1531.823	-0.0054	-3.5	8.79	64861.3	5.86	HUMAN	B4DS13	Eukaryotic translation initiation factor 4B
5485	dirMS_041712_NAR_20mM_plus.16583.16583.2	2	12.79	0	1.41E+05		(K)TVDNFV	(K)T V|D N F/V/A L/A/T/G E K(G)		185.9	682.8565	1364.706	0.0001	0.1	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
5486	dirMS_041712_NAR_30mM_plus2.5507.5528.2	2	12.79	0	1.51E+05	M67m	(R)AmNGES	(R)A/m|N/G/E/S/L/D/G R(Q)	m:Oxidized methionine	82.97	533.2363	1049.468	15.9973	2.2	4.37	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
5487	dirMS_041712_NAR_30mM_plus2.7355.7376.2	2	12.79	0	1.79E+05		(K)MSAAQ/	(K)M/S|A/A Q A/L/K(K)		93.1	410.2229	819.439	-0.0008	-0.9	8.5	533778	5.74	HUMAN	Q15149	Plectin
5488	dirMS_041712_NAR_40mM_plus2.12567.12567.3	3	12.79	1	1.28E+05		(K)LLQSIGC	(K)L L/Q/S I/G Q A P E S I/S E K E L/K(L)		141.22	657.359	1970.08	-0.018	-9.1	4.79	60972	5.25	HUMAN	A6NCK0	NEDD8-activating enzyme E1 regulatory subunit
5489	dirMS_041712_NAR_40mM_plus2.15145.15145.3	3	12.79	1	2.11E+04		(R)TIAQDY(	(R)T I|A/Q/D/Y G V L/K A D E/G I S F R(G)		155.8	661.6783	1983.018	0.0022	1.1	4.56	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
5490	dirMS_041712_NAR_40mM_plus2.7986.7986.2	2	12.79	0	1.36E+05		(R)ELNITAA	(R)E L/N/I|T/A/A|K(E)		106.93	430.2474	859.488	-0.0008	-1	6.1	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
5491	dirMS_041712_NAR_20mM_minus.14431.14431.2	2	12.78	0	2.22E+05		(K)DAGVIA(	(K)D A G\V/I/A|G L N V L R(I)		198.2	599.3503	1197.695	-0.0017	-1.4	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
5492	dirMS_041712_NAR_50mM_minus2.15191.15191.3	3	12.78	0	4.42E+05		(R)DGLAFN	(R)D G/L|A/F/N/A/L I H R(H)		155.28	409.5594	1226.664	-0.0004	-0.3	6.74	146974	5.55	HUMAN	C9JRP8	Spectrin beta chain, non-erythrocytic 4
5493	dirMS_041712_NAR_60mM_minus.10577.10620.3	3	12.78	0	5.02E+05	M368m	(K)LAQANC	(K)L/A|Q/A/N G/W/G V m V/S H R(S)	m:Oxidized methionine	119	514.591	1525.769	15.9892	-3.7	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
5494	dirMS_041712_NAR_120mM_plus.9453.9576.4	4	12.78	2	5.78E+05		(K)LITYGSD	(K)L/I/T/Y/G/S D R T E A\L K/R(M)		102.88	406.4764	1622.886	-0.0023	-1.4	8.59	15838.9	7.03	HUMAN	H0Y5U0	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
5495	dirMS_041712_NAR_20mM_plus.12261.12261.2	2	12.78	0	4.61E+04		(K)VALSSET	(K)V A|L/S/S E/T E V A L/A R(D)		157.62	673.3693	1345.732	-0.0008	-0.6	4.53	246695.2	5.91	HUMAN	E7EVA0	Microtubule-associated protein
5496	dirMS_041712_NAR_20mM_plus.13660.13660.2	2	12.78	0	1.80E+05	M98m	(R)TLTIVDT	(R)T L|T|I|V/D T G I G m T K(A)	m:Oxidized methionine	166.4	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
5497	dirMS_041712_NAR_20mM_plus.16516.16752.2	2	12.78	0	1.85E+05		(K)IAFAITAI	(K)I/A|F|A/I/T A I K(G)		185.4	474.2987	947.592	-0.0023	-2.4	8.75	17718.4	10.99	HUMAN	P62269	40S ribosomal protein S18
5498	dirMS_041712_NAR_20mM_plus.9335.9335.2	2	12.78	0	1.86E+05		(K)SVTNED'	(K)S V|T/N E/D|V|T Q/E E L G G/A/K(T)		136	838.9014	1676.797	-0.0018	-1.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
5499	dirMS_041712_NAR_30mM_plus2.10503.10503.2	2	12.78	0	5.44E+05		(K)ACQIFVF	(K)A/C|Q/I|F V/R(N)	C:Carbamidomethylation	108.75	447.2386	893.466	0.0037	4.2	9.79	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
5500	dirMS_041712_NAR_30mM_plus2.16739.16739.2	2	12.78	0	3.06E+05		(K)SNQQLV	(K)S N/Q/Q L/V/D I I E K(V)		141.15	643.8504	1286.695	-0.0015	-1.2	4.37	22568.6	6.35	HUMAN	B3KQ25	Proteasome activator complex subunit 3
5501	dirMS_041712_NAR_40mM_plus2.10253.10253.2	2	12.78	0	6.81E+04		(R)GYFDEEI	(R)G Y|F/D/E/E M N R(V)		124.8	580.7366	1160.468	-0.0018	-1.5	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
5502	dirMS_041712_NAR_50mM_plus2.9997.9997.3	3	12.78	1	2.08E+05		(R)ILNEKVN	(R)I/L|N/E/K V N T/P T T/T V Y R(C)		119.87	583.6557	1748.954	-0.0016	-0.9	8.59	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
5503	dirMS_041712_NAR_60mM_plus.16574.16574.3	3	12.78	1	1.56E+05		(R)VAGGPC	(R)V/A/G G P Q/M I/Q L S/L D G K/R(L)		143.02	557.3061	1669.905	-0.0017	-1	8.72	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
5504	dirMS_041712_NAR_20mM_minus.14426.14426.2	2	12.77	0	2.26E+05		(K)DAGVIA(	(K)D A\G\V/I|A/G\L N V L/R(I)		198.18	599.3503	1197.695	-0.0017	-1.4	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
5505	dirMS_041712_NAR_30mM_minus2.7152.7152.2	2	12.77	0	3.86E+05		(K)QQTLEA	(K)Q Q|T/L/E/A E/E/A/K(R)		93.4	573.7846	1146.564	-0.0018	-1.6	4.25	76925.9	4.46	HUMAN	A8MV58	Drebrin
5506	dirMS_041712_NAR_50mM_minus2.9846.9846.3	3	12.77	0	3.27E+05	M147m	(K)LQmEAF	(K)L/Q|m/E A P H\I/I V/G T P G R(V)	m:Oxidized methionine	124.77	545.6267	1618.873	15.9922	-1.7	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
5507	dirMS_041712_NAR_60mM_minus.15748.15748.3	3	12.77	1	2.90E+05		(R)IDTRNEL	(R)I/D|T R N E L E|S/Y/A Y S L K(N)		148.02	601.3049	1801.897	0.0035	1.9	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
5508	dirMS_041712_NAR_60mM_minus.18745.18745.3	3	12.77	1	1.29E+05		(K)IILDLISE	(K)I I|L/D L/I/S E S P I K/G R(A)		166.15	518.6442	1553.926	-0.0081	-5.2	6.07	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
5509	dirMS_041712_NAR_60mM_minus.19826.19879.3	3	12.77	1	1.80E+06		(K)EIIDLVLI	(K)E I/I/D/L/V L/D/R I/R(K)		179.9	452.2739	1354.805	0.0019	1.4	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
5510	dirMS_041712_NAR_20mM_plus.18747.18747.3	3	12.77	0	1.30E+05		(K)IYVDDGI	(K)I Y V D D G L/I/S L Q/V K(Q)		200.6	488.2764	1462.815	-0.0005	-0.4	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
5511	dirMS_041712_NAR_30mM_plus2.10191.10191.2	2	12.77	0	2.33E+05		(K)TAVCDIF	(K)T A|V|C/D/I/P|P R(G)	C:Carbamidomethylation	105.85	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
5512	dirMS_041712_NAR_30mM_plus2.5992.5992.2	2	12.77	0	9.97E+04		(R)QLAEED	(R)Q L/A/E/E/D A/A R(Q)		85.77	501.7464	1002.485	0.0005	0.5	4.14	533778	5.74	HUMAN	Q15149	Plectin
5513	dirMS_041712_NAR_40mM_plus2.15259.15259.3	3	12.77	0	1.17E+05		(R)IETMLGI	(R)I E|T/M\L G D V/A/V/A|V H P K(D)		156.27	527.286	1579.851	-0.0078	-4.9	5.32	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
5514	dirMS_041712_NAR_120mM_minus.12099.12117.2	2	12.76	0	2.74E+05		(R)HEIVQTI	(R)H|E|I|V/Q T L/S L/K(D)		120	584.3388	1167.673	-0.0029	-2.5	6.75	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
5515	dirMS_041712_NAR_120mM_minus.20842.20842.4	4	12.76	1	5.83E+05		(R)SLHDAL(	(R)S L H D\A L|C/V/L A Q/T V K D/S R(T)	C:Carbamidomethylation	173.1	479.0049	1912.991	0.0068	3.6	6.47	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
5516	dirMS_041712_NAR_30mM_minus2.16346.16346.2	2	12.76	0	1.70E+05		(R)GLGLDD	(R)G L\G\L/D/D/A|L/E/P R(Q)		141.95	578.299	1155.6	-0.0097	-8.4	4.03	51326.8	5.49	HUMAN	Q9Y230	RuvB-like 2
5517	dirMS_041712_NAR_40mM_minus2.14343.14343.3	3	12.76	0	1.23E+05		(R)GTEDITS	(R)G T|E/D|I|T S P H G I P L D|L|L D R(V)		168.55	650.3366	1948.997	-0.0022	-1.1	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
5518	dirMS_041712_NAR_60mM_minus.16035.16082.3	3	12.76	1	2.88E+05		(K)ELKIDIIP	(K)E L K I D I|I|P/N/P Q E/R(T)		149	522.2935	1564.869	-0.0034	-2.2	4.68	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
5519	dirMS_041712_NAR_60mM_minus.16834.16834.3	3	12.76	1	2.85E+05		(R)GQFSTD	(R)G Q|F/S/T D E L/V/A E/V E/K R(N)		153.92	569.9569	1707.855	0.0013	0.8	4.41	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
5520	dirMS_041712_NAR_20mM_plus.6676.6676.2	2	12.76	0	7.77E+04	M357m	(K)AELDDTI	(K)A E|L/D/D|T/P m R(G)	m:Oxidized methionine	110.62	532.24	1047.478	15.9952	0.3	4.03	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
5521	dirMS_041712_NAR_30mM_plus2.10209.10267.2	2	12.76	0	9.93E+05		(R)GLDVED	(R)G L|D|V/E D|V/K(F)		108.08	437.7293	874.452	-0.0003	-0.4	4.03	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
5522	dirMS_041712_NAR_30mM_plus2.13517.13710.2	2	12.76	0	1.10E+06		(R)ANTFVA	(R)A N|T|F/V/A/E/L/K(G)		124.65	496.774	992.541	-0.0004	-0.4	6.05	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
5523	dirMS_041712_NAR_40mM_plus2.11398.11398.3	3	12.76	0	3.79E+05		(R)MPLPAP	(R)M/P\L/P A/P S L S H Q/P/P P A\P R(V)		133.63	598.3202	1792.953	-0.0066	-3.7	9.52	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
5524	dirMS_041712_NAR_50mM_plus2.9457.9457.3	3	12.76	1	1.35E+05		(R)GAVIATI	(R)G A/V|I/A T/E\L K N N S Y K(L)		116.82	503.2738	1507.812	-0.0046	-3.1	8.5	20123.7	9.25	HUMAN	B0QYA3	Eukaryotic translation initiation factor 3 subunit D (Fragment)
5525	dirMS_041712_NAR_60mM_plus.17097.17097.3	3	12.76	0	9.47E+05	T2573t	(R)ELSNFEL	(R)E L S N F E\L|T|L S/P D G t R(V)	t:N-acetylglucosamine (T)	145.6	627.9721	1678.828	203.0735	-3.1	4.14	352805	4.89	HUMAN	Q5SZK8	FRAS1-related extracellular matrix protein 2
5526	dirMS_041712_NAR_20mM_minus.8139.8139.2	2	12.75	0	3.12E+05	M239m	(K)EITALAP	(K)E I/T\A|L|A/P S T m K(I)	m:Oxidized methionine	131.35	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
5527	dirMS_041712_NAR_50mM_minus2.12536.12536.3	3	12.75	0	1.41E+05		(K)LQNQLC	(K)L Q|N Q/L Q/G A I V/I E R P N V K(W)		139.15	640.7016	1920.103	-0.0123	-6.4	8.75	49472.3	6.75	HUMAN	O75351	Vacuolar protein sorting-associated protein 4B
5528	dirMS_041712_NAR_50mM_minus2.5628.5628.3	3	12.75	1	3.66E+05		(K)DSYVGD	(K)D S|Y/V G/D E A/Q S K R(G)		92.95	452.2119	1354.623	-0.0022	-1.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
5529	dirMS_041712_NAR_120mM_plus.19983.19983.4	4	12.75	1	6.21E+05		(K)AAIDWF	(K)A/A|I/D/W F D G K E F/H G N I I/K(V)		158.17	491.0027	1960.992	-0.0026	-1.3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
5530	dirMS_041712_NAR_120mM_plus.7382.7382.3	3	12.75	0	1.08E+05		(K)CIGKPG(	(K)C/I/G/K/P G G S/L/D N/S E Q K(C)	C:Carbamidomethylation	92.13	530.5901	1589.759	-0.003	-1.9	6.07	9122.2	9.22	HUMAN	K7EIT2	Mitochondrial import inner membrane translocase subunit Tim13
5531	dirMS_041712_NAR_20mM_plus.14810.14810.2	2	12.75	0	1.26E+05		(K)FANPFP/	(K)F A|N|P F/P/A A V R(G)		173.87	545.2958	1089.584	0.0003	0.3	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
5532	dirMS_041712_NAR_30mM_plus2.11052.11096.2	2	12.75	0	3.42E+05		(R)MVIEYA	(R)M/V|I/E/Y A/R(L)		111.27	441.231	881.455	-0.0002	-0.3	5.75	63566.6	6.3	HUMAN	P07686	Beta-hexosaminidase subunit beta
5533	dirMS_041712_NAR_30mM_plus2.12894.13071.2	2	12.75	0	6.25E+05		(K)STLTDSL	(K)S T|L/T|D/S L V/C/K(A)	C:Carbamidomethylation	121.22	562.2876	1123.566	0.0016	1.4	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
5534	dirMS_041712_NAR_30mM_plus2.21244.21244.2	2	12.75	0	8.25E+03		(R)GAFQNL	(R)G A/F|Q/N/L/F\Q/S V/R(E)		164.77	633.8315	1266.659	-0.0032	-2.5	9.75	68629.9	5.59	HUMAN	E7EVX6	Androgen receptor
5535	dirMS_041712_NAR_30mM_plus2.21409.21409.2	2	12.75	0	4.06E+04		(R)GAFQNL	(R)G A/F|Q/N L/F Q/S V R(E)		168.1	633.8315	1266.659	-0.0032	-2.5	9.75	68629.9	5.59	HUMAN	E7EVX6	Androgen receptor
5536	dirMS_041712_NAR_30mM_plus2.6141.6155.2	2	12.75	0	1.34E+05		(R)ESNCYD	(R)E S/N/C/Y/D/P E/R(V)	C:Carbamidomethylation	86.4	585.2299	1169.453	-0.0003	-0.2	4.14	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
5537	dirMS_041712_NAR_40mM_plus2.14285.14354.3	3	12.75	1	7.99E+05		(R)IINEPTA	(R)I/I|N\E/P T A/A A I/A/Y G L D K K(V)		149.77	596.6671	1787.99	-0.0034	-1.9	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
5538	dirMS_041712_NAR_60mM_plus.19898.19898.3	3	12.75	1	1.53E+05		(R)GMLREI	(R)G M/L/R E D A|V/L E Y L K(I)		163.87	512.9411	1536.809	-0.0003	-0.2	4.68	67933	6.08	HUMAN	P26038	Moesin
5539	dirMS_041712_NAR_20mM_minus.11103.11103.2	2	12.74	0	8.39E+04		(K)VIDPATA	(K)V I/D|P A T\A/T S V D\L R(D)		158.43	679.3706	1357.732	0.0018	1.3	4.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
5540	dirMS_041712_NAR_30mM_minus2.18341.18341.3	3	12.74	0	5.14E+05		(R)QAQEYE	(R)Q A Q\E\Y|E/A|L/L|N I K(V)		154.65	473.9196	1419.748	-0.0036	-2.5	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5541	dirMS_041712_NAR_30mM_minus2.19032.19032.3	3	12.74	0	1.63E+05		(K)SYELPDC	(K)S Y E L|P D G Q\V/I/T\I/G N E R(F)		158.77	597.6343	1790.892	-0.0036	-2	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
5542	dirMS_041712_NAR_120mM_plus.8228.8238.2	2	12.74	1	3.43E+05		(K)FSEVLKR	(K)F/S|E/V L K/R(L)		96.78	439.7584	878.509	0.0001	0.1	8.75	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
5543	dirMS_041712_NAR_20mM_plus.9359.9359.2	2	12.74	0	6.69E+04		(K)TGQEIP\	(K)T G Q/E/I|P/V N V R(F)		135.92	556.8027	1112.606	-0.0077	-6.9	5.66	28051.5	4.98	HUMAN	J3QKT2	Cytosolic non-specific dipeptidase (Fragment)
5544	dirMS_041712_NAR_30mM_plus2.15369.15664.2	2	12.74	0	3.39E+06		(R)QITVND	(R)Q I|T|V/N/D/L/P V G R(S)		133.12	606.3403	1211.674	-0.0009	-0.8	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
5545	dirMS_041712_NAR_40mM_plus2.10243.10243.2	2	12.74	0	6.81E+04		(R)GYFDEEI	(R)G Y|F/D E/E/M N/R(V)		124.8	580.7366	1160.468	-0.0018	-1.5	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
5546	dirMS_041712_NAR_50mM_plus2.14577.14577.3	3	12.74	1	1.32E+05		(K)NLKVTA'	(K)N L/K V T A|V|P T L L K(Y)		144.67	432.9459	1296.825	-0.0018	-1.4	10	11462.8	5.18	HUMAN	I3L2R6	Thioredoxin domain-containing protein 17
5547	dirMS_041712_NAR_50mM_plus2.17950.17950.3	3	12.74	1	1.07E+05		(K)TVDNFV	(K)T V|D/N F/V A L A/T G E K G F G Y K(N)		161.83	639.6639	1916.975	0.0019	1	5.73	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
5548	dirMS_041712_NAR_60mM_plus.13908.13908.3	3	12.74	1	9.19E+05		(K)TTVKDLS	(K)T T/V K D L S E|L/G/S/V/R(T)		129.45	468.9268	1404.769	-0.0034	-2.4	5.74	533778	5.74	HUMAN	Q15149	Plectin
5549	dirMS_041712_NAR_60mM_plus.7143.7143.3	3	12.74	0	3.22E+05		(K)IFSGSSH	(K)I/F/S G/S/S H/Q D L S Q K(I)		95.45	478.5718	1433.702	-0.0011	-0.8	6.74	18741.7	9.49	HUMAN	B1ALA7	Phosphoribosyl pyrophosphate synthetase 1
5550	dirMS_041712_NAR_120mM_minus.8873.8873.3	3	12.73	0	8.92E+05		(K)HTGPNS	(K)H T G P N\S P D/T|A/N/D G/F V/R(L)		103.08	562.2599	1684.767	-0.0022	-1.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
5551	dirMS_041712_NAR_40mM_minus2.12115.12115.3	3	12.73	1	9.22E+04		(K)IIVDELK(	(K)I/I|V D/E L K Q/E\V/I S T S S K(A)		154.43	597.0023	1788.995	-0.003	-1.7	4.68	30149.5	5.96	HUMAN	D6RAC2	Guanine nucleotide-binding protein subunit beta-2-like 1
5552	dirMS_041712_NAR_40mM_minus2.13535.13535.3	3	12.73	0	3.00E+04		(K)YVDTPF(	(K)Y/V/D T/P F G K P S D A L I/L G K(I)		163.33	607.6637	1820.979	-0.0027	-1.5	5.96	33699.1	7.18	HUMAN	B4DUC8	S-methyl-5'-thioadenosine phosphorylase
5553	dirMS_041712_NAR_40mM_minus2.14151.14152.3	3	12.73	1	2.95E+05		(K)VIAATNI	(K)V/I\A|A/T N R V D I\L/D/P A L L/R(S)		167.82	617.3653	1850.086	-0.0045	-2.4	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
5554	dirMS_041712_NAR_60mM_minus.14780.14780.3	3	12.73	1	5.91E+05		(K)TDKTLVI	(K)T D K T L V|L/L/M G/K(E)		142.57	406.9088	1218.713	-0.0008	-0.6	8.26	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b

5555	dirMS_041712_NAR_60mM_minus.5692.5789.2	2	12.73	1	4.42E+06		(K)DSYVGD	(K)D/S Y|V/G D|E/A Q S K R(G)		87.58	677.8144	1354.623	-0.0018	-1.3	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
5556	dirMS_041712_NAR_60mM_minus.7257.7461.3	3	12.73	1	6.21E+05	M136m M	(K)VKEGm	(K)V K\E G m N|I/V/E/A m E/R(F)	m:Oxidized methionine	100.3	513.25	1505.745	31.9904	0.4	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
5557	dirMS_041712_NAR_120mM_plus.12742.13176.3	3	12.73	0	1.20E+06		(K)HYGPGV	(K)H Y G P G\W|V|S/M/A/N A G K(D)		121.02	492.2383	1474.69	0.0108	7.3	8.6	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
5558	dirMS_041712_NAR_120mM_plus.15413.15815.3	3	12.73	0	2.59E+06		(K)HFSVEG	(K)H F\S\V\E|G\Q|L E/F/R(A)		135.42	450.2258	1348.664	-0.0016	-1.2	5.4	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
5559	dirMS_041712_NAR_20mM_plus.12550.12550.2	2	12.73	0	1.19E+05		(K)IISNASC	(K)I I|S/N|A/S C T T/N C L\A|P L A K(V)	C:Carbamidomethylation	159.55	917.4626	1833.92	-0.0018	-1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
5560	dirMS_041712_NAR_30mM_plus2.10018.10319.2	2	12.73	0	1.51E+06		(R)GVNVSA	(R)G V|N|V/S A L/S/R(D)		105.73	451.7509	902.505	-0.0109	-12.1	9.75	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
5561	dirMS_041712_NAR_30mM_plus2.19294.19592.2	2	12.73	0	8.40E+05		(K)GFGGIG	(K)G F|G/G|I/G/G I L/R(Y)		155.32	473.7749	946.547	-0.0044	-4.6	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
5562	dirMS_041712_NAR_40mM_plus2.11033.11033.3	3	12.73	0	6.44E+04		(K)SLYVAEY	(K)S L|Y/V/A E Y H S E P V E D E K P(-)		130.75	664.6419	1991.923	-0.0121	-6.1	4.25	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
5563	dirMS_041712_NAR_50mM_plus2.19300.19300.3	3	12.73	0	5.40E+05		(K)HLLQAP	(K)H L\L Q A\P L D D A/Q|E/I L/Q/A R(F)		169.5	644.3484	1931.035	-0.0039	-2	4.54	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
5564	dirMS_041712_NAR_50mM_plus2.19865.19865.3	3	12.73	1	2.65E+05		(K)DRDVTF	(K)D R D V T F\S|P A|T/I/E N E L I/K(F)		172.68	650.0048	1948.002	-0.0024	-1.2	4.32	8027.1	8.38	HUMAN	H7C2D6	Mesencephalic astrocyte-derived neurotrophic factor (Fragment)
5565	dirMS_041712_NAR_50mM_plus2.9284.9284.3	3	12.73	1	2.83E+05		(K)LTDCVV	(K)L/T/D C V V M R D P A S/K(R)	C:Carbamidomethylation	116.45	497.917	1491.729	0.007	4.7	5.96	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
5566	dirMS_041712_NAR_50mM_plus2.9473.9554.3	3	12.73	0	5.99E+05		(K)GAVDG	(K)G A|V|D/G G L/S/I/P H/S T K(R)		117.25	446.9057	1338.701	0.0013	1	6.74	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
5567	dirMS_041712_NAR_50mM_plus2.9474.9474.3	3	12.73	1	5.41E+05		(K)GILAAD	(K)G I/L/A/A/D E S/T/G S I A K R(L)		116.73	496.9389	1488.802	0.0005	0.3	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
5568	dirMS_041712_NAR_60mM_plus.12757.12757.3	3	12.73	1	9.60E+05	M232m	(R)MSmKE	(R)M S m K E V D E/Q|M/L/N V|Q N K(N)	m:Oxidized methionine	123.5	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
5569	dirMS_041712_NAR_60mM_plus.16418.16544.3	3	12.73	1	3.69E+05		(-)MKLNISF	(-)M K L N I S|F|P/A/T G/C Q K(L)	C:Carbamidomethylation	142.85	532.2733	1594.808	-0.0026	-1.7	10	10471.9	5.4	HUMAN	A2A3R7	40S ribosomal protein S6
5570	dirMS_041712_NAR_20mM_minus.12065.12065.2	2	12.72	0	7.40E+05	M313m	(R)TVQSLEI	(R)T V/Q|S L/E/I\D/L/D/S m R(N)	m:Oxidized methionine	170.25	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5571	dirMS_041712_NAR_40mM_minus2.10721.10856.3	3	12.72	0	2.22E+05		(R)DLSHIG	(R)D L S H\I G D A|V|V/I/S/C/A K(D)	C:Carbamidomethylation	147.08	528.9384	1584.805	-0.0044	-2.8	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
5572	dirMS_041712_NAR_40mM_minus2.11259.11259.3	3	12.72	0	4.48E+04		(R)EALAEA	(R)E A L/A/E/A/A L E/S P R P A L/V/R(S)		149.25	598.3347	1792.992	-0.002	-1.1	4.79	22148.2	5.87	HUMAN	B3KY21	Na(+)/H(+) exchange regulatory cofactor NHE-RF1
5573	dirMS_041712_NAR_50mM_minus2.12299.12336.3	3	12.72	1	1.19E+05		(K)ILQEYIT	(K)I/L|Q|E/Y/I/T Q Q S N K L E T G K(S)		138.22	665.0228	1993.06	-0.0062	-3.1	6.14	28001.7	5.46	HUMAN	K7EJJ1	AP-1 complex subunit mu-2 (Fragment)
5574	dirMS_041712_NAR_50mM_minus2.19056.19056.3	3	12.72	1	1.34E+06		(R)KEGGLG	(R)K\E G G L G P L N\I|P L L/A/D V T R(R)		187.5	621.6941	1863.07	-0.0021	-1.1	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
5575	dirMS_041712_NAR_50mM_minus2.9494.9494.3	3	12.72	0	1.82E+05		(R)AIGSASE	(R)A I|G S A/S E G A/Q S S L Q E V Y/H/K(S)		122.55	654.6559	1961.956	-0.0032	-1.6	5.4	20148.5	4.65	HUMAN	B4E2V4	Proteasome (Prosome, macropain) subunit, alpha type, 5, isoform CRA_c
5576	dirMS_041712_NAR_120mM_plus.8374.8384.3	3	12.72	1	5.02E+05		(R)VREEEIE	(R)V R E E\E\I|E|V/D/S/R(V)		97.32	454.2277	1360.67	-0.0018	-1.3	4.25	73601.9	9.46	HUMAN	Q14978	Nucleolar and coiled-body phosphoprotein 1
5577	dirMS_041712_NAR_20mM_plus.13968.13968.2	2	12.72	0	7.16E+04		(R)FLICTDV	(R)F L|I|C/T D V/A A R(G)	C:Carbamidomethylation	168.13	583.3065	1165.603	0.0023	2	5.84	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
5578	dirMS_041712_NAR_30mM_plus2.12414.12414.2	2	12.72	0	6.65E+05		(R)FGISSVP	(R)F/G\I/S/S/V/P T/K(G)		117.7	468.2629	935.52	-0.0011	-1.2	8.75	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
5579	dirMS_041712_NAR_30mM_plus2.13416.13488.2	2	12.72	0	8.55E+05		(K)EITALAP	(K)E I|T/A|L/A P S/T M K(I)		123.35	581.307	1161.618	-0.0117	-10	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
5580	dirMS_041712_NAR_30mM_plus2.13466.13466.2	2	12.72	0	1.26E+06		(R)MVPAGI	(R)M V/P\A/G M G A G L/E/R(M)		123.2	594.797	1188.586	0.0003	0.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
5581	dirMS_041712_NAR_40mM_plus2.18852.18852.3	3	12.72	0	6.10E+05		(R)DYLHLP	(R)D Y L H L P/P E\I\V|P A T L R(R)		176.92	578.6565	1733.959	-0.0035	-2	5.32	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
5582	dirMS_041712_NAR_40mM_plus2.5442.5442.2	2	12.72	0	2.74E+04		(K)TYGQST	(K)T/Y/G Q/S\T Y S R(Q)		88.83	531.7462	1062.485	0.0001	0.1	8.25	14693.3	4.69	HUMAN	C9JLS9	26S protease regulatory subunit 7 (Fragment)
5583	dirMS_041712_NAR_50mM_plus2.13405.13405.3	3	12.72	0	1.74E+05		(K)LGDVYV	(K)L/G D\V/Y V/N\D/A/F G T A H R(A)		138.82	545.6029	1634.792	0.002	1.2	5.21	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
5584	dirMS_041712_NAR_50mM_plus2.15942.15942.3	3	12.72	1	1.41E+05		(K)VSEQGL	(K)V/S/E/Q G L/I E I L K K(V)		151.65	452.944	1356.81	0.0078	5.7	6.11	12899.6	6.59	HUMAN	K7EL31	Programmed cell death protein 5
5585	dirMS_041712_NAR_50mM_plus2.7181.7181.3	3	12.72	0	1.04E+06		(R)EATNPP	(R)E A T N/P P V/I Q E E/K/P K(K)		103.55	527.282	1579.833	-0.0012	-0.7	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
5586	dirMS_041712_NAR_60mM_plus.17702.17702.3	3	12.72	1	3.22E+05		(K)EIIDPVL	(K)E I/I/D P V L D R I/R(K)		149.82	446.9288	1338.774	-0.0021	-1.6	4.56	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
5587	dirMS_041712_NAR_60mM_plus.6914.6933.3	3	12.72	1	4.23E+05		(R)AAEEAE	(R)A/A|E/E/A/E/E/A/R V Q A E/R(E)		94.67	520.2564	1558.746	0.0091	5.8	4.33	533778	5.74	HUMAN	Q15149	Plectin
5588	dirMS_041712_NAR_30mM_minus2.7681.7681.2	2	12.71	0	2.31E+05		(R)QDVDN	(R)Q D|V/D/N/A/S L/A R(L)		96.17	544.7694	1088.533	-0.0016	-1.4	4.21	49709.6	5.19	HUMAN	B0YJC4	Vimentin
5589	dirMS_041712_NAR_40mM_minus2.11004.11004.3	3	12.71	0	7.92E+05		(R)QVSASE	(R)Q V|S/A S E L\H T/S G/I/L/G P E T L R(D)		148.75	665.6822	1995.051	-0.0185	-9.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
5590	dirMS_041712_NAR_50mM_minus2.14560.14560.3	3	12.71	0	3.68E+05		(R)LASTLV	(R)L A|S/T L/V/H L\G E\Y/Q A A|V/D G A/R(K)		150.95	657.6803	1971.029	-0.0031	-1.6	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
5591	dirMS_041712_NAR_50mM_minus2.17904.17904.3	3	12.71	1	2.31E+05		(K)LALFQA	(K)L A|L|F Q/A I/G K E V/V D R(A)		170.53	520.3043	1558.895	0.0032	2	6.07	266161	5.68	HUMAN	E9PPU0	Epiplakin
5592	dirMS_041712_NAR_60mM_minus.15702.15702.3	3	12.71	1	3.12E+05		(K)VAAIRGI	(K)V/A|A I R G E V/T/A/A/D/L/F N S R(V)		147.35	597.3237	1789.956	0.001	0.6	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
5593	dirMS_041712_NAR_50mM_plus2.11591.11591.3	3	12.71	1	1.31E+05		(K)IGRIEDV	(K)I G R I E D\V\T|P\I|P S D/S T R(R)		128.73	585.9784	1755.924	-0.0029	-1.7	4.56	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
5594	dirMS_041712_NAR_60mM_plus.16431.16431.3	3	12.71	0	4.55E+05		(R)EAYPGD	(R)E A Y/P/G D V F/Y/L/H S R(L)		142.63	518.5855	1553.738	0.0036	2.3	5.32	48851.3	9.2	HUMAN	K7EK63	ATP synthase subunit alpha, mitochondrial
5595	dirMS_041712_NAR_60mM_plus.20136.20136.3	3	12.71	1	6.74E+04		(K)KSVEEV	(K)K S V E E\V A S E|I/Q|P/F L R(G)		165.4	577.9775	1731.928	-0.0096	-5.6	4.79	334221.3	6.44	HUMAN	P15924	Desmoplakin
5596	dirMS_041712_NAR_30mM_minus2.17795.17795.2	2	12.7	0	3.94E+05		(K)GNFNYI	(K)G N|F/N/Y|I/E/F T R(I)		151.3	630.8052	1260.601	0.0024	1.9	6	20513.6	4.62	HUMAN	J3QRS3	Myosin regulatory light chain 12A
5597	dirMS_041712_NAR_50mM_minus2.9390.9390.3	3	12.7	1	1.31E+05	M15m	(K)mLVSGA	(K)m L/V/S/G/A/G D I K L T\K(D)	m:Oxidized methionine	121.65	450.2541	1332.756	15.9922	-2	8.35	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
5598	dirMS_041712_NAR_60mM_minus.11212.11212.3	3	12.7	1	9.28E+05	M232m	(R)MSmKE	(R)M/S m K E V D E Q|M/L/N V Q/N K(N)	m:Oxidized methionine	122.78	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
5599	dirMS_041712_NAR_60mM_minus.11468.11468.3	3	12.7	0	2.41E+04		(K)TKPYIQ	(K)T K/P Y I Q/V D|I/G G G Q\T/K(T)		123.8	535.6216	1604.864	-0.014	-8.7	8.17	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
5600	dirMS_041712_NAR_60mM_minus.15467.15467.3	3	12.7	1	2.13E+05		(R)ASLISAV	(R)A/S/L/I/S/A/V S D K/L R(W)		146.08	420.5811	1259.732	-0.003	-2.4	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
5601	dirMS_041712_NAR_60mM_minus.9555.9555.3	3	12.7	1	2.46E+05		(R)QERYEIE	(R)Q E\R Y E\I/E|E/T E T V/T K(S)		112.57	585.6185	1754.844	-0.0034	-1.9	4.32	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
5602	dirMS_041712_NAR_120mM_plus.8211.8211.3	3	12.7	1	2.71E+06		(R)AAPGAE	(R)A A|P G A E F A/P N K/R(R)		96.73	410.2196	1228.643	0.001	0.8	8.79	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
5603	dirMS_041712_NAR_20mM_plus.13721.13721.2	2	12.7	0	6.17E+05		(R)GALQNI	(R)G A/L\Q|N|I|I\P A S T G A A K(A)		167.23	706.3975	1411.79	-0.0026	-1.9	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
5604	dirMS_041712_NAR_30mM_plus2.18286.18286.2	2	12.7	0	3.65E+05		(R)SQVEEEI	(R)S Q|V|E/E E/L F/S V/R(V)		149.37	661.8302	1322.659	-0.0055	-4.2	4.25	533778	5.74	HUMAN	Q15149	Plectin
5605	dirMS_041712_NAR_30mM_plus2.7225.7225.2	2	12.7	0	3.05E+05		(K)GSAITG	(K)G S\A|I/T/G P V A K(E)		92.77	450.7605	900.515	-0.0012	-1.3	8.75	8956.4	10.28	HUMAN	J3KTJ3	60S ribosomal protein L23
5606	dirMS_041712_NAR_40mM_plus2.14881.14881.3	3	12.7	1	2.18E+04		(K)VTADVI	(K)V/T|A|D/V/I N A A E K L Q V V G R(A)		154.18	595.0062	1783.007	-0.0032	-1.8	6.04	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
5607	dirMS_041712_NAR_40mM_plus2.19981.19981.3	3	12.7	1	1.55E+06		(R)ELAILLG	(R)E L|A/I/L/L G M L D/P A E/K D E K(G)		189.1	629.003	1884.999	-0.0042	-2.3	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
5608	dirMS_041712_NAR_50mM_plus2.22145.22152.3	3	12.7	1	5.40E+05		(R)ELAILLG	(R)E L/A|I/L/L/G M L D/P A E K D E K(G)		190.32	629.004	1884.999	-0.0012	-0.7	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
5609	dirMS_041712_NAR_50mM_plus2.7100.7100.3	3	12.7	1	3.75E+04		(R)ASVDTK	(R)A S V D T K E\A\E/G\A|P Q V/E A G K(R)		103.02	596.2908	1786.882	-0.0239	-13.4	4.41	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
5610	dirMS_041712_NAR_30mM_minus2.13532.13590.2	2	12.69	0	5.88E+05		(K)TCTFILR	(K)T/C|T|F I/L/R(G)	C:Carbamidomethylation	127.43	455.7458	910.481	0.0028	3.1	9.41	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
5611	dirMS_041712_NAR_40mM_minus2.13522.13522.3	3	12.69	1	1.96E+05		(K)LGVQVV	(K)L/G/V/Q/V/V/I/T D P E K/L D Q I R(Q)		163.38	641.7007	1923.091	-0.0034	-1.8	4.56	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
5612	dirMS_041712_NAR_60mM_minus.18591.18591.3	3	12.69	0	1.66E+05		(K)KPGGFD	(K)K P G G F D\I/S L/F\Y/R(D)		165.1	467.2495	1399.737	-0.0029	-2.1	8.59	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
5613	dirMS_041712_NAR_60mM_minus.9600.9735.3	3	12.69	1	5.37E+05		(R)IITEGFE	(R)I I|T E/G F/E A/A/K E K(A)		113.88	445.91	1335.716	0	0	4.79	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
5614	dirMS_041712_NAR_120mM_plus.9390.9390.3	3	12.69	1	3.91E+05		(K)STFREES	(K)S/T/F|R E E/S|P L R(I)		102.63	407.8773	1221.622	-0.0049	-4	5.87	53030.7	11.3	HUMAN	E9PJA7	Bcl-2-associated transcription factor 1
5615	dirMS_041712_NAR_20mM_plus.18076.18076.2	2	12.69	0	1.69E+05		(K)VANVSL	(K)V/A/N|V|S L L A/L Y/K(G)		195.5	595.8558	1190.714	-0.01	-8.4	8.56	15978.4	10.84	HUMAN	P62266	40S ribosomal protein S23
5616	dirMS_041712_NAR_20mM_plus.7440.7440.2	2	12.69	0	1.14E+05		(K)AQYEDI	(K)A Q|Y/E/D/I/A N R(S)		120.38	540.2601	1079.512	0.0013	1.2	4.37	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
5617	dirMS_041712_NAR_30mM_plus2.7816.7816.2	2	12.69	0	4.12E+05		(K)CNLLAE	(K)C N|L|L/A/E/K(Q)	C:Carbamidomethylation	94.87	424.2213	847.434	0.0011	1.3	6	40209.9	5.43	HUMAN	C9JV77	Alpha-2-HS-glycoprotein
5618	dirMS_041712_NAR_50mM_plus2.16945.16945.3	3	12.69	0	7.80E+05		(R)QYYTLL	(R)Q Y\Y T|L/L N Q/A/P D|M L H R(K)		156.93	621.6447	1862.922	-0.0022	-1.2	6.74	4335.1	9.82	HUMAN	E5RH00	Ras GTPase-activating protein-binding protein 1
5619	dirMS_041712_NAR_120mM_minus.11769.11803.3	3	12.68	1	2.46E+05		(R)RGLLED	(R)R\G L L\E\D|V|Q/E/G/R(T)		118.47	424.562	1271.67	0.0012	0.9	4.68	266161	5.68	HUMAN	E9PPU0	Epiplakin
5620	dirMS_041712_NAR_50mM_minus2.10516.10516.3	3	12.68	0	1.12E+05	M271m	(R)DLSYCLS	(R)D L/S/Y/C L S G m Y/D H/R(Y)	C:Carbamidomethylation m:Oxid	128.07	544.8966	1616.683	15.9921	-1.7	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
5621	dirMS_041712_NAR_60mM_minus.18216.18348.3	3	12.68	1	4.80E+05		(K)TQLNLLI	(K)T Q|L N\L/L/L/D/K L R(S)		163.37	442.9403	1326.81	-0.004	-3	8.41	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
5622	dirMS_041712_NAR_60mM_minus.6052.6052.3	3	12.68	1	2.45E+06		(K)DSYVGD	(K)D S/Y/V/G D E/A Q S K/R(G)		90.63	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
5623	dirMS_041712_NAR_120mM_plus.11641.11662.4	4	12.68	1	8.44E+05		(R)KVSQPIE	(R)K\V S Q|P/I/E/G H A A/S F A/Q F K(M)		113.75	461.9971	1844.965	0.0012	0.7	8.6	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
5624	dirMS_041712_NAR_50mM_plus2.17613.17613.3	3	12.68	1	1.27E+06		(R)VTFSGLF	(R)V/T|F/S G L R D T V T/P G E L L K(A)		160.82	611.6724	1833.012	-0.009	-4.9	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
5625	dirMS_041712_NAR_50mM_plus2.9777.9777.3	3	12.68	1	1.99E+05		(R)AGTGVD	(R)A/G/T/G/V/D N V D/L E/A A T R K(G)		118.75	539.6108	1616.824	-0.006	-3.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
5626	dirMS_041712_NAR_60mM_plus.19393.19393.3	3	12.68	1	4.90E+05		(K)TVTAMD	(K)T/V|T A/M D V/V/Y A L K\R(Q)		160.25	489.6071	1466.804	0.0032	2.2	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
5627	dirMS_041712_NAR_40mM_minus2.12086.12086.3	3	12.67	1	5.22E+03		(R)IINEPTA	(R)I I|N/E/P/T A A A I/A/Y G L D/K R(E)		153.6	606.0008	1815.996	-0.0085	-4.7	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
5628	dirMS_041712_NAR_40mM_minus2.15126.15126.3	3	12.67	0	7.32E+05		(K)ALIEVLQ	(K)A L|I/E|V/L Q/P L I/A/E H Q A R(R)		175.28	601.0146	1801.033	-0.0038	-2.1	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
5629	dirMS_041712_NAR_50mM_minus2.12482.12482.3	3	12.67	1	3.32E+05		(K)LYEQILA	(K)L/Y\E Q\I/L|A|E N E K L K(A)		139.12	530.9592	1590.874	-0.0107	-6.7	4.79	22046.7	5.8	HUMAN	H0YIM2	Protein phosphatase 1 regulatory subunit 12A (Fragment)
5630	dirMS_041712_NAR_50mM_minus2.17021.17021.3	3	12.67	0	6.32E+04		(K)YAPLHL	(K)Y A/P\L/H/L/V/P L I E R(L)		164.78	474.2781	1420.831	-0.0113	-8	6.75	147553.6	6.73	HUMAN	E7EVF4	Cytoplasmic FMR1-interacting protein 2
5631	dirMS_041712_NAR_20mM_plus.18651.18651.2	2	12.67	0	2.19E+05		(K)IYVDDGI	(K)I/Y\V/D D\G L/I/S L/Q V|K(Q)		200.58	731.9068	1462.815	-0.0088	-6	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
5632	dirMS_041712_NAR_20mM_plus.9482.9482.2	2	12.67	0	9.59E+04		(R)ALEESN	(R)A L|E/E/S/N Y E L E|G K(I)		136.52	691.3246	1381.648	-0.0062	-4.5	4.09	59054.3	5.14	HUMAN	P13645	Keratin, type I cytoskeletal 10
5633	dirMS_041712_NAR_30mM_plus2.11899.11908.2	2	12.67	0	3.51E+05		(K)YAIGSLN	(K)Y/A|I/G/S/L\N E G R(I)		115.68	540.2736	1079.548	-0.0081	-7.5	6	36309.7	5.86	HUMAN	B4DQ51	Short/branched chain-specific acyl-CoA dehydrogenase, mitochondrial
5634	dirMS_041712_NAR_30mM_plus2.16720.16720.2	2	12.67	0	5.99E+04		(R)AALQELI	(R)A/A|L/Q E L/L S/K(G)		140.78	486.7894	972.572	-0.0009	-0.9	6.05	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
5635	dirMS_041712_NAR_30mM_plus2.17572.17797.2	2	12.67	0	2.65E+06		(K)MIFVGI	(K)M/I|F/V/G I/K(K)		144.85	404.2433	807.48	-0.0004	-0.5	8.5	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
5636	dirMS_041712_NAR_30mM_plus2.21563.21563.2	2	12.67	0	2.68E+05		(R)EADDIVI	(R)E A/D/D I/V/N W L K(K)		167.63	601.81	1202.605	0.0075	6.3	4.03	26363.4	4.91	HUMAN	I3L312	Protein disulfide-isomerase (Fragment)
5637	dirMS_041712_NAR_40mM_plus2.17592.17592.3	3	12.67	0	1.61E+05		(R)VYAILTH	(R)V/Y/A|I L T H G I/F S G P A I S/R(I)		169.55	601.3376	1801.996	0.0023	1.3	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
5638	dirMS_041712_NAR_50mM_plus2.10849.10986.3	3	12.67	0	4.89E+05		(R)EALLSSA	(R)E A/L|L/S/S A/V D H G S D E V K(F)		124.7	552.9403	1656.807	-0.0012	-0.7	4.31	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
5639	dirMS_041712_NAR_50mM_plus2.16681.16681.3	3	12.67	1	5.82E+05		(K)DANAKL	(K)D A|N A K L S E\L|E/A/A L/Q R(A)		155.78	543.6256	1628.86	0.002	1.2	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
5640	dirMS_041712_NAR_50mM_plus2.16810.17325.3	3	12.67	1	3.79E+06	M148m	(R)LDLAGR	(R)L/D|L\A/G R D L/T/D/Y L/m/K(I)	m:Oxidized methionine	157.9	547.2842	1623.841	15.997	1.3	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
5641	dirMS_041712_NAR_120mM_minus.11555.11556.3	3	12.66	2	4.62E+05		(K)QAGPAS	(K)Q/A|G/P/A/S/V/P L R T E E E F K/K(F)		117.17	629.6696	1886.997	-0.0028	-1.5	6.23	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
5642	dirMS_041712_NAR_20mM_minus.14675.14703.3	3	12.66	0	3.68E+05		(K)LAVEAL	(K)L A\V E\A L S S L/D/G D/L/A/G R(Y)		201.3	529.6163	1586.838	-0.0041	-2.6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
5643	dirMS_041712_NAR_20mM_minus.8150.8150.2	2	12.66	0	3.12E+05	M239m	(K)EITALAP	(K)E I|T A/L/A/P S T m K(I)	m:Oxidized methionine	131.35	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
5644	dirMS_041712_NAR_30mM_minus2.13072.13091.2	2	12.66	0	5.96E+05		(R)GGEPQ	(R)G G\E/P/Q/G|P P F I K(Y)		124.8	563.7964	1126.589	-0.0036	-3.2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
5645	dirMS_041712_NAR_30mM_minus2.9472.9510.2	2	12.66	0	2.19E+05		(R)YMELEQ	(R)Y/M|E|L/E/Q/R(Y)		105.65	484.7299	968.451	0.0019	2	4.53	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
5646	dirMS_041712_NAR_50mM_minus2.12367.12367.3	3	12.66	0	2.32E+05		(K)AASDIA	(K)A A/S D\I/A/M T E L/P/P T H P I R(L)		138.97	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
5647	dirMS_041712_NAR_50mM_minus2.9483.9483.3	3	12.66	0	1.82E+05		(R)AIGSASE	(R)A/I/G S/A S E G A Q/S S L/Q E/V Y H K(S)		122.55	654.6559	1961.956	-0.0032	-1.6	5.4	20148.5	4.65	HUMAN	B4E2V4	Proteasome (Prosome, macropain) subunit, alpha type, 5, isoform CRA_c
5648	dirMS_041712_NAR_60mM_minus.11721.11721.3	3	12.66	1	7.51E+05	M546m	(K)QmADT	(K)Q m/A D/T G K L/N T/L/L Q/R(A)	m:Oxidized methionine	124.67	535.6216	1588.848	16.0027	4.8	8.75	91324.5	5.75	HUMAN	Q00839	Heterogeneous nuclear ribonucleoprotein U
5649	dirMS_041712_NAR_60mM_minus.16919.16976.3	3	12.66	1	2.55E+05		(K)MFGIDR	(K)M/F|G I/D R D A|I/A/Q A V R(G)		154.57	521.6047	1562.811	-0.0112	-7.2	5.71	63448.4	7.29	HUMAN	B4E022	Transketolase
5650	dirMS_041712_NAR_120mM_plus.11527.11527.4	4	12.66	2	2.22E+06		(K)QAGPAS	(K)Q A/G P/A S V/P L R T E E E/F/K K(F)		113.4	472.5046	1886.997	-0.0005	-0.3	6.23	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
5651	dirMS_041712_NAR_120mM_plus.8456.8456.4	4	12.66	0	3.85E+05		(K)LLETTDR	(K)L/L/E/T/T D R P D/G H Q N N L/R(S)		97.58	470.4895	1878.942	-0.0055	-2.9	5.38	82375.7	4.6	HUMAN	B7ZAV6	Importin subunit beta-1
5652	dirMS_041712_NAR_120mM_plus.9326.9387.3	3	12.66	0	1.03E+06		(K)EFHLNE	(K)E F H L N\E|S/G/D/P/S S K(S)		102.32	482.8884	1446.65	0.0011	0.7	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
5653	dirMS_041712_NAR_20mM_plus.18375.18375.2	2	12.66	0	1.22E+05		(R)GVVQEL	(R)G V|V|Q/E\L/Q\Q|A I/S K(L)		198.05	650.3656	1299.727	-0.0028	-2.1	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
5654	dirMS_041712_NAR_30mM_plus2.11958.11958.2	2	12.66	0	1.09E+05		(R)TPVSEDI	(R)T/P|V|S E D M L G/R(V)		115.97	552.7679	1104.535	-0.0069	-6.2	4.37	27142.6	6.66	HUMAN	C9J5E3	V-type proton ATPase subunit B, kidney isoform
5655	dirMS_041712_NAR_30mM_plus2.19305.19841.2	2	12.66	0	2.25E+06		(R)ALLFIPR	(R)A L|L|F/I/P R(R)		156.72	415.2703	829.529	0.0039	4.7	9.79	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
5656	dirMS_041712_NAR_30mM_plus2.21811.21811.2	2	12.66	0	2.18E+05		(R)NSILAQ	(R)N S|I|L\A|Q|V L D Q/S\A R(A)		170.17	707.8889	1414.765	0.0057	4	5.84	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
5657	dirMS_041712_NAR_50mM_plus2.14755.14755.3	3	12.66	1	4.12E+06		(R)ELISNAS	(R)E L|I/S N/A/S D A L D K I R(L)		145.58	515.6136	1544.828	-0.0016	-1	4.56	5582.4	4.81	HUMAN	F8W026	Endoplasmin (Fragment)
5658	dirMS_041712_NAR_50mM_plus2.15929.15929.3	3	12.66	1	6.95E+05		(R)SSISILE	(R)S S/I/S/I/L E Q E K/V V/A/Q Q\I\R(Q)		151.57	643.3614	1928.081	-0.0115	-5.9	5.87	58152.9	9.31	HUMAN	D6REB5	Alpha-L-iduronidase
5659	dirMS_041712_NAR_50mM_plus2.19297.19297.3	3	12.66	1	4.32E+05		(R)LKVPPAI	(R)L K|V/P P A I\N|Q\F/T Q/A L D R(Q)		169.82	604.3351	1811.017	-0.0266	-14.7	8.75	30166.2	10.79	HUMAN	P62424	60S ribosomal protein L7a
5660	dirMS_041712_NAR_20mM_minus.12190.12190.2	2	12.65	0	5.41E+05	M185m	(K)LAVNm	(K)L A|V/N m V/P\F P R(L)	m:Oxidized methionine	171.12	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
5661	dirMS_041712_NAR_30mM_minus2.12677.12677.2	2	12.65	0	2.59E+05		(R)TLSGME	(R)T L|S|G M/E/S Y/C V R(A)	C:Carbamidomethylation	122.08	651.795	1302.582	0.001	0.8	5.66	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
5662	dirMS_041712_NAR_30mM_minus2.5280.5280.2	2	12.65	0	5.96E+05		(R)TDTGEP	(R)T D|T/G|E P M G R(G)		82.45	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
5663	dirMS_041712_NAR_40mM_minus2.6431.6431.3	3	12.65	1	1.94E+05		(K)GAVAED	(K)G A/V|A\E/D G D/E L R T E/P E A/K(K)		104.53	596.2893	1786.845	0.008	4.5	4.08	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)

5664	dirMS_041712_NAR_50mM_minus2.15494.15494.3	3	12.65	1	1.73E+05		(K)DVLFLK	(K)D V|L/F/L/K D/C/V/G P E V E/K(A)	C:Carbamidomethylation	156.42	583.3014	1747.893	-0.0039	-2.2	4.32	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
5665	dirMS_041712_NAR_50mM_minus2.16618.16618.3	3	12.65	1	1.61E+05		(K)TVTAM	(K)T V|T/A/M D/V/V/Y A L K R(Q)		162.78	489.6051	1466.804	-0.0028	-1.9	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
5666	dirMS_041712_NAR_60mM_minus.7608.7608.3	3	12.65	1	5.65E+05		(R)YLAEVA	(R)Y L/A E V/A/A/G/D D/K/K(G)		102.07	427.222	1279.653	-0.0014	-1.1	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
5667	dirMS_041712_NAR_120mM_plus.17053.17271.4	4	12.65	1	1.15E+06		(R)VLISSLK	(R)V L\I/S/S L/K D C L/H/G I E/A/K(S)	C:Carbamidomethylation	142.77	446.4951	1782.978	-0.0197	-11	6.72	26261.9	9.78	HUMAN	F5GWE6	Cleavage and polyadenylation-specificity factor subunit 7
5668	dirMS_041712_NAR_120mM_plus.17106.17439.3	3	12.65	1	1.04E+06		(R)KVNNA	(R)K\V N N A D D\F|P/N/L/F R(Q)		143.2	517.2637	1549.776	0.0008	0.5	5.96	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
5669	dirMS_041712_NAR_120mM_plus.21469.21469.3	3	12.65	1	3.04E+05		(R)KVESLW	(R)K V E S L\W|P/I/F R(I)		165.78	425.5799	1274.726	-0.0004	-0.3	8.75	14138.1	9.89	HUMAN	C9JNV2	Protein BUD31 homolog
5670	dirMS_041712_NAR_120mM_plus.8714.8714.2	2	12.65	0	8.36E+05		(K)HFVALS	(K)H/F|V/A L S/T N T T/K(V)		99.1	609.8311	1218.648	0.0072	5.9	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
5671	dirMS_041712_NAR_20mM_plus.10784.10784.2	2	12.65	0	8.63E+04		(R)FLEQQN	(R)F L/E/Q Q|N Q V|L/Q\T/K(W)		146.73	738.3942	1475.785	-0.0041	-2.8	6	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
5672	dirMS_041712_NAR_20mM_plus.16544.16544.2	2	12.65	0	1.35E+05		(K)TVDNFV	(K)T V|D/N/F|V/A L A T G E K(G)		185.85	682.8565	1364.706	0.0001	0.1	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
5673	dirMS_041712_NAR_20mM_plus.17975.17975.2	2	12.65	0	1.12E+05		(K)VDFPQD	(K)V D/F/P Q D/Q L/T/A L/T G R(I)		195.42	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
5674	dirMS_041712_NAR_30mM_plus2.11299.11299.2	2	12.65	0	6.77E+05		(K)LTVDSAI	(K)L/T|V/D S A I A R(D)		112.97	473.2687	945.536	-0.0062	-6.6	5.84	334221.3	6.44	HUMAN	P15924	Desmoplakin
5675	dirMS_041712_NAR_30mM_plus2.17164.17630.2	2	12.65	0	6.70E+05		(R)GLVGIEF	(R)G L|V|G/I E/F/K(E)		144.35	431.7495	862.503	-0.0116	-13.4	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
5676	dirMS_041712_NAR_30mM_plus2.17605.17605.2	2	12.65	0	3.91E+05		(R)LSYTQLL	(R)L/S|Y/T Q/L L R(R)		145.58	497.2902	993.573	0.0004	0.4	8.75	533778	5.74	HUMAN	Q15149	Plectin
5677	dirMS_041712_NAR_30mM_plus2.18362.18362.2	2	12.65	0	2.25E+05		(K)GVEGLI	(K)G V|E G L|I|D I/E N P\N R(V)		149.43	713.3669	1425.733	-0.0067	-4.7	4.14	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
5678	dirMS_041712_NAR_40mM_plus2.19290.19290.3	3	12.65	1	1.93E+05		(K)TSAQVV	(K)T S/A/Q/V/V L/D G L/V D K I G D/V K(C)		180.37	619.6811	1857.033	-0.004	-2.2	4.43	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
5679	dirMS_041712_NAR_40mM_plus2.6251.6251.2	2	12.65	0	4.38E+05		(K)NAGFTP	(K)N A|G/F/T/P Q E R(Q)		96.23	510.2487	1019.491	-0.0004	-0.4	6	29474.8	6.94	HUMAN	G3V3M6	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
5680	dirMS_041712_NAR_40mM_plus2.8000.8041.3	3	12.65	1	1.36E+05		(K)GAVAED	(K)G A/V|A|E/D G D E L R T E P E/A/K(K)		107.38	596.2867	1786.845	0.0002	0.1	4.08	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
5681	dirMS_041712_NAR_50mM_plus2.10108.10108.3	3	12.65	0	6.15E+05		(K)VGQEIE	(K)V/G Q/E/I E V R P G I V S K(D)		121.05	504.2907	1510.859	-0.0012	-0.8	6.11	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
5682	dirMS_041712_NAR_50mM_plus2.12463.12463.3	3	12.65	1	2.64E+05		(R)SVELNP	(R)S V/E/L/N/P T Q K D L V/L K(I)		133.58	528.6368	1583.9	-0.0045	-2.8	5.79	198852.6	5.95	HUMAN	A6NKT7	RanBP2-like and GRIP domain-containing protein 3
5683	dirMS_041712_NAR_50mM_plus2.21003.21003.3	3	12.65	0	4.42E+06		(R)AGKPVI	(R)A G K\P V I\C\A T|Q|M|L E/S M I K(K)	C:Carbamidomethylation	179.65	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
5684	dirMS_041712_NAR_60mM_plus.11993.11993.3	3	12.65	0	3.20E+05		(R)LQAQQ	(R)L Q|A Q Q D|A/V/N I V C/H S K(T)	C:Carbamidomethylation	119.92	570.957	1710.859	-0.0027	-1.6	6.74	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
5685	dirMS_041712_NAR_60mM_plus.7699.7699.2	2	12.65	1	7.47E+05		(R)VITEEEK	(R)V/I/T E/E/E/K/N F K(A)		97.92	618.8282	1236.647	0.0021	1.7	4.79	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
5686	dirMS_041712_NAR_120mM_minus.4988.4988.3	3	12.64	1	5.89E+05		(R)AAEEED	(R)A/A/E E/E D E A D/P K R(Q)		79.32	453.8716	1359.602	-0.002	-1.5	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
5687	dirMS_041712_NAR_20mM_minus.13607.13607.2	2	12.64	0	1.30E+05		(K)ALQQGL	(K)A L/Q Q|G/L V G L/E L/K(E)		187.4	634.8811	1268.757	-0.0023	-1.8	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
5688	dirMS_041712_NAR_30mM_minus2.13956.13956.2	2	12.64	0	1.66E+05		(K)NVIGLQ	(K)N V|I/G/L/Q/M G/T N R(G)		129.38	601.8183	1202.631	-0.0017	-1.4	9.75	22562.2	8.8	HUMAN	P37802	Transgelin-2
5689	dirMS_041712_NAR_30mM_minus2.17823.17823.2	2	12.64	0	2.89E+05		(R)NNLAGA	(R)N\N\L|A/G A/E E L/F/A R(K)		151.62	652.8358	1304.659	0.005	3.8	4.53	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
5690	dirMS_041712_NAR_30mM_minus2.9001.9312.2	2	12.64	0	1.95E+07		(K)VIDDTN	(K)V/I|D|D/T N I/T/R(L)		104	523.7834	1046.548	0.0119	11.3	4.21	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5691	dirMS_041712_NAR_50mM_minus2.6899.6899.3	3	12.64	0	5.92E+05		(R)EATNPP	(R)E A/T/N/P/P V I Q E/E K/P K(K)		105.52	527.2846	1579.833	0.0066	4.2	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
5692	dirMS_041712_NAR_60mM_minus.10006.10006.3	3	12.64	0	1.56E+06		(R)EIVHIQA	(R)E/I V H I Q A G/Q/C/G/N Q I/G/A K(F)	C:Carbamidomethylation	115.57	608.3099	1822.923	-0.0077	-4.2	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
5693	dirMS_041712_NAR_60mM_minus.11962.11962.3	3	12.64	1	3.03E+06	M72m	(R)TEmENE	(R)T\E/m E N E/F V L I/K K(D)	m:Oxidized methionine	126.87	499.5941	1480.772	15.9962	0.8	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
5694	dirMS_041712_NAR_20mM_plus.19343.19343.2	2	12.64	0	8.40E+04		(R)ALIAGG	(R)A L I|A/G/G/G A|P E I E L A L R(L)		205.1	775.9467	1550.89	-0.0039	-2.5	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
5695	dirMS_041712_NAR_30mM_plus2.10680.10680.2	2	12.64	0	3.56E+05		(K)ATAVVD	(K)A T/A|V/V D/G/A F K(E)		109.4	489.7656	978.525	-0.0015	-1.6	5.88	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
5696	dirMS_041712_NAR_40mM_plus2.13162.13162.3	3	12.64	0	1.97E+05		(R)DLSHIG	(R)D/L S H I G D A\V|V/I/S C A/K(D)	C:Carbamidomethylation	144.35	528.9395	1584.805	-0.0011	-0.7	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
5697	dirMS_041712_NAR_40mM_plus2.16123.16123.2	2	12.64	0	1.50E+05		(R)YLTVAA	(R)Y/L|T/V/A A V F/R(G)		162.03	520.2997	1039.593	-0.0014	-1.3	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
5698	dirMS_041712_NAR_50mM_plus2.15687.15751.3	3	12.64	1	1.23E+05		(K)ELKIDIIP	(K)E L K\I D I\I|P/N/P Q E/R(T)		150.97	522.2931	1564.869	-0.0046	-2.9	4.68	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
5699	dirMS_041712_NAR_60mM_plus.13029.13030.3	3	12.64	0	3.45E+05		(K)YTVQDE	(K)Y/T|V/Q|D E S H/S E W\V/S C V R(F)	C:Carbamidomethylation	124.82	661.296	1981.871	0.0026	1.3	4.65	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
5700	dirMS_041712_NAR_120mM_minus.16703.16953.4	4	12.63	0	9.04E+05		(K)HLEINP	(K)H L\E\I\N P D H/S\I/I|E/T L/R(Q)		146.58	447.4904	1786.945	-0.0049	-2.7	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
5701	dirMS_041712_NAR_30mM_minus2.13114.13260.2	2	12.63	0	3.53E+05		(K)LQQFFN	(K)L Q|Q|F/F|N E/R(I)		125.18	541.2823	1081.543	0.0148	13.7	6	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
5702	dirMS_041712_NAR_30mM_minus2.13493.13717.2	2	12.63	0	4.15E+05		(K)LSSLPFQ	(K)L/S|S/L/P F Q/K(I)		127.68	460.2646	919.525	-0.0028	-3.1	8.75	12272.7	5.08	HUMAN	H3BRV9	Nuclear transport factor 2 (Fragment)
5703	dirMS_041712_NAR_30mM_minus2.14038.14038.2	2	12.63	0	2.72E+05		(K)CDFPIM	(K)C/D|F|P I|M|K(F)	C:Carbamidomethylation	129.67	455.7144	910.416	0.0054	5.9	5.84	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
5704	dirMS_041712_NAR_30mM_minus2.6973.7029.2	2	12.63	0	2.06E+05	M88m	(K)DVDEAY	(K)D V|D|E/A/Y m N/K(V)	m:Oxidized methionine	92.7	550.7326	1084.462	15.9964	1.3	4.03	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
5705	dirMS_041712_NAR_30mM_minus2.9974.9974.2	2	12.63	0	1.44E+05		(R)SSTETCY	(R)S S T/E/T/C Y S/A I/P K(A)	C:Carbamidomethylation	108.25	672.31	1343.615	-0.002	-1.5	5.72	258215.9	5.48	HUMAN	E7EN95	Filamin-B
5706	dirMS_041712_NAR_50mM_minus2.10820.10820.3	3	12.63	1	6.04E+05		(R)IAEFTTN	(R)I A|E/F/T T N L T E E E E K S K(S)		130.4	623.6418	1868.912	-0.0015	-0.8	4.32	227783.5	5.5	HUMAN	P35579	Myosin-9
5707	dirMS_041712_NAR_20mM_plus.16749.16749.2	2	12.63	0	1.86E+05		(R)ELLIIGG	(R)E L L|I/I/G/G V A A R(D)		186.42	556.3437	1111.683	-0.0032	-2.9	6.1	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
5708	dirMS_041712_NAR_20mM_plus.16969.16969.2	2	12.63	0	2.65E+05		(K)VQIAVA	(K)V Q|I|A\V/A|N A Q/E L\L/Q/R(M)		187.98	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
5709	dirMS_041712_NAR_30mM_plus2.12833.12833.2	2	12.63	0	1.98E+05		(K)LVPVLSA	(K)L V|P V/L/S A K(A)		120.23	413.7745	826.54	0.0021	2.5	8.75	37710.6	6.36	HUMAN	P37837	Transaldolase
5710	dirMS_041712_NAR_30mM_plus2.14145.14145.2	2	12.63	0	5.38E+04		(K)YGEPGE	(K)Y G\E|P G E V/F I N K(G)		127.15	626.8136	1252.621	-0.0009	-0.7	4.53	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
5711	dirMS_041712_NAR_30mM_plus2.5456.5456.2	2	12.63	0	3.75E+04		(K)SAAQAA	(K)S A/A Q/A A A|Q/T\N S N A/A G K(Q)		82.75	730.8568	1460.709	-0.0025	-1.7	8.47	45021.6	8.74	HUMAN	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein
5712	dirMS_041712_NAR_30mM_plus2.8248.8248.2	2	12.63	0	1.36E+06		(K)QGGGG	(K)Q G G G G|G/G G/S/V/P G I E R(M)		97.17	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
5713	dirMS_041712_NAR_40mM_plus2.9842.9842.3	3	12.63	0	2.12E+05		(R)AAEDPV	(R)A A|E|D|P V A/A/A P R P L P A G G R(L)		121.25	572.6438	1715.919	-0.0019	-1.1	6.12	73966.7	10.21	HUMAN	B3KWK6	Alpha-L-iduronidase
5714	dirMS_041712_NAR_50mM_plus2.20912.20912.3	3	12.63	0	3.65E+06		(R)AGKPVI	(R)A G K\P V I\C A/T/Q|M\L/E/S M I K(K)	C:Carbamidomethylation	179.23	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
5715	dirMS_041712_NAR_30mM_minus2.16560.16560.2	2	12.62	0	3.67E+05	M185m	(K)LAVNm	(K)L A|V/N/m/V|P\F P R(L)	m:Oxidized methionine	142.78	580.3178	1143.634	15.994	-0.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
5716	dirMS_041712_NAR_30mM_minus2.9924.9924.2	2	12.62	0	1.44E+05		(R)SSTETCY	(R)S S/T|E/T C/Y S A I|P K(A)	C:Carbamidomethylation	108.25	672.31	1343.615	-0.002	-1.5	5.72	258215.9	5.48	HUMAN	E7EN95	Filamin-B
5717	dirMS_041712_NAR_120mM_plus.6729.6741.3	3	12.62	1	6.52E+05		(R)NKQTYS	(R)N K Q T\Y|S|T/E/P N N L K(A)		88.83	512.9261	1536.765	-0.0015	-1	8.5	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
5718	dirMS_041712_NAR_120mM_plus.9119.9119.3	3	12.62	1	2.52E+05		(R)LRECELS	(R)L R E C/E\L|S|P G V N R(D)	C:Carbamidomethylation	100.88	477.2447	1429.722	-0.0021	-1.5	6.14	57188.9	5.97	HUMAN	H7C3A1	Serrate RNA effector molecule homolog (Fragment)
5719	dirMS_041712_NAR_20mM_plus.16647.16647.2	2	12.62	0	1.58E+05		(R)LLEAQIA	(R)L L\E\A/Q|I|A/T\G G I I D/P K(E)		185.68	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
5720	dirMS_041712_NAR_20mM_plus.16923.16923.3	3	12.62	0	3.15E+05		(K)VQIAVA	(K)V Q\I A V A\N A Q/E/L/L Q R(M)		187.82	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
5721	dirMS_041712_NAR_30mM_plus2.22047.22192.2	2	12.62	0	2.65E+05		(K)LISLFQA	(K)L/I|S\L/F/Q A\M/K(K)		171.08	525.8042	1050.602	-0.0005	-0.5	8.75	533778	5.74	HUMAN	Q15149	Plectin
5722	dirMS_041712_NAR_30mM_plus2.6030.6030.2	2	12.62	0	1.59E+05		(K)TYGQST	(K)T Y|G|Q/S T Y S R(Q)		85.9	531.7464	1062.485	0.0005	0.4	8.25	14693.3	4.69	HUMAN	C9JLS9	26S protease regulatory subunit 7 (Fragment)
5723	dirMS_041712_NAR_40mM_plus2.9848.9848.3	3	12.62	0	5.27E+04	M376m	(K)mAPVPL	(K)m A|P V/P L D/D/S N R P A S L T K(D)	m:Oxidized methionine	122.05	609.9795	1811.932	15.9919	-1.6	5.71	53030.7	11.3	HUMAN	E9PJA7	Bcl-2-associated transcription factor 1
5724	dirMS_041712_NAR_50mM_plus2.20197.20236.3	3	12.62	0	5.30E+05		(R)QARPTY	(R)Q/A R P T Y\A|T|A|M/L/Q/S L L K(-)		174.57	597.9962	1791.979	-0.0045	-2.5	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
5725	dirMS_041712_NAR_50mM_plus2.9140.9140.3	3	12.62	0	1.50E+05		(R)NDIASHI	(R)N/D\I|A S H/P P V E/G S Y|A P R(R)		114.92	570.6114	1709.824	-0.0045	-2.6	5.32	26398.4	5.21	HUMAN	H7C597	Staphylococcal nuclease domain-containing protein 1 (Fragment)
5726	dirMS_041712_NAR_60mM_plus.9810.9850.3	3	12.62	0	7.41E+05		(R)QQEGFK	(R)Q Q/E/G F/K/P N Y M E/N R(E)		109.35	547.5879	1640.749	0.0006	0.4	6.14	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
5727	dirMS_041712_NAR_60mM_plus.9829.9829.3	3	12.62	1	1.29E+06		(K)EAALSTA	(K)E A/A/L/S T/A L/S E K/R(T)		109.78	425.898	1275.69	-0.0109	-8.5	6.24	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
5728	dirMS_041712_NAR_30mM_minus2.14775.14898.2	2	12.61	0	2.52E+05		(R)YLIEIAK	(R)Y/L|I/E/I/A/K(N)		134.45	425.2556	849.508	-0.0041	-4.8	6	41736.1	5.41	HUMAN	A8KAH5	IST1 homolog
5729	dirMS_041712_NAR_30mM_minus2.17638.17638.2	2	12.61	0	1.67E+05		(R)NGGQIL	(R)N/G/G Q|I|L I/A D L/R(G)		149.57	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
5730	dirMS_041712_NAR_30mM_minus2.19621.19621.2	2	12.61	0	4.38E+05		(R)ASLSLW	(R)A S/L/S L/W/Q A M E/K(G)		162.85	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
5731	dirMS_041712_NAR_40mM_minus2.10905.10905.3	3	12.61	0	1.10E+05	M56m	(K)VAIVKP	(K)V/A|I/V/K/P G V/P m E I V L N K(E)	m:Oxidized methionine	147.05	575.0112	1707.024	15.9953	0.2	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
5732	dirMS_041712_NAR_40mM_minus2.11473.11473.3	3	12.61	0	1.87E+05		(K)LVTSIGD	(K)L V|T/S I/G/D V V N H D/P V V G D R(L)		150.45	631.3335	1891.987	-0.0013	-0.7	4.41	27786.2	5.93	HUMAN	H0Y4Z6	Phosphorylase (Fragment)
5733	dirMS_041712_NAR_50mM_minus2.9373.9373.3	3	12.61	0	6.84E+04		(R)AASIFG	(R)A A/S|I/F/G G A K/P V D/T A A R(E)		121.62	511.2773	1531.823	-0.0054	-3.5	8.79	64861.3	5.86	HUMAN	B4DS13	Eukaryotic translation initiation factor 4B
5734	dirMS_041712_NAR_60mM_minus.10245.10245.3	3	12.61	1	2.36E+04	M88m	(K)DVDEAY	(K)D V/D\E/A Y/m N K/V/E L E/S/R(L)	m:Oxidized methionine	116.03	605.2791	1797.832	15.9904	-2.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
5735	dirMS_041712_NAR_60mM_minus.8098.8098.3	3	12.61	1	4.11E+05		(R)YLAEVA	(R)Y/L/A|E/V/A T/G E K R(A)		104.48	412.8902	1236.658	-0.0022	-1.8	6.14	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
5736	dirMS_041712_NAR_60mM_minus.9679.9679.3	3	12.61	0	3.48E+05		(R)QLSQAG	(R)Q L|S/Q/A/G/S F S D\G T H G G L R(Y)		113.6	573.2781	1717.825	-0.0055	-3.2	6.74	266161	5.68	HUMAN	E9PPU0	Epiplakin
5737	dirMS_041712_NAR_30mM_plus2.10208.10591.2	2	12.61	0	1.14E+06		(R)GLDVED	(R)G L|D|V/E D|V/K(F)		108.2	437.7293	874.452	-0.0003	-0.4	4.03	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
5738	dirMS_041712_NAR_30mM_plus2.12567.12883.2	2	12.61	0	3.83E+05		(K)IGVTVLS	(K)I/G|V|T/V/L/S R(I)		119.77	422.7657	844.525	-0.001	-1.1	9.75	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
5739	dirMS_041712_NAR_30mM_plus2.17506.17506.2	2	12.61	0	3.69E+05		(K)SFNLSAL	(K)S F/N|L/S/A L E/K(H)		144.53	504.7726	1008.536	0.0019	1.9	5.72	82756.6	5.34	HUMAN	C9JIF9	Acylamino-acid-releasing enzyme
5740	dirMS_041712_NAR_30mM_plus2.20171.20171.2	2	12.61	0	1.12E+05		(K)TNVALM	(K)T N/V|A/L|M/C M L/R(E)	C:Carbamidomethylation	159.55	604.8021	1208.595	0.0021	1.7	9.41	71929.1	5.1	HUMAN	C9JAQ9	U5 small nuclear ribonucleoprotein 200 kDa helicase
5741	dirMS_041712_NAR_50mM_plus2.15213.15213.3	3	12.61	0	2.43E+04		(K)VALLLLD	(K)V A\L|L/L/L|D/Q/G A S P H A A A K(N)		147.53	558.9877	1674.954	-0.0052	-3.1	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
5742	dirMS_041712_NAR_60mM_plus.11236.11236.3	3	12.61	0	1.93E+06		(R)EIVHIQA	(R)E/I V\H I Q\A/G/Q/C/G N Q|I/G A K(F)	C:Carbamidomethylation	116.42	608.311	1822.923	-0.0044	-2.4	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
5743	dirMS_041712_NAR_60mM_plus.13679.13679.3	3	12.61	1	5.75E+05		(R)ISVYYNE	(R)I/S/V|Y/Y N E A/T G G K Y V P/R(A)		128.33	606.3113	1816.923	-0.0035	-1.9	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
5744	dirMS_041712_NAR_60mM_plus.15055.15055.3	3	12.61	0	5.61E+05		(R)YLDLHD	(R)Y/L/D/L H/D/C Y L/K(Y)	C:Carbamidomethylation	135	447.2169	1339.635	0.001	0.8	5.21	52796.2	5.19	HUMAN	E7EUT8	Splicing factor 3A subunit 3
5745	dirMS_041712_NAR_20mM_minus.9271.9289.3	3	12.6	0	3.43E+05		(R)AQIFAN	(R)A Q\I\F\A\N/T|V/D N A/R(I)		142.32	440.5612	1319.67	-0.0012	-0.9	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5746	dirMS_041712_NAR_30mM_minus2.14527.14527.2	2	12.6	0	4.83E+05		(R)TFEDFV	(R)T/F|E/D/F/V/R(I)		133.2	457.2246	913.441	0.0005	0.6	4.37	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
5747	dirMS_041712_NAR_50mM_minus2.12556.12556.3	3	12.6	0	2.96E+05		(K)AASDIA	(K)A A\S/D I/A|M T E\L/P P T/H/P I R(L)		139.5	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
5748	dirMS_041712_NAR_50mM_minus2.8323.8323.3	3	12.6	1	2.09E+05		(K)GILAAD	(K)G I|L/A/A|D E/S T/G S I/A K R(L)		114.97	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
5749	dirMS_041712_NAR_120mM_plus.8364.8364.2	2	12.6	1	3.54E+05		(K)YEKDIAA	(K)Y E/K/D/I/A A Y R(A)		97.17	564.7869	1128.568	-0.0019	-1.7	6.07	25064.5	5.62	HUMAN	P09429	High mobility group protein B1
5750	dirMS_041712_NAR_20mM_plus.14105.14105.2	2	12.6	0	7.05E+04	M313m	(R)TVQSLEI	(R)T V/Q|S/L/E/I D\L D S m R(N)	m:Oxidized methionine	169.18	761.8738	1506.747	15.9935	-0.9	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5751	dirMS_041712_NAR_30mM_plus2.21369.21394.2	2	12.6	0	3.00E+06		(K)FLPLFDR	(K)F L|P/L F/D/R(V)		166.02	454.2621	907.504	0.0133	14.7	5.84	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
5752	dirMS_041712_NAR_40mM_plus2.5715.5715.2	2	12.6	0	1.12E+05		(R)FSSSSGY	(R)F/S|S|S/S/G Y G G G S S R(V)		90.98	618.2686	1235.529	0.0012	1	8.75	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
5753	dirMS_041712_NAR_50mM_plus2.14618.14618.3	3	12.6	1	6.09E+05		(R)ELVFKED	(R)E L/V/F/K E D G Q/E/Y A Q|V I/K(M)		144.92	632.6588	1895.975	-0.0131	-6.9	4.41	14568.9	5.17	HUMAN	A6NJH9	Eukaryotic translation initiation factor 1A, Y-chromosomal
5754	dirMS_041712_NAR_50mM_plus2.16338.16338.3	3	12.6	1	4.23E+05		(K)DVLFLK	(K)D V/L|F/L K/D C V/G P E V E/K(A)	C:Carbamidomethylation	154.42	583.3027	1747.893	0	0	4.32	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
5755	dirMS_041712_NAR_50mM_plus2.16717.16809.3	3	12.6	0	1.14E+05		(K)AQDGSH	(K)A/Q|D/G S H/P L/S L/Q D L I E K(V)		155.92	584.2981	1750.897	-0.0173	-9.9	4.54	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
5756	dirMS_041712_NAR_120mM_minus.20544.20544.3	3	12.59	1	3.46E+05		(R)LDLAGR	(R)L/D|L/A/G R D L T D Y/L M/K(I)		169.02	541.9508	1623.841	-0.0032	-2	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
5757	dirMS_041712_NAR_30mM_minus2.11718.11718.2	2	12.59	0	2.43E+05		(R)MAIESA	(R)M/A|I/E/S A G F K(L)		117.25	477.2411	953.476	-0.0012	-1.2	5.75	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
5758	dirMS_041712_NAR_30mM_minus2.19550.19686.2	2	12.59	0	4.75E+05		(R)ASLSLW	(R)A S/L/S|L/W\Q/A/M/E/K(G)		162.73	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
5759	dirMS_041712_NAR_30mM_minus2.5777.5777.2	2	12.59	0	6.55E+04		(K)TSETLSC	(K)T\S|E|T L/S/Q A G Q/K(A)		85.58	575.2877	1149.575	-0.0065	-5.6	5.66	25978.5	4.91	HUMAN	C9J502	Prostate leucine zipper variant 2
5760	dirMS_041712_NAR_50mM_minus2.9426.9533.2	2	12.59	1	7.15E+05		(R)DGKLVS	(R)D/G K|L|V|S E/S\S D V\L|P K(-)		121.97	737.3927	1473.78	-0.0014	-0.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
5761	dirMS_041712_NAR_60mM_minus.11396.11396.3	3	12.59	1	8.92E+05	M232m	(R)MSmKE	(R)M/S m K E V|D E\Q|M|L/N V Q N K(N)	m:Oxidized methionine	122.82	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
5762	dirMS_041712_NAR_60mM_minus.5032.5060.3	3	12.59	1	2.11E+05		(R)MQNDT	(R)M/Q|N/D/T A E/N E T T E K E\E K(S)		82.83	632.9407	1896.813	-0.0052	-2.7	4.14	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
5763	dirMS_041712_NAR_120mM_plus.22981.22981.3	3	12.59	1	4.83E+05		(K)GLAPDL	(K)G L|A|P D/L/P E D L Y H L I K K(A)		174.03	608.0076	1822.011	-0.0027	-1.5	5.38	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
5764	dirMS_041712_NAR_20mM_plus.17828.17828.2	2	12.59	0	1.67E+05		(K)GADFLV	(K)G A D\F L|V|T E/V/E/N G G\S L G S K(K)		195	890.4414	1779.876	-0.0004	-0.2	4.14	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
5765	dirMS_041712_NAR_30mM_plus2.13662.13706.2	2	12.59	0	1.80E+05		(R)YYGYTG	(R)Y/Y|G/Y T|G/A F R(C)		124.72	549.2571	1097.505	0.0019	1.7	8.5	78507.3	9.14	HUMAN	E7EQB2	Kaliocin-1 (Fragment)
5766	dirMS_041712_NAR_30mM_plus2.14375.14539.2	2	12.59	0	3.62E+05		(K)TLPQMF	(K)T/L|P Q/M/F T/K(T)		128.93	483.2645	965.513	0.0093	9.6	8.41	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
5767	dirMS_041712_NAR_50mM_plus2.6705.6705.3	3	12.59	1	3.61E+04		(K)VVSETN	(K)V V|S/E T/N D/T K V/L/R(H)		100.07	454.2516	1360.743	-0.0028	-2.1	6.04	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
5768	dirMS_041712_NAR_60mM_plus.19194.19194.3	3	12.59	1	1.15E+04		(R)AGEAGK	(R)A G E/A/G/K L E E V/M|Q E L R(A)		159.08	553.9525	1659.837	0.0059	3.6	4.49	54918.3	5.61	HUMAN	Q9BR76	Coronin-1B
5769	dirMS_041712_NAR_30mM_minus2.15355.15355.2	2	12.58	0	4.30E+05	M2249m	(K)MSIYQA	(K)M/S|I/Y/Q A m/W K(G)	m:Oxidized methionine	136.15	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
5770	dirMS_041712_NAR_50mM_minus2.17248.17248.3	3	12.58	0	1.05E+06	M195m	(R)LHFFmP	(R)L H\F F m|P G|F\A/P L T S R(G)	m:Oxidized methionine	167.33	546.2872	1620.835	16.0115	10.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
5771	dirMS_041712_NAR_60mM_minus.16912.16912.3	3	12.58	1	2.73E+05		(R)GQFSTD	(R)G Q|F/S/T/D E L V A E V E K R(N)		153.97	569.9569	1707.855	0.0013	0.8	4.41	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
5772	dirMS_041712_NAR_20mM_plus.9002.9002.2	2	12.58	0	2.22E+05		(K)VTADVI	(K)V/T|A/D V|I N A A E K(L)		132.65	565.806	1130.605	-0.0005	-0.4	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase

5773	dirMS_041712_NAR_30mM_plus2.8109.8109.2	2	12.58	0	1.34E+06		(K)QGGGG	(K)Q/G G\G/G/G/G G S\V/P G I/E R(M)		97.15	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
5774	dirMS_041712_NAR_30mM_plus2.8517.8684.2	2	12.58	0	4.73E+05		(R)AVNYFS	(R)A/V|N/Y/F/S/K(V)		98.93	414.7159	828.425	-0.0005	-0.6	8.63	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
5775	dirMS_041712_NAR_50mM_plus2.10721.10722.3	3	12.58	1	2.46E+06		(R)MQKEIT	(R)M Q K E I T/A|L|A|P/S T M K(I)		124.03	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
5776	dirMS_041712_NAR_50mM_plus2.18720.18720.3	3	12.58	0	1.19E+06		(R)LGFHLP	(R)L G F H L P/L\E|V/A/Y Q R(G)		167.38	514.9522	1542.843	-0.0007	-0.4	6.75	533778	5.74	HUMAN	Q15149	Plectin
5777	dirMS_041712_NAR_50mM_plus2.19847.19847.3	3	12.58	0	7.56E+04		(K)ILFIFIDSI	(K)I/L|F|I/F I D/S D H T D N Q R(I)		172.73	611.9758	1833.913	-0.0001	-0.1	4.41	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
5778	dirMS_041712_NAR_50mM_plus2.20554.20554.3	3	12.58	1	1.36E+05		(R)GGPNIIT	(R)G G/P/N/I/I/T L/A D/I V K D P V S\R(T)		176.98	622.3526	1865.049	-0.0058	-3.1	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
5779	dirMS_041712_NAR_50mM_plus2.7425.7425.3	3	12.58	1	2.93E+05		(R)IVEQDT	(R)I V|E/Q/D T M/P P K G V R(H)		105.32	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
5780	dirMS_041712_NAR_50mM_plus2.7798.7798.3	3	12.58	1	1.02E+05		(K)ELQAAG	(K)E L\Q|A A/G K/S/P/E D/L/E R(L)		106.55	514.9321	1542.776	0.0059	3.8	4.41	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
5781	dirMS_041712_NAR_60mM_plus.12463.12810.3	3	12.58	1	3.93E+06		(K)VKLEAEI	(K)V K L E\A E|I|A/T/Y/R(R)		123.08	431.5782	1292.721	-0.0008	-0.6	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5782	dirMS_041712_NAR_20mM_minus.12218.12218.2	2	12.57	0	1.37E+05		(K)LVSIGAE	(K)L V|S|I/G\A E E I V D/G N A K(M)		171.23	757.9044	1514.806	-0.0045	-3	4.14	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
5783	dirMS_041712_NAR_30mM_minus2.18181.18181.2	2	12.57	0	2.92E+04		(R)LINLVGE	(R)L I|N\L/V/G E S L/R(L)		153.3	557.3333	1113.663	-0.0033	-3	6	119157.2	5.4	HUMAN	B0UX83	HLA-B associated transcript 3
5784	dirMS_041712_NAR_50mM_minus2.7899.7899.3	3	12.57	1	1.50E+05		(K)TAVCDIF	(K)T A/V/C/D/I/P/P R G L K(M)	C:Carbamidomethylation	111.93	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
5785	dirMS_041712_NAR_60mM_minus.14132.14204.3	3	12.57	1	4.08E+05	M320m	(K)YmACCL	(K)Y/m|A|C C L L Y R G D\V\V/P K(E)	C:Carbamidomethylation m:Oxid	138.77	620.9608	1844.886	15.9823	-6.8	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
5786	dirMS_041712_NAR_120mM_plus.14135.14639.3	3	12.57	1	2.83E+06		(R)QLREYQ	(R)Q L/R E Y\Q/E/L/M N V K(L)		128.7	517.6042	1550.8	-0.0015	-1	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
5787	dirMS_041712_NAR_20mM_plus.7939.7939.2	2	12.57	0	4.38E+03		(R)GLANPE	(R)G L\A|N/P\E/P A/P E P K(V)		124.33	610.3183	1219.632	-0.0024	-2	4.53	54333.1	6.51	HUMAN	H0Y5S1	Protein transport protein Sec16A (Fragment)
5788	dirMS_041712_NAR_30mM_plus2.14471.14471.2	2	12.57	0	1.82E+04		(R)VATWF	(R)V A|T/W/F/N Q/P A/R(K)		128.88	595.3077	1189.611	-0.0031	-2.6	9.72	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
5789	dirMS_041712_NAR_30mM_plus2.19600.19600.2	2	12.57	0	2.69E+05		(K)APDFVF	(K)A P/D|F/V|F/Y/A P R(L)		156.67	591.8008	1182.594	0.0001	0.1	5.88	71218.8	6.3	HUMAN	A7YIJ8	Radixin
5790	dirMS_041712_NAR_30mM_plus2.9032.9073.2	2	12.57	0	3.30E+05		(K)ALELDQ	(K)A L|E|L/D/Q E/R(K)		101.05	487.2518	973.495	0.0014	1.5	4.14	71218.8	6.3	HUMAN	A7YIJ8	Radixin
5791	dirMS_041712_NAR_40mM_plus2.11462.11462.2	2	12.57	0	6.40E+04		(R)SVPTWL	(R)S/V|P T/W L K(L)		133.45	415.7412	830.477	-0.0019	-2.3	8.47	12573.5	10.39	HUMAN	E9PS50	40S ribosomal protein S13 (Fragment)
5792	dirMS_041712_NAR_40mM_plus2.9681.9681.3	3	12.57	0	1.97E+05		(R)AAEDPV	(R)A/A|E/D/P V A/A A/P R P L P A G G R(L)		120.92	572.6438	1715.919	-0.0019	-1.1	6.12	73966.7	10.21	HUMAN	B3KWK6	Alpha-L-iduronidase
5793	dirMS_041712_NAR_50mM_plus2.10600.10600.3	3	12.57	0	5.07E+05		(K)MIVDPV	(K)M I|V\D/P V/E P H G E M K(F)		123.22	494.5783	1481.713	0.0076	5.2	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
5794	dirMS_041712_NAR_50mM_plus2.11823.11926.3	3	12.57	1	3.79E+05		(K)IGRIEDV	(K)I G R I E D\V\T|P\I|P/S/D S T R(R)		130.28	585.9784	1755.924	-0.0029	-1.7	4.56	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
5795	dirMS_041712_NAR_50mM_plus2.18604.18604.3	3	12.57	0	3.58E+05		(R)LLLDGA	(R)L L/L/D G A/P L I A I/H/K(A)		165.82	458.622	1373.852	-0.0001	0	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
5796	dirMS_041712_NAR_60mM_plus.11138.11138.3	3	12.57	1	2.86E+05		(R)LRGPSG	(R)L R G P S G G G E E|P A|L|S/Q/Y Q R(L)		115.92	634.6529	1901.946	-0.0023	-1.2	6.14	80080.5	5.54	HUMAN	J3KMX1	Nuclear pore complex protein Nup88 (Fragment)
5797	dirMS_041712_NAR_60mM_plus.12478.12617.3	3	12.57	1	3.93E+06		(K)VKLEAEI	(K)V K\L E\A E|I|A/T Y R(R)		123.08	431.5782	1292.721	-0.0008	-0.6	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5798	dirMS_041712_NAR_50mM_minus2.11314.11314.3	3	12.56	1	4.87E+05		(K)ILIANTG	(K)I/L/I/A N T/G M/D/T D/K I K(I)		133.38	511.6179	1532.835	0.0039	2.5	5.96	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
5799	dirMS_041712_NAR_20mM_plus.14775.14775.2	2	12.56	0	1.17E+05		(K)FANPFP	(K)F A/N|P F/P A A V R(G)		173.78	545.2958	1089.584	0.0003	0.3	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
5800	dirMS_041712_NAR_30mM_plus2.10026.10026.2	2	12.56	0	3.07E+05		(K)LAEQFP	(K)L A|E/Q/F/P R(Q)		105.68	430.7352	860.462	0.0006	0.7	6	15778.8	9.12	HUMAN	E9PL10	Transcription factor BTF3 homolog 4
5801	dirMS_041712_NAR_30mM_plus2.10115.10254.2	2	12.56	0	7.52E+05		(K)FVIATST	(K)F/V|I|A T/S/T/K(I)		107.07	433.7497	866.498	-0.0061	-7	8.75	25891.4	10.67	HUMAN	F8W181	60S ribosomal protein L6 (Fragment)
5802	dirMS_041712_NAR_30mM_plus2.19177.19177.2	2	12.56	0	2.42E+05		(R)LTAEDLF	(R)L T/A/E D/L/F/E/A R(I)		153.35	582.796	1164.59	-0.0048	-4.1	4.14	533778	5.74	HUMAN	Q15149	Plectin
5803	dirMS_041712_NAR_30mM_plus2.20917.21165.2	2	12.56	0	4.83E+05		(K)AIDLFTD	(K)A I|D|L/F T/D\A\I/K(L)		164.68	553.8012	1106.609	-0.0141	-12.7	4.21	18141.9	4.7	HUMAN	F6VDH7	Hsc70-interacting protein (Fragment)
5804	dirMS_041712_NAR_30mM_plus2.7658.8132.2	2	12.56	0	5.88E+06		(K)NMMAA	(K)N M|M|A|A|C D|P/R(H)	C:Carbamidomethylation	94.58	533.2174	1065.427	0.0001	0.1	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
5805	dirMS_041712_NAR_30mM_plus2.8277.8277.2	2	12.56	0	2.73E+05		(K)EIAENAL	(K)E I/A/E/N A L/G K(H)		96.92	472.755	944.505	-0.002	-2.1	4.53	36982.9	6.37	HUMAN	P31942	Heterogeneous nuclear ribonucleoprotein H3
5806	dirMS_041712_NAR_30mM_plus2.9608.9767.2	2	12.56	0	7.73E+05		(K)AELDDT	(K)A E|L|D|D/T/P M/R(G)		104.82	524.2438	1047.478	0.0028	2.7	4.03	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
5807	dirMS_041712_NAR_40mM_plus2.17965.17965.3	3	12.56	0	1.63E+04	N86n	(K)LEQLVn	(K)L E Q|L V n V T D D/L L I Y K(I)	n:N-acetylglucosamine (N)	172.2	660.3654	1775.979	203.1027	11.8	4.03	48624.6	5.98	HUMAN	Q969V4	Tektin-1
5808	dirMS_041712_NAR_50mM_plus2.19275.19275.3	3	12.56	0	8.48E+05		(R)DFNHIN	(R)D F/N H I N\V|E\L/S L/L/G K(K)		170.1	533.6223	1598.854	-0.0013	-0.8	5.32	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
5809	dirMS_041712_NAR_50mM_plus2.6025.6025.3	3	12.56	1	1.87E+05		(R)AIEAAP	(R)A I|E/A A/P Q E/P E Q K R(S)		95.88	489.5906	1466.76	-0.0025	-1.7	4.79	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
5810	dirMS_041712_NAR_50mM_plus2.8636.8636.3	3	12.56	0	1.10E+06		(R)LESGMC	(R)L/E|S G M/Q/N M/S I H/T K(T)		112.92	492.5704	1475.698	-0.0015	-1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
5811	dirMS_041712_NAR_60mM_plus.4778.4778.3	3	12.56	1	3.22E+05		(K)AGADEE	(K)A/G\A/D/E E R A E\T A R(L)		79.42	425.868	1275.592	-0.0029	-2.3	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
5812	dirMS_041712_NAR_60mM_plus.5755.5755.3	3	12.56	0	1.87E+05		(R)STFETE	(R)S/T|F/E/T/E/H A G Q R(D)		88.4	421.5294	1262.576	-0.0024	-1.9	5.38	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
5813	dirMS_041712_NAR_20mM_minus.7194.7194.2	2	12.55	0	1.40E+05		(K)VTLTSEE	(K)V T|L/T/S/E E/E A/R(L)		119.73	567.785	1134.564	-0.001	-0.9	4.25	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
5814	dirMS_041712_NAR_30mM_minus2.10472.10615.2	2	12.55	0	1.47E+06		(R)GLTSVIN	(R)G L|T|S/V/I/N Q K(L)		111.3	480.2794	959.552	-0.0005	-0.5	8.75	36923.1	5.71	HUMAN	P07195	L-lactate dehydrogenase B chain
5815	dirMS_041712_NAR_30mM_minus2.17786.17786.2	2	12.55	0	1.60E+05		(R)VPFSLLR	(R)V/P/F/S L L/R(G)		151.43	416.2578	831.509	-0.0004	-0.5	9.72	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
5816	dirMS_041712_NAR_30mM_minus2.18551.18551.2	2	12.55	0	4.01E+05		(R)QAQEYE	(R)Q A|Q/E/Y/E A L L/N I K(V)		154.8	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5817	dirMS_041712_NAR_40mM_minus2.12236.12236.3	3	12.55	0	1.61E+05		(R)LQQELD	(R)L Q/Q E/L D/D L/T/V/D L D H Q\R(Q)		155.02	646.6596	1937.956	0.0079	4.1	4.03	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
5818	dirMS_041712_NAR_50mM_minus2.10685.10685.3	3	12.55	0	2.71E+05		(K)VFEGNR	(K)V/F|E/G N R P T/N S I V F T K(L)		129.15	570.3032	1708.902	-0.0066	-3.9	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
5819	dirMS_041712_NAR_50mM_minus2.16680.16680.3	3	12.55	1	1.61E+05		(K)TVTAMD	(K)T V/T A M D V V/Y A L/K/R(Q)		162.78	489.6051	1466.804	-0.0028	-1.9	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
5820	dirMS_041712_NAR_60mM_minus.11536.11536.3	3	12.55	0	6.83E+04	M186m	(K)NmQNV	(K)N m\Q N V E H\V/P L S/L D/R(A)	m:Oxidized methionine	124.27	556.6111	1651.822	15.9967	1.1	5.32	26717.1	8.65	HUMAN	P20618	Proteasome subunit beta type-1
5821	dirMS_041712_NAR_60mM_minus.13254.13254.3	3	12.55	0	5.71E+04		(R)NLDIER	(R)N/L|D\I/E R P T Y T N L N/R(L)		133.1	573.6304	1718.882	-0.0054	-3.1	6.07	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
5822	dirMS_041712_NAR_20mM_plus.12408.12408.2	2	12.55	0	1.87E+05		(R)GVEICIA	(R)G V E|I/C/I/A T/P G R(L)	C:Carbamidomethylation	158.58	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
5823	dirMS_041712_NAR_20mM_plus.14977.14977.2	2	12.55	0	8.31E+04		(K)VVNIVP	(K)V V|N/I/V P V I A K(A)		174.67	526.3453	1051.687	-0.0041	-3.9	8.72	22387.6	9.64	HUMAN	K7EK18	Septin-9 (Fragment)
5824	dirMS_041712_NAR_20mM_plus.17594.17594.2	2	12.55	0	1.53E+04		(K)ITNLTQ	(K)I T|N L/T Q/Q L/E Q A/S I\V K(K)		193.05	843.4752	1685.943	-0.0001	-0.1	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
5825	dirMS_041712_NAR_20mM_plus.18663.18663.2	2	12.55	0	1.55E+05	M332m	(R)IVSQLLT	(R)I/V|S/Q/L/L/T L/m D G\L/K(Q)	m:Oxidized methionine	199.52	723.9145	1430.829	15.993	-1.3	5.84	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
5826	dirMS_041712_NAR_30mM_plus2.11457.11781.2	2	12.55	0	1.50E+06		(K)LVGYLD	(K)L/V|G/Y/L/D/R(N)		114.23	418.2367	835.467	-0.0011	-1.3	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
5827	dirMS_041712_NAR_30mM_plus2.19668.19848.2	2	12.55	0	2.00E+05		(R)IIPGFM	(R)I/I|P/G F/M/C Q/G G D F T R(H)	C:Carbamidomethylation	157.72	799.8749	1598.745	-0.0029	-1.8	5.84	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
5828	dirMS_041712_NAR_30mM_plus2.21812.21812.2	2	12.55	0	1.28E+05		(K)YLFTLIR	(K)Y/L/F/T L/I/R(A)		170.02	463.2766	925.551	-0.0046	-5	8.75	103914.7	5.19	HUMAN	B4DZ67	Nuclear pore complex protein Nup107
5829	dirMS_041712_NAR_30mM_plus2.21836.21836.2	2	12.55	0	1.55E+05		(K)ANFLQN	(K)A N|F|L/Q/N/M/I E D R(T)		170.25	675.8282	1350.647	0.0021	1.5	4.37	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
5830	dirMS_041712_NAR_50mM_plus2.12041.12041.3	3	12.55	0	1.54E+05		(R)ISLGMP	(R)I S L/G M|P V/G P N A H K(V)		131.02	440.9073	1320.709	-0.0019	-1.5	8.76	98282.7	5.49	HUMAN	E9PPJ0	Splicing factor 3B subunit 2
5831	dirMS_041712_NAR_60mM_plus.12318.12319.3	3	12.55	1	2.56E+04		(R)VFDKEG	(R)V/F|D K E G\N G T|V/M/G A E/I/R(H)		120.43	574.9548	1722.848	0.0019	1.1	4.68	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
5832	dirMS_041712_NAR_30mM_minus2.9948.9948.2	2	12.54	0	1.44E+05		(R)SSTETCY	(R)S S/T/E/T/C Y S/A/I|P K(A)	C:Carbamidomethylation	108.25	672.31	1343.615	-0.002	-1.5	5.72	258215.9	5.48	HUMAN	E7EN95	Filamin-B
5833	dirMS_041712_NAR_40mM_minus2.11306.11306.3	3	12.54	0	7.68E+04		(K)SIEIPRP	(K)S I/E/I/P R P\V D G V/E V/P G C G K(I)	C:Carbamidomethylation	149.55	637.0036	1908.985	0.0115	6	4.68	34243.5	4.88	HUMAN	K7ENG2	Splicing factor U2AF 65 kDa subunit
5834	dirMS_041712_NAR_50mM_minus2.16652.16652.3	3	12.54	1	2.46E+05		(R)SELELTL	(R)S E|L/E/L T L/G K L E Q/V R(S)		163.55	538.9725	1614.906	-0.0032	-2	4.78	533778	5.74	HUMAN	Q15149	Plectin
5835	dirMS_041712_NAR_60mM_minus.5116.5116.3	3	12.54	0	3.25E+06	M434m M4	(R)LESGmC	(R)L/E|S G/m Q N/m S I/H/T K(T)	m:Oxidized methionine	84.12	503.2336	1475.698	31.9881	-1.1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
5836	dirMS_041712_NAR_20mM_plus.11944.11944.2	2	12.54	0	1.12E+05		(R)IYVVDV	(R)I Y|V/V/D/V/G S E/P R(A)		156.08	617.3237	1233.647	-0.0073	-5.9	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
5837	dirMS_041712_NAR_30mM_plus2.9621.9798.2	2	12.54	0	3.44E+06		(R)AVVIVDI	(R)A V|V|I/V/D/D/R(G)		103.6	443.7534	886.499	0.0003	0.3	4.21	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
5838	dirMS_041712_NAR_40mM_plus2.15144.15415.3	3	12.54	0	4.85E+05		(K)FTISDHP	(K)F/T|I/S D H/P Q/P I D/P L L K(N)		156.65	574.3118	1720.927	-0.006	-3.5	5.21	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
5839	dirMS_041712_NAR_40mM_plus2.5577.5577.2	2	12.54	0	4.33E+04		(R)FLEQQN	(R)F/L|E/Q/Q|N K(I)		89.93	453.7354	906.468	-0.0044	-4.9	6	49709.6	5.19	HUMAN	B0YJC4	Vimentin
5840	dirMS_041712_NAR_50mM_plus2.11251.11251.3	3	12.54	1	4.13E+05		(R)MLFKD	(R)M L|F/K D D Y/P/S/S/P P K(C)		127.05	508.9188	1524.74	0.0016	1	5.71	20685.4	9.18	HUMAN	B0QYN7	SUMO-conjugating enzyme UBC9
5841	dirMS_041712_NAR_50mM_plus2.16469.16469.3	3	12.54	0	5.57E+05		(R)QVVQGI	(R)Q V|V/Q|G L L/S E/T Y L E/A H R(I)		154.53	614.9984	1842.971	0.0098	5.3	5.4	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
5842	dirMS_041712_NAR_50mM_plus2.19636.19636.3	3	12.54	1	5.70E+04		(K)LKEAELL	(K)L K E A E L\L|E|P L/M/P/A I R(A)		171.37	574.9989	1722.982	-0.0001	-0.1	4.79	56164.6	6.01	HUMAN	E9PP73	Coatomer subunit beta (Fragment)
5843	dirMS_041712_NAR_50mM_plus2.21805.21805.3	3	12.54	0	3.68E+05		(K)AYNMVI	(K)A/Y/N/M V/D I\I/H S V V D/E R(E)		185.85	587.6346	1760.864	0.0257	14.6	4.54	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
5844	dirMS_041712_NAR_120mM_minus.13296.13296.4	4	12.53	1	8.85E+05		(K)SVHSSV	(K)S V H\S S V|P\L/L/N S K\D/P I/D R(I)		127.12	466.7525	1863.992	-0.0041	-2.2	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
5845	dirMS_041712_NAR_30mM_minus2.10645.10645.2	2	12.53	0	8.37E+05		(K)GSDFDC	(K)G S|D/F/D/C/E L/R(L)	C:Carbamidomethylation	111.43	549.7307	1098.452	0.0021	1.9	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
5846	dirMS_041712_NAR_30mM_minus2.10858.11154.2	2	12.53	0	3.32E+05		(K)MLVSGA	(K)M/L|V|S|G A G D|I/K(L)		113.32	495.7683	990.529	0.0005	0.5	5.59	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
5847	dirMS_041712_NAR_40mM_minus2.9625.9625.2	2	12.53	0	1.24E+06		(R)VAPEEH	(R)V A/P E E H|P V L/L T E A/P L N/P K(A)		139.8	977.5343	1954.064	-0.0031	-1.6	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
5848	dirMS_041712_NAR_60mM_minus.15769.15769.3	3	12.53	1	1.01E+05		(R)ISGLIYE	(R)I/S|G L/I/Y E E T R G V/L K(V)		147.93	526.6326	1577.89	-0.0065	-4.1	6.14	11367.1	11.36	HUMAN	P62805	Histone H4
5849	dirMS_041712_NAR_120mM_plus.10172.10604.2	2	12.53	1	2.25E+06		(R)VKYETEL	(R)V/K|Y|E/T E/L\A M R(Q)		107.58	620.3237	1239.64	-0.0001	0	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5850	dirMS_041712_NAR_120mM_plus.11126.11126.3	3	12.53	0	1.33E+06		(R)GSAVHC	(R)G/S/A V/H Q L/S/E E L R(C)		111.18	442.5657	1325.681	0.0017	1.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
5851	dirMS_041712_NAR_50mM_plus2.6023.6024.3	3	12.53	1	2.93E+05		(K)TGQAPG	(K)T/G/Q|A/P G Y/S Y/T/A A N K N K(G)		95.93	557.6102	1670.813	0.0028	1.7	9.52	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
5852	dirMS_041712_NAR_30mM_minus2.17809.17847.2	2	12.52	0	6.65E+04		(K)IFFAGDT	(K)I/F|F/A/G D T/I/P K(S)		151.17	554.8038	1108.604	-0.0034	-3.1	5.84	258215.9	5.48	HUMAN	E7EN95	Filamin-B
5853	dirMS_041712_NAR_40mM_minus2.12027.12067.3	3	12.52	1	5.22E+03		(R)IINEPTA	(R)I/I\N|E/P T A A/A/I/A Y G L D/K R(E)		153.6	606.0008	1815.996	-0.0085	-4.7	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
5854	dirMS_041712_NAR_60mM_minus.14877.14877.3	3	12.52	0	3.84E+05		(K)WIGLDL	(K)W I/G L/D L/S/N G K/P/R(D)		143.42	452.5849	1355.743	-0.0029	-2.1	8.75	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
5855	dirMS_041712_NAR_60mM_minus.9296.9296.3	3	12.52	0	4.37E+04		(R)IQFKPD	(R)I/Q|F K/P D/D/G/T T P E R(I)		111.73	501.9209	1503.744	0.0043	2.9	4.56	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
5856	dirMS_041712_NAR_120mM_plus.10766.10773.2	2	12.52	1	2.27E+06		(R)LASYLD	(R)L/A|S Y L D|R/V/R(S)		109.83	546.8117	1092.616	0.0001	0.1	8.75	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5857	dirMS_041712_NAR_20mM_plus.7903.7903.2	2	12.52	0	1.26E+05		(K)VEIIAND	(K)V E\I|I|A|N D\Q G N R(T)		124.55	614.8177	1228.628	0.0001	0.1	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
5858	dirMS_041712_NAR_30mM_plus2.13579.13616.2	2	12.52	0	1.37E+06		(K)VLLPEY	(K)V L|L|P E/Y/G G T K(V)		125.05	538.8034	1076.599	0.0009	0.8	5.97	5189.9	4.56	HUMAN	B8ZZ54	10 kDa heat shock protein, mitochondrial
5859	dirMS_041712_NAR_30mM_plus2.15359.15854.2	2	12.52	0	9.53E+05		(R)YPVNSV	(R)Y/P/V/N/S V/N I/L/K(A)		134.13	573.8278	1146.652	-0.0034	-3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
5860	dirMS_041712_NAR_30mM_plus2.22318.22318.2	2	12.52	0	3.79E+05		(R)VGNLGL	(R)V G N\L|G/L A/T/S/F F/N E\R(N)		172.8	762.8926	1524.781	-0.0026	-1.7	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
5861	dirMS_041712_NAR_40mM_plus2.10712.10712.3	3	12.52	1	4.18E+05		(R)DGKLVS	(R)D G K L\V\S\E|S/S/D/V L/P K(-)		128.6	491.9315	1473.78	0.0004	0.3	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
5862	dirMS_041712_NAR_40mM_plus2.11402.11402.3	3	12.52	1	1.39E+04		(R)LLIVSTT	(R)L L|I/V/S T T P Y/S E K D/T K(Q)		133.43	565.6432	1694.921	-0.006	-3.6	6.07	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
5863	dirMS_041712_NAR_50mM_plus2.16573.16636.3	3	12.52	0	1.44E+05		(R)DVQIGD	(R)D V\Q|I|G D/I/V/T V/G E C R P L S K(T)	C:Carbamidomethylation	155.08	662.6825	1986.033	0.0005	0.2	4.56	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
5864	dirMS_041712_NAR_50mM_plus2.9658.9658.3	3	12.52	1	3.85E+05		(K)ALIEME	(K)A L/I/E/M E K Q/Q Q D Q V D/R(N)		118.65	610.9732	1830.901	0.0036	2	4.32	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)
5865	dirMS_041712_NAR_60mM_plus.12959.12959.3	3	12.52	1	1.36E+06		(K)NQVAM	(K)N Q|V|A/M/N/P T N T V/F D A K R(L)		124.48	602.6367	1805.896	-0.0007	-0.4	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
5866	dirMS_041712_NAR_60mM_plus.13126.13249.3	3	12.52	0	8.43E+05	M1m	(-)mVNHF	(-)m V/N H\F/I/A E|F K(R)	m:Oxidized methionine	125.8	417.8778	1235.624	15.9947	-0.2	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
5867	dirMS_041712_NAR_60mM_plus.16722.16722.2	2	12.52	0	7.98E+05		(R)EHALLA	(R)E/H|A|L/L/A/Y\T L G\V/K(Q)		143.97	657.8735	1314.742	-0.0019	-1.4	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
5868	dirMS_041712_NAR_30mM_minus2.11847.12070.3	3	12.51	0	4.86E+05		(K)GISQEQ	(K)G I\S\Q/E\Q|M/Q E/F/R(A)		118.83	451.547	1352.626	0.0001	0.1	4.53	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
5869	dirMS_041712_NAR_30mM_minus2.16595.16595.2	2	12.51	0	2.83E+05		(R)ASLEAAI	(R)A S L E A/A/I/A/D/A E Q R(G)		143.85	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
5870	dirMS_041712_NAR_30mM_minus2.17774.17796.2	2	12.51	0	2.08E+05		(R)TEMDW	(R)T/E|M/D/W V/L/K(H)		151.1	511.2565	1021.502	0.0034	3.4	4.37	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
5871	dirMS_041712_NAR_30mM_minus2.18388.18388.3	3	12.51	0	5.33E+05		(R)QAQEYE	(R)Q A\Q E\Y|E/A/L/L N I K(V)		154.7	473.9196	1419.748	-0.0036	-2.5	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5872	dirMS_041712_NAR_40mM_minus2.11838.11838.3	3	12.51	0	1.02E+04		(K)LVEALC	(K)L V/E/A L/C/A E/H Q I N L/I K(V)	C:Carbamidomethylation	152.93	584.3199	1750.952	-0.0069	-3.9	5.4	14914.1	6.84	HUMAN	P25398	40S ribosomal protein S12
5873	dirMS_041712_NAR_50mM_minus2.8455.8455.3	3	12.51	1	1.45E+05		(K)LTSDDVI	(K)L/T|S/D D V/K E Q I/Y/K(L)		115.95	480.252	1438.742	-0.001	-0.7	4.56	12573.5	10.39	HUMAN	E9PS50	40S ribosomal protein S13 (Fragment)
5874	dirMS_041712_NAR_60mM_minus.14614.14885.3	3	12.51	1	3.80E+05		(K)STFVLDE	(K)S/T|F/V/L/D E F K R(K)		142.47	414.5567	1241.652	0.0031	2.5	5.79	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
5875	dirMS_041712_NAR_60mM_minus.17752.17752.3	3	12.51	1	4.16E+05	M148m	(R)LDLAGR	(R)L/D|L|A/G R D L T D Y L m/K(I)	m:Oxidized methionine	159.32	547.2829	1623.841	15.9931	-1.1	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
5876	dirMS_041712_NAR_120mM_plus.17950.18179.3	3	12.51	1	4.31E+05		(K)YRGFTIP	(K)Y/R G F T\I|P/E/A F R(G)		148.27	452.9069	1356.706	0.0003	0.2	8.75	27264.5	5.09	HUMAN	O00299	Chloride intracellular channel protein 1
5877	dirMS_041712_NAR_20mM_plus.10657.10657.2	2	12.51	0	6.90E+04	M61m	(K)NQVAm	(K)N Q\V|A|m|N/P T N T V/F/D A\K(R)	m:Oxidized methionine	146.22	833.3977	1649.795	15.9929	-1.2	5.84	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
5878	dirMS_041712_NAR_20mM_plus.16669.16669.2	2	12.51	0	6.46E+04		(R)TVELSIP	(R)T V E\L|S/I|P A/D P\A N L D S E A K(I)		186.08	935.4704	1869.944	-0.0105	-5.6	3.91	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
5879	dirMS_041712_NAR_20mM_plus.17823.17823.3	3	12.51	0	1.83E+05		(R)TVQSLEI	(R)T V Q\S L E|I D/L/D S M R(N)		194.83	502.9236	1506.747	0.0094	6.2	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5880	dirMS_041712_NAR_30mM_plus2.12293.12352.2	2	12.51	0	2.85E+05		(K)MMEIM	(K)M/M|E|I|M T/R(E)		117.57	456.2155	911.415	0.009	9.9	5.75	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
5881	dirMS_041712_NAR_30mM_plus2.16182.16182.2	2	12.51	0	1.77E+05		(R)VEVTEFE	(R)V E|V/T E F/E D I/K(S)		137.82	604.8021	1208.604	-0.0076	-6.3	4	30992.3	4.14	HUMAN	B2REB8	Protein SET

5882	dirMS_041712_NAR_30mM_plus2.17922.17922.2	2	12.51	0	6.24E+04		(K)TFEVCDI	(K)T F|E|V/C D\L/P/V R(A)	C:Carbamidomethylation	147.03	618.3057	1235.609	-0.0048	-3.9	4.37	99900.1	5.04	HUMAN	B4DZI8	Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b
5883	dirMS_041712_NAR_30mM_plus2.19492.19492.2	2	12.51	0	1.17E+05		(K)VQIAVA	(K)V Q/I|A\V/A N A Q E\L\L|Q\R(M)		155.75	776.9425	1552.881	-0.0028	-1.8	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
5884	dirMS_041712_NAR_30mM_plus2.21967.22066.2	2	12.51	0	1.54E+05		(R)LVFGFL	(R)L V|F/G/F/L/N G R(A)		171.07	511.7906	1022.578	-0.0043	-4.2	9.75	10585.9	6.9	HUMAN	G3V2H3	Purine nucleoside phosphorylase (Fragment)
5885	dirMS_041712_NAR_30mM_plus2.6050.6050.2	2	12.51	0	1.82E+05		(R)DSEIMQ	(R)D/S|E|I/M Q Q K(Q)		86	489.7318	978.456	0.0003	0.3	4.37	5215.9	10.07	HUMAN	B5MCG1	Small EDRK-rich factor 2
5886	dirMS_041712_NAR_40mM_plus2.14965.15036.3	3	12.51	0	2.29E+05		(R)EVIDLLK	(R)E V|I/D L/L/K/P D Q V/E G I Q K(S)		155.13	608.6749	1824.011	-0.0012	-0.6	4.32	156557.7	5.52	HUMAN	Q86UP2	Kinectin
5887	dirMS_041712_NAR_40mM_plus2.15272.15376.3	3	12.51	0	3.14E+05		(K)GVTIIGP	(K)G V/T|I|I/G/P A T V/G G I K P G C F K(I)	C:Carbamidomethylation	156.28	624.683	1872.041	-0.0067	-3.6	10	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
5888	dirMS_041712_NAR_50mM_plus2.11689.11689.3	3	12.51	1	1.92E+05		(K)TGQPMI	(K)T\G\Q/P/M I N/L/Y T D R E T G K(L)		129.08	608.6361	1823.896	-0.0019	-1	5.73	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
5889	dirMS_041712_NAR_50mM_plus2.13793.13793.3	3	12.51	1	4.77E+05		(R)SILKIDD	(R)S I|L K I D D\V/V/N T R(-)		140.5	458.2605	1372.78	-0.0125	-9.1	5.68	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
5890	dirMS_041712_NAR_50mM_plus2.14714.14714.3	3	12.51	1	9.20E+05		(K)MQSAAI	(K)M/Q/S A A F S I/A\A D V K D|V K(A)		145.55	560.9581	1680.863	-0.0028	-1.7	5.72	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
5891	dirMS_041712_NAR_60mM_plus.13931.14436.3	3	12.51	1	1.02E+06		(R)SGKAPIL	(R)S G K A P I\L|I|A|T/D/V/A\S R(G)		131.57	500.2895	1498.859	-0.0048	-3.2	8.46	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
5892	dirMS_041712_NAR_30mM_minus2.10134.10159.2	2	12.5	0	1.30E+06		(R)TFEGIDF	(R)T F|E|G I/D|P/K(K)		109	453.7335	906.457	0.003	3.3	4.37	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
5893	dirMS_041712_NAR_30mM_minus2.14064.14064.2	2	12.5	0	1.82E+05		(R)VPELFA	(R)V/P/E L/F/A N R(G)		129.85	473.2631	945.515	0.0037	3.9	5.97	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
5894	dirMS_041712_NAR_30mM_minus2.8631.8631.2	2	12.5	0	4.89E+05	M281m	(R)AEAESm	(R)A E|A/E|S m Y Q I/K(Y)	m:Oxidized methionine	101.12	593.2765	1169.551	15.995	0.1	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
5895	dirMS_041712_NAR_40mM_minus2.13129.13203.3	3	12.5	1	2.01E+05	M148m	(R)LDLAGR	(R)L/D|L|A/G R D L T/D/Y L m/K(I)	m:Oxidized methionine	161.12	547.2822	1623.841	15.991	-2.4	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
5896	dirMS_041712_NAR_40mM_minus2.9435.9435.3	3	12.5	1	4.72E+04		(K)AGTEEA	(K)A/G\T E/E A I/V Y/S/D I D L K K(L)		138.08	584.64	1751.906	-0.0007	-0.4	4.32	31006.8	6.85	HUMAN	Q9NQR4	Omega-amidase NIT2
5897	dirMS_041712_NAR_50mM_minus2.15428.15428.3	3	12.5	0	7.78E+04		(R)DLTPEHI	(R)D L/T|P/E\H L/P L L R(N)		155.98	435.2497	1303.737	-0.0023	-1.8	5.32	38779.2	5.93	HUMAN	Q96C86	m7GpppX diphosphatase
5898	dirMS_041712_NAR_20mM_plus.12891.12891.2	2	12.5	0	1.48E+05		(R)LVVPAS	(R)L V|V|P A S Q C G S L I G K(G)	C:Carbamidomethylation	161.62	714.8991	1428.788	0.003	2.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
5899	dirMS_041712_NAR_20mM_plus.14970.14970.2	2	12.5	0	1.45E+05		(K)VLEQLT	(K)V L\E|Q/L/T/G\Q/T|P V/F/S K(A)		174.65	773.9244	1546.848	-0.006	-3.9	5.97	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
5900	dirMS_041712_NAR_20mM_plus.6989.6989.2	2	12.5	0	1.09E+05		(K)AGFAGD	(K)A G F|A/G D/D A/P R(A)		114.77	488.7307	976.448	0.0058	6	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
5901	dirMS_041712_NAR_30mM_plus2.19199.19199.2	2	12.5	0	2.07E+05		(K)YPQLLP	(K)Y/P/Q|L|L|P G I R(G)		153.25	528.814	1056.62	0.0007	0.6	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
5902	dirMS_041712_NAR_30mM_plus2.6411.6412.2	2	12.5	0	1.01E+05		(R)SVSPCS	(R)S V|S|P C/S N V/E S R(L)	C:Carbamidomethylation	87.83	611.2799	1221.553	-0.0003	-0.2	5.72	99885.2	12.36	HUMAN	I3L182	Serine/arginine repetitive matrix protein 2 (Fragment)
5903	dirMS_041712_NAR_40mM_plus2.5886.5886.2	2	12.5	0	6.04E+04		(K)SGYLSSE	(K)S G Y|L|S|S/E/R(L)		92.52	449.7162	898.427	-0.0014	-1.5	5.72	65692.2	5.7	HUMAN	E7EQR4	Ezrin
5904	dirMS_041712_NAR_50mM_plus2.17454.17454.3	3	12.5	0	6.18E+05		(K)VLISSLQ	(K)V/L|I/S/S L/Q D C L H G I E/S K(S)	C:Carbamidomethylation	159.32	600.3189	1798.937	0.0054	3	5.32	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
5905	dirMS_041712_NAR_50mM_plus2.20215.20215.3	3	12.5	0	5.21E+05		(R)QARPTY	(R)Q/A R P T/Y A|T|A|M/L Q S L L K(-)		174.58	597.9962	1791.979	-0.0045	-2.5	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
5906	dirMS_041712_NAR_50mM_plus2.21774.21774.3	3	12.5	0	3.20E+05		(K)AYNMVI	(K)A Y/N M/V D I I/H S/V V D/E R(E)		185.7	587.6346	1760.864	0.0257	14.6	4.54	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
5907	dirMS_041712_NAR_60mM_plus.20388.20388.3	3	12.5	1	4.21E+05		(K)NAAGAL	(K)N/A/A/G A/L D L L/K E/L K(N)		166.93	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
5908	dirMS_041712_NAR_60mM_plus.21703.21703.3	3	12.5	0	8.78E+04		(R)LHFFMP	(R)L H F F M\P G\F|A/P\L/T/S R(G)		181.67	540.9492	1620.835	-0.0025	-1.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
5909	dirMS_041712_NAR_120mM_minus.8936.8936.2	2	12.49	0	5.86E+05		(K)HFVALS	(K)H/F|V|A L/S T/N T T K(V)		103.32	609.8267	1218.648	-0.0016	-1.3	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
5910	dirMS_041712_NAR_30mM_minus2.15471.15471.2	2	12.49	0	3.81E+05		(R)AAPFSLE	(R)A A|P/F/S/L/E Y R(V)		138.3	527.2782	1053.536	0.0128	12.1	6.04	33115.9	5.54	HUMAN	Q15181	Inorganic pyrophosphatase
5911	dirMS_041712_NAR_30mM_minus2.18593.18593.2	2	12.49	0	3.07E+05		(K)YPQLLP	(K)Y/P\Q/L|L/P G I R(G)		155.38	528.816	1056.62	0.0047	4.4	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
5912	dirMS_041712_NAR_40mM_minus2.10943.10943.3	3	12.49	0	1.84E+05		(R)DLSHIGI	(R)D L S H I G\D A\V|V|I/S C A K(D)	C:Carbamidomethylation	147.38	528.9384	1584.805	-0.0044	-2.8	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
5913	dirMS_041712_NAR_40mM_minus2.14523.14523.3	3	12.49	1	1.11E+06	M116m	(R)ELAILLG	(R)E L A|I/L L/G m L/D/P A E K D E K(G)	m:Oxidized methionine	171	634.338	1884.999	16.0008	3.1	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
5914	dirMS_041712_NAR_40mM_minus2.9259.9259.3	3	12.49	0	1.31E+05		(K)VQASLA	(K)V Q|A|S L/A A N T/F/T\I/T G H A E/T K(Q)		137.35	654.0087	1960.013	-0.0019	-1	6.72	11802.2	5.6	HUMAN	D6RDG3	Transcription factor BTF3 (Fragment)
5915	dirMS_041712_NAR_50mM_minus2.14103.14103.3	3	12.49	0	3.40E+05		(K)SPAPPLI	(K)S P A|P/P L/L\H/V A A L G Q K(Q)		148.45	500.2911	1498.874	-0.0153	-10.2	8.49	17549.1	10.39	HUMAN	E5RFJ3	DBIRD complex subunit KIAA1967 (Fragment)
5916	dirMS_041712_NAR_60mM_minus.12287.12287.3	3	12.49	0	2.05E+05		(K)LAQANC	(K)L A/Q/A N/G W/G V/M\V S H R(S)		128.17	509.2631	1525.769	0.0055	3.6	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
5917	dirMS_041712_NAR_20mM_plus.17529.17529.2	2	12.49	0	3.20E+04		(K)LFVTND	(K)L F|V|T|N\D A A T I/L R(E)		192.63	667.3752	1333.747	-0.0043	-3.2	5.84	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
5918	dirMS_041712_NAR_30mM_plus2.18704.18704.2	2	12.49	0	9.94E+04		(R)GLPWSC	(R)G L/P W/S C S A D/E/V/M R(F)	C:Carbamidomethylation	151.4	754.3298	1507.667	-0.0145	-9.6	4.37	49548	5.89	HUMAN	P55795	Heterogeneous nuclear ribonucleoprotein H2
5919	dirMS_041712_NAR_40mM_plus2.16167.16167.3	3	12.49	0	4.11E+04		(K)VLISSLQ	(K)V L|I/S S L Q/D C L H G I E/S K(S)	C:Carbamidomethylation	161.47	600.3172	1798.937	0.0003	0.2	5.32	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
5920	dirMS_041712_NAR_50mM_plus2.22195.22195.3	3	12.49	1	5.40E+05		(R)ELAILLG	(R)E L/A/I/L|L G M L D/P A E K D E K(G)		190.32	629.004	1884.999	-0.0012	-0.7	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
5921	dirMS_041712_NAR_60mM_plus.17614.17614.3	3	12.49	1	4.55E+05		(R)AKELLG	(R)A K E L L/G Q/G/L/L/L/R(S)		148.83	437.6093	1310.815	-0.0021	-1.6	8.79	106155.7	5.45	HUMAN	B5ME19	Eukaryotic translation initiation factor 3 subunit C
5922	dirMS_041712_NAR_120mM_minus.7931.7931.2	2	12.48	1	6.37E+04		(K)VAAYDK	(K)V/A/A|Y/D K L E K(T)		97.5	518.7878	1036.567	0.001	1	6.04	227783.5	5.5	HUMAN	P35579	Myosin-9
5923	dirMS_041712_NAR_30mM_minus2.12631.12631.2	2	12.48	0	2.85E+05		(R)NLGLYVI	(R)N/L/G L/Y V/K(T)		122.08	403.7423	806.477	0.0003	0.3	8.59	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
5924	dirMS_041712_NAR_50mM_minus2.9738.9738.3	3	12.48	1	9.58E+04		(K)NVDILKI	(K)N V|D/I L/K/D P E/T V K(Q)		123.92	457.5912	1370.753	0.0065	4.7	4.56	124524.8	5.71	HUMAN	O14980	Exportin-1
5925	dirMS_041712_NAR_60mM_minus.15948.15948.3	3	12.48	0	1.65E+04		(K)LFCIPVH	(K)L F/C I/P V/H/G I R(S)	C:Carbamidomethylation	148.82	404.5628	1211.672	0.0021	1.7	9.75	29040.9	5.88	HUMAN	H0YBL1	Inositol monophosphatase 1 (Fragment)
5926	dirMS_041712_NAR_60mM_minus.18283.18283.3	3	12.48	1	1.37E+05		(R)SELELTL	(R)S E|L/E/L T L/G K L E Q V R(S)		163.05	538.9724	1614.906	-0.0035	-2.1	4.78	533778	5.74	HUMAN	Q15149	Plectin
5927	dirMS_041712_NAR_20mM_plus.15597.15597.3	3	12.48	0	8.77E+03		(R)SSFYVN	(R)S/S F Y V N G\L/T/L/G G Q K(C)		179.37	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
5928	dirMS_041712_NAR_20mM_plus.8959.9044.2	2	12.48	0	4.41E+05	M161m	(K)LLIEmEC	(K)L/L|I/E/m/E/Q R(L)	m:Oxidized methionine	132.8	524.278	1031.555	15.9933	-1.5	4.53	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
5929	dirMS_041712_NAR_30mM_plus2.17063.17063.2	2	12.48	0	2.27E+05		(K)ACGNFG	(K)A C|G/N F/G|I P/C E L R(V)	C:Carbamidomethylation	142.65	697.3237	1393.635	0.005	3.6	6.05	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
5930	dirMS_041712_NAR_30mM_plus2.19980.20174.2	2	12.48	0	4.61E+06		(R)YLTVAA	(R)Y L|T/V/A/A\V F/R(G)		160.38	520.2996	1039.593	-0.0016	-1.5	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
5931	dirMS_041712_NAR_40mM_plus2.15291.15291.3	3	12.48	0	3.09E+05		(K)GVTIIGP	(K)G V T I|I/G/P A T V G G I K P G C F K(I)	C:Carbamidomethylation	156.3	624.683	1872.041	-0.0067	-3.6	10	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
5932	dirMS_041712_NAR_50mM_plus2.14931.14931.3	3	12.48	0	5.02E+05		(K)TTISVAH	(K)T T|I/S V A/H L/L A A/R(Q)		146.45	418.2499	1252.737	-0.002	-1.6	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
5933	dirMS_041712_NAR_50mM_plus2.20457.20457.3	3	12.48	1	1.04E+04		(K)SSVLESL	(K)S S/V|L/E S/L/V G R D L L P|R(G)		175.6	547.6436	1640.933	-0.0167	-10.2	5.79	19884.2	4.87	HUMAN	B4DDQ3	Dynamin-1-like protein
5934	dirMS_041712_NAR_60mM_plus.17918.17979.3	3	12.48	1	2.30E+05		(R)YRVPDV	(R)Y R V P D\V\L\V\A|D/P/P I A R(L)		150.93	560.9839	1680.943	-0.006	-3.6	5.96	96499.9	5.43	HUMAN	F5H6X6	Neutral alpha-glucosidase AB
5935	dirMS_041712_NAR_30mM_minus2.20152.20245.2	2	12.47	0	6.55E+05		(K)IGFPWSI	(K)I/G|F|P/W/S E/I R(N)		171.88	552.7932	1104.584	-0.0045	-4.1	6	71218.8	6.3	HUMAN	A7YIJ8	Radixin
5936	dirMS_041712_NAR_30mM_minus2.9700.9898.2	2	12.47	0	4.05E+05		(R)LTPEEIEI	(R)L/T|P/E/E/I E/R(M)		108.18	493.7642	986.515	0.0058	5.9	4.25	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
5937	dirMS_041712_NAR_60mM_minus.14909.14909.3	3	12.47	1	2.10E+05		(K)IDSRLEQ	(K)I/D/S R L E Q\Y T/S/A/I E G T K(S)		142.88	604.3095	1810.918	-0.0042	-2.3	4.68	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
5938	dirMS_041712_NAR_60mM_minus.16479.16479.3	3	12.47	1	1.28E+05		(K)WVAIQS	(K)W V/A I Q/S V/S A W/P E K R(G)		151.87	552.9674	1656.886	0.002	1.2	8.75	6412.4	9.52	HUMAN	J3KSS4	Cytosolic non-specific dipeptidase (Fragment)
5939	dirMS_041712_NAR_120mM_plus.12620.12620.3	3	12.47	1	8.32E+05		(K)VKLEAEI	(K)V K L E\A E|I/A/T Y/R(R)		119.97	431.5774	1292.721	-0.0032	-2.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5940	dirMS_041712_NAR_20mM_plus.10412.10412.2	2	12.47	0	7.55E+04		(R)IEDVTPI	(R)I E D\V T|P I|P S D/S T R(R)		144.53	715.3607	1429.717	-0.0028	-2	4.03	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
5941	dirMS_041712_NAR_20mM_plus.14670.14670.2	2	12.47	0	1.37E+05		(K)LVILANN	(K)L V|I\L/A\N/N C/P A L R(K)	C:Carbamidomethylation	172.6	677.3851	1353.767	-0.0042	-3.1	9.75	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
5942	dirMS_041712_NAR_20mM_plus.18983.18983.2	2	12.47	0	4.98E+04		(R)NLTALGI	(R)N L T A/L/G|L N L V/A|S\G G T A K(A)		201.53	800.4534	1599.906	-0.0069	-4.3	8.75	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
5943	dirMS_041712_NAR_30mM_plus2.8947.8947.2	2	12.47	0	7.09E+05		(R)GMGPG	(R)G M|G/P/G T/P A G Y G/R(G)		100.33	560.7657	1120.52	0.0037	3.3	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
5944	dirMS_041712_NAR_50mM_plus2.10729.10729.3	3	12.47	0	4.20E+05		(K)TSEVDL	(K)T/S|E/V/D/L A K/P L V K(F)		123.78	433.922	1299.752	-0.0004	-0.3	5.73	17178.3	5.63	HUMAN	C9IZF9	Programmed cell death 6-interacting protein (Fragment)
5945	dirMS_041712_NAR_120mM_minus.10642.10642.3	3	12.46	1	2.46E+05		(R)YLAEFA	(R)Y/L/A E F/A T/G N D R K(E)		111.73	462.2338	1384.686	0.0013	0.9	6.07	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
5946	dirMS_041712_NAR_120mM_minus.14582.14666.4	4	12.46	1	2.55E+06		(K)LDKSQI	(K)L D K S Q I H D\I\V\L|V/G/G/S/T R(I)		133.8	460.2577	1838.013	-0.0041	-2.2	6.75	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
5947	dirMS_041712_NAR_120mM_minus.7471.7471.4	4	12.46	0	2.90E+05		(R)IHEGCEI	(R)I H\E\G C/E E/P/A T/H N\A L A/K(I)	C:Carbamidomethylation	95	444.9637	1776.833	-0.0004	-0.2	5.32	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
5948	dirMS_041712_NAR_30mM_minus2.10347.10490.2	2	12.46	0	7.58E+05		(R)IIALDGD	(R)I/I|A|L/D/G D/T/K(N)		111.05	473.2631	945.525	-0.0062	-6.6	4.21	63448.4	7.29	HUMAN	B4E022	Transketolase
5949	dirMS_041712_NAR_30mM_minus2.8370.8370.2	2	12.46	0	4.65E+05		(K)SFQQSSI	(K)S\F/Q/Q/S/S L S R(D)		100.35	520.2591	1039.517	-0.0058	-5.6	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
5950	dirMS_041712_NAR_50mM_minus2.6925.6925.3	3	12.46	0	3.00E+04	M315m	(R)GICEDES	(R)G I|C/E D\E S S H G V I/m E K(F)	C:Carbamidomethylation m:Oxid	105.93	569.5836	1690.741	15.9951	0.1	4.4	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
5951	dirMS_041712_NAR_60mM_minus.16034.16034.3	3	12.46	1	2.88E+05		(K)ELKIDIIP	(K)E L/K I D I\I/P/N/P Q/E R(T)		149	522.2935	1564.869	-0.0034	-2.2	4.68	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
5952	dirMS_041712_NAR_60mM_minus.18462.18462.3	3	12.46	1	1.29E+05		(R)RFDEILE	(R)R F D E\I\L\E|A/S/D/G I M/V A/R(G)		164.42	607.9739	1821.916	-0.0092	-5.1	4.32	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
5953	dirMS_041712_NAR_60mM_minus.18585.18585.3	3	12.46	1	3.27E+04		(R)VYEFLD	(R)V/Y/E\F/L D K L D/V V/R(S)		165.28	499.2763	1495.815	-0.0012	-0.8	4.56	41296.9	9.52	HUMAN	B4DT72	26S proteasome non-ATPase regulatory subunit 3
5954	dirMS_041712_NAR_20mM_plus.11037.11037.2	2	12.46	0	1.17E+05		(K)EITALAP	(K)E I/T/A L/A P S/T/M K(I)		148.15	581.3129	1161.618	0.0001	0.1	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
5955	dirMS_041712_NAR_30mM_plus2.14294.14470.2	2	12.46	0	2.70E+05		(K)IVVLLQR	(K)I/V|V|L\L/Q/R(L)		128.32	420.7864	840.567	-0.001	-1.2	9.75	28772.3	6.28	HUMAN	A6NJG9	Proteasome activator complex subunit 1
5956	dirMS_041712_NAR_30mM_plus2.20355.20767.3	3	12.46	0	1.23E+06		(R)TVQSLEI	(R)T V\Q\S L E/I/D|L/D/S M/R(N)		162.2	502.9201	1506.747	-0.0011	-0.7	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5957	dirMS_041712_NAR_50mM_plus2.12383.12406.3	3	12.46	1	7.86E+05		(K)IEVEKPF	(K)I/E|V/E K/P F A I/A/K E(-)		133.12	458.5944	1373.767	0.0012	0.8	5.01	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
5958	dirMS_041712_NAR_50mM_plus2.19824.19824.3	3	12.46	0	3.20E+05		(K)ILFIFIDSI	(K)I L/F/I|F I D S D H/T/D N Q R(I)		172.75	611.9758	1833.913	-0.0001	-0.1	4.41	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
5959	dirMS_041712_NAR_60mM_plus.11516.11518.3	3	12.46	1	4.52E+05		(K)TCVFEKI	(K)T/C|V|F/E/K E N D|P/S V M R(S)	C:Carbamidomethylation	117.33	571.2635	1711.778	-0.0019	-1.1	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
5960	dirMS_041712_NAR_60mM_plus.12056.12056.2	2	12.46	1	7.93E+05		(K)MKEIAE	(K)M/K|E|I/A/E A/Y L/G K(T)		120.2	626.8335	1252.661	-0.0009	-0.7	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
5961	dirMS_041712_NAR_20mM_minus.12064.12384.3	3	12.45	0	2.99E+06	M313m	(R)TVQSLEI	(R)T V\Q S L\E\I|D|L/D/S m R(N)	m:Oxidized methionine	170.78	508.2517	1506.747	15.9937	-0.8	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
5962	dirMS_041712_NAR_30mM_minus2.8169.8169.2	2	12.45	0	2.35E+06		(R)GTLDPV	(R)G T|L/D|P V E K(A)		99.83	429.7348	858.457	0.0056	6.5	4.37	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
5963	dirMS_041712_NAR_40mM_minus2.14233.14233.3	3	12.45	0	3.15E+04		(K)GVTIAS	(K)G V T|I/A/S|G\G V L/P N I H P E L L A K(K)		168.03	662.715	1986.138	-0.0078	-3.9	6.75	17631.5	10.76	HUMAN	D6RCF2	Histone H2A
5964	dirMS_041712_NAR_50mM_minus2.14287.14455.3	3	12.45	0	4.31E+05		(R)QIFHPE	(R)Q I F H/P E\Q L/I/T/G K(E)		149.72	470.9286	1410.774	-0.0027	-1.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
5965	dirMS_041712_NAR_50mM_minus2.9601.9601.3	3	12.45	0	1.82E+05		(R)AIGSASE	(R)A/I|G S A/S E G A Q S/S L Q E V Y H K(S)		122.55	654.6559	1961.956	-0.0032	-1.6	5.4	20148.5	4.65	HUMAN	B4E2V4	Proteasome (Prosome, macropain) subunit, alpha type, 5, isoform CRA_c
5966	dirMS_041712_NAR_60mM_minus.11848.11848.3	3	12.45	0	3.46E+05	M42m	(K)GVGISVI	(K)G V|G I/S V/L/E m S H R(S)	m:Oxidized methionine	126.42	434.2267	1284.673	15.9927	-1.7	6.75	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
5967	dirMS_041712_NAR_60mM_minus.9495.9495.3	3	12.45	0	3.19E+05		(R)QLSQAG	(R)Q L/S Q/A/G/S F S D G T/H/G G L R(Y)		113.52	573.2781	1717.825	-0.0055	-3.2	6.74	266161	5.68	HUMAN	E9PPU0	Epiplakin
5968	dirMS_041712_NAR_120mM_plus.12677.12677.4	4	12.45	2	8.69E+05		(K)KGTVEG	(K)K G T V E G\F|E/P A D N K C L L/R(A)	C:Carbamidomethylation	118.95	484.2468	1933.98	-0.0147	-7.6	6.18	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
5969	dirMS_041712_NAR_120mM_plus.17057.17057.4	4	12.45	2	1.52E+06		(R)GFCFITF	(R)G F/C F/I/T F K E/E E/P V K K(I)	C:Carbamidomethylation	142.78	465.4906	1858.941	-0.0002	-0.1	6.23	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
5970	dirMS_041712_NAR_20mM_plus.10617.10617.2	2	12.45	0	3.55E+04		(R)LLVVTDI	(R)L L\V/V|T/D/P R(A)		145.98	456.7796	912.551	0.0006	0.7	5.84	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
5971	dirMS_041712_NAR_20mM_plus.12804.12804.2	2	12.45	0	3.06E+05	M316m	(R)ISEQFTA	(R)I/S/E Q/F/T/A m/F\R(R)	m:Oxidized methionine	161.37	623.3012	1229.598	15.9968	1.5	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
5972	dirMS_041712_NAR_20mM_plus.14074.14074.2	2	12.45	0	2.41E+05		(R)AALQELI	(R)A A/L/Q/E L L/S K(G)		168.72	486.789	972.572	-0.0017	-1.7	6.05	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
5973	dirMS_041712_NAR_20mM_plus.16398.16398.2	2	12.45	0	3.49E+05		(K)LGGSAV	(K)L G\G S/A/V|I S L E/G K|P L(-)		185.32	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
5974	dirMS_041712_NAR_20mM_plus.17504.17504.3	3	12.45	0	1.19E+05		(R)TTVPQLI	(R)T T V P Q|L|L/A/S V/Q R(W)		191.87	438.2581	1312.758	0.0014	1.1	9.41	266161	5.68	HUMAN	E9PPU0	Epiplakin
5975	dirMS_041712_NAR_20mM_plus.18810.18810.2	2	12.45	0	1.58E+05		(R)IITLTGP	(R)I/I/T|L/T/G P T N A I F K(A)		200.47	694.9091	1388.815	-0.0039	-2.8	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
5976	dirMS_041712_NAR_30mM_plus2.19617.19617.2	2	12.45	0	6.40E+05		(K)GFGGIG	(K)G F/G G\I|G G I\L R(Y)		155.58	473.7749	946.547	-0.0044	-4.6	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
5977	dirMS_041712_NAR_50mM_plus2.14020.14020.3	3	12.45	1	1.18E+06		(K)ALQQGL	(K)A/L|Q/Q G L V/G L E L K E K(L)		142.07	509.3022	1525.895	-0.0028	-1.8	6.18	266161	5.68	HUMAN	E9PPU0	Epiplakin
5978	dirMS_041712_NAR_30mM_minus2.11001.11133.2	2	12.44	0	3.32E+05		(K)MLVSGA	(K)M/L|V/S/G/A/G D I K(L)		113.32	495.7683	990.529	0.0005	0.5	5.59	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
5979	dirMS_041712_NAR_30mM_minus2.15633.15633.2	2	12.44	0	3.51E+05		(K)LLYNNV	(K)L/L|Y/N/N V|S N F G\R(L)		137.97	648.8355	1296.67	-0.0058	-4.5	8.75	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
5980	dirMS_041712_NAR_30mM_minus2.19854.20002.2	2	12.44	0	1.54E+06		(R)LFFLQV	(R)L/F/F|L/Q/V K(E)		167.3	447.7757	894.545	-0.0006	-0.7	8.75	71218.8	6.3	HUMAN	A7YIJ8	Radixin
5981	dirMS_041712_NAR_30mM_minus2.8484.8561.2	2	12.44	0	5.61E+05		(K)IDDVVN	(K)I/D|D|V/V/N T/R(-)		101.05	466.2472	931.484	0.0028	3	4.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
5982	dirMS_041712_NAR_50mM_minus2.14313.14313.3	3	12.44	1	2.08E+05		(R)DLAALG	(R)D L|A/A/L/G D K V N S/L/G E/T A E R(L)		149.15	620.3204	1858.95	-0.0038	-2.1	4.32	285798.6	5.23	HUMAN	A6NG51	Spectrin alpha chain, non-erythrocytic 1
5983	dirMS_041712_NAR_50mM_minus2.7168.7211.3	3	12.44	1	1.25E+05		(K)VDDSSEI	(K)V/D|D/S/S E D K T E/F T V/K(N)		107.78	533.9173	1599.738	-0.0011	-0.7	4.11	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
5984	dirMS_041712_NAR_60mM_minus.10627.10627.3	3	12.44	0	1.44E+05	M271m	(R)DLNYCF	(R)D L|N/Y/C F/S G m S D H R(Y)	C:Carbamidomethylation m:Oxid	119.2	539.8863	1601.647	15.9972	1.4	5.21	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
5985	dirMS_041712_NAR_120mM_plus.18110.18110.3	3	12.44	1	4.00E+05		(K)YRGFTIP	(K)Y R G F T\I|P/E/A/F R(G)		148.27	452.9069	1356.706	0.0003	0.2	8.75	27264.5	5.09	HUMAN	O00299	Chloride intracellular channel protein 1
5986	dirMS_041712_NAR_120mM_plus.8942.8942.3	3	12.44	0	2.13E+06		(K)HTGPNS	(K)H T\G P N\S P/D|T|A/N/D/G F V R(L)		99.53	562.26	1684.767	-0.0019	-1.2	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
5987	dirMS_041712_NAR_20mM_plus.13745.13745.2	2	12.44	0	1.96E+05		(K)APILIATI	(K)A/P I/L|I|A/T D/V A S R(G)		166.73	613.8559	1226.71	-0.0058	-4.7	5.88	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
5988	dirMS_041712_NAR_20mM_plus.17061.17061.2	2	12.44	0	4.44E+04		(R)AIGIGAY	(R)A I/G\I|G/A Y L\V R(L)		188.57	516.8123	1032.62	-0.0027	-2.6	8.79	9731	5.19	HUMAN	E9PEW7	Acetyl-CoA carboxylase 2
5989	dirMS_041712_NAR_20mM_plus.18809.18809.2	2	12.44	0	1.04E+05		(K)LTVYTTL	(K)L/T/V/Y/T T L/I|D V\T K(G)		200.83	683.8948	1366.783	-0.0005	-0.4	5.83	42194.9	8.75	HUMAN	E7EMM4	Acid ceramidase
5990	dirMS_041712_NAR_30mM_plus2.21439.21439.2	2	12.44	0	3.26E+05		(R)NSYLEVI	(R)N/S/Y|L/E/V/L/L K(L)		167.7	539.8092	1078.614	-0.0032	-2.9	6	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6

5991	dirMS_041712_NAR_30mM_plus2.6745.6745.2	2	12.44	0	2.64E+05		(R)FQTMEE	(R)F/Q|T/M E|E K(K)		89.95	456.7106	912.413	0.0008	0.9	4.53	40551.6	10.15	HUMAN	G5E9G0	60S ribosomal protein L3
5992	dirMS_041712_NAR_40mM_plus2.11020.11020.3	3	12.44	0	6.82E+04		(R)LLELGPK	(R)L/L|E/L/G P K/P E V A/Q Q T R(K)		131.02	560.318	1678.949	-0.0092	-5.5	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
5993	dirMS_041712_NAR_40mM_plus2.8505.8505.2	2	12.44	0	8.22E+04		(K)DVNQQI	(K)D V/N/Q/Q E/F/V/R(A)		110.82	567.78	1134.554	-0.0011	-1	4.37	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
5994	dirMS_041712_NAR_40mM_plus2.9001.9049.2	2	12.44	0	1.05E+05		(K)FYEQFSK	(K)F/Y|E/Q|F/S/K(N)		115.03	474.7301	948.446	0.0068	7.1	6	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
5995	dirMS_041712_NAR_50mM_plus2.10987.10987.3	3	12.44	0	4.42E+05		(R)EALLSSA	(R)E A|L/L/S/S A V D H G S D/E V/K(F)		124.83	552.9403	1656.807	-0.0012	-0.7	4.31	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
5996	dirMS_041712_NAR_50mM_plus2.18543.18779.3	3	12.44	0	4.45E+05		(R)DVCTELI	(R)D V|C|T/E L/L/P L I/K/P Q G R(V)	C:Carbamidomethylation	166.58	580.3229	1738.952	0.0021	1.2	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
5997	dirMS_041712_NAR_120mM_minus.4994.4994.3	3	12.43	1	5.82E+05		(R)AAEEED	(R)A A|E E E/D\E A/D/P K R(Q)		79.33	453.8716	1359.602	-0.002	-1.5	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
5998	dirMS_041712_NAR_120mM_minus.9137.9137.3	3	12.43	0	7.27E+05		(K)HTGPNS	(K)H T G P N\S P D T\A/N/D/G F V/R(L)		103.4	562.2599	1684.767	-0.0022	-1.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
5999	dirMS_041712_NAR_20mM_minus.9290.9290.3	3	12.43	0	3.43E+05		(R)AQIFAN	(R)A Q\I F A N T/V/D/N A R(I)		142.32	440.5612	1319.67	-0.0012	-0.9	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
6000	dirMS_041712_NAR_30mM_minus2.13958.13958.2	2	12.43	0	2.88E+05	M313m	(K)NSLESYA	(K)N S|L/E/S/Y/A F/N m K(A)	m:Oxidized methionine	128.98	660.3011	1303.599	15.9962	1	6	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
6001	dirMS_041712_NAR_30mM_minus2.14648.14751.2	2	12.43	0	3.50E+05		(R)LAVEAL\	(R)L/A|V|E/A L V/R(T)		134.08	435.7729	870.541	-0.0022	-2.5	6	65558.6	9.87	HUMAN	G3V1S7	Hyaluronan synthase 1
6002	dirMS_041712_NAR_30mM_minus2.18900.18900.2	2	12.43	0	1.91E+05		(K)CFSVLGF	(K)C/F/S V/L/G F/C K(S)	C:Carbamidomethylation	157.42	559.2673	1117.517	0.0104	9.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
6003	dirMS_041712_NAR_50mM_minus2.9683.9683.3	3	12.43	1	1.97E+05		(R)ALEEAM	(R)A L|E/E/A/M E Q K A E L E/R(L)		122.57	549.6072	1646.805	0.0016	1	4.33	227783.5	5.5	HUMAN	P35579	Myosin-9
6004	dirMS_041712_NAR_20mM_plus.12532.12532.3	3	12.43	0	3.48E+05		(K)IISNASC	(K)I I\S N\A\S/C T T/N C L/A/P/L A/K(V)	C:Carbamidomethylation	159.53	611.9768	1833.92	-0.0039	-2.1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
6005	dirMS_041712_NAR_30mM_plus2.12072.12178.3	3	12.43	0	2.56E+06		(R)AQIFAN	(R)A Q\I\F\A N T/V/D/N A/R(I)		116.83	440.5613	1319.67	-0.0009	-0.7	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
6006	dirMS_041712_NAR_30mM_plus2.15022.15174.2	2	12.43	0	8.46E+05		(R)AGLQFP	(R)A G/L|Q|F|P V/G/R(I)		132.1	472.7711	944.531	0.0037	3.9	9.79	6891.8	11.07	HUMAN	A8MQC5	Histone H2A
6007	dirMS_041712_NAR_30mM_plus2.17523.17523.2	2	12.43	0	9.20E+04		(K)VFQFLN	(K)V/F|Q/F L\N A K(C)		144.02	483.7736	966.541	-0.0008	-0.8	8.72	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
6008	dirMS_041712_NAR_30mM_plus2.5470.5470.2	2	12.43	0	3.75E+04		(K)SAAQAA	(K)S A A/Q|A/A\A/Q T N S N A A|G K(Q)		82.75	730.8568	1460.709	-0.0025	-1.7	8.47	45021.6	8.74	HUMAN	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein
6009	dirMS_041712_NAR_40mM_plus2.12189.12189.3	3	12.43	0	2.41E+05		(K)VQASLA	(K)V Q|A|S L/A A N T F T I T G H A E T/K(Q)		137.67	654.0104	1960.013	0.0032	1.6	6.72	11802.2	5.6	HUMAN	D6RDG3	Transcription factor BTF3 (Fragment)
6010	dirMS_041712_NAR_50mM_plus2.20827.20827.3	3	12.43	1	7.61E+04		(K)TSAQVV	(K)T S\A/Q/V/V L D G L V D K I G D/V K(C)		178.37	619.6814	1857.033	-0.0031	-1.7	4.43	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
6011	dirMS_041712_NAR_60mM_plus.15045.15045.3	3	12.43	1	2.99E+04		(R)ELAFQIS	(R)E L|A/F/Q/I/S/K E Y E/R(F)		135.27	504.9258	1512.769	-0.0064	-4.3	4.79	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
6012	dirMS_041712_NAR_120mM_minus.4810.4810.3	3	12.42	1	5.38E+05		(K)AGADEE	(K)A/G|A/D/E E R A E T\A/R(L)		77.15	425.8687	1275.592	-0.0008	-0.7	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
6013	dirMS_041712_NAR_30mM_minus2.16070.16070.2	2	12.42	0	1.41E+05		(K)GCSFLPD	(K)G C/S\F L/P D|P Y Q K(Q)	C:Carbamidomethylation	141.02	656.3051	1311.604	-0.0009	-0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
6014	dirMS_041712_NAR_30mM_minus2.16923.16923.2	2	12.42	0	1.37E+05		(R)IMNTFS\	(R)I/M/N/T F/S V V/P/S P K(V)		145.95	660.3534	1319.703	-0.0033	-2.5	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
6015	dirMS_041712_NAR_40mM_minus2.15016.15016.3	3	12.42	1	5.46E+05		(R)GDLGIEI	(R)G D/L G|I|E I/P A E K V F L A Q K(M)		173.02	610.0109	1828.022	-0.0033	-1.8	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
6016	dirMS_041712_NAR_50mM_minus2.12650.12650.3	3	12.42	1	3.93E+05		(K)NTVELL\	(K)N/T|V|E L/L/V/E D K G N Q V Y R(C)		140.42	626.3309	1876.976	0.0018	1	4.68	258215.9	5.48	HUMAN	E7EN95	Filamin-B
6017	dirMS_041712_NAR_50mM_minus2.7231.7231.3	3	12.42	0	1.54E+05	M378m M:	(K)mIVDPV	(K)m I/V D/P V E/P H G\E/m K(F)	m:Oxidized methionine	107.92	505.2416	1481.713	31.9975	5.1	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
6018	dirMS_041712_NAR_60mM_minus.16854.16854.3	3	12.42	0	2.46E+05	S78s M80n	(R)YFSLsLm	(R)Y F S L/s|L/m/S G A\L/A V N Q\K(I)	s:N-acetylglucosamine (S) m:	153.75	649.9986	1728.899	219.0823	4.1	8.59	102603.5	4.86	HUMAN	Q9Y5F6	Protocadherin gamma-C5
6019	dirMS_041712_NAR_120mM_plus.10507.10507.3	3	12.42	1	3.83E+05		(K)KGENYV	(K)K G E\N Y/V/Y|I/N/E A T/R(H)		108.4	519.5943	1556.77	-0.002	-1.3	6.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
6020	dirMS_041712_NAR_120mM_plus.23982.23982.4	4	12.42	2	2.56E+05		(R)RGVMLA	(R)R G\V\M\L\A\V/D A/V/I/A E L K K(Q)		179.9	429.0075	1713.009	-0.001	-0.6	8.59	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
6021	dirMS_041712_NAR_20mM_plus.12127.12127.2	2	12.42	0	2.63E+05		(K)YGEPGE'	(K)Y/G|E|P|G E V/F I/N/K(G)		156.1	626.8223	1252.621	0.0165	13.2	4.53	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
6022	dirMS_041712_NAR_20mM_plus.12305.12305.2	2	12.42	0	1.37E+05		(R)GVEICIA	(R)G V\E\I|C/I A/T/P G R(L)	C:Carbamidomethylation	158.27	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
6023	dirMS_041712_NAR_20mM_plus.13476.13476.2	2	12.42	0	1.49E+05	M273m	(K)mISDAIF	(K)m I/S|D A I/P E L K(A)	m:Oxidized methionine	165.25	566.7967	1116.597	15.9892	-5	4.37	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
6024	dirMS_041712_NAR_20mM_plus.14521.14521.3	3	12.42	0	1.44E+05		(R)LQEAGIL	(R)L Q E/A G\I\L/S\A/E/E L Q R(L)		171.72	519.6131	1556.828	-0.0031	-2	4.25	533778	5.74	HUMAN	Q15149	Plectin
6025	dirMS_041712_NAR_20mM_plus.18106.18140.2	2	12.42	0	1.01E+05		(R)AILVDLE	(R)A I L|V/D|L|E|P\G T M D S V/R(S)		196.62	808.419	1615.836	-0.0053	-3.3	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
6026	dirMS_041712_NAR_30mM_plus2.19847.19967.2	2	12.42	1	4.48E+05		(K)EKLEATI	(K)E K L\E A T\I\N/E|L|V(-)		158.27	629.8458	1258.689	-0.0046	-3.6	4.25	9680	5.77	HUMAN	B1ALW1	Thioredoxin
6027	dirMS_041712_NAR_40mM_plus2.16105.16302.3	3	12.42	0	6.30E+05		(R)FGVPVIA	(R)F G|V|P V/I/A D/G G I Q N V/G H I/A K(A)		162.53	631.3436	1892.039	-0.0226	-12	6.74	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
6028	dirMS_041712_NAR_50mM_plus2.15809.15887.3	3	12.42	1	8.21E+05		(R)VRLGDV	(R)V R L G D V\I\S\I\Q|P C/P D V\K(Y)	C:Carbamidomethylation	151.38	599.3276	1795.974	-0.0052	-2.9	5.93	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
6029	dirMS_041712_NAR_50mM_plus2.7184.7184.3	3	12.42	0	1.68E+05		(R)SGSSQEI	(R)S G S|S Q/E L/D V/K/P S/A/S P Q E R(S)		103.85	634.6443	1901.92	-0.0016	-0.8	4.68	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
6030	dirMS_041712_NAR_60mM_plus.11933.11933.3	3	12.42	1	2.18E+05		(K)VYVGNL	(K)V/Y|V/G N L G T G A/G K G E L E R(A)		118.25	573.9701	1719.902	-0.0067	-3.9	6.11	27155.8	11.98	HUMAN	C9JAB2	Serine/arginine-rich-splicing factor 7
6031	dirMS_041712_NAR_60mM_plus.20434.20434.3	3	12.42	0	3.20E+04		(R)IHFPLAT	(R)I H|F P L A T Y/A|P/V I/S A E K(A)		167.23	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
6032	dirMS_041712_NAR_60mM_plus.5756.5756.3	3	12.42	0	1.87E+05		(R)STFETEH	(R)S/T|F E/T/E/H/A G Q R(D)		88.4	421.5294	1262.576	-0.0024	-1.9	5.38	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
6033	dirMS_041712_NAR_120mM_minus.10799.10821.3	3	12.41	1	5.64E+05		(K)LRETAEA	(K)L R E T A E\A/D|V|A/S L/N R(R)		113.7	515.6051	1544.803	-0.002	-1.3	4.68	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
6034	dirMS_041712_NAR_40mM_minus2.11255.11255.3	3	12.41	1	1.21E+05		(K)VIDPATA	(K)V I|D/P A T A/T S V D L R D I K(I)		149.38	571.9828	1713.938	-0.0043	-2.5	4.43	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
6035	dirMS_041712_NAR_50mM_minus2.12130.12130.3	3	12.41	0	9.09E+03		(K)AASAGV	(K)A A/S/A G/V/P Y H G E/V P V S L/A R(A)		135.98	594.315	1780.934	-0.0036	-2	6.79	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
6036	dirMS_041712_NAR_60mM_minus.18718.18718.3	3	12.41	0	2.88E+05		(K)TFLVWV	(K)T F|L|V/W/V/N E E D/H L R(V)		165.82	553.2818	1657.833	-0.0024	-1.5	4.65	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
6037	dirMS_041712_NAR_120mM_plus.20344.20629.4	4	12.41	2	6.56E+05		(K)LTVEDLE	(K)L T\V/E/D/L E/K E R D F Y/F/G K(L)		160.85	498.0043	1988.996	-0.001	-0.5	4.51	30169.7	5.02	HUMAN	Q15691	Microtubule-associated protein RP/EB family member 1
6038	dirMS_041712_NAR_20mM_plus.14790.14790.2	2	12.41	0	1.12E+05		(K)LLGELLQ	(K)L L|G|E L/L Q D N A\K(L)		173.67	607.3421	1213.679	-0.0018	-1.4	4.37	35556.4	9.3	HUMAN	F2Z393	Transaldolase
6039	dirMS_041712_NAR_20mM_plus.17052.17052.2	2	12.41	0	1.36E+05		(K)FATEAAI	(K)F A\T\E/A/A I/T\I L R(I)		188.82	603.3442	1205.689	-0.0077	-6.4	6	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
6040	dirMS_041712_NAR_30mM_plus2.13976.13976.2	2	12.41	0	2.12E+05		(K)NFGIGQ	(K)N/F|G\I/G Q D I Q/P K(R)		126.03	608.8192	1216.632	-0.0009	-0.8	5.84	30166.2	10.79	HUMAN	P62424	60S ribosomal protein L7a
6041	dirMS_041712_NAR_30mM_plus2.7290.7379.2	2	12.41	0	4.11E+05		(K)SLESINSI	(K)S L|E/S/I/N S/R(L)		92.93	453.2369	905.469	-0.0022	-2.4	5.72	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
6042	dirMS_041712_NAR_40mM_plus2.8027.8027.2	2	12.41	0	2.11E+05		(R)AVVIVDI	(R)A V/V|I/V/D/D/R(G)		108.22	443.7528	886.499	-0.0009	-1.1	4.21	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
6043	dirMS_041712_NAR_40mM_minus2.13830.13830.3	3	12.4	1	4.48E+04		(K)FGEVVD	(K)F G/E|V/V D C T L/K L D/P I T G R(S)	C:Carbamidomethylation	165.3	640.6656	1919.989	-0.0073	-3.8	4.56	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
6044	dirMS_041712_NAR_60mM_minus.16668.16668.3	3	12.4	1	8.10E+04		(R)RDDGTG	(R)R D D G T G Q L|L|L/P L S D/A R(K)		152.85	576.307	1726.908	-0.0018	-1	4.43	533778	5.74	HUMAN	Q15149	Plectin
6045	dirMS_041712_NAR_20mM_plus.9422.9422.2	2	12.4	0	1.86E+05		(K)SVTNED'	(K)S V/T\N E|D V/T Q/E E L/G G A/K(T)		136	838.9014	1676.797	-0.0018	-1.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
6046	dirMS_041712_NAR_30mM_plus2.6180.6295.2	2	12.4	0	5.49E+05		(K)IVEMSTS	(K)I/V|E|M/S T/S/K(T)		87.1	447.7285	894.46	-0.0104	-11.6	6	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
6047	dirMS_041712_NAR_30mM_plus2.9000.9000.2	2	12.4	0	3.86E+05		(R)CSEQVQ	(R)C/S|E|Q/V/Q/D F\T/K(C)	C:Carbamidomethylation	100.43	621.2771	1241.547	0.0002	0.2	4.37	13533.5	9.82	HUMAN	H7C3D8	COX assembly mitochondrial protein homolog (Fragment)
6048	dirMS_041712_NAR_40mM_plus2.11281.11281.3	3	12.4	0	2.83E+04		(K)AGVSISV	(K)A/G V/S|I/S V V H G/N L S E E A A K(Q)		132.63	589.9796	1767.924	0.0007	0.4	5.4	50949.8	9.28	HUMAN	P36551	Coproporphyrinogen-III oxidase, mitochondrial
6049	dirMS_041712_NAR_60mM_plus.17322.17322.3	3	12.4	0	2.04E+05		(K)THLPGF\	(K)T H L\P G F\V|E|Q\A/E A L K(A)		147.35	513.9442	1539.817	0.0015	1	5.37	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
6050	dirMS_041712_NAR_120mM_minus.13662.13680.3	3	12.39	0	4.02E+05		(R)AWGPG	(R)A/W|G P/G L/H/G G I V G/R(S)		129.03	426.2349	1276.691	-0.0008	-0.6	9.8	258215.9	5.48	HUMAN	E7EN95	Filamin-B
6051	dirMS_041712_NAR_30mM_minus2.17090.17090.2	2	12.39	0	8.20E+04		(K)FAEAFEA	(K)F A|E/A/F E/A I|P R(A)		146.93	575.7971	1150.589	-0.0022	-1.9	4.53	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
6052	dirMS_041712_NAR_30mM_minus2.5864.5864.2	2	12.39	0	5.74E+04		(R)LAEAEET	(R)L A/E/A|E E|T/A R(T)		86.62	495.2478	989.49	-0.0015	-1.5	4.25	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
6053	dirMS_041712_NAR_50mM_minus2.14874.14874.3	3	12.39	0	4.12E+05		(K)QLEAIDC	(K)Q L/E A/I D Q L/H L/E Y A/K(R)		152.43	557.6327	1670.875	0.0087	5.2	4.65	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
6054	dirMS_041712_NAR_60mM_minus.8643.8643.3	3	12.39	0	2.74E+05		(R)LAQGHT	(R)L/A|Q G H/T T V/D E/L A/R(R)		107.93	470.9153	1410.734	-0.0022	-1.6	5.32	533778	5.74	HUMAN	Q15149	Plectin
6055	dirMS_041712_NAR_60mM_minus.9339.9339.3	3	12.39	1	2.25E+05	M230m M:	(R)mSMKE\	(R)m S M\K E V\D E Q|m|L/N|V|Q N/K(N)	m:Oxidized methionine	111.92	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
6056	dirMS_041712_NAR_20mM_plus.18085.18085.2	2	12.39	0	1.64E+05		(K)VANVSL	(K)V A|N\V/S L/L A L/Y K(G)		195.52	595.8558	1190.714	-0.01	-8.4	8.56	15978.4	10.84	HUMAN	P62266	40S ribosomal protein S23
6057	dirMS_041712_NAR_30mM_plus2.11322.11365.2	2	12.39	0	1.51E+05		(R)LVDMM	(R)L/V|D/M/M/E/R(G)		112.18	447.2119	893.422	-0.0054	-6.1	4.37	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
6058	dirMS_041712_NAR_30mM_plus2.16097.16097.2	2	12.39	0	1.26E+05		(K)LALASLG	(K)L/A|L/A/S L G\Y/E K(S)		136.85	532.8002	1064.599	-0.0055	-5.2	6	96649	6.13	HUMAN	Q8WUM4	Programmed cell death 6-interacting protein
6059	dirMS_041712_NAR_40mM_plus2.18204.18204.3	3	12.39	1	2.86E+05		(R)VAAKLE'	(R)V A A\K L\E V/A|P/I/S D I I A/I K(S)		174.02	584.3591	1751.068	-0.005	-2.8	6.04	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
6060	dirMS_041712_NAR_60mM_plus.16929.16929.3	3	12.39	1	2.15E+05		(K)YMACCL	(K)Y/M/A/C C L L Y R G D\V V/P K(E)	C:Carbamidomethylation	145.85	615.6325	1844.886	-0.0026	-1.4	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
6061	dirMS_041712_NAR_120mM_minus.5364.5464.3	3	12.38	1	9.04E+05		(R)NDDDEE	(R)N/D|D/D/E/E/E A A\R E/R(R)		82.93	483.5345	1448.588	0.0005	0.4	3.95	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
6062	dirMS_041712_NAR_20mM_minus.14116.14116.2	2	12.38	0	1.39E+06		(K)SYELPDC	(K)S Y E|L|P D G/Q/V I/T I/G N E R(F)		194.13	895.9481	1790.892	-0.003	-1.7	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
6063	dirMS_041712_NAR_50mM_minus2.12194.12206.3	3	12.38	1	3.81E+05	M356m	(K)VGEVIVT	(K)V/G|E|V/I/V/T K D D A m L L K(G)	m:Oxidized methionine	137.88	549.6316	1630.908	15.9718	-14	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
6064	dirMS_041712_NAR_50mM_minus2.14814.14814.3	3	12.38	1	3.01E+05		(R)EAVTEIL	(R)E A/V/T/E I|L G I/E P D R E K(G)		152.28	566.9683	1698.891	-0.0005	-0.3	4.25	25685.9	6.4	HUMAN	E9PGT1	Translin
6065	dirMS_041712_NAR_50mM_minus2.16495.16495.3	3	12.38	1	1.87E+04		(R)EVQLEEI	(R)E V/Q/L/E E/L/E A A R D L V S K(E)		161.82	610.3273	1828.965	0.0023	1.2	4.25	45984.6	6.24	HUMAN	B4E1G6	Galactokinase
6066	dirMS_041712_NAR_60mM_minus.17563.17594.3	3	12.38	1	2.36E+05		(K)GPREEIV	(K)G P R E E I\V|Y|L|P/C I Y R(N)	C:Carbamidomethylation	157.97	588.9733	1764.91	-0.0048	-2.7	6.14	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
6067	dirMS_041712_NAR_60mM_minus.19321.19321.3	3	12.38	0	1.03E+06		(R)SLHDALC	(R)S L H D A L\C|V/L/A Q T/V\K(D)	C:Carbamidomethylation	171.23	518.9484	1554.831	-0.0002	-0.1	6.46	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
6068	dirMS_041712_NAR_60mM_minus.8695.8695.3	3	12.38	0	2.74E+05		(R)LAQGHT	(R)L/A\Q\G H/T/T/V/D/E L A R(R)		107.93	470.9153	1410.734	-0.0022	-1.6	5.32	533778	5.74	HUMAN	Q15149	Plectin
6069	dirMS_041712_NAR_120mM_plus.16280.16280.4	4	12.38	1	9.89E+05		(R)ALEHFTI	(R)A L\E/H/F/T D L/Y/D I/K/R(A)		138.33	405.9647	1620.838	-0.0011	-0.7	5.38	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
6070	dirMS_041712_NAR_120mM_plus.5248.5353.3	3	12.38	1	7.24E+05	M117m	(K)EmQLRC	(K)E m/Q/L/R Q/E/E/E R(R)	m:Oxidized methionine	80.92	455.2145	1347.632	15.9968	1.4	4.49	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
6071	dirMS_041712_NAR_30mM_plus2.18484.18484.2	2	12.38	0	1.65E+05		(K)QFLSQFI	(K)Q F|L|S/Q/F/E M Q S R(K)		150.25	700.8358	1400.663	0.0016	1.2	6	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
6072	dirMS_041712_NAR_30mM_plus2.22359.22420.2	2	12.38	0	3.76E+05		(R)VGNLGL	(R)V G N|L/G/L|A|T/S/F F\N E R(N)		172.82	762.8926	1524.781	-0.0026	-1.7	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
6073	dirMS_041712_NAR_30mM_plus2.5417.5417.2	2	12.38	0	1.51E+05	M67m	(R)AmNGES	(R)A/m|N/G/E S/L D G R(Q)	m:Oxidized methionine	82.97	533.2363	1049.468	15.9973	2.2	4.37	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
6074	dirMS_041712_NAR_40mM_plus2.12255.12255.2	2	12.38	0	1.06E+05		(R)VLQALE(	(R)V L|Q/A/L E G L K(M)		138.8	485.8002	970.593	0	0	5.97	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
6075	dirMS_041712_NAR_40mM_plus2.12294.12294.3	3	12.38	0	1.63E+05		(K)QLTEED(	(K)Q L/T/E/E/D/G V H S V I E\E N I K(C)		138.75	647.3228	1939.961	-0.0069	-3.5	4.25	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
6076	dirMS_041712_NAR_50mM_plus2.11843.11843.3	3	12.38	1	4.35E+05		(K)QIDLSTV	(K)Q I\D L/S T/V/D\L K K(L)		130.47	420.5781	1259.72	-0.0008	-0.6	5.96	21156.2	9.41	HUMAN	P55145	Mesencephalic astrocyte-derived neurotrophic factor
6077	dirMS_041712_NAR_50mM_plus2.13093.13225.3	3	12.38	1	9.93E+05		(R)GYSFTTT	(R)G Y|S|F/T/T T A\E R E I V/R(D)		137.88	543.9455	1629.823	-0.0012	-0.7	6.14	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
6078	dirMS_041712_NAR_50mM_plus2.7188.7188.3	3	12.38	1	3.91E+04		(R)IVEQDTI	(R)I/V\E/Q/D T M/P P K G V/R(H)		103.58	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
6079	dirMS_041712_NAR_50mM_plus2.9012.9012.3	3	12.38	1	3.60E+05		(K)TAVCDIF	(K)T/A/V/C D/I/P P R G L/K(M)	C:Carbamidomethylation	114.93	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
6080	dirMS_041712_NAR_60mM_plus.12255.12274.3	3	12.38	1	2.23E+05		(R)VIACFDS	(R)V/I/A/C/F/D/S L/K G R(C)	C:Carbamidomethylation	120.97	422.5606	1265.667	0.0002	0.1	8.72	23656.6	9.69	HUMAN	B4E3F7	Muscleblind-like protein 2
6081	dirMS_041712_NAR_120mM_minus.17764.17764.3	3	12.37	1	1.82E+05		(R)AGKLDP	(R)A G K L D|P/H|L|V L D Q L R(C)		151.52	525.6385	1574.901	-0.0004	-0.2	6.79	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
6082	dirMS_041712_NAR_30mM_minus2.14055.14122.2	2	12.37	0	2.84E+05		(R)NLVDNI'	(R)N L|V|D|N/I|T/G Q R(L)		130	565.3015	1129.596	-0.0003	-0.3	5.84	533778	5.74	HUMAN	Q15149	Plectin
6083	dirMS_041712_NAR_30mM_minus2.18446.18446.2	2	12.37	0	4.47E+05		(R)QAQEYE	(R)Q/A\Q E/Y/E/A/L/L/N I K(V)		154.67	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
6084	dirMS_041712_NAR_40mM_minus2.11290.11290.3	3	12.37	0	2.05E+04		(K)VALLLLD	(K)V/A/L\L/L/L/D Q G A S P H A A/A K(N)		150	558.9882	1674.954	-0.0037	-2.2	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
6085	dirMS_041712_NAR_50mM_minus2.9428.9446.2	2	12.37	1	7.15E+05		(R)DGKLVS	(R)D/G K|L\V|S/E/S S\D\V L|P K(-)		121.97	737.3927	1473.78	-0.0014	-0.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
6086	dirMS_041712_NAR_60mM_minus.15560.15560.3	3	12.37	1	1.92E+05		(R)ASLISAV	(R)A S|L|I/S A V S/D K L R(W)		146.22	420.5811	1259.732	-0.003	-2.4	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
6087	dirMS_041712_NAR_120mM_plus.8192.8210.3	3	12.37	1	2.71E+06		(R)AAPGAE	(R)A A|P/G A E F A/P N K/R(R)		96.73	410.2196	1228.643	0.001	0.8	8.79	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
6088	dirMS_041712_NAR_20mM_plus.18353.18353.2	2	12.37	0	1.22E+05		(R)GVVQEL	(R)G V/V/Q/E/L|Q\Q A I/S K(L)		198.05	650.3656	1299.727	-0.0028	-2.1	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
6089	dirMS_041712_NAR_20mM_plus.18695.18695.2	2	12.37	0	1.63E+05		(R)IITLTGPT	(R)I I|T/L/T|G/P T N A I/F K(A)		200.35	694.9091	1388.815	-0.0039	-2.8	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
6090	dirMS_041712_NAR_20mM_plus.6746.6746.3	3	12.37	0	1.25E+05	M136m	(R)LVAGEm	(R)L V A\G E m G Q\N\E/P/D/Q G G Q R(G)	m:Oxidized methionine	111.45	601.2753	1785.818	15.9929	-1.1	4.14	17508.7	8.03	HUMAN	Q5H928	3-hydroxyacyl-CoA dehydrogenase type-2
6091	dirMS_041712_NAR_30mM_plus2.13042.13282.2	2	12.37	0	1.65E+06		(R)MVVPAA	(R)M/V|V|P A A L/K(V)		123.12	414.7506	828.501	-0.0072	-8.7	8.5	23633.9	11.02	HUMAN	P40429	60S ribosomal protein L13a
6092	dirMS_041712_NAR_30mM_plus2.13952.13952.2	2	12.37	0	1.87E+05		(K)NFGIGQ	(K)N F|G|I/G\Q D/I Q P K(R)		126.08	608.8192	1216.632	-0.0009	-0.8	5.84	30166.2	10.79	HUMAN	P62424	60S ribosomal protein L7a
6093	dirMS_041712_NAR_30mM_plus2.18251.18251.2	2	12.37	0	5.29E+05		(R)GYISPYF	(R)G Y\I|S|P/Y F I N T S K(G)		149.7	695.3554	1389.705	-0.0014	-1	8.5	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
6094	dirMS_041712_NAR_40mM_plus2.17550.17550.3	3	12.37	1	5.30E+05		(R)GLLPGLL	(R)G L/L|P G L L/P A/P/A/D K L T P K(G)		170.55	567.6811	1701.031	-0.0022	-1.3	8.59	153084.9	5.55	HUMAN	Q6P2E9	Enhancer of mRNA-decapping protein 4
6095	dirMS_041712_NAR_60mM_plus.16110.16190.3	3	12.37	1	6.05E+05		(R)IKIGDPL	(R)I K/I G D\P\L|L/E D/T R(M)		141.57	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
6096	dirMS_041712_NAR_60mM_plus.6931.6931.3	3	12.37	1	3.73E+05		(K)DGGFCE	(K)D/G/G/F/C/E V C\K/K(L)	C:Carbamidomethylation	94.72	400.5114	1199.518	0.0013	1.1	6.07	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
6097	dirMS_041712_NAR_120mM_minus.9538.9623.3	3	12.36	0	8.55E+05		(K)SPQYCQ	(K)S P/Q|Y C/Q/V I/H/R(L)	C:Carbamidomethylation	106.37	429.8855	1287.626	0.0157	12.2	8.49	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
6098	dirMS_041712_NAR_120mM_minus.9731.9731.3	3	12.36	1	3.92E+05		(K)YAGKDG	(K)Y/A/G K/D G Y N Y/T L/S/K(T)		107.57	493.9089	1479.711	0.0007	0.5	8.38	11854.4	6.57	HUMAN	P31949	Protein S100-A11
6099	dirMS_041712_NAR_20mM_minus.11601.11601.2	2	12.36	0	2.23E+05		(R)GDLGIEI	(R)G D L/G|I|E/I|P A E K(V)		163.93	571.3078	1141.61	-0.0016	-1.4	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)

6100	dirMS_041712_NAR_20mM_minus.9315.9320.2	2	12.36	0	5.70E+05		(K)YEELQSL	(K)Y E|E|L/Q/S L/A/G K(H)		143.25	569.2917	1137.579	-0.0025	-2.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
6101	dirMS_041712_NAR_30mM_minus2.9155.9311.2	2	12.36	0	6.20E+05		(K)TVGATA	(K)T V|G|A|T/A/L P R(L)		104.73	443.2601	885.515	-0.0023	-2.6	9.41	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
6102	dirMS_041712_NAR_40mM_minus2.10441.10923.3	3	12.36	0	2.23E+05		(R)DLSHIG	(R)D L/S H I G D A|V|V|I/S C A K(D)	C:Carbamidomethylation	147.1	528.9384	1584.805	-0.0044	-2.8	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
6103	dirMS_041712_NAR_40mM_minus2.11323.11323.3	3	12.36	1	1.21E+05		(K)VIDPAT	(K)V I|D|P A T A T|S V D L R D/I/K(I)		149.38	571.9828	1713.938	-0.0043	-2.5	4.43	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
6104	dirMS_041712_NAR_40mM_minus2.11612.11612.3	3	12.36	1	1.33E+04		(R)DLAALG	(R)D L|A/A\L/G D K V\N S L/G E T A E R(L)		151.8	620.3199	1858.95	-0.0053	-2.9	4.32	285798.6	5.23	HUMAN	A6NG51	Spectrin alpha chain, non-erythrocytic 1
6105	dirMS_041712_NAR_50mM_minus2.13192.13192.3	3	12.36	1	3.21E+05		(R)ALPAVQ	(R)A L/P A V Q Q/N/N L/D E D L I R K(L)		142.87	646.3522	1937.045	-0.003	-1.6	4.56	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
6106	dirMS_041712_NAR_50mM_minus2.14547.14547.3	3	12.36	1	1.40E+05		(R)GDVVPK	(R)G D V/V/P/K D V N/A A/I/A T I K(T)		150.42	537.6375	1610.911	-0.0133	-8.2	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
6107	dirMS_041712_NAR_50mM_minus2.18832.18832.3	3	12.36	1	2.24E+06		(R)LIALLEVI	(R)L/I|A L/L/E/V L/S Q K R(M)		183.72	461.6289	1382.873	-0.0008	-0.6	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
6108	dirMS_041712_NAR_60mM_minus.18769.18769.3	3	12.36	1	2.67E+05		(K)NAAGAL	(K)N A|A/G/A/L/D L/L K\E L/K(N)		166.87	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
6109	dirMS_041712_NAR_120mM_plus.14365.14913.4	4	12.36	1	4.09E+06		(K)LDKSQI	(K)L D K S Q I H D\I\V\L\V|G/G/S/T R(I)		130.45	460.2603	1838.013	0.0063	3.4	6.75	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
6110	dirMS_041712_NAR_120mM_plus.18194.18234.4	4	12.36	1	1.39E+06		(K)YYITIIDA	(K)Y Y\I T I/I/D/A/P G H R D F I/K(N)		148.93	481.2587	1922.017	-0.0041	-2.1	6.75	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
6111	dirMS_041712_NAR_120mM_plus.9392.9411.3	3	12.36	2	4.46E+05		(K)LTDCVVI	(K)L/T|D|C/V/V M R D/P A S K R(S)	C:Carbamidomethylation	102.65	549.9483	1647.831	-0.0002	-0.1	8.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
6112	dirMS_041712_NAR_20mM_plus.11506.11506.2	2	12.36	0	1.69E+05		(R)YALYDA	(R)Y A|L/Y/D/A T Y E T/K(E)		151.57	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
6113	dirMS_041712_NAR_30mM_plus2.10045.10045.2	2	12.36	0	2.67E+05		(R)ELSEQL	(R)E L|S E/Q/L/G Q/A E R(A)		105.82	630.3143	1259.623	-0.0013	-1	4.25	266161	5.68	HUMAN	E9PPU0	Epiplakin
6114	dirMS_041712_NAR_30mM_plus2.11659.11659.2	2	12.36	0	5.70E+05		(R)AMGEQ	(R)A/M/G E/Q/A V|A L A/R(A)		114.4	558.7944	1116.583	-0.0015	-1.3	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
6115	dirMS_041712_NAR_30mM_plus2.12224.12438.2	2	12.36	0	6.65E+05		(R)FGISSVP	(R)F/G|I|S/S V/P T/K(G)		117.7	468.2629	935.52	-0.0011	-1.2	8.75	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
6116	dirMS_041712_NAR_30mM_plus2.18022.18022.2	2	12.36	0	2.32E+05		(R)QITLNDI	(R)Q I/T/L/N/D L P V/G R(S)		147.83	613.3465	1225.69	-0.0042	-3.4	5.84	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
6117	dirMS_041712_NAR_30mM_plus2.19788.19788.3	3	12.36	0	1.41E+05		(K)GFAFVQ	(K)G F\A/F V Q/Y/V/N E R(N)		157.38	443.8907	1329.659	-0.0011	-0.8	6	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
6118	dirMS_041712_NAR_50mM_plus2.14362.14542.3	3	12.36	0	2.26E+06		(K)LQMEA	(K)L Q|M/E A/P/H I/I/V/G T P G/R(V)		143.97	540.2948	1618.873	-0.0035	-2.2	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
6119	dirMS_041712_NAR_50mM_plus2.17021.17021.3	3	12.36	1	3.71E+05		(K)LSKNEV	(K)L S K N E V L M/V|N I|G/S L/S T G/G R(V)		157	659.0229	1975.064	-0.0099	-5	8.75	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
6120	dirMS_041712_NAR_50mM_plus2.17494.17494.3	3	12.36	1	5.25E+05		(K)VKLAAV	(K)V K L A\A V D A T V/N Q|V/L/A S R(Y)		160.33	585.6736	1755.012	-0.0061	-3.5	8.72	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
6121	dirMS_041712_NAR_60mM_plus.12232.12361.3	3	12.36	1	6.83E+05		(R)YGEPSE	(R)Y/G|E|P/S E/V F I N R D/R(G)		121.23	527.9264	1581.766	-0.0009	-0.6	4.68	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
6122	dirMS_041712_NAR_120mM_minus.12624.12624.3	3	12.35	0	7.44E+05		(K)TFTAWC	(K)T F/T/A/W/C N S H/L/R(K)	C:Carbamidomethylation	122.28	464.8871	1392.648	-0.001	-0.7	9.44	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
6123	dirMS_041712_NAR_20mM_minus.9647.9647.2	2	12.35	0	2.40E+05	M33m	(K)VAGmD	(K)V A/G m/D/V/E|L T/V E/E R(N)	m:Oxidized methionine	147.48	732.355	1447.71	15.993	-1.3	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
6124	dirMS_041712_NAR_30mM_minus2.17160.17160.2	2	12.35	0	2.76E+05		(R)LLNTFLE	(R)L L|N T/F L\E R(L)		146.9	503.2871	1005.573	-0.0058	-5.8	6	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
6125	dirMS_041712_NAR_40mM_minus2.13910.13910.3	3	12.35	0	5.98E+04		(R)LLAEIGA	(R)L/L|A E|I|G A\V/T L V S A P\R P D S R(H)		165.87	655.7064	1965.113	-0.0081	-4.1	6.07	27279.2	9.51	HUMAN	A9C4B9	tRNA splicing endonuclease 34 homolog (S. cerevisiae) (Fragment)
6126	dirMS_041712_NAR_60mM_minus.11723.11746.3	3	12.35	1	2.27E+05		(K)KLEEEQI	(K)K L\E E E Q\I\I|L/E/D Q N C K(L)	C:Carbamidomethylation	125.35	630.3154	1888.932	-0.0004	-0.2	4.25	227783.5	5.5	HUMAN	P35579	Myosin-9
6127	dirMS_041712_NAR_60mM_minus.15875.15934.3	3	12.35	1	3.10E+05		(K)ELKIDIIP	(K)E L K I D I|I|P/N/P Q E R(T)		148.9	522.2935	1564.869	-0.0034	-2.2	4.68	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
6128	dirMS_041712_NAR_120mM_plus.11454.11454.3	3	12.35	2	7.36E+05		(K)QAGPAS	(K)Q A|G/P A/S/V/P L R T E E E F K K(F)		113.4	629.6702	1886.997	-0.001	-0.5	6.23	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
6129	dirMS_041712_NAR_20mM_plus.11390.11529.2	2	12.35	0	2.68E+06		(K)DVNAA	(K)D V|N|A|A/I/A/T I K(T)		150.2	508.292	1015.578	-0.0015	-1.5	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
6130	dirMS_041712_NAR_20mM_plus.18733.18733.3	3	12.35	0	1.30E+05		(K)IYVDDGI	(K)I Y V D D G L|I/S L Q V K(Q)		200.6	488.2764	1462.815	-0.0005	-0.4	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
6131	dirMS_041712_NAR_20mM_plus.18763.18763.3	3	12.35	0	1.15E+05		(K)VIGNQS	(K)V I G N Q S L V/N/E/L A/F/T A R(K)		200.67	577.9842	1731.939	-0.0008	-0.4	5.97	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
6132	dirMS_041712_NAR_30mM_plus2.14357.14357.2	2	12.35	0	2.38E+05		(K)DSNFAG	(K)D S N/F/A/G D L/V/R(N)		128.13	547.2595	1093.527	-0.0155	-14.2	4.21	103258.6	6.54	HUMAN	Q86XP3	ATP-dependent RNA helicase DDX42
6133	dirMS_041712_NAR_30mM_plus2.17535.17536.2	2	12.35	0	7.85E+05		(K)NLYIISV	(K)N/L|Y|I/I/S V/K(G)		144.45	475.2893	949.572	-0.0004	-0.4	8.59	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
6134	dirMS_041712_NAR_40mM_plus2.13511.13511.3	3	12.35	0	3.39E+05		(R)VAPDEH	(R)V/A|P D E H P I L L/T/E A/P\L N P K(I)		145.4	652.0252	1954.064	-0.0034	-1.7	4.65	42344.8	5.39	HUMAN	Q562R1	Beta-actin-like protein 2
6135	dirMS_041712_NAR_40mM_plus2.18349.18349.3	3	12.35	1	1.13E+05		(K)MFEIVF	(K)M F E|I/V F/E D/P K I/P G E/K(Q)		174.45	593.6385	1778.903	-0.0024	-1.3	4.41	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
6136	dirMS_041712_NAR_40mM_plus2.19723.19723.3	3	12.35	0	3.56E+05		(R)DLLDTVI	(R)D L|L/D T/V L/P H L/Y N E T K(V)		185.2	590.9774	1770.927	-0.0096	-5.4	4.54	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
6137	dirMS_041712_NAR_40mM_plus2.6445.6445.2	2	12.35	0	8.18E+04		(R)VTDALN	(R)V T|D/A|L/N A T R(A)		96.73	480.7594	960.511	0.0006	0.7	5.81	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
6138	dirMS_041712_NAR_60mM_plus.12593.12895.3	3	12.35	1	1.28E+06		(K)DLFPYEE	(K)D/L|F/P/Y/E E S K E K(F)		123.67	462.2281	1384.663	0.0067	4.8	4.41	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
6139	dirMS_041712_NAR_60mM_plus.17755.17755.3	3	12.35	1	1.13E+05		(K)WVAIQS	(K)W/V/A\I/Q S V/S A W P E K R(G)		150.05	552.9655	1656.886	-0.0037	-2.2	8.75	6412.4	9.52	HUMAN	J3KSS4	Cytosolic non-specific dipeptidase (Fragment)
6140	dirMS_041712_NAR_120mM_minus.20008.20008.3	3	12.34	0	7.83E+04		(R)INLWHL	(R)I/N|L W/H L\E/I T D/R(S)		165.22	470.5897	1409.754	0.001	0.7	5.32	52204.6	5.82	HUMAN	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
6141	dirMS_041712_NAR_30mM_minus2.10262.10461.2	2	12.34	0	1.03E+06		(R)LVSVLQ	(R)L/V|S|V/L/Q/N K(M)		111	450.7779	900.551	-0.0028	-3.1	8.75	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
6142	dirMS_041712_NAR_30mM_minus2.14708.14708.2	2	12.34	0	5.00E+05		(R)TFEDFV	(R)T/F/E/D|F V/R(I)		133.23	457.2246	913.441	0.0005	0.6	4.37	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
6143	dirMS_041712_NAR_30mM_minus2.16154.16154.2	2	12.34	0	3.19E+05	M185m	(K)LAVNm	(K)L A|V|N m/V|P F/P R(L)	m:Oxidized methionine	142.33	580.3178	1143.634	15.994	-0.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
6144	dirMS_041712_NAR_50mM_minus2.12253.12291.3	3	12.34	1	3.25E+05		(K)SIQEIQE	(K)S I|Q/E/I/Q/E/L D/K/D D E S L R(K)		138.1	639.9828	1917.94	-0.0061	-3.2	4.02	18289.2	5.09	HUMAN	A8MXW0	Rho GDP-dissociation inhibitor 1
6145	dirMS_041712_NAR_50mM_minus2.15093.15093.3	3	12.34	1	1.33E+05		(K)VSEQGL	(K)V/S/E/Q G/L/I E|I L K K(V)		154.37	452.9385	1356.81	-0.0087	-6.4	6.11	12899.6	6.59	HUMAN	K7EL31	Programmed cell death protein 5
6146	dirMS_041712_NAR_50mM_minus2.15797.15797.3	3	12.34	0	3.64E+05		(K)LYGPTNI	(K)L/Y/G P T/N F/S/P\I/I N H V A R(F)		158.22	600.3221	1798.96	-0.0081	-4.5	8.75	60985.3	5.6	HUMAN	O75131	Copine-3
6147	dirMS_041712_NAR_50mM_minus2.16962.16962.3	3	12.34	0	6.67E+04		(K)YAPLHL	(K)Y A|P L/H/L\V/P L I E R(L)		164.72	474.2781	1420.831	-0.0113	-8	6.75	147553.6	6.73	HUMAN	E7EVF4	Cytoplasmic FMR1-interacting protein 2
6148	dirMS_041712_NAR_60mM_minus.13721.13721.3	3	12.34	1	2.57E+05		(K)KAEAAA	(K)K\A/E A A\A\S A\L|A/D A/D A/D/L E E R(L)		136.4	639.6429	1916.92	-0.0054	-2.8	4.02	25103.6	5.88	HUMAN	O43633	Charged multivesicular body protein 2a
6149	dirMS_041712_NAR_60mM_minus.14401.14401.3	3	12.34	0	3.65E+05		(R)VWYVS	(R)V/W|Y V/S/N/I/D G T H I A K(T)		140.38	534.9461	1602.828	-0.0037	-2.3	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
6150	dirMS_041712_NAR_20mM_plus.13624.13765.2	2	12.34	0	2.14E+05		(K)APILIAT	(K)A/P\I/L|I|A/T D/V A S R(G)		166.6	613.8559	1226.71	-0.0058	-4.7	5.88	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
6151	dirMS_041712_NAR_20mM_plus.13943.13943.2	2	12.34	0	6.90E+04		(K)IEVLEEEI	(K)I E|V/L/E E/E L R(L)		168.03	565.3132	1129.61	0.0092	8.1	4.09	334221.3	6.44	HUMAN	P15924	Desmoplakin
6152	dirMS_041712_NAR_20mM_plus.16802.16802.2	2	12.34	0	9.64E+04		(R)SSIAGLL	(R)S/S I/A/G L/L/L K(A)		187.07	451.2885	901.572	-0.002	-2.2	8.47	533778	5.74	HUMAN	Q15149	Plectin
6153	dirMS_041712_NAR_30mM_plus2.21946.21946.2	2	12.34	0	1.03E+05		(K)NFYFLE	(K)N F|Y|F/L E/M N T R(L)		170.5	667.8205	1334.62	0.0139	10.4	6	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
6154	dirMS_041712_NAR_30mM_plus2.22048.22134.2	2	12.34	0	1.40E+05		(K)ETLLAM	(K)E/T/L/L/A/M/F/K(Y)		170.98	476.7621	952.517	-0.0003	-0.3	6.1	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
6155	dirMS_041712_NAR_50mM_plus2.16828.16828.3	3	12.34	0	7.42E+05		(R)QYYTLL	(R)Q Y Y/T/L/L N Q/A/P D\M L/H R(K)		156.87	621.6447	1862.922	-0.0022	-1.2	6.74	4335.1	9.82	HUMAN	E5RH00	Ras GTPase-activating protein-binding protein 1
6156	dirMS_041712_NAR_60mM_plus.7369.7369.2	2	12.34	1	1.58E+06		(R)AAPGAE	(R)A A/P/G A/E/F A P N K R(R)		96.2	614.8248	1228.643	-0.001	-0.8	8.79	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
6157	dirMS_041712_NAR_60mM_plus.8955.8955.3	3	12.34	1	7.38E+05		(R)VVDSME	(R)V/V|D/S M E D E V Q R/R(L)		105.27	488.2367	1462.696	0.0001	0.1	4.32	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
6158	dirMS_041712_NAR_120mM_minus.7525.7551.3	3	12.33	1	2.18E+05		(K)SKAEAE	(K)S K A E A\E/S|L|Y/Q/S K(Y)		95.33	447.558	1340.669	-0.0098	-7.3	5.86	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
6159	dirMS_041712_NAR_20mM_minus.8586.8586.2	2	12.33	0	8.30E+04		(R)YEIEETE	(R)Y/E|I\E|E/T/E/T V T K(S)		134.9	671.3246	1341.642	-0.0001	-0.1	4.09	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
6160	dirMS_041712_NAR_30mM_minus2.13406.13406.2	2	12.33	0	2.45E+05		(K)QYGNE	(K)Q Y/G/N E V/F/L/A/K(L)		126.23	584.7961	1168.6	-0.0148	-12.6	6	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
6161	dirMS_041712_NAR_30mM_minus2.16776.17226.2	2	12.33	0	4.65E+05		(R)NILGGT	(R)N I|L|G/G\T V F/R(E)		146.67	488.7803	976.557	-0.0041	-4.2	9.75	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
6162	dirMS_041712_NAR_30mM_minus2.7625.7625.2	2	12.33	0	8.10E+04		(R)SDEGQL	(R)S D|E/G/Q|L/S/P A T R(G)		95.82	580.7788	1160.554	-0.0039	-3.3	4.37	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
6163	dirMS_041712_NAR_50mM_minus2.7338.7338.3	3	12.33	0	1.34E+05		(K)STAGDT	(K)S T|A G D/T H/L/G G E D F D/N R(M)		108.48	564.5808	1691.726	0.0023	1.3	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
6164	dirMS_041712_NAR_60mM_minus.10829.10829.3	3	12.33	1	5.44E+05	M239m	(R)MSMKE	(R)M/S|M K E V D E\Q\m|L/N/V\Q/N K(N)	m:Oxidized methionine	119.9	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
6165	dirMS_041712_NAR_60mM_minus.14393.14393.3	3	12.33	1	1.30E+06		(R)MSMKE	(R)M S\M K E V D E/Q|M/L/N V Q N K(N)		140.47	641.9701	1923.897	-0.0015	-0.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
6166	dirMS_041712_NAR_60mM_minus.17467.17467.3	3	12.33	1	4.55E+06		(R)VSFELFA	(R)V/S|F E/L F A D K V/P K(T)		157.68	460.5911	1379.757	0.0018	1.3	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
6167	dirMS_041712_NAR_60mM_minus.6113.6113.3	3	12.33	1	2.99E+05		(K)ETEGDV	(K)E T E/G D/V/T S V K/D/A/K(I)		92.5	460.2267	1378.67	-0.0041	-3	4.32	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
6168	dirMS_041712_NAR_20mM_plus.12774.12774.2	2	12.33	0	1.15E+05		(R)LVVPAS	(R)L V|V|P A S Q C\G S/L I G K(G)	C:Carbamidomethylation	161.33	714.8991	1428.788	0.003	2.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
6169	dirMS_041712_NAR_20mM_plus.13664.13664.2	2	12.33	0	3.55E+05		(R)VLQALE	(R)V/L|Q/A L E/G L K(M)		165.33	485.8004	970.593	0.0004	0.4	5.97	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
6170	dirMS_041712_NAR_30mM_plus2.15377.15935.2	2	12.33	0	4.09E+06		(R)YIEIFK(S	(R)Y/I|E I/F/K(S)		135.57	406.7314	812.455	0.0003	0.3	6	24249.1	6.99	HUMAN	D6RBM0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
6171	dirMS_041712_NAR_30mM_plus2.18783.19055.2	2	12.33	0	3.71E+05		(R)IYISLLK(	(R)I/Y|I/S/L/L/K(E)		152.37	425.2732	849.544	-0.0053	-6.2	8.59	105417.2	6.41	HUMAN	C9JZR2	Catenin delta-1
6172	dirMS_041712_NAR_30mM_plus2.20143.20143.2	2	12.33	0	1.74E+05		(R)MLDMG	(R)M L/D|M/G|F/E/P Q I R(K)		159.27	668.8241	1336.639	0.0021	1.6	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
6173	dirMS_041712_NAR_40mM_plus2.10640.10640.2	2	12.33	0	7.56E+04		(R)LSESQLS	(R)L/S\E/S/Q/L/S F R(R)		127.93	533.7789	1066.553	-0.0022	-2.1	6	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
6174	dirMS_041712_NAR_40mM_plus2.17433.17433.3	3	12.33	0	1.53E+05		(R)VYAILTH	(R)V/Y|A\I L T H G I|F S/G P A I|S R(I)		169.28	601.3376	1801.996	0.0023	1.3	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
6175	dirMS_041712_NAR_50mM_plus2.14798.14798.3	3	12.33	0	1.17E+06		(R)EHALLA	(R)E\H A\L\L/A|Y/T/L/G V K(Q)		145.75	438.9176	1314.742	-0.0034	-2.6	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
6176	dirMS_041712_NAR_50mM_plus2.19695.19695.3	3	12.33	1	1.81E+05		(R)TSLLTLE	(R)T S/L/L/T/L E D V K Q E L I/K(L)		172.07	577.3359	1729.995	-0.0014	-0.8	4.68	156316.8	8.61	HUMAN	Q7Z478	ATP-dependent RNA helicase DHX29
6177	dirMS_041712_NAR_50mM_plus2.22127.22127.3	3	12.33	1	2.51E+05		(R)KEGGLG	(R)K E G G L G P\L N\I|P L L/A/D V T R(R)		189.68	621.6925	1863.07	-0.0069	-3.7	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
6178	dirMS_041712_NAR_50mM_plus2.7507.7585.3	3	12.33	1	3.52E+05		(R)VVASDK	(R)V/V|A/S D K/E/T/Y E/L\R(Y)		105.87	470.5836	1409.727	0.0092	6.5	4.68	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
6179	dirMS_041712_NAR_60mM_plus.17393.17415.3	3	12.33	1	4.10E+05		(R)ISGLIYEE	(R)I/S|G L|I/Y/E E T R G V L K(V)		148.38	526.634	1577.89	-0.0023	-1.4	6.14	11367.1	11.36	HUMAN	P62805	Histone H4
6180	dirMS_041712_NAR_30mM_minus2.7141.7141.2	2	12.32	0	4.82E+05		(K)DAQGQI	(K)D A/Q/G\Q/P/G L E R(A)		92.98	535.762	1070.523	-0.0058	-5.4	4.37	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
6181	dirMS_041712_NAR_50mM_minus2.10221.10221.3	3	12.32	0	4.65E+05	M147m	(K)LQmEA	(K)L Q/m/E A P/H I/I/V/G/T P G R(V)	m:Oxidized methionine	125.83	545.6267	1618.873	15.9922	-1.7	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
6182	dirMS_041712_NAR_50mM_minus2.12887.12887.3	3	12.32	1	1.80E+05		(K)GGELVY	(K)G G E|L|V|Y/T D S E/A R D V F E K(A)		141.5	638.9739	1914.908	-0.0008	-0.4	4.18	533778	5.74	HUMAN	Q15149	Plectin
6183	dirMS_041712_NAR_60mM_minus.17160.17160.3	3	12.32	1	3.06E+05		(K)DANAKL	(K)D A/N A K L S\E\L/E|A/A/L Q R(A)		156.02	543.6239	1628.86	-0.0031	-1.9	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
6184	dirMS_041712_NAR_20mM_plus.16663.16663.2	2	12.32	0	1.54E+05		(R)LLEAQIA	(R)L L E|A|Q|I|A/T G G I I/D\P K(E)		185.72	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
6185	dirMS_041712_NAR_20mM_plus.7057.7057.2	2	12.32	0	4.35E+05		(R)IQEAGT	(R)I/Q|E/A/G T E\V/V K(A)		115.37	537.2946	1073.584	-0.0018	-1.7	4.53	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
6186	dirMS_041712_NAR_30mM_plus2.20796.20796.2	2	12.32	0	2.22E+05		(K)GGIVG	(K)G G I|V|G/M/T L/P I A/R(D)		162.7	592.8453	1184.682	0.0013	1.1	9.75	27150.8	7.95	HUMAN	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2
6187	dirMS_041712_NAR_30mM_plus2.6271.6271.2	2	12.32	0	8.62E+04		(K)EVYPEA	(K)E/V|Y/P E/A/R(K)		87.3	432.2218	863.426	0.0106	12.2	4.53	17921.1	9.84	HUMAN	H7BZW6	Histone deacetylase complex subunit SAP18 (Fragment)
6188	dirMS_041712_NAR_50mM_plus2.15350.15350.3	3	12.32	1	1.10E+05		(R)VEKIPG	(R)V/E K I/P\G G\I|I/E/D S C V\L R(G)	C:Carbamidomethylation	147.42	595.6548	1784.958	-0.0076	-4.3	4.68	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
6189	dirMS_041712_NAR_50mM_plus2.6095.6095.3	3	12.32	1	6.55E+04		(R)NTDVA	(R)N T/D V/A/Q/S P E A/P K Q E A P A K(K)		96.33	627.6463	1880.935	-0.0105	-5.6	4.68	152868.9	8.79	HUMAN	Q9P2E9	Ribosome-binding protein 1
6190	dirMS_041712_NAR_60mM_plus.7252.7252.3	3	12.32	0	3.00E+05		(K)ITPAHD	(K)I/T|P A/H D/Q N D Y/E/V G Q R(H)		96.68	581.6074	1742.809	-0.0016	-0.9	4.54	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
6191	dirMS_041712_NAR_120mM_minus.13522.13651.3	3	12.31	0	5.66E+05		(K)YNPTW	(K)Y N|P/T W/H/C\I/V G/R(N)	C:Carbamidomethylation	128.55	468.2346	1402.669	0.0208	14.8	8.75	10536.9	6.9	HUMAN	P63167	Dynein light chain 1, cytoplasmic
6192	dirMS_041712_NAR_30mM_minus2.14707.14749.2	2	12.31	0	4.87E+05		(K)IAWALSI	(K)I/A|W|A/L S/R(K)		133.35	408.7427	816.473	0.0055	6.7	9.75	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
6193	dirMS_041712_NAR_40mM_minus2.14365.14365.3	3	12.31	0	1.77E+04		(R)GTEDITS	(R)G T/E D I/T/S/P H G I/P\L D\L L/D/R(V)		169.05	650.3366	1948.997	-0.0022	-1.1	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
6194	dirMS_041712_NAR_60mM_minus.10552.10552.3	3	12.31	1	1.96E+04		(K)TAPFDS	(K)T A/P F/D/S R F P/N Q N Q T R(N)		118.3	593.6163	1778.857	-0.0225	-12.7	9.26	12263.5	6.83	HUMAN	J3KPM8	Cytochrome c oxidase subunit 6B1
6195	dirMS_041712_NAR_60mM_minus.14884.14884.3	3	12.31	1	5.61E+05		(K)TDKTLVI	(K)T/D K T/L\V|L/L/M/G/K(E)		142.63	406.9088	1218.713	-0.0008	-0.6	8.26	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
6196	dirMS_041712_NAR_20mM_plus.13570.13570.2	2	12.31	0	1.60E+05	M98m	(R)TLTIVDT	(R)T L|T|I/V|D T G I G m T K(A)	m:Oxidized methionine	165.92	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
6197	dirMS_041712_NAR_30mM_plus2.16044.16088.2	2	12.31	0	7.19E+05		(R)YLCGLG	(R)Y L/C/G/L/G A V G/G V R(L)	C:Carbamidomethylation	137.47	611.3189	1221.641	-0.0103	-8.5	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
6198	dirMS_041712_NAR_30mM_plus2.16978.17238.2	2	12.31	0	1.37E+06		(K)NLYIISV	(K)N L|Y|I/I/S V/K(G)		143.5	475.2893	949.572	-0.0004	-0.4	8.59	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
6199	dirMS_041712_NAR_40mM_plus2.10839.10839.3	3	12.31	0	2.22E+05		(R)LLEAQA	(R)L L|E/A Q A/C T/G G I/I H P T T G Q K(L)	C:Carbamidomethylation	128.95	665.6807	1995.033	-0.0052	-2.6	6.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
6200	dirMS_041712_NAR_50mM_plus2.12542.12542.3	3	12.31	1	3.06E+05		(R)SGVGLS	(R)S\G/V/G L/S S Y/L S T E K D A S\P/K(T)		133.63	609.3102	1825.918	-0.0018	-1	5.79	64248.4	9.08	HUMAN	Q9BW04	Specifically androgen-regulated gene protein
6201	dirMS_041712_NAR_50mM_plus2.18840.18840.3	3	12.31	0	4.20E+05		(R)AGLGSG	(R)A G/L/G/S/G/L/S L/S/G L V/H P/E\L S R(S)		167.15	617.3412	1850.013	-0.004	-2.2	6.79	73325.2	9.19	HUMAN	F5H2A9	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial
6202	dirMS_041712_NAR_60mM_plus.10079.10079.2	2	12.31	0	2.03E+06		(K)GIVEFSG	(K)G I/V|E|F/S G K/P A A R(K)		111.3	616.3425	1231.679	-0.0016	-1.3	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
6203	dirMS_041712_NAR_60mM_plus.15212.15212.3	3	12.31	1	3.82E+05		(K)SLEELRL	(K)S L|E/E L\R\L E D/Y Q/A N R(K)		135.75	579.2911	1735.861	-0.0022	-1.3	4.41	178367.2	6.03	HUMAN	J3KP29	Nuclear pore complex protein Nup98-Nup96
6204	dirMS_041712_NAR_60mM_plus.16757.16757.3	3	12.31	0	1.09E+06		(K)TTISVAH	(K)T T/I/S V A/H/L L A A/R(Q)		144.38	418.2478	1252.737	-0.0083	-6.7	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
6205	dirMS_041712_NAR_60mM_plus.20123.20123.3	3	12.31	0	2.36E+05		(K)ALSAIAD	(K)A L|S|A/I/A D L L/T/N E H E R(V)		165.23	551.6246	1652.86	-0.001	-0.6	4.65	105417.2	6.41	HUMAN	C9JZR2	Catenin delta-1
6206	dirMS_041712_NAR_40mM_minus2.9027.9064.3	3	12.3	1	9.47E+04		(K)LAEIGA	(K)L/A|E|I|G A|P I Q G N R E E L V E R(L)		136.07	665.3586	1994.066	-0.0053	-2.6	4.49	38572.2	6.31	HUMAN	E9PJ04	Splicing factor 3B subunit 2 (Fragment)
6207	dirMS_041712_NAR_50mM_minus2.11951.11951.3	3	12.3	1	3.61E+05		(K)AVLFCLS	(K)A V/L/F C\L/S E D K K(N)	C:Carbamidomethylation	136.03	437.2326	1309.682	0.0012	0.9	6.11	22956	8.8	HUMAN	E9PK25	Cofilin-1
6208	dirMS_041712_NAR_50mM_minus2.9429.9429.3	3	12.3	0	1.82E+05		(R)LQAQQ	(R)L Q|A Q/Q D A|V N/I/V C H S K(T)	C:Carbamidomethylation	121.82	570.9573	1710.859	-0.0018	-1.1	6.74	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)

6209	dirMS_041712_NAR_60mM_minus.14825.14825.3	3	12.3	0	3.63E+05		(R)AVAIDLF	(R)A V|A I/D L/P/G L G H/S K(E)		142.55	426.578	1277.721	-0.0018	-1.4	6.79	19983.6	8.14	HUMAN	B4DQI4	Alpha/beta hydrolase domain-containing protein 14B
6210	dirMS_041712_NAR_60mM_minus.18893.18894.3	3	12.3	1	3.85E+06		(R)LDLAGR	(R)L/D|L/A/G R D L/T D Y L/M/K(I)		167.88	541.9507	1623.841	-0.0035	-2.2	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
6211	dirMS_041712_NAR_20mM_plus.17512.17512.2	2	12.3	0	5.69E+04		(K)LAAVDA	(K)L A\A\V/D A/T/V\N Q V/L/A S R(Y)		192.35	764.4257	1527.849	-0.0048	-3.1	5.84	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
6212	dirMS_041712_NAR_30mM_plus2.18252.18252.2	2	12.3	0	5.29E+05		(R)GYISPYF	(R)G Y|I/S/P/Y F I|N T S K(G)		149.7	695.3554	1389.705	-0.0014	-1	8.5	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
6213	dirMS_041712_NAR_30mM_plus2.7441.7465.2	2	12.3	0	2.14E+05		(R)EYENEL	(R)E Y/E/N/E/L/A/K(V)		93.48	498.2399	995.468	0.0045	4.5	4.25	334221.3	6.44	HUMAN	P15924	Desmoplakin
6214	dirMS_041712_NAR_50mM_plus2.12138.12260.3	3	12.3	1	1.20E+06		(K)ASLENSI	(K)A/S|L/E/N S\L R E V E/A/R(Y)		132.27	491.9313	1473.766	0.0138	9.3	4.79	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
6215	dirMS_041712_NAR_50mM_plus2.19045.19045.3	3	12.3	0	8.17E+05		(R)CRPDQL	(R)C R P D Q\L T|G L|S|L/L/P L S E K(A)	C:Carbamidomethylation	167.72	643.0148	1927.032	-0.0019	-1	6.07	533778	5.74	HUMAN	Q15149	Plectin
6216	dirMS_041712_NAR_30mM_minus2.11869.12046.2	2	12.29	0	1.63E+05		(R)LSEDYG	(R)L/S|E/D/Y/G V L K(T)		118.88	512.2719	1023.536	0.0008	0.8	4.37	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
6217	dirMS_041712_NAR_30mM_minus2.13321.13321.2	2	12.29	0	9.82E+05		(K)DVNAAI	(K)D\V|N A/A/I/A T/I K(T)		126.43	508.2928	1015.578	0.0001	0.1	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
6218	dirMS_041712_NAR_30mM_minus2.18303.18303.2	2	12.29	0	4.10E+05		(R)QAQEYE	(R)Q/A/Q|E Y/E A L\L\N/I/K(V)		154.6	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
6219	dirMS_041712_NAR_50mM_minus2.12110.12110.3	3	12.29	0	9.09E+03		(K)AASAGV	(K)A A/S/A/G V/P Y/H G E/V/P V S L A R(A)		135.98	594.315	1780.934	-0.0036	-2	6.79	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
6220	dirMS_041712_NAR_60mM_minus.4727.4727.3	3	12.29	1	1.35E+06		(R)AAEEED	(R)A A|E/E E/D/E A D|P K/R(Q)		78.07	453.872	1359.602	-0.0008	-0.6	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
6221	dirMS_041712_NAR_60mM_minus.9431.9446.3	3	12.29	1	2.46E+05		(R)QERYEIE	(R)Q E R Y\E\I|E|E|T/E/T V T K(S)		112.57	585.6185	1754.844	-0.0034	-1.9	4.32	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
6222	dirMS_041712_NAR_60mM_minus.9832.9832.3	3	12.29	0	4.34E+05		(K)LQVEEVI	(K)L/Q/V E/E V/H/Q L S R(-)		114.55	446.5761	1337.717	-0.0034	-2.6	5.4	14571.2	5.15	HUMAN	F5GX50	Diablo homolog, mitochondrial (Fragment)
6223	dirMS_041712_NAR_120mM_plus.8207.8207.2	2	12.29	0	4.30E+05		(R)DHFEEA	(R)D H|F|E/E A|M R(F)		96.32	517.7288	1034.436	0.0143	13.8	4.65	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
6224	dirMS_041712_NAR_20mM_plus.14485.14485.2	2	12.29	0	1.36E+05		(R)FIDTTLA	(R)F/I|D\T T L/A I T/S R(F)		171.58	619.3413	1237.679	-0.0034	-2.7	5.84	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
6225	dirMS_041712_NAR_20mM_plus.16854.16854.2	2	12.29	0	3.34E+05		(K)VQIAVA	(K)V Q|I|A V/A\N A/Q E L L/Q|R(M)		187.42	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
6226	dirMS_041712_NAR_20mM_plus.17543.17543.2	2	12.29	0	1.44E+04	M199m	(K)SmVPVC	(K)S m|V|P V Q/V Q L D V|P V/V K(V)	m:Oxidized methionine	192.52	827.4624	1637.93	15.988	-4.2	5.55	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
6227	dirMS_041712_NAR_20mM_plus.9193.9193.2	2	12.29	0	4.54E+04		(R)IIYGGSV	(R)I I|Y/G/G/S V/T/G A/T C K(E)	C:Carbamidomethylation	135.4	663.8412	1326.672	0.0029	2.2	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
6228	dirMS_041712_NAR_20mM_plus.9931.9931.2	2	12.29	0	2.43E+05		(K)VASGCLI	(K)V A/S|G C/L D I N S/S V/K(G)	C:Carbamidomethylation	139.72	675.3376	1349.673	-0.005	-3.7	5.81	56837	7.19	HUMAN	E7ETT1	Propionyl-CoA carboxylase beta chain, mitochondrial
6229	dirMS_041712_NAR_30mM_plus2.13723.13724.2	2	12.29	0	1.97E+05		(K)VANVEL	(K)V/A|N|V/E/L/Y Y/R(A)		124.78	563.7923	1126.589	-0.0118	-10.5	5.97	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
6230	dirMS_041712_NAR_40mM_plus2.12480.12480.3	3	12.29	1	3.43E+04	M357m	(R)ALAEIAK	(R)A L|A/E|I|A K A E/L D/D/T/P m R(G)	m:Oxidized methionine	139.65	587.3006	1743.895	15.9927	-1.3	4.32	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
6231	dirMS_041712_NAR_50mM_plus2.14920.15222.3	3	12.29	1	9.38E+05		(K)TVGVEP	(K)T V|G|V/E/P A A D G K G V V V V I/K(R)		147.45	580.0056	1738.011	-0.0087	-5	5.73	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
6232	dirMS_041712_NAR_50mM_plus2.18402.18403.3	3	12.29	1	5.45E+05		(K)VIAATN	(K)V/I|A|A/T N R V|D I L/D/P A L L R(S)		164.5	617.3645	1850.086	-0.0069	-3.7	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
6233	dirMS_041712_NAR_50mM_plus2.19348.19348.3	3	12.29	1	4.32E+05		(R)LKVPPAI	(R)L K\V|P/P A I|N|Q/F/T Q/A L D R(Q)		169.82	604.3351	1811.017	-0.0266	-14.7	8.75	30166.2	10.79	HUMAN	P62424	60S ribosomal protein L7a
6234	dirMS_041712_NAR_50mM_plus2.9034.9370.3	3	12.29	1	1.17E+06		(K)TAVCDI	(K)T/A|V|C D I/P/P R G L K(M)	C:Carbamidomethylation	116.33	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
6235	dirMS_041712_NAR_20mM_minus.12196.12196.2	2	12.28	0	1.08E+06	M313m	(R)TVQSLEI	(R)T V/Q/S\L|E/I\D/L/D\S m R(N)	m:Oxidized methionine	170.82	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
6236	dirMS_041712_NAR_40mM_minus2.8282.8282.3	3	12.28	1	4.74E+04		(K)VAVVAG	(K)V A V/V/A/G Y G D V/G\K G/C A Q A L R(G)	C:Carbamidomethylation	129.07	630.9989	1890.985	-0.0033	-1.7	8.56	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
6237	dirMS_041712_NAR_50mM_minus2.10204.10204.3	3	12.28	0	1.60E+05	M392m	(K)EmNPAL	(K)E m\N/P A/L|G I|D C L H K(G)	C:Carbamidomethylation m:Oxid	125.95	505.2416	1497.719	15.9914	-2.3	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
6238	dirMS_041712_NAR_60mM_minus.15223.15223.2	2	12.28	0	4.20E+05		(R)EHALLA	(R)E/H|A|L|L/A Y T L G V K(Q)		144.65	657.873	1314.742	-0.0029	-2.2	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
6239	dirMS_041712_NAR_60mM_minus.7580.7580.3	3	12.28	1	1.06E+05	M195m	(R)GSNmDI	(R)G S/N/m/D/F R E/P T E/E E R(A)	m:Oxidized methionine	102.05	571.578	1696.723	15.9963	0.8	4.25	27441.6	6.68	HUMAN	Q15056	Eukaryotic translation initiation factor 4H
6240	dirMS_041712_NAR_20mM_plus.13168.13168.2	2	12.28	0	6.52E+04		(R)IGGGID	(R)I/G G\G/I/D V\P V P R(H)		163.1	540.3131	1079.621	-0.0018	-1.7	5.84	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
6241	dirMS_041712_NAR_20mM_plus.7354.7488.2	2	12.28	0	2.44E+05		(R)TVGIVGI	(R)T V|G|I|V/G N Q/P K(V)		119.85	506.7922	1012.579	-0.0014	-1.4	8.41	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
6242	dirMS_041712_NAR_30mM_plus2.11700.11700.2	2	12.28	0	1.28E+06		(R)GGGGNI	(R)G G G G|N F/G/P G/P G S N F R(G)		114.4	689.3175	1377.629	-0.0017	-1.2	9.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
6243	dirMS_041712_NAR_30mM_plus2.14940.14999.2	2	12.28	0	6.25E+05		(R)SLLLSVN	(R)S L|L|L|S/V N\A/R(G)		132	486.7894	972.584	-0.0121	-12.5	9.47	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
6244	dirMS_041712_NAR_30mM_plus2.21844.21844.3	3	12.28	0	3.70E+05		(R)NSILAQ	(R)N S\I\L A\Q/V|L/D Q S A R(A)		170.02	472.2638	1414.765	0.012	8.5	5.84	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
6245	dirMS_041712_NAR_50mM_plus2.11398.11398.3	3	12.28	0	4.19E+05		(K)GFVEFA	(K)G F|V/E F/A A K/P/P A/R(K)		127.83	430.5716	1289.7	0.0002	0.1	8.75	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
6246	dirMS_041712_NAR_50mM_plus2.15309.15309.3	3	12.28	1	5.10E+05		(K)TKDGQII	(K)T K D G Q I|L|P V/P N/V V V R(D)		148.65	545.6573	1634.959	-0.0015	-0.9	8.41	56825.2	9.49	HUMAN	Q9P258	Protein RCC2
6247	dirMS_041712_NAR_50mM_plus2.16156.16156.3	3	12.28	1	4.90E+04		(R)EGIVTAT	(R)E G I|V/T/A T E Q E V K E D I A K(L)		152.25	620.658	1859.96	-0.0002	-0.1	4.25	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
6248	dirMS_041712_NAR_50mM_plus2.17878.17878.3	3	12.28	0	2.57E+05		(K)YAPLHL	(K)Y A/P L H/L\V|P/L I E R(L)		162.08	474.2819	1420.831	0.0001	0	6.75	147553.6	6.73	HUMAN	E7EVF4	Cytoplasmic FMR1-interacting protein 2
6249	dirMS_041712_NAR_60mM_plus.18643.18643.3	3	12.28	1	2.32E+05		(R)RGDINLI	(R)R G D I N L\L M|L/G D/P G T A K(S)		154.67	557.6331	1670.889	-0.0047	-2.8	5.96	78390.7	9.27	HUMAN	B1AHB1	DNA replication licensing factor MCM5
6250	dirMS_041712_NAR_60mM_plus.6487.6489.3	3	12.28	1	2.39E+05		(R)LTQEPES	(R)L/T/Q E/P E/S I R K(W)		92.45	400.8875	1200.658	-0.0103	-8.6	6.14	8409.9	4.52	HUMAN	H0Y9Q6	Clathrin light chain B (Fragment)
6251	dirMS_041712_NAR_20mM_minus.9752.9752.2	2	12.27	0	1.57E+05		(K)LSELEPG	(K)L/S E|L/E/P G T G D L R(F)		147.78	643.8318	1286.659	-0.0023	-1.8	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
6252	dirMS_041712_NAR_30mM_minus2.7991.7991.2	2	12.27	0	1.67E+05		(K)SLAAEEE	(K)S/L|A|A E E E/A A R(Q)		96.75	523.7597	1046.511	0.0008	0.8	4.25	533778	5.74	HUMAN	Q15149	Plectin
6253	dirMS_041712_NAR_60mM_minus.8461.8461.3	3	12.27	0	1.10E+05		(K)VDNDEN	(K)V/D|N/D E/N E H Q L S L R(T)		107.02	523.5817	1568.73	0.0006	0.4	4.31	6862.5	4.32	HUMAN	E5RGW4	Nucleophosmin (Fragment)
6254	dirMS_041712_NAR_120mM_plus.10036.10036.4	4	12.27	2	1.97E+06		(K)MQASIE	(K)M Q|A S I E K/G G S L/P K V/E/A K(F)		105.72	443.9944	1772.958	-0.0017	-1	8.25	32745.6	4.64	HUMAN	P06748	Nucleophosmin
6255	dirMS_041712_NAR_120mM_plus.10508.10508.3	3	12.27	1	3.83E+05		(K)KGENYV	(K)K\G E N Y\V|Y/I/N/E A T/R(H)		108.4	519.5943	1556.77	-0.002	-1.3	6.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
6256	dirMS_041712_NAR_120mM_plus.12488.12714.2	2	12.27	0	7.62E+05		(K)HLSVND	(K)H/L|S|V|N D|L/P V G R(S)		119.22	603.8321	1206.659	-0.002	-1.7	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
6257	dirMS_041712_NAR_20mM_plus.17151.17151.2	2	12.27	0	8.69E+04		(K)VLDIIATI	(K)V L|D/I/I A/T I N K(G)		189.92	550.3381	1099.672	-0.0032	-2.9	5.81	19639	5.52	HUMAN	H0YA83	Beta-hexosaminidase subunit beta (Fragment)
6258	dirMS_041712_NAR_30mM_plus2.10932.10932.2	2	12.27	0	3.75E+05		(K)YSGTLNI	(K)Y/S/G T/L N L/D R(V)		110.9	519.7636	1038.521	-0.0015	-1.5	5.83	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
6259	dirMS_041712_NAR_30mM_plus2.13702.13702.2	2	12.27	0	9.93E+04		(K)LNCNPE	(K)L N|C|N/P E L/F R(C)	C:Carbamidomethylation	124.87	581.7885	1162.567	0.0024	2	6	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
6260	dirMS_041712_NAR_30mM_plus2.15756.15756.2	2	12.27	0	3.67E+05		(K)ELIPTEE	(K)E L|I/P T/E/E A L R(L)		135.82	585.8217	1170.637	-0.0004	-0.3	4.25	533778	5.74	HUMAN	Q15149	Plectin
6261	dirMS_041712_NAR_30mM_plus2.18828.19275.3	3	12.27	0	3.71E+06		(R)QAQEYE	(R)Q A Q\E\Y|E|A|L/L/N I K(V)		153.43	473.9205	1419.748	-0.0009	-0.6	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
6262	dirMS_041712_NAR_40mM_plus2.11988.12024.3	3	12.27	1	2.31E+05		(R)VVDALG	(R)V/V/D/A L/G N A I/D/G K G P I G S/K(T)		137.1	570.9838	1710.939	-0.0016	-1	5.93	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
6263	dirMS_041712_NAR_50mM_plus2.11734.12110.3	3	12.27	0	4.59E+06		(R)NLDIERF	(R)N/L|D|I/E R/P T Y/T N L N R(L)		131.23	573.6314	1718.882	-0.0024	-1.4	6.07	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
6264	dirMS_041712_NAR_50mM_plus2.19259.19259.3	3	12.27	0	8.39E+05		(R)DFNHIN	(R)D F N/H I\N\V|E|L/S L/L G K(K)		170.08	533.6223	1598.854	-0.0013	-0.8	5.32	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
6265	dirMS_041712_NAR_50mM_plus2.20570.20570.3	3	12.27	1	2.60E+05		(R)GGPNIIT	(R)G G/P\N\I|I/T L A D I V K D/P V S R(T)		176.9	622.3526	1865.049	-0.0058	-3.1	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
6266	dirMS_041712_NAR_50mM_plus2.9999.10100.3	3	12.27	1	5.74E+05	M322m	(K)TGQPmI	(K)T/G\Q|P/m/I N/L Y T D R E\T G K(L)	m:Oxidized methionine	120.18	613.9672	1823.896	15.9914	-1.9	5.73	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
6267	dirMS_041712_NAR_60mM_plus.12360.12360.3	3	12.27	1	4.80E+05		(R)TSDVGG	(R)T/S|D|V/G G Y Y/Y E K I|E R(T)		121.22	560.6017	1679.791	-0.0006	-0.4	4.68	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
6268	dirMS_041712_NAR_60mM_plus.15208.15452.3	3	12.27	1	1.61E+06		(K)NREPVQ	(K)N R E\P\V\Q|L|E/T/L/S I/R(G)		137.18	518.9516	1554.86	-0.0196	-12.6	6.14	8392.6	11.84	HUMAN	J3QLI9	Small nuclear ribonucleoprotein Sm D1
6269	dirMS_041712_NAR_30mM_minus2.10057.10198.2	2	12.26	0	1.92E+06		(R)VPVDVA	(R)V/P|V/D/V/A Y R(R)		109.4	459.7564	918.504	0.0012	1.3	5.8	266161	5.68	HUMAN	E9PPU0	Epiplakin
6270	dirMS_041712_NAR_30mM_minus2.11205.11474.2	2	12.26	0	3.18E+06		(K)SCNCLLL	(K)S/C|N/C L/L|L/K(V)	C:Carbamidomethylation	115.4	504.2543	1007.501	0.0001	0.1	8.47	47510.4	7.04	HUMAN	P06733	Alpha-enolase
6271	dirMS_041712_NAR_50mM_minus2.17139.17139.3	3	12.26	1	3.18E+05		(K)AILILDNI	(K)A I|L|I/L D N\D/G D R L F A K(Y)		165.27	558.6442	1673.922	-0.004	-2.4	4.43	18430.9	4.79	HUMAN	F8VS17	Coatomer subunit zeta-1
6272	dirMS_041712_NAR_120mM_plus.18483.18505.4	4	12.26	1	1.57E+06		(K)FQIPPN	(K)F Q\I/P/P/N|A E L/K/Y E L H/L K(S)		150.05	485.7703	1940.064	-0.0046	-2.4	6.75	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
6273	dirMS_041712_NAR_30mM_plus2.12106.12106.2	2	12.26	0	2.80E+05		(R)LAVYIDF	(R)L/A|V|Y I D|R(V)		116.78	425.239	849.483	-0.0122	-14.3	5.83	74423.5	6.57	HUMAN	P02545	Prelamin-A/C
6274	dirMS_041712_NAR_30mM_plus2.13828.13828.2	2	12.26	0	1.34E+05		(R)TIAQDY	(R)T/I|A/Q/D Y G V L/K(A)		126.35	554.3087	1107.604	0.0057	5.1	5.5	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
6275	dirMS_041712_NAR_30mM_plus2.22537.22537.2	2	12.26	0	6.10E+04		(R)LEGLTD	(R)L E G\L|T/D/E\I|N\F L/R(Q)		174.63	710.3766	1419.748	-0.0019	-1.3	4.14	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
6276	dirMS_041712_NAR_40mM_plus2.11117.11117.2	2	12.26	0	5.49E+04		(R)DVQEIFF	(R)D V/Q/E/I F R(L)		131.53	453.7354	906.468	-0.0044	-4.9	4.37	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
6277	dirMS_041712_NAR_40mM_plus2.14921.14921.3	3	12.26	0	8.33E+04		(R)LLIHQSL	(R)L L/I/H Q S L/A/G/G I/I G V/K(G)		154.33	506.9819	1518.937	-0.0055	-3.6	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
6278	dirMS_041712_NAR_40mM_plus2.6111.6111.2	2	12.26	0	5.66E+04		(R)QAFPNT	(R)Q A/F/P/N T N R(W)		94.88	474.2383	947.469	0	0	9.75	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
6279	dirMS_041712_NAR_50mM_plus2.12944.13222.3	3	12.26	1	1.56E+06	M356m	(K)VGEVIV	(K)V/G|E|V|I|V/T K D D/A m L L K(G)	m:Oxidized methionine	137.15	549.6381	1630.908	15.9913	-2.2	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
6280	dirMS_041712_NAR_50mM_plus2.17767.17768.3	3	12.26	1	7.54E+05		(K)FGEVVD	(K)F/G|E|V/V/D C T L K L D/P I T G R(S)	C:Carbamidomethylation	161.67	640.6666	1919.989	-0.0043	-2.2	4.56	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
6281	dirMS_041712_NAR_60mM_plus.12166.12166.3	3	12.26	1	1.01E+06	M232m	(R)MSmKE	(R)M S\m K E V D E Q\M|L\N/V/Q/N K(N)	m:Oxidized methionine	120.57	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
6282	dirMS_041712_NAR_30mM_minus2.11102.11102.2	2	12.25	0	6.41E+05		(K)VAGQD	(K)V/A|G Q|D/G S V/V Q/F K(I)		113.98	617.824	1234.643	-0.0019	-1.5	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
6283	dirMS_041712_NAR_30mM_minus2.16267.16287.2	2	12.25	0	2.50E+05		(R)LLGWIQ	(R)L/L|G\W/I/Q N/K(L)		142.25	486.2861	971.567	-0.0024	-2.4	8.75	67046.8	9.38	HUMAN	F8WE98	Filamin-A (Fragment)
6284	dirMS_041712_NAR_30mM_minus2.20022.20028.2	2	12.25	0	2.44E+04		(K)SLNILTA	(K)S L|N|I|L/T/A F Q K(K)		168.82	567.8283	1134.652	-0.0024	-2.1	8.47	18172.6	7.77	HUMAN	F8VY02	Endoplasmic reticulum resident protein 29
6285	dirMS_041712_NAR_40mM_minus2.11388.11388.3	3	12.25	0	1.98E+05		(K)LVTSIGD	(K)L V|T/S I/G/D V V N/H D P V V G D R(L)		150.33	631.3335	1891.987	-0.0013	-0.7	4.41	27786.2	5.93	HUMAN	H0Y4Z6	Phosphorylase (Fragment)
6286	dirMS_041712_NAR_40mM_minus2.11777.11921.3	3	12.25	1	5.04E+05		(K)VALNVS	(K)V A\L/N|V|S/C A N L/L D K D/I G S K(S)	C:Carbamidomethylation	153.28	639.6749	1917.011	-0.0008	-0.4	5.93	9239.5	7.98	HUMAN	E5RFT7	Copine-3 (Fragment)
6287	dirMS_041712_NAR_50mM_minus2.12213.12251.3	3	12.25	1	1.52E+05	M331m	(R)YGSDIVI	(R)Y G|S|D|I|V/P F/S K V D E E Q m K(Y)	m:Oxidized methionine	137.82	663.3194	1971.937	16.0068	6	4.32	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
6288	dirMS_041712_NAR_60mM_minus.13609.13628.3	3	12.25	0	3.60E+05		(K)ILQGGV	(K)I L|Q/G G\V/G/I/P H I R(S)		136.02	420.5931	1259.758	0.0065	5.1	9.75	9772.1	9.6	HUMAN	D6RGE5	Casein kinase I isoform alpha
6289	dirMS_041712_NAR_120mM_plus.5486.5486.3	3	12.25	1	4.01E+05		(K)CDSSPD	(K)C D|S/S|P|D S A E/D/V R K(V)	C:Carbamidomethylation	81.9	489.2122	1465.622	-0.0003	-0.2	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
6290	dirMS_041712_NAR_20mM_plus.17130.17472.2	2	12.25	0	1.44E+06		(R)VLITTDL	(R)V L|I/T/T/D L/L/A R(G)		191	557.8442	1114.683	-0.0019	-1.7	5.81	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
6291	dirMS_041712_NAR_20mM_plus.17676.17676.2	2	12.25	0	3.53E+03		(R)FLGTEVI	(R)F L|G/T/E V L L/R(L)		193.65	524.3108	1047.62	-0.0054	-5.1	6	103045.5	7.1	HUMAN	B9ZVT1	RNA-binding protein 12B
6292	dirMS_041712_NAR_20mM_plus.17714.17714.2	2	12.25	0	1.56E+05		(R)SLVPAAI	(R)S L|V|P A|A/E L L E S R(V)		194.3	642.8613	1284.716	-0.0005	-0.4	4.53	533778	5.74	HUMAN	Q15149	Plectin
6293	dirMS_041712_NAR_30mM_plus2.10241.10241.2	2	12.25	0	3.19E+05		(K)LVIEEAE	(K)L V|I/E/E/A/E R(S)		106.78	479.7648	958.52	0.0019	2	4.25	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
6294	dirMS_041712_NAR_40mM_plus2.14959.15019.3	3	12.25	1	1.82E+05		(R)EGIVTAT	(R)E G\I|V|T/A/T/E/Q E V K E D I A K(L)		155.1	620.6583	1859.96	0.0007	0.4	4.25	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
6295	dirMS_041712_NAR_50mM_plus2.20094.20094.3	3	12.25	0	2.96E+05		(R)DYLHLPI	(R)D Y L H L\P P E\I|V/P A T L R(R)		173.92	578.658	1733.959	0.001	0.6	5.32	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
6296	dirMS_041712_NAR_50mM_plus2.9885.9886.3	3	12.25	0	9.98E+04		(K)GIVEFAS	(K)G I|V/E/F/A/S K P A A R(K)		119.48	415.9028	1245.695	-0.0012	-0.9	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
6297	dirMS_041712_NAR_60mM_plus.17656.17656.3	3	12.25	1	4.51E+05		(R)LMDLLG	(R)L/M|D/L/L/G E\G L K R(S)		149.2	415.5712	1244.703	-0.0041	-3.3	6.07	52817.9	6.2	HUMAN	F5H3T8	Arginine--tRNA ligase, cytoplasmic
6298	dirMS_041712_NAR_30mM_minus2.10753.10856.2	2	12.24	0	3.05E+05		(R)FVTLSAT	(R)F V|T|L/S A T/N A K(T)		112.58	526.2919	1051.578	-0.0017	-1.6	8.75	72873.4	5.73	HUMAN	Q96S55	ATPase WRNIP1
6299	dirMS_041712_NAR_30mM_minus2.11027.11027.2	2	12.24	0	5.27E+05		(R)FASGGC	(R)F A|S G|G C D N L|I K(L)	C:Carbamidomethylation	113.53	591.2858	1181.562	0.0024	2	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
6300	dirMS_041712_NAR_30mM_minus2.12539.12539.2	2	12.24	0	5.07E+05		(R)GQVVSL	(R)G Q|V|V/S/L I/R(M)		122.25	436.2706	871.536	-0.0021	-2.4	9.75	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
6301	dirMS_041712_NAR_30mM_minus2.13873.13896.2	2	12.24	0	3.52E+05		(R)LAGLFNI	(R)L/A|G\L/F/N E/Q/R(K)		129.13	524.2789	1047.558	-0.0076	-7.3	6	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
6302	dirMS_041712_NAR_50mM_minus2.13276.13276.3	3	12.24	0	4.26E+05		(R)EQTLSPT	(R)E Q/T/L/S/P T/I/T S G L/H N\I A R(S)		143.47	613.3274	1837.977	-0.009	-4.9	6.85	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
6303	dirMS_041712_NAR_60mM_minus.10874.10874.3	3	12.24	1	2.16E+05		(K)VTVAGL	(K)V/T|V/A/G L A/G K/D/P V Q C S R(D)	C:Carbamidomethylation	121	553.2923	1657.869	-0.0067	-4	8.72	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
6304	dirMS_041712_NAR_120mM_plus.7038.7038.3	3	12.24	1	1.35E+05		(R)NKQTYS	(R)N K Q T\Y/S/T E/P N/N L K(A)		90.25	512.9261	1536.765	-0.0015	-1	8.5	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
6305	dirMS_041712_NAR_20mM_plus.10780.10780.2	2	12.24	0	1.18E+05		(R)AGTGVD	(R)A G T G V|D\N\V|D/L E/A A/T\R(K)		146.88	744.8731	1488.729	0.01	6.7	4.03	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
6306	dirMS_041712_NAR_30mM_plus2.21190.21190.2	2	12.24	0	2.85E+05		(R)FDAMPF	(R)F D|A\M/P F T L R(A)		166.32	549.276	1097.545	-0.0001	-0.1	5.84	42088	5.39	HUMAN	F8VTY8	Proliferation-associated protein 2G4
6307	dirMS_041712_NAR_30mM_plus2.21521.21548.2	2	12.24	0	2.79E+05		(R)EADDIVI	(R)E A|D/D/I/V/N W/L/K(K)		167.58	601.81	1202.605	0.0075	6.3	4.03	26363.4	4.91	HUMAN	I3L312	Protein disulfide-isomerase (Fragment)
6308	dirMS_041712_NAR_50mM_plus2.21012.21012.3	3	12.24	0	4.33E+06		(R)AGKPVI	(R)A G K P V I\C A|T\Q|M/L/E S M I K(K)	C:Carbamidomethylation	179.7	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
6309	dirMS_041712_NAR_60mM_plus.15097.15117.3	3	12.24	0	5.71E+05		(K)LSMKPE	(K)L S|M/K/P E/P L F R(S)		135.85	406.5616	1217.671	-0.0008	-0.7	8.75	75482.2	6.34	HUMAN	D6RA32	Microtubule-associated protein 1B (Fragment)
6310	dirMS_041712_NAR_60mM_plus.17875.17875.3	3	12.24	0	2.66E+05		(R)LLIHQSL	(R)L L/I/H Q S\L/A|G G I I G V K(G)		150.48	506.9815	1518.937	-0.0067	-4.4	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
6311	dirMS_041712_NAR_120mM_minus.13275.13275.4	4	12.23	1	7.94E+05		(K)SVHSSVI	(K)S V H S S V|P/L L N S K D/P I D/R(I)		127	466.7525	1863.992	-0.0041	-2.2	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
6312	dirMS_041712_NAR_120mM_minus.18401.18401.3	3	12.23	0	1.60E+05		(R)FHQLDI	(R)F H Q\L\D\I/D D|L/Q/S I R(A)		155.3	533.9425	1599.813	0.0004	0.3	4.41	24897.7	9.84	HUMAN	A8MTM1	Carbonyl reductase [NADPH] 1
6313	dirMS_041712_NAR_20mM_minus.10073.10073.2	2	12.23	0	1.24E+05		(R)YALYDA	(R)Y/A|L/Y/D A T Y E T K(E)		150.82	669.3156	1337.626	-0.0021	-1.5	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
6314	dirMS_041712_NAR_30mM_minus2.15320.15320.2	2	12.23	0	5.64E+05	M2249m	(K)MSIYQA	(K)M/S/I/Y/Q/A m W K(G)	m:Oxidized methionine	135.95	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
6315	dirMS_041712_NAR_30mM_minus2.17800.18110.2	2	12.23	0	5.59E+05		(K)VFLENVI	(K)V/F|L/E/N/V I/R(D)		152	495.2924	989.578	-0.0003	-0.3	5.97	11367.1	11.36	HUMAN	P62805	Histone H4
6316	dirMS_041712_NAR_50mM_minus2.17481.17481.3	3	12.23	1	3.07E+05		(K)GYPPED	(K)G Y/P/P/E/D/I F N\L V/G K K(V)		167.35	526.2832	1576.837	-0.0019	-1.2	6.07	40763.2	6.29	HUMAN	Q9NR45	Sialic acid synthase
6317	dirMS_041712_NAR_50mM_minus2.9635.9635.3	3	12.23	1	2.92E+05		(R)ALEEAM	(R)A L/E|E/A/M E Q K/A E L E R(L)		122.23	549.6072	1646.805	0.0016	1	4.33	227783.5	5.5	HUMAN	P35579	Myosin-9

6318	dirMS_041712_NAR_60mM_minus.12047.12047.3	3	12.23	1	5.65E+05		(R)ISVYYNE	(R)I/S/V/Y/Y N E/A/T G G K Y V/P R(A)		127.47	606.3103	1816.923	-0.0065	-3.6	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
6319	dirMS_041712_NAR_60mM_minus.18420.18420.3	3	12.23	1	1.29E+05		(R)RFDEILE	(R)R F D E I\L\E|A|S/D/G|I/M V A R(G)		164.42	607.9739	1821.916	-0.0092	-5.1	4.32	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
6320	dirMS_041712_NAR_120mM_plus.10659.10659.3	3	12.23	1	7.19E+05		(R)FYKNEG	(R)F/Y|K N E G\G T/W S V E/K(V)		109.07	515.5841	1544.738	-0.0002	-0.2	6.14	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
6321	dirMS_041712_NAR_120mM_plus.20636.21103.4	4	12.23	2	1.12E+07		(R)TLAEIAK	(R)T/L\A\E/I/A/K V E L D/N M/P L R G K(Q)		163.07	500.2814	1998.105	-0.0015	-0.7	5.85	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
6322	dirMS_041712_NAR_20mM_plus.14927.14927.2	2	12.23	0	1.23E+05		(R)ILNVPQ	(R)I/L/N|V/P/Q/E L/Y E K(G)		174.48	673.3693	1345.736	-0.0049	-3.6	4.53	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
6323	dirMS_041712_NAR_20mM_plus.18682.18682.3	3	12.23	0	1.88E+04		(R)APVPAS	(R)A P V P A S E\L\L/A/S/G V L/S R(A)		199.92	522.9655	1566.885	-0.003	-1.9	6.05	533778	5.74	HUMAN	Q15149	Plectin
6324	dirMS_041712_NAR_20mM_plus.7401.7401.2	2	12.23	0	2.86E+05		(K)TGQAP	(K)T G Q|A|P G/Y S Y T A A N K(N)		119.52	714.8394	1428.675	-0.0039	-2.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
6325	dirMS_041712_NAR_30mM_plus2.18176.18176.2	2	12.23	0	2.06E+05		(R)QITLND	(R)Q I/T\L|N/D\L/P V/G R(S)		147.97	613.3465	1225.69	-0.0042	-3.4	5.84	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
6326	dirMS_041712_NAR_30mM_plus2.23524.23524.2	2	12.23	0	1.80E+05		(R)IAIYELLF	(R)I/A|I/Y E L L/F K(E)		190.25	555.3331	1109.661	-0.0016	-1.4	6	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
6327	dirMS_041712_NAR_30mM_plus2.9391.9391.2	2	12.23	0	6.90E+05		(K)SVEAAA	(K)S V|E/A|A/A/E L S/A K(D)		103.03	538.2855	1075.563	0.0007	0.7	4.53	12131.5	11.14	HUMAN	F5GXR3	Parathymosin
6328	dirMS_041712_NAR_40mM_plus2.16562.16562.3	3	12.23	1	2.47E+05		(R)VTFSGL	(R)V/T|F S G L R D T V T/P G E L L K(A)		163.87	611.6744	1833.012	-0.003	-1.6	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
6329	dirMS_041712_NAR_40mM_plus2.5533.5533.2	2	12.23	0	2.45E+05	M299m	(K)NmMAA	(K)N m|M A|A/C/D|P R(H)	C:Carbamidomethylation m:Oxid	89.2	541.2145	1065.427	15.9943	-0.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
6330	dirMS_041712_NAR_50mM_plus2.11845.11845.3	3	12.23	1	3.79E+05		(K)IGRIEDV	(K)I G R I E D V\T|P I|P S/D S T/R(R)		130.28	585.9784	1755.924	-0.0029	-1.7	4.56	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
6331	dirMS_041712_NAR_50mM_plus2.16889.16889.3	3	12.23	1	8.57E+05		(K)LFTAESL	(K)L F|T/A E S L/I G L K N P E/K(S)		157.48	553.9791	1659.932	-0.0089	-5.3	6.14	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
6332	dirMS_041712_NAR_50mM_minus2.10704.10704.3	3	12.22	0	2.72E+05		(K)VFEGNR	(K)V/F/E|G N R P T N S I V F T K(L)		129.18	570.3032	1708.902	-0.0066	-3.9	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
6333	dirMS_041712_NAR_50mM_minus2.11262.11262.3	3	12.22	1	1.86E+05		(R)DNKQA	(R)D N K Q A\G|V/F/E/P/T I V K(V)		132.05	515.9485	1545.827	0.0038	2.5	6.07	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
6334	dirMS_041712_NAR_50mM_minus2.11415.11415.3	3	12.22	0	2.35E+04		(R)LIAEQP	(R)L I|A E Q/P/P/H L T P/G I R(E)		133.68	514.6309	1541.88	-0.0017	-1.1	6.75	20915.7	6.45	HUMAN	C9JBI3	Phosphoserine phosphatase (Fragment)
6335	dirMS_041712_NAR_50mM_minus2.12778.12778.3	3	12.22	1	4.16E+05	M100m	(K)QGGLG	(K)Q G G\L|G P/m N\I|P L/V/S D P K R(T)	m:Oxidized methionine	140.45	598.988	1778.958	15.9913	-2	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
6336	dirMS_041712_NAR_50mM_minus2.14959.14959.3	3	12.22	1	9.63E+05		(R)DVDFEL	(R)D V|D F/E L/I K V E/G K(V)		153.85	464.5852	1391.742	-0.0006	-0.4	4.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
6337	dirMS_041712_NAR_60mM_minus.11308.11308.3	3	12.22	1	2.07E+05		(K)FADLSE	(K)F/A/D|L/S\E/A/A N R N N D A L R(Q)		122.5	592.9581	1776.862	-0.0026	-1.5	4.56	49709.6	5.19	HUMAN	B0YJC4	Vimentin
6338	dirMS_041712_NAR_60mM_minus.12203.12203.3	3	12.22	0	3.77E+05		(K)VTNEFV	(K)V/T/N E/F V/H/I/N N L K(L)		127.53	476.5974	1427.764	0.0135	9.5	6.72	18317.8	6.19	HUMAN	B7Z3E2	Serine/threonine-protein phosphatase 6 catalytic subunit
6339	dirMS_041712_NAR_120mM_plus.8136.8136.3	3	12.22	1	4.76E+05		(R)SSDVSW	(R)S/S/D|V/S/W S D T R|R(T)		95.73	432.5393	1295.598	0.0059	4.5	5.68	116336.3	8.59	HUMAN	G3V220	Transcription elongation regulator 1
6340	dirMS_041712_NAR_20mM_plus.17562.17562.3	3	12.22	0	6.52E+04		(K)ITNLTQ	(K)I T N L T Q\Q/L/E/Q/A S I V/K(K)		192.92	562.6523	1685.943	-0.0009	-0.5	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
6341	dirMS_041712_NAR_30mM_plus2.11100.11182.2	2	12.22	0	5.13E+05		(K)AVLENA	(K)A V|L/E/N A/L/R(N)		111.05	443.2607	885.515	-0.0011	-1.3	6.05	33605.6	6.56	HUMAN	A6NJ11	Ubiquitin fusion degradation protein 1 homolog
6342	dirMS_041712_NAR_30mM_plus2.13848.13921.2	2	12.22	0	4.01E+05		(K)TIFQGIA	(K)T/I|F Q/G I A/A/K(V)		125.82	474.7784	948.551	-0.0018	-1.9	8.41	52385	7.18	HUMAN	B4DQJ8	6-phosphogluconate dehydrogenase, decarboxylating
6343	dirMS_041712_NAR_30mM_plus2.15955.16310.2	2	12.22	0	3.42E+06		(R)YIEIFK(S	(R)Y/I|E I/F/K(S)		135.82	406.7314	812.455	0.0003	0.3	6	24249.1	6.99	HUMAN	D6RBM0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
6344	dirMS_041712_NAR_30mM_plus2.7035.7057.2	2	12.22	0	2.58E+05		(K)MAQFD	(K)M|A|Q/F/D/A K(K)		91.35	405.6961	810.381	0.0035	4.3	5.59	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
6345	dirMS_041712_NAR_30mM_plus2.7325.7373.2	2	12.22	0	7.14E+04		(R)EVIINSR	(R)E V|I|I/N/S/R(F)		93.52	415.7394	830.473	-0.0015	-1.8	6.1	15838.9	7.03	HUMAN	H0Y5U0	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
6346	dirMS_041712_NAR_30mM_plus2.8939.8939.2	2	12.22	0	1.86E+05		(R)QPLGAT	(R)Q P/L|G/A/T S/G A/S L K(T)		100.28	565.3227	1129.621	0.017	15	8.75	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
6347	dirMS_041712_NAR_40mM_plus2.10666.10666.2	2	12.22	0	7.56E+04		(R)LSESQLS	(R)L/S/E|S/Q/L/S/F R(R)		127.93	533.7789	1066.553	-0.0022	-2.1	6	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
6348	dirMS_041712_NAR_40mM_plus2.14072.14072.3	3	12.22	1	8.78E+04		(R)STGLELE	(R)S T|G\L/E L E/T/P S L/V/P V K K(N)		148.73	566.6552	1697.968	-0.0173	-10.2	5.86	34828	9.96	HUMAN	F5H5K4	Serine/threonine-protein phosphatase 1 regulatory subunit 10
6349	dirMS_041712_NAR_50mM_plus2.13559.13559.3	3	12.22	0	1.58E+07		(R)LIDLHSP	(R)L/I/D L/H/S/P S E\I V K(Q)		138.68	450.9258	1350.763	0.0001	0.1	5.32	7304.3	9.39	HUMAN	G3XAN0	40S ribosomal protein S20
6350	dirMS_041712_NAR_60mM_plus.12373.12373.2	2	12.22	0	4.51E+05		(R)HVFGES	(R)H/V|F/G E S D E/L I/G Q K(V)		121.58	729.8644	1458.722	-0.0008	-0.6	4.65	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
6351	dirMS_041712_NAR_30mM_minus2.11564.11564.2	2	12.21	0	3.67E+05		(K)EIAEAYL	(K)E I/A/E/A Y L/G/K(T)		115.85	497.265	993.525	-0.0024	-2.4	4.53	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
6352	dirMS_041712_NAR_30mM_minus2.9616.9633.2	2	12.21	1	7.36E+05		(K)AIYKGP	(K)A I|Y K/G P G S E|A|G|P(-)		106.8	573.7932	1146.579	0.0002	0.1	6.04	30492.9	5.26	HUMAN	P21964	Catechol O-methyltransferase
6353	dirMS_041712_NAR_40mM_minus2.8309.8309.3	3	12.21	0	3.89E+03		(R)LLELGPK	(R)L L/E/L G/P K/P E/V A Q Q\T R(K)		129.42	560.3204	1678.949	-0.002	-1.2	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
6354	dirMS_041712_NAR_50mM_minus2.18177.18177.3	3	12.21	1	2.47E+05		(K)LKEAELL	(K)L K E A E L\L|E|P L/M/P A I R(A)		172.7	574.9957	1722.982	-0.0097	-5.6	4.79	56164.6	6.01	HUMAN	E9PP73	Coatomer subunit beta (Fragment)
6355	dirMS_041712_NAR_50mM_minus2.5851.5851.3	3	12.21	1	4.33E+04		(R)AIEAAP	(R)A I|E/A/A/P Q E/P E/Q K R(S)		95.43	489.5922	1466.76	0.0023	1.5	4.79	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
6356	dirMS_041712_NAR_120mM_plus.15728.15862.4	4	12.21	2	9.72E+05		(K)VGLQVV	(K)V G L/Q|V/V/A V/K A/P G F G D N R K(N)		136.27	464.5161	1855.055	-0.0123	-6.6	9.99	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
6357	dirMS_041712_NAR_120mM_plus.17378.17400.4	4	12.21	1	7.85E+04		(R)GFGHIG	(R)G F G H I\G I A\V|P/D V/Y/S A C K/R(F)	C:Carbamidomethylation	144.95	487.5024	1946.991	-0.0028	-1.4	8.6	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
6358	dirMS_041712_NAR_120mM_plus.6632.6632.2	2	12.21	0	3.07E+05		(R)SHEGET	(R)S/H|E|G E/T\A Y I R(V)		88.3	581.7777	1162.549	-0.0006	-0.5	5.38	16510	11.51	HUMAN	J3KSR8	Serine/arginine-rich-splicing factor 1 (Fragment)
6359	dirMS_041712_NAR_20mM_plus.13548.13548.2	2	12.21	0	1.62E+05	M98m	(R)TLTIVDT	(R)T L|T I/V/D/T G I/G m\T K(A)	m:Oxidized methionine	165.88	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
6360	dirMS_041712_NAR_20mM_plus.17172.17172.2	2	12.21	0	8.06E+04		(K)VNIIPIIA	(K)V/N/I|I|P I/I A K(A)		189.38	490.8283	980.65	-0.001	-1	8.72	51212	5.84	HUMAN	A6NFQ9	Septin-8
6361	dirMS_041712_NAR_30mM_plus2.11918.12001.2	2	12.21	0	2.07E+05		(R)GLLGDA	(R)G L|L|G/D/A/P N D|P R(G)		115.62	562.7857	1124.57	-0.0053	-4.7	4.21	63055.8	6.41	HUMAN	E7EWR4	Cleavage stimulation factor subunit 2
6362	dirMS_041712_NAR_30mM_plus2.14125.14126.2	2	12.21	0	3.23E+05		(R)YVDIAIP	(R)Y V|D|I/A|I\P C/N/N K(G)	C:Carbamidomethylation	127.05	653.8256	1306.646	-0.0021	-1.6	5.83	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
6363	dirMS_041712_NAR_30mM_plus2.14455.14597.2	2	12.21	0	5.52E+05		(K)TIIFVET	(K)T/I|I|F V E/T/K(R)		129.5	475.7798	950.556	-0.0034	-3.6	5.66	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
6364	dirMS_041712_NAR_30mM_plus2.16629.16629.2	2	12.21	0	3.86E+04		(K)LGEWV	(K)L/G|E|W/V|G L C K(I)	C:Carbamidomethylation	140.05	531.2766	1061.545	0.0011	1	6	14914.1	6.84	HUMAN	P25398	40S ribosomal protein S12
6365	dirMS_041712_NAR_30mM_plus2.21205.21205.2	2	12.21	0	1.87E+05		(R)QTLMW	(R)Q/T/L\M/W/S A T/W/P K(E)		165.82	674.8389	1348.672	-0.0013	-1	8.75	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
6366	dirMS_041712_NAR_30mM_plus2.21728.21728.2	2	12.21	0	8.29E+04		(K)GLVQAL	(K)G L/V/Q A L/G\L/S/N F/N S R(Q)		169.4	738.3989	1475.796	-0.006	-4.1	9.75	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
6367	dirMS_041712_NAR_30mM_plus2.9663.9806.2	2	12.21	0	1.36E+06		(R)QLSSGV	(R)Q L/S/S/G/V/S E/I/R(H)		104.9	538.2855	1075.574	-0.0105	-9.8	6	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
6368	dirMS_041712_NAR_60mM_plus.9852.9852.3	3	12.21	1	2.90E+05		(K)SEEQLK	(K)S/E|E\Q L K/E E/G I E/Y K(V)		109.28	527.9264	1581.764	0.0004	0.2	4.32	43928.7	6.58	HUMAN	B4DHG0	Dihydrolipoyl dehydrogenase, mitochondrial
6369	dirMS_041712_NAR_30mM_minus2.18561.18561.2	2	12.2	0	6.44E+04		(R)SSIAGLL	(R)S S/I/A/G L/L/L/K(A)		155.6	451.2891	901.572	-0.0008	-0.9	8.47	533778	5.74	HUMAN	Q15149	Plectin
6370	dirMS_041712_NAR_50mM_minus2.12274.12274.3	3	12.2	1	1.53E+05		(K)ASLAET	(K)A/S/L|A/E/T D K I T/L E V A K(L)		137.92	530.2953	1588.879	-0.0079	-5	4.68	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
6371	dirMS_041712_NAR_50mM_minus2.14806.14806.3	3	12.2	0	3.91E+04		(K)IAILTCP	(K)I/A I|L/T|C/P F E/P P K P K(T)	C:Carbamidomethylation	152.75	537.6375	1610.898	0.0005	0.3	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
6372	dirMS_041712_NAR_60mM_minus.10939.10939.3	3	12.2	1	1.26E+05		(K)KVEAQL	(K)K V E A Q|L|Q|E/L Q/V K(F)		121.12	471.6068	1412.811	-0.0049	-3.5	6.14	227783.5	5.5	HUMAN	P35579	Myosin-9
6373	dirMS_041712_NAR_30mM_plus2.10190.10225.2	2	12.2	0	6.87E+05		(R)SPSTLLP	(R)S/P|S/T L L|P/K(K)		107.73	421.7559	842.498	0.0063	7.5	8.47	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
6374	dirMS_041712_NAR_30mM_plus2.16112.16468.2	2	12.2	0	1.29E+06		(K)EGALDL	(K)E G A|L/D/L/S/G L/R(A)		138.2	515.7855	1030.553	0.011	10.6	4.37	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
6375	dirMS_041712_NAR_30mM_plus2.18333.18333.2	2	12.2	0	1.64E+04		(K)VVNSIL	(K)V/V/N/S/I L A F/R(E)		149.52	509.8031	1018.604	-0.0055	-5.4	9.72	56564.1	6.56	HUMAN	B4DNW0	Aminoacylase-1
6376	dirMS_041712_NAR_30mM_plus2.20245.20502.2	2	12.2	0	3.00E+05		(R)TTLLPGL	(R)T T|L|L/P/G L L K(T)		160.85	478.3126	955.619	-0.0007	-0.8	8.41	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
6377	dirMS_041712_NAR_30mM_plus2.22655.22707.2	2	12.2	0	5.16E+05		(K)LAAFWL	(K)L/A|A/F/W/L M K(A)		176.55	490.2728	979.543	-0.005	-5.2	8.75	32535.6	9.19	HUMAN	B4DZW6	Regulator of microtubule dynamics protein 1
6378	dirMS_041712_NAR_50mM_plus2.18339.18587.3	3	12.2	1	3.49E+05		(R)GDSVIV	(R)G D/S|V|I/V V L R N P L I/A|G K(-)		165.37	550.9999	1650.99	-0.005	-3	8.75	6144.3	10.23	HUMAN	K7EJB5	Small nuclear ribonucleoprotein Sm D2
6379	dirMS_041712_NAR_50mM_plus2.21599.21599.3	3	12.2	0	1.01E+05		(K)THLPLA	(K)T H L\P L A\L\L|P/Q T L L/D/Q K(V)		183.97	601.0191	1801.058	-0.0154	-8.6	6.41	22243.5	7.91	HUMAN	E9PKR8	Sulfotransferase 1A2 (Fragment)
6380	dirMS_041712_NAR_50mM_plus2.6748.6749.3	3	12.2	0	1.60E+05		(K)IGEEEIQ	(K)I/G|E E/E I/Q K/P E E K(V)		100.35	476.9126	1428.722	0.0016	1.1	4.32	81733.5	5.24	HUMAN	E9PAW1	Splicing factor 3A subunit 1
6381	dirMS_041712_NAR_60mM_plus.18306.18306.3	3	12.2	1	9.04E+05		(K)EVNKFQ	(K)E V/N K F Q/M\A|Y S/N L L R(A)		152.87	571.6293	1712.879	-0.0055	-3.2	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
6382	dirMS_041712_NAR_60mM_plus.7694.7694.3	3	12.2	1	7.88E+05		(K)TPKGPS	(K)T/P K/G P S S|V/E D/I K(A)		98.27	419.894	1257.669	-0.0011	-0.8	5.73	32745.6	4.64	HUMAN	P06748	Nucleophosmin
6383	dirMS_041712_NAR_120mM_minus.18687.18687.4	4	12.19	1	4.42E+05		(K)FQIPPN	(K)F Q\I|P/P N/A E/L K Y E L H L/K(S)		157	485.7686	1940.064	-0.0114	-5.9	6.75	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
6384	dirMS_041712_NAR_120mM_minus.5387.5425.3	3	12.19	0	1.24E+05		(R)YIDTEH	(R)Y/I D/T E/H/G/G S/Q A R(F)		82.93	445.2092	1333.613	-0.0001	-0.1	5.32	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
6385	dirMS_041712_NAR_20mM_minus.14425.14425.2	2	12.19	0	2.52E+05		(R)APGSGL	(R)A/P|G S G L A/L\L|P L K(I)		198.32	568.8551	1136.704	-0.0008	-0.7	8.8	266161	5.68	HUMAN	E9PPU0	Epiplakin
6386	dirMS_041712_NAR_20mM_minus.8919.8919.2	2	12.19	0	2.41E+04		(K)LVSESSD	(K)L/V|S E/S S D V L/P K(-)		138.67	587.321	1173.636	-0.0014	-1.2	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
6387	dirMS_041712_NAR_30mM_minus2.10501.10501.2	2	12.19	0	3.43E+05		(K)SAVGFD	(K)S/A|V/G/F D|Y Q/G K(T)		111.15	536.2608	1071.511	0.0038	3.5	5.55	25153.2	6.6	HUMAN	H7C314	Src substrate cortactin (Fragment)
6388	dirMS_041712_NAR_30mM_minus2.11756.11858.2	2	12.19	0	5.17E+05		(K)LNFAVA	(K)L/N|F|A\V/A/S/R(K)		117.85	439.2467	877.489	-0.0029	-3.3	9.75	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
6389	dirMS_041712_NAR_30mM_minus2.15844.15844.2	2	12.19	0	1.25E+05		(R)TINEVEN	(R)T I|N E|V/E/N Q I L T R(D)		139.6	715.3834	1429.765	-0.005	-3.5	4.53	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
6390	dirMS_041712_NAR_40mM_minus2.14104.14104.3	3	12.19	0	6.49E+05		(R)IHFPLAT	(R)I H F P L A T\Y|A|P/V/I/S A E K(A)		167.75	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
6391	dirMS_041712_NAR_50mM_minus2.10183.10183.3	3	12.19	0	1.63E+05	M392m	(K)EmNPAL	(K)E m/N/P A L|G I|D C L/H/K(G)	C:Carbamidomethylation m:Oxid	125.93	505.2416	1497.719	15.9914	-2.3	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
6392	dirMS_041712_NAR_50mM_minus2.15763.15763.3	3	12.19	0	1.03E+05	M41m	(K)mLDAED	(K)m L/D/A E D/I/V G T L R P D|E\K(A)	m:Oxidized methionine	157.65	606.6366	1801.9	15.9952	0.2	4.1	21601.4	6.27	HUMAN	K7EJH8	Alpha-actinin-4 (Fragment)
6393	dirMS_041712_NAR_50mM_minus2.17954.17954.3	3	12.19	1	1.70E+05		(K)AIDLFTD	(K)A I|D|L F T|D A/I K/L N P R(L)		171.33	529.6358	1586.89	0.0028	1.8	6	18141.9	4.7	HUMAN	F6VDH7	Hsc70-interacting protein (Fragment)
6394	dirMS_041712_NAR_60mM_minus.12139.12139.3	3	12.19	1	3.77E+05		(K)AAAGKA	(K)A/A/A G K|A E L E|L E/L|G R(I)		127.53	476.5974	1427.785	-0.0076	-5.3	4.79	533778	5.74	HUMAN	Q15149	Plectin
6395	dirMS_041712_NAR_60mM_minus.14250.14250.3	3	12.19	1	2.87E+05		(K)VFGPGI	(K)V/F/G/P G I/E G/K/D/V F R(E)		139.95	474.2636	1420.758	0.0179	12.6	6.04	258215.9	5.48	HUMAN	E7EN95	Filamin-B
6396	dirMS_041712_NAR_60mM_minus.6439.6439.3	3	12.19	1	6.33E+04		(R)GTDDSP	(R)G T|D D/S P K D S Q/E/D L Q E/R(H)		94.48	607.2707	1819.794	0.0035	1.9	3.96	23420.8	4.74	HUMAN	Q5H9L2	Transcription elongation factor A protein-like 5
6397	dirMS_041712_NAR_30mM_plus2.22771.22771.3	3	12.19	0	4.63E+05		(R)ELSDFIS	(R)E L S D F I/S/Y/L Q/R(E)		177.23	457.5693	1370.695	-0.0017	-1.2	4.37	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
6398	dirMS_041712_NAR_40mM_plus2.11392.11392.3	3	12.19	2	1.28E+05		(K)VEVDLD	(K)V E/V/D/L D Q T Q R E R/K(M)		133.28	539.2829	1615.84	-0.0057	-3.5	4.78	107120	9.75	HUMAN	Q7Z7M9	Polypeptide N-acetylgalactosaminyltransferase 5
6399	dirMS_041712_NAR_40mM_plus2.9009.9009.3	3	12.19	0	4.93E+04		(K)VVQVSA	(K)V V|Q|V/S|A G D S H T/A A L T D D/G R(V)		115.07	633.6448	1898.92	-0.0004	-0.2	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
6400	dirMS_041712_NAR_50mM_plus2.18376.18376.2	2	12.19	0	6.12E+05		(R)IHFPLAT	(R)I H|F|P L A/T Y/A P\V I S A E/K(A)		164.83	878.9842	1756.963	-0.0021	-1.2	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
6401	dirMS_041712_NAR_50mM_plus2.19449.19449.3	3	12.19	0	3.28E+04		(K)LVLIGSN	(K)L V|L/I/G/S N/H S L P F L K(F)		170.82	513.3073	1537.91	-0.0027	-1.8	8.76	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
6402	dirMS_041712_NAR_50mM_plus2.6740.7000.3	3	12.19	1	8.73E+05		(K)IVADKD	(K)I/V|A/D/K/D Y S\V/T A N S K(I)		101.47	504.2628	1510.775	-0.0009	-0.6	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
6403	dirMS_041712_NAR_60mM_plus.15397.15397.3	3	12.19	1	3.92E+05		(R)SLIANLA	(R)S L|I/A N L|A A/A/N C Y K/K(E)	C:Carbamidomethylation	137.4	512.9411	1536.82	-0.0115	-7.5	9.7	36978.6	6.33	HUMAN	B7Z800	Adenosine kinase
6404	dirMS_041712_NAR_60mM_plus.15463.15463.3	3	12.19	0	2.24E+05		(R)ILHCLGL	(R)I L H C L G\L/A/E E/I Q K(Y)	C:Carbamidomethylation	137.7	508.6121	1523.825	-0.0033	-2.2	5.4	33713.1	6.06	HUMAN	P53004	Biliverdin reductase A
6405	dirMS_041712_NAR_60mM_plus.19955.19955.3	3	12.19	1	1.53E+05		(R)GMLRED	(R)G M|L R E D A|V/L/E\Y L K(I)		163.87	512.9411	1536.809	-0.0003	-0.2	4.68	67933	6.08	HUMAN	P26038	Moesin
6406	dirMS_041712_NAR_20mM_minus.13480.13480.2	2	12.18	0	6.41E+05		(K)DAGTIA	(K)D A G T|I/A|G L/N V L R(I)		185.02	600.3403	1199.674	-0.0009	-0.8	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
6407	dirMS_041712_NAR_30mM_minus2.9453.9453.2	2	12.18	0	1.01E+06		(K)QADVNL	(K)Q A/D|V|N/L V N A K(L)		105.43	536.2917	1071.579	-0.0032	-3	5.84	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
6408	dirMS_041712_NAR_120mM_plus.8240.8259.3	3	12.18	1	6.03E+05		(R)DQGGF	(R)D Q|G/G/F/G D/R/N E Y/G S R(I)		96.88	519.8934	1557.668	-0.002	-1.3	4.56	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
6409	dirMS_041712_NAR_30mM_plus2.11054.11055.2	2	12.18	0	2.55E+05		(R)YYPTED	(R)Y/Y|P/T/E D/V P R(K)		111.17	570.2716	1139.537	-0.0008	-0.7	4.37	7289.7	11.65	HUMAN	F8VR69	60S ribosomal protein L6 (Fragment)
6410	dirMS_041712_NAR_30mM_plus2.6008.6008.2	2	12.18	0	9.97E+04		(R)QLAEED	(R)Q\L|A|E/E/D/A A/R(Q)		85.77	501.7464	1002.485	0.0005	0.5	4.14	533778	5.74	HUMAN	Q15149	Plectin
6411	dirMS_041712_NAR_30mM_plus2.9420.9736.2	2	12.18	0	7.30E+05		(R)GGGQII	(R)G G\G\Q|I|I|P T A/R(R)		104.25	485.2772	969.548	-0.0005	-0.5	9.75	15036.9	7.16	HUMAN	K7EJ74	116 kDa U5 small nuclear ribonucleoprotein component (Fragment)
6412	dirMS_041712_NAR_50mM_plus2.13097.13097.3	3	12.18	1	1.45E+06		(R)VVDALG	(R)V/V/V|D|A L/G N A I D G K G P I G S K(T)		137.43	570.9829	1710.939	-0.0043	-2.5	5.93	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
6413	dirMS_041712_NAR_60mM_plus.18391.18391.3	3	12.18	1	8.52E+05		(K)EVNKFQ	(K)E V N K/F Q M/A/Y S/N/L L R(A)		152.93	571.6293	1712.879	-0.0055	-3.2	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
6414	dirMS_041712_NAR_120mM_minus.14136.14136.3	3	12.17	0	4.33E+05		(K)NRPTSIS	(K)N R P T S\I|S|W/D/G L D S G K(L)		130.63	544.9369	1632.798	-0.0015	-0.9	5.96	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
6415	dirMS_041712_NAR_120mM_minus.16828.16828.3	3	12.17	0	4.25E+05		(K)HLEINP	(K)H/L|E I N|P D|H|S|I I/E T L R(Q)		146.58	596.3176	1786.945	-0.0064	-3.6	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
6416	dirMS_041712_NAR_20mM_minus.12105.12105.2	2	12.17	0	3.90E+05	M185m	(K)LAVNm	(K)L A|V/N/m V/P F P R(L)	m:Oxidized methionine	170.83	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
6417	dirMS_041712_NAR_20mM_minus.8232.8232.2	2	12.17	0	1.47E+05		(K)DVGSLA	(K)D V/G/S/L/A/S/V Q R(Y)		132.08	516.2772	1031.548	-0.0009	-0.8	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin
6418	dirMS_041712_NAR_30mM_minus2.9996.9996.2	2	12.17	0	2.19E+05		(R)GVTIKPT	(R)G V|T|I|K/P T V D/D/D(-)		108.62	580.294	1159.584	-0.0034	-2.9	4.17	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
6419	dirMS_041712_NAR_50mM_minus2.5757.5757.3	3	12.17	1	9.21E+04		(K)LEEAEK	(K)L E|E\A E K/A A\D/E/S E R(G)		94.08	492.8982	1476.681	-0.0012	-0.8	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
6420	dirMS_041712_NAR_60mM_minus.11044.11248.3	3	12.17	1	3.17E+06		(R)DGKLVS	(R)D G K\L\V\S\E|S/S/D/V L/P K(-)		122.2	491.927	1473.78	-0.0131	-8.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
6421	dirMS_041712_NAR_60mM_minus.7011.7011.3	3	12.17	1	3.61E+05		(K)LDEREA	(K)L/D|E R E/A/G I T E K(V)		98.2	420.8852	1260.643	-0.002	-1.6	4.41	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
6422	dirMS_041712_NAR_60mM_minus.9059.9313.3	3	12.17	1	1.02E+06		(R)ETAEAD	(R)E T|A/E/A D/V/A S L N R R(I)		111.37	477.9107	1431.719	-0.0011	-0.8	4.68	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
6423	dirMS_041712_NAR_120mM_plus.20426.20426.3	3	12.17	0	2.75E+05		(R)INLWHL	(R)I/N/L W/H/L E/I/T D R(S)		159.63	470.5889	1409.754	-0.0014	-1	5.32	52204.6	5.82	HUMAN	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
6424	dirMS_041712_NAR_20mM_plus.11284.11284.2	2	12.17	0	1.52E+05		(R)YALYDA	(R)Y A\L|Y/D/A/T Y\E T|K(E)		150.42	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
6425	dirMS_041712_NAR_20mM_plus.19356.19356.3	3	12.17	0	9.30E+04		(R)ALIAGG	(R)A L\I A G G G A|P E/I/E L A/L/R(L)		205.05	517.6345	1550.89	-0.0011	-0.7	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
6426	dirMS_041712_NAR_30mM_plus2.12947.12947.2	2	12.17	0	3.14E+05		(K)QQIQSI	(K)Q Q|I/Q/S I/Q/Q\S\I/E R(L)		120.75	729.3893	1457.771	0.0006	0.4	6	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)

6427	dirMS_041712_NAR_30mM_plus2.18456.18564.2	2	12.17	0	5.13E+05		(R)GFVDDII	(R)G F\V/D D/I|I|Q|P S/S T R(A)		150.37	717.8617	1434.722	-0.0062	-4.3	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
6428	dirMS_041712_NAR_30mM_plus2.4037.4037.2	2	12.17	0	6.13E+05	M299m M:	(K)NmmAA	(K)N m/m/A|A C D|P R(H)	C:Carbamidomethylation m:Oxid	67.88	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
6429	dirMS_041712_NAR_50mM_plus2.11420.11420.3	3	12.17	1	2.61E+05		(K)CATITPD	(K)C/A|T|I/T/P D/E A R V E E F/K(L)	C:Carbamidomethylation	127.75	589.2842	1765.843	-0.0045	-2.5	4.41	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
6430	dirMS_041712_NAR_50mM_plus2.18183.18183.3	3	12.17	1	1.61E+06		(R)ELIKVLEI	(R)E L/I K V\L\E E A/N Q|A/I N/P/K(L)		163.62	603.6741	1809.012	-0.0039	-2.2	4.79	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
6431	dirMS_041712_NAR_50mM_plus2.18582.18638.3	3	12.17	0	3.58E+05		(R)LLLDGAI	(R)L/L|L D/G A/P L I A I H K(A)		165.82	458.622	1373.852	-0.0001	0	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
6432	dirMS_041712_NAR_50mM_plus2.18737.18737.3	3	12.17	1	4.36E+05		(K)AAIDWF	(K)A A/I/D/W F/D/G K E F S G N P I K(V)		167.18	632.3186	1894.933	0.0079	4.1	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
6433	dirMS_041712_NAR_50mM_plus2.19197.19197.3	3	12.17	1	4.32E+05		(R)LKVPPAI	(R)L K\V/P P A I\N\Q/F|T Q A L/D R(Q)		169.82	604.3351	1811.017	-0.0266	-14.7	8.75	30166.2	10.79	HUMAN	P62424	60S ribosomal protein L7a
6434	dirMS_041712_NAR_50mM_plus2.21672.21672.3	3	12.17	0	1.01E+05		(K)THLPLAL	(K)T H L P L A\L\L/P Q/T/L L D Q K(V)		183.97	601.0191	1801.058	-0.0154	-8.6	6.41	22243.5	7.91	HUMAN	E9PKR8	Sulfotransferase 1A2 (Fragment)
6435	dirMS_041712_NAR_60mM_plus.8908.8908.3	3	12.17	1	8.20E+05		(R)SSGGSYI	(R)S S|G G S Y R D S Y/D|S/Y|A\T/H N E(-)		104.85	665.9403	1995.795	0.0112	5.6	4.81	18647.7	9.51	HUMAN	Q14011	Cold-inducible RNA-binding protein
6436	dirMS_041712_NAR_60mM_plus.9361.9361.2	2	12.17	0	5.11E+05		(K)QEYDES	(K)Q E|Y D|E/S/G/P S I/V/H R(K)		107.15	758.8546	1516.703	-0.0007	-0.5	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
6437	dirMS_041712_NAR_60mM_plus.9805.9805.3	3	12.17	1	1.29E+06		(K)EAALSTA	(K)E A/A/L/S/T A/L/S E/K R(T)		109.78	425.898	1275.69	-0.0109	-8.5	6.24	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
6438	dirMS_041712_NAR_30mM_minus2.18154.18154.2	2	12.16	0	1.96E+05		(K)VADIGLA	(K)V A/D\I|G/L A A W G/R(K)		152.82	564.8076	1128.616	-0.0081	-7.2	5.81	48285.8	5.93	HUMAN	P23526	Adenosylhomocysteinase
6439	dirMS_041712_NAR_60mM_minus.14061.14061.3	3	12.16	1	3.30E+05		(R)QATKDA	(R)Q A T K D A G T\I/A/G/L/N V/L R(I)		138.87	543.3073	1627.913	-0.0052	-3.2	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
6440	dirMS_041712_NAR_20mM_plus.12232.12594.2	2	12.16	0	2.42E+05		(K)DLAGSII	(K)D L|A|G/S I/I/G K(G)		158.25	437.2558	873.504	0.0003	0.4	5.84	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
6441	dirMS_041712_NAR_20mM_plus.14098.14098.3	3	12.16	0	4.03E+05	M313m	(R)TVQSLEI	(R)T V\Q S L E|I/D L/D S m/R(N)	m:Oxidized methionine	168.7	508.2519	1506.747	15.9943	-0.4	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
6442	dirMS_041712_NAR_30mM_plus2.14123.14183.2	2	12.16	0	2.55E+05		(R)AMADA	(R)A/M|A/D/A/L/L E/R(G)		127.22	495.2615	989.508	0.0073	7.4	4.37	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
6443	dirMS_041712_NAR_30mM_plus2.17986.17986.2	2	12.16	0	5.84E+05		(R)EQLAIAE	(R)E Q/L/A/I/A/E F A R(S)		148.18	574.3083	1147.611	-0.0013	-1.1	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
6444	dirMS_041712_NAR_30mM_plus2.5955.5955.2	2	12.16	0	3.57E+04		(R)VGPNAF	(R)V/G/P/N A P E/E K(K)		85.55	470.7391	940.473	-0.0025	-2.7	4.53	66105.7	7.3	HUMAN	A8MQB8	Fragile X mental retardation protein 1
6445	dirMS_041712_NAR_40mM_plus2.10284.10284.2	2	12.16	0	6.93E+04		(R)EYQELM	(R)E Y/Q/E L/M/N/V K(L)		125.03	577.2823	1153.556	0.0015	1.3	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
6446	dirMS_041712_NAR_40mM_plus2.8714.8779.2	2	12.16	0	4.09E+05		(K)VCADLIF	(K)V/C|A/D L/I/R(G)	C:Carbamidomethylation	113.22	423.7286	846.45	-0.0003	-0.3	5.81	6885.1	10.56	HUMAN	E5RJX2	40S ribosomal protein S20
6447	dirMS_041712_NAR_50mM_plus2.12458.12458.3	3	12.16	0	2.04E+05		(K)AIIKPQY	(K)A I/I K/P Q/Y V D Q I/P/K(A)		133.23	504.9637	1512.878	-0.0019	-1.3	8.54	47949	9.16	HUMAN	D6R9I9	ATP-binding cassette sub-family E member 1
6448	dirMS_041712_NAR_50mM_plus2.18233.18233.2	2	12.16	0	5.46E+05		(R)IHFPLAT	(R)I/H|F|P L/A T/Y/A/P V I S A E K(A)		164.65	878.9842	1756.963	-0.0021	-1.2	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
6449	dirMS_041712_NAR_60mM_plus.16576.16576.3	3	12.16	0	3.86E+05		(R)EAYPGD	(R)E A/Y/P G D V/F Y/L H S R(L)		142.97	518.5855	1553.738	0.0036	2.3	5.32	48851.3	9.2	HUMAN	K7EK63	ATP synthase subunit alpha, mitochondrial
6450	dirMS_041712_NAR_60mM_plus.7643.7643.3	3	12.16	0	1.38E+06	M80m	(R)TICSHVC	(R)T/I/C S/H/V Q N/m I K(G)	C:Carbamidomethylation m:Oxid	97.92	449.5594	1330.661	16.003	6	8.44	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
6451	dirMS_041712_NAR_120mM_minus.13173.13557.4	4	12.15	1	1.07E+06		(K)SVHSSVI	(K)S V H S S V|P/L/L/N S K/D/P I D/R(I)		127.33	466.7525	1863.992	-0.0041	-2.2	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
6452	dirMS_041712_NAR_20mM_minus.9673.9673.2	2	12.15	0	2.50E+05	M33m	(K)VAGmDV	(K)V A/G m/D V/E/L T/V/E/E R(N)	m:Oxidized methionine	147.53	732.355	1447.71	15.993	-1.3	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
6453	dirMS_041712_NAR_30mM_minus2.16514.16514.2	2	12.15	0	4.38E+05	M185m	(K)LAVNmV	(K)L/A|V|N m V/P F\P R(L)	m:Oxidized methionine	142.67	580.3178	1143.634	15.994	-0.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
6454	dirMS_041712_NAR_50mM_minus2.13223.13223.3	3	12.15	0	1.63E+05		(K)MLDAED	(K)M/L|D A E/D I V G T A R P D/E K(A)		143.47	587.2894	1759.853	0.0006	0.3	4.1	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
6455	dirMS_041712_NAR_20mM_plus.9926.9926.2	2	12.15	0	2.42E+05		(K)LVSESSD	(K)L/V/S\E S S D/V L/P K(-)		140.25	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
6456	dirMS_041712_NAR_30mM_plus2.13253.13291.2	2	12.15	0	8.79E+05		(K)NSGVLM	(K)N|S|G/V|L/M V/V/K(C)		123	473.7749	946.539	0.0035	3.7	8.75	9148.5	9.4	HUMAN	C9JES7	COX assembly mitochondrial protein homolog
6457	dirMS_041712_NAR_40mM_plus2.18232.18232.3	3	12.15	0	3.43E+05		(R)EAVELPI	(R)E A/V E/L/P L T H/F E L Y K(Q)		173.8	563.6336	1688.889	-0.0032	-1.9	4.75	47479.5	5.09	HUMAN	P43686	26S protease regulatory subunit 6B
6458	dirMS_041712_NAR_40mM_plus2.6995.6995.2	2	12.15	0	1.27E+05		(R)MGPVM	(R)M/G/P/V/M/D R(M)		100.62	403.1892	805.37	0.0016	2	5.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
6459	dirMS_041712_NAR_50mM_plus2.10874.10874.3	3	12.15	1	8.35E+05		(R)DISTNKV	(R)D I|S T N K V E Q|I/P/Y G E R(I)		124.1	583.6304	1748.881	-0.0047	-2.7	4.68	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
6460	dirMS_041712_NAR_50mM_plus2.19084.19084.3	3	12.15	0	7.46E+05		(K)LLYDLAD	(K)L/L|Y/D\L A D/Q L H A A V\G A S R(A)		168.47	604.9965	1812.96	0.0147	8.1	5.21	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
6461	dirMS_041712_NAR_50mM_plus2.8251.8251.3	3	12.15	1	3.49E+05		(R)VAVEAK	(R)V A/V E A/K N/P A/D L/P K(L)		110.53	451.2563	1351.758	-0.0036	-2.7	6.04	96306.4	6.41	HUMAN	P13639	Elongation factor 2
6462	dirMS_041712_NAR_50mM_plus2.8758.8758.3	3	12.15	0	7.58E+05		(R)AALAHS	(R)A A L A H S E E|V|T|A/S Q V/A A\T K(T)		113.45	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
6463	dirMS_041712_NAR_60mM_plus.10248.10248.3	3	12.15	1	1.48E+06		(K)IFRDGEE	(K)I F/R D\G E\E\A|G|A|Y D/G P R(T)		111.47	551.593	1652.766	-0.0019	-1.1	4.32	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
6464	dirMS_041712_NAR_30mM_minus2.14479.14543.2	2	12.14	0	5.00E+05		(R)TFEDFVI	(R)T/F|E/D/F V/R(I)		133.23	457.2246	913.441	0.0005	0.6	4.37	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
6465	dirMS_041712_NAR_30mM_minus2.16221.16450.2	2	12.14	0	2.75E+05		(R)LLGWIQ	(R)L/L|G W/I/Q|N K(L)		142.35	486.2861	971.567	-0.0024	-2.4	8.75	67046.8	9.38	HUMAN	F8WE98	Filamin-A (Fragment)
6466	dirMS_041712_NAR_30mM_minus2.16413.16413.2	2	12.14	0	2.21E+05		(R)ASLEAAI	(R)A S L E/A/A|I/A/D/A\E Q R(G)		143.47	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
6467	dirMS_041712_NAR_30mM_minus2.18574.18574.2	2	12.14	0	3.87E+05		(R)QAQEYE	(R)Q/A Q E/Y/E/A L/L/N I K(V)		154.83	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
6468	dirMS_041712_NAR_60mM_minus.13389.13389.3	3	12.14	1	9.36E+04		(K)DTDSEEI	(K)D/T|D/S E/E E I R E A F R(V)		134.33	532.9108	1596.714	0.0042	2.6	4.08	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
6469	dirMS_041712_NAR_60mM_minus.18154.18154.3	3	12.14	1	1.61E+05		(R)IRVESLL	(R)I R V E S\L\L|V T A/I S K(A)		162.52	476.9628	1428.878	-0.0046	-3.2	8.75	91730	7.16	HUMAN	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15
6470	dirMS_041712_NAR_60mM_minus.18622.18622.3	3	12.14	0	2.86E+05		(K)LHDNLII	(K)L H D N L\I|I/S/D\L E N T V K(K)		165.83	575.3117	1723.922	-0.0019	-1.1	4.54	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
6471	dirMS_041712_NAR_60mM_minus.9094.9094.3	3	12.14	1	1.62E+05	M232m M:	(R)MSmKEV	(R)M/S/m K E\V D/E\Q|m/L/N/V Q/N\K(N)	m:Oxidized methionine	110.57	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
6472	dirMS_041712_NAR_120mM_plus.14908.14971.2	2	12.14	0	3.44E+06		(R)DWSHYI	(R)D/W/S H|Y|F/K(I)		132.03	491.725	982.442	0.001	1	6.74	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
6473	dirMS_041712_NAR_120mM_plus.4626.4626.3	3	12.14	0	6.19E+05		(R)THSQGG	(R)T H S Q G G|Y/G S Q/G Y/K(Y)		74.07	457.2092	1369.613	-0.0001	-0.1	8.2	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
6474	dirMS_041712_NAR_120mM_plus.7252.7252.3	3	12.14	1	3.21E+05	M462m	(R)KAYGGA	(R)K A Y G G\A|Y/D\V/m/S S K(H)	m:Oxidized methionine	91.37	464.8863	1376.651	15.9929	-1.5	8.43	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
6475	dirMS_041712_NAR_20mM_plus.18315.18472.2	2	12.14	1	1.35E+05		(K)DIGFIKLI	(K)D I|G|F/I/K/L D(-)		198.13	460.7578	920.509	-0.0004	-0.5	4.53	6904.9	11.35	HUMAN	P62273	40S ribosomal protein S29
6476	dirMS_041712_NAR_30mM_plus2.6794.6794.2	2	12.14	0	1.50E+05		(K)VPLTQA	(K)V/P/L/T/Q A/T R(G)		90.48	443.2607	885.515	-0.0011	-1.3	9.72	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
6477	dirMS_041712_NAR_40mM_plus2.9776.9776.3	3	12.14	0	2.44E+05		(R)AAEDPV	(R)A A|E/D/P/V A/A A P R\P L P A G G R(L)		121.12	572.6438	1715.919	-0.0019	-1.1	6.12	73966.7	10.21	HUMAN	B3KWK6	Alpha-L-iduronidase
6478	dirMS_041712_NAR_50mM_plus2.10637.10805.3	3	12.14	1	6.61E+05		(K)GCGVVK	(K)G C|G V V K F E/S|P E/V/A E R(A)	C:Carbamidomethylation	123.88	555.2753	1663.811	0.0005	0.3	4.79	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
6479	dirMS_041712_NAR_50mM_plus2.17641.17641.3	3	12.14	0	3.57E+05		(R)LLLDIPL	(R)L/L|L D\I/P L Q T/P H K(L)		160.8	463.2819	1387.831	0.0004	0.3	6.74	198852.6	5.95	HUMAN	A6NKT7	RanBP2-like and GRIP domain-containing protein 3
6480	dirMS_041712_NAR_60mM_plus.9767.9767.3	3	12.14	1	4.50E+05		(R)QDSAAV	(R)Q/D S/A/A V/G\F/D/Y K E K(L)		108.93	486.5682	1457.691	-0.0007	-0.4	4.56	61756.2	5.24	HUMAN	Q14247	Src substrate cortactin
6481	dirMS_041712_NAR_120mM_minus.7111.7111.3	3	12.13	1	6.92E+05		(K)LEEAEKA	(K)L/E|E/A E K/A A/D E S E R(G)		93.33	492.8986	1476.681	0	0	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
6482	dirMS_041712_NAR_30mM_minus2.16495.16495.2	2	12.13	0	6.44E+04	M2243m	(K)mSIYQA	(K)m S|I|Y/Q/A/M W K(G)	m:Oxidized methionine	144.38	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
6483	dirMS_041712_NAR_50mM_minus2.17034.17034.3	3	12.13	0	2.33E+05		(K)TVSGVN	(K)T V/S\G V/N G/P/L V/I L D H V/K(V)		164.72	549.9835	1647.943	-0.0069	-4.2	6.41	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
6484	dirMS_041712_NAR_50mM_minus2.7740.7740.3	3	12.13	1	5.68E+04		(R)LGAAPE	(R)L/G|A\A/P/E E E S A Y V A/G E/K R(Q)		111.32	592.9614	1776.876	-0.0066	-3.7	4.5	30276.7	5	HUMAN	F2Z2K0	NSFL1 cofactor p47
6485	dirMS_041712_NAR_60mM_minus.13962.13962.3	3	12.13	0	3.42E+05		(K)LHLGTT	(K)L H\L G T T Q\N/S|L/T/E A D F R(E)		137.48	601.6438	1802.903	0.0137	7.6	5.32	49472.3	6.75	HUMAN	O75351	Vacuolar protein sorting-associated protein 4B
6486	dirMS_041712_NAR_60mM_minus.18525.18761.3	3	12.13	0	2.58E+05		(R)DFLLKPE	(R)D F|L/L/K/P E L L R(A)		165.43	415.25	1243.741	-0.0054	-4.4	6.07	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
6487	dirMS_041712_NAR_60mM_minus.6107.6107.3	3	12.13	1	1.45E+06		(K)DSYVGD	(K)D S Y/V/G D E/A Q S/K/R(G)		90.98	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
6488	dirMS_041712_NAR_60mM_minus.7053.7053.3	3	12.13	1	3.04E+05		(R)ELFESST	(R)E L/F/E/S/S/T N N N K D/T K(Q)		98.72	542.9247	1626.761	-0.001	-0.6	4.68	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
6489	dirMS_041712_NAR_120mM_plus.15730.15730.4	4	12.13	2	9.72E+05		(K)VGLQVV	(K)V/G L/Q/V V/A/V K A/P G F G D/N R K(N)		136.27	464.5161	1855.055	-0.0123	-6.6	9.99	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
6490	dirMS_041712_NAR_20mM_plus.16631.17031.2	2	12.13	0	2.63E+05		(R)IVLLDSS	(R)I/V|L|L/D/S S L|E/Y K(K)		186.98	640.36	1279.714	-0.0017	-1.3	4.37	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
6491	dirMS_041712_NAR_20mM_plus.17664.17664.2	2	12.13	0	1.28E+05		(K)LATQSN	(K)L A T Q S N E\I|T I|P/V T F E S R(A)		193.23	953.4986	1905.992	-0.0017	-0.9	4.53	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
6492	dirMS_041712_NAR_20mM_plus.8534.8534.2	2	12.13	0	4.73E+04		(K)EAESSPI	(K)E A E/S/S/P/F V E/R(L)		128.55	575.7771	1150.537	0.0094	8.2	4.25	92752.5	4.76	HUMAN	P14625	Endoplasmin
6493	dirMS_041712_NAR_30mM_plus2.19933.19933.2	2	12.13	0	6.43E+05		(R)NAVWA	(R)N A|V|W/A|L\S N L\C R(G)	C:Carbamidomethylation	157.37	652.3414	1303.658	0.018	13.8	9.75	37228.9	5.22	HUMAN	C9JYI4	Importin subunit alpha-1 (Fragment)
6494	dirMS_041712_NAR_30mM_plus2.21194.21194.2	2	12.13	0	1.82E+05		(R)QTLMW	(R)Q T/L|M/W/S/A T W/P K(E)		165.78	674.8389	1348.672	-0.0013	-1	8.75	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
6495	dirMS_041712_NAR_40mM_plus2.9419.9419.2	2	12.13	0	6.70E+04		(K)SISISVAF	(K)S\I|S/I/S/V A/R(G)		118.4	416.7466	832.489	-0.0028	-3.3	9.47	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
6496	dirMS_041712_NAR_50mM_plus2.21220.21220.3	3	12.13	0	2.16E+06		(R)AGKPVI	(R)A G K P V/I C\A\T/Q/M L/E/S/M I K(K)	C:Carbamidomethylation	180.62	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
6497	dirMS_041712_NAR_60mM_plus.17708.17708.3	3	12.13	0	1.41E+05		(R)NHLLPD	(R)N H L L P/D\I\V/T|C V/Q/S S R(K)	C:Carbamidomethylation	149.65	580.3035	1738.891	0.0055	3.1	6.74	20940.9	10.04	HUMAN	Q9BSD7	Cancer-related nucleoside-triphosphatase
6498	dirMS_041712_NAR_60mM_plus.9880.9880.3	3	12.13	1	2.90E+05		(K)SEEQLKE	(K)S/E|E Q/L K E E G I E Y/K(V)		109.28	527.9264	1581.764	0.0004	0.2	4.32	43928.7	6.58	HUMAN	B4DHG0	Dihydrolipoyl dehydrogenase, mitochondrial
6499	dirMS_041712_NAR_120mM_minus.8158.8158.3	3	12.12	0	3.22E+04		(K)HSGPNS	(K)H S\G P N S\A|D S A/N/D/G F/V R(L)		98.87	544.2477	1630.72	0.0081	5	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
6500	dirMS_041712_NAR_120mM_minus.8770.8770.3	3	12.12	0	5.76E+05		(R)THYSNIE	(R)T\H Y S N\I\E|A|N/E/S/E/E V R(Q)		102.13	593.2723	1777.799	0.0036	2	4.48	21983.3	4.68	HUMAN	K7EIV0	Calpain small subunit 1
6501	dirMS_041712_NAR_20mM_minus.13224.13224.2	2	12.12	0	9.37E+04	M329m	(K)ALELNm	(K)A L|E/L/N/m L S L K(G)	m:Oxidized methionine	182.92	574.3232	1131.644	15.9949	0	6.05	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
6502	dirMS_041712_NAR_40mM_minus2.11238.11238.3	3	12.12	1	1.92E+04	M250m	(R)DSDIIED	(R)D S/D|I/I/E D V/m V K D L Q/K(L)	m:Oxidized methionine	149.23	588.6311	1747.878	16.0005	3.2	4.04	55757.3	5.55	HUMAN	O94919	Endonuclease domain-containing 1 protein
6503	dirMS_041712_NAR_50mM_minus2.11651.11725.3	3	12.12	0	3.27E+04	M425m M4	(R)VFITDDF	(R)V/F|I/T D/D F H/D m m P K(Y)	m:Oxidized methionine	134.58	543.2416	1595.723	31.987	-1.7	4.41	92752.5	4.76	HUMAN	P14625	Endoplasmin
6504	dirMS_041712_NAR_50mM_minus2.15954.15954.3	3	12.12	0	9.69E+04		(K)INLEAAE	(K)I/N|L E/A A E L G E/I/S D/I H T K(L)		158.72	618.326	1852.965	-0.0016	-0.9	4.4	84268.2	6.32	HUMAN	Q9UHD2	Serine/threonine-protein kinase TBK1
6505	dirMS_041712_NAR_60mM_minus.9109.9109.2	2	12.12	0	9.67E+05		(K)QEYDES	(K)Q E/Y/D/E S/G P S/I/V/H R(K)		110.35	758.8539	1516.703	-0.0021	-1.4	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
6506	dirMS_041712_NAR_120mM_plus.12538.12538.2	2	12.12	0	7.55E+05		(K)HLSVND	(K)H/L|S/V|N D L/P V G R(S)		119.22	603.8321	1206.659	-0.002	-1.7	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
6507	dirMS_041712_NAR_20mM_plus.10035.10303.2	2	12.12	0	1.43E+06		(K)LVSESSD	(K)L V|S/E/S\S D/V L|P K(-)		143.17	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
6508	dirMS_041712_NAR_30mM_plus2.21826.21826.3	3	12.12	0	3.70E+05		(R)NSILAQV	(R)N S I\L/A Q V/L/D Q/S/A R(A)		170.02	472.2638	1414.765	0.012	8.5	5.84	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
6509	dirMS_041712_NAR_50mM_plus2.5982.5984.3	3	12.12	1	2.51E+06		(R)AQLGGF	(R)A Q|L/G/G/P E A\A/K S D/E T A A K(-)		95.82	548.6114	1643.824	-0.0039	-2.3	4.68	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
6510	dirMS_041712_NAR_50mM_plus2.9906.9923.3	3	12.12	1	4.21E+05	M477m	(R)TLKIPAm	(R)T/L|K I|P A m/T I/A K(N)	m:Oxidized methionine	119.58	401.5718	1186.723	15.9781	-14	10	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
6511	dirMS_041712_NAR_60mM_plus.7277.7277.3	3	12.12	1	1.19E+06		(K)IQDKEGI	(K)I Q/D K E G I/P/P D Q Q R(L)		95.9	508.5982	1523.781	-0.0012	-0.8	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
6512	dirMS_041712_NAR_120mM_minus.8078.8078.3	3	12.11	2	1.87E+05		(R)ASVDTK	(R)A S/V/D/T K E A\E\G A|P Q/V/E A G K R(L)		98.33	648.3315	1942.983	-0.0029	-1.5	4.87	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
6513	dirMS_041712_NAR_120mM_minus.9995.10190.3	3	12.11	0	4.01E+06		(R)QSVEND	(R)Q S/V/E N D/I/H/G L/R(K)		109.3	423.2169	1267.639	-0.0028	-2.2	5.32	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
6514	dirMS_041712_NAR_30mM_minus2.8759.9025.2	2	12.11	0	3.60E+05		(K)IIAPAEQ	(K)I/I|A|P/A E Q/K(I)		102.88	435.2563	869.509	-0.0038	-4.3	6	496093.1	6.13	HUMAN	Q8NCM8	Cytoplasmic dynein 2 heavy chain 1
6515	dirMS_041712_NAR_40mM_minus2.12876.12876.3	3	12.11	0	3.35E+05		(R)DVQIGD	(R)D V|Q|I/G D/I V T V/G E C R P L S K(T)	C:Carbamidomethylation	159.67	662.684	1986.033	0.005	2.5	4.56	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
6516	dirMS_041712_NAR_40mM_minus2.8150.8150.2	2	12.11	0	7.00E+04		(R)IVLQIDN	(R)I V/L Q/I/D/N A R(L)		128.1	521.3059	1041.605	-0.0006	-0.6	5.84	20842.9	5.32	HUMAN	C9JM50	Keratin, type I cytoskeletal 19 (Fragment)
6517	dirMS_041712_NAR_50mM_minus2.16794.16794.3	3	12.11	0	2.43E+05		(R)LGIEGLS	(R)L/G|I/E/G L S L H N V L/K(L)		164.17	464.9452	1392.821	0.0001	0.1	6.75	177928	5.42	HUMAN	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1
6518	dirMS_041712_NAR_120mM_plus.10233.10652.3	3	12.11	1	1.44E+06		(R)LQRLEDI	(R)L/Q/R L E/D/E/L|N/R(A)		108.18	429.2327	1285.686	-0.0023	-1.8	4.68	334221.3	6.44	HUMAN	P15924	Desmoplakin
6519	dirMS_041712_NAR_120mM_plus.4633.4633.3	3	12.11	0	6.19E+05		(R)THSQGG	(R)T\H S Q G G|Y|G/S/Q/G Y K(Y)		74.07	457.2092	1369.613	-0.0001	-0.1	8.2	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
6520	dirMS_041712_NAR_20mM_plus.13858.13858.2	2	12.11	0	1.26E+05	M62m	(R)DASLmV	(R)D A S\L\m\V/T\N D G/A/T I/L/K(N)	m:Oxidized methionine	167.72	782.8922	1548.794	15.9833	-7.4	4.21	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
6521	dirMS_041712_NAR_20mM_plus.18223.18223.2	2	12.11	0	1.70E+05		(R)LTGQLFI	(R)L T/G/Q/L|F/L/G G S I V K(G)		197.02	666.8962	1332.789	-0.0034	-2.6	8.75	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
6522	dirMS_041712_NAR_30mM_plus2.12837.12837.2	2	12.11	0	1.82E+05		(K)SKPVFSE	(K)S K|P V F\S/E/S\L|S D(-)		120.22	598.2946	1195.584	-0.0022	-1.8	4.67	11226.4	5.09	HUMAN	O60220	Mitochondrial import inner membrane translocase subunit Tim8 A
6523	dirMS_041712_NAR_30mM_plus2.7945.7945.2	2	12.11	0	2.20E+05		(K)IAVAAQ	(K)I/A|V/A/A/Q N C Y/K(V)	C:Carbamidomethylation	96.05	569.2905	1137.572	0.0016	1.4	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
6524	dirMS_041712_NAR_40mM_plus2.10711.10711.3	3	12.11	1	4.18E+05		(R)DGKLVS	(R)D G K L V\S\E|S/S D/V/L/P/K(-)		128.6	491.9315	1473.78	0.0004	0.3	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
6525	dirMS_041712_NAR_40mM_plus2.14001.14001.3	3	12.11	0	1.01E+05		(R)LVLEVAC	(R)L/V|L/E/V A Q/H L/G E S T V R(T)		149.03	550.9762	1650.917	-0.0033	-2	5.4	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
6526	dirMS_041712_NAR_40mM_plus2.8980.8980.2	2	12.11	0	1.19E+05		(R)GYSFTTT	(R)G Y/S|F/T/T/T\A/E R(E)		114.9	566.7672	1132.527	0.0002	0.2	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
6527	dirMS_041712_NAR_50mM_plus2.12039.12039.3	3	12.11	0	3.79E+05		(K)FSVCVLC	(K)F/S|V/C/V/L G D Q Q\H C D E\A K(A)	C:Carbamidomethylation	131.38	631.6129	1892.827	-0.0024	-1.3	4.54	25002	10.06	HUMAN	P62906	60S ribosomal protein L10a
6528	dirMS_041712_NAR_60mM_plus.17297.17297.3	3	12.11	0	9.95E+05		(R)QIFHPEC	(R)Q I/F/H P E/Q L I/T G/K(E)		147.17	470.9225	1410.774	-0.021	-14.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
6529	dirMS_041712_NAR_60mM_plus.5576.5576.2	2	12.11	0	4.83E+04		(K)TATPQQ	(K)T A/T/P Q Q\A Q E|V\H/E K(L)		87.62	733.8625	1466.723	-0.0057	-3.9	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
6530	dirMS_041712_NAR_120mM_minus.11749.11749.3	3	12.1	0	5.95E+05		(R)STYYWP	(R)S T|Y/Y/W/P R P/R(R)		118.05	409.2126	1225.611	0.012	9.8	9.98	13152.8	4.23	HUMAN	A1L429	G antigen 12B/C/D/E
6531	dirMS_041712_NAR_20mM_minus.11122.11122.2	2	12.1	0	2.39E+05		(K)LSELEAA	(K)L/S E|L|E\A/A\L Q R(A)		159.33	565.3134	1129.621	-0.0016	-1.5	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
6532	dirMS_041712_NAR_30mM_minus2.10003.10003.2	2	12.1	0	1.30E+06		(R)ANFENL	(R)A/N|F/E N L A/K(E)		109	453.7335	906.468	-0.0082	-9.1	6.05	35720	5.34	HUMAN	B4E358	Src substrate cortactin
6533	dirMS_041712_NAR_30mM_minus2.14820.14962.2	2	12.1	0	4.03E+05		(R)LPLEAAL	(R)L/P|L/E/A A L/R(C)		134.78	441.7731	882.541	-0.0018	-2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
6534	dirMS_041712_NAR_30mM_minus2.17763.17763.2	2	12.1	0	1.59E+04		(R)SLAALSC	(R)S L|A A\L/S/Q I/A/Y/Q/R(N)		150.98	660.8642	1320.727	-0.0059	-4.5	8.46	64225	6.66	HUMAN	E7EX44	Caldesmon
6535	dirMS_041712_NAR_40mM_minus2.12780.12780.3	3	12.1	1	1.47E+04		(R)LDQEVA	(R)L/D/Q/E/V/A E V/D/K N I E L L K(K)		158.83	619.3351	1856.001	-0.0104	-5.6	4.18	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein

6536	dirMS_041712_NAR_50mM_minus2.10319.10319.3	3	12.1	0	1.32E+05		(K)NAQLNI	(K)N A Q L/N/I E L|E/A A/H/H(-)		127.2	487.2478	1459.729	0	0	5.23	13452	8.89	HUMAN	F5H246	Protein NAMPTL
6537	dirMS_041712_NAR_50mM_minus2.12238.12238.3	3	12.1	1	3.31E+05		(R)VVDALG	(R)V/V/D/A L/G/N A\I/D G K G P I G S K(T)		138.07	570.9819	1710.939	-0.0073	-4.3	5.93	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
6538	dirMS_041712_NAR_50mM_minus2.9281.9281.3	3	12.1	1	6.52E+05		(K)VTVAGL	(K)V/T|V/A/G L A G K|D P V Q C S R(D)	C:Carbamidomethylation	121.4	553.2936	1657.869	-0.0028	-1.7	8.72	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
6539	dirMS_041712_NAR_20mM_plus.14108.14108.2	2	12.1	0	7.05E+04	M313m	(R)TVQSLEI	(R)T V/Q/S\L/E/I D L/D/S m R(N)	m:Oxidized methionine	169.18	761.8738	1506.747	15.9935	-0.9	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
6540	dirMS_041712_NAR_20mM_plus.18953.18953.3	3	12.1	0	1.01E+05		(R)AAVPSG	(R)A A V/P S G A S T G I/Y E/A/L/E L/R(D)		201.5	602.3183	1804.944	-0.0036	-2	4.53	43048.9	4.99	HUMAN	B7Z2X9	Enolase
6541	dirMS_041712_NAR_30mM_plus2.10607.10783.2	2	12.1	0	1.01E+06		(R)GCAVVE	(R)G C|A|V/V/E|F/K(M)	C:Carbamidomethylation	109.38	455.2298	909.45	0.0025	2.7	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
6542	dirMS_041712_NAR_30mM_plus2.11994.12029.2	2	12.1	1	5.36E+05		(R)LQKLPTS	(R)L/Q|K|L|P T/S|M(-)		116.08	459.2593	917.513	-0.0011	-1.2	8.75	9148.5	9.4	HUMAN	C9JES7	COX assembly mitochondrial protein homolog
6543	dirMS_041712_NAR_30mM_plus2.12606.12606.2	2	12.1	0	5.61E+05		(K)NAGVEC	(K)N A|G|V|E|G S L I V E K(I)		118.43	608.3313	1215.658	-0.0026	-2.2	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
6544	dirMS_041712_NAR_30mM_plus2.18062.18062.2	2	12.1	0	2.28E+05		(R)QITLNDI	(R)Q I/T/L/N/D L/P V/G R(S)		147.85	613.3465	1225.69	-0.0042	-3.4	5.84	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
6545	dirMS_041712_NAR_40mM_plus2.17771.17771.3	3	12.1	0	1.46E+05		(R)LPVPPLC	(R)L P/V/P/P L Q Q S L D H Y L K(A)		171.22	583.3378	1747.974	0.0247	14.1	6.74	18575.3	9.69	HUMAN	A6PVN3	Carnitine O-acetyltransferase
6546	dirMS_041712_NAR_50mM_plus2.10845.10845.3	3	12.1	1	2.46E+06		(R)MQKEIT	(R)M/Q/K E I T\A|L|A/P S T M K(I)		124.03	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
6547	dirMS_041712_NAR_60mM_plus.18581.18581.3	3	12.1	1	1.52E+05		(R)CRVDLP	(R)C R V D\L|P/L|A V L/S K(M)	C:Carbamidomethylation	154.35	457.599	1370.782	0	0	8.75	7765.6	8.23	HUMAN	H3BSA6	dCTP pyrophosphatase 1
6548	dirMS_041712_NAR_30mM_minus2.10824.11075.2	2	12.09	0	2.51E+06		(R)TSASIILR	(R)T/S|A|S I/I L/R(G)		112.08	430.7619	860.52	-0.0035	-4	9.41	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
6549	dirMS_041712_NAR_30mM_minus2.12723.12741.2	2	12.09	0	2.31E+05		(R)DTYVSSI	(R)D T|Y|V/S S/F/P R(A)		122.43	536.2608	1071.511	0.0038	3.5	5.83	34425.5	9.08	HUMAN	P23193	Transcription elongation factor A protein 1
6550	dirMS_041712_NAR_40mM_minus2.11604.11604.3	3	12.09	0	1.30E+04	M95m	(K)GIEILTDI	(K)G I/E/I/L T/D/m S/R P V E L S D/R(E)	m:Oxidized methionine	151.05	649.6701	1930.99	16.0055	5.4	4.32	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
6551	dirMS_041712_NAR_50mM_minus2.16719.16719.3	3	12.09	1	2.06E+04		(R)VTFSGLI	(R)V/T|F/S G L R D T V T/P G E L L K(A)		163.35	611.672	1833.012	-0.0102	-5.6	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
6552	dirMS_041712_NAR_60mM_minus.13617.13618.3	3	12.09	1	1.80E+05		(K)QMADT	(K)Q M/A/D/T/G/K L/N T L/L Q R(A)		135.92	530.2846	1588.848	-0.0083	-5.2	8.75	91324.5	5.75	HUMAN	Q00839	Heterogeneous nuclear ribonucleoprotein U
6553	dirMS_041712_NAR_60mM_minus.14763.14763.3	3	12.09	0	2.66E+05		(K)YYITIIDA	(K)Y Y I/T I/I/D/A/P G H R(D)		142.87	473.5815	1418.743	-0.0127	-9	6.74	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
6554	dirMS_041712_NAR_60mM_minus.19729.19744.3	3	12.09	0	4.74E+06		(R)LHFFMP	(R)L H\F F\M\P G\F|A|P\L T S R(G)		179.25	540.9491	1620.835	-0.0028	-1.7	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
6555	dirMS_041712_NAR_20mM_plus.12485.12485.2	2	12.09	0	1.88E+05		(R)GVEICIA	(R)G V\E|I|C/I/A|T P G/R(L)	C:Carbamidomethylation	158.73	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
6556	dirMS_041712_NAR_20mM_plus.14288.14288.2	2	12.09	0	5.25E+04		(K)LIINSLYK	(K)L/I|I/N S\L Y K(N)		169.95	482.2962	963.587	-0.0022	-2.3	8.59	5582.4	4.81	HUMAN	F8W026	Endoplasmin (Fragment)
6557	dirMS_041712_NAR_30mM_plus2.16845.16944.2	2	12.09	0	5.02E+05		(K)FVADGII	(K)F/V|A/D/G/I/F/K(A)		141.87	448.7485	896.488	0.0021	2.3	5.84	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
6558	dirMS_041712_NAR_30mM_plus2.21930.21930.2	2	12.09	0	1.03E+05		(K)NFYFLEN	(K)N F/Y|F/L E M/N T R(L)		170.5	667.8205	1334.62	0.0139	10.4	6	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
6559	dirMS_041712_NAR_40mM_plus2.18086.18086.3	3	12.09	1	1.23E+05		(K)LIQLMEI	(K)L/I/Q/L/M/E E I M A E K E/N/K(T)		172.53	606.982	1818.934	-0.0025	-1.4	4.49	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
6560	dirMS_041712_NAR_50mM_plus2.10195.10195.3	3	12.09	0	6.15E+05		(K)VGQEIE\	(K)V/G|Q|E I/E V R P G/I V S K(D)		121.05	504.2907	1510.859	-0.0012	-0.8	6.11	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
6561	dirMS_041712_NAR_50mM_plus2.17342.17424.3	3	12.09	1	9.23E+05		(R)VYAEDP	(R)V/Y|A E/D/P Y K S F/G L/P S I G R(L)		159.32	633.6509	1898.965	-0.0265	-14	6.04	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
6562	dirMS_041712_NAR_50mM_plus2.17819.17952.3	3	12.09	1	1.98E+05		(K)VLTLSDI	(K)V/L|T|L S D D/L E R T I E/E R(V)		162.37	596.9838	1788.934	0.0031	1.7	4.18	49678.3	5.41	HUMAN	P55010	Eukaryotic translation initiation factor 5
6563	dirMS_041712_NAR_60mM_plus.20057.20119.3	3	12.09	1	5.02E+05		(R)GFKDQI	(R)G F K D Q\I|Y/D/I/F/Q/K(L)		164.73	501.2609	1501.769	-0.0004	-0.3	5.96	26945.8	8.07	HUMAN	J3KSZ0	Eukaryotic initiation factor 4A-I (Fragment)
6564	dirMS_041712_NAR_60mM_plus.9471.9471.3	3	12.09	0	4.80E+05		(K)QADNPI	(K)Q A/D\N/P H V/A/L/Y Q A R(F)		107.52	494.9186	1482.745	-0.0036	-2.4	6.74	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
6565	dirMS_041712_NAR_30mM_minus2.14068.14068.2	2	12.08	0	3.06E+05		(R)LAGLFNI	(R)L/A|G/L/F N E/Q R(K)		129.7	524.2789	1047.558	-0.0076	-7.3	6	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
6566	dirMS_041712_NAR_30mM_minus2.16513.16513.2	2	12.08	0	4.38E+05	M185m	(K)LAVNm\	(K)L A|V/N/m V|P\F P R(L)	m:Oxidized methionine	142.67	580.3178	1143.634	15.994	-0.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
6567	dirMS_041712_NAR_50mM_minus2.16082.16305.3	3	12.08	1	4.74E+05		(K)LFTAESL	(K)L F|T/A/E S L I/G L K N/P E K(S)		160.67	553.9759	1659.932	-0.0185	-11.1	6.14	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
6568	dirMS_041712_NAR_50mM_minus2.16690.16828.3	3	12.08	1	1.60E+05		(K)NIPIPTLI	(K)N I|P/I/P T L K D/F A K(A)		163.38	452.9385	1356.789	0.0124	9.1	8.59	20960.6	7.05	HUMAN	H0YKU1	Tropomodulin-3 (Fragment)
6569	dirMS_041712_NAR_60mM_minus.6550.6550.3	3	12.08	1	4.07E+04		(K)SPPREG	(K)S P P R E G S Q G E/L|T/P A N S Q S R(M)		95.02	666.6591	1997.964	-0.0008	-0.4	5.87	53941.6	6.3	HUMAN	C9JFE4	COP9 signalosome complex subunit 1
6570	dirMS_041712_NAR_20mM_plus.18355.18355.3	3	12.08	0	8.80E+04	M36m	(K)NIPmTLI	(K)N I|P/m T\L E L\L|Q S T/R(I)	m:Oxidized methionine	197.85	511.28	1515.82	16.0055	6.9	6	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
6571	dirMS_041712_NAR_30mM_plus2.11186.11186.2	2	12.08	0	1.42E+05		(K)SVTNED	(K)S V/T|N\E/D/V/T Q E/E L/G G A K(T)		111.78	838.9006	1676.797	-0.0034	-2	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
6572	dirMS_041712_NAR_50mM_plus2.20033.20033.3	3	12.08	1	5.31E+05		(-)MDELQL	(-)M/D/E/L Q L F/R/G D/T V L L K(G)		173.25	593.3209	1777.952	-0.0035	-2	4.56	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
6573	dirMS_041712_NAR_50mM_plus2.7373.7373.3	3	12.08	1	1.96E+05	M32m	(K)GGImLP	(K)G G/I/m/L|P E K S Q G K(V)	m:Oxidized methionine	104.6	420.8922	1244.667	15.9953	0.3	8.59	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
6574	dirMS_041712_NAR_60mM_plus.12207.12242.3	3	12.08	1	1.23E+06		(R)LNDSILC	(R)L/N|D/S/I L/Q A T E Q R/R(R)		120.47	515.2771	1543.819	-0.0019	-1.3	6.07	334221.3	6.44	HUMAN	P15924	Desmoplakin
6575	dirMS_041712_NAR_60mM_plus.20309.20309.3	3	12.08	1	4.21E+05		(K)NAAGAL	(K)N/A/A/G/A L D L L/K E L K(N)		166.93	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
6576	dirMS_041712_NAR_120mM_minus.7822.7822.3	3	12.07	1	2.74E+06	M281m	(R)SRAEAE	(R)S R A E\A\E|S m/Y Q I/K(Y)	m:Oxidized methionine	96.75	476.8951	1412.684	15.9869	-5.6	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
6577	dirMS_041712_NAR_120mM_minus.9419.9767.3	3	12.07	1	6.94E+06		(R)SRAEAE	(R)S R A E\A\E|S|M/Y Q/I/K(Y)		107.13	471.5662	1412.684	0.0002	0.1	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
6578	dirMS_041712_NAR_30mM_minus2.11969.11969.2	2	12.07	0	7.50E+05		(K)SIYYITGI	(K)S\I|Y/Y/I T G E S/K(E)		119.15	580.7949	1160.583	-0.0009	-0.7	5.72	16789.1	8.77	HUMAN	H0Y5S7	Heat shock protein HSP 90-beta (Fragment)
6579	dirMS_041712_NAR_30mM_minus2.14101.14101.2	2	12.07	0	5.74E+05		(R)SEQFINL	(R)S E|Q|F|I N L R(E)		130.7	503.7677	1006.532	-0.0035	-3.5	5.72	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
6580	dirMS_041712_NAR_50mM_minus2.10366.10366.3	3	12.07	0	1.66E+05		(K)LQAEAP	(K)L/Q/A E A P/H I/V V/G T P G R(V)		127.08	515.6179	1544.854	-0.0152	-9.8	6.75	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
6581	dirMS_041712_NAR_50mM_minus2.8355.8355.3	3	12.07	1	8.27E+04	M61m	(K)NQVAm	(K)N\Q|V/A m/N P T N T V/F D A K R(L)	m:Oxidized methionine	114.92	607.968	1805.896	15.9932	-1	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
6582	dirMS_041712_NAR_60mM_minus.18651.18651.3	3	12.07	0	1.23E+05		(R)IDILDSA	(R)I/D|I/L/D S A/L L R P G R(I)		165.33	480.2832	1438.838	-0.0026	-1.8	5.96	44954.5	8.44	HUMAN	A8K3Z3	26S protease regulatory subunit 8
6583	dirMS_041712_NAR_60mM_minus.7067.7067.3	3	12.07	1	3.61E+05		(K)LDEREA	(K)L/D/E/R E A G\I T E/K(V)		98.2	420.8852	1260.643	-0.002	-1.6	4.41	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
6584	dirMS_041712_NAR_120mM_plus.11413.11516.3	3	12.07	0	7.29E+05		(R)STYYWP	(R)S/T|Y/Y/W/P R P R(R)		113.28	409.2097	1225.611	0.0033	2.7	9.98	13152.8	4.23	HUMAN	A1L429	G antigen 12B/C/D/E
6585	dirMS_041712_NAR_120mM_plus.7235.7235.3	3	12.07	1	3.21E+05	M462m	(R)KAYGGA	(R)K\A Y G G A\Y|D|V/m/S S/K(H)	m:Oxidized methionine	91.37	464.8863	1376.651	15.9929	-1.5	8.43	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
6586	dirMS_041712_NAR_20mM_plus.16885.16895.2	2	12.07	0	1.86E+05		(R)IVLLDSS	(R)I/V|L/L/D S S L\E Y|K(K)		187.52	640.36	1279.714	-0.0017	-1.3	4.37	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
6587	dirMS_041712_NAR_20mM_plus.7302.7324.2	2	12.07	0	3.31E+05	M281m	(R)AEAESm	(R)A E|A|E/S/m Y Q/I/K(Y)	m:Oxidized methionine	118.62	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
6588	dirMS_041712_NAR_30mM_plus2.10785.10868.2	2	12.07	0	3.53E+05		(K)SLLSAEE	(K)S L|L/S/A/E E A/A/K(Q)		109.93	509.7774	1018.542	0.006	5.9	4.53	102679.8	6.75	HUMAN	Q7KZF4	Staphylococcal nuclease domain-containing protein 1
6589	dirMS_041712_NAR_30mM_plus2.13537.13597.2	2	12.07	0	2.02E+05		(R)LIIAGTS	(R)L I|I/A|G/T S/A Y A R(L)		124.3	568.322	1135.647	-0.0103	-9	8.75	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
6590	dirMS_041712_NAR_30mM_plus2.16048.16532.2	2	12.07	0	1.13E+06		(R)IFIGTFK	(R)I/F|I/G T/F/K(A)		138.43	413.2445	825.487	-0.0052	-6.3	8.75	25246.3	11.45	HUMAN	B3KVR1	Small nuclear ribonucleoprotein-associated protein
6591	dirMS_041712_NAR_30mM_plus2.16770.16770.2	2	12.07	0	3.06E+05		(K)SNQQLV	(K)S N/Q|Q|L/V/D I I/E K(V)		141.15	643.8504	1286.695	-0.0015	-1.2	4.37	22568.6	6.35	HUMAN	B3KQ25	Proteasome activator complex subunit 3
6592	dirMS_041712_NAR_30mM_plus2.18493.18493.2	2	12.07	0	7.81E+04		(R)VVNVSS	(R)V V|N V/S S I/M/S V R(A)		149.77	595.8347	1190.656	0.006	5	9.72	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
6593	dirMS_041712_NAR_30mM_plus2.20104.20104.2	2	12.07	0	1.72E+05		(R)MLDMG	(R)M L|D/M/G\F/E/P Q I/R(K)		159.2	668.8241	1336.639	0.0021	1.6	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
6594	dirMS_041712_NAR_60mM_plus.11378.11378.3	3	12.07	0	4.60E+06		(R)GSAVHC	(R)G/S/A/V/H/Q/L/S E E L R(C)		116.45	442.5666	1325.681	0.0044	3.4	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
6595	dirMS_041712_NAR_50mM_minus2.14214.14214.3	3	12.06	1	2.08E+05		(R)DLAALG	(R)D L|A|A/L/G D K V N S/L|G E T A E R(L)		149.15	620.3204	1858.95	-0.0038	-2.1	4.32	285798.6	5.23	HUMAN	A6NG51	Spectrin alpha chain, non-erythrocytic 1
6596	dirMS_041712_NAR_50mM_minus2.16702.16702.3	3	12.06	1	9.23E+04		(R)DSEQVA	(R)D\S|E/Q/V/A E/L K Q/E L A T L K(S)		163.05	601.3217	1801.954	-0.0036	-2	4.41	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
6597	dirMS_041712_NAR_60mM_minus.15622.15622.3	3	12.06	1	1.72E+05		(R)GRLPLLA	(R)G R L\P\L\L|A\V/C D Y K(Q)	C:Carbamidomethylation	146.87	468.9273	1404.767	0.0006	0.4	8.59	533778	5.74	HUMAN	Q15149	Plectin
6598	dirMS_041712_NAR_60mM_minus.18060.18092.3	3	12.06	1	2.77E+05		(R)TRIEGLL	(R)T R I E G\L|L|A/A/F/P\K(L)		161.67	439.2618	1315.773	-0.0024	-1.8	8.41	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
6599	dirMS_041712_NAR_20mM_plus.11541.11541.2	2	12.06	0	1.79E+05		(K)VGLQVV	(K)V/G|L/Q|V V|A V/K(A)		151.72	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
6600	dirMS_041712_NAR_30mM_plus2.18459.18485.2	2	12.06	0	6.04E+04		(K)NLGTAL	(K)N L|G/T/A/L/A/E L/R(T)		150	529.3028	1057.6	-0.0017	-1.6	6	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
6601	dirMS_041712_NAR_30mM_plus2.19640.19640.2	2	12.06	0	6.82E+05		(R)LIDFLEC	(R)L/I|D/F/L\E/C G/K(T)	C:Carbamidomethylation	155.7	547.7808	1094.555	-0.0007	-0.7	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
6602	dirMS_041712_NAR_40mM_plus2.11463.11464.3	3	12.06	0	7.03E+04		(K)TVPEEL\	(K)T V|P/E E L V/K/P E E/L S K(Y)		133.57	533.2936	1597.868	-0.0021	-1.3	4.49	27945.7	6.25	HUMAN	F5GY56	Pre-mRNA-processing factor 19 (Fragment)
6603	dirMS_041712_NAR_40mM_plus2.12711.12711.3	3	12.06	0	2.65E+05		(K)AASDIAI	(K)A A|S D I/A/M\T E L/P P T H P I R(L)		140.77	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
6604	dirMS_041712_NAR_40mM_plus2.19266.19339.3	3	12.06	1	4.28E+05		(K)LLPLVSD	(K)L L|P/L/V/S D E V F I R D/V A K(V)		180.72	605.3503	1814.042	-0.0059	-3.2	4.56	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
6605	dirMS_041712_NAR_40mM_plus2.5857.5910.2	2	12.06	0	1.19E+05		(K)LLEGEES	(K)L/L|E|G E E/S R(I)		92.77	466.739	932.468	0.0024	2.5	4.25	49709.6	5.19	HUMAN	B0YJC4	Vimentin
6606	dirMS_041712_NAR_60mM_plus.16384.16571.3	3	12.06	1	5.89E+05		(R)VTPTRTI	(R)V/T|P T R T E I\I/I/L/A T R(T)		142.97	528.653	1583.948	-0.0035	-2.2	9.57	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
6607	dirMS_041712_NAR_60mM_plus.9520.9520.3	3	12.06	0	1.05E+06		(K)GHENVE	(K)G H E\N V\E\A\A|Q/A/E Y I E K(F)		108.07	563.2692	1687.792	0.0008	0.5	4.48	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
6608	dirMS_041712_NAR_120mM_minus.17639.17639.3	3	12.05	2	1.89E+05		(R)GYSFTTI	(R)G Y/S\F/T/T/T A E R E I V R D/I K(E)		150.63	662.6807	1986.029	-0.0015	-0.8	6.18	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
6609	dirMS_041712_NAR_30mM_minus2.19403.19522.2	2	12.05	0	2.44E+05		(R)ILVATNL	(R)I/L|V/A/T/N L/F G R(G)		162.07	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
6610	dirMS_041712_NAR_50mM_minus2.14980.14980.3	3	12.05	1	8.94E+05		(R)IINEPTA.	(R)I I|N|E P T A A A I/A Y G L D/K R(E)		152.67	606.0022	1815.996	-0.0043	-2.4	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
6611	dirMS_041712_NAR_50mM_minus2.15744.15744.3	3	12.05	0	6.81E+04		(K)LLDSSTV	(K)L|L/D S/S T/V T H/L F K(I)		157.6	454.2542	1360.747	0.001	0.7	6.74	25746.2	6.77	HUMAN	B4DXJ9	Proteasome (Prosome, macropain) subunit, alpha type, 6, isoform CRA_a
6612	dirMS_041712_NAR_120mM_plus.8859.8859.3	3	12.05	0	5.55E+05		(R)FACHSA	(R)F A|C/H/S/A/S L/T\V R(N)	C:Carbamidomethylation	99.62	416.8772	1248.615	0.0017	1.3	9.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
6613	dirMS_041712_NAR_20mM_plus.13455.13455.2	2	12.05	0	9.69E+04		(R)AELIVQF	(R)A E|L|I/V Q/P E L K(Y)		164.3	570.3361	1139.667	-0.0021	-1.9	4.53	334221.3	6.44	HUMAN	P15924	Desmoplakin
6614	dirMS_041712_NAR_20mM_plus.15893.15893.2	2	12.05	0	1.21E+05		(R)GTPLISP	(R)G T|P L|I/S P L I K(W)		181.08	519.8306	1038.656	-0.0018	-1.8	8.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
6615	dirMS_041712_NAR_30mM_plus2.10467.10467.2	2	12.05	0	5.36E+04		(K)TAVCDIF	(K)T A\V|C/D/I|P|P/R(G)	C:Carbamidomethylation	108.98	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
6616	dirMS_041712_NAR_40mM_plus2.6168.6168.3	3	12.05	1	3.14E+04		(R)AQLGGF	(R)A Q|L/G G P/E A A K S D E T A A/K(-)		95.22	548.6136	1643.824	0.0027	1.7	4.68	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
6617	dirMS_041712_NAR_40mM_plus2.9252.9252.3	3	12.05	0	7.25E+03	M115m	(R)VmLGET	(R)V m|L/G E/T N/P A D S K P G/T I R(G)	m:Oxidized methionine	117.13	601.3077	1785.916	15.9922	-1.5	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
6618	dirMS_041712_NAR_60mM_plus.16905.16948.3	3	12.05	1	2.15E+05		(K)YMACCL	(K)Y/M|A/C/C L L/Y R G D V V/P K(E)	C:Carbamidomethylation	145.85	615.6325	1844.886	-0.0026	-1.4	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
6619	dirMS_041712_NAR_60mM_plus.17805.17867.3	3	12.05	1	7.75E+05		(K)KYDAFL	(K)K\Y/D A\F\L|A/S E/S L I/K(Q)		150.5	495.6047	1484.8	0	0	6.07	25002	10.06	HUMAN	P62906	60S ribosomal protein L10a
6620	dirMS_041712_NAR_60mM_plus.18462.18462.3	3	12.05	1	1.58E+05		(R)CRVDLP	(R)C R V D\L|P/L A V/L/S K(M)	C:Carbamidomethylation	154.05	457.599	1370.782	0	0	8.75	7765.6	8.23	HUMAN	H3BSA6	dCTP pyrophosphatase 1
6621	dirMS_041712_NAR_120mM_minus.18024.18024.3	3	12.04	1	2.86E+05		(R)ARFEELI	(R)A R\F E E\L\N|A/D/L F/R(G)		153.08	494.2561	1480.754	-0.0006	-0.4	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
6622	dirMS_041712_NAR_120mM_minus.8351.8390.3	3	12.04	1	4.70E+05		(R)ASRDEIF	(R)A S R D\E\I|F/A/Q/S K(E)		99.97	417.8786	1251.633	-0.0115	-9.2	6.12	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
6623	dirMS_041712_NAR_20mM_minus.10386.10386.2	2	12.04	0	9.30E+04		(R)NTGIICT	(R)N T/G\I|I/C T/I/G P A S/R(S)	C:Carbamidomethylation	152.63	680.3561	1359.705	0	0	9.75	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
6624	dirMS_041712_NAR_30mM_minus2.7638.7655.2	2	12.04	0	2.88E+05		(R)ELAQQI	(R)E L/A/Q/Q/I/Q/K(V)		96.05	479.2746	957.536	0.0056	5.8	6.1	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
6625	dirMS_041712_NAR_30mM_minus2.8547.8708.2	2	12.04	0	1.06E+06		(R)SYSDPPI	(R)S/Y|S|D P/P L/K(F)		101.68	453.7335	906.457	0.003	3.3	5.55	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
6626	dirMS_041712_NAR_40mM_minus2.8217.8217.3	3	12.04	0	1.68E+05		(R)LLEAQA	(R)L L|E/A/Q A/C T G G I I H P T T G Q K(L)	C:Carbamidomethylation	128.68	665.6822	1995.033	-0.0007	-0.4	6.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
6627	dirMS_041712_NAR_120mM_plus.18220.18220.4	4	12.04	1	6.50E+05		(R)ILEFFGLI	(R)I/L|E/F F G L K/K/E E C P A V R(L)	C:Carbamidomethylation	148.63	484.7638	1936.036	-0.0027	-1.4	6.23	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
6628	dirMS_041712_NAR_20mM_plus.13816.13816.2	2	12.04	0	2.44E+05	M98m	(R)TLTIVDT	(R)T L/T\I/V/D T G I G|m T K(A)	m:Oxidized methionine	167.3	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
6629	dirMS_041712_NAR_20mM_plus.14129.14129.2	2	12.04	0	2.12E+05		(R)AALQELI	(R)A A/L/Q/E L/L/S K(G)		168.92	486.789	972.572	-0.0017	-1.7	6.05	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
6630	dirMS_041712_NAR_40mM_plus2.17860.17860.3	3	12.04	0	1.42E+05		(R)DIKPQN	(R)D I K P Q N\L/L|L/D|P D T A V\L K(L)		170.92	631.6874	1893.069	-0.0215	-11.4	4.43	47257	9.38	HUMAN	P49841	Glycogen synthase kinase-3 beta
6631	dirMS_041712_NAR_50mM_plus2.11491.11491.3	3	12.04	1	2.53E+05		(R)ICCDLD\	(R)I/C/C D L D V/L/A/S/K K(V)	C:Carbamidomethylation	128.2	474.5801	1421.713	0.013	9.2	5.96	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
6632	dirMS_041712_NAR_30mM_minus2.13806.13806.2	2	12.03	0	2.22E+05		(R)SISLYYT	(R)S I|S/L/Y/Y/T/G E/K(G)		128.27	580.7949	1160.583	-0.0009	-0.7	5.72	32503.1	5.29	HUMAN	H7BY16	Nucleolin (Fragment)
6633	dirMS_041712_NAR_30mM_minus2.9699.9699.2	2	12.03	0	3.50E+05		(R)SSENPN	(R)S/S E/N/P/N E V/F/R(F)		107.32	589.7805	1178.544	0.0101	8.6	4.53	96697.4	4.91	HUMAN	P45974	Ubiquitin carboxyl-terminal hydrolase 5
6634	dirMS_041712_NAR_50mM_minus2.8740.8740.3	3	12.03	1	8.70E+04		(R)LLDEEEA	(R)L L|D/E/E E A/T D N D L R A K(F)		117.43	577.9535	1731.84	0.0064	3.7	4.02	96649	6.13	HUMAN	Q8WUM4	Programmed cell death 6-interacting protein
6635	dirMS_041712_NAR_60mM_minus.10674.10674.3	3	12.03	1	5.44E+05	M232m	(R)MSmKE\	(R)M/S m K E V D E/Q M|L N V Q/N K(N)	m:Oxidized methionine	119.9	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
6636	dirMS_041712_NAR_60mM_minus.9673.9673.3	3	12.03	1	5.37E+05		(R)IITEGFE	(R)I I|T E/G/F/E A A K E K(A)		113.88	445.91	1335.716	0	0	4.79	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
6637	dirMS_041712_NAR_120mM_plus.13456.13477.4	4	12.03	2	2.50E+05		(R)RLEGED	(R)R L E G\E D S A R E\T|P/I/G/L V/P/K(E)		123.5	492.5177	1967.056	-0.0067	-3.4	4.87	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
6638	dirMS_041712_NAR_120mM_plus.8894.8894.3	3	12.03	0	2.91E+05		(K)VTWDGI	(K)V/T|W/D/G H/S/G S M A R(T)		100.18	435.2046	1303.585	0.0145	11.1	6.71	81733.5	5.24	HUMAN	E9PAW1	Splicing factor 3A subunit 1
6639	dirMS_041712_NAR_20mM_plus.10652.10652.2	2	12.03	0	4.78E+04		(K)GILAADI	(K)G I/L|A/A|D/E S T G S I A K(R)		145.93	666.8531	1332.7	-0.0016	-1.2	4.37	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
6640	dirMS_041712_NAR_20mM_plus.12391.12511.2	2	12.03	0	1.78E+05		(K)TIIFVETI	(K)T I|I/F V/E T K(R)		158.87	475.7818	950.556	0.0006	0.6	5.66	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
6641	dirMS_041712_NAR_30mM_plus2.14101.14273.2	2	12.03	0	5.28E+05		(R)SEQFINL	(R)S E|Q|F/I|N/L/R(E)		126.98	503.7693	1006.532	-0.0003	-0.3	5.72	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
6642	dirMS_041712_NAR_30mM_plus2.15755.15755.2	2	12.03	0	2.11E+05		(K)LLPPYLR	(K)L\L/P/P/Y/L/R(V)		135.38	436.2709	871.54	-0.0055	-6.3	8.75	55805.4	6.7	HUMAN	P43490	Nicotinamide phosphoribosyltransferase
6643	dirMS_041712_NAR_30mM_plus2.21697.21697.2	2	12.03	0	3.32E+05		(R)FSWNV\	(R)F S/W/N/V W/P S S R(L)		169.18	633.3085	1265.606	0.0035	2.8	9.75	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
6644	dirMS_041712_NAR_40mM_plus2.16098.16098.3	3	12.03	0	3.15E+05		(K)VAIVKPC	(K)V/A|I V K P G V/P|M E/I V L N K(E)		161.32	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)

6645	dirMS_041712_NAR_40mM_plus2.17854.17854.3	3	12.03	0	1.66E+05		(K)LAKPLSS	(K)L/A K P L S S L\T/P L I M A A K(E)		171.7	552.0052	1653.997	0.0039	2.3	10	24711.4	5.19	HUMAN	H7C1X3	PAK-2p34 (Fragment)
6646	dirMS_041712_NAR_40mM_plus2.7620.7620.2	2	12.03	0	1.66E+05		(R)SGYFDEI	(R)S G|Y/F D/E/R(Y)		104.47	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
6647	dirMS_041712_NAR_40mM_plus2.9016.9016.2	2	12.03	0	8.93E+04		(K)GSDFDC	(K)G S/D/F/D/C E/L R(L)	C:Carbamidomethylation	115.47	549.7296	1098.452	-0.0001	-0.1	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
6648	dirMS_041712_NAR_50mM_plus2.15494.15494.3	3	12.03	0	1.51E+06		(R)LASTLVH	(R)L A|S T L/V H L G E Y/Q A/A/V D/G A/R(K)		149.68	657.6802	1971.029	-0.0034	-1.7	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
6649	dirMS_041712_NAR_60mM_plus.12243.12394.3	3	12.03	0	9.17E+05		(K)TKPYIQV	(K)T K|P Y\I Q\V/D|I/G/G G Q T K(T)		121.42	535.6249	1604.864	-0.0041	-2.6	8.17	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
6650	dirMS_041712_NAR_60mM_plus.18453.18453.3	3	12.03	1	7.09E+05		(R)IRIDSLS	(R)I R I D\S\L\S\A\Q|L/S\Q L Q|K(Q)		153.97	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
6651	dirMS_041712_NAR_60mM_plus.7390.7390.2	2	12.03	1	1.58E+06		(R)AAPGAE	(R)A/A/P/G A|E/F A\P N K R(R)		96.2	614.8248	1228.643	-0.001	-0.8	8.79	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
6652	dirMS_041712_NAR_120mM_minus.7093.7093.3	3	12.02	1	3.74E+05		(K)DSYVGD	(K)D\S/Y|V/G D E/A Q S K/R(G)		92.47	452.2134	1354.623	0.0023	1.7	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
6653	dirMS_041712_NAR_120mM_minus.7296.7296.3	3	12.02	1	1.49E+06		(R)CREMDE	(R)C R E\M/D|E/Q/I/R(L)	C:Carbamidomethylation	93.97	412.8591	1236.546	0.0168	13.6	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
6654	dirMS_041712_NAR_120mM_minus.8557.8557.3	3	12.02	1	4.19E+05		(R)LKVTEG	(R)L/K V\T E G G E/P/Y/R(L)		100.63	416.885	1248.658	-0.0178	-14.3	6.14	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
6655	dirMS_041712_NAR_30mM_minus2.13749.13849.2	2	12.02	0	2.22E+05		(R)SISLYYT	(R)S I|S|L/Y/Y T G E/K(G)		128.27	580.7949	1160.583	-0.0009	-0.7	5.72	32503.1	5.29	HUMAN	H7BY16	Nucleolin (Fragment)
6656	dirMS_041712_NAR_30mM_minus2.16174.16174.2	2	12.02	0	3.40E+05	M185m	(K)LAVNm	(K)L A\V/N m V|P/F P R(L)	m:Oxidized methionine	142.37	580.3178	1143.634	15.994	-0.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
6657	dirMS_041712_NAR_50mM_minus2.14167.14167.3	3	12.02	1	1.31E+05		(R)QFVPIK	(R)Q F/V|P I/K V E Q/I/E/A/G T P G R(L)		148.68	623.6775	1869.023	-0.0049	-2.6	6.14	55287.2	6.08	HUMAN	B2R5P6	Thioredoxin reductase 1, cytoplasmic
6658	dirMS_041712_NAR_50mM_minus2.7421.7421.3	3	12.02	0	4.47E+04		(R)IYDLNKF	(R)I/Y|D/L N K/P E A E/P/K(E)		109.18	472.9187	1416.737	0.0046	3.3	4.68	28733.7	4.82	HUMAN	B0AZV0	Serine-threonine kinase receptor-associated protein
6659	dirMS_041712_NAR_60mM_minus.17174.17272.3	3	12.02	1	1.10E+05		(R)CRVDLP	(R)C R V D\L|P\L|A\V/L/S/K(M)	C:Carbamidomethylation	156	457.5982	1370.782	-0.0024	-1.7	8.75	7765.6	8.23	HUMAN	H3BSA6	dCTP pyrophosphatase 1
6660	dirMS_041712_NAR_60mM_minus.7842.7843.3	3	12.02	1	4.71E+05		(K)IQDKEGI	(K)I Q D K E G|I|P/P/D Q Q R(L)		103.4	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
6661	dirMS_041712_NAR_20mM_plus.13962.13962.2	2	12.02	0	6.12E+04		(K)IVPNVLL	(K)I V/P N/V L L/E Q G K(A)		167.72	605.3616	1209.72	-0.0042	-3.5	6	50659.2	7.87	HUMAN	B4DJV2	Citrate synthase
6662	dirMS_041712_NAR_20mM_plus.17475.17475.3	3	12.02	0	2.28E+05	M90m	(R)LFVGNLI	(R)L F V/G N\L\P/P D I/T/E/E E m R(K)	m:Oxidized methionine	192.4	625.9762	1859.921	15.9933	-0.9	4	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
6663	dirMS_041712_NAR_20mM_plus.7481.7489.2	2	12.02	0	2.40E+05		(K)VTLTSEE	(K)V/T|L/T/S E E E A/R(L)		119.92	567.7865	1134.564	0.002	1.8	4.25	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
6664	dirMS_041712_NAR_20mM_plus.9041.9041.2	2	12.02	0	4.38E+05	M161m	(K)LLIEmEC	(K)L L|I/E m E/Q/R(L)	m:Oxidized methionine	132.78	524.278	1031.555	15.9933	-1.5	4.53	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
6665	dirMS_041712_NAR_30mM_plus2.11815.11832.2	2	12.02	0	5.94E+04		(R)GCTATL	(R)G/C|T|A/T/L|G N F\A K(A)	C:Carbamidomethylation	116.57	570.2807	1139.551	0.0028	2.4	8.75	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
6666	dirMS_041712_NAR_30mM_plus2.14328.14328.2	2	12.02	0	3.57E+05		(R)ELAFQIS	(R)E L/A/F/Q/I/S K(E)		128.28	468.2629	935.52	-0.0011	-1.2	6.1	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
6667	dirMS_041712_NAR_40mM_plus2.9981.9981.2	2	12.02	0	2.48E+05		(K)EQFAWI	(K)E/Q|F/A/W/R(H)		122.88	418.706	836.405	-0.0002	-0.3	6.1	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
6668	dirMS_041712_NAR_50mM_plus2.11778.11778.3	3	12.02	1	7.42E+05		(R)INVYYNI	(R)I N|V|Y/Y|N/E A T G G K Y V/P R(A)		130.43	615.3151	1843.934	-0.003	-1.6	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
6669	dirMS_041712_NAR_50mM_plus2.18803.18803.3	3	12.02	1	6.22E+05	M1m	(-)mDELQLI	(-)m/D|E|L/Q/L F R G D T V L L K(G)	m:Oxidized methionine	166.62	598.6527	1777.952	15.9919	-1.7	4.56	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
6670	dirMS_041712_NAR_50mM_plus2.8537.8537.3	3	12.02	1	2.16E+04		(R)AIDSSNL	(R)A I|D|S S N L K/D D/Y/S T A Q R(V)		111.82	595.2868	1783.846	0.0002	0.1	4.43	46656.7	9.19	HUMAN	Q5JVF3	PCI domain-containing protein 2
6671	dirMS_041712_NAR_60mM_plus.15412.15412.3	3	12.02	0	3.46E+05		(K)DCGATV	(K)D C/G A T/W/V/V/L G H S E/R(R)	C:Carbamidomethylation	137.57	529.5842	1586.738	0	0	5.32	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
6672	dirMS_041712_NAR_50mM_minus2.13686.13686.3	3	12.01	1	1.15E+05		(K)LTEDKAI	(K)L/T/E D K A D V Q/S/I/I/G L Q/R(F)		146.42	595.9939	1785.97	-0.0034	-1.9	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
6673	dirMS_041712_NAR_50mM_minus2.7481.7481.3	3	12.01	1	3.43E+04		(K)ATQPET	(K)A T Q/P E/T/T E E V T D/L K/R(Q)		109.37	573.2875	1717.86	-0.0123	-7.2	4.41	72152.1	5.27	HUMAN	A0MZ66	Shootin-1
6674	dirMS_041712_NAR_60mM_minus.7962.7962.3	3	12.01	1	4.84E+05		(R)YLAEVA	(R)Y/L/A E/V A T G E K R(A)		104.27	412.8902	1236.658	-0.0022	-1.8	6.14	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
6675	dirMS_041712_NAR_20mM_plus.7868.7868.2	2	12.01	0	1.21E+05		(K)VEIIAND	(K)V E|I|I|A/N D Q G N R(T)		124.5	614.8177	1228.628	0.0001	0.1	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
6676	dirMS_041712_NAR_20mM_plus.9827.9827.2	2	12.01	0	6.20E+03		(K)IIEEAPAI	(K)I I/E|E|A|P|A P G I K(S)		139.02	569.3276	1137.651	-0.0035	-3.1	4.53	66923.1	6.88	HUMAN	E9PG35	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (Fragment)
6677	dirMS_041712_NAR_30mM_plus2.11808.11871.2	2	12.01	0	7.54E+05		(R)SSTDSLP	(R)S S/T D|S|L/P/G P I\S|R(Q)		115.18	608.8101	1216.617	-0.0039	-3.2	5.55	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
6678	dirMS_041712_NAR_30mM_plus2.12513.12998.2	2	12.01	0	1.44E+06		(R)TIGISVD	(R)T I|G|I|S V D|P/R(R)		120.87	479.2725	957.536	0.0014	1.4	5.5	14749.1	12.2	HUMAN	J3QSB4	60S ribosomal protein L13 (Fragment)
6679	dirMS_041712_NAR_30mM_plus2.17871.18016.2	2	12.01	0	3.59E+05		(R)NGGQIL	(R)N G|G|Q|I|L I/A/D/L R(G)		147.35	585.3347	1169.664	-0.0016	-1.3	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
6680	dirMS_041712_NAR_30mM_plus2.23389.23531.2	2	12.01	0	2.11E+06		(R)DLPLLLF	(R)D L|P|L/L/L/F R(T)		189.25	493.8049	986.603	-0.0008	-0.8	5.84	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
6681	dirMS_041712_NAR_30mM_plus2.8820.8944.2	2	12.01	0	1.17E+06		(K)FCLDNG	(K)F/C|L/D/N/G A/K(S)	C:Carbamidomethylation	100.02	462.7168	924.424	0.0019	2.1	5.84	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
6682	dirMS_041712_NAR_40mM_plus2.10417.10417.2	2	12.01	0	9.40E+04		(K)IGGIGTV	(K)I/G/G I|G\T V/P V G/R(V)		125.75	513.3081	1025.61	-0.0013	-1.2	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
6683	dirMS_041712_NAR_40mM_plus2.18444.18444.3	3	12.01	1	2.56E+04		(R)IAEVGG	(R)I A|E\V/G G V/P Y L L/P L V N Q K K(V)		174.58	646.716	1938.142	-0.0088	-4.5	8.5	18803.3	5.55	HUMAN	E9PIP1	Ester hydrolase C11orf54 (Fragment)
6684	dirMS_041712_NAR_50mM_plus2.13282.13282.3	3	12.01	1	2.49E+05		(R)GYISPYF	(R)G Y/I/S/P Y/F I/N T S K G Q K(C)		137.03	568.292	1702.88	-0.0185	-10.8	9.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
6685	dirMS_041712_NAR_50mM_plus2.16353.16353.3	3	12.01	0	2.89E+05		(K)ACQSIYF	(K)A/C|Q S I/Y/P L H/D V F V R(K)	C:Carbamidomethylation	154.4	568.9562	1704.853	0.0014	0.8	6.79	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
6686	dirMS_041712_NAR_60mM_plus.11416.11416.3	3	12.01	1	4.52E+05		(K)TCVFEKE	(K)T C|V F E/K E N/D|P S V M R(S)	C:Carbamidomethylation	117.33	571.2635	1711.778	-0.0019	-1.1	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
6687	dirMS_041712_NAR_20mM_minus.14894.14894.2	2	12	0	1.93E+06		(K)EIIDLVLI	(K)E I|I|D/L/V/L D/R(I)		204.03	543.3133	1085.62	-0.0008	-0.7	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
6688	dirMS_041712_NAR_30mM_minus2.16557.16557.2	2	12	0	2.80E+05		(R)ASLEAAI	(R)A S L E/A|A/I/A\D/A E Q/R(G)		143.7	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
6689	dirMS_041712_NAR_30mM_minus2.16910.16910.2	2	12	0	3.31E+05		(K)FANPFP	(K)F A/N|P F/P A A V R(G)		146.35	545.2937	1089.584	-0.0039	-3.5	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
6690	dirMS_041712_NAR_50mM_minus2.17494.17494.3	3	12	0	1.03E+06	M195m	(R)LHFFmP	(R)L H F\F m\P\G|F A|P L T S/R(G)	m:Oxidized methionine	167.33	546.2872	1620.835	16.0115	10.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
6691	dirMS_041712_NAR_50mM_minus2.7936.7936.3	3	12	0	8.88E+04		(K)TAVEHA	(K)T/A|V E/H A T\D E D\I L A/K(G)		112.23	504.9229	1512.754	0.0001	0.1	4.31	288852.1	5.33	HUMAN	E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein
6692	dirMS_041712_NAR_60mM_minus.15767.15767.3	3	12	1	2.94E+05		(R)IDTRNEL	(R)I/D|T R\N E\L/E|S/Y/A Y S L K(N)		148.03	601.3049	1801.897	0.0035	1.9	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
6693	dirMS_041712_NAR_60mM_minus.8472.8472.3	3	12	1	8.38E+04	M375m	(K)GVAINm	(K)G V/A/I/N/m V T E\E D K R(T)	m:Oxidized methionine	107.37	493.2448	1461.737	15.9832	-7.9	4.68	46381.4	5.32	HUMAN	P60842	Eukaryotic initiation factor 4A-I
6694	dirMS_041712_NAR_20mM_plus.11579.11579.2	2	12	0	1.25E+05	M402m	(R)mAFGAT	(R)m A|F|G A/T L D V/K(T)	m:Oxidized methionine	152.47	534.7743	1052.545	15.9968	1.8	5.59	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
6695	dirMS_041712_NAR_20mM_plus.6012.6012.3	3	12	0	1.02E+06	M295m M	(R)mGQmA	(R)m G Q m A m/G G|A|m/G I/N N R(G)	m:Oxidized methionine	100.27	534.8861	1538.67	63.9743	-3.4	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
6696	dirMS_041712_NAR_30mM_plus2.10997.10997.2	2	12	0	3.75E+05		(K)YSGTLNI	(K)Y/S/G/T/L N L D R(V)		110.9	519.7636	1038.521	-0.0015	-1.5	5.83	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
6697	dirMS_041712_NAR_30mM_plus2.17286.17830.2	2	12	0	2.26E+06		(K)FLDGIYV	(K)F/L|D|G\I/Y V/S E K(G)		145.7	585.8057	1170.604	0	0	4.37	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
6698	dirMS_041712_NAR_30mM_plus2.6177.6179.2	2	12	0	3.03E+05		(K)SNNSMA	(K)S N|N/S|M/A Q/A/M/K(G)		86.65	541.2441	1081.477	0.0044	4.1	8.47	25103.6	5.88	HUMAN	O43633	Charged multivesicular body protein 2a
6699	dirMS_041712_NAR_30mM_plus2.9718.9908.2	2	12	0	1.76E+07		(K)LAADDF	(K)L/A|A\D D/F/R(T)		104.83	404.2048	807.399	0.0028	3.4	4.21	48845.9	4.72	HUMAN	C4AM86	Keratin, type I cuticular Ha5
6700	dirMS_041712_NAR_40mM_plus2.13880.13880.3	3	12	1	4.04E+05		(R)QVFGEA	(R)Q V F/G E A T K Q/P G I/T F I A/A K(F)		147.57	636.0176	1906.043	-0.005	-2.6	8.59	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
6701	dirMS_041712_NAR_60mM_plus.11136.11136.3	3	12	1	4.49E+05	M230m M	(R)mSmKE	(R)m S m K E V D E|Q|M|L/N V/Q\N K(N)	m:Oxidized methionine	115.73	652.6326	1923.897	31.986	-2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
6702	dirMS_041712_NAR_60mM_plus.7450.7502.3	3	12	0	8.79E+05		(R)AAHSEG	(R)A A H\S\E G N\T|T/A/G L/D/M/R(E)		96.75	510.9035	1530.697	-0.0006	-0.4	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
6703	dirMS_041712_NAR_120mM_minus.11445.11445.4	4	11.99	2	1.39E+06	M105m	(R)AQKDEE	(R)A Q K D E E K m E|I|Q E/I/Q/L K(E)	m:Oxidized methionine	116.63	494.7536	1960.006	15.987	-4	4.58	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
6704	dirMS_041712_NAR_20mM_minus.13322.13322.2	2	11.99	0	5.30E+05		(K)DAGTIA	(K)D A|G T/I/A|G L N V L/R(I)		184.67	600.3403	1199.674	-0.0009	-0.8	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
6705	dirMS_041712_NAR_30mM_minus2.15632.15632.2	2	11.99	0	3.51E+05		(K)LLYNNV	(K)L L|Y/N/N/V/S/N/F G R(L)		137.97	648.8355	1296.67	-0.0058	-4.5	8.75	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
6706	dirMS_041712_NAR_50mM_minus2.10509.10509.3	3	11.99	0	3.82E+04		(K)VFEGNR	(K)V/F/E/G N R P T N S I V F T/K(L)		128.28	570.3032	1708.902	-0.0066	-3.9	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
6707	dirMS_041712_NAR_50mM_minus2.16907.16972.3	3	11.99	1	2.31E+05		(K)SLLGKD	(K)S/L/L|G K/D\V L F/L/K(D)		164.22	411.5911	1232.761	-0.0025	-2.1	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
6708	dirMS_041712_NAR_60mM_minus.11610.11611.3	3	11.99	0	5.56E+05		(K)RPGAAL	(K)R P G A A\L|D|P/G/C/V L\A K(M)	C:Carbamidomethylation	124.2	475.5992	1424.768	0.0152	10.7	8.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
6709	dirMS_041712_NAR_60mM_minus.17642.17642.3	3	11.99	0	1.17E+05		(R)GGHVVE	(R)G G H V V E G L A/G E|L|E/Q/L/R(A)		158.32	555.2959	1663.876	-0.0031	-1.8	4.75	106088.3	5.78	HUMAN	P10275	Androgen receptor
6710	dirMS_041712_NAR_120mM_plus.10226.10226.3	3	11.99	0	1.19E+06		(R)ILRPWQ	(R)I/L/R/P W Q/S/S E T R(S)		106.72	458.2486	1372.733	-0.0019	-1.4	9.6	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
6711	dirMS_041712_NAR_20mM_plus.13786.13786.2	2	11.99	0	2.57E+05		(R)GDLGIEI	(R)G D|L/G/I\E I/P A E/K(V)		166.83	571.3075	1141.61	-0.0022	-1.9	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
6712	dirMS_041712_NAR_20mM_plus.18749.18749.3	3	11.99	0	1.07E+05	M80m	(R)APLPDL	(R)A P L P D L\Y|P/F G/T m\R(G)	m:Oxidized methionine	200.42	498.5865	1477.751	15.9941	-0.5	5.88	81122.9	9.03	HUMAN	H3BLZ8	Probable ATP-dependent RNA helicase DDX17
6713	dirMS_041712_NAR_30mM_plus2.12121.12239.3	3	11.99	0	1.23E+06		(K)EVDEQN	(K)E V D E Q\M|L/N/V/Q N K(N)		116.97	482.9009	1446.689	-0.0012	-0.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
6714	dirMS_041712_NAR_30mM_plus2.6109.6112.2	2	11.99	0	3.03E+05	M299m	(K)NmMAA	(K)N m|M|A|A/C D|P/R(H)	C:Carbamidomethylation m:Oxid	86.65	541.2163	1065.427	15.9979	2.8	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
6715	dirMS_041712_NAR_30mM_plus2.6281.6281.2	2	11.99	0	3.24E+04		(K)LAPEYEK	(K)L A|P E/Y/E/K(A)		86.52	425.2221	849.435	0.0017	2	4.53	73273.4	4.96	HUMAN	P13667	Protein disulfide-isomerase A4
6716	dirMS_041712_NAR_40mM_plus2.8125.8125.2	2	11.99	0	1.94E+05		(K)SFYMQF	(K)S F/Y/M Q/R(C)		108.45	416.1954	831.382	0.0017	2.1	8.46	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
6717	dirMS_041712_NAR_50mM_plus2.12879.12879.3	3	11.99	0	3.15E+05		(K)EMNPAL	(K)E M/N\P A L/G|I D/C L H K(G)	C:Carbamidomethylation	135.47	499.9106	1497.719	-0.0016	-1.1	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
6718	dirMS_041712_NAR_60mM_plus.8533.8533.3	3	11.99	0	6.38E+05		(K)EHDPVG	(K)E H D\P V G Q|M/V/N N P K(I)		102.25	488.9052	1464.69	0.0111	7.6	5.32	86098.8	5.31	HUMAN	B4DUC5	Exportin-2
6719	dirMS_041712_NAR_20mM_minus.8913.8913.2	2	11.98	0	1.36E+05		(R)LEQYTS	(R)L E Q/Y/T/S A I/E\G T K(S)		138	670.3403	1339.674	-0.0007	-0.5	4.53	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
6720	dirMS_041712_NAR_60mM_minus.10508.10508.3	3	11.98	1	1.71E+04		(R)YAAVTQ	(R)Y/A|A/V T Q F E A T D A R R(A)		118.3	533.5999	1598.792	-0.007	-4.4	6.07	54259.7	5.17	HUMAN	A6NEC2	Puromycin-sensitive aminopeptidase-like protein
6721	dirMS_041712_NAR_60mM_minus.20002.20002.3	3	11.98	1	7.77E+05		(R)LIALLEVI	(R)L/I/A L/L/E V/L/S Q K R(M)		182.08	461.6287	1382.873	-0.0014	-1	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
6722	dirMS_041712_NAR_60mM_minus.9319.9319.3	3	11.98	0	9.34E+04		(K)GHENVE	(K)G H E\N\V\E\A\A|Q/A\E Y I/E K(F)		111.78	563.2673	1687.792	-0.0049	-2.9	4.48	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
6723	dirMS_041712_NAR_20mM_plus.14065.14065.2	2	11.98	0	8.16E+04		(K)LSILYPA	(K)L S I|L/Y/P/A T T G R(N)		168.68	596.3406	1191.673	0.0007	0.6	8.75	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
6724	dirMS_041712_NAR_30mM_plus2.18910.18991.2	2	11.98	0	1.87E+05		(K)LNLGTV	(K)L N|L|G/T/V/G F/Y/R(T)		152.8	570.3123	1139.621	-0.0034	-3	8.75	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
6725	dirMS_041712_NAR_30mM_plus2.18946.18970.2	2	11.98	0	1.87E+05		(K)LNLGTV	(K)L/N|L|G/T/V|G/F Y R(T)		152.8	570.3123	1139.621	-0.0034	-3	8.75	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
6726	dirMS_041712_NAR_30mM_plus2.21204.21204.2	2	11.98	0	3.22E+05		(R)GVVQEL	(R)G V|V|Q/E\L/Q/Q A|I/S/K(L)		165.82	650.3632	1299.727	-0.0076	-5.8	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
6727	dirMS_041712_NAR_30mM_plus2.21926.21926.2	2	11.98	0	2.34E+05		(R)EGDVLT	(R)E G D\V|L/T L/L E/S/E R(E)		170.72	680.8538	1360.696	0.0049	3.6	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
6728	dirMS_041712_NAR_40mM_plus2.19902.19902.3	3	11.98	0	4.60E+05	M166m	(K)VLDFEHI	(K)V/L|D F/E/H F L/P m L Q T V A K(N)	m:Oxidized methionine	187.63	635.3379	1888.004	15.9954	0.3	5.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
6729	dirMS_041712_NAR_50mM_plus2.12978.12978.3	3	11.98	1	3.89E+05		(K)LAEIGAF	(K)L A|E/I/G A/P/I Q G N R E E L V E R(L)		135.98	665.3593	1994.066	-0.0032	-1.6	4.49	38572.2	6.31	HUMAN	E9PJ04	Splicing factor 3B subunit 2 (Fragment)
6730	dirMS_041712_NAR_60mM_plus.18608.18608.3	3	11.98	1	1.43E+05		(R)CRVDLP	(R)C R V D\L|P/L|A\V L S K(M)	C:Carbamidomethylation	154.47	457.599	1370.782	0	0	8.75	7765.6	8.23	HUMAN	H3BSA6	dCTP pyrophosphatase 1
6731	dirMS_041712_NAR_20mM_minus.11649.11649.2	2	11.97	0	1.62E+05		(R)VEVTEFI	(R)V/E|V|T/E/F/E D\I K(S)		164.68	604.8043	1208.604	-0.0032	-2.6	4	30992.3	4.14	HUMAN	B2REB8	Protein SET
6732	dirMS_041712_NAR_30mM_minus2.11042.11081.2	2	11.97	0	3.32E+05		(K)MLVSGA	(K)M/L|V/S/G A G D/I K(L)		113.32	495.7683	990.529	0.0005	0.5	5.59	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
6733	dirMS_041712_NAR_30mM_minus2.18984.18984.2	2	11.97	0	2.20E+05		(K)SYELPD	(K)S Y E|L|P D G Q V/I\T I G\N E R(F)		158.72	895.9492	1790.892	-0.0008	-0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
6734	dirMS_041712_NAR_40mM_minus2.14125.14125.3	3	11.97	0	6.72E+05		(R)IHFPLAT	(R)I H F/P L A T\Y/A|P V I S A E K(A)		167.78	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
6735	dirMS_041712_NAR_50mM_minus2.14920.14920.3	3	11.97	0	3.98E+05		(K)QLEAID	(K)Q L/E/A/I D Q L H L E/Y A K(R)		152.47	557.6327	1670.875	0.0087	5.2	4.65	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
6736	dirMS_041712_NAR_50mM_minus2.15464.15464.3	3	11.97	0	3.28E+05		(R)LSFQHD	(R)L/S F Q H D P E|T/S/V|L V L R(K)		156.07	580.9793	1740.928	-0.0046	-2.6	5.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
6737	dirMS_041712_NAR_50mM_minus2.18088.18088.3	3	11.97	1	6.74E+05		(R)VLEALLP	(R)V L/E A L L/P L K/G L E/E R(V)		172.47	527.3171	1579.942	-0.005	-3.2	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
6738	dirMS_041712_NAR_50mM_minus2.7741.7741.3	3	11.97	1	5.68E+04		(R)LGAAPE	(R)L/G/A/A|P E/E/E S A/Y V A/G E K R(Q)		111.32	592.9614	1776.876	-0.0066	-3.7	4.5	30276.7	5	HUMAN	F2Z2K0	NSFL1 cofactor p47
6739	dirMS_041712_NAR_60mM_minus.10263.10263.3	3	11.97	1	2.36E+04	M88m	(K)DVDEAY	(K)D V|D E/A Y m N K/V/E/L E S R(L)	m:Oxidized methionine	116.03	605.2791	1797.832	15.9904	-2.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
6740	dirMS_041712_NAR_60mM_minus.9344.9344.3	3	11.97	0	1.02E+06		(K)QEYDES	(K)Q E Y/D E/S/G/P/S I V/H/R(K)		111.27	506.2391	1516.703	0.0001	0.1	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
6741	dirMS_041712_NAR_20mM_plus.10449.10449.2	2	11.97	0	1.88E+05	M592m M	(R)mGPAm	(R)m G/P A m/G P/A L|G A G I E/R(M)	m:Oxidized methionine	144.65	730.3568	1427.713	31.993	2.1	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
6742	dirMS_041712_NAR_20mM_plus.11269.11269.2	2	11.97	0	1.37E+05		(K)STGGAP	(K)S T/G G A|P T F N V/T V/T K(T)		150.13	690.3592	1379.717	-0.0054	-3.9	8.47	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
6743	dirMS_041712_NAR_20mM_plus.15762.15762.2	2	11.97	0	4.98E+03		(R)SSFYVN	(R)S S F|Y/V|N/G L/T L/G G Q K(C)		180.83	735.8818	1470.759	-0.0024	-1.6	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
6744	dirMS_041712_NAR_30mM_plus2.20186.20549.2	2	11.97	0	2.47E+05		(R)FLGTEVI	(R)F/L|G T|E/V L/L/R(L)		160.98	524.3115	1047.62	-0.004	-3.8	6	103045.5	7.1	HUMAN	B9ZVT1	RNA-binding protein 12B
6745	dirMS_041712_NAR_30mM_plus2.21589.21675.2	2	11.97	0	6.04E+05		(R)IIWQFIK	(R)I/I|W Q F/I/K(E)		169.2	474.2886	947.571	-0.0014	-1.5	8.75	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
6746	dirMS_041712_NAR_60mM_plus.12881.12904.3	3	11.97	1	5.27E+05		(R)LYPPSAE	(R)L Y|P/P S A E/Y/P D/L R/K(H)		124.07	516.9402	1548.806	0.0004	0.2	6.07	16450.4	6.98	HUMAN	C9J8F6	Creatine kinase U-type, mitochondrial (Fragment)
6747	dirMS_041712_NAR_60mM_plus.15162.15162.3	3	11.97	1	4.21E+05		(K)SLEELRL	(K)S L|E/E/L R L E D/Y Q A N R(K)		135.65	579.2911	1735.861	-0.0022	-1.3	4.41	178367.2	6.03	HUMAN	J3KP29	Nuclear pore complex protein Nup98-Nup96
6748	dirMS_041712_NAR_120mM_minus.13306.13306.4	4	11.96	0	3.25E+05		(R)VLSAPPI	(R)V L\S A/P P/H F H/F G/Q T N R(T)		126.85	427.7219	1707.871	-0.0056	-3.3	9.74	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
6749	dirMS_041712_NAR_120mM_minus.15445.15445.3	3	11.96	2	9.57E+05		(R)ALKDEEI	(R)A/L/K|D/E E K M E\L\Q\E I Q\L K(E)		137.72	649.0139	1945.031	-0.0039	-2	4.58	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
6750	dirMS_041712_NAR_120mM_minus.15953.15953.2	2	11.96	0	2.14E+05		(R)HIEIFTDI	(R)H I|E/I/F T/D\L S S R(F)		141.03	659.3422	1317.68	-0.0026	-2	5.32	14818.5	4.73	HUMAN	C9JZ81	X-ray repair cross-complementing protein 5 (Fragment)
6751	dirMS_041712_NAR_120mM_minus.6109.6109.3	3	11.96	1	5.60E+05		(K)TCEESSF	(K)T/C|E/E/S/S/F C/K R(Q)	C:Carbamidomethylation	86.8	435.1849	1303.541	-0.0004	-0.3	5.81	10576.1	11.44	HUMAN	E9PRF8	Neutral alpha-glucosidase AB
6752	dirMS_041712_NAR_40mM_minus2.8924.8924.3	3	11.96	1	5.45E+04		(R)IVAPGK	(R)I V/A/P G K/G I/L A A/D E S T G S I A K(R)		135.25	633.355	1898.059	-0.0089	-4.7	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
6753	dirMS_041712_NAR_50mM_minus2.11261.11305.3	3	11.96	1	4.95E+05	M327m	(R)VAGGP	(R)V/A|G/G/P Q/m I/Q/L S L D G K R(L)	m:Oxidized methionine	131.88	562.6354	1669.905	15.9862	-5.1	8.72	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1

6754	dirMS_041712_NAR_60mM_minus.11319.11319.3	3	11.96	1	9.28E+05	M230m	(R)mSMKE	(R)m S M K E V D\E/Q|M|L/N V|Q N K(N)	m:Oxidized methionine	122.78	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
6755	dirMS_041712_NAR_60mM_minus.13313.13313.3	3	11.96	1	4.79E+05		(K)TKEVYEL	(K)T K E V Y E|L|L/D/S P G K(V)		134.4	493.5966	1478.774	0.0015	1	4.68	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
6756	dirMS_041712_NAR_60mM_minus.7968.7968.3	3	11.96	1	4.26E+05		(K)IQDKEGI	(K)I Q D K E\G I|P/P D Q Q R(L)		103.95	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
6757	dirMS_041712_NAR_120mM_plus.21067.21067.4	4	11.96	0	3.50E+05		(K)ALEHAF	(K)A L/E H A/F Q L E/H I/M D/L T R(L)		163.77	481.7493	1923.975	0.0008	0.4	5.27	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
6758	dirMS_041712_NAR_20mM_plus.12567.12567.2	2	11.96	0	1.41E+05		(R)GVEICIA	(R)G V E|I/C|I/A/T|P\G R(L)	C:Carbamidomethylation	159.07	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
6759	dirMS_041712_NAR_20mM_plus.14302.14302.3	3	11.96	0	7.24E+03		(R)VPTANV	(R)V P T A N V S\V V/D/L/T/C R(L)	C:Carbamidomethylation	169.75	510.9348	1530.795	-0.0046	-3	5.81	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
6760	dirMS_041712_NAR_20mM_plus.16757.16757.3	3	11.96	0	2.96E+05		(K)VQIAVA	(K)V Q I A/V\A N A|Q/E/L/L/Q R(M)		186.87	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
6761	dirMS_041712_NAR_30mM_plus2.10687.10936.2	2	11.96	0	4.94E+06		(R)QTVAVG	(R)Q/T/V/A/V/G V/I/K(A)		110.18	457.7881	914.567	0.002	2.2	8.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
6762	dirMS_041712_NAR_60mM_plus.10109.10109.3	3	11.96	1	1.48E+06		(K)IFRDGEE	(K)I/F R D G E\E\A G/A/Y/D/G P R(T)		111.47	551.593	1652.766	-0.0019	-1.1	4.32	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
6763	dirMS_041712_NAR_60mM_plus.8396.8504.3	3	11.96	1	2.08E+06		(K)EAIEGTY	(K)E A|I/E G T/Y/I D/K/K(C)		102.38	422.8929	1266.658	0.0065	5.2	4.68	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
6764	dirMS_041712_NAR_20mM_minus.10611.10611.2	2	11.95	0	1.04E+05		(K)FLIPNAS	(K)F L|I|P N\A S Q A E/S K(V)		154.47	652.8447	1304.685	-0.0024	-1.8	6	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
6765	dirMS_041712_NAR_30mM_minus2.15431.15610.2	2	11.95	0	2.78E+05		(R)IDYIAGL	(R)I/D|Y\I|A|G L D/S R(G)		137.83	561.7944	1122.579	0.0026	2.3	4.21	14613.6	6.73	HUMAN	G5E9J2	Adenine phosphoribosyltransferase
6766	dirMS_041712_NAR_50mM_minus2.13491.13491.3	3	11.95	0	4.82E+05		(K)SLTNDW	(K)S L|T|N/D W E D H L/A V K(H)		144.27	509.9192	1527.744	-0.0008	-0.5	4.53	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
6767	dirMS_041712_NAR_50mM_minus2.16042.16042.3	3	11.95	1	8.40E+04		(K)LQVDAL	(K)L/Q/V D A/L/I D T\I K/K(S)		159.23	452.9385	1356.81	-0.0087	-6.4	5.96	234333.2	6.01	HUMAN	J3KNX9	Unconventional myosin-XVIIIa
6768	dirMS_041712_NAR_50mM_minus2.17951.17951.3	3	11.95	1	2.28E+05	M116m	(R)ELAILLG	(R)E L/A/I/L/L/G m L D/P A E K D/E K(G)	m:Oxidized methionine	170.82	634.3353	1884.999	15.9927	-1.2	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
6769	dirMS_041712_NAR_60mM_minus.8043.8043.3	3	11.95	1	2.63E+04		(R)YLAEVA	(R)Y/L/A/E V/A/C G D D/R K(Q)	C:Carbamidomethylation	104.8	466.2187	1396.652	-0.011	-7.9	4.56	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
6770	dirMS_041712_NAR_60mM_minus.9937.9969.3	3	11.95	1	2.53E+05		(K)QTLENE	(K)Q/T/L/E/N E R G E L A N E/V/K(V)		115.13	577.2903	1729.872	-0.0152	-8.8	4.49	227783.5	5.5	HUMAN	P35579	Myosin-9
6771	dirMS_041712_NAR_20mM_plus.16846.16846.2	2	11.95	0	3.45E+05		(K)VQIAVA	(K)V Q|I|A/V\A/N A Q E/L\L Q R(M)		187.37	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
6772	dirMS_041712_NAR_50mM_plus2.9954.9954.3	3	11.95	1	3.10E+05	T3700t	(K)DSGLTS	(K)D/S G|L|T S V G T D t F R L(-)	t:N-acetylglucosamine (T)	119.77	557.9454	1468.728	203.0938	8.6	4.21	409090.1	5.82	HUMAN	Q15911	Zinc finger homeobox protein 3
6773	dirMS_041712_NAR_60mM_plus.18741.18741.3	3	11.95	1	3.96E+06		(R)VSFELFA	(R)V/S/F E/L/F/A/D K V/P K(T)		155.83	460.5914	1379.757	0.0027	2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
6774	dirMS_041712_NAR_120mM_minus.20071.20071.4	4	11.94	0	3.63E+05		(K)LAFPSPF	(K)L A|F/P S/P F G/H L S E/G F|S H S R(W)		165.95	493.9968	1972.966	-0.0011	-0.5	6.92	16196.2	9.92	HUMAN	C9JRJ8	Sequestosome-1 (Fragment)
6775	dirMS_041712_NAR_120mM_minus.6283.6380.3	3	11.94	1	1.05E+06		(R)TEERAEL	(R)T/E|E/R A E\L A/E/S/R(C)		89	430.8806	1290.628	-0.0012	-0.9	4.49	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
6776	dirMS_041712_NAR_120mM_minus.8691.8691.3	3	11.94	0	5.76E+05		(R)THYSNIE	(R)T\H Y\S N I\E\A|N/E/S/E\E/V/R(Q)		102.13	593.2723	1777.799	0.0036	2	4.48	21983.3	4.68	HUMAN	K7EIV0	Calpain small subunit 1
6777	dirMS_041712_NAR_30mM_minus2.16578.16578.2	2	11.94	0	2.83E+05		(R)ASLEAAI	(R)A S L E|A/A|I/A/D/A E Q R(G)		143.77	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
6778	dirMS_041712_NAR_40mM_minus2.8234.8241.3	3	11.94	1	5.29E+05		(R)DVVICP	(R)D V|V/I/C/P D/A S L E D A K K(E)	C:Carbamidomethylation	129.32	553.9467	1659.826	-0.0003	-0.2	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
6779	dirMS_041712_NAR_50mM_minus2.7729.7729.3	3	11.94	0	4.07E+04	M409m	(K)VLAmSG	(K)V L|A\m/S G D/P N/Y/L H/R(M)	m:Oxidized methionine	111.03	496.9173	1472.732	16.0059	7.4	6.71	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
6780	dirMS_041712_NAR_60mM_minus.11302.11421.3	3	11.94	1	3.98E+05		(R)ELLTLDE	(R)E L\L/T/L D E K D/P/R(R)		123.5	443.573	1328.706	-0.0012	-0.9	4.32	9591.1	10.94	HUMAN	A8MXK4	40S ribosomal protein S9
6781	dirMS_041712_NAR_60mM_minus.11936.11936.3	3	11.94	1	8.76E+04		(R)YETSSTS	(R)Y E/T/S/S/T S A G D R Y D S L L G R(S)		126.58	659.9681	1977.915	-0.0251	-12.7	4.56	22046.7	5.8	HUMAN	H0YIM2	Protein phosphatase 1 regulatory subunit 12A (Fragment)
6782	dirMS_041712_NAR_120mM_plus.13724.13724.3	3	11.94	1	4.38E+05		(R)LWDLTT	(R)L/W/D/L T T G T T T R R(F)		125.25	474.2499	1420.754	-0.0192	-13.5	9.6	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
6783	dirMS_041712_NAR_20mM_plus.18197.18197.3	3	11.94	0	1.36E+05		(R)AILVDLE	(R)A I\L V D L/E/P G T M D/S V R(S)		196.55	539.2833	1615.836	-0.0006	-0.4	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
6784	dirMS_041712_NAR_30mM_plus2.12584.12756.2	2	11.94	0	3.88E+05		(K)LVPVLSA	(K)L/V|P/V/L S A K(A)		119.3	413.7745	826.54	0.0021	2.5	8.75	37710.6	6.36	HUMAN	P37837	Transaldolase
6785	dirMS_041712_NAR_30mM_plus2.17841.17841.2	2	11.94	0	5.57E+05		(R)IMNTFS	(R)I/M/N/T/F/S V V/P S P K(V)		145.7	660.3537	1319.703	-0.0027	-2	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
6786	dirMS_041712_NAR_30mM_plus2.18059.18149.2	2	11.94	0	4.72E+05		(K)LLLWSQ	(K)L/L|L/W/S Q/R(M)		147.95	458.2693	915.541	-0.0097	-10.6	9.75	22576.6	9.45	HUMAN	E9PKG0	Plectin (Fragment)
6787	dirMS_041712_NAR_40mM_plus2.11126.11126.3	3	11.94	0	9.07E+04		(R)VLVASS	(R)V/L|V/A/S S V/V/A/G E S Q K P E L K(A)		131.88	614.3443	1841.038	-0.0195	-10.6	6.11	61441.6	5.93	HUMAN	G8JLE9	Fragile X mental retardation protein 1
6788	dirMS_041712_NAR_40mM_plus2.14850.14850.3	3	11.94	0	5.25E+05		(K)IAILTCP	(K)I/A|I/L T/C/P F E/P/P K/P K(T)	C:Carbamidomethylation	153.58	537.6381	1610.898	0.0023	1.4	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
6789	dirMS_041712_NAR_40mM_plus2.9443.9443.2	2	11.94	0	9.68E+04		(R)ISVYYNE	(R)I/S/V/Y/Y N E A/T G G K(Y)		118.55	651.3206	1301.637	-0.0033	-2.5	6	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
6790	dirMS_041712_NAR_60mM_plus.15607.15607.3	3	11.94	0	2.27E+05		(R)NFDLTA	(R)N F\D L/T A I/P C/A N H K(M)	C:Carbamidomethylation	138.13	500.9145	1500.726	0.0026	1.7	6.74	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
6791	dirMS_041712_NAR_60mM_plus.15957.15957.3	3	11.94	0	5.20E+05		(R)VWYVSN	(R)V W|Y V S N/I D G T H I A K(T)		139.92	534.9464	1602.828	-0.0028	-1.8	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
6792	dirMS_041712_NAR_60mM_plus.16926.16926.3	3	11.94	0	8.46E+05		(K)TTISVAH	(K)T/T|I/S V A H/L L A A/R(Q)		144.68	418.2478	1252.737	-0.0083	-6.7	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
6793	dirMS_041712_NAR_20mM_minus.9773.9773.2	2	11.93	0	1.57E+05		(K)LSELEPG	(K)L S E L|E|P G T G D/L R(F)		147.78	643.8318	1286.659	-0.0023	-1.8	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
6794	dirMS_041712_NAR_50mM_minus2.5786.5786.3	3	11.93	0	1.15E+05		(K)TVEAEA	(K)T V|E A E/A A/H G T V|T/R(H)		94.6	447.8956	1341.676	-0.0035	-2.6	5.37	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
6795	dirMS_041712_NAR_20mM_plus.12459.12459.2	2	11.93	0	5.73E+04		(K)LLQLVED	(K)L L|Q L/V/E D/R(G)		157.63	493.2863	985.568	-0.0023	-2.4	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
6796	dirMS_041712_NAR_20mM_plus.8850.8850.2	2	11.93	0	1.30E+05		(K)VLEEAN	(K)V/L|E E/A|N Q|A\I/N/P K(L)		131.6	663.353	1325.706	-0.0072	-5.5	4.53	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
6797	dirMS_041712_NAR_30mM_plus2.14710.14710.2	2	11.93	0	3.22E+05		(R)YQETFN	(R)Y Q|E|T F N V/I/E/R(C)		129.92	649.8225	1298.638	0.0002	0.1	4.53	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
6798	dirMS_041712_NAR_30mM_plus2.16776.16932.2	2	11.93	0	4.32E+05		(K)GCSFLPD	(K)G C|S/F/L|P D/P Y Q\K(Q)	C:Carbamidomethylation	140.87	656.306	1311.604	0.0009	0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
6799	dirMS_041712_NAR_30mM_plus2.18661.18661.2	2	11.93	0	1.75E+05		(K)TVLSNV	(K)T V|L|S N/V/Q E/E L D R(M)		150.95	701.8633	1402.717	0.0021	1.5	4.14	45232	5.78	HUMAN	B4DZP4	Cytoplasmic dynein 1 light intermediate chain 2
6800	dirMS_041712_NAR_30mM_plus2.6131.6150.2	2	11.93	0	2.57E+05		(K)INYTEGF	(K)I/N|Y/T/E/G/R(A)		86.48	426.7164	852.421	0.0045	5.3	6	16867	10.86	HUMAN	K7ELR7	Glucose-6-phosphate isomerase (Fragment)
6801	dirMS_041712_NAR_30mM_plus2.6292.6292.2	2	11.93	0	1.43E+05		(R)FGGSGS	(R)F/G\G/S/G S/Q/V/D/S A R(M)		87.52	584.2731	1167.539	0	0	5.84	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
6802	dirMS_041712_NAR_40mM_plus2.7120.7120.2	2	11.93	0	8.31E+04		(R)AVDFAE	(R)A V|D/F/A E/R(H)		101.7	404.2049	807.399	0.003	3.7	4.37	24115.6	11.59	HUMAN	E9PIZ3	60S ribosomal protein L8
6803	dirMS_041712_NAR_50mM_plus2.16270.16270.3	3	11.93	1	1.17E+06		(K)CEFQDA	(K)C E/F Q D\A\Y/V/L L S E K K(I)	C:Carbamidomethylation	152.42	577.2866	1729.847	-0.0013	-0.8	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
6804	dirMS_041712_NAR_60mM_plus.15359.15359.3	3	11.93	1	2.67E+04		(R)KVIGIEC	(R)K V\I G\I\E C/S/S/I/S D/Y\A V/K(I)	C:Carbamidomethylation	136.72	590.3097	1768.915	-0.0004	-0.2	6.07	12798.3	6.06	HUMAN	E9PI83	Protein arginine N-methyltransferase 1 (Fragment)
6805	dirMS_041712_NAR_120mM_minus.11432.11432.4	4	11.92	1	7.67E+05	M216m	(K)ASIHEA	(K)A/S/I/H/E A W\T D/G K/E A m L K(H)	m:Oxidized methionine	116.6	451.4752	1786.879	15.9997	2.7	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
6806	dirMS_041712_NAR_30mM_minus2.11701.11764.2	2	11.92	0	3.24E+05		(K)SCAHDW	(K)S C|A H D\W\V|Y|E(-)	C:Carbamidomethylation	117.45	583.7323	1166.457	0.0002	0.2	4.71	8782.8	5.3	HUMAN	F6XY72	Nucleoside diphosphate kinase
6807	dirMS_041712_NAR_30mM_minus2.11799.11800.2	2	11.92	0	3.73E+05		(K)MTISQQ	(K)M/T|I/S/Q/Q E F G/R(T)		117.87	598.7911	1196.573	0.0021	1.7	5.75	21119.9	4.34	HUMAN	H0Y3Y9	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
6808	dirMS_041712_NAR_30mM_minus2.14781.14781.2	2	11.92	0	1.82E+05		(K)NLQEAE	(K)N L/Q/E/A E/E W Y/K(S)		133.95	655.3063	1309.606	-0.0006	-0.4	4.25	49709.6	5.19	HUMAN	B0YJC4	Vimentin
6809	dirMS_041712_NAR_60mM_minus.16815.16815.3	3	11.92	0	1.02E+05		(K)ICDQWD	(K)I/C D Q\W D\A|L/G S L/T H S R(R)	C:Carbamidomethylation	153.88	586.9446	1758.823	-0.0035	-2	5.21	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
6810	dirMS_041712_NAR_120mM_plus.18257.18257.4	4	11.92	1	1.06E+06		(K)EMVELP	(K)E M/V/E/L/P L R H/P A L F K(A)		149.07	420.7376	1679.93	-0.0016	-0.9	6.86	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
6811	dirMS_041712_NAR_120mM_plus.5614.5649.3	3	11.92	1	1.36E+05		(R)ALCDYK	(R)A/L|C D/Y/K Q D/Q/K(I)	C:Carbamidomethylation	82.62	423.5365	1268.594	0.001	0.8	6.01	334221.3	6.44	HUMAN	P15924	Desmoplakin
6812	dirMS_041712_NAR_20mM_plus.10095.10142.2	2	11.92	0	4.14E+04		(K)LVSESSD	(K)L/V|S|E|S S\D\V L/P K(-)		142.18	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
6813	dirMS_041712_NAR_20mM_plus.11036.11036.2	2	11.92	0	1.17E+05		(K)EITALAP	(K)E I/T A/L/A P/S/T M/K(I)		148.15	581.3129	1161.618	0.0001	0.1	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
6814	dirMS_041712_NAR_40mM_plus2.11128.11128.3	3	11.92	0	9.07E+04		(R)VLVASS	(R)V L|V/A/S S V/V A G E S Q K P E L/K(A)		131.88	614.3443	1841.038	-0.0195	-10.6	6.11	61441.6	5.93	HUMAN	G8JLE9	Fragile X mental retardation protein 1
6815	dirMS_041712_NAR_50mM_plus2.20202.20202.3	3	11.92	0	3.26E+05		(R)NEVSFV	(R)N E/V/S F V/I/H N L P V L/A K(M)		174.42	560.6531	1679.948	-0.0032	-1.9	6.75	35663.7	5.91	HUMAN	B4DWK0	Selenide, water dikinase 1
6816	dirMS_041712_NAR_50mM_plus2.21707.21707.3	3	11.92	0	1.12E+05		(R)GLAPVQ	(R)G L/A|P V Q A Y L/H I P D I I K(V)		184.93	583.336	1748.011	-0.0171	-9.8	6.74	58266.4	9.46	HUMAN	B4DN00	Pyruvate carboxylase, mitochondrial
6817	dirMS_041712_NAR_50mM_plus2.8999.8999.3	3	11.92	1	1.12E+05		(R)ALSTTAS	(R)A L|S T/T A/S T A A/F D K Q/P Q S R(E)		114.4	627.3202	1879.951	-0.0048	-2.5	8.79	48446.2	8.53	HUMAN	C9J8T0	Selenocysteine-specific elongation factor
6818	dirMS_041712_NAR_60mM_plus.11803.11803.3	3	11.92	0	6.55E+05		(R)GISEETT	(R)G I|S E/E T/T/T/G V H N L Y K(M)		119.12	550.2735	1648.818	-0.0117	-7.1	5.4	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
6819	dirMS_041712_NAR_60mM_plus.6451.6451.3	3	11.92	0	2.48E+05		(R)CGETGH	(R)C/G E|T G H/V/A/I/N C S K(T)	C:Carbamidomethylation	92.37	478.2118	1432.631	-0.0099	-6.9	6.75	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
6820	dirMS_041712_NAR_120mM_minus.9920.9942.3	3	11.91	1	8.35E+04		(R)RLDECE	(R)R L D\E C|E|E|A/F/Q/G T K(V)	C:Carbamidomethylation	108.6	528.2437	1582.717	0	0	4.41	22568.6	6.35	HUMAN	B3KQ25	Proteasome activator complex subunit 3
6821	dirMS_041712_NAR_20mM_minus.12060.12356.3	3	11.91	0	2.99E+06	M313m	(R)TVQSLEI	(R)T\V\Q\S\L\E\I/D|L/D/S m R(N)	m:Oxidized methionine	170.78	508.2517	1506.747	15.9937	-0.8	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
6822	dirMS_041712_NAR_20mM_minus.7269.7269.2	2	11.91	0	2.46E+04		(K)IAVAAQ	(K)I/A|V|A/A/Q N C Y K(V)	C:Carbamidomethylation	120.58	569.2917	1137.572	0.004	3.5	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
6823	dirMS_041712_NAR_20mM_minus.9462.9462.3	3	11.91	0	1.18E+04	M175m	(R)LEQGQA	(R)L E Q G Q A\I/D D L/m/P\A/Q K(-)	m:Oxidized methionine	144.5	558.2794	1656.826	15.9975	1.5	4.03	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
6824	dirMS_041712_NAR_40mM_minus2.11310.11310.3	3	11.91	0	1.76E+05		(K)LVTSIGD	(K)L V|T S I/G/D V V N H D/P V V G D/R(L)		150.22	631.3335	1891.987	-0.0013	-0.7	4.41	27786.2	5.93	HUMAN	H0Y4Z6	Phosphorylase (Fragment)
6825	dirMS_041712_NAR_40mM_minus2.9798.9798.2	2	11.91	0	2.04E+06		(R)VAPEEH	(R)V/A/P E E|H|P V L L T\E A|P L N/P K(A)		140.28	977.5343	1954.064	-0.0031	-1.6	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
6826	dirMS_041712_NAR_50mM_minus2.13338.13338.3	3	11.91	0	5.21E+05		(K)SLTNDW	(K)S L|T/N D W/E D H L A V/K(H)		144.18	509.9192	1527.744	-0.0008	-0.5	4.53	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
6827	dirMS_041712_NAR_50mM_minus2.16009.16384.3	3	11.91	1	3.24E+07	M148m	(R)LDLAGR	(R)L/D|L|A/G R D L/T D Y L/m/K(I)	m:Oxidized methionine	160.03	547.2838	1623.841	15.9958	0.5	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
6828	dirMS_041712_NAR_50mM_minus2.9279.9279.3	3	11.91	1	2.01E+05		(K)GITEQQ	(K)G I|T E/Q Q K\E/G/L E I V K(M)		120.58	524.6237	1571.864	-0.0074	-4.7	4.79	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
6829	dirMS_041712_NAR_60mM_minus.5504.5504.3	3	11.91	1	6.90E+04		(R)GSCSTE	(R)G S|C/S/T E V E K E T Q E/K(M)	C:Carbamidomethylation	86.75	537.9095	1611.717	-0.0027	-1.7	4.49	13871.4	9.22	HUMAN	O75348	V-type proton ATPase subunit G 1
6830	dirMS_041712_NAR_60mM_minus.8145.8145.3	3	11.91	1	6.51E+04		(K)SLVSDKT	(K)S L|V|S/D K T S\I S E/K(V)		105.47	431.9006	1293.69	-0.0024	-1.8	5.79	58791	9.93	HUMAN	E9PDI4	Ladinin-1
6831	dirMS_041712_NAR_120mM_plus.4600.4600.3	3	11.91	0	6.19E+05		(R)THSQGG	(R)T H S Q G G|Y/G S/Q/G Y/K(Y)		74.07	457.2092	1369.613	-0.0001	-0.1	8.2	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
6832	dirMS_041712_NAR_30mM_plus2.13609.13695.2	2	11.91	0	1.05E+06		(K)LITPAVV	(K)L I|T|P/A/V/V/S\E R(L)		124.33	542.8172	1084.636	-0.009	-8.3	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
6833	dirMS_041712_NAR_30mM_plus2.21787.21881.2	2	11.91	0	6.86E+05		(K)NGFLLD	(K)N G|F|L|L/D/G F/P R(T)		170.28	568.3022	1135.59	0.0077	6.7	5.84	21283.1	6.45	HUMAN	F8VY04	Adenylate kinase 2, mitochondrial
6834	dirMS_041712_NAR_30mM_plus2.22309.22309.2	2	11.91	0	3.79E+05		(R)VGNLGL	(R)V G\N\L|G L|A/T S/F F\N E R(N)		172.8	762.8926	1524.781	-0.0026	-1.7	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
6835	dirMS_041712_NAR_50mM_plus2.20119.20119.3	3	11.91	1	1.08E+05		(K)SVISGGL	(K)S V|I/S/G G L/D A L/E F I G K K(T)		174.18	545.3096	1633.916	-0.0017	-1	5.79	22133.2	4.82	HUMAN	E5RGF9	Protein FAM114A2 (Fragment)
6836	dirMS_041712_NAR_60mM_plus.6962.6962.3	3	11.91	0	3.29E+05		(R)GPFRPEI	(R)G P/F R P E|P/G D G G E/K(M)		94.62	448.2174	1342.639	-0.001	-0.7	4.68	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
6837	dirMS_041712_NAR_120mM_minus.11731.11828.3	3	11.9	1	2.46E+05		(R)RGLLED	(R)R G L\L\E|D\V|Q/E/G R(T)		118.47	424.562	1271.67	0.0012	0.9	4.68	266161	5.68	HUMAN	E9PPU0	Epiplakin
6838	dirMS_041712_NAR_30mM_minus2.7108.7256.2	2	11.9	0	7.11E+05		(K)ESPQEIA	(K)E S/P/Q/E/I/A/R(K)		93.87	465.2366	929.469	-0.0028	-3	4.53	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
6839	dirMS_041712_NAR_50mM_minus2.15282.15282.3	3	11.9	1	4.51E+05		(K)GADFLV	(K)G A|D/F/L\V|T E V E N G G S L G S K K(G)		155.55	636.662	1907.971	0.0005	0.3	4.68	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
6840	dirMS_041712_NAR_60mM_minus.14803.14803.3	3	11.9	0	2.66E+05		(K)YYITIIDA	(K)Y Y I/T/I|I/D/A/P G H R(D)		142.87	473.5815	1418.743	-0.0127	-9	6.74	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
6841	dirMS_041712_NAR_60mM_minus.19896.19896.3	3	11.9	0	4.40E+06		(R)LHFFMP	(R)L H F F M P/G|F|A|P\L T S R(G)		179.95	540.9491	1620.835	-0.0028	-1.7	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
6842	dirMS_041712_NAR_120mM_plus.17013.17013.4	4	11.9	2	1.32E+06		(R)YEEIVKE	(R)Y/E E I V K E V/S T/Y/I/K K(I)		142.25	432.9909	1728.942	-0.0001	0	6.23	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
6843	dirMS_041712_NAR_20mM_plus.10566.10566.2	2	11.9	0	5.11E+04		(R)ELAEDG	(R)E L/A E/D/G Y/S G\V E/V R(V)		145.7	712.3373	1423.67	-0.0026	-1.9	4	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
6844	dirMS_041712_NAR_20mM_plus.12069.12069.2	2	11.9	0	5.20E+04		(K)VVLVLA	(K)V V|L/V/L/A G R(Y)		156.4	413.778	826.551	-0.0022	-2.6	9.72	4480.4	11.2	HUMAN	K7ERY7	60S ribosomal protein L27
6845	dirMS_041712_NAR_20mM_plus.13373.13373.2	2	11.9	0	4.59E+05	M148m	(R)DLTDYL	(R)D/L|T/D/Y\L|m K(I)	m:Oxidized methionine	164.65	507.7439	998.486	15.9942	-0.7	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
6846	dirMS_041712_NAR_30mM_plus2.19972.19972.2	2	11.9	0	5.38E+05		(R)NAVWA	(R)N A|V|W/A\L S N L C R(G)	C:Carbamidomethylation	157.48	652.3414	1303.658	0.018	13.8	9.75	37228.9	5.22	HUMAN	C9JYI4	Importin subunit alpha-1 (Fragment)
6847	dirMS_041712_NAR_30mM_plus2.7311.7312.2	2	11.9	0	3.05E+05		(K)LAGESES	(K)L/A|G\E/S/E/S N L/R(K)		92.98	538.2715	1075.538	-0.0021	-2	4.53	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
6848	dirMS_041712_NAR_50mM_plus2.15959.15959.3	3	11.9	1	6.35E+05		(K)LALDIEI	(K)L/A\L/D I/E/I/A/T Y R K(L)		151.7	469.2726	1405.805	-0.0017	-1.2	6.07	49564	5.84	HUMAN	E9PAX3	Glial fibrillary acidic protein
6849	dirMS_041712_NAR_50mM_plus2.16482.16483.3	3	11.9	0	7.49E+05		(K)ANIVHLI	(K)A N\I/V H L M|L|S S|P E Q I Q/K(Q)		154.68	603.3265	1807.974	-0.0085	-4.7	6.79	104619	5.75	HUMAN	F8W904	Exportin-2
6850	dirMS_041712_NAR_50mM_plus2.16526.16526.3	3	11.9	1	2.21E+05		(R)STVRDID	(R)S T V R D I\D|P Q/N D/L/T|F L R(I)		154.87	630.6609	1889.972	-0.0034	-1.8	4.43	16537.8	6.59	HUMAN	B1AKR6	Dynein light chain roadblock-type 1
6851	dirMS_041712_NAR_50mM_plus2.18507.18507.3	3	11.9	0	4.12E+05		(R)VYAILTH	(R)V/Y|A/I/L T/H/G I F S G P A I S R(I)		165.83	601.3347	1801.996	-0.0064	-3.5	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
6852	dirMS_041712_NAR_50mM_plus2.6443.6443.3	3	11.9	1	1.97E+05		(K)IVSGKD	(K)I/V|S G/K D Y N/V/T A N S K(L)		98.92	499.2611	1495.775	-0.0064	-4.2	8.5	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
6853	dirMS_041712_NAR_50mM_plus2.7426.7426.3	3	11.9	1	2.93E+05		(R)IVEQDTI	(R)I/V|E Q/D T M/P/P K G V R(H)		105.32	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
6854	dirMS_041712_NAR_50mM_plus2.9159.9263.3	3	11.9	1	2.65E+05		(K)EVPAVP	(K)E V/P A/V/P E/T L K K(K)		115.48	404.2395	1210.704	-0.0002	-0.2	6.24	29282.3	10.71	HUMAN	P18124	60S ribosomal protein L7
6855	dirMS_041712_NAR_50mM_plus2.9703.9703.3	3	11.9	1	3.85E+05		(K)ALIEME	(K)A/L|I/E M/E K Q Q Q/D Q V D R(N)		118.65	610.9732	1830.901	0.0036	2	4.32	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)
6856	dirMS_041712_NAR_60mM_plus.11037.11037.3	3	11.9	1	6.48E+05		(R)AVDERF	(R)A/V|D/E\R F/P G C\M/Q G R(T)	C:Carbamidomethylation	115.12	508.237	1522.689	0.0075	4.9	6.12	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
6857	dirMS_041712_NAR_60mM_plus.13634.13685.3	3	11.9	1	7.33E+05		(R)FNVPVS	(R)F/N|V|P V/S L/E S\K K(A)		128.48	416.571	1247.699	-0.001	-0.8	8.59	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
6858	dirMS_041712_NAR_60mM_plus.17854.17854.3	3	11.9	0	2.66E+05		(R)LLIHQSL	(R)L L/I H/Q S\L|A G/G I/I G V K(G)		150.48	506.9815	1518.937	-0.0067	-4.4	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
6859	dirMS_041712_NAR_60mM_plus.6407.6408.3	3	11.9	1	4.32E+05		(R)ARSDEG	(R)A R S D E/G\Q|L|S/P A/T R(G)		92.5	463.233	1387.692	-0.008	-5.8	6.12	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
6860	dirMS_041712_NAR_40mM_minus2.15135.15135.3	3	11.89	0	7.39E+05		(K)ALIEVLQ	(K)A/L/I/E/V/L Q/P L I/A E/H Q A R(R)		175.3	601.0146	1801.033	-0.0038	-2.1	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
6861	dirMS_041712_NAR_40mM_minus2.15968.16019.3	3	11.89	0	1.60E+06	M166m	(K)VLDFEHI	(K)V/L|D F E H F L|P m/L Q T V A K(N)	m:Oxidized methionine	187.72	635.3376	1888.004	15.9945	-0.2	5.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
6862	dirMS_041712_NAR_60mM_minus.6494.6494.3	3	11.89	1	8.87E+04		(K)SESPKEP	(K)S E|S/P K E\P/E Q L R(K)		94.9	433.8887	1299.654	-0.0024	-1.8	4.78	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1

6863	dirMS_041712_NAR_20mM_plus.15903.15903.2	2	11.89	0	5.02E+05		(R)GNPTVE	(R)G N|P T/V/E V/D L F T S K(G)		180.5	703.861	1406.716	-0.0015	-1	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
6864	dirMS_041712_NAR_20mM_plus.16465.16465.2	2	11.89	0	1.40E+05		(R)QAQEYE	(R)Q/A\Q E/Y/E/A L L N/I/K(V)		184.52	710.3754	1419.748	-0.0043	-3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
6865	dirMS_041712_NAR_30mM_plus2.12047.12082.2	2	11.89	0	6.57E+05		(R)GFSIPEC	(R)G F|S|I|P E C Q K(L)	C:Carbamidomethylation	116.08	533.2595	1065.503	0.0084	7.9	6	50659.2	7.87	HUMAN	B4DJV2	Citrate synthase
6866	dirMS_041712_NAR_30mM_plus2.18150.18150.2	2	11.89	0	2.14E+05		(R)QITLNDI	(R)Q I/T/L/N D/L/P V G R(S)		147.93	613.3465	1225.69	-0.0042	-3.4	5.84	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
6867	dirMS_041712_NAR_30mM_plus2.9133.9557.2	2	11.89	0	1.05E+06		(K)SVEAAA	(K)S V|E|A|A/A/E/L/S A K(D)		104.75	538.2855	1075.563	0.0007	0.7	4.53	12131.5	11.14	HUMAN	F5GXR3	Parathymosin
6868	dirMS_041712_NAR_40mM_plus2.13029.13029.3	3	11.89	0	2.15E+05		(R)VVLSVSS	(R)V V|L/S V/S S G G Q H T V/L L V/K(D)		143.55	575.0089	1723.011	0.0009	0.5	8.73	45424.7	7.24	HUMAN	P18754	Regulator of chromosome condensation
6869	dirMS_041712_NAR_50mM_plus2.5648.5648.3	3	11.89	1	1.06E+06		(K)TAGPIAS	(K)T A|G P I/A/S A Q\K Q/P A G K(V)		91.9	475.5987	1424.786	-0.0041	-2.8	10	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
6870	dirMS_041712_NAR_50mM_plus2.8757.8757.3	3	11.89	0	7.58E+05		(R)AALAHS	(R)A A/L\A H S E E\V T/A|S Q V|A/A T K(T)		113.45	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
6871	dirMS_041712_NAR_60mM_plus.7807.7871.3	3	11.89	1	2.85E+06		(R)LKSTCIY	(R)L K S T C|I|Y G G A/P K(G)	C:Carbamidomethylation	98.97	432.2316	1294.682	-0.0021	-1.7	9.7	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
6872	dirMS_041712_NAR_120mM_minus.6901.6901.3	3	11.88	1	2.11E+07		(R)TKTEISE	(R)T K T E I/S/E/M/N R(N)		92.55	403.5363	1208.594	0.0004	0.3	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
6873	dirMS_041712_NAR_120mM_minus.8417.8455.3	3	11.88	1	2.08E+05		(R)LREDEN	(R)L R E D\E N\A\E|P V/G T T/Y Q/K(T)		100.38	617.3002	1849.893	-0.0066	-3.6	4.41	76925.9	4.46	HUMAN	A8MV58	Drebrin
6874	dirMS_041712_NAR_30mM_minus2.17469.17469.2	2	11.88	0	2.34E+05		(R)NGGQIL	(R)N G\G\Q|I/L I/A D/L/R(G)		149.18	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
6875	dirMS_041712_NAR_40mM_minus2.8795.8837.3	3	11.88	1	2.33E+05		(R)IVLAND	(R)I/V|L/A/N D P D/A D R L A V/A E K(Q)		134.3	603.9966	1809.97	0.0047	2.6	4.23	32837.5	6.16	HUMAN	B4E0G8	Phosphoglucomutase-2
6876	dirMS_041712_NAR_40mM_minus2.8941.8941.3	3	11.88	1	5.45E+04		(R)IVAPGK	(R)I V|A/P G/K G I L A/A/D E/S T G S I A K(R)		135.25	633.355	1898.059	-0.0089	-4.7	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
6877	dirMS_041712_NAR_50mM_minus2.9097.9116.3	3	11.88	0	1.99E+05		(K)VGQEIE	(K)V/G|Q/E/I/E V R/P G I V S K(D)		120.43	504.2902	1510.859	-0.0027	-1.8	6.11	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
6878	dirMS_041712_NAR_60mM_minus.13631.13631.3	3	11.88	1	1.80E+05		(K)QMADT	(K)Q/M A D/T/G K/L/N T L/L/Q R(A)		135.92	530.2846	1588.848	-0.0083	-5.2	8.75	91324.5	5.75	HUMAN	Q00839	Heterogeneous nuclear ribonucleoprotein U
6879	dirMS_041712_NAR_60mM_minus.14373.14373.3	3	11.88	1	1.30E+06		(R)MSMKE	(R)M S M/K E V D E\Q|M/L/N V Q/N K(N)		140.47	641.9701	1923.897	-0.0015	-0.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
6880	dirMS_041712_NAR_60mM_minus.18654.18654.3	3	11.88	1	1.15E+05		(K)IILDLISE	(K)I I/L/D L/I/S E S P I/K G R(A)		166	518.6442	1553.926	-0.0081	-5.2	6.07	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
6881	dirMS_041712_NAR_60mM_minus.18684.18781.3	3	11.88	0	2.97E+05		(K)LHDNLII	(K)L H D N L\I|I/S/D\L/E N T V/K(K)		165.95	575.3117	1723.922	-0.0019	-1.1	4.54	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
6882	dirMS_041712_NAR_60mM_minus.7961.8075.3	3	11.88	1	4.84E+05		(R)YLAEVA	(R)Y/L|A/E/V/A T G E K R(A)		104.27	412.8902	1236.658	-0.0022	-1.8	6.14	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
6883	dirMS_041712_NAR_120mM_plus.18866.18866.4	4	11.88	0	3.40E+05		(K)APIRPDI	(K)A P I R P D/I V/N F/V/H/T N L R(K)		151.78	466.2639	1862.04	-0.0058	-3.1	9.65	18988.7	11.2	HUMAN	H3BTP7	60S ribosomal protein L4 (Fragment)
6884	dirMS_041712_NAR_20mM_plus.17584.17621.2	2	11.88	0	1.28E+05		(K)LATQSN	(K)L A T Q/S\N\E|I/T\I|P V T F E/S R(A)		193.23	953.4986	1905.992	-0.0017	-0.9	4.53	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
6885	dirMS_041712_NAR_20mM_plus.18135.18193.2	2	11.88	0	1.72E+05		(K)DAGVIA	(K)D A\G\V|I/A|G L N V L/R(I)		196.72	599.3505	1197.695	-0.0013	-1.1	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
6886	dirMS_041712_NAR_30mM_plus2.12164.12164.2	2	11.88	0	7.36E+05		(K)VNLLYS	(K)V/N|L/L Y S/R(D)		117.3	432.7483	864.494	-0.0045	-5.2	8.72	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
6887	dirMS_041712_NAR_30mM_plus2.8321.8556.2	2	11.88	0	9.70E+05		(R)LGLGEG	(R)L/G|L|G/E/G A E E K(S)		98.92	501.7639	1002.51	0.0103	10.3	4.25	40096.8	9.24	HUMAN	C9JW69	Regulator of chromosome condensation (Fragment)
6888	dirMS_041712_NAR_40mM_plus2.18154.18173.2	2	11.88	0	8.61E+04		(R)SLDMDS	(R)S L|D|M/D/S/I\I A E/V K(A)		173.07	660.8385	1320.671	-0.0018	-1.4	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
6889	dirMS_041712_NAR_40mM_plus2.6102.6102.2	2	11.88	0	1.72E+04		(R)ENPYYD	(R)E N|P/Y Y/D/S R(V)		94.68	522.2253	1043.443	0.0005	0.4	4.37	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
6890	dirMS_041712_NAR_50mM_plus2.13394.13414.3	3	11.88	1	1.15E+06		(K)IINADSE	(K)I/I|N/A/D/S E D/P K Y I I N V K(Q)		138.8	611.3256	1831.98	-0.0178	-9.7	4.56	14693.3	4.69	HUMAN	C9JLS9	26S protease regulatory subunit 7 (Fragment)
6891	dirMS_041712_NAR_50mM_plus2.18505.18505.2	2	11.88	0	5.42E+05		(R)IHFPLAT	(R)I H|F|P/L A T Y A/P V I\S\A E K(A)		164.98	878.9842	1756.963	-0.0021	-1.2	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
6892	dirMS_041712_NAR_50mM_plus2.20360.20360.3	3	11.88	1	1.84E+05		(R)GGPNIIT	(R)G G/P N/I|I/T L A\D I V K D/P V S R(T)		176.12	622.3526	1865.049	-0.0058	-3.1	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
6893	dirMS_041712_NAR_50mM_plus2.6921.6921.3	3	11.88	1	8.65E+05		(K)IVADKD	(K)I/V/A D K D Y/S V/T/A N S K(I)		101.45	504.2628	1510.775	-0.0009	-0.6	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
6894	dirMS_041712_NAR_50mM_plus2.9909.9911.3	3	11.88	0	7.05E+04		(R)AAEDPV	(R)A A|E|D|P/V A/A/A P R P L P A G G R(L)		119.42	572.6392	1715.919	-0.0157	-9.1	6.12	73966.7	10.21	HUMAN	B3KWK6	Alpha-L-iduronidase
6895	dirMS_041712_NAR_60mM_plus.12609.12609.3	3	11.88	0	4.99E+05		(K)VLAMSG	(K)V L/A|M S G D/P N Y L H/R(M)		121.75	491.5805	1472.732	-0.0045	-3.1	6.71	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
6896	dirMS_041712_NAR_120mM_minus.10257.10299.3	3	11.87	0	5.52E+05		(R)LESGM	(R)L/E|S G M Q/N M/S I/H T K(T)		110.28	492.571	1475.698	0.0003	0.2	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
6897	dirMS_041712_NAR_120mM_minus.12100.12100.3	3	11.87	0	2.17E+05		(R)QADFEA	(R)Q A/D/F E A/H/N I L/R(E)		119.82	438.5572	1313.66	-0.0026	-2	5.32	66612.6	7.28	HUMAN	F8W720	GMP synthase [glutamine-hydrolyzing]
6898	dirMS_041712_NAR_30mM_minus2.11617.11735.2	2	11.87	0	5.66E+05		(R)NLQDA	(R)N L|Q|D|A/M/Q/V/C R(N)	C:Carbamidomethylation	117.25	617.7907	1234.567	0.0074	6	5.84	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
6899	dirMS_041712_NAR_50mM_minus2.14881.14881.3	3	11.87	1	1.72E+05		(R)ALASQL	(R)A L|A/S Q/L Q/D S L K D/L K(A)		152.73	510.6213	1529.853	-0.004	-2.6	6	124367.7	5.51	HUMAN	P18206	Vinculin
6900	dirMS_041712_NAR_60mM_minus.14893.14932.3	3	11.87	1	3.83E+05		(R)IKIGDPL	(R)I K I G D\P\L|L|E/D/T/R(M)		142.83	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
6901	dirMS_041712_NAR_20mM_plus.12255.12280.2	2	11.87	0	9.16E+04	M78m	(K)TLVLLm	(K)T L|V/L/L/m G K(E)	m:Oxidized methionine	157.5	445.7707	874.543	15.9911	-4.3	8.41	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
6902	dirMS_041712_NAR_20mM_plus.13744.13744.2	2	11.87	0	1.96E+05		(K)APILIAT	(K)A/P/I|L|I/A/T/D V A S/R(G)		166.73	613.8559	1226.71	-0.0058	-4.7	5.88	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
6903	dirMS_041712_NAR_20mM_plus.13780.13853.2	2	11.87	0	6.96E+04		(R)VEVTEF	(R)V/E|V|T/E/F E D/I K(S)		167.18	604.8056	1208.604	-0.0006	-0.5	4	30992.3	4.14	HUMAN	B2REB8	Protein SET
6904	dirMS_041712_NAR_20mM_plus.6883.6883.2	2	11.87	0	4.03E+05	M132m	(R)DmVGIA	(R)D m|V|G/I/A Q T G S G K(T)	m:Oxidized methionine	112.9	590.2864	1163.573	15.993	-1.6	5.84	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
6905	dirMS_041712_NAR_30mM_plus2.11660.11661.2	2	11.87	0	5.70E+05		(R)AMGEQ	(R)A M/G\E|Q/A/V/A/L A/R(A)		114.4	558.7944	1116.583	-0.0015	-1.3	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
6906	dirMS_041712_NAR_30mM_plus2.13950.14161.2	2	11.87	0	9.22E+05		(K)SIPTLISR	(K)S I|P/T/L/I S/R(L)		126.3	443.7727	886.536	0.0025	2.8	9.47	40096.8	9.24	HUMAN	C9JW69	Regulator of chromosome condensation (Fragment)
6907	dirMS_041712_NAR_40mM_plus2.12704.12716.3	3	11.87	1	5.65E+04		(K)VLCGGD	(K)V L|C G G D I\Y|V/P E D/P K L K(D)	C:Carbamidomethylation	141.33	601.6538	1802.936	0.0111	6.2	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
6908	dirMS_041712_NAR_50mM_plus2.18193.18193.3	3	11.87	1	1.26E+05		(K)IILDLISE	(K)I I/L D L/I/S E/S P I K G R(A)		164	518.6453	1553.926	-0.0048	-3.1	6.07	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
6909	dirMS_041712_NAR_50mM_plus2.8434.8434.3	3	11.87	0	5.53E+05		(R)ASGNYA	(R)A/S/G/N Y/A T V/I S H N P/E T K(K)		111.85	563.6145	1688.824	0.0051	3	6.79	24115.6	11.59	HUMAN	E9PIZ3	60S ribosomal protein L8
6910	dirMS_041712_NAR_120mM_minus.12045.12045.4	4	11.86	0	2.96E+05		(K)TGTIVVE	(K)T G\T/I/V/V/E/G/H E L H D E D/I/R(L)		119.67	480.7433	1919.946	0.0056	2.9	4.49	132902.3	5.82	HUMAN	J3KR24	Isoleucine--tRNA ligase, cytoplasmic
6911	dirMS_041712_NAR_30mM_minus2.7794.8256.2	2	11.86	0	1.73E+06		(K)LLEAET	(K)L/L|E|A/E/T Q/R(Q)		98.72	480.2603	959.516	-0.0023	-2.4	4.53	266161	5.68	HUMAN	E9PPU0	Epiplakin
6912	dirMS_041712_NAR_50mM_minus2.9561.9561.3	3	11.86	1	3.07E+05		(R)ALEEAM	(R)A L|E/E/A/M E Q/K A E L/E R(L)		122.18	549.6072	1646.805	0.0016	1	4.33	227783.5	5.5	HUMAN	P35579	Myosin-9
6913	dirMS_041712_NAR_60mM_minus.10961.10961.3	3	11.86	0	2.66E+05		(R)ALPESL	(R)A L/P E/S L/G Q/H A L R(S)		121.3	431.2376	1291.712	-0.0135	-10.4	6.79	31463.6	5.53	HUMAN	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1
6914	dirMS_041712_NAR_60mM_minus.18782.18782.3	3	11.86	1	2.67E+05		(K)NAAGAL	(K)N A|A/G/A L/D L L K E L K(N)		166.87	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
6915	dirMS_041712_NAR_60mM_minus.6163.6163.3	3	11.86	1	7.53E+05		(K)DSYVGD	(K)D S|Y|V/G D/E A Q S K R(G)		92.53	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
6916	dirMS_041712_NAR_30mM_plus2.7383.7383.2	2	11.86	1	2.13E+05		(R)YSGGNY	(R)Y/S|G G N Y/R D N|Y/D|N(-)		93.03	719.2864	1437.567	-0.001	-0.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
6917	dirMS_041712_NAR_50mM_plus2.15032.15032.3	3	11.86	1	1.14E+05		(R)LLDAQL	(R)L L|D|A/Q|L/A T G G L V C P A R R(L)	C:Carbamidomethylation	147.2	604.3351	1810.996	-0.0049	-2.7	9.6	266161	5.68	HUMAN	E9PPU0	Epiplakin
6918	dirMS_041712_NAR_50mM_plus2.16520.16520.3	3	11.86	0	2.19E+05		(K)FTISDHP	(K)F/T|I/S D H P Q P I D/P L/L K(N)		154.8	574.3119	1720.927	-0.0057	-3.3	5.21	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
6919	dirMS_041712_NAR_50mM_plus2.19925.19925.3	3	11.86	0	8.05E+05		(K)LNEHFL	(K)L N E H F L N/T/T/D/F/L D/T I K(S)		173.27	640.9957	1920.97	0.0024	1.2	4.54	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
6920	dirMS_041712_NAR_60mM_plus.5081.5081.3	3	11.86	1	3.95E+05		(R)AAEDDE	(R)A/A|E/D/D E D D D/V/D/T K K(Q)		83.53	522.5529	1565.645	-0.0008	-0.5	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
6921	dirMS_041712_NAR_60mM_plus.7532.7532.3	3	11.86	0	4.71E+05		(R)SSGHSSS	(R)S S G/H S S S E\L/S/P D A V E K(A)		97.02	539.584	1616.74	-0.0024	-1.5	4.65	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
6922	dirMS_041712_NAR_60mM_plus.8945.8945.3	3	11.86	1	8.20E+05		(R)SSGGSY	(R)S S/G G/S Y R D S Y\D\S/Y A T/H N/E(-)		104.85	665.9403	1995.795	0.0112	5.6	4.81	18647.7	9.51	HUMAN	Q14011	Cold-inducible RNA-binding protein
6923	dirMS_041712_NAR_30mM_minus2.15195.15195.2	2	11.85	0	7.59E+04		(R)QITVND	(R)Q I/T V/N D/L/P V G R(S)		136.35	606.3404	1211.674	-0.0007	-0.6	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
6924	dirMS_041712_NAR_30mM_minus2.9291.9336.2	2	11.85	0	3.53E+05		(K)CAADLG	(K)C/A|A|D/L/G\L N K(G)	C:Carbamidomethylation	104.88	481.2466	961.477	0.0088	9.1	5.84	13915.8	6.43	HUMAN	P49773	Histidine triad nucleotide-binding protein 1
6925	dirMS_041712_NAR_50mM_minus2.13738.13738.3	3	11.85	0	5.66E+05		(R)DLSHIG	(R)D L S H I G D\A\V|V|I/S C A K(D)	C:Carbamidomethylation	146.12	528.9397	1584.805	-0.0005	-0.3	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
6926	dirMS_041712_NAR_50mM_minus2.14524.14524.3	3	11.85	0	1.91E+04		(K)VALLLLD	(K)V/A/L|L L L D/Q/G/A S P H A A A K(N)		150.97	558.9883	1674.954	-0.0034	-2	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
6927	dirMS_041712_NAR_60mM_minus.15896.15896.3	3	11.85	1	3.50E+04		(R)KDDPVT	(R)K\D D P V\T N/L/N N\A|F/E/V A E K(Y)		148.48	635.317	1903.94	-0.0032	-1.7	4.32	21601.4	6.27	HUMAN	K7EJH8	Alpha-actinin-4 (Fragment)
6928	dirMS_041712_NAR_60mM_minus.16795.16893.3	3	11.85	1	3.66E+05		(K)ILLAELE	(K)I/L/L|A/E L/E/Q/L K G Q G K(S)		154.27	513.9734	1539.911	-0.0048	-3.1	6.14	49709.6	5.19	HUMAN	B0YJC4	Vimentin
6929	dirMS_041712_NAR_20mM_plus.17138.17138.2	2	11.85	0	9.11E+04		(R)AIVAIEN	(R)A I/V\A|I\E\N|P A D V S V I/S S R(N)		189.05	870.9764	1740.949	-0.0035	-2	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
6930	dirMS_041712_NAR_20mM_plus.18564.18564.3	3	11.85	0	4.98E+03		(K)LAVEALS	(K)L A V E A L S S/L/D G D|L A/G R(Y)		199.18	529.6164	1586.838	-0.0038	-2.4	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
6931	dirMS_041712_NAR_20mM_plus.7950.7950.2	2	11.85	0	5.64E+04		(K)SVTEQG	(K)S V|T|E Q/G A\E L/S N E E R(N)		124.88	774.8589	1548.714	-0.0031	-2	4.09	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
6932	dirMS_041712_NAR_30mM_plus2.10297.10297.2	2	11.85	0	2.98E+04		(K)TAVCDI	(K)T A|V/C/D I|P\P/R(G)	C:Carbamidomethylation	106.05	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
6933	dirMS_041712_NAR_30mM_plus2.14374.14374.2	2	11.85	0	2.16E+05		(K)ASEGPA	(K)A S/E/G/P A/F/F/P G R(C)		127.95	568.2831	1135.553	0.0058	5.1	6.05	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
6934	dirMS_041712_NAR_30mM_plus2.19108.19108.2	2	11.85	0	2.07E+05		(K)YPQLLP	(K)Y/P/Q L|L|P G I/R(G)		153.25	528.814	1056.62	0.0007	0.6	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
6935	dirMS_041712_NAR_40mM_plus2.17861.17861.3	3	11.85	0	1.42E+05		(R)DIKPQN	(R)D I K P Q N\L|L/L/D/P D T A V/L K(L)		170.92	631.6874	1893.069	-0.0215	-11.4	4.43	47257	9.38	HUMAN	P49841	Glycogen synthase kinase-3 beta
6936	dirMS_041712_NAR_50mM_plus2.19491.19777.3	3	11.85	0	6.79E+05		(R)EAVELPL	(R)E A\V/E/L/P L/T H/F E L Y K(Q)		171.62	563.6357	1688.889	0.0031	1.9	4.75	47479.5	5.09	HUMAN	P43686	26S protease regulatory subunit 6B
6937	dirMS_041712_NAR_50mM_plus2.20993.20993.3	3	11.85	0	5.51E+04		(R)LHFFMP	(R)L H F F M|P G F|A|P|L T S R(G)		179.42	540.9498	1620.835	-0.0007	-0.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
6938	dirMS_041712_NAR_60mM_plus.12314.12375.3	3	11.85	0	5.29E+05		(K)EDLYLK	(K)E D/L/Y/L/K/P I/Q R(T)		121.37	425.5789	1274.71	0.0118	9.3	6.17	96306.4	6.41	HUMAN	P13639	Elongation factor 2
6939	dirMS_041712_NAR_60mM_plus.6758.6759.3	3	11.85	1	4.02E+06		(R)KTGQAP	(R)K\T G|Q A|P G\Y|S|Y T A A/N K(N)		94.02	519.5996	1556.77	0.0139	8.9	9.53	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
6940	dirMS_041712_NAR_120mM_minus.12080.12080.3	3	11.84	1	2.45E+05		(R)MQKEIT	(R)M Q K\E I T A|L/A/P/S T M K(I)		119.85	516.9425	1548.812	0.0005	0.3	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
6941	dirMS_041712_NAR_20mM_minus.10730.10730.2	2	11.84	0	1.89E+05		(R)TTPSYV	(R)T T/P S Y/V\A/F T/D/T E R(L)		154.68	744.3547	1487.701	0.0009	0.6	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
6942	dirMS_041712_NAR_30mM_minus2.15987.15987.2	2	11.84	0	2.34E+05		(K)ELPELLQ	(K)E L/P E/L/L Q/R(N)		140.12	499.2869	997.568	-0.0011	-1.2	4.53	96649	6.13	HUMAN	Q8WUM4	Programmed cell death 6-interacting protein
6943	dirMS_041712_NAR_30mM_minus2.9578.9711.2	2	11.84	0	1.26E+06		(K)EAESSP	(K)E\A|E/S/S/P F V E/R(L)		107.62	575.7705	1150.537	-0.0038	-3.3	4.25	92752.5	4.76	HUMAN	P14625	Endoplasmin
6944	dirMS_041712_NAR_40mM_minus2.8796.8796.3	3	11.84	1	6.30E+03		(K)DVDEAY	(K)D V/D/E|A|Y M N/K/V E L E S R(L)		134.07	599.947	1797.832	-0.0059	-3.3	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
6945	dirMS_041712_NAR_60mM_minus.12629.13142.3	3	11.84	0	9.18E+05		(K)GIHPTIIS	(K)G I\H\P T I\I/S/E/S F/Q K(A)		132.28	486.2642	1456.78	-0.0014	-1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
6946	dirMS_041712_NAR_60mM_minus.4799.4799.3	3	11.84	1	7.13E+05	M137m	(R)mQNDT	(R)m/Q|N/D/T/A E N E/T T E K E\E K(S)	m:Oxidized methionine	79.37	638.2735	1896.813	15.9932	-0.9	4.14	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
6947	dirMS_041712_NAR_60mM_minus.6182.6182.3	3	11.84	1	6.66E+05		(K)DSYVGD	(K)D\S/Y/V/G D E/A/Q S K R(G)		92.85	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
6948	dirMS_041712_NAR_120mM_plus.7221.7221.3	3	11.84	1	3.21E+05	M462m	(R)KAYGGA	(R)K\A Y G G\A|Y/D|V/m S S K(H)	m:Oxidized methionine	91.37	464.8863	1376.651	15.9929	-1.5	8.43	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
6949	dirMS_041712_NAR_20mM_plus.13564.13564.2	2	11.84	0	2.03E+05		(R)GDLGIEI	(R)G D|L/G|I/E I/P A E K(V)		166.5	571.3075	1141.61	-0.0022	-1.9	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
6950	dirMS_041712_NAR_20mM_plus.17128.17129.2	2	11.84	0	2.50E+05		(K)LFLVQL	(K)L|F|L|V/Q/L Q E/K(A)		189.67	559.3342	1117.662	-0.0004	-0.4	6	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
6951	dirMS_041712_NAR_30mM_plus2.8701.8701.2	2	11.84	0	1.81E+05		(R)VGDYGS	(R)V/G/D|Y|G S/L/S G R(E)		99.42	505.7477	1010.49	-0.002	-2	5.8	34552	6.72	HUMAN	Q9UBR2	Cathepsin Z
6952	dirMS_041712_NAR_40mM_plus2.18841.18841.3	3	11.84	1	4.26E+05		(R)TLAEIAK	(R)T L|A/E\I/A/K/V E/L D N M/P L/R(G)		176.73	604.9967	1812.989	-0.0132	-7.3	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
6953	dirMS_041712_NAR_50mM_plus2.9495.9584.3	3	11.84	0	8.00E+05		(K)YIQQTK	(K)Y/I|Q|Q/T K/P L T L E R(T)		117.03	497.2822	1489.837	-0.0053	-3.5	8.59	26283.8	8.96	HUMAN	O43809	Cleavage and polyadenylation specificity factor subunit 5
6954	dirMS_041712_NAR_60mM_plus.11894.11913.3	3	11.84	1	2.04E+05		(K)IIEDQQE	(K)I/I|E/D/Q Q\E/S L/N K W K(S)		119.47	544.2896	1630.843	0.0107	6.6	4.68	41995	5.77	HUMAN	E9PFH8	Lupus La protein
6955	dirMS_041712_NAR_60mM_plus.16412.16412.3	3	11.84	1	6.29E+05		(K)AAVEW	(K)A/A|V/E/W F/D G K/D F Q G S K(L)		142.77	562.2762	1684.797	0.0175	10.4	4.56	65213.5	9.57	HUMAN	B0QYK0	Ewing sarcoma breakpoint region 1
6956	dirMS_041712_NAR_60mM_plus.20588.20670.3	3	11.84	1	7.14E+05		(R)LDLAGR	(R)L/D|L/A/G R D L/T D/Y L/M K(I)		168.28	541.9516	1623.841	-0.0008	-0.5	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
6957	dirMS_041712_NAR_120mM_minus.20553.20553.3	3	11.83	1	3.46E+05		(R)LDLAGR	(R)L/D|L\A/G R D L T D Y\L M K(I)		169.02	541.9508	1623.841	-0.0032	-2	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
6958	dirMS_041712_NAR_30mM_minus2.8532.8647.2	2	11.83	0	4.75E+05		(R)YLSNAY	(R)Y/L|S|N A/Y A/R(E)		101.35	479.2437	957.479	0.0013	1.3	8.59	27264.5	5.09	HUMAN	O00299	Chloride intracellular channel protein 1
6959	dirMS_041712_NAR_60mM_minus.18999.18999.3	3	11.83	0	5.02E+05		(R)LGFHLPL	(R)L G F H L P L|E|V/A/Y/Q/R(G)		168.45	514.9512	1542.843	-0.0037	-2.4	6.75	533778	5.74	HUMAN	Q15149	Plectin
6960	dirMS_041712_NAR_20mM_plus.12771.12771.2	2	11.83	0	2.85E+05	M316m	(R)ISEQFTA	(R)I/S\E Q/F/T/A/m F R(R)	m:Oxidized methionine	161.28	623.3012	1229.598	15.9968	1.5	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
6961	dirMS_041712_NAR_30mM_plus2.11478.11538.2	2	11.83	0	2.10E+05		(K)MLVSGA	(K)M/L|V|S/G A G D|I/K(L)		113.55	495.7686	990.529	0.0011	1.1	5.59	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
6962	dirMS_041712_NAR_30mM_plus2.20403.20403.2	2	11.83	0	3.00E+05		(R)TTLLPGL	(R)T T|L|L/P G/L L K(T)		160.85	478.3126	955.619	-0.0007	-0.8	8.41	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
6963	dirMS_041712_NAR_50mM_plus2.6988.6988.3	3	11.83	1	6.65E+05		(K)IVADKD	(K)I V|A D K D/Y/S/V/T/A N S K(I)		101.85	504.2628	1510.775	-0.0009	-0.6	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
6964	dirMS_041712_NAR_60mM_plus.16203.16203.3	3	11.83	0	5.21E+05		(K)WIGLDL	(K)W/I/G L/D|L/S N/G K/P R(D)		141.92	452.5864	1355.743	0.0016	1.2	8.75	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
6965	dirMS_041712_NAR_120mM_minus.9729.9729.3	3	11.82	1	6.41E+05		(R)AREQAE	(R)A R E\Q A E\A\E|V/A/S L/N\R(R)		107.8	515.2649	1543.782	-0.0022	-1.4	4.79	11017	4.8	HUMAN	D6R904	Tropomyosin alpha-3 chain
6966	dirMS_041712_NAR_30mM_minus2.18286.18286.2	2	11.82	0	8.12E+04		(K)SCDFLSS	(K)S C/D|F/L/S S/F R(D)	C:Carbamidomethylation	153.88	559.7501	1118.494	-0.0006	-0.5	5.55	42963.5	5.19	HUMAN	P35237	Serpin B6
6967	dirMS_041712_NAR_50mM_minus2.8460.8460.3	3	11.82	1	8.44E+04		(K)NVSEEL	(K)N V/S E E\L D R T/P/P E V/S K(K)		115.98	567.289	1699.85	0.0027	1.6	4.41	136658.9	5.13	HUMAN	Q15393	Splicing factor 3B subunit 3
6968	dirMS_041712_NAR_60mM_minus.16242.16242.3	3	11.82	1	4.38E+05		(K)NIYVLQE	(K)N/I/Y|V L Q E L D N P G A K/R(I)		150.72	577.3128	1729.923	0.0007	0.4	6.07	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
6969	dirMS_041712_NAR_60mM_minus.16773.16817.3	3	11.82	1	2.85E+05		(R)GQFSTD	(R)G Q\F/S/T/D/E L/V/A/E V E K R(N)		153.92	569.9569	1707.855	0.0013	0.8	4.41	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
6970	dirMS_041712_NAR_60mM_minus.9757.9757.2	2	11.82	1	4.41E+05		(R)LQAEIE	(R)L/Q/A E/I/E/G L/K G Q R(A)		114.13	671.3768	1341.748	-0.0022	-1.6	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
6971	dirMS_041712_NAR_120mM_plus.12836.12836.3	3	11.82	0	8.27E+05		(K)HYGPGV	(K)H Y\G P G W/V/S/M A/N A G K(D)		121.25	492.2383	1474.69	0.0108	7.3	8.6	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B

6972	dirMS_041712_NAR_120mM_plus.20242.20242.3	3	11.82	0	2.78E+05		(R)INLWHL	(R)I/N L/W/H/L/E I/T D/R(S)		159.48	470.5889	1409.754	-0.0014	-1	5.32	52204.6	5.82	HUMAN	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
6973	dirMS_041712_NAR_120mM_plus.6458.6622.2	2	11.82	0	4.57E+05		(K)HQPTAII	(K)H/Q|P T A\I|I|A/K(T)		87.75	489.7897	978.573	-0.001	-1	8.76	63448.4	7.29	HUMAN	B4E022	Transketolase
6974	dirMS_041712_NAR_120mM_plus.7039.7058.3	3	11.82	0	4.26E+05		(K)SQFSDKI	(K)S Q|F/S D K/P/V/Q D/R(G)		90.13	436.2209	1306.639	0.0095	7.3	5.68	13194	9.99	HUMAN	E9PI70	Chitinase domain-containing protein 1 (Fragment)
6975	dirMS_041712_NAR_120mM_plus.9677.9723.3	3	11.82	0	2.28E+06	S71s	(R)IEQFsQE	(R)I/E Q/F s/Q|E H S V|K(K)	s:N-acetylglucosamine (S)	104.1	512.2541	1331.659	203.0887	6.1	5.4	104355.7	8.97	HUMAN	Q2TBE0	CWF19-like protein 2
6976	dirMS_041712_NAR_20mM_plus.8448.8448.2	2	11.82	0	1.04E+05	M607m M(	(R)mGLAm	(R)m G\L|A/m/G|G G G G A S/F D R(A)	m:Oxidized methionine	128.17	708.3061	1383.614	31.9905	0.5	5.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
6977	dirMS_041712_NAR_30mM_plus2.11602.11875.2	2	11.82	0	1.69E+06		(R)NTDEM	(R)N T|D/E|M/V/E/L/R(I)		114.77	553.7615	1106.515	0.0011	1	4.14	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
6978	dirMS_041712_NAR_30mM_plus2.15048.15231.2	2	11.82	0	5.29E+05		(R)IAAYLFK	(R)I/A|A/Y\L/F/K(G)		132.15	413.2445	825.487	-0.0052	-6.3	8.59	15830.9	5.16	HUMAN	J3KRF5	Clathrin heavy chain 1 (Fragment)
6979	dirMS_041712_NAR_30mM_plus2.20305.20305.3	3	11.82	0	4.89E+05		(K)SYELPD	(K)S\Y\E\L|P D\G Q\V\I|T I/G N E R(F)		159.92	597.6334	1790.892	-0.0063	-3.5	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
6980	dirMS_041712_NAR_30mM_plus2.21167.21167.2	2	11.82	0	3.30E+05		(R)GVVQEL	(R)G V|V\Q/E L|Q Q A I|S K(L)		165.77	650.3632	1299.727	-0.0076	-5.8	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
6981	dirMS_041712_NAR_30mM_plus2.21451.21451.2	2	11.82	0	1.58E+05		(R)VFIGNL	(R)V F|I/G N L N/T L V V K(K)		167.38	658.8983	1316.794	-0.0043	-3.3	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
6982	dirMS_041712_NAR_40mM_plus2.12764.12764.2	2	11.82	0	1.31E+05		(K)YMACCL	(K)Y/M|A|C/C L/L/Y/R(G)	C:Carbamidomethylation	141.83	625.28	1249.553	0.0001	0.1	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
6983	dirMS_041712_NAR_50mM_plus2.15605.15605.3	3	11.82	1	1.01E+06		(R)KVPGVT	(R)K\V P G V T A I\E|L/D/E/D T/G T F R(I)		149.87	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
6984	dirMS_041712_NAR_50mM_plus2.6620.6641.3	3	11.82	0	2.83E+05		(K)TIEAEAA	(K)T I|E/A/E/A A/H/G T V/T R(H)		99.78	452.5685	1355.691	-0.0004	-0.3	5.37	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
6985	dirMS_041712_NAR_60mM_plus.6764.6764.2	2	11.82	1	4.77E+05		(K)GPSSVEI	(K)G P|S|S V/E D I K A K(M)		93.85	565.8054	1130.605	-0.0017	-1.5	6.07	32745.6	4.64	HUMAN	P06748	Nucleophosmin
6986	dirMS_041712_NAR_60mM_plus.8628.8628.3	3	11.82	1	1.43E+06		(K)MQASIE	(K)M|Q/A/S I/E K G G S L/P K(V)		103.27	449.2449	1345.714	0.0057	4.3	8.35	32745.6	4.64	HUMAN	P06748	Nucleophosmin
6987	dirMS_041712_NAR_30mM_minus2.7579.7579.2	2	11.81	0	7.71E+04		(K)NCTYTQ	(K)N/C|T/Y/T Q/V/Q T R(S)	C:Carbamidomethylation	95.8	635.7938	1270.584	-0.0041	-3.3	8.75	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
6988	dirMS_041712_NAR_40mM_minus2.15121.15121.3	3	11.81	0	7.24E+05		(K)ALIEVLQ	(K)A L I/E\V L/Q/P L I/A E/H Q A R(R)		175.28	601.0146	1801.033	-0.0038	-2.1	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
6989	dirMS_041712_NAR_60mM_minus.11419.11419.3	3	11.81	1	8.45E+05	M232m	(R)MSmKE	(R)M/S m K E V D E/Q|M/L|N|V Q N K(N)	m:Oxidized methionine	122.85	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
6990	dirMS_041712_NAR_60mM_minus.11571.11608.3	3	11.81	0	2.25E+05		(K)ADDGR	(K)A/D|D/G R P F/P Q V/I/K(S)		124.53	448.2371	1342.711	-0.0146	-10.9	6	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
6991	dirMS_041712_NAR_60mM_minus.13864.13864.3	3	11.81	1	2.04E+05		(R)IQLVEEE	(R)I/Q|L/V/E E E L D R A/Q E R(L)		137.75	576.6347	1727.892	-0.0027	-1.6	4.25	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
6992	dirMS_041712_NAR_60mM_minus.15211.15417.3	3	11.81	1	4.91E+04		(K)YMACCL	(K)Y/M|A/C/C L/L Y R G D V V/P K(E)	C:Carbamidomethylation	145.53	615.6321	1844.886	-0.0038	-2.1	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
6993	dirMS_041712_NAR_60mM_minus.16685.16685.3	3	11.81	1	1.80E+05		(K)VSEQGL	(K)V/S E Q G\L I E I L K/K(V)		152.83	452.9408	1356.81	-0.0018	-1.4	6.11	12899.6	6.59	HUMAN	K7EL31	Programmed cell death protein 5
6994	dirMS_041712_NAR_60mM_minus.5123.5123.3	3	11.81	1	4.62E+04		(R)GGARVE	(R)G G A R V\E|P A/D A/S/G T E K(A)		82.98	482.2368	1444.703	-0.0068	-4.7	4.68	54713.8	5.69	HUMAN	P49189	4-trimethylaminobutyraldehyde dehydrogenase
6995	dirMS_041712_NAR_120mM_plus.13639.13714.3	3	11.81	0	1.60E+06		(R)NLDIER	(R)N/L|D/I/E R/P T Y/T/N L N R(L)		125.65	573.6317	1718.882	-0.0015	-0.9	6.07	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
6996	dirMS_041712_NAR_20mM_plus.14626.14626.2	2	11.81	0	3.89E+04	M185m	(K)LAVNm	(K)L A|V/N/m\V/P F P/R(L)	m:Oxidized methionine	172.75	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
6997	dirMS_041712_NAR_30mM_plus2.7687.7712.2	2	11.81	0	4.24E+05		(K)AVVVVD	(K)A V/V|V/V/D/D/R(G)		94.38	436.7447	872.484	-0.0015	-1.7	4.21	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
6998	dirMS_041712_NAR_50mM_plus2.7428.7428.3	3	11.81	1	2.93E+05		(R)IVEQDT	(R)I/V/E/Q/D T/M/P P K G V/R(H)		105.32	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
6999	dirMS_041712_NAR_50mM_plus2.8684.8684.3	3	11.81	0	1.34E+05		(K)VVQVSA	(K)V V/Q/V|S/A G D/S H T/A A L/T D D G R(V)		113.03	633.6509	1898.92	0.0179	9.4	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
7000	dirMS_041712_NAR_60mM_plus.11966.12029.3	3	11.81	1	2.27E+06		(K)VELDN	(K)V/E|L/D N M/P L R G/K(Q)		119.92	424.5617	1271.678	-0.0071	-5.6	6.04	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
7001	dirMS_041712_NAR_60mM_plus.16637.16637.3	3	11.81	0	1.92E+05		(R)LSQYQE	(R)L/S\Q/Y Q/E P L/H L/P G V/R(V)		143.7	546.297	1636.881	-0.0041	-2.5	6.75	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
7002	dirMS_041712_NAR_120mM_minus.5646.5646.3	3	11.8	1	1.23E+05		(K)CDSSPD	(K)C D S|S/P/D S/A/E D V R K(V)	C:Carbamidomethylation	83.98	489.2132	1465.622	0.0027	1.8	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
7003	dirMS_041712_NAR_30mM_minus2.12554.12554.2	2	11.8	0	2.01E+05		(K)YALSVG	(K)Y A|L/S/V/G Y/R(H)		122.23	464.7493	928.489	0.0026	2.8	8.59	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
7004	dirMS_041712_NAR_20mM_plus.11416.11416.2	2	11.8	0	2.35E+05		(K)VGLQVV	(K)V/G|L/Q/V/V A/V/K(A)		151.23	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
7005	dirMS_041712_NAR_20mM_plus.12864.12864.2	2	11.8	0	1.41E+05		(R)LVVPAS	(R)L V/V|P A S/Q C G S L I/G K(G)	C:Carbamidomethylation	161.55	714.8991	1428.788	0.003	2.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
7006	dirMS_041712_NAR_30mM_plus2.5749.5749.2	2	11.8	0	2.46E+05		(R)QSSGAS	(R)Q S|S G A|S/S/S S F/S/S/S/R(A)		84.3	681.3013	1361.593	0.0025	1.9	9.75	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
7007	dirMS_041712_NAR_60mM_plus.5393.5393.3	3	11.8	0	3.82E+05	M21m	(R)SGSmD	(R)S G|S/m/D/P S G A/H/P S V R(Q)	m:Oxidized methionine	86.25	467.5464	1384.627	15.9973	1.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
7008	dirMS_041712_NAR_120mM_minus.9937.10003.3	3	11.79	1	6.70E+05		(R)SRNTDE	(R)S\R N T D\E|M|V/E/L/R(I)		108.62	450.5556	1349.648	0.0045	3.3	4.68	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
7009	dirMS_041712_NAR_30mM_minus2.16139.16139.2	2	11.79	1	1.55E+05		(R)FVLSQA	(R)F/V|L/S Q A/K D E L(-)		141.43	575.3113	1149.615	0.0003	0.3	4.37	41053.3	5.58	HUMAN	Q86UY0	TXNDC5 protein
7010	dirMS_041712_NAR_30mM_minus2.6190.6190.2	2	11.79	0	2.84E+05		(K)TSEVNC	(K)T|S|E/V|N C Y R(C)	C:Carbamidomethylation	88	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
7011	dirMS_041712_NAR_30mM_minus2.7849.7849.2	2	11.79	0	4.01E+04		(K)TDEGIA	(K)T D/E/G I/A Y R(G)		97.15	462.7203	924.442	-0.0088	-9.5	4.37	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
7012	dirMS_041712_NAR_50mM_minus2.16034.16034.3	3	11.79	1	4.43E+06		(R)VSFELFA	(R)V/S/F E L/F/A D K\V/P K(T)		159.72	460.5908	1379.757	0.0009	0.7	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
7013	dirMS_041712_NAR_50mM_minus2.6772.6772.3	3	11.79	0	5.92E+05		(R)EATNPP	(R)E A T N/P P V/I/Q E E K P/K(K)		105.52	527.2846	1579.833	0.0066	4.2	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
7014	dirMS_041712_NAR_60mM_minus.10399.10399.3	3	11.79	1	2.88E+04		(K)SPFEVS	(K)S P/F/E|V\S V D K|A Q G D A S K(V)		117.73	555.6083	1664.813	-0.0023	-1.4	4.56	258215.9	5.48	HUMAN	E7EN95	Filamin-B
7015	dirMS_041712_NAR_60mM_minus.12081.12081.3	3	11.79	1	2.33E+05		(R)VVNGK	(R)V/V|N G K/V/E Y F L/K(W)		127.17	432.5826	1295.736	-0.0026	-2	8.47	11857.8	9.63	HUMAN	B8ZZ43	Chromobox homolog 3 (HP1 gamma homolog, Drosophila), isoform CRA_b
7016	dirMS_041712_NAR_60mM_minus.15584.15584.3	3	11.79	1	1.72E+05		(R)GRLPLL	(R)G R L\P L\L|A|V/C D/Y K(Q)	C:Carbamidomethylation	146.87	468.9273	1404.767	0.0006	0.4	8.59	533778	5.74	HUMAN	Q15149	Plectin
7017	dirMS_041712_NAR_20mM_plus.17992.17992.2	2	11.79	0	1.93E+05		(K)GADFLV	(K)G A D\F L\V|T|E V/E|N G G S L G S K(K)		195.23	890.4414	1779.876	-0.0004	-0.2	4.14	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
7018	dirMS_041712_NAR_20mM_plus.7405.7405.3	3	11.79	0	2.14E+05		(K)TGQAP	(K)T G Q A|P G|Y S/Y/T/A A N K(N)		119.53	476.8963	1428.675	-0.001	-0.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
7019	dirMS_041712_NAR_30mM_plus2.11455.11455.2	2	11.79	0	3.67E+05		(R)NGDFLP	(R)N/G D/F/L/P T|R(L)		113.58	460.2391	919.463	0.0077	8.4	5.84	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
7020	dirMS_041712_NAR_30mM_plus2.11809.11853.2	2	11.79	0	7.54E+05		(R)SSTDSLP	(R)S S\T/D/S|L/P/G\P I\S R(Q)		115.18	608.8101	1216.617	-0.0039	-3.2	5.55	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
7021	dirMS_041712_NAR_30mM_plus2.11812.11812.2	2	11.79	0	1.33E+05		(R)INVYYNE	(R)I N|V|Y/Y\N E A/T G G K(Y)		115.12	664.8272	1328.648	-0.001	-0.7	6	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
7022	dirMS_041712_NAR_30mM_plus2.20769.20769.2	2	11.79	0	7.52E+05		(R)TVQSLEI	(R)T V/Q|S|L|E I D L\D S M/R(N)		162.3	753.8768	1506.747	-0.0005	-0.3	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
7023	dirMS_041712_NAR_40mM_plus2.6216.6216.2	2	11.79	0	4.16E+05		(K)NAGFTP	(K)N A|G/F/T/P Q E R(Q)		96.18	510.2487	1019.491	-0.0004	-0.4	6	29474.8	6.94	HUMAN	G3V3M6	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
7024	dirMS_041712_NAR_50mM_plus2.14449.14449.3	3	11.79	1	5.76E+05		(R)SEGVVA	(R)S E|G V V/A/V L L/T K K(S)		144.37	415.2585	1243.762	-0.0011	-0.9	8.31	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
7025	dirMS_041712_NAR_50mM_plus2.5421.5421.3	3	11.79	1	5.11E+04		(R)DASTLQ	(R)D A/S/T L/Q/S Q K A E G T G D A K(-)		89.17	569.61	1706.819	-0.0037	-2.2	4.56	9538.7	10.48	HUMAN	O00479	High mobility group nucleosome-binding domain-containing protein 4
7026	dirMS_041712_NAR_50mM_plus2.6562.6562.3	3	11.79	0	6.49E+05	M434m	(R)LESGm	(R)L/E|S/G m Q/N M/S I/H T K(T)	m:Oxidized methionine	98.9	497.9026	1475.698	15.9951	0.1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
7027	dirMS_041712_NAR_50mM_plus2.9913.9913.3	3	11.79	1	1.41E+05		(K)TCVFEKE	(K)T C|V/F/E K E N D/P S V M R(S)	C:Carbamidomethylation	119.48	571.2629	1711.778	-0.0037	-2.1	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
7028	dirMS_041712_NAR_60mM_plus.11287.11491.3	3	11.79	0	1.67E+06		(K)AQVARP	(K)A Q|V/A/R P G G D T I/F/G/K(I)		116.72	472.9241	1416.759	-0.0016	-1.2	8.79	7323.5	9.4	HUMAN	D6RC06	Histidine triad nucleotide-binding protein 1
7029	dirMS_041712_NAR_60mM_plus.12374.12374.3	3	11.79	1	7.40E+05		(K)YGQISE	(K)Y/G/Q/I/S E\V/V/V V K D R(E)		121.27	497.9427	1491.817	-0.003	-2	6.07	28815.3	9.52	HUMAN	B4E2X2	Cold-inducible RNA-binding protein
7030	dirMS_041712_NAR_60mM_plus.5361.5361.3	3	11.79	1	7.94E+04		(K)VSQGVE	(K)V/S|Q/G V E D|G P D T K R(A)		85.7	463.233	1387.681	0.0032	2.3	4.56	33726	7.84	HUMAN	B3KNJ4	SUMO-1 activating enzyme subunit 1, isoform CRA_a
7031	dirMS_041712_NAR_120mM_minus.10030.10030.3	3	11.78	0	5.96E+05		(R)HGESAV	(R)H G E\S A\W|N/L/E/N/R(F)		109.4	438.2098	1312.603	0.012	9.1	5.4	28917.5	6.68	HUMAN	P18669	Phosphoglycerate mutase 1
7032	dirMS_041712_NAR_120mM_minus.11488.11488.2	2	11.78	0	7.46E+05		(R)GSAVH	(R)G S A V/H|Q|L/S E E|L R(C)		116.68	663.3434	1325.681	-0.0013	-1	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
7033	dirMS_041712_NAR_20mM_minus.11052.11052.2	2	11.78	0	1.49E+06	M92m	(R)ImNTFS	(R)I m/N/T/F S/V/V/P/S P K(V)	m:Oxidized methionine	157.23	668.3513	1319.703	15.9925	-1.8	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
7034	dirMS_041712_NAR_20mM_minus.11131.11131.2	2	11.78	0	8.06E+04		(K)VIDPAT	(K)V I/D|P A/T A T S V D/L R(D)		158.48	679.3706	1357.732	0.0018	1.3	4.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
7035	dirMS_041712_NAR_40mM_minus2.10877.10877.3	3	11.78	0	4.63E+05		(R)DAGEGL	(R)D A|G E|G\L/L A V Q I T D Q E G K P K(R)		147.63	657.0157	1969.024	0.0089	4.5	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
7036	dirMS_041712_NAR_40mM_minus2.11588.11690.3	3	11.78	1	1.36E+05		(K)TVGVEP	(K)T V\G V|E/P A A D G K/G V V V V/I/K(R)		152.03	580.008	1738.011	-0.0015	-0.8	5.73	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
7037	dirMS_041712_NAR_50mM_minus2.11390.11390.3	3	11.78	1	1.24E+05		(K)LSAEKVE	(K)L/S/A E K V E\I/A/T/L T R(E)		133.27	477.6106	1430.821	-0.0041	-2.8	6.14	26661.1	7.81	HUMAN	H0YL69	Proteasome subunit alpha type (Fragment)
7038	dirMS_041712_NAR_50mM_minus2.13549.13549.3	3	11.78	1	5.31E+05		(K)LTEDKA	(K)L T/E D K A D/V Q|S|I I/G L Q R(F)		144.8	595.9939	1785.97	-0.0034	-1.9	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
7039	dirMS_041712_NAR_50mM_minus2.13977.13977.3	3	11.78	1	5.22E+05	M85m	(K)TVTAmD	(K)T V|T A/m D/V/V/Y A L K R(Q)	m:Oxidized methionine	148.28	494.9385	1466.804	15.9974	1.7	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
7040	dirMS_041712_NAR_50mM_minus2.14291.14291.3	3	11.78	1	2.08E+05		(R)DLAALG	(R)D L|A|A/L/G D K V/N S L G E T/A E R(L)		149.15	620.3204	1858.95	-0.0038	-2.1	4.32	285798.6	5.23	HUMAN	A6NG51	Spectrin alpha chain, non-erythrocytic 1
7041	dirMS_041712_NAR_50mM_minus2.17888.17888.3	3	11.78	0	2.19E+05		(R)LGFHLP	(R)L G F/H L\P L/E|V/A Y Q/R(G)		170.25	514.953	1542.843	0.0017	1.1	6.75	533778	5.74	HUMAN	Q15149	Plectin
7042	dirMS_041712_NAR_50mM_minus2.5949.5949.3	3	11.78	1	4.40E+04		(R)AQLGGP	(R)A Q|L|G G P E A A K S D E/T A A K(-)		96.13	548.6119	1643.824	-0.0024	-1.4	4.68	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
7043	dirMS_041712_NAR_20mM_plus.13216.13216.3	3	11.78	0	5.65E+04		(R)ALEAEQ	(R)A L E A\E Q/V|E I T V/G R(F)		163.2	472.2552	1414.754	-0.0026	-1.8	4.25	266161	5.68	HUMAN	E9PPU0	Epiplakin
7044	dirMS_041712_NAR_20mM_plus.14213.14213.2	2	11.78	0	6.30E+05	M185m	(K)LAVNm	(K)L A|V/N m/V|P F/P R(L)	m:Oxidized methionine	170.55	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
7045	dirMS_041712_NAR_20mM_plus.18510.18510.3	3	11.78	0	2.24E+05		(R)LSVEEA	(R)L S V E E A V A A\G\V/V|G/G E I Q E\K(L)		198.52	629.0001	1884.991	-0.0056	-2.9	4.09	266161	5.68	HUMAN	E9PPU0	Epiplakin
7046	dirMS_041712_NAR_20mM_plus.7878.7878.2	2	11.78	0	1.21E+05		(K)VEIIAND	(K)V E|I|I/A N D/Q G N R(T)		124.5	614.8177	1228.628	0.0001	0.1	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
7047	dirMS_041712_NAR_30mM_plus2.12354.12354.2	2	11.78	0	8.33E+04		(K)MADEAI	(K)M/A|D/E/A|I L|Q E/R(E)		116.57	588.2906	1175.573	0.0014	1.2	4.14	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
7048	dirMS_041712_NAR_40mM_plus2.7540.7540.2	2	11.78	0	5.87E+04		(R)SLQSVAI	(R)S L/Q/S V A/E/E R(A)		104.55	509.7615	1018.516	-0.0006	-0.6	4.53	20623.6	11.46	HUMAN	E7EQV9	Ribosomal protein L15 (Fragment)
7049	dirMS_041712_NAR_50mM_plus2.11314.11314.3	3	11.78	1	2.98E+05		(R)ETGVDL	(R)E T G V/D/L/T/K D/N M/A/L Q R(V)		127.18	564.2856	1690.843	-0.0006	-0.4	4.56	73964.5	5.87	HUMAN	P38646	Stress-70 protein, mitochondrial
7050	dirMS_041712_NAR_50mM_plus2.14488.14488.3	3	11.78	0	1.06E+06		(R)ETHSAL	(R)E T H S A/L G|P A/L/Q A A/F K(L)		144.3	514.2745	1540.812	-0.0029	-1.9	6.85	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
7051	dirMS_041712_NAR_50mM_plus2.7799.7799.3	3	11.78	1	1.02E+05		(K)ELQAAG	(K)E L Q|A/A\G K/S/P E D/L E/R(L)		106.55	514.9321	1542.776	0.0059	3.8	4.41	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
7052	dirMS_041712_NAR_50mM_plus2.8357.8357.3	3	11.78	0	9.05E+04		(K)QQSIAG	(K)Q Q/S I/A/G S/A D S\K/P I D\V S R(L)		110.42	586.971	1758.898	0.0004	0.2	5.96	34637.3	8.91	HUMAN	Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1
7053	dirMS_041712_NAR_120mM_minus.10626.10626.3	3	11.77	1	2.46E+05		(R)YLAEFAT	(R)Y/L/A/E F/A/T G N D R K(E)		111.73	462.2338	1384.686	0.0013	0.9	6.07	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
7054	dirMS_041712_NAR_120mM_minus.13869.13869.4	4	11.77	1	1.62E+06		(K)ASIHEA	(K)A S|I/H/E/A W T D/G K E A M L/K(H)		129.97	447.476	1786.879	0.0029	1.6	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
7055	dirMS_041712_NAR_120mM_minus.13872.13872.4	4	11.77	1	1.62E+06		(K)ASIHEA	(K)A/S\I/H/E\A W T D G/K/E A M L K(H)		129.97	447.476	1786.879	0.0029	1.6	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
7056	dirMS_041712_NAR_20mM_minus.12576.12576.2	2	11.77	0	2.76E+05	M185m	(K)LAVNm	(K)L A/V|N m/V/P/F P R(L)	m:Oxidized methionine	173.25	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
7057	dirMS_041712_NAR_30mM_minus2.12565.12565.2	2	11.77	0	9.26E+04		(R)GYFDEE	(R)G Y|F|D/E E/M N R(V)		121.7	580.7374	1160.468	-0.0002	-0.2	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
7058	dirMS_041712_NAR_30mM_minus2.16050.16050.2	2	11.77	0	1.41E+05		(K)GCSFLP	(K)G C|S|F L|P D/P Y Q K(Q)	C:Carbamidomethylation	141.02	656.3051	1311.604	-0.0009	-0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
7059	dirMS_041712_NAR_30mM_minus2.18903.18903.2	2	11.77	0	6.82E+04		(K)APDFVF	(K)A/P/D/F|V/F Y A/P R(L)		157.32	591.8008	1182.594	0.0001	0.1	5.88	71218.8	6.3	HUMAN	A7YIJ8	Radixin
7060	dirMS_041712_NAR_40mM_minus2.12222.12222.3	3	11.77	1	5.07E+05		(R)IIAFVGS	(R)I I|A\F/V/G S/P V E D N E K D L V K(L)		156	658.3553	1973.059	-0.0076	-3.9	4.32	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
7061	dirMS_041712_NAR_50mM_minus2.10285.10285.3	3	11.77	0	2.72E+05		(R)TFIAIKP	(R)T F|I A I/K/P D/G V Q R(G)		126.83	448.923	1344.763	-0.009	-6.7	8.41	6640.6	8.25	HUMAN	C9K028	Nucleoside diphosphate kinase A (Fragment)
7062	dirMS_041712_NAR_50mM_minus2.14459.14459.3	3	11.77	1	1.40E+05		(R)GDVVPK	(R)G D V|V|P K D V N A|A/I A T I/K(T)		150.42	537.6375	1610.911	-0.0133	-8.2	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
7063	dirMS_041712_NAR_60mM_minus.9810.9810.3	3	11.77	1	2.36E+05		(R)LKAEAE	(R)L K A E A\E\L|L/Q/Q Q K(E)		114.67	466.9338	1398.795	-0.0083	-5.9	6.14	533778	5.74	HUMAN	Q15149	Plectin
7064	dirMS_041712_NAR_120mM_plus.8735.8735.3	3	11.77	0	2.74E+06		(K)HTGPNS	(K)H T\G P N S\P/D T|A/N D/G/F V/R(L)		99.25	562.26	1684.767	-0.0019	-1.2	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
7065	dirMS_041712_NAR_20mM_plus.17634.17634.2	2	11.77	0	3.49E+04	M199m	(K)SmVPV	(K)S m V/P V/Q/V\Q L D V/P V V K(V)	m:Oxidized methionine	192.93	827.4624	1637.93	15.988	-4.2	5.55	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
7066	dirMS_041712_NAR_30mM_plus2.21573.21573.2	2	11.77	0	2.71E+05		(R)NIPMLF	(R)N\I|P/M L/F V R(G)		167.78	495.2847	989.56	0.002	2.1	9.75	11845.2	4.58	HUMAN	P62310	U6 snRNA-associated Sm-like protein LSm3
7067	dirMS_041712_NAR_60mM_plus.14999.15257.3	3	11.77	1	4.36E+05		(K)SLEELRL	(K)S L|E/E/L R L E D|Y/Q/A N R(K)		135.6	579.2911	1735.861	-0.0022	-1.3	4.41	178367.2	6.03	HUMAN	J3KP29	Nuclear pore complex protein Nup98-Nup96
7068	dirMS_041712_NAR_120mM_minus.13181.13181.4	4	11.76	0	2.31E+05		(R)VLSAPPH	(R)V L|S/A/P/P H F H F G Q/T N R(T)		126.17	427.7219	1707.871	-0.0056	-3.3	9.74	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
7069	dirMS_041712_NAR_20mM_minus.14383.14418.2	2	11.76	0	2.36E+05		(K)DAGVIA	(K)D A/G\V|I|A|G L N V L R(I)		198.13	599.3503	1197.695	-0.0017	-1.4	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
7070	dirMS_041712_NAR_20mM_minus.6168.6168.2	2	11.76	0	2.49E+04		(K)DSYVGD	(K)D S Y|V|G D/E A Q S K(R)		102.87	599.7642	1198.522	-0.0011	-0.9	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
7071	dirMS_041712_NAR_30mM_minus2.18304.18304.2	2	11.76	0	4.10E+05		(R)QAQEYE	(R)Q A Q/E Y/E/A/L/L/N I/K(V)		154.6	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
7072	dirMS_041712_NAR_30mM_minus2.7333.7333.2	2	11.76	0	1.61E+05		(R)AQAAGS	(R)A Q|A|A/G\S S V L/R(E)		94.8	480.2603	959.527	-0.0135	-14.1	9.79	38843.2	6.48	HUMAN	Q96EK9	Protein KTI12 homolog
7073	dirMS_041712_NAR_40mM_minus2.6986.6986.2	2	11.76	0	5.85E+05		(R)GYSFTTT	(R)G Y|S F/T/T/T/A E R(E)		111.95	566.7661	1132.527	-0.002	-1.8	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
7074	dirMS_041712_NAR_50mM_minus2.17601.17984.3	3	11.76	1	3.19E+06		(R)LDLAGR	(R)L/D|L|A/G R D L T D/Y L/M K(I)		170.1	541.9562	1623.841	0.013	8	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
7075	dirMS_041712_NAR_50mM_minus2.7959.7959.3	3	11.76	0	8.88E+04		(K)TAVEHA	(K)T A|V|E/H A T D E D I/L A K(G)		112.23	504.9229	1512.754	0.0001	0.1	4.31	288852.1	5.33	HUMAN	E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein
7076	dirMS_041712_NAR_50mM_minus2.8544.8544.3	3	11.76	0	1.58E+06		(R)EIVHIQA	(R)E/I/V H I Q A G/Q/C/G N Q I/G A K(F)	C:Carbamidomethylation	116.8	608.3087	1822.923	-0.0113	-6.2	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
7077	dirMS_041712_NAR_60mM_minus.15830.15830.3	3	11.76	1	3.91E+05		(K)KANLQI	(K)K A N L Q I D\Q\I|N/T|D L N L/E R(S)		148.05	666.6911	1998.061	-0.0027	-1.3	4.56	227783.5	5.5	HUMAN	P35579	Myosin-9
7078	dirMS_041712_NAR_120mM_plus.8142.8142.3	3	11.76	1	5.38E+05		(K)IVSGKD	(K)I/V|S G K/D Y N/V/T A N S K(L)		96.72	499.263	1495.775	-0.0007	-0.4	8.5	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
7079	dirMS_041712_NAR_20mM_plus.14692.14692.2	2	11.76	0	6.83E+04		(R)IMNTFS	(R)I M/N/T/F/S/V/V|P S/P K(V)		173.27	660.3527	1319.703	-0.0047	-3.5	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
7080	dirMS_041712_NAR_20mM_plus.17908.17908.2	2	11.76	0	1.65E+05		(R)TVQSLEI	(R)T V|Q|S/L/E|I D/L D S M R(N)		194.95	753.8776	1506.747	0.0011	0.7	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18

7081	dirMS_041712_NAR_40mM_plus2.9004.9004.2	2	11.76	0	1.19E+05		(R)GYSFTTT	(R)G Y/S|F/T\T T/A E R(E)		114.9	566.7672	1132.527	0.0002	0.2	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
7082	dirMS_041712_NAR_50mM_plus2.10913.10913.3	3	11.76	1	4.68E+05		(R)ALRETLF	(R)A L R\E T L|P\A|E Q/D L T T K(N)		125.08	562.6377	1685.907	-0.0083	-4.9	4.68	26790	6.25	HUMAN	F5GX11	Proteasome subunit alpha type-1
7083	dirMS_041712_NAR_60mM_plus.17820.17820.3	3	11.76	0	2.66E+05		(R)LLIHQSL	(R)L/L/I H Q S\L/A/G G I/I G V K(G)		150.48	506.9815	1518.937	-0.0067	-4.4	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
7084	dirMS_041712_NAR_120mM_minus.11727.11877.4	4	11.75	1	3.82E+05		(R)DFTVSAI	(R)D F|T/V/S A M/H/G D M D Q K E/R(D)		118.4	467.458	1866.811	-0.0007	-0.4	4.66	26945.8	8.07	HUMAN	J3KSZ0	Eukaryotic initiation factor 4A-I (Fragment)
7085	dirMS_041712_NAR_30mM_minus2.13682.13891.2	2	11.75	0	3.35E+05		(K)SPAQILII	(K)S/P/A|Q/I/L/I/R(F)		128.45	449.2751	897.552	-0.0087	-9.7	9.47	23434.6	5.78	HUMAN	G3V1C1	1,5-anhydro-D-fructose reductase
7086	dirMS_041712_NAR_50mM_minus2.14944.14944.3	3	11.75	1	1.54E+05		(R)LLTTIGK	(R)L/L/T\T I/G/K/D L D/F E K(A)		152.73	498.2798	1492.826	-0.0009	-0.6	4.56	98682.1	4.86	HUMAN	C9JF13	Eukaryotic translation initiation factor 4 gamma 1 (Fragment)
7087	dirMS_041712_NAR_60mM_minus.7976.7976.3	3	11.75	1	4.69E+05		(R)YLAEVA	(R)Y/L/A E V A/T/G E K R(A)		104.32	412.8902	1236.658	-0.0022	-1.8	6.14	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
7088	dirMS_041712_NAR_120mM_plus.6449.6449.2	2	11.75	1	2.84E+05		(R)SIAKEGF	(R)S/I|A K/E/G F E\K(I)		87.12	504.7715	1008.536	-0.0003	-0.3	5.86	17213.7	10.05	HUMAN	B7Z712	60 kDa heat shock protein, mitochondrial
7089	dirMS_041712_NAR_20mM_plus.12251.12336.3	3	11.75	0	2.90E+05		(K)VNQIGS	(K)V N\Q\I G S V|T|E/S/I/Q/A/C K(L)	C:Carbamidomethylation	157.67	545.2781	1633.821	-0.0016	-1	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
7090	dirMS_041712_NAR_20mM_plus.12649.12649.2	2	11.75	0	9.34E+04	M91m	(R)AITGASL	(R)A I|T\G/A/S L/A D/I m A/K(R)	m:Oxidized methionine	159.93	639.3398	1261.682	15.9903	-3.6	5.88	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
7091	dirMS_041712_NAR_20mM_plus.19013.19013.2	2	11.75	0	1.91E+05		(R)STGEAF	(R)S T G E A\F|V/Q/F/A S/Q\E I/A E K(A)		202.2	921.4477	1841.892	-0.0035	-1.9	4.25	24249.1	6.99	HUMAN	D6RBM0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
7092	dirMS_041712_NAR_30mM_plus2.8616.8616.2	2	11.75	0	6.11E+05		(K)VTMQN	(K)V T|M/Q/N/L/N D R(L)		99.2	545.7703	1090.531	0.0024	2.2	5.81	51902.9	5.09	HUMAN	P02533	Keratin, type I cytoskeletal 14
7093	dirMS_041712_NAR_40mM_plus2.16129.16251.3	3	11.75	0	4.11E+04		(K)VLISSLQ	(K)V L|I|S S L Q/D C L/H/G I E S/K(S)	C:Carbamidomethylation	161.47	600.3172	1798.937	0.0003	0.2	5.32	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
7094	dirMS_041712_NAR_50mM_plus2.10079.10079.3	3	11.75	0	4.13E+05		(R)MVQVH	(R)M/V|Q/V/H E L/G C E G I/S K(S)	C:Carbamidomethylation	120.23	529.5984	1586.767	0.0141	8.9	5.38	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
7095	dirMS_041712_NAR_50mM_plus2.13443.13443.3	3	11.75	0	9.05E+05		(R)TVVTGIE	(R)T V|V/T/G I/E M F H K(S)		138.55	421.225	1261.661	-0.0005	-0.4	6.41	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
7096	dirMS_041712_NAR_60mM_plus.15297.15297.3	3	11.75	1	1.76E+05		(R)VEVTEFE	(R)V E|V/T E F E D/I K S G Y R(I)		136.78	557.9447	1671.822	-0.0029	-1.7	4.41	30992.3	4.14	HUMAN	B2REB8	Protein SET
7097	dirMS_041712_NAR_60mM_plus.7151.7195.3	3	11.75	1	4.16E+05	M136m M:	(K)VKEGmN	(K)V K E/G m N\I|V/E/A/m/E R(F)	m:Oxidized methionine	95.72	513.2511	1505.745	31.9937	2.5	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
7098	dirMS_041712_NAR_120mM_minus.10825.10825.2	2	11.74	1	1.13E+06		(K)IKIIAPPE	(K)I/K|I|I/A\P P E R(K)		113.33	518.8303	1036.651	0.002	1.9	8.75	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
7099	dirMS_041712_NAR_20mM_minus.12492.12492.2	2	11.74	0	9.66E+05	M256m	(R)SLDmDS	(R)S L\D|m D S/I I A/E V/K(A)	m:Oxidized methionine	172.42	668.8364	1320.671	15.994	-0.7	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
7100	dirMS_041712_NAR_20mM_minus.9656.9656.2	2	11.74	0	5.91E+03		(K)DVNAAL	(K)D V|N/A A/I/A T/I K(T)		146.73	508.2919	1015.578	-0.0017	-1.7	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
7101	dirMS_041712_NAR_30mM_minus2.11234.11286.2	2	11.74	0	3.89E+05		(R)NTDEM	(R)N T|D/E|M/V/E/L/R(I)		115.05	553.7611	1106.515	0.0003	0.2	4.14	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
7102	dirMS_041712_NAR_30mM_minus2.16135.16135.2	2	11.74	0	2.98E+05	M185m	(K)LAVNm	(K)L A|V/N/m\V/P F/P R(L)	m:Oxidized methionine	142.3	580.3178	1143.634	15.994	-0.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
7103	dirMS_041712_NAR_50mM_minus2.12739.12920.3	3	11.74	1	3.99E+05		(R)LSEDYG	(R)L/S|E/D/Y G V/L/K T D E/G I A Y R(G)		141.55	643.6561	1928.96	-0.0063	-3.2	4.32	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
7104	dirMS_041712_NAR_50mM_minus2.13365.13365.3	3	11.74	0	2.46E+05		(K)VIQYLAY	(K)V/I/Q Y L A/Y/V A/S S H K(S)		144.78	493.6043	1478.8	-0.0018	-1.2	8.48	227783.5	5.5	HUMAN	P35579	Myosin-9
7105	dirMS_041712_NAR_50mM_minus2.14921.14969.3	3	11.74	1	1.58E+05		(R)LLTTIGK	(R)L/L/T/T/I/G K/D L D/F E K(A)		152.72	498.2798	1492.826	-0.0009	-0.6	4.56	98682.1	4.86	HUMAN	C9JF13	Eukaryotic translation initiation factor 4 gamma 1 (Fragment)
7106	dirMS_041712_NAR_120mM_plus.17425.17463.3	3	11.74	1	4.15E+05		(R)RTVQSLI	(R)R T V Q S\L/E|I/D/L/D/S M R(N)		144.22	554.9524	1662.848	-0.0053	-3.2	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
7107	dirMS_041712_NAR_20mM_plus.17083.17083.2	2	11.74	0	9.18E+04		(R)AVLVDLI	(R)A V\L|V D L|E|P/G T M D S V R(S)		189.4	801.414	1601.82	0.0004	0.2	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
7108	dirMS_041712_NAR_20mM_plus.18027.18027.2	2	11.74	0	3.23E+05		(R)ILVATNL	(R)I L|V/A/T N L/F/G R(G)		194.98	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
7109	dirMS_041712_NAR_30mM_plus2.22660.22742.2	2	11.74	0	5.16E+05		(K)LAAFWL	(K)L/A|A/F|W L M/K(A)		176.55	490.2728	979.543	-0.005	-5.2	8.75	32535.6	9.19	HUMAN	B4DZW6	Regulator of microtubule dynamics protein 1
7110	dirMS_041712_NAR_50mM_plus2.16025.16025.3	3	11.74	1	1.20E+06		(K)CEFQDA	(K)C E|F Q D A Y|V/L/L S E K K(I)	C:Carbamidomethylation	152.32	577.2866	1729.847	-0.0013	-0.8	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
7111	dirMS_041712_NAR_50mM_plus2.6851.6851.3	3	11.74	1	7.87E+05		(K)IVADKD	(K)I/V/A D K D/Y S V/T A/N S K(I)		101.32	504.2628	1510.775	-0.0009	-0.6	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
7112	dirMS_041712_NAR_60mM_plus.18602.18602.3	3	11.74	1	2.46E+05		(R)RGDINLI	(R)R G D I N L L|M|L/G D/P G T A K(S)		154.6	557.6331	1670.889	-0.0047	-2.8	5.96	78390.7	9.27	HUMAN	B1AHB1	DNA replication licensing factor MCM5
7113	dirMS_041712_NAR_120mM_minus.13537.13537.4	4	11.73	1	7.85E+05		(K)SVHSSVI	(K)S V H S S\V/P\L L N S/K/D/P I D/R(I)		127.8	466.7525	1863.992	-0.0041	-2.2	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
7114	dirMS_041712_NAR_120mM_minus.6562.6564.3	3	11.73	1	3.16E+05		(R)LNGTLRI	(R)L/N|G/T/L/R E D D/N/R(I)		90.27	434.8858	1302.64	0.0032	2.4	4.56	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
7115	dirMS_041712_NAR_30mM_minus2.12221.12221.2	2	11.73	0	2.15E+05		(R)TIGISVD	(R)T I/G|I/S V D|P R(R)		119.17	479.2746	957.536	0.0056	5.8	5.5	14749.1	12.2	HUMAN	J3QSB4	60S ribosomal protein L13 (Fragment)
7116	dirMS_041712_NAR_30mM_minus2.16957.16957.2	2	11.73	0	1.97E+05	M2243m	(K)mSIYQA	(K)m S/I|Y Q/A M|W K(G)	m:Oxidized methionine	145.78	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
7117	dirMS_041712_NAR_40mM_minus2.14335.14335.3	3	11.73	1	1.72E+05		(K)GNAGGI	(K)G N\A G G I/Q/P D L L I S L T A P K/K(S)		169.3	631.6945	1893.08	-0.0114	-6	8.59	32016.3	7.83	HUMAN	Q8NCW5	NAD(P)H-hydrate epimerase
7118	dirMS_041712_NAR_30mM_plus2.12130.12130.2	2	11.73	0	1.34E+06		(K)GIYAVGI	(K)G I/Y|A|V/G D V C G K(A)	C:Carbamidomethylation	117.58	569.7798	1138.556	-0.0038	-3.3	5.83	56826.6	9.16	HUMAN	P00390	Glutathione reductase, mitochondrial
7119	dirMS_041712_NAR_30mM_plus2.4815.4815.2	2	11.73	0	7.69E+05	M571m	(R)mGANSI	(R)m/G\A|N S/L/E/R(M)	m:Oxidized methionine	76.47	447.2119	877.42	15.9969	2.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
7120	dirMS_041712_NAR_30mM_plus2.7292.7374.2	2	11.73	0	3.37E+05		(K)DYAESV	(K)D Y|A|E|S V/G/R(K)		93.07	448.71	896.411	0.0019	2.1	4.37	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
7121	dirMS_041712_NAR_20mM_minus.13248.13248.3	3	11.72	0	2.65E+05		(K)VGINYQ	(K)V G I N Y Q|P P T V|V/P G G D L A/K(V)		183.15	608.9971	1824.985	-0.0087	-4.8	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
7122	dirMS_041712_NAR_30mM_minus2.17925.17925.2	2	11.72	0	1.77E+05		(R)YVANIFF	(R)Y V/A/N I F|P Y/K(G)		151.4	557.7997	1114.593	-0.001	-0.9	8.5	23312.3	5.53	HUMAN	B4DFH3	Inorganic pyrophosphatase 2, mitochondrial
7123	dirMS_041712_NAR_30mM_minus2.8737.8965.2	2	11.72	0	5.41E+05		(K)SDPVVS	(K)S D/P/V|V/S Y/R(E)		102.65	461.7315	922.463	-0.0071	-7.7	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
7124	dirMS_041712_NAR_40mM_minus2.11170.11170.3	3	11.72	0	3.79E+05		(R)DAGEGL	(R)D A|G E|G/L/L A V Q I T D Q/E G K P K(R)		148.32	657.0157	1969.024	0.0089	4.5	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
7125	dirMS_041712_NAR_40mM_minus2.13595.13595.3	3	11.72	1	1.19E+05		(R)CITDPQ	(R)C I/T/D/P Q T/G L C L L/P L K E K(K)	C:Carbamidomethylation	164.02	662.684	1986.04	-0.0024	-1.2	6.07	533778	5.74	HUMAN	Q15149	Plectin
7126	dirMS_041712_NAR_50mM_minus2.13260.13260.3	3	11.72	0	4.36E+05		(R)EQTLSP	(R)E Q T/L/S/P T I/T S G L H N\I A R(S)		143.43	613.3274	1837.977	-0.009	-4.9	6.85	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
7127	dirMS_041712_NAR_50mM_minus2.15938.15938.3	3	11.72	1	2.34E+04	M132m	(R)TLAEIAK	(R)T L|A/E/I A K V E L D/N m P L R(G)	m:Oxidized methionine	158.85	610.3273	1812.989	15.9786	-8.9	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
7128	dirMS_041712_NAR_50mM_minus2.16073.16073.3	3	11.72	1	4.43E+06		(R)VSFELFA	(R)V/S/F E L/F A D/K V P K(T)		159.72	460.5908	1379.757	0.0009	0.7	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
7129	dirMS_041712_NAR_50mM_minus2.16994.16994.3	3	11.72	0	1.55E+05		(R)LLEVLSG	(R)L/L|E/V/L S G E\I L P K P/T K(G)		165.35	546.3329	1636.988	-0.0042	-2.6	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
7130	dirMS_041712_NAR_60mM_minus.10728.11168.3	3	11.72	1	2.04E+06		(R)FPGQLN	(R)F/P|G Q|L/N/A/D L/R K(L)		121.02	420.2346	1258.69	-0.001	-0.8	8.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
7131	dirMS_041712_NAR_60mM_minus.18152.18152.3	3	11.72	0	9.48E+04		(R)NSVSNF	(R)N S|V/S/N F/L/H S L E R(G)		162.5	468.2409	1402.707	0.0008	0.6	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
7132	dirMS_041712_NAR_60mM_minus.7284.7284.3	3	11.72	0	2.51E+06	M434m	(R)LESGmC	(R)L/E/S G m\Q N M/S I/H T K(T)	m:Oxidized methionine	98.97	497.9023	1475.698	15.9942	-0.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
7133	dirMS_041712_NAR_120mM_plus.6716.6716.2	2	11.72	0	3.07E+05		(R)SHEGET	(R)S/H|E|G\E T A/Y I R(V)		88.3	581.7777	1162.549	-0.0006	-0.5	5.38	16510	11.51	HUMAN	J3KSR8	Serine/arginine-rich-splicing factor 1 (Fragment)
7134	dirMS_041712_NAR_20mM_plus.15156.15156.2	2	11.72	0	2.75E+05		(K)LLCGLLA	(K)L L/C/G L L/A E R(L)	C:Carbamidomethylation	176.7	522.7971	1044.587	-0.0001	-0.1	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
7135	dirMS_041712_NAR_20mM_plus.16498.16498.2	2	11.72	0	2.41E+05		(R)ADLIAYL	(R)A/D/L/I/A Y L/K(K)		184.43	453.7678	906.529	-0.0012	-1.3	5.88	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
7136	dirMS_041712_NAR_20mM_plus.16664.16664.2	2	11.72	0	1.54E+05		(R)LLEAQIA	(R)L L\E A/Q|I/A/T/G G I I D|P K(E)		185.72	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
7137	dirMS_041712_NAR_20mM_plus.16693.16693.2	2	11.72	0	2.39E+05		(K)VQIAVA	(K)V Q|I A/V/A\N A Q E L/L Q R(M)		186.53	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
7138	dirMS_041712_NAR_20mM_plus.18112.18112.2	2	11.72	0	1.31E+05	M153m	(K)VVTYGm	(K)V V T|Y/G|m/A N L L T G P K(R)	m:Oxidized methionine	196.32	740.3997	1463.793	15.9995	3.1	8.56	28454.5	6.24	HUMAN	B0AZP7	Synaptic vesicle membrane protein VAT-1 homolog
7139	dirMS_041712_NAR_20mM_plus.8632.8700.2	2	11.72	0	2.34E+05		(R)VPPPPPI	(R)V/P|P/P/P P I A R(A)		130.57	472.2851	943.572	-0.0094	-10	9.72	32085.2	8.93	HUMAN	B4DY08	Heterogeneous nuclear ribonucleoproteins C1/C2
7140	dirMS_041712_NAR_30mM_plus2.16867.16987.2	2	11.72	0	2.05E+05		(R)VFSGLV	(R)V/F|S/G L/V|S/T G L K(V)		141.95	554.322	1107.641	-0.0041	-3.7	8.72	96306.4	6.41	HUMAN	P13639	Elongation factor 2
7141	dirMS_041712_NAR_40mM_plus2.11721.11721.2	2	11.72	0	1.99E+05		(R)FPGQLN	(R)F/P/G Q/L N/A D\L R(K)		135.38	565.7995	1130.595	-0.0036	-3.1	5.84	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
7142	dirMS_041712_NAR_40mM_plus2.12621.12621.3	3	11.72	0	3.46E+05		(K)AASDIAI	(K)A A\S D I/A/M/T E L/P P T H P I/R(L)		140.4	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
7143	dirMS_041712_NAR_50mM_plus2.12022.12022.3	3	11.72	0	4.17E+05		(K)QADLYIS	(K)Q A/D L Y I/S/E/G L/H/P\R(I)		131.4	500.2606	1498.765	0.0024	1.6	5.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
7144	dirMS_041712_NAR_50mM_plus2.19977.20227.3	3	11.72	0	2.96E+05		(R)DYLHLPI	(R)D Y L H L\P P E|I|V|P/A T L R(R)		173.92	578.658	1733.959	0.001	0.6	5.32	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
7145	dirMS_041712_NAR_50mM_plus2.7508.7508.3	3	11.72	1	2.58E+05		(K)SEETLDE	(K)S E|E/T/L|D E G P/P K/Y T K(S)		105.8	531.9261	1593.764	-0.0005	-0.3	4.41	25233.4	9.34	HUMAN	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3
7146	dirMS_041712_NAR_50mM_plus2.9757.9757.3	3	11.72	0	9.82E+04		(K)YIQQTKI	(K)Y/I/Q/Q/T K/P L T L E R(T)		118.75	497.2822	1489.837	-0.0053	-3.5	8.59	26283.8	8.96	HUMAN	O43809	Cleavage and polyadenylation specificity factor subunit 5
7147	dirMS_041712_NAR_60mM_plus.15657.15750.3	3	11.72	1	4.34E+05		(K)KSDIDEI	(K)K S D I D E\I|V\L|V/G|G S T R(I)		138.32	530.2831	1588.854	-0.0193	-12.2	4.56	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
7148	dirMS_041712_NAR_60mM_plus.9032.9032.3	3	11.72	0	1.59E+06		(K)EFHLNES	(K)E F H\L N\E/S/G D/P S/S K(S)		105.52	482.8882	1446.65	0.0005	0.3	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
7149	dirMS_041712_NAR_30mM_minus2.16750.16750.2	2	11.71	0	2.22E+05		(R)FFMGN	(R)F F/M/G/N Q V L/K(V)		145.18	542.2866	1083.566	0.0004	0.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
7150	dirMS_041712_NAR_30mM_minus2.18159.18159.2	2	11.71	1	1.13E+05		(R)LVLDSVI	(R)L/V|L/D/S V K L\E A(-)		152.92	543.8223	1086.641	-0.0032	-2.9	4.37	10137.3	4.59	HUMAN	E5RIW3	Tubulin-specific chaperone A
7151	dirMS_041712_NAR_30mM_minus2.7007.7007.2	2	11.71	0	1.47E+05		(K)ISTVVSS	(K)I/S/T/V/V/S S K(E)		92.48	410.7405	820.477	-0.0037	-4.6	8.75	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
7152	dirMS_041712_NAR_50mM_minus2.7724.7724.3	3	11.71	0	2.44E+05		(R)LESGMC	(R)L/E|S G/M Q N|M/S/I H T K(T)		111.27	492.5712	1475.698	0.0009	0.6	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
7153	dirMS_041712_NAR_120mM_plus.7670.7670.3	3	11.71	0	4.62E+05		(R)SGSMDF	(R)S G|S/M/D/P/S G A/H P S V R(Q)		93.92	462.218	1384.627	0.0121	8.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
7154	dirMS_041712_NAR_20mM_plus.6436.6436.2	2	11.71	0	2.02E+05	M216m	(R)DLmACA	(R)D L/m/A/C/A Q T G S G K(T)	C:Carbamidomethylation m:Oxid	107.72	627.776	1238.55	15.9943	-0.5	5.84	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
7155	dirMS_041712_NAR_30mM_plus2.10861.10965.2	2	11.71	0	1.19E+06		(R)GLTSVIN	(R)G L|T|S/V/I/N Q K(L)		110.87	480.2785	959.552	-0.0023	-2.4	8.75	36923.1	5.71	HUMAN	P07195	L-lactate dehydrogenase B chain
7156	dirMS_041712_NAR_30mM_plus2.16043.16043.2	2	11.71	0	3.73E+05		(K)EIIDPVLI	(K)E I\I/D/P\V/L D/R(I)		136.75	535.2996	1069.589	0.0031	2.9	4.03	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
7157	dirMS_041712_NAR_30mM_plus2.19639.19639.2	2	11.71	0	4.14E+05		(K)LLQDFFI	(K)L/L|Q D/F/F|N G R(D)		156.85	555.2902	1109.574	-0.0007	-0.6	5.84	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
7158	dirMS_041712_NAR_30mM_plus2.8960.8960.2	2	11.71	0	1.86E+05		(R)QPLGAT	(R)Q P/L|G/A/T S/G A S/L/K(T)		100.28	565.3227	1129.621	0.017	15	8.75	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
7159	dirMS_041712_NAR_50mM_plus2.12431.12431.3	3	11.71	0	3.93E+05		(R)LDDTVH	(R)L/D D/T V/H V|V/I A|T P G R(I)		133.35	498.2741	1492.812	-0.0041	-2.7	5.21	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
7160	dirMS_041712_NAR_50mM_plus2.16271.16271.3	3	11.71	1	1.17E+06		(K)CEFQDA	(K)C E/F Q D/A Y V/L/L S/E/K K(I)	C:Carbamidomethylation	152.42	577.2866	1729.847	-0.0013	-0.8	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
7161	dirMS_041712_NAR_50mM_plus2.20805.20805.3	3	11.71	0	2.59E+06		(R)AGKPVI	(R)A G K P\V I C\A/T\Q|M/L/E S M I/K(K)	C:Carbamidomethylation	178.87	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
7162	dirMS_041712_NAR_60mM_plus.8472.8472.2	2	11.71	0	4.27E+05		(R)FACHSA	(R)F/A/C/H/S/A\S L T/V R(N)	C:Carbamidomethylation	102.73	624.8118	1248.615	0.001	0.8	9.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
7163	dirMS_041712_NAR_120mM_minus.10026.10026.2	2	11.7	0	5.19E+05		(K)HIYYITG	(K)H/I|Y/Y I T|G E T K(D)		109.03	612.8167	1224.626	0.0002	0.2	6.75	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
7164	dirMS_041712_NAR_50mM_minus2.12661.12661.3	3	11.7	1	2.05E+05	M2709m	(K)ISmPDID	(K)I/S m/P D I D/L/N L K G P/K(V)	m:Oxidized methionine	139.8	519.6148	1540.84	15.9895	-3.5	5.96	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
7165	dirMS_041712_NAR_50mM_minus2.15790.15790.3	3	11.7	1	8.21E+04		(K)DANAKL	(K)D A/N A\K L S E/L E/A A/L/Q/R(A)		158.97	543.6248	1628.86	-0.0004	-0.2	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
7166	dirMS_041712_NAR_50mM_minus2.7422.7422.3	3	11.7	0	3.24E+04		(K)ATAGDT	(K)A/T|A G/D T H L|G G E D F D/N R(L)		109.13	559.2493	1675.731	0.0027	1.6	4.22	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
7167	dirMS_041712_NAR_50mM_minus2.9531.9531.3	3	11.7	1	1.31E+05		(R)MQKEIT	(R)M/Q K E I T A|L|A/P/S T M K(I)		122.2	516.9426	1548.812	0.0008	0.5	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
7168	dirMS_041712_NAR_20mM_plus.10667.10667.3	3	11.7	0	7.11E+04	M175m	(R)LEQGQA	(R)L E Q\G Q\A I/D/D\L/m/P A Q K(-)	m:Oxidized methionine	146.07	558.2795	1656.826	15.9978	1.7	4.03	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
7169	dirMS_041712_NAR_20mM_plus.11968.12044.2	2	11.7	0	1.20E+05		(R)IYVVDV	(R)I/Y|V|V|D/V/G S E P R(A)		156.17	617.3237	1233.647	-0.0073	-5.9	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
7170	dirMS_041712_NAR_20mM_plus.16639.16639.2	2	11.7	0	6.29E+04		(R)TVELSIP	(R)T V E/L S/I|P A/D/P\A N L\D S E A K(I)		186	935.4704	1869.944	-0.0105	-5.6	3.91	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
7171	dirMS_041712_NAR_20mM_plus.18837.18837.2	2	11.7	0	2.45E+05		(K)IYVDDGI	(K)I Y|V/D D/G L/I/S L Q V K(Q)		200.73	731.9068	1462.815	-0.0088	-6	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
7172	dirMS_041712_NAR_30mM_plus2.18198.18198.2	2	11.7	0	2.68E+05		(R)VNPALA	(R)V N|P A/L/A E L N L R(S)		147.93	605.3509	1209.695	-0.0005	-0.4	5.97	20026.6	4.67	HUMAN	E9PIK5	Ribonuclease inhibitor (Fragment)
7173	dirMS_041712_NAR_40mM_plus2.10996.10996.3	3	11.7	0	6.82E+04		(R)LLELGPK	(R)L/L|E/L/G P K P E V A Q Q T R(K)		131.02	560.318	1678.949	-0.0092	-5.5	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
7174	dirMS_041712_NAR_40mM_plus2.6434.6434.2	2	11.7	0	1.41E+05		(K)SLESINSI	(K)S L|E/S I N S R(L)		96.83	453.2358	905.469	-0.0044	-4.8	5.72	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
7175	dirMS_041712_NAR_50mM_plus2.16276.16276.3	3	11.7	1	2.67E+04		(K)GADFLV	(K)G A|D/F/L|V/T E V/E N G G S L G S K K(G)		153.22	636.6618	1907.971	-0.0001	0	4.68	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
7176	dirMS_041712_NAR_30mM_minus2.13915.14012.2	2	11.69	0	2.05E+05		(R)AFFSEVE	(R)A/F|F|S/E V/E R(R)		129.48	492.7447	984.479	0.0036	3.7	4.53	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
7177	dirMS_041712_NAR_30mM_minus2.5463.5603.2	2	11.69	0	1.13E+06	M139m	(R)LmDQNI	(R)L/m|D/Q/N L/K(C)	m:Oxidized methionine	84.93	439.2266	861.45	15.9961	1.3	5.84	26611.3	4.47	HUMAN	A6NL28	Putative tropomyosin alpha-3 chain-like protein
7178	dirMS_041712_NAR_20mM_plus.17807.17807.2	2	11.69	0	1.86E+05		(R)SLVPAAI	(R)S L|V/P A A E L\L/E/S R(V)		194.62	642.8613	1284.716	-0.0005	-0.4	4.53	533778	5.74	HUMAN	Q15149	Plectin
7179	dirMS_041712_NAR_20mM_plus.18475.18475.3	3	11.69	0	5.84E+03		(K)VVVQVL	(K)V V V Q\V L/A|E|E/P E A V L K(G)		199.15	541.6507	1622.936	0.0012	0.7	4.26	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
7180	dirMS_041712_NAR_30mM_plus2.16679.16906.2	2	11.69	0	5.48E+05		(R)FNVPVS	(R)F N|V|P V/S L E/S K(K)		140.52	560.3022	1119.604	-0.0073	-6.5	6	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
7181	dirMS_041712_NAR_30mM_plus2.6017.6017.3	3	11.69	0	6.78E+04		(R)GGSGGS	(R)G G S G G S Y/G G G G S G G\G/Y/G/G G S G S R(G)		85.83	597.9128	1791.728	-0.0039	-2.2	8.59	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
7182	dirMS_041712_NAR_30mM_plus2.7252.7252.2	2	11.69	0	1.34E+05		(K)AAAAAA	(K)A A|A|A|A/A\A\L Q A K(S)		92.78	478.7844	956.552	0.0092	9.6	8.8	37884.5	11.27	HUMAN	H3BM89	60S ribosomal protein L4
7183	dirMS_041712_NAR_40mM_plus2.5914.5914.2	2	11.69	0	1.03E+05		(R)SPDNPM	(R)S/P|D|N|P M N Q R(A)		93.47	529.7368	1058.468	-0.002	-1.9	5.55	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
7184	dirMS_041712_NAR_50mM_plus2.11336.11336.3	3	11.69	1	2.98E+05		(R)ETGVDL	(R)E T/G V/D L T/K D N M/A/L/Q R(V)		127.18	564.2856	1690.843	-0.0006	-0.4	4.56	73964.5	5.87	HUMAN	P38646	Stress-70 protein, mitochondrial
7185	dirMS_041712_NAR_50mM_plus2.13187.13187.3	3	11.69	1	9.66E+05		(R)ELNITAA	(R)E L/N/I|T A/A K E I E/V/G G G R(K)		137.7	552.9671	1656.892	-0.0048	-2.9	4.79	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
7186	dirMS_041712_NAR_50mM_plus2.21514.21514.3	3	11.69	1	1.97E+05		(R)LIALLEVI	(R)L/I/A|L/L E/V L S Q/K R(M)		183.25	461.6293	1382.873	0.0004	0.3	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
7187	dirMS_041712_NAR_60mM_plus.15226.15226.3	3	11.69	1	2.48E+05		(-)MKVELCS	(-)M/K V/E L|C/S|F/S/G Y K(I)	C:Carbamidomethylation	136.28	483.5686	1448.691	0	0	8.26	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
7188	dirMS_041712_NAR_60mM_plus.17012.17276.3	3	11.69	0	1.11E+06		(R)QIFHPE	(R)Q I/F H/P E Q/L/I/T G K(E)		146.98	470.9225	1410.774	-0.021	-14.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
7189	dirMS_041712_NAR_20mM_minus.10297.10297.2	2	11.68	0	2.40E+04		(R)AQAALA	(R)A Q|A|A/L/A V/N I S A A R(G)		152.12	628.3558	1255.712	-0.0074	-5.9	9.79	58479.6	6.23	HUMAN	P40227	T-complex protein 1 subunit zeta

7190	dirMS_041712_NAR_20mM_minus.7650.7650.2	2	11.68	0	6.88E+05	M239m	(K)EVDEQ	(K)E V/D E/Q/m L N|V|Q/N/K(N)	m:Oxidized methionine	125.07	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
7191	dirMS_041712_NAR_30mM_minus2.9885.9885.2	2	11.68	0	8.17E+04		(R)LEDAAD	(R)L/E|D|A|A/D/V Y R(G)		108.18	526.2618	1051.506	0.0109	10.3	4.03	102525.8	7.33	HUMAN	Q9BXJ9	N-alpha-acetyltransferase 15, NatA auxiliary subunit
7192	dirMS_041712_NAR_50mM_minus2.17646.17646.3	3	11.68	0	2.09E+05		(R)DVCTEL	(R)D V|C/T E L L/P/L/I K/P Q\G R(V)	C:Carbamidomethylation	168.85	580.3212	1738.952	-0.003	-1.7	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
7193	dirMS_041712_NAR_60mM_minus.12243.12243.3	3	11.68	0	8.91E+04		(R)LFFQPH	(R)L F/F Q/P/H/Q A G L S K(V)		128.12	458.2502	1372.737	-0.0011	-0.8	8.76	8684.1	9.22	HUMAN	C9J0F6	Ubiquitin-like modifier-activating enzyme 5 (Fragment)
7194	dirMS_041712_NAR_60mM_minus.9932.9932.3	3	11.68	1	5.63E+05	M230m M	(R)mSmKE	(R)m S m K E V D\E/Q|M|L/N\V Q/N K(N)	m:Oxidized methionine	114.97	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
7195	dirMS_041712_NAR_120mM_plus.5097.5097.3	3	11.68	1	1.28E+05		(K)MSSPED	(K)M S|S/P/E D D/S D/T K R(L)		79.25	456.5294	1367.574	-0.0007	-0.5	4.23	103309.5	5.34	HUMAN	A0AV56	SAFB protein
7196	dirMS_041712_NAR_30mM_plus2.12203.12329.2	2	11.68	0	5.04E+05		(K)GLVEDT	(K)G L|V|E/D/T L/R(Q)		117.57	451.7509	902.494	0.0004	0.4	4.37	533778	5.74	HUMAN	Q15149	Plectin
7197	dirMS_041712_NAR_30mM_plus2.14251.14251.2	2	11.68	0	2.88E+05		(K)ASEGPA	(K)A S E/G|P A/F|F/P G R(C)		127.82	568.2831	1135.553	0.0058	5.1	6.05	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
7198	dirMS_041712_NAR_30mM_plus2.19752.19752.2	2	11.68	0	2.28E+05		(K)GFAFVQ	(K)G F/A F/V/Q|Y V N E R(N)		157.53	665.3326	1329.659	-0.0007	-0.5	6	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
7199	dirMS_041712_NAR_40mM_plus2.13289.13289.3	3	11.68	0	2.92E+05		(K)NLPPSG	(K)N L/P P S\G A V\P V/T/G I/P P H V V K(V)		144.43	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
7200	dirMS_041712_NAR_50mM_plus2.18407.18407.3	3	11.68	0	2.22E+05		(R)IDILDSA	(R)I/D/I L/D/S/A L L R P G R(I)		164.5	480.2828	1438.838	-0.0038	-2.6	5.96	44954.5	8.44	HUMAN	A8K3Z3	26S protease regulatory subunit 8
7201	dirMS_041712_NAR_120mM_minus.11627.11627.4	4	11.67	2	9.96E+05		(R)SGKYDL	(R)S G K Y\D\L/D|F K S P D D/P/S/R(Y)		117.92	457.4692	1826.855	-0.0006	-0.3	4.58	47510.4	7.04	HUMAN	P06733	Alpha-enolase
7202	dirMS_041712_NAR_60mM_minus.11397.11397.3	3	11.67	1	8.92E+05	M232m	(R)MSmKE	(R)M S m K E V D E/Q|M|L/N V\Q/N K(N)	m:Oxidized methionine	122.82	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
7203	dirMS_041712_NAR_60mM_minus.16930.16930.3	3	11.67	1	3.01E+05		(R)LKLPAV	(R)L K L P A V|V/T/A/D/L R(L)		154.07	432.6056	1295.805	-0.0023	-1.8	8.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
7204	dirMS_041712_NAR_120mM_plus.10205.10205.3	3	11.67	0	1.20E+06		(R)ILRPWQ	(R)I/L/R P W Q/S S/E/T R(S)		106.67	458.2486	1372.733	-0.0019	-1.4	9.6	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
7205	dirMS_041712_NAR_20mM_plus.15255.15255.2	2	11.67	0	5.88E+04		(R)EQLAIAE	(R)E Q/L/A|I/A E/F A R(S)		176.1	574.312	1147.611	0.0061	5.3	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
7206	dirMS_041712_NAR_20mM_plus.16416.16416.2	2	11.67	0	1.40E+05		(R)QAQEYE	(R)Q A Q/E\Y/E/A/L/L/N I/K(V)		184.52	710.3754	1419.748	-0.0043	-3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
7207	dirMS_041712_NAR_20mM_plus.16973.16973.2	2	11.67	0	6.33E+04		(K)VLTPELY	(K)V L\T|P/E L Y/A E/L R(A)		188.15	652.3664	1303.726	-0.0001	-0.1	4.53	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
7208	dirMS_041712_NAR_30mM_plus2.10130.10130.2	2	11.67	0	5.34E+04		(R)IGLIQGN	(R)I/G/L|I/Q/G N R(V)		107.95	435.7618	870.516	0.0007	0.9	9.75	18719.9	6.91	HUMAN	F8VP00	6-phosphofructokinase, muscle type (Fragment)
7209	dirMS_041712_NAR_30mM_plus2.17207.17505.2	2	11.67	0	5.09E+05		(K)SFNLSAL	(K)S F|N|L/S/A L E/K(H)		144.05	504.7726	1008.536	0.0019	1.9	5.72	82756.6	5.34	HUMAN	C9JIF9	Acylamino-acid-releasing enzyme
7210	dirMS_041712_NAR_50mM_plus2.14358.14358.3	3	11.67	1	8.83E+05		(K)ATLPSPD	(K)A T/L/P/S/P D K L/P G F K(M)		143.57	457.5906	1370.768	-0.0106	-7.7	8.64	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
7211	dirMS_041712_NAR_50mM_plus2.17857.17857.3	3	11.67	0	2.57E+05		(K)YAPLHL	(K)Y/A/P|L H/L/V/P/L I E R(L)		162.08	474.2819	1420.831	0.0001	0	6.75	147553.6	6.73	HUMAN	E7EVF4	Cytoplasmic FMR1-interacting protein 2
7212	dirMS_041712_NAR_50mM_plus2.21769.21769.3	3	11.67	0	1.07E+04		(R)LHFFMP	(R)L H F F\M|P G F|A|P|L T S/R(G)		184.08	540.9498	1620.835	-0.0007	-0.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
7213	dirMS_041712_NAR_60mM_plus.15432.15432.3	3	11.67	1	8.12E+05		(R)FVNVVP	(R)F V\N V V/P/T F G K/K(K)		137.72	412.5761	1235.715	-0.0009	-0.7	10	10904.6	11.56	HUMAN	E9PR30	40S ribosomal protein S30
7214	dirMS_041712_NAR_60mM_plus.15622.15647.3	3	11.67	0	1.71E+05		(R)ILHGLGF	(R)I L H G L G F\T|P/A/M Q R(K)		138.35	480.9305	1440.778	-0.0011	-0.7	9.75	27043.5	6.34	HUMAN	C9JHK9	ATP-binding cassette sub-family F member 2 (Fragment)
7215	dirMS_041712_NAR_50mM_minus2.7435.7435.3	3	11.66	1	8.03E+04		(R)VAVEAK	(R)V/A|V E/A/K N/P A D L/P K(L)		109.27	451.2571	1351.758	-0.0012	-0.9	6.04	96306.4	6.41	HUMAN	P13639	Elongation factor 2
7216	dirMS_041712_NAR_60mM_minus.8078.8078.3	3	11.66	1	1.12E+05		(K)VLTQER	(K)V/L|T Q E/R V S E S G/K(Y)		105.03	444.903	1332.712	-0.0173	-13	6.11	22724.2	6.51	HUMAN	F5H6S6	Zinc finger protein 10 (Fragment)
7217	dirMS_041712_NAR_120mM_plus.12374.12411.3	3	11.66	0	1.40E+06		(R)HVFGES	(R)H V\F G\E|S D|E|L|I/G Q K(V)		118.93	486.9124	1458.722	0.0003	0.2	4.65	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
7218	dirMS_041712_NAR_30mM_plus2.19014.19014.2	2	11.66	0	1.87E+05		(K)LNLGTV	(K)L N|L/G/T|V G/F Y\R(T)		152.8	570.3123	1139.621	-0.0034	-3	8.75	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
7219	dirMS_041712_NAR_30mM_plus2.7232.7232.2	2	11.66	0	1.34E+05		(K)AAAAAA	(K)A A|A|A/A/A\A L Q A/K(S)		92.78	478.7844	956.552	0.0092	9.6	8.8	37884.5	11.27	HUMAN	H3BM89	60S ribosomal protein L4
7220	dirMS_041712_NAR_50mM_plus2.17060.17060.3	3	11.66	1	3.91E+05		(K)TLNDM	(K)T\L/N/D/M R Q E Y E Q\L I/A K(N)		157.17	617.98	1851.927	-0.0015	-0.8	4.68	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
7221	dirMS_041712_NAR_50mM_plus2.8098.8098.3	3	11.66	1	2.64E+05	M227m M	(R)mQKEIT	(R)m/Q\K E I\T A\L/A|P S T m K(I)	m:Oxidized methionine	108.98	527.6045	1548.812	31.9865	-2.1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
7222	dirMS_041712_NAR_60mM_plus.18353.18353.3	3	11.66	1	2.86E+05		(K)LLQDFF	(K)L/L|Q/D/F/F N G R D L N K(S)		152.75	527.2793	1579.823	0.0006	0.4	5.96	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
7223	dirMS_041712_NAR_120mM_minus.7063.7063.3	3	11.65	1	1.81E+05		(K)EAAEVL	(K)E A/A/E/V/L/Q N N R R(L)		92.83	433.8957	1299.676	-0.0038	-3	6.24	21184.9	7.82	HUMAN	P61081	NEDD8-conjugating enzyme Ubc12
7224	dirMS_041712_NAR_40mM_minus2.14329.14329.3	3	11.65	0	1.23E+05		(R)GTEDITS	(R)G T|E/D I/T/S P/H G I/P L/D\L L D R(V)		168.55	650.3366	1948.997	-0.0022	-1.1	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
7225	dirMS_041712_NAR_40mM_minus2.14358.14358.3	3	11.65	1	1.87E+05		(R)GLLPGL	(R)G L\L/P\G L L P\A P/A D K L T P K(G)		169.4	567.6813	1701.031	-0.0016	-0.9	8.59	153084.9	5.55	HUMAN	Q6P2E9	Enhancer of mRNA-decapping protein 4
7226	dirMS_041712_NAR_60mM_minus.10092.10092.3	3	11.65	0	3.76E+06		(R)GSAVHC	(R)G S/A V/H Q/L/S/E/E L R(C)		116.52	442.5648	1325.681	-0.001	-0.7	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
7227	dirMS_041712_NAR_60mM_minus.7701.8055.3	3	11.65	1	8.85E+05		(K)IQDKEGI	(K)I/Q D K E G\I|P/P/D/Q Q R(L)		102.97	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
7228	dirMS_041712_NAR_120mM_plus.10646.10646.3	3	11.65	1	9.74E+06		(R)VKYETEL	(R)V/K Y E\T/E/L/A M/R(Q)		108.02	413.8849	1239.64	0	0	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
7229	dirMS_041712_NAR_20mM_plus.13065.13065.2	2	11.65	0	7.40E+04		(R)VCEEIAII	(R)V/C/E/E I A I/I/P S K(K)	C:Carbamidomethylation	162.67	629.8346	1258.671	-0.0092	-7.3	4.53	21927.8	9.55	HUMAN	H0YK46	40S ribosomal protein S17 (Fragment)
7230	dirMS_041712_NAR_20mM_plus.13829.13848.2	2	11.65	0	2.82E+05		(R)INEILSN	(R)I/N|E|I|L/S N A L K(R)		167.63	557.8267	1114.647	-0.0005	-0.5	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
7231	dirMS_041712_NAR_20mM_plus.17502.17502.2	2	11.65	0	1.44E+04	M199m	(K)SmVPV	(K)S m|V|P V/Q V/Q/L D V/P V V K(V)	m:Oxidized methionine	192.52	827.4624	1637.93	15.988	-4.2	5.55	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
7232	dirMS_041712_NAR_40mM_plus2.11985.11985.2	2	11.65	0	2.48E+05		(K)LSELEAA	(K)L/S|E/L/E A/A/L Q R(A)		136.62	565.3103	1129.621	-0.0078	-6.9	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
7233	dirMS_041712_NAR_50mM_plus2.12060.12060.3	3	11.65	0	3.79E+05		(K)FSVCVL	(K)F/S V/C/V/L/G D Q Q H C D E A K(A)	C:Carbamidomethylation	131.38	631.6129	1892.827	-0.0024	-1.3	4.54	25002	10.06	HUMAN	P62906	60S ribosomal protein L10a
7234	dirMS_041712_NAR_50mM_plus2.16748.16748.3	3	11.65	1	1.06E+06		(R)LFVGNL	(R)L F|V/G N L/P P D I T E E E M R/K(L)		155.3	663.3447	1988.016	0.0038	1.9	4.41	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
7235	dirMS_041712_NAR_50mM_plus2.16909.17256.3	3	11.65	1	1.35E+06		(K)LFTAESL	(K)L/F|T A/E S\L/I G L K N P E/K(S)		158.05	553.9791	1659.932	-0.0089	-5.3	6.14	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
7236	dirMS_041712_NAR_50mM_plus2.18570.18570.3	3	11.65	1	2.79E+04		(K)LFPGFEI	(K)L F|P/G F E I E T/V K N N L R(I)		165.57	592.986	1776.964	-0.0208	-11.7	6.14	62566.6	6.59	HUMAN	E9PCI3	Asparagine synthetase
7237	dirMS_041712_NAR_50mM_plus2.19327.19327.3	3	11.65	0	9.44E+04		(K)TIADLEL	(K)T/I/A/D/L E L/H Y/Q E F I R(N)		169.88	583.3027	1747.901	-0.0078	-4.5	4.65	334221.3	6.44	HUMAN	P15924	Desmoplakin
7238	dirMS_041712_NAR_60mM_plus.6699.6699.3	3	11.65	0	8.87E+05		(K)LVDQSG	(K)L/V/D Q/S G/P P H E/P/K(F)		93.93	435.2257	1303.664	-0.0015	-1.2	5.32	142137.5	9.17	HUMAN	E7ENU4	Double-stranded RNA-specific adenosine deaminase
7239	dirMS_041712_NAR_30mM_minus2.14457.14476.2	2	11.64	0	2.39E+05		(R)YYFEGIK	(R)Y/Y|F/E/G I K(Q)		132.38	460.2363	919.456	0.0093	10.1	6	23092.1	6.93	HUMAN	G3V438	Activator of 90 kDa heat shock protein ATPase homolog 1 (Fragment)
7240	dirMS_041712_NAR_30mM_minus2.14864.14864.2	2	11.64	0	1.40E+05		(R)WALSQS	(R)W A|L/S/Q S N/P S A L R(E)		134.55	665.3481	1329.691	-0.0021	-1.5	9.75	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
7241	dirMS_041712_NAR_50mM_minus2.12316.12316.3	3	11.64	1	4.17E+04		(K)QLGGSV	(K)Q L/G G/S/V/E L/V/D I G K Q K(L)		138.1	524.2969	1570.88	-0.0038	-2.4	6.07	9475.6	4.64	HUMAN	J3KRD5	Cytosolic non-specific dipeptidase (Fragment)
7242	dirMS_041712_NAR_30mM_plus2.18193.18193.2	2	11.64	0	3.13E+05		(R)SQVEEE	(R)S Q|V/E|E E L\F/S V/R(V)		149.2	661.8302	1322.659	-0.0055	-4.2	4.25	533778	5.74	HUMAN	Q15149	Plectin
7243	dirMS_041712_NAR_30mM_plus2.19092.19589.2	2	11.64	0	1.87E+06		(R)SSIAGLL	(R)S S|I/A/G L/L/L K(A)		155.65	451.2894	901.572	-0.0002	-0.2	8.47	533778	5.74	HUMAN	Q15149	Plectin
7244	dirMS_041712_NAR_30mM_plus2.19180.19180.2	2	11.64	0	2.35E+05		(K)TVDNFV	(K)T V|D/N/F|V/A/L A T G E K(G)		154.42	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
7245	dirMS_041712_NAR_30mM_plus2.21587.21587.2	2	11.64	0	3.32E+05		(R)NSYLEV	(R)N S|Y/L|E V L/L/K(L)		168.03	539.8092	1078.614	-0.0032	-2.9	6	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
7246	dirMS_041712_NAR_30mM_plus2.22154.22154.2	2	11.64	0	1.75E+05		(K)GLSSLLC	(K)G L/S S/L/L|C/N F/T K(S)	C:Carbamidomethylation	171.83	620.3199	1239.64	-0.0077	-6.2	8.75	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
7247	dirMS_041712_NAR_30mM_plus2.22557.22568.3	3	11.64	0	1.19E+06		(R)LEGLTDE	(R)L E\G L T\D\E|I/N F/L R(Q)		175.42	473.9205	1419.748	-0.0009	-0.6	4.14	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
7248	dirMS_041712_NAR_40mM_plus2.5860.5860.2	2	11.64	0	1.61E+05	M367m	(R)FGSGmN	(R)F/G|S/G m N M G R(I)	m:Oxidized methionine	92.73	486.7054	956.408	15.9958	1	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
7249	dirMS_041712_NAR_50mM_plus2.10808.10808.3	3	11.64	1	4.28E+05		(K)NQLTSN	(K)N Q|L/T S/N/P E/N T/V/F/D A K R(L)		124.88	611.9758	1833.909	0.0039	2.1	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
7250	dirMS_041712_NAR_50mM_plus2.11332.11356.3	3	11.64	1	4.23E+05		(R)LYPPSAE	(R)L Y|P/P S A E Y/P D/L R K(H)		127.25	516.9418	1548.806	0.0052	3.3	6.07	16450.4	6.98	HUMAN	C9J8F6	Creatine kinase U-type, mitochondrial (Fragment)
7251	dirMS_041712_NAR_50mM_plus2.11424.11424.3	3	11.64	1	7.45E+05		(K)LAEQAE	(K)L/A|E/Q/A E R Y D D M A A A/M K(A)		127.98	604.9469	1812.825	0.0007	0.4	4.32	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
7252	dirMS_041712_NAR_50mM_plus2.13363.13363.3	3	11.64	0	1.99E+05		(K)LVRPPV	(K)L/V|R P P V\Q\V|Y/G I E G R(Y)		138.6	528.3069	1582.906	-0.0002	-0.2	8.75	8249.6	10.2	HUMAN	H7C086	ATP synthase subunit O, mitochondrial (Fragment)
7253	dirMS_041712_NAR_50mM_plus2.20953.20953.3	3	11.64	0	3.54E+05		(K)HSQFIGY	(K)H S Q F|I G\Y|P I|T L/F V E K(E)		179.45	593.6536	1778.948	-0.0013	-0.8	6.75	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
7254	dirMS_041712_NAR_50mM_plus2.21779.21779.3	3	11.64	1	1.26E+05		(K)TENPLIL	(K)T E/N/P L I/L I/D E V D K\I G R(G)		185.57	609.0045	1825.007	-0.0076	-4.2	4.32	86039.3	5.74	HUMAN	F5GZ27	Lon protease homolog
7255	dirMS_041712_NAR_60mM_plus.10444.10466.2	2	11.64	1	2.92E+05		(K)IKIIAPPE	(K)I/K|I|I/A\P P E/R(K)		112.38	518.8301	1036.651	0.0016	1.5	8.75	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
7256	dirMS_041712_NAR_60mM_plus.20376.20376.3	3	11.64	1	4.21E+05		(K)NAAGAL	(K)N A|A/G\A/L D L/L K E/L K(N)		166.93	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
7257	dirMS_041712_NAR_60mM_plus.8381.8381.3	3	11.64	1	2.51E+05		(R)TERFGQ	(R)T E R F G Q\G G\A|G|P/V\G/G Q G P R(G)		101.95	576.6232	1727.857	-0.0022	-1.2	9.26	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
7258	dirMS_041712_NAR_120mM_minus.10050.10050.4	4	11.63	1	1.65E+05		(R)AQGEPV	(R)A Q\G E/P V/A/G/H E S P K I/P Y E K(Q)		109.07	484.9989	1936.976	-0.0025	-1.3	5.5	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
7259	dirMS_041712_NAR_30mM_minus2.11946.11946.2	2	11.63	0	3.64E+05		(R)IATGSFL	(R)I/A|T/G S F L K(R)		118.15	418.7451	836.488	-0.0047	-5.6	8.75	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
7260	dirMS_041712_NAR_50mM_minus2.14801.14801.3	3	11.63	0	3.07E+04		(K)GQYFGE	(K)G Q/Y/F/G E/L A L/V T/N K P R(A)		152.52	564.9709	1692.907	-0.0086	-5.1	8.59	10305.6	6.94	HUMAN	H7C330	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
7261	dirMS_041712_NAR_20mM_plus.16563.16563.3	3	11.63	0	6.48E+04	M137m M	(R)IIGATDS	(R)I I\G A T D/S S G/E/L/m/F L/m K(W)	m:Oxidized methionine	185.8	582.2872	1712.86	31.9873	-1.5	4.37	19439.5	4.97	HUMAN	B5MD17	Chromobox protein homolog 1 (Fragment)
7262	dirMS_041712_NAR_20mM_plus.18045.18045.2	2	11.63	0	1.32E+05		(R)LFDQAF	(R)L F|D Q/A/F/G L/P R(L)		195.55	582.3166	1163.621	0.0052	4.4	5.84	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
7263	dirMS_041712_NAR_30mM_plus2.10192.10192.2	2	11.63	0	2.33E+05		(K)TAVCDI	(K)T A\V/C/D|I/P\P R(G)	C:Carbamidomethylation	105.85	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
7264	dirMS_041712_NAR_30mM_plus2.14791.14846.2	2	11.63	0	1.52E+06		(R)LADALQ	(R)L/A|D|A/L/Q/E L/R(A)		130.85	514.7896	1028.574	-0.0016	-1.5	4.37	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
7265	dirMS_041712_NAR_30mM_plus2.17431.17431.2	2	11.63	0	4.00E+05		(K)SFNLSAL	(K)S/F|N/L/S A L/E K(H)		144.32	504.7726	1008.536	0.0019	1.9	5.72	82756.6	5.34	HUMAN	C9JIF9	Acylamino-acid-releasing enzyme
7266	dirMS_041712_NAR_30mM_plus2.17507.17565.2	2	11.63	0	9.20E+04		(K)VFQFLN	(K)V/F|Q|F L/N\A/K(C)		144.02	483.7736	966.541	-0.0008	-0.8	8.72	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
7267	dirMS_041712_NAR_40mM_plus2.19787.19792.3	3	11.63	0	3.68E+05		(R)DLLDTV	(R)D L\L/D/T/V/L/P H L Y N E T K(V)		185.23	590.9774	1770.927	-0.0096	-5.4	4.54	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
7268	dirMS_041712_NAR_50mM_plus2.16272.16272.3	3	11.63	1	1.17E+06		(K)CEFQDA	(K)C E/F\Q/D A Y|V L/L S E K K(I)	C:Carbamidomethylation	152.42	577.2866	1729.847	-0.0013	-0.8	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
7269	dirMS_041712_NAR_50mM_plus2.20055.20055.3	3	11.63	0	2.83E+05		(R)LQSLPF	(R)L Q S L/P F/A L/T/H/L/N L K(A)		173.82	532.3178	1594.931	0.0073	4.6	8.76	175851.7	5.01	HUMAN	Q14160	Protein scribble homolog
7270	dirMS_041712_NAR_60mM_plus.11286.11286.2	2	11.63	0	2.12E+06		(K)GIVEFAS	(K)G I|V|E/F/A S K/P A A R(K)		116.18	623.3504	1245.695	-0.0015	-1.2	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
7271	dirMS_041712_NAR_60mM_plus.17469.17469.3	3	11.63	1	3.74E+05		(R)KVPGVT	(R)K\V P G V T A\I\E|L/D/E/D/T|G T/F R(I)		148.18	650.0017	1948.002	-0.0117	-6	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
7272	dirMS_041712_NAR_120mM_minus.20120.20157.4	4	11.62	0	4.58E+05		(K)LAFPSPF	(K)L A\F/P/S/P/F G H L/S E/G F S H S R(W)		166.2	493.9968	1972.966	-0.0011	-0.5	6.92	16196.2	9.92	HUMAN	C9JRJ8	Sequestosome-1 (Fragment)
7273	dirMS_041712_NAR_20mM_minus.13157.13157.3	3	11.62	0	2.65E+05		(K)VGINYQ	(K)V G I N Y Q/P P T V|V/P/G G D L A K(V)		183.15	608.9971	1824.985	-0.0087	-4.8	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
7274	dirMS_041712_NAR_30mM_minus2.7011.7011.2	2	11.62	0	2.00E+05	M88m	(K)DVDEAY	(K)D V|D E|A/Y m\N K(V)	m:Oxidized methionine	92.67	550.7326	1084.462	15.9964	1.3	4.03	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
7275	dirMS_041712_NAR_40mM_minus2.6148.6163.2	2	11.62	0	1.51E+05		(K)AQYEDI	(K)A/Q|Y/E|D/I/A\N R(S)		101.52	540.2599	1079.512	0.0009	0.8	4.37	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
7276	dirMS_041712_NAR_50mM_minus2.16603.16603.3	3	11.62	0	1.40E+05		(K)VSHLLGI	(K)V S H L/L G I\N/V/T D/F T R(G)		162.18	524.6237	1571.854	0.0025	1.6	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
7277	dirMS_041712_NAR_50mM_minus2.9705.9705.3	3	11.62	0	2.51E+05		(K)TSEVDL	(K)T/S|E/V D L A/K/P L V/K(F)		123.18	433.9205	1299.752	-0.0049	-3.8	5.73	17178.3	5.63	HUMAN	C9IZF9	Programmed cell death 6-interacting protein (Fragment)
7278	dirMS_041712_NAR_60mM_minus.8605.8605.3	3	11.62	0	2.74E+05		(R)LAQGHT	(R)L/A|Q\G|H/T T V D/E L A/R(R)		107.93	470.9153	1410.734	-0.0022	-1.6	5.32	533778	5.74	HUMAN	Q15149	Plectin
7279	dirMS_041712_NAR_120mM_plus.17268.17318.3	3	11.62	2	1.00E+06		(R)NLKASLE	(R)N/L|K/A|S L E/N S L R E V E|A R(Y)		143.48	610.332	1828.988	-0.0061	-3.3	6.23	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
7280	dirMS_041712_NAR_120mM_plus.9068.9113.3	3	11.62	1	1.06E+06		(R)EQAEEE	(R)E/Q/A/E E|E/R/Y F R(A)		101.13	452.8785	1356.618	0.0031	2.3	4.5	12248.6	9.34	HUMAN	Q9UII2	ATPase inhibitor, mitochondrial
7281	dirMS_041712_NAR_20mM_plus.19141.19141.3	3	11.62	0	1.90E+05		(K)TLETQS	(K)T L E T Q S A\L|G/P A/L Q A A F K(L)		202.63	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
7282	dirMS_041712_NAR_20mM_plus.19363.19363.3	3	11.62	0	9.30E+04		(R)ALIAGG	(R)A L\I\A G G G A/P E/I/E/L A/L R(L)		205.05	517.6345	1550.89	-0.0011	-0.7	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
7283	dirMS_041712_NAR_20mM_plus.7537.7537.2	2	11.62	0	2.93E+04		(K)VTLTSEE	(K)V/T/L/T/S E/E E A R(L)		120.93	567.7865	1134.564	0.002	1.8	4.25	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
7284	dirMS_041712_NAR_20mM_plus.9071.9071.2	2	11.62	0	4.50E+05		(K)VIPELNG	(K)V I|P/E L/N G K(L)		133.23	435.2573	869.509	-0.0018	-2	5.97	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
7285	dirMS_041712_NAR_30mM_plus2.16047.16222.2	2	11.62	0	2.79E+05		(K)MDQAII	(K)M D|Q|A/I/I|F/C R(T)	C:Carbamidomethylation	137.37	577.2809	1153.549	0.0053	4.6	5.59	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
7286	dirMS_041712_NAR_30mM_plus2.19200.19200.2	2	11.62	0	2.26E+05		(R)LTAEDLF	(R)L/T/A|E D/L\F/E A R(I)		153.4	582.796	1164.59	-0.0048	-4.1	4.14	533778	5.74	HUMAN	Q15149	Plectin
7287	dirMS_041712_NAR_40mM_plus2.16119.16161.3	3	11.62	0	5.18E+05		(R)FGVPVI	(R)F G\V|P/V/I A D/G G I Q N V/G H I A K(A)		162.3	631.3436	1892.039	-0.0226	-12	6.74	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
7288	dirMS_041712_NAR_50mM_plus2.6769.6769.3	3	11.62	0	1.60E+05		(K)IGEEEIQ	(K)I/G/E E E/I Q/K/P E E K(V)		100.35	476.9126	1428.722	0.0016	1.1	4.32	81733.5	5.24	HUMAN	E9PAW1	Splicing factor 3A subunit 1
7289	dirMS_041712_NAR_120mM_minus.10926.10926.3	3	11.61	1	6.07E+05		(R)FYKNEG	(R)F/Y/K N E\G G T/W/S V E/K(V)		113.78	515.5834	1544.738	-0.0023	-1.5	6.14	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
7290	dirMS_041712_NAR_120mM_minus.17515.17515.3	3	11.61	1	2.98E+05		(R)RAPFDL	(R)R A P F\D|L|F E/N/K(K)		150.67	412.8849	1236.637	0.003	2.4	6.07	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
7291	dirMS_041712_NAR_120mM_minus.7164.7164.2	2	11.61	1	1.52E+05		(K)GSSLKIE	(K)G/S/S|L/K/I/E/E R(A)		93.25	509.7795	1018.553	-0.001	-1	6.14	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
7292	dirMS_041712_NAR_30mM_minus2.17206.17206.2	2	11.61	0	2.60E+05		(R)LLNTFLE	(R)L/L|N|T F/L E R(L)		146.97	503.2871	1005.573	-0.0058	-5.8	6	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
7293	dirMS_041712_NAR_50mM_minus2.10825.10825.3	3	11.61	1	1.97E+05		(K)NQVAM	(K)N Q|V|A/M/N P T/N T\V/F D A K R(L)		129.22	602.6379	1805.896	0.0029	1.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
7294	dirMS_041712_NAR_50mM_minus2.17819.17819.3	3	11.61	1	2.28E+05	M116m	(R)ELAILLG	(R)E L/A/I/L/L/G m L D/P A E K/D E K(G)	m:Oxidized methionine	170.82	634.3353	1884.999	15.9927	-1.2	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
7295	dirMS_041712_NAR_60mM_minus.10629.10629.3	3	11.61	0	1.31E+05		(R)HLVCSS	(R)H L\V C S S G G N A|G\I/A/A A Y\A A/R(K)	C:Carbamidomethylation	119.23	615.9709	1845.902	-0.0043	-2.3	8.75	18015.6	9.05	HUMAN	F8VYZ3	Serine dehydratase-like (Fragment)
7296	dirMS_041712_NAR_60mM_minus.11614.11614.3	3	11.61	0	1.53E+05		(K)DLQHPN	(K)D L/Q H/P/N E/F I R(G)		124.7	423.5497	1268.638	-0.0037	-2.9	5.32	15826.6	6.3	HUMAN	E9PKQ1	Coatomer subunit beta (Fragment)
7297	dirMS_041712_NAR_20mM_plus.7404.7404.2	2	11.61	0	2.86E+05		(K)TGQAPG	(K)T G Q|A|P G Y/S Y T A A N/K(N)		119.52	714.8394	1428.675	-0.0039	-2.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
7298	dirMS_041712_NAR_30mM_plus2.7626.7628.2	2	11.61	0	2.84E+05		(R)YLSNAY	(R)Y/L|S|N A Y/A|R(E)		94.2	479.2438	957.479	0.0015	1.5	8.59	27264.5	5.09	HUMAN	O00299	Chloride intracellular channel protein 1

7299	dirMS_041712_NAR_30mM_plus2.8971.8971.2	2	11.61	0	3.86E+05		(R)CSEQVQ	(R)C S|E/Q|V/Q/D\F|T K(C)	C:Carbamidomethylation	100.43	621.2771	1241.547	0.0002	0.2	4.37	13533.5	9.82	HUMAN	H7C3D8	COX assembly mitochondrial protein homolog (Fragment)
7300	dirMS_041712_NAR_40mM_plus2.17920.17920.3	3	11.61	1	7.73E+04	M116m	(R)ELAILLG	(R)E L/A/I/L/L/G m L D P A E K D E K(G)	m:Oxidized methionine	171.67	634.3333	1884.999	15.9867	-4.3	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
7301	dirMS_041712_NAR_50mM_plus2.10154.10154.3	3	11.61	1	2.94E+05		(R)VLTVINC	(R)V L|T/V/I N Q T Q K E N L|R(K)		120.45	552.6527	1655.944	-0.0003	-0.2	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
7302	dirMS_041712_NAR_50mM_plus2.13750.13750.3	3	11.61	0	1.60E+06		(K)DLAGCII	(K)D L/A|G C I/H/G L S N V/K(L)	C:Carbamidomethylation	140.37	461.9061	1383.705	-0.0012	-0.8	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
7303	dirMS_041712_NAR_50mM_plus2.20473.20473.3	3	11.61	1	2.66E+05		(R)GGPNIIT	(R)G G P\N/I/I/T L A D I V K D/P V S R(T)		176.7	622.3526	1865.049	-0.0058	-3.1	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
7304	dirMS_041712_NAR_60mM_plus.12041.12041.2	2	11.61	1	7.93E+05		(K)MKEIAE	(K)M K|E/I/A/E A/Y L/G K(T)		120.2	626.8335	1252.661	-0.0009	-0.7	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
7305	dirMS_041712_NAR_60mM_plus.5723.5723.3	3	11.61	1	3.86E+04		(R)TLEEKEC	(R)T L/E E/K E/Q E E/A R(L)		87.77	454.555	1361.654	-0.0039	-2.8	4.32	95923.1	9.67	HUMAN	Q9BUQ8	Probable ATP-dependent RNA helicase DDX23
7306	dirMS_041712_NAR_60mM_plus.7651.7651.2	2	11.61	1	7.47E+05		(R)VITEEEK	(R)V/I|T|E/E E K N\F/K(A)		97.92	618.8282	1236.647	0.0021	1.7	4.79	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
7307	dirMS_041712_NAR_120mM_minus.13421.13421.4	4	11.6	1	9.79E+05		(K)SVHSSVI	(K)S V H S S V|P|L L N S K D/P I D R(I)		127.5	466.7525	1863.992	-0.0041	-2.2	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
7308	dirMS_041712_NAR_120mM_minus.13977.13977.4	4	11.6	1	1.60E+06		(K)ASIHEAV	(K)A/S/I/H E A/W/T D/G K E A M L K(H)		129.98	447.476	1786.879	0.0029	1.6	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
7309	dirMS_041712_NAR_40mM_minus2.8077.8109.2	2	11.6	0	7.00E+04		(R)IVLQIDN	(R)I V|L/Q|I/D/N A R(L)		128.1	521.3059	1041.605	-0.0006	-0.6	5.84	20842.9	5.32	HUMAN	C9JM50	Keratin, type I cytoskeletal 19 (Fragment)
7310	dirMS_041712_NAR_50mM_minus2.13955.14101.3	3	11.6	1	5.56E+05	M85m	(K)TVTAmD	(K)T V|T/A/m/D V/V/Y A L K/R(Q)	m:Oxidized methionine	148.35	494.9385	1466.804	15.9974	1.7	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
7311	dirMS_041712_NAR_50mM_minus2.14941.14941.3	3	11.6	0	4.19E+05		(K)IAILTCPF	(K)I/A|I/L T C P F\E/P/P K P K(T)	C:Carbamidomethylation	153.32	537.6375	1610.898	0.0005	0.3	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
7312	dirMS_041712_NAR_50mM_minus2.5752.5760.3	3	11.6	1	9.21E+04		(K)LEEAEKA	(K)L/E|E|A/E K/A/A D/E S E R(G)		94.08	492.8982	1476.681	-0.0012	-0.8	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
7313	dirMS_041712_NAR_60mM_minus.12207.12207.3	3	11.6	1	2.17E+05		(K)SGYLAGI	(K)S G Y|L/A G D/K/L|L/P Q/R(V)		127.73	473.258	1417.78	-0.0203	-14.3	8.31	67933	6.08	HUMAN	P26038	Moesin
7314	dirMS_041712_NAR_60mM_minus.17965.18101.3	3	11.6	1	2.77E+05		(R)TRIEGLL	(R)T R I\E G\L|L/A/A F/P/K(L)		161.67	439.2618	1315.773	-0.0024	-1.8	8.41	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
7315	dirMS_041712_NAR_120mM_plus.6258.6382.3	3	11.6	1	5.04E+05		(R)ARSDEG	(R)A R S D E\G Q|L|S/P A T R(G)		86.7	463.2395	1387.692	0.0115	8.3	6.12	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
7316	dirMS_041712_NAR_120mM_plus.6608.6625.2	2	11.6	1	3.09E+05		(K)GKFEDM	(K)G/K|F/E D\M/A/K(A)		88.22	463.2276	925.445	0.0031	3.4	6.07	24408.7	5.92	HUMAN	B2RPK0	Putative high mobility group protein B1-like 1
7317	dirMS_041712_NAR_20mM_plus.13904.13904.2	2	11.6	0	2.12E+05	M98m	(R)TLTIVDT	(R)T/L|T/I V/D T G\I|G m T K(A)	m:Oxidized methionine	167.5	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
7318	dirMS_041712_NAR_20mM_plus.17979.17979.2	2	11.6	0	1.93E+05		(K)GADFLV	(K)G A D\F L|V|T E/V|E/N G G S L G S K(K)		195.23	890.4414	1779.876	-0.0004	-0.2	4.14	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
7319	dirMS_041712_NAR_30mM_plus2.19781.19781.2	2	11.6	0	2.91E+05		(K)LFLVQLC	(K)L/F|L/V Q L Q E/K(A)		157.37	559.3295	1117.662	-0.0098	-8.8	6	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
7320	dirMS_041712_NAR_40mM_plus2.11299.11329.3	3	11.6	0	1.67E+05		(R)SVIDPVF	(R)S V|I D P V/P A/P V G D/S H V D G A A K(S)		132.95	644.3327	1930.987	-0.0033	-1.7	4.41	58326.8	5.7	HUMAN	Q13177	Serine/threonine-protein kinase PAK 2
7321	dirMS_041712_NAR_40mM_plus2.17519.17519.3	3	11.6	0	2.09E+04		(R)IHFPLAT	(R)I H F P/L A T\Y/A|P/V I S A E K(A)		169.42	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
7322	dirMS_041712_NAR_40mM_plus2.7693.7693.2	2	11.6	0	1.48E+05		(R)SGYFDEI	(R)S G|Y|F D/E/R(Y)		104.58	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
7323	dirMS_041712_NAR_50mM_plus2.13941.13941.3	3	11.6	1	6.51E+05		(K)GGELVY	(K)G G E/L|V/Y/T D S E A R D V F E/K(A)		141.45	638.9735	1914.908	-0.002	-1.1	4.18	533778	5.74	HUMAN	Q15149	Plectin
7324	dirMS_041712_NAR_60mM_plus.11237.11237.3	3	11.6	0	1.50E+06		(K)YIQQTKI	(K)Y I/Q Q T K|P\L/T L E/R(T)		115.95	497.2818	1489.837	-0.0065	-4.3	8.59	26283.8	8.96	HUMAN	O43809	Cleavage and polyadenylation specificity factor subunit 5
7325	dirMS_041712_NAR_30mM_minus2.12026.12026.2	2	11.59	0	3.30E+05		(K)GLVQAL	(K)G L|V/Q/A/L Q T K(V)		118.73	479.288	957.573	-0.004	-4.2	8.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
7326	dirMS_041712_NAR_50mM_minus2.18504.18504.3	3	11.59	1	1.47E+06		(R)VISGVLC	(R)V I/S\G V/L/Q/L/G N I V F K K(E)		177	539.0018	1614.994	-0.0033	-2	10	227783.5	5.5	HUMAN	P35579	Myosin-9
7327	dirMS_041712_NAR_50mM_minus2.6238.6238.3	3	11.59	0	2.41E+05	M434m	(R)LESGmC	(R)L/E|S G m Q N/M/S I/H T K(T)	m:Oxidized methionine	98.83	497.9018	1475.698	15.9927	-1.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
7328	dirMS_041712_NAR_60mM_minus.11697.11949.3	3	11.59	1	7.36E+05		(K)DLFPYEE	(K)D L|F/P/Y/E/E S K E K(F)		125.8	462.2282	1384.663	0.007	5	4.41	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
7329	dirMS_041712_NAR_60mM_minus.16441.16441.3	3	11.59	1	8.35E+04		(R)VRLGDV	(R)V R L G/D V I S|I\Q|P C P D V/K(Y)	C:Carbamidomethylation	151.82	599.3265	1795.974	-0.0085	-4.8	5.93	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
7330	dirMS_041712_NAR_60mM_minus.16957.16957.3	3	11.59	1	2.53E+05		(R)GQFSTD	(R)G Q|F/S T/D E L V/A E/V E K R(N)		154.03	569.9569	1707.855	0.0013	0.8	4.41	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
7331	dirMS_041712_NAR_120mM_plus.10786.10820.3	3	11.59	1	7.48E+04		(K)KYEFGES	(K)K\Y E\F\G|E/S\D/L/R(S)		109.63	415.205	1243.595	0.0051	4.1	4.68	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
7332	dirMS_041712_NAR_20mM_plus.16770.16770.2	2	11.59	0	2.97E+05		(K)VQIAVA	(K)V Q|I\A|V|A\N/A Q E/L L/Q R(M)		186.92	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
7333	dirMS_041712_NAR_20mM_plus.9433.9433.2	2	11.59	0	1.86E+05		(K)SVTNED	(K)S V/T/N/E/D/V/T\Q\E E/L G G A K(T)		136	838.9014	1676.797	-0.0018	-1.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
7334	dirMS_041712_NAR_30mM_plus2.16957.16957.2	2	11.59	0	2.53E+05	M313m	(R)TVQSLEI	(R)T V/Q\S L/E I D/L/D S m R(N)	m:Oxidized methionine	142.07	761.8741	1506.747	15.9941	-0.5	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
7335	dirMS_041712_NAR_30mM_plus2.18367.18526.2	2	11.59	0	6.04E+04		(K)NLGTAL	(K)N L|G|T/A/L/A E L/R(T)		150	529.3028	1057.6	-0.0017	-1.6	6	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
7336	dirMS_041712_NAR_30mM_plus2.20877.21348.2	2	11.59	0	4.30E+06		(K)FLPLFDR	(K)F L|P/L F D/R(V)		165.65	454.2621	907.504	0.0133	14.7	5.84	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
7337	dirMS_041712_NAR_30mM_plus2.21941.21941.2	2	11.59	0	2.38E+05		(R)EGDVLT	(R)E G\D\V/L/T/L/L/E S E R(E)		170.73	680.8538	1360.696	0.0049	3.6	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
7338	dirMS_041712_NAR_30mM_plus2.5434.5434.2	2	11.59	0	1.84E+05		(R)TDTGEP	(R)T/D|T\G/E\P M/G/R(G)		82.82	482.2128	963.42	-0.0017	-1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
7339	dirMS_041712_NAR_40mM_plus2.10651.10651.2	2	11.59	0	1.63E+05		(R)GLQDVL	(R)G L/Q/D\V/L R(T)		128.13	400.7336	800.462	-0.0026	-3.2	5.84	54099	7.15	HUMAN	B4DX20	T-complex protein 1 subunit zeta-2
7340	dirMS_041712_NAR_50mM_plus2.14500.14500.3	3	11.59	1	3.88E+06		(K)VGEVIVT	(K)V/G|E|V/I V/T K D D A M/L/L K(G)		145.3	544.3052	1630.908	-0.0074	-4.5	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
7341	dirMS_041712_NAR_50mM_plus2.15200.15200.3	3	11.59	1	1.01E+06		(R)GDVVPK	(R)G D/V\V/P/K D V N A/A/I/A T I K(T)		147.92	537.6393	1610.911	-0.0079	-4.9	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
7342	dirMS_041712_NAR_50mM_plus2.15353.15353.3	3	11.59	1	7.54E+05		(K)EAFSLFD	(K)E A F/S/L/F/D/K D G D G T I T/T K(E)		149.33	615.6348	1844.891	-0.0014	-0.8	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
7343	dirMS_041712_NAR_50mM_plus2.18567.18567.3	3	11.59	1	5.28E+05		(K)TGISDVF	(K)T G|I/S/D V|F A K N D/L/A V V D/V R(I)		166.27	640.3449	1919.023	-0.0031	-1.6	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
7344	dirMS_041712_NAR_120mM_minus.6859.6859.2	2	11.58	1	2.58E+06		(R)TKTEISEI	(R)T/K|T|E I/S E M N R(N)		92.45	604.8012	1208.594	0.0012	1	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
7345	dirMS_041712_NAR_20mM_minus.13920.13920.2	2	11.58	0	8.14E+05		(K)VLTPELY	(K)V L|T/P E/L Y A E L R(A)		191.32	652.3653	1303.726	-0.0023	-1.8	4.53	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
7346	dirMS_041712_NAR_20mM_minus.14700.14700.2	2	11.58	0	1.82E+05		(K)TAVETA	(K)T A|V|E/T A/V/L\L L R(I)		201.32	593.3613	1185.72	-0.0048	-4.1	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
7347	dirMS_041712_NAR_40mM_minus2.11884.11884.3	3	11.58	0	2.40E+05		(K)DAGEGL	(K)D A|G/E/G L L A V Q I T D/P E G K|P K(K)		153.83	646.6785	1938.018	0.0031	1.6	4.32	283472.4	5.71	HUMAN	P21333	Filamin-A
7348	dirMS_041712_NAR_50mM_minus2.6966.6966.3	3	11.58	0	3.75E+04		(R)LIQSHPE	(R)L/I|Q S/H/P E S A E D/L Q E K(C)		106.3	575.2885	1723.85	0.0012	0.7	4.4	285798.6	5.23	HUMAN	A6NG51	Spectrin alpha chain, non-erythrocytic 1
7349	dirMS_041712_NAR_50mM_minus2.8435.8435.3	3	11.58	1	1.02E+05		(R)YESLTDF	(R)Y E/S L T/D/P S K L/D S/G K(E)		116.12	513.9233	1539.754	0.0017	1.1	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
7350	dirMS_041712_NAR_60mM_minus.13231.13231.3	3	11.58	1	2.81E+05	M194m	(R)KLQEEEI	(R)K L Q E E E\L\L|A/T/Q/V D/m R(A)	m:Oxidized methionine	133.93	606.9793	1802.932	15.9917	-1.8	4.41	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
7351	dirMS_041712_NAR_30mM_plus2.15095.15167.2	2	11.58	0	1.06E+06		(R)NFDEILR	(R)N/F|D/E/I/L/R(V)		131.83	453.7343	906.468	-0.0066	-7.3	4.37	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
7352	dirMS_041712_NAR_40mM_plus2.18744.18744.3	3	11.58	0	9.38E+04		(R)NEVSFVI	(R)N/E/V/S F V/I|H N L P V L/A K(M)		176.03	560.6533	1679.948	-0.0026	-1.5	6.75	35663.7	5.91	HUMAN	B4DWK0	Selenide, water dikinase 1
7353	dirMS_041712_NAR_50mM_plus2.19424.19424.3	3	11.58	1	3.94E+05		(K)ILDVASL	(K)I/L/D/V/A|S L E V L N E V N R R(S)		169.97	614.0109	1840.029	-0.0105	-5.7	4.68	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
7354	dirMS_041712_NAR_60mM_plus.8210.8210.3	3	11.58	1	7.31E+05		(K)AAYEAEI	(K)A/A/Y/E A E/L/G D/A R K(T)		100.93	431.8884	1293.643	0.0073	5.6	4.68	74423.5	6.57	HUMAN	P02545	Prelamin-A/C
7355	dirMS_041712_NAR_120mM_minus.15383.15383.3	3	11.57	2	9.57E+05		(R)ALKDEEI	(R)A L|K/D E E/K M\E\L/Q/E I Q L K(E)		137.72	649.0139	1945.031	-0.0039	-2	4.58	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
7356	dirMS_041712_NAR_30mM_minus2.14203.14357.2	2	11.57	0	3.75E+05		(K)IMMEFE	(K)I/M|M/E/F E/R(Q)		130.8	478.2237	955.438	0.0025	2.7	4.53	25103.6	5.88	HUMAN	O43633	Charged multivesicular body protein 2a
7357	dirMS_041712_NAR_50mM_minus2.10401.10401.3	3	11.57	0	2.78E+05	M35m	(K)AASDIA	(K)A/A|S D/I A m/T E L/P/P T\H P I R(L)	m:Oxidized methionine	127.6	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
7358	dirMS_041712_NAR_50mM_minus2.7712.7712.3	3	11.57	0	1.57E+04		(K)VVQVSA	(K)V V Q|V/S A/G D S H T A A/L T D D G R(V)		111.02	633.641	1898.92	-0.0118	-6.2	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
7359	dirMS_041712_NAR_50mM_minus2.9369.9369.3	3	11.57	1	1.36E+05		(R)QEEELQ	(R)Q E/E/E/L/Q A K D E E L L/K(V)		121.4	567.9554	1701.854	-0.0025	-1.5	4.14	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
7360	dirMS_041712_NAR_120mM_plus.10447.10447.3	3	11.57	1	6.02E+05		(K)KGENYV	(K)K G E N\Y\V|Y|I/N/E A T R(H)		108.07	519.5943	1556.77	-0.002	-1.3	6.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
7361	dirMS_041712_NAR_20mM_plus.9091.9091.2	2	11.57	0	1.11E+06	M239m	(K)EITALAP	(K)E/I/T/A/L/A|P S T m K(I)	m:Oxidized methionine	132.7	589.309	1161.618	15.9923	-2.2	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
7362	dirMS_041712_NAR_30mM_plus2.20918.20918.2	2	11.57	0	2.16E+05		(K)VFSIGPV	(K)V/F|S/I/G P V F R(A)		164.43	511.2941	1021.583	-0.002	-2	9.72	57534.6	6.11	HUMAN	P14868	Aspartate--tRNA ligase, cytoplasmic
7363	dirMS_041712_NAR_40mM_plus2.14918.14918.3	3	11.57	0	1.82E+05		(K)GLPQTA	(K)G L/P/Q T A V C N L/N I T L/P A/H K(K)	C:Carbamidomethylation	154.48	649.6838	1947.048	-0.0112	-5.7	8.76	112066.5	5.59	HUMAN	B1AQT2	Ankyrin 3, node of Ranvier (Ankyrin G)
7364	dirMS_041712_NAR_50mM_plus2.20265.20285.3	3	11.57	0	1.29E+05		(R)AFIDPLG	(R)A F|I/D|P L/G L P D/R P F Y/R(H)		175.4	592.986	1776.943	0.0003	0.2	6	84557.3	6.5	HUMAN	Q04609	Glutamate carboxypeptidase 2
7365	dirMS_041712_NAR_60mM_plus.7105.7105.2	2	11.57	0	2.35E+05	M437m	(R)LESGMC	(R)L/E|S/G M Q/N m/S I/H/T\K(T)	m:Oxidized methionine	94.93	746.3495	1475.698	15.9936	-0.9	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
7366	dirMS_041712_NAR_120mM_minus.9117.9117.3	3	11.56	0	7.83E+05		(K)HTGPNS	(K)H T G P N S|P D|T/A/N D/G F V/R(L)		103.35	562.2599	1684.767	-0.0022	-1.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
7367	dirMS_041712_NAR_30mM_minus2.14821.14821.2	2	11.56	0	5.43E+04		(R)WQAVL	(R)W Q/A|V/L\A Q/T D/V R(Q)		134.45	643.846	1286.685	-0.0004	-0.3	5.84	533778	5.74	HUMAN	Q15149	Plectin
7368	dirMS_041712_NAR_30mM_minus2.17716.17716.2	2	11.56	0	1.59E+04		(R)SLAALSC	(R)S L A\A|L\S/Q/I/A\Y Q R(N)		150.98	660.8642	1320.727	-0.0059	-4.5	8.46	64225	6.66	HUMAN	E7EX44	Caldesmon
7369	dirMS_041712_NAR_30mM_minus2.18435.18435.2	2	11.56	0	1.26E+05		(K)GLGILSL	(K)G/L/G/I L/S L K(Q)		154.32	400.7655	800.524	-0.0003	-0.4	8.75	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
7370	dirMS_041712_NAR_40mM_minus2.11313.11313.3	3	11.56	0	2.99E+06		(R)VAPEEH	(R)V/A|P E E H/P V L L/T/E A/P L N/P K(A)		148.87	652.0263	1954.064	-0.0001	0	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
7371	dirMS_041712_NAR_40mM_minus2.14283.14283.3	3	11.56	0	2.72E+05		(R)DVCTELI	(R)D V|C/T/E L L/P L I K/P/Q G R(V)	C:Carbamidomethylation	168.95	580.3211	1738.952	-0.0033	-1.9	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
7372	dirMS_041712_NAR_50mM_minus2.8875.8875.3	3	11.56	1	7.29E+04		(K)TAVCDIF	(K)T A/V/C D/I/P P R G L K(M)	C:Carbamidomethylation	117.77	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
7373	dirMS_041712_NAR_60mM_minus.17320.17320.3	3	11.56	0	3.22E+05		(K)GSDHSA	(K)G S D H S A S L E|P G E L/A/E L V R(S)		156.83	622.9764	1866.919	-0.0045	-2.4	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
7374	dirMS_041712_NAR_20mM_plus.18067.18067.2	2	11.56	0	9.96E+04		(K)VDFPQD	(K)V/D\F/P Q|D Q/L T A L T/G R(I)		195.73	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
7375	dirMS_041712_NAR_20mM_plus.18858.18858.2	2	11.56	0	1.00E+05		(K)LTVYTTL	(K)L T\V|Y/T/T L/I D\V T K(G)		200.88	683.8948	1366.783	-0.0005	-0.4	5.83	42194.9	8.75	HUMAN	E7EMM4	Acid ceramidase
7376	dirMS_041712_NAR_30mM_plus2.18716.18760.2	2	11.56	0	2.59E+05		(K)AITGFDI	(K)A I|T|G/F/D/D P F S G K(T)		151.77	627.8052	1254.6	0.003	2.4	4.21	334221.3	6.44	HUMAN	P15924	Desmoplakin
7377	dirMS_041712_NAR_30mM_plus2.7087.7099.2	2	11.56	0	6.70E+05		(K)AQCPIVI	(K)A Q|C/P I V/E/R(L)	C:Carbamidomethylation	92.52	486.7542	972.493	0.008	8.2	6.05	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
7378	dirMS_041712_NAR_40mM_plus2.19955.19955.3	3	11.56	0	4.60E+05	M166m	(K)VLDFEHI	(K)V L/D F E/H F\L|P m L Q T V A K(N)	m:Oxidized methionine	187.63	635.3379	1888.004	15.9954	0.3	5.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
7379	dirMS_041712_NAR_40mM_plus2.6390.6390.2	2	11.56	0	1.96E+05		(K)TEISEMI	(K)T E|I/S/E/M N R(N)		96.38	490.2351	979.451	0.0116	11.8	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
7380	dirMS_041712_NAR_40mM_plus2.6641.6763.2	2	11.56	0	5.39E+05		(R)FFSDCK(	(R)F/F|S/D/C K(I)	C:Carbamidomethylation	99.92	402.1734	803.339	0.0003	0.3	5.84	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
7381	dirMS_041712_NAR_50mM_plus2.19366.19567.3	3	11.56	1	9.05E+05		(R)ASLEAAI	(R)A S/L/E|A/A/I A/D A E Q R G E L A I K(D)		170.58	652.6835	1956.04	-0.0037	-1.9	4.41	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
7382	dirMS_041712_NAR_60mM_plus.11361.11361.3	3	11.56	0	3.70E+05		(R)SLGTAD	(R)S L|G T/A D/V H F/E/R(K)		116.88	411.2075	1231.607	0.0014	1.1	5.3	27557.2	11.05	HUMAN	E9PB61	THO complex subunit 4
7383	dirMS_041712_NAR_40mM_minus2.8203.8203.3	3	11.55	0	1.68E+05		(R)LLEAQA	(R)L L|E|A/Q/A C/T G G I/I H P T/T G Q K(L)	C:Carbamidomethylation	128.68	665.6822	1995.033	-0.0007	-0.4	6.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
7384	dirMS_041712_NAR_50mM_minus2.7291.7291.3	3	11.55	0	1.66E+05		(R)ETPHSP	(R)E T P H S P G V|E D/A P I/A K(V)		107.98	516.5936	1547.77	-0.0038	-2.4	4.65	67446.5	5.63	HUMAN	F8VQE1	LIM domain and actin-binding protein 1
7385	dirMS_041712_NAR_60mM_minus.16106.16106.3	3	11.55	1	3.04E+04		(K)LPFPIID	(K)L/P|F/P I I D/D R N R(E)		149.15	452.5849	1355.743	-0.0029	-2.1	5.96	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
7386	dirMS_041712_NAR_20mM_plus.13980.13980.2	2	11.55	0	1.34E+05		(R)GGIVDE	(R)G G I|V|D E G A L/L/R(A)		167.83	550.3066	1099.611	-0.0047	-4.3	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
7387	dirMS_041712_NAR_20mM_plus.16845.16845.2	2	11.55	0	3.45E+05		(K)VQIAVA	(K)V Q/I\A/V|A/N/A Q E L L Q R(M)		187.37	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
7388	dirMS_041712_NAR_20mM_plus.7229.7229.2	2	11.55	0	3.74E+05	M532m M	(R)mVPAG	(R)m V/P/A G/m G A G L E/R(M)	m:Oxidized methionine	117.58	610.7907	1188.586	31.9877	-1.7	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
7389	dirMS_041712_NAR_30mM_plus2.11879.12120.2	2	11.55	0	2.15E+06		(K)STELLIR(	(K)S T|E/L|L/I/R(K)		116.03	416.2501	831.493	-0.0005	-0.6	5.72	14166.5	11.62	HUMAN	B4DEB1	Histone H3
7390	dirMS_041712_NAR_30mM_plus2.14476.14476.3	3	11.55	0	1.03E+04		(K)VNQIGS	(K)V N Q I G S V T|E/S/I/Q/A/C/K(L)	C:Carbamidomethylation	127.72	545.28	1633.821	0.0041	2.5	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
7391	dirMS_041712_NAR_40mM_plus2.20057.20062.3	3	11.55	1	5.88E+05		(K)EGGLGP	(K)E G G L/G/P/L/N/I/P L\L A D/V T R R(L)		189.8	631.0288	1891.076	-0.0041	-2.2	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
7392	dirMS_041712_NAR_40mM_plus2.7772.7772.2	2	11.55	0	4.23E+04		(R)VLNTNII	(R)V L|N T|N/I D G R(R)		105.73	501.2719	1001.537	-0.0009	-0.9	5.81	17718.4	10.99	HUMAN	P62269	40S ribosomal protein S18
7393	dirMS_041712_NAR_50mM_plus2.13646.13646.3	3	11.55	1	7.51E+05		(K)LIQEIVD	(K)L I/Q E I|V D K/S/G V V R(V)		140.07	485.9552	1455.853	-0.0019	-1.3	6.07	66105.7	7.3	HUMAN	A8MQB8	Fragile X mental retardation protein 1
7394	dirMS_041712_NAR_60mM_plus.10882.10882.3	3	11.55	1	2.49E+06		(K)TAVCDIF	(K)T/A|V C/D I/P P R G L K(M)	C:Carbamidomethylation	115.02	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
7395	dirMS_041712_NAR_60mM_plus.16778.16778.3	3	11.55	1	8.72E+05		(R)STNKGT.	(R)S T\N K G T A Y\T/F F|T/P G N L K(Q)		144.73	616.3117	1846.933	-0.0128	-7	9.7	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
7396	dirMS_041712_NAR_60mM_plus.19474.19474.3	3	11.55	1	5.90E+05		(K)TVTAMD	(K)T V|T A/M/D V/V Y A L K/R(Q)		160.52	489.6071	1466.804	0.0032	2.2	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
7397	dirMS_041712_NAR_120mM_minus.4518.4518.2	2	11.54	0	7.35E+05		(R)HSDGNL	(R)H/S|D/G N L C\V|K(V)	C:Carbamidomethylation	73.95	515.2423	1029.478	-0.0009	-0.9	6.74	7781.8	6.82	HUMAN	E9PE20	Signal recognition particle 9 kDa protein
7398	dirMS_041712_NAR_20mM_minus.13265.13265.2	2	11.54	0	8.06E+04		(K)SILFVPT	(K)S I\L/F/V/P\T S A P R(G)		183.42	594.3411	1187.678	-0.0034	-2.8	9.47	92752.5	4.76	HUMAN	P14625	Endoplasmin
7399	dirMS_041712_NAR_40mM_minus2.16065.16065.3	3	11.54	1	7.11E+05		(R)ELAILLG	(R)E L/A I/L/L/G M L D/P A E K D/E K(G)		189.47	629.0034	1884.999	-0.003	-1.6	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
7400	dirMS_041712_NAR_50mM_minus2.15632.15632.3	3	11.54	1	4.82E+05		(K)QGGLGF	(K)Q G\G L G/P M N I|P L V/S D P K R(T)		157.48	593.6566	1778.958	-0.0029	-1.6	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
7401	dirMS_041712_NAR_50mM_minus2.15960.15960.3	3	11.54	0	2.34E+04	N338n	(R)TIAGIIYE	(R)T I|A/G I I Y/E n/Y L/L S R(K)	n:N-acetylglucosamine (N)	158.85	610.3273	1625.89	203.0776	-1	5.66	154994.1	8.19	HUMAN	A3KN83	Protein strawberry notch homolog 1
7402	dirMS_041712_NAR_60mM_minus.15684.15684.3	3	11.54	1	5.41E+05	M81m	(K)EVNKFQ	(K)E V|N/K F Q m A/Y S/N L L/R(A)	m:Oxidized methionine	146.82	576.9619	1712.879	15.9923	-1.5	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
7403	dirMS_041712_NAR_60mM_minus.18815.18815.3	3	11.54	0	2.56E+05		(K)LHDNLII	(K)L H D N L\I|I/S/D/L/E N T V/K(K)		166.17	575.3117	1723.922	-0.0019	-1.1	4.54	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
7404	dirMS_041712_NAR_20mM_plus.16538.16538.2	2	11.54	0	1.71E+05		(R)LLEAQIA	(R)L L E/A\Q/I/A/T G G I I D|P K(E)		185.43	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
7405	dirMS_041712_NAR_30mM_plus2.14817.15061.2	2	11.54	0	8.87E+05		(K)NMVLFT	(K)N/M|V|L F/T/R(Q)		131.22	440.7384	880.471	-0.0014	-1.6	9.75	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1
7406	dirMS_041712_NAR_40mM_plus2.13823.13823.3	3	11.54	1	2.27E+05		(R)GDVVPK	(R)G D V/V/P K D V N/A/A/I A T I/K(T)		147.52	537.6381	1610.911	-0.0115	-7.1	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
7407	dirMS_041712_NAR_40mM_plus2.14807.14807.3	3	11.54	0	3.03E+05		(R)IEGDMI	(R)I/E|G/D M I V/C A A Y A H E L P/K(Y)	C:Carbamidomethylation	153.93	639.6498	1916.925	0.0104	5.4	4.65	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5

7408	dirMS_041712_NAR_40mM_plus2.19265.19265.3	3	11.54	1	1.93E+05		(K)TSAQVV	(K)T/S|A Q|V/V L D G L V D K I G D/V K(C)		180.37	619.6811	1857.033	-0.004	-2.2	4.43	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
7409	dirMS_041712_NAR_50mM_plus2.11294.11294.3	3	11.54	1	3.14E+05		(R)DLDRIA	(R)D L/D R I A/G\Q|V/A/A A N K(K)		126.77	481.2661	1441.776	0.008	5.5	5.96	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
7410	dirMS_041712_NAR_50mM_plus2.11497.11497.3	3	11.54	1	1.25E+06		(K)NQVAM	(K)N Q|V|A/M/N/P T/N T V F D A K R(L)		127.8	602.6354	1805.896	-0.0046	-2.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
7411	dirMS_041712_NAR_60mM_plus.16189.16189.3	3	11.54	1	1.12E+06		(K)TDKTLVL	(K)T D K T L V|L/L/M/G K(E)		141.08	406.908	1218.713	-0.0032	-2.6	8.26	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
7412	dirMS_041712_NAR_60mM_plus.8106.8214.3	3	11.54	1	6.15E+05		(R)KQSTDE	(R)K|Q S\T D\E|E|V|T/S L A/K(S)		100.87	479.2461	1435.728	-0.0037	-2.6	4.68	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
7413	dirMS_041712_NAR_120mM_minus.8831.8984.3	3	11.53	0	7.27E+05		(R)RPELEDS	(R)R P\E\L|E|D/S/T/L/R(Y)		102.42	405.8796	1215.633	-0.0085	-7	4.68	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
7414	dirMS_041712_NAR_30mM_minus2.14374.14374.2	2	11.53	0	7.55E+04		(R)TPYGASI	(R)T/P|Y/G|A/S I F\Q S/K(E)		131.18	599.8093	1198.61	0.0011	0.9	8.26	44815.8	6.62	HUMAN	B3KQ29	Transducin-like enhancer protein 4
7415	dirMS_041712_NAR_40mM_minus2.12297.12297.3	3	11.53	0	2.18E+05		(R)GAPPSSI	(R)G A/P/P S S N I E D/F H G L L/P\K(G)		155.63	593.6401	1778.907	-0.0014	-0.8	5.32	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
7416	dirMS_041712_NAR_50mM_minus2.13219.13219.3	3	11.53	1	2.73E+04		(K)VVSSSIV	(K)V/V|S S S I V D K/Y/I/G E S\A R(L)		142.6	570.6413	1709.907	0.0025	1.5	6.04	29938.9	6.07	HUMAN	H0YJC0	26S protease regulatory subunit 10B (Fragment)
7417	dirMS_041712_NAR_50mM_minus2.5188.5188.3	3	11.53	1	8.82E+04		(R)MQNDT	(R)M/Q|N D/T A E/N E/T T E K E E K(S)		86.63	632.9425	1896.813	0.0002	0.1	4.14	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
7418	dirMS_041712_NAR_60mM_minus.9373.9380.3	3	11.53	1	1.86E+05		(R)KTLDELS	(R)K\T L D\E\L|S|Q|G T T T/V K(E)		112.08	507.6079	1520.817	-0.0075	-4.9	6.07	266161	5.68	HUMAN	E9PPU0	Epiplakin
7419	dirMS_041712_NAR_20mM_plus.11418.11418.2	2	11.53	0	2.12E+05		(R)YALYDA	(R)Y A|L|Y/D A T Y E T K(E)		151.12	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
7420	dirMS_041712_NAR_20mM_plus.17104.17104.2	2	11.53	0	5.46E+05		(R)VLITTDL	(R)V/L/I/T|T D/L L A R(G)		190.23	557.8442	1114.683	-0.0019	-1.7	5.81	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
7421	dirMS_041712_NAR_30mM_plus2.13252.13314.2	2	11.53	0	8.79E+05		(K)NSGVLM	(K)N/S|G|V|L/M V/V/K(C)		123	473.7749	946.539	0.0035	3.7	8.75	9148.5	9.4	HUMAN	C9JES7	COX assembly mitochondrial protein homolog
7422	dirMS_041712_NAR_30mM_plus2.18594.18658.2	2	11.53	0	1.98E+05		(K)ELEFYLR	(K)E L/E/F/Y/L/R(K)		151.03	485.2559	969.504	0.0005	0.5	4.53	24490	10.56	HUMAN	P62241	40S ribosomal protein S8
7423	dirMS_041712_NAR_30mM_plus2.22024.22024.2	2	11.53	0	1.71E+05		(R)WQFLTL	(R)W\Q/F/L\T L/R(E)		170.9	482.2695	963.541	-0.0093	-9.7	9.75	132493.1	6.53	HUMAN	B4DER1	Leucine--tRNA ligase, cytoplasmic
7424	dirMS_041712_NAR_30mM_plus2.9017.9017.2	2	11.53	0	2.40E+05		(R)SGQGAF	(R)S G/Q|G A/F/G/N M C/R(G)	C:Carbamidomethylation	100.87	592.7504	1184.494	0	0	9.47	18988.7	11.2	HUMAN	H3BTP7	60S ribosomal protein L4 (Fragment)
7425	dirMS_041712_NAR_50mM_plus2.11517.11517.3	3	11.53	1	2.80E+06	M72m	(R)TEmENE	(R)T/E/m E N\E F V L\I/K/K(D)	m:Oxidized methionine	127.98	499.5943	1480.772	15.9968	1.2	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
7426	dirMS_041712_NAR_60mM_plus.11052.11052.3	3	11.53	1	9.67E+05		(R)KTEELEE	(R)K T E E L E E E/S/F/P E/R(S)		115.75	541.5897	1622.754	0.0001	0.1	4.2	108720.9	10.17	HUMAN	Q9Y2W1	Thyroid hormone receptor-associated protein 3
7427	dirMS_041712_NAR_60mM_plus.14809.14828.3	3	11.53	1	9.63E+04		(R)KFLDGIY	(R)K\F L D\G\I|Y|V/S E/K(G)		133.93	433.5671	1298.699	-0.0123	-9.5	6.07	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
7428	dirMS_041712_NAR_60mM_plus.16670.16670.2	2	11.53	0	8.01E+05		(R)EHALLA	(R)E H|A\L|L|A/Y T L/G V K(Q)		143.88	657.8735	1314.742	-0.0019	-1.4	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
7429	dirMS_041712_NAR_50mM_minus2.5862.5862.3	3	11.52	1	4.33E+04		(R)AIEAAP	(R)A I/E/A A/P Q E/P E Q K/R(S)		95.43	489.5922	1466.76	0.0023	1.5	4.79	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
7430	dirMS_041712_NAR_60mM_minus.12010.12010.3	3	11.52	1	2.51E+05		(R)GLAGLG	(R)G L|A/G|L G D\V/A E V R K(S)		127.02	428.9126	1284.727	-0.0038	-2.9	6.07	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
7431	dirMS_041712_NAR_20mM_plus.10689.10829.2	2	11.52	0	1.66E+05		(R)LQAEIEG	(R)L Q|A/E/I E/G L/K(G)		146.82	500.7867	1000.567	-0.0012	-1.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
7432	dirMS_041712_NAR_20mM_plus.14585.14585.2	2	11.52	0	1.40E+05		(R)FIDTTLA	(R)F I/D T T L/A|I T S R(F)		171.95	619.3413	1237.679	-0.0034	-2.7	5.84	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
7433	dirMS_041712_NAR_30mM_plus2.12025.12066.2	2	11.52	0	3.80E+05		(R)DINLDVI	(R)D I|N|L/D/V N/R(I)		116.67	479.7542	958.495	0.0059	6.1	4.21	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
7434	dirMS_041712_NAR_30mM_plus2.13237.13237.2	2	11.52	0	2.83E+05		(R)TNEGVIE	(R)T N|E|G V/I E F/R(S)		122.2	532.7727	1064.537	0.001	1	4.53	39700.2	11.49	HUMAN	Q13247	Serine/arginine-rich splicing factor 6
7435	dirMS_041712_NAR_30mM_plus2.18508.18508.2	2	11.52	0	1.65E+05		(K)QFLSQFI	(K)Q/F|L|S Q F/E/M\Q S R(K)		150.25	700.8358	1400.663	0.0016	1.2	6	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
7436	dirMS_041712_NAR_40mM_plus2.15935.15935.3	3	11.52	0	2.88E+05		(K)VAIVKP	(K)V/A/I|V K P G V|P M E I V/L/N K(E)		160.9	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
7437	dirMS_041712_NAR_40mM_plus2.16128.16148.3	3	11.52	0	4.11E+04		(K)VLISSLQ	(K)V L\I|S/S/L Q D C L H/G I/E/S K(S)	C:Carbamidomethylation	161.47	600.3172	1798.937	0.0003	0.2	5.32	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
7438	dirMS_041712_NAR_40mM_plus2.16695.17004.2	2	11.52	0	2.73E+05		(K)FLPLFDR	(K)F/L|P/L F D/R(V)		165.5	454.255	907.504	-0.0009	-1	5.84	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
7439	dirMS_041712_NAR_40mM_plus2.9967.9988.2	2	11.52	0	2.48E+05		(K)EQFAWI	(K)E Q|F/A/W/R(H)		122.88	418.706	836.405	-0.0002	-0.3	6.1	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
7440	dirMS_041712_NAR_50mM_plus2.10710.10710.3	3	11.52	1	2.43E+05		(R)LLQTSNI	(R)L/L|Q/T S N I/T/K L E Q K(K)		124.02	505.9621	1515.874	-0.0023	-1.5	8.59	20207.3	8.69	HUMAN	B1AKS5	Serine/threonine-protein kinase PAK 3 (Fragment)
7441	dirMS_041712_NAR_50mM_plus2.11230.11230.3	3	11.52	1	4.13E+05		(R)MLFKDD	(R)M/L/F/K D D Y|P S S P\P K(C)		127.05	508.9188	1524.74	0.0016	1	5.71	20685.4	9.18	HUMAN	B0QYN7	SUMO-conjugating enzyme UBC9
7442	dirMS_041712_NAR_50mM_plus2.7731.7951.3	3	11.52	0	2.10E+05		(R)DGQVIN	(R)D G\Q|V|I/N/E/T S/Q H H D D L E(-)		106.82	612.9457	1836.8	0.0231	12.6	4.28	53707.8	5.06	HUMAN	P08670	Vimentin
7443	dirMS_041712_NAR_60mM_plus.15010.15010.3	3	11.52	0	7.90E+05		(R)SCTVNIN	(R)S C/T/V/N\I/M/F G T/P Q E H R(N)	C:Carbamidomethylation	135.17	592.9433	1776.816	-0.0003	-0.1	6.47	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
7444	dirMS_041712_NAR_60mM_plus.17576.17576.3	3	11.52	0	4.55E+05		(R)FDASFF	(R)F D/A S F/F/G/V H/P/K(Q)		149.22	417.8778	1251.616	0.0032	2.5	6.74	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
7445	dirMS_041712_NAR_120mM_minus.10509.10931.2	2	11.51	1	3.38E+06		(R)VKYETEL	(R)V/K|Y|E/T E/L/A M R(Q)		113.43	620.3232	1239.64	-0.0011	-0.9	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
7446	dirMS_041712_NAR_20mM_minus.9736.9736.2	2	11.51	0	2.50E+05	M33m	(K)VAGmD	(K)V/A/G/m/D/V E|L T V E E R(N)	m:Oxidized methionine	147.53	732.355	1447.71	15.993	-1.3	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
7447	dirMS_041712_NAR_30mM_minus2.13595.13595.2	2	11.51	0	1.14E+06		(K)VMYGF	(K)V/M|Y/G\F C S V K(D)	C:Carbamidomethylation	127.72	545.7611	1090.506	0.0089	8.2	8.56	76925.9	4.46	HUMAN	A8MV58	Drebrin
7448	dirMS_041712_NAR_30mM_minus2.14477.14477.2	2	11.51	0	2.19E+05		(K)QVSVFQ	(K)Q V|S V/F Q/A M K(K)		132.58	519.2752	1037.545	-0.0017	-1.6	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
7449	dirMS_041712_NAR_50mM_minus2.12185.12185.3	3	11.51	0	1.95E+05		(K)FADEHV	(K)F/A/D E H V/P G S/P F T V K(I)		137.67	510.9256	1530.759	0.0035	2.3	5.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
7450	dirMS_041712_NAR_50mM_minus2.17661.17661.3	3	11.51	0	2.03E+05		(R)DVCTELI	(R)D V|C/T E L\L/P L I/K/P Q G R(V)	C:Carbamidomethylation	168.88	580.3212	1738.952	-0.003	-1.7	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
7451	dirMS_041712_NAR_60mM_minus.16599.16599.3	3	11.51	1	8.10E+04		(R)RDDGTG	(R)R D D G T G Q\L\L|L/P L S D/A R(K)		152.85	576.307	1726.908	-0.0018	-1	4.43	533778	5.74	HUMAN	Q15149	Plectin
7452	dirMS_041712_NAR_60mM_minus.6561.6561.3	3	11.51	1	9.19E+04		(-)MDSETD	(-)M/D/S E T/D/M/V R Q I R(A)		95.25	494.235	1480.688	0.0022	1.5	4.56	28693	5.27	HUMAN	E9PJ36	Vacuolar protein sorting-associated protein 51 homolog (Fragment)
7453	dirMS_041712_NAR_120mM_plus.20412.20412.4	4	11.51	1	2.36E+07		(K)AAIDWF	(K)A/A/I/D/W/F D G K/E F H G N I I K(V)		159.37	491.0027	1960.992	-0.0026	-1.3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
7454	dirMS_041712_NAR_20mM_plus.10487.10487.2	2	11.51	0	1.10E+05	M267m	(R)LITLEEE	(R)L I|T/L/E E E m T K(Y)	m:Oxidized methionine	145.17	611.8175	1206.629	15.9991	3.4	4.25	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
7455	dirMS_041712_NAR_20mM_plus.10990.10990.2	2	11.51	0	2.60E+04		(R)IVLQIDN	(R)I/V|L Q/I/D N A R(L)		148.23	521.3056	1041.605	-0.0012	-1.1	5.84	20842.9	5.32	HUMAN	C9JM50	Keratin, type I cytoskeletal 19 (Fragment)
7456	dirMS_041712_NAR_20mM_plus.17689.17689.2	2	11.51	0	7.13E+04		(R)AVLDALI	(R)A V|L/D A L/L|E G K(A)		193.83	514.8011	1028.599	-0.0037	-3.6	4.37	332906.7	4.86	HUMAN	E9PGC8	MAP1 light chain LC2
7457	dirMS_041712_NAR_20mM_plus.9421.9421.2	2	11.51	0	1.86E+05		(K)SVTNED	(K)S V/T/N/E/D\V/T Q\E E L G G A K(T)		136	838.9014	1676.797	-0.0018	-1.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
7458	dirMS_041712_NAR_30mM_plus2.12550.12550.2	2	11.51	0	2.27E+05		(R)SMSFQG	(R)S M|S/F/Q/G I R(Q)		118.85	463.233	925.456	0.0027	2.9	9.47	334221.3	6.44	HUMAN	P15924	Desmoplakin
7459	dirMS_041712_NAR_30mM_plus2.17716.17716.2	2	11.51	0	3.14E+05		(K)SLEDQV	(K)S L|E|D Q/V/E M L R(T)		145.83	610.3003	1219.599	-0.0054	-4.4	4.14	61161.1	4.34	HUMAN	K7ELL7	Glucosidase 2 subunit beta
7460	dirMS_041712_NAR_40mM_plus2.18273.18273.3	3	11.51	0	3.35E+05		(R)EAVELPI	(R)E A/V E L/P L/T/H F E L Y\K(Q)		173.83	563.6336	1688.889	-0.0032	-1.9	4.75	47479.5	5.09	HUMAN	P43686	26S protease regulatory subunit 6B
7461	dirMS_041712_NAR_60mM_plus.10464.10485.3	3	11.51	0	9.97E+05		(K)YAVTTG	(K)Y A|V/T/T/G D/H G I I/R(T)		112.45	434.9004	1302.68	0.0066	5	6.74	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
7462	dirMS_041712_NAR_60mM_plus.15754.15767.3	3	11.51	1	1.13E+06		(R)KSEIEYY	(R)K|S E I\E|Y|Y/A/M L A K(T)		139.77	482.5882	1445.735	0.0156	10.8	6.14	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
7463	dirMS_041712_NAR_60mM_plus.9680.9824.3	3	11.51	0	4.99E+06		(R)QSVEND	(R)Q S/V/E N D/I/H/G\L R(K)		109.7	423.2195	1267.639	0.005	4	5.32	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
7464	dirMS_041712_NAR_120mM_minus.14110.14293.3	3	11.5	2	1.13E+06		(K)VLAGDK	(K)V/L|A/G D/K/N F I T A E E L R|R(E)		131.63	611.338	1832.003	-0.003	-1.7	6.15	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
7465	dirMS_041712_NAR_30mM_minus2.14544.14683.2	2	11.5	0	4.20E+05		(K)DLAGSII	(K)D L|A|G/S I/I/G K(G)		133.1	437.2551	873.504	-0.0011	-1.2	5.84	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
7466	dirMS_041712_NAR_30mM_minus2.14734.14734.2	2	11.5	0	3.78E+05		(K)DLAGSII	(K)D L|A/G S I I G K(G)		133.23	437.2551	873.504	-0.0011	-1.2	5.84	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
7467	dirMS_041712_NAR_30mM_minus2.17508.17508.2	2	11.5	0	2.23E+05		(R)NGGQIL	(R)N G G Q|I/L I/A D/L/R(G)		149.25	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
7468	dirMS_041712_NAR_30mM_minus2.7650.7650.2	2	11.5	0	2.31E+05		(R)QDVDN	(R)Q D|V/D/N|A/S L/A/R(L)		96.17	544.7694	1088.533	-0.0016	-1.4	4.21	49709.6	5.19	HUMAN	B0YJC4	Vimentin
7469	dirMS_041712_NAR_50mM_minus2.12366.12366.3	3	11.5	0	2.32E+05		(K)AASDIA	(K)A A/S D I A/M T/E L/P P T/H P I R(L)		138.97	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
7470	dirMS_041712_NAR_50mM_minus2.13243.13243.3	3	11.5	1	5.24E+05		(K)ATLPSPD	(K)A T|L/P/S/P D K L/P G F K(M)		144.18	457.5912	1370.768	-0.0088	-6.4	8.64	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
7471	dirMS_041712_NAR_50mM_minus2.13497.13497.3	3	11.5	1	1.31E+05		(K)IDSRLEQ	(K)I D|S R L E Q|Y/T\S A/I E/G T K(S)		144.68	604.3145	1810.918	0.0108	6	4.68	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
7472	dirMS_041712_NAR_60mM_minus.11317.11317.3	3	11.5	1	9.28E+05	M232m	(R)MSmKE	(R)M S m K E V D\E Q\M|L/N\V Q/N K(N)	m:Oxidized methionine	122.78	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
7473	dirMS_041712_NAR_60mM_minus.14344.14442.3	3	11.5	1	3.16E+05		(K)KSDIDEI	(K)K S D I\D E I|V|L|V/G/G S T R(I)		139.77	530.2846	1588.854	-0.0148	-9.3	4.56	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
7474	dirMS_041712_NAR_20mM_plus.13724.13724.2	2	11.5	0	2.05E+05		(K)APILIAT	(K)A/P I/L|I|A/T|D V A S R(G)		166.67	613.8559	1226.71	-0.0058	-4.7	5.88	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
7475	dirMS_041712_NAR_20mM_plus.16751.16751.2	2	11.5	0	2.02E+05		(R)IVLLDSS	(R)I V|L|L/D S S L|E Y/K(K)		186.72	640.36	1279.714	-0.0017	-1.3	4.37	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
7476	dirMS_041712_NAR_30mM_plus2.10259.10386.2	2	11.5	0	3.62E+05		(K)LVIEEAE	(K)L/V|I|E/E A E/R(S)		107.45	479.7648	958.52	0.0019	2	4.25	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
7477	dirMS_041712_NAR_30mM_plus2.16003.16041.2	2	11.5	0	1.54E+06		(R)MGAGM	(R)M/G/A|G|M|G/F/G\L E R(M)		137.47	563.2636	1125.518	0.002	1.7	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
7478	dirMS_041712_NAR_30mM_plus2.6261.6339.2	2	11.5	0	3.88E+05		(R)QIDNPD	(R)Q I|D/N/P/D|Y/K(G)		87.23	496.7371	992.468	-0.0014	-1.4	4.21	28545.1	4.5	HUMAN	K7EJB9	Calreticulin (Fragment)
7479	dirMS_041712_NAR_40mM_plus2.17547.17547.3	3	11.5	0	1.65E+05		(R)VYAILTH	(R)V Y/A I\L T H G I/F S G/P A I/S R(I)		169.45	601.3376	1801.996	0.0023	1.3	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
7480	dirMS_041712_NAR_50mM_plus2.13836.13836.3	3	11.5	0	1.48E+06		(K)DLAGCII	(K)D/L|A|G C I/H G L S N V K(L)	C:Carbamidomethylation	140.47	461.9061	1383.705	-0.0012	-0.8	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
7481	dirMS_041712_NAR_50mM_plus2.14297.14297.3	3	11.5	0	1.11E+06		(R)IVATKPL	(R)I/V|A/T K/P L Y V|A L A/Q R(K)		143.7	514.9831	1542.937	-0.0019	-1.2	9.99	65918.2	9.74	HUMAN	E7EQV3	Polyadenylate-binding protein 1
7482	dirMS_041712_NAR_60mM_plus.17861.17878.3	3	11.5	1	1.90E+05		(K)LKEVFSN	(K)L K E V F S/M/A/G\V/V V/R(A)		150.6	478.9419	1434.814	-0.0026	-1.8	8.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
7483	dirMS_041712_NAR_60mM_plus.7421.7421.3	3	11.5	0	5.01E+05		(R)SSGHSSS	(R)S S/G H S S S E\L/S|P/D A V E K(A)		96.95	539.584	1616.74	-0.0024	-1.5	4.65	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
7484	dirMS_041712_NAR_60mM_plus.9009.9138.3	3	11.5	0	1.59E+06		(K)EFHLNES	(K)E F H\L N\E/S/G D/P S/S K(S)		105.52	482.8882	1446.65	0.0005	0.3	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
7485	dirMS_041712_NAR_30mM_minus2.5483.5483.2	2	11.49	0	7.97E+05	M139m	(R)LmDQNI	(R)L/m/D/Q/N L K(C)	m:Oxidized methionine	84.67	439.2266	861.45	15.9961	1.3	5.84	26611.3	4.47	HUMAN	A6NL28	Putative tropomyosin alpha-3 chain-like protein
7486	dirMS_041712_NAR_50mM_minus2.9539.9539.3	3	11.49	1	3.07E+05		(R)ALEEAM	(R)A L|E E/A/M/E/Q K|A E L E R(L)		122.18	549.6072	1646.805	0.0016	1	4.33	227783.5	5.5	HUMAN	P35579	Myosin-9
7487	dirMS_041712_NAR_50mM_minus2.9745.9745.3	3	11.49	0	1.99E+05	M147m	(K)LQmEAP	(K)L/Q|m/E A P H\I I V G T/P G R(V)	m:Oxidized methionine	124.25	545.6267	1618.873	15.9922	-1.7	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
7488	dirMS_041712_NAR_60mM_minus.9041.9041.3	3	11.49	1	1.94E+06	M227m M	(R)mQKEIT	(R)m Q K E I T A/L|A|P/S T m K(I)	m:Oxidized methionine	109.72	527.6044	1548.812	31.9862	-2.3	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
7489	dirMS_041712_NAR_120mM_plus.17430.17430.4	4	11.49	2	2.04E+06		(R)NLKASLE	(R)N L|K/A S/L E/N S\L R E V E/A R(Y)		143.85	458.0016	1828.988	-0.003	-1.6	6.23	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
7490	dirMS_041712_NAR_120mM_plus.9660.9740.4	4	11.49	1	3.49E+06		(R)STGKGI	(R)S T G K G\I\V/E/F/A/S K/P A A R(K)		104.22	405.4784	1618.891	0.0006	0.4	9.99	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
7491	dirMS_041712_NAR_20mM_plus.16724.16759.2	2	11.49	0	2.12E+05		(R)IVLLDSS	(R)I/V|L|L/D/S S L\E Y K(K)		186.72	640.36	1279.714	-0.0017	-1.3	4.37	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
7492	dirMS_041712_NAR_20mM_plus.17107.17107.2	2	11.49	0	9.48E+04		(R)AVLVDLI	(R)A V\L V/D/L/E/P/G T M D S V R(S)		189.43	801.414	1601.82	0.0004	0.2	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
7493	dirMS_041712_NAR_20mM_plus.8103.8103.2	2	11.49	0	4.05E+05	M239m	(K)EVDEQm	(K)E V/D/E/Q/m L/N V/Q/N K(N)	m:Oxidized methionine	125.13	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
7494	dirMS_041712_NAR_30mM_plus2.10323.10323.2	2	11.49	0	2.86E+05		(R)LNQDQL	(R)L/N|Q/D/Q L\D A V/S\K(Y)		107.42	615.819	1230.632	-0.0017	-1.4	4.21	20235.4	6.77	HUMAN	E9PLA9	Caprin-1 (Fragment)
7495	dirMS_041712_NAR_30mM_plus2.13041.13323.2	2	11.49	0	1.43E+06		(K)FSVSPV	(K)F/S|V/S/P|V V/R(V)		122.87	445.759	890.509	0.0013	1.5	9.75	96306.4	6.41	HUMAN	P13639	Elongation factor 2
7496	dirMS_041712_NAR_30mM_plus2.18004.18004.2	2	11.49	0	2.34E+05		(R)QITLNDI	(R)Q I/T/L/N/D L/P V/G R(S)		147.82	613.3465	1225.69	-0.0042	-3.4	5.84	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
7497	dirMS_041712_NAR_30mM_plus2.19866.19922.2	2	11.49	1	4.34E+05		(K)EKLEATI	(K)E K L E A\T/I\N\E|L|V(-)		158.22	629.8458	1258.689	-0.0046	-3.6	4.25	9680	5.77	HUMAN	B1ALW1	Thioredoxin
7498	dirMS_041712_NAR_30mM_plus2.6720.6765.2	2	11.49	0	2.64E+05		(R)FQTMEE	(R)F/Q|T/M/E|E/K(K)		89.95	456.7106	912.413	0.0008	0.9	4.53	40551.6	10.15	HUMAN	G5E9G0	60S ribosomal protein L3
7499	dirMS_041712_NAR_50mM_plus2.10228.10228.3	3	11.49	0	3.81E+05		(R)NSNLVG	(R)N S|N/L/V/G A A/H/E E L Q Q S R(I)		120.75	584.9601	1752.862	0.0034	1.9	5.4	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
7500	dirMS_041712_NAR_50mM_plus2.21360.21360.3	3	11.49	1	4.92E+05	M145m	(R)GVmLA	(R)G V|m\L A/V D A V/I\A E L K K(Q)	m:Oxidized methionine	182.35	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
7501	dirMS_041712_NAR_50mM_plus2.9175.9260.3	3	11.49	1	7.57E+05	M239m	(R)MQKEIT	(R)M Q|K E I T A\L|A|P S T m/K(I)	m:Oxidized methionine	115.63	522.2726	1548.812	15.9908	-2.6	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
7502	dirMS_041712_NAR_30mM_minus2.12518.12518.2	2	11.48	0	5.00E+05		(R)GQVVSL	(R)G Q|V/V|S L I/R(M)		122.23	436.2706	871.536	-0.0021	-2.4	9.75	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
7503	dirMS_041712_NAR_50mM_minus2.11480.11480.3	3	11.48	1	9.59E+04		(R)LLIVSTT	(R)L L|I/V/S/T T/P Y S/E K D T K(Q)		133.12	565.6428	1694.921	-0.0072	-4.3	6.07	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
7504	dirMS_041712_NAR_50mM_minus2.13647.13647.3	3	11.48	0	4.59E+04		(K)MLDAED	(K)M/L/D/A\E D I V N T A/R P D E K(A)		144.98	606.2965	1816.875	0.0004	0.2	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
7505	dirMS_041712_NAR_50mM_minus2.16934.17014.3	3	11.48	0	1.44E+05		(K)TVSGVN	(K)T V|S/G|V/N G P L V/I/L D H V K(V)		164.98	549.9835	1647.943	-0.0069	-4.2	6.41	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
7506	dirMS_041712_NAR_50mM_minus2.18190.18190.3	3	11.48	0	1.53E+06		(K)ALESPER	(K)A L|E/S/P E R P/F L A I/L/G G A K(V)		173.87	590.3356	1768.996	-0.0033	-1.9	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
7507	dirMS_041712_NAR_50mM_minus2.9134.9134.3	3	11.48	0	1.99E+05		(K)VGQEIE	(K)V/G/Q/E I E/V R P G/I\V/S K(D)		120.43	504.2902	1510.859	-0.0027	-1.8	6.11	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
7508	dirMS_041712_NAR_60mM_minus.6528.6528.3	3	11.48	1	7.68E+03		(R)KTGQAP	(R)K\T G/Q A P G\Y/S|Y T/A A N K(N)		94.83	519.5963	1556.77	0.004	2.6	9.53	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
7509	dirMS_041712_NAR_60mM_minus.9091.9091.3	3	11.48	1	1.62E+05	M232m M	(R)MSmKE	(R)M/S m K E V\D E/Q\m|L/N/V Q N K(N)	m:Oxidized methionine	110.57	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
7510	dirMS_041712_NAR_120mM_plus.9792.9792.3	3	11.48	0	9.06E+05		(R)HGESAV	(R)H G E S A|W\N/L E N R(F)		104.47	438.2077	1312.603	0.0057	4.3	5.4	28917.5	6.68	HUMAN	P18669	Phosphoglycerate mutase 1
7511	dirMS_041712_NAR_20mM_plus.13876.13876.2	2	11.48	0	1.34E+05		(R)GGIVDE	(R)G G I|V/D|E G/A L L/R(A)		167.83	550.3066	1099.611	-0.0047	-4.3	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
7512	dirMS_041712_NAR_20mM_plus.17960.17960.2	2	11.48	0	1.12E+05		(K)VDFPQD	(K)V D/F/P Q D\Q L T A/L/T G R(I)		195.37	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
7513	dirMS_041712_NAR_20mM_plus.19228.19228.2	2	11.48	0	1.70E+04		(R)ALIAGG	(R)A L I|A/G/G/G A|P E I E L A L R(L)		203.82	775.9467	1550.89	-0.0039	-2.5	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
7514	dirMS_041712_NAR_30mM_plus2.10343.10468.2	2	11.48	0	5.36E+04		(K)TAVCDIF	(K)T A|V|C/D I/P|P R(G)	C:Carbamidomethylation	108.98	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
7515	dirMS_041712_NAR_30mM_plus2.13698.13737.2	2	11.48	0	6.12E+05		(R)IAAQTLL	(R)I/A|A|Q|T L/L/G T A K(M)		124.75	543.8267	1086.652	-0.0056	-5.2	8.75	14626.5	7.07	HUMAN	B5MD87	Pyrroline-5-carboxylate reductase 3
7516	dirMS_041712_NAR_30mM_plus2.19429.19429.2	2	11.48	0	1.85E+04		(K)MNEFLE	(K)M N|E|F\L/E N F E K(N)		155.87	650.7974	1300.588	-0.0003	-0.2	4.25	28580.2	9.35	HUMAN	Q9UFN0	Protein NipSnap homolog 3A

7517	dirMS_041712_NAR_30mM_plus2.5951.5951.2	2	11.48	0	3.25E+04		(R)LEGGSG	(R)L E|G|G\S G/G D S E/V Q/R(T)		85.37	645.797	1290.592	-0.0053	-4.1	4.14	44954.5	8.44	HUMAN	A8K3Z3	26S protease regulatory subunit 8
7518	dirMS_041712_NAR_50mM_plus2.20161.20161.3	3	11.48	1	1.14E+05		(R)FLIPVLN	(R)F L|I/P/V L N G L E K K(E)		174.58	457.6182	1370.841	-0.0006	-0.4	8.59	142001.7	5.82	HUMAN	Q92797	Symplekin
7519	dirMS_041712_NAR_60mM_plus.11466.11548.3	3	11.48	1	1.25E+06		(K)FGQYNK	(K)F/G/Q|Y N K E D|P/T S F R(L)		117.23	530.2507	1588.739	-0.0015	-0.9	6.07	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
7520	dirMS_041712_NAR_60mM_plus.11687.11687.3	3	11.48	0	2.19E+05		(K)TGNLGN	(K)T/G\N/L/G N/V V/H I E/R(F)		118.37	436.9042	1308.702	-0.0038	-2.9	6.41	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
7521	dirMS_041712_NAR_60mM_plus.15728.15747.3	3	11.48	1	4.04E+05		(K)KSDIDEI	(K)K\S D I D E\I\V\L|V/G/G S T/R(I)		138.4	530.2831	1588.854	-0.0193	-12.2	4.56	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
7522	dirMS_041712_NAR_20mM_minus.12279.12295.2	2	11.47	0	4.28E+05	M73m	(R)AVLVDLI	(R)A V L\V|D L|E|P/G T m D S V R(S)	m:Oxidized methionine	172.15	809.4088	1601.82	15.99	-3	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
7523	dirMS_041712_NAR_20mM_minus.6400.6400.2	2	11.47	0	1.57E+05		(R)VLADPSI	(R)V L|A/D/P S D D/T/K(G)		107.4	530.7615	1060.516	0	0	3.93	266161	5.68	HUMAN	E9PPU0	Epiplakin
7524	dirMS_041712_NAR_30mM_minus2.19898.19898.2	2	11.47	0	1.47E+06		(R)LFFLQVK	(R)L F|F\L/Q V K(E)		167.23	447.7757	894.545	-0.0006	-0.7	8.75	71218.8	6.3	HUMAN	A7YIJ8	Radixin
7525	dirMS_041712_NAR_50mM_minus2.12757.12757.3	3	11.47	1	3.86E+05		(K)NTVELLV	(K)N T|V|E/L/L/V E/D K G N Q V Y R(C)		140.47	626.3309	1876.976	0.0018	1	4.68	258215.9	5.48	HUMAN	E7EN95	Filamin-B
7526	dirMS_041712_NAR_50mM_minus2.14962.14962.3	3	11.47	0	4.22E+05		(K)IAILTCPF	(K)I/A\I L\T/C/P F E/P P K/P K(T)	C:Carbamidomethylation	153.37	537.6375	1610.898	0.0005	0.3	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
7527	dirMS_041712_NAR_60mM_minus.14930.14930.3	3	11.47	0	2.66E+05		(K)YYITIIDA	(K)Y Y I T/I/I D/A/P G H/R(D)		142.87	473.5815	1418.743	-0.0127	-9	6.74	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
7528	dirMS_041712_NAR_120mM_plus.12642.12642.3	3	11.47	1	9.12E+05		(K)VKLEAEI	(K)V K L E A\E|I|A/T/Y R(R)		120.07	431.5774	1292.721	-0.0032	-2.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
7529	dirMS_041712_NAR_20mM_plus.13547.13996.2	2	11.47	0	2.84E+05	M98m	(R)TLTIVDT	(R)T L|T|I|V/D T G I G m/T K(A)	m:Oxidized methionine	167.02	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
7530	dirMS_041712_NAR_30mM_plus2.19938.19938.2	2	11.47	0	2.17E+05		(K)GFAFVQ	(K)G F|A\F/V/Q/Y/V/N E R(N)		157.67	665.3326	1329.659	-0.0007	-0.5	6	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
7531	dirMS_041712_NAR_30mM_plus2.20221.20221.2	2	11.47	0	1.71E+05		(K)NIEDVIA	(K)N I|E|D V I/A Q/G I\G K(L)		160.45	628.8445	1256.685	-0.0028	-2.2	4.37	9098.8	4.38	HUMAN	H0YDD8	60S acidic ribosomal protein P2 (Fragment)
7532	dirMS_041712_NAR_30mM_plus2.6183.6183.2	2	11.47	0	1.67E+05		(K)VSDYEM	(K)V/S|D/Y/E/M/K(L)		86.68	436.1974	871.387	0.0009	1.1	4.37	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
7533	dirMS_041712_NAR_30mM_plus2.9501.9501.2	2	11.47	0	2.55E+05		(R)LAAVDV	(R)L/A|A|V|D V/S A R(A)		103.58	451.2545	901.51	-0.0084	-9.4	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin
7534	dirMS_041712_NAR_40mM_plus2.19719.19777.3	3	11.47	1	4.44E+05		(R)ILDDDTI	(R)I/L\D/D/D T/I/I/T T L E N L K R(E)		185.12	625.0111	1873.028	-0.0089	-4.8	4.23	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
7535	dirMS_041712_NAR_50mM_plus2.10599.10599.3	3	11.47	0	5.07E+05		(K)MIVDPV	(K)M/I/V D/P V/E/P H G E M/K(F)		123.22	494.5783	1481.713	0.0076	5.2	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
7536	dirMS_041712_NAR_50mM_plus2.13150.13150.3	3	11.47	0	3.85E+05		(K)VQASLA	(K)V Q|A/S L A A N T/F/T\I T G H A/E T K(Q)		137.68	654.0087	1960.013	-0.0019	-1	6.72	11802.2	5.6	HUMAN	D6RDG3	Transcription factor BTF3 (Fragment)
7537	dirMS_041712_NAR_50mM_plus2.20426.20448.3	3	11.47	1	4.12E+05		(R)VISGVLC	(R)V I|S G V L/Q L G/N I/V/F K K(E)		176.1	539.0011	1614.994	-0.0054	-3.3	10	227783.5	5.5	HUMAN	P35579	Myosin-9
7538	dirMS_041712_NAR_50mM_plus2.7652.7652.3	3	11.47	1	1.64E+05		(K)VDDSSEI	(K)V/D/D/S S E D K/T E F T V K(N)		106.45	533.9169	1599.738	-0.0023	-1.4	4.11	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
7539	dirMS_041712_NAR_40mM_minus2.13628.13628.3	3	11.46	1	3.98E+05		(R)VTFSGLF	(R)V T|F/S/G/L R D T V T/P G E L L K(A)		164.73	611.6742	1833.012	-0.0036	-2	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
7540	dirMS_041712_NAR_50mM_minus2.14922.14922.3	3	11.46	1	2.72E+05		(K)NIYVLQE	(K)N I/Y V/L Q/E L D/N P G A K R(I)		152.63	577.3116	1729.923	-0.0029	-1.7	6.07	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
7541	dirMS_041712_NAR_50mM_minus2.15513.15513.3	3	11.46	0	4.57E+05		(R)DGLAFN	(R)D G L/A/F/N/A|L/I/H/R(H)		155.65	409.5594	1226.664	-0.0004	-0.3	6.74	146974	5.55	HUMAN	C9JRP8	Spectrin beta chain, non-erythrocytic 4
7542	dirMS_041712_NAR_60mM_minus.15661.15661.3	3	11.46	1	5.60E+05	M81m	(K)EVNKFQ	(K)E V|N K F Q/m A/Y/S/N L L R(A)	m:Oxidized methionine	146.78	576.9619	1712.879	15.9923	-1.5	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
7543	dirMS_041712_NAR_60mM_minus.16103.16512.3	3	11.46	1	7.09E+05		(K)EIIDPVLI	(K)E I|I/D P V/L D/R I R(K)		151.38	446.9287	1338.774	-0.0024	-1.8	4.56	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
7544	dirMS_041712_NAR_120mM_plus.25672.25672.3	3	11.46	1	4.77E+05		(R)GVMLAV	(R)G V/M|L/A V/D A V/I/A E L K K(Q)		193.27	519.6402	1556.908	-0.002	-1.3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
7545	dirMS_041712_NAR_20mM_plus.13593.13593.2	2	11.46	0	5.50E+04		(K)IFVGGLS	(K)I F|V/G G|L S P D T\P E E K(I)		165.28	744.8731	1488.758	-0.0191	-12.8	4.14	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
7546	dirMS_041712_NAR_20mM_plus.19358.19358.3	3	11.46	0	2.32E+05		(R)LAGTQP	(R)L A G T Q P L E|V L/E/A/V Q R(S)		204.48	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
7547	dirMS_041712_NAR_20mM_plus.7779.7779.2	2	11.46	0	8.55E+04		(K)AQAAAF	(K)A Q/A\A|A/P A S V/P A Q A P K(R)		123.6	689.3745	1377.748	-0.0068	-4.9	8.8	17808.8	11.77	HUMAN	P47914	60S ribosomal protein L29
7548	dirMS_041712_NAR_30mM_plus2.16925.16925.2	2	11.46	0	3.58E+05		(K)SNQQLV	(K)S N Q/Q|L/V/D/I/I E/K(V)		141.33	643.8504	1286.695	-0.0015	-1.2	4.37	22568.6	6.35	HUMAN	B3KQ25	Proteasome activator complex subunit 3
7549	dirMS_041712_NAR_30mM_plus2.19112.19254.2	2	11.46	0	1.14E+06		(R)SSIAGLL	(R)S S|I|A/G L/L/L/K(A)		155.03	451.2894	901.572	-0.0002	-0.2	8.47	533778	5.74	HUMAN	Q15149	Plectin
7550	dirMS_041712_NAR_30mM_plus2.8813.8872.2	2	11.46	0	3.99E+05		(K)ITSEIPQT	(K)I/T|S/E|I|P Q T E R(M)		100.2	587.3094	1173.611	0.0005	0.5	4.53	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
7551	dirMS_041712_NAR_40mM_plus2.18328.18328.3	3	11.46	1	1.07E+05		(K)MFEIVFE	(K)M/F|E\I V F E D/P K I P G E K(Q)		174.38	593.6385	1778.903	-0.0024	-1.3	4.41	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
7552	dirMS_041712_NAR_50mM_plus2.19842.19842.3	3	11.46	1	2.72E+05		(K)DRDVTF	(K)D R D V T\F|S|P A|T I/E N E L I K(F)		172.65	650.0048	1948.002	-0.0024	-1.2	4.32	8027.1	8.38	HUMAN	H7C2D6	Mesencephalic astrocyte-derived neurotrophic factor (Fragment)
7553	dirMS_041712_NAR_50mM_plus2.19995.19995.3	3	11.46	1	1.59E+05		(K)EIEELKEI	(K)E I E E L K E L L/P/E/I R(E)		173.57	537.6393	1610.9	0.0034	2.1	4.33	30121.3	4.2	HUMAN	E9PRH9	Nuclear autoantigenic sperm protein (Fragment)
7554	dirMS_041712_NAR_50mM_plus2.7097.7097.3	3	11.46	0	3.21E+05	T374t	(R)TAAtLAT	(R)T|A|A t L/A/T H E L/R(A)	t:N-acetylglucosamine (T)	103.07	462.9074	1183.643	203.0647	-10.6	6.41	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
7555	dirMS_041712_NAR_50mM_plus2.9015.9015.3	3	11.46	1	1.62E+05		(R)LGAAPE	(R)L/G/A\A/P E E E S A Y V A G E/K R(Q)		114.3	592.9628	1776.876	-0.0024	-1.4	4.5	30276.7	5	HUMAN	F2Z2K0	NSFL1 cofactor p47
7556	dirMS_041712_NAR_60mM_plus.13822.13822.3	3	11.46	0	1.56E+06		(K)LAQANG	(K)L/A|Q/A/N G W/G V/M V S H R(S)		129.07	509.2606	1525.769	-0.002	-1.3	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
7557	dirMS_041712_NAR_60mM_plus.19465.19465.3	3	11.46	1	4.46E+04		(R)SLADIAR	(R)S L|A/D I/A R/E/E A S\N F R(S)		159.53	526.9346	1578.787	0.0022	1.4	4.68	20458.8	4.99	HUMAN	G3V4X5	Proteasome subunit alpha type-3
7558	dirMS_041712_NAR_20mM_minus.11162.11162.2	2	11.45	0	2.60E+05		(K)LSELEAA	(K)L/S/E|L/E A A L/Q R(A)		159.42	565.3134	1129.621	-0.0016	-1.5	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
7559	dirMS_041712_NAR_20mM_minus.9759.9759.2	2	11.45	0	2.50E+05	M33m	(K)VAGmD	(K)V A/G m/D V/E/L/T V E\E R(N)	m:Oxidized methionine	147.53	732.355	1447.71	15.993	-1.3	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
7560	dirMS_041712_NAR_40mM_minus2.6169.6169.2	2	11.45	0	1.51E+05		(K)AQYEDI	(K)A Q|Y/E/D\I A N/R(S)		101.52	540.2599	1079.512	0.0009	0.8	4.37	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
7561	dirMS_041712_NAR_50mM_minus2.17883.17883.3	3	11.45	1	9.75E+03		(K)TFVNITP	(K)T F/V N/I/T|P A E V G V L V/G K D/R(S)		170.58	639.0247	1915.065	-0.0052	-2.7	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
7562	dirMS_041712_NAR_120mM_plus.14579.14580.3	3	11.45	1	1.47E+06		(R)KFLDGIY	(R)K F L D G\I|Y/V/S E/K(G)		130.58	433.5709	1298.699	-0.0009	-0.7	6.07	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
7563	dirMS_041712_NAR_120mM_plus.20405.20406.4	4	11.45	2	6.12E+05		(K)LTVEDLE	(K)L/T\V/E/D/L E K E R D F Y F G/K(L)		160.78	498.0043	1988.996	-0.001	-0.5	4.51	30169.7	5.02	HUMAN	Q15691	Microtubule-associated protein RP/EB family member 1
7564	dirMS_041712_NAR_20mM_plus.8343.8343.2	2	11.45	0	1.06E+05		(K)TAVCDIF	(K)T A/V|C/D|I/P|P R(G)	C:Carbamidomethylation	127.63	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
7565	dirMS_041712_NAR_30mM_plus2.13779.13822.2	2	11.45	0	7.37E+05		(K)LGIYEAN	(K)L/G|I/Y E/A M K(I)		125.47	462.7408	924.486	-0.0116	-12.5	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
7566	dirMS_041712_NAR_30mM_plus2.14692.14692.2	2	11.45	0	3.22E+05		(R)YQETFN	(R)Y/Q|E|T F N V/I/E/R(C)		129.92	649.8225	1298.638	0.0002	0.1	4.53	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
7567	dirMS_041712_NAR_40mM_plus2.9041.9041.2	2	11.45	0	1.94E+05		(K)LQQWYI	(K)L/Q|Q|W/Y/R(E)		115.2	447.2352	893.463	0.0003	0.3	8.75	12797.5	10.58	HUMAN	K7EIL4	Glucose-6-phosphate isomerase (Fragment)
7568	dirMS_041712_NAR_50mM_plus2.10763.10763.3	3	11.45	1	2.46E+06		(R)MQKEIT	(R)M Q K E I T A|L/A|P/S/T M K(I)		124.03	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
7569	dirMS_041712_NAR_50mM_plus2.11486.11486.3	3	11.45	0	4.19E+05		(K)GFVEFA	(K)G F|V/E F A A/K/P/P A/R(K)		127.83	430.5716	1289.7	0.0002	0.1	8.75	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
7570	dirMS_041712_NAR_50mM_plus2.14705.14750.3	3	11.45	1	8.16E+05	M85m	(K)TVTAmD	(K)T\V|T/A/m D V/V/Y/A L K R(Q)	m:Oxidized methionine	145.5	494.9387	1466.804	15.998	2.1	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
7571	dirMS_041712_NAR_60mM_plus.12332.12332.3	3	11.45	1	6.83E+05		(R)YGEPSE	(R)Y/G|E|P S E V/F I\N R D R(G)		121.23	527.9264	1581.766	-0.0009	-0.6	4.68	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
7572	dirMS_041712_NAR_60mM_plus.16657.16657.3	3	11.45	1	7.16E+05		(R)STNKGT.	(R)S T N K G T A Y\T|F/F/T/P G N L K(Q)		144.52	616.3117	1846.933	-0.0128	-7	9.7	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
7573	dirMS_041712_NAR_120mM_minus.13274.13274.4	4	11.44	1	7.94E+05		(K)SVHSSVI	(K)S V H S S V|P/L/L/N S K D/P I D R(I)		127	466.7525	1863.992	-0.0041	-2.2	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
7574	dirMS_041712_NAR_120mM_minus.8063.8063.3	3	11.44	1	7.83E+05		(K)IQDKEGI	(K)I Q/D K E G\I/P/P/D Q Q R(L)		97.97	508.5981	1523.781	-0.0015	-1	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
7575	dirMS_041712_NAR_30mM_minus2.9070.9089.2	2	11.44	0	1.36E+05	M328m	(K)ALmDEV	(K)A/L|m/D E V|V K(A)	m:Oxidized methionine	103.57	460.7407	904.481	15.9933	-1.8	4.37	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
7576	dirMS_041712_NAR_50mM_minus2.12628.12628.3	3	11.44	0	6.48E+05		(K)AGVVGF	(K)A/G\V|V/G/P E L H E Q L L S A/E K(A)		139.3	592.9866	1776.949	-0.0038	-2.1	4.75	533778	5.74	HUMAN	Q15149	Plectin
7577	dirMS_041712_NAR_50mM_minus2.14683.14830.3	3	11.44	1	1.72E+06		(K)AGTQIEI	(K)A G/T|Q/I/E/N I D/E D F R D G L/K(L)		152.02	640.9832	1920.93	0.0053	2.8	4.11	59872.5	4.85	HUMAN	F5GXS2	Alpha-actinin-4
7578	dirMS_041712_NAR_50mM_minus2.14684.14831.3	3	11.44	1	1.72E+06		(K)AGTQIEI	(K)A G/T|Q/I|E/N I/D E D F R D G L K(L)		152.02	640.9832	1920.93	0.0053	2.8	4.11	59872.5	4.85	HUMAN	F5GXS2	Alpha-actinin-4
7579	dirMS_041712_NAR_50mM_minus2.15673.15673.3	3	11.44	0	1.75E+05		(R)QVVQGI	(R)Q V|V/Q|G L\L S E T Y/L E A H/R(I)		156.95	614.9953	1842.971	0.0005	0.3	5.4	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
7580	dirMS_041712_NAR_50mM_minus2.9660.9660.3	3	11.44	0	3.15E+05		(R)EALLSSA	(R)E A|L\L/S/S A/V D H G S D E V K(F)		123.72	552.9403	1656.807	-0.0012	-0.7	4.31	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
7581	dirMS_041712_NAR_120mM_plus.8036.8036.3	3	11.44	2	2.08E+05	M53m	(K)LTDCVV	(K)L/T/D/C V/V m/R D P A S K R(S)	C:Carbamidomethylation m:Oxid	95.88	555.2807	1647.831	15.997	1.3	8.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
7582	dirMS_041712_NAR_120mM_plus.9514.9514.3	3	11.44	0	3.32E+05		(K)QEYDES	(K)Q E Y D E/S/G P S\I/V/H/R(K)		102.88	506.2393	1516.703	0.0007	0.5	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
7583	dirMS_041712_NAR_120mM_plus.9996.9996.3	3	11.44	1	2.90E+06		(R)LQAEIEG	(R)L/Q|A E/I/E/G L/K G Q R(A)		106.25	447.9207	1341.748	-0.0009	-0.7	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
7584	dirMS_041712_NAR_20mM_plus.10445.10445.2	2	11.44	0	1.04E+05		(K)VQISPDS	(K)V Q\I/S/P D/S G G L/P E R(S)		144.55	677.8458	1354.696	-0.0118	-8.7	4.37	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
7585	dirMS_041712_NAR_20mM_plus.11557.11557.2	2	11.44	0	1.46E+05		(K)LITPAVV	(K)L I|T/P A V V S E/R(L)		151.45	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
7586	dirMS_041712_NAR_20mM_plus.17668.17701.2	2	11.44	0	8.14E+04		(R)TTLLPGL	(R)T/T|L/L/P G L L/K(T)		193.85	478.3131	955.619	0.0003	0.3	8.41	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
7587	dirMS_041712_NAR_30mM_plus2.12031.12076.2	2	11.44	0	6.57E+05		(K)GCGTVL	(K)G/C|G T|V/L/L/S/G/P R(K)	C:Carbamidomethylation	116.2	558.7944	1116.583	-0.0015	-1.3	9.75	14643	11.93	HUMAN	F8VUA6	60S ribosomal protein L18 (Fragment)
7588	dirMS_041712_NAR_30mM_plus2.17366.17366.3	3	11.44	0	1.07E+06		(R)ASLEAAI	(R)A S L E A A\I/A/D/A E/Q/R(G)		144.33	448.8963	1344.675	-0.001	-0.8	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
7589	dirMS_041712_NAR_30mM_plus2.19373.19373.2	2	11.44	0	1.15E+05		(K)VQIAVA	(K)V Q/I/A/V/A/N A/Q/E L L Q R(M)		155.63	776.9425	1552.881	-0.0028	-1.8	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
7590	dirMS_041712_NAR_30mM_plus2.20493.20493.2	2	11.44	0	9.21E+04		(K)TENLLGS	(K)T E|N|L|L/G S Y F/P K(K)		161.27	634.8311	1268.652	0.0028	2.2	5.66	28772.3	6.28	HUMAN	A6NJG9	Proteasome activator complex subunit 1
7591	dirMS_041712_NAR_40mM_plus2.13407.13407.3	3	11.44	0	2.53E+05		(R)LSAMLV	(R)L S/A\M L V/P V T/P E V K P K(R)		145.73	536.9848	1608.939	0.0005	0.3	8.59	31524.1	4.5	HUMAN	P82970	High mobility group nucleosome-binding domain-containing protein 5
7592	dirMS_041712_NAR_40mM_plus2.19333.19333.3	3	11.44	0	1.75E+05		(R)LQQAQL	(R)L Q/Q/A Q\L/Y/P I A/I F I K P\K(S)		180.67	624.3737	1871.115	-0.0088	-4.7	9.7	94175.4	6.59	HUMAN	Q5JUW8	Discs, large homolog 3 (Neuroendocrine-dlg, Drosophila)
7593	dirMS_041712_NAR_50mM_plus2.10043.10216.3	3	11.44	0	6.15E+05		(K)VGQEIE	(K)V/G|Q|E I E/V R/P G I V/S K(D)		121.05	504.2907	1510.859	-0.0012	-0.8	6.11	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
7594	dirMS_041712_NAR_50mM_plus2.13609.13761.3	3	11.44	1	1.04E+06		(R)IQLVEEE	(R)I/Q|L/V/E E E L D/R A Q E/R(L)		140.12	576.6349	1727.892	-0.0021	-1.2	4.25	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
7595	dirMS_041712_NAR_60mM_plus.15225.15225.3	3	11.44	0	4.29E+05		(-)MVNHFI	(-)M/V N|H F I A E/F/K(R)		137.47	412.5464	1235.624	0.0005	0.4	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
7596	dirMS_041712_NAR_120mM_minus.17758.17875.3	3	11.43	1	8.28E+05		(R)RAPFDLI	(R)R A\P F D\L|F E/N/R(K)		152.73	422.2193	1264.643	0.0001	0	6.07	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
7597	dirMS_041712_NAR_20mM_minus.12374.12374.2	2	11.43	0	5.67E+05	M73m	(R)AVLVDLI	(R)A V L/V|D\L/E|P G T\m D S V R(S)	m:Oxidized methionine	172.47	809.4088	1601.82	15.99	-3	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
7598	dirMS_041712_NAR_60mM_minus.17937.17937.3	3	11.43	0	3.59E+03		(R)GGYVLH	(R)G G/Y\V/L H I/G T I/Y G D L K(V)		161.65	535.9574	1605.863	-0.0059	-3.7	6.74	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
7599	dirMS_041712_NAR_60mM_minus.9486.9486.3	3	11.43	1	8.25E+05		(K)TFDQLTI	(K)T F|D Q\L/T/P D E S K E R(L)		113.5	522.5846	1565.744	-0.0049	-3.2	4.32	17272.1	6.63	HUMAN	E9PJD5	Reticulocalbin-1
7600	dirMS_041712_NAR_120mM_plus.10446.10446.3	3	11.43	1	6.02E+05		(K)KGENYV	(K)K G E N Y V\Y|I/N/E A T R(H)		108.07	519.5943	1556.77	-0.002	-1.3	6.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
7601	dirMS_041712_NAR_20mM_plus.10816.10816.2	2	11.43	0	8.63E+04		(R)FLEQQN	(R)F L E\Q Q N Q/V|L/Q/T/K(W)		146.73	738.3942	1475.785	-0.0041	-2.8	6	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
7602	dirMS_041712_NAR_20mM_plus.10865.10865.2	2	11.43	0	2.19E+05	M33m	(K)VAGmD	(K)V/A/G/m D/V/E/L\T V/E/E/R(N)	m:Oxidized methionine	147.28	732.3555	1447.71	15.994	-0.6	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
7603	dirMS_041712_NAR_20mM_plus.10930.10930.2	2	11.43	0	2.19E+05	M33m	(K)VAGmD	(K)V/A/G m D|V|E L/T V E/E R(N)	m:Oxidized methionine	147.28	732.3555	1447.71	15.994	-0.6	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
7604	dirMS_041712_NAR_20mM_plus.9059.9059.2	2	11.43	0	2.66E+05		(R)VLTVINC	(R)V L/T|V/I/N Q T Q K(E)		133.07	572.3399	1143.673	-0.0007	-0.6	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
7605	dirMS_041712_NAR_30mM_plus2.11789.11937.2	2	11.43	0	9.24E+04		(R)GCTATL	(R)G C|T|A/T/L/G N/F\A/K(A)	C:Carbamidomethylation	114.95	570.2807	1139.551	0.0028	2.4	8.75	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
7606	dirMS_041712_NAR_30mM_plus2.21575.21575.2	2	11.43	0	2.63E+05		(R)EADDIVI	(R)E A\D D I|V/N W L/K(K)		167.65	601.81	1202.605	0.0075	6.3	4.03	26363.4	4.91	HUMAN	I3L312	Protein disulfide-isomerase (Fragment)
7607	dirMS_041712_NAR_30mM_plus2.22273.22273.2	2	11.43	0	2.11E+05		(K)NSSYFVE	(K)N S\S Y F/V/E/W I/P N/N V K(V)		171.9	848.9189	1696.833	-0.0024	-1.4	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
7608	dirMS_041712_NAR_40mM_plus2.12797.12797.3	3	11.43	0	1.02E+04		(R)LSSPCIV	(R)L/S/S/P C/I M V/V N H D A S S I P R(L)	C:Carbamidomethylation	141.52	661.6617	1982.979	-0.0081	-4.1	6.74	87267.9	6.33	HUMAN	Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase
7609	dirMS_041712_NAR_50mM_plus2.9434.9434.3	3	11.43	0	2.40E+05	M389m	(K)MIVDPV	(K)M I|V D/P V/E/P H G E m K(F)	m:Oxidized methionine	116.62	499.9106	1481.713	16.0045	6.4	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
7610	dirMS_041712_NAR_60mM_plus.11911.11911.3	3	11.43	0	3.36E+04		(R)NSNLVG	(R)N S/N/L|V/G A/A H E/E L Q Q S R(I)		119.55	584.9576	1752.862	-0.0041	-2.3	5.4	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
7611	dirMS_041712_NAR_120mM_minus.19719.19719.3	3	11.42	1	1.50E+05		(K)GTKHLSI	(K)G T K H|L/S/P Y A T L T V G D S S H K(T)		163.08	667.0203	1999.024	0.022	11	8.51	123367.7	5.57	HUMAN	Q9BSJ8	Extended synaptotagmin-1
7612	dirMS_041712_NAR_40mM_minus2.11022.11022.3	3	11.42	0	4.77E+05		(R)DAGEGL	(R)D A|G\E|G/L/L A/V Q I/T D Q E G K P K(R)		148.03	657.0157	1969.024	0.0089	4.5	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
7613	dirMS_041712_NAR_40mM_minus2.5901.5901.2	2	11.42	0	1.27E+06		(K)AGFAGD	(K)A/G F|A/G/D D/A P R(A)		98.13	488.7279	976.448	0.0002	0.2	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
7614	dirMS_041712_NAR_40mM_minus2.9438.9438.3	3	11.42	0	9.99E+04		(K)AASDIAN	(K)A A|S D|I/A/M T E/L/P P T H/P I R(L)		138.25	607.3174	1819.937	0.0006	0.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
7615	dirMS_041712_NAR_50mM_minus2.14175.14175.3	3	11.42	0	1.56E+05	M13m	(R)DLISHDE	(R)D L/I/S H/D E\m/F S/D I Y K(I)	m:Oxidized methionine	149.13	576.9343	1712.784	16.0047	5.7	4.22	19709.1	4.83	HUMAN	P13693	Translationally-controlled tumor protein
7616	dirMS_041712_NAR_120mM_plus.20606.20606.4	4	11.42	1	2.15E+05		(K)AAIDWF	(K)A A|I/D W F/D G K E F H/G N I I K(V)		161.23	491.0027	1960.992	-0.0026	-1.3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
7617	dirMS_041712_NAR_20mM_plus.12070.12070.2	2	11.42	0	4.67E+04		(K)LVPVGY	(K)L V/P/V G Y/G I R(K)		156.53	487.2934	973.583	-0.0034	-3.5	8.75	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
7618	dirMS_041712_NAR_20mM_plus.16560.16560.2	2	11.42	0	1.72E+05		(R)LLEAQIA	(R)L L/E\A\Q/I/A/T G G I I D\P K(E)		185.52	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
7619	dirMS_041712_NAR_20mM_plus.6731.6731.3	3	11.42	0	1.25E+05	M136m	(R)LVAGEm	(R)L V A G E/m G Q\N E/P/D/Q/G G Q R(G)	m:Oxidized methionine	111.45	601.2753	1785.818	15.9929	-1.1	4.14	17508.7	8.03	HUMAN	Q5H928	3-hydroxyacyl-CoA dehydrogenase type-2
7620	dirMS_041712_NAR_30mM_plus2.12627.12627.2	2	11.42	0	9.15E+05		(R)YSGSYNI	(R)Y/S/G/S Y/N D/Y L R(A)		119.53	619.2776	1237.548	-0.0005	-0.4	5.83	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
7621	dirMS_041712_NAR_30mM_plus2.20011.20011.2	2	11.42	0	2.34E+05		(K)LALFQAI	(K)L A/L|F/Q A\I/G K(E)		158.55	480.795	960.588	-0.005	-5.2	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
7622	dirMS_041712_NAR_40mM_plus2.16003.16003.3	3	11.42	1	1.97E+05		(K)LGVQVV	(K)L/G\V|Q/V/V I T D/P E K L D Q I R(Q)		160.97	641.701	1923.091	-0.0025	-1.3	4.56	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
7623	dirMS_041712_NAR_40mM_plus2.8964.8964.2	2	11.42	0	1.19E+05		(R)GYSFTTI	(R)G Y/S|F/T/T T A E/R(E)		114.9	566.7672	1132.527	0.0002	0.2	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
7624	dirMS_041712_NAR_50mM_plus2.10996.10996.3	3	11.42	0	1.94E+05		(K)ADDGRF	(K)A/D/D/G/R P F/P Q\V/I/K(S)		125.1	448.2419	1342.711	-0.0002	-0.2	6	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
7625	dirMS_041712_NAR_50mM_plus2.11802.11802.3	3	11.42	1	4.58E+05		(R)ISVYYNE	(R)I/S/V/Y/Y N/E A T/G/G K Y V P/R(A)		130.37	606.3123	1816.923	-0.0005	-0.3	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain

7626	dirMS_041712_NAR_60mM_plus.9271.9271.3	3	11.42	1	1.31E+06		(R)FNEVAA	(R)F/N\E/V/A/A Q Y/S E D/K A/R(Q)		106.1	543.2616	1627.771	-0.0008	-0.5	4.68	14236.2	10.25	HUMAN	F5H1P5	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4
7627	dirMS_041712_NAR_60mM_plus.9935.9957.3	3	11.42	1	1.14E+06		(K)VSSVFKI	(K)V/S|S V/F/K/D/E A T V R(M)		109.73	446.5716	1337.706	-0.0057	-4.3	6.04	58229.7	4.46	HUMAN	F8W7I9	Ran GTPase-activating protein 1
7628	dirMS_041712_NAR_20mM_minus.7295.7295.2	2	11.41	0	1.32E+05	M374m	(R)mAPTPII	(R)m A|P/T/P I/P T R(S)	m:Oxidized methionine	121.02	500.2679	983.534	15.9943	-0.7	9.5	76925.9	4.46	HUMAN	A8MV58	Drebrin
7629	dirMS_041712_NAR_30mM_minus2.12236.12236.2	2	11.41	0	1.26E+05		(R)TLSGME	(R)T/L/S/G M/E/S/Y C V R(A)	C:Carbamidomethylation	119.52	651.795	1302.582	0.001	0.8	5.66	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
7630	dirMS_041712_NAR_30mM_minus2.15683.15683.2	2	11.41	0	2.70E+04	M1342m	(R)ASLSLW	(R)A S/L/S/L/W Q/A/m E K(G)	m:Oxidized methionine	138.55	640.3185	1263.64	15.9895	-4.2	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
7631	dirMS_041712_NAR_40mM_minus2.14995.14995.3	3	11.41	1	7.94E+04		(R)VLEALLP	(R)V L|E/A L L/P L/K G L E E R(V)		173.35	527.317	1579.942	-0.0053	-3.4	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
7632	dirMS_041712_NAR_50mM_minus2.11854.11854.3	3	11.41	1	1.47E+05	T663t	(R)LIKEAGS	(R)L I|K/E/A\G S A M N H Q t R(T)	t:N-acetylglucosamine (T)	135.78	586.9724	1555.801	203.1017	12.7	8.76	84554.5	5.47	HUMAN	Q86VM9-2	Isoform 2 of Zinc finger CCCH domain-containing protein 18
7633	dirMS_041712_NAR_60mM_minus.14352.14352.3	3	11.41	1	2.27E+05		(R)IQLVEEE	(R)I Q|L/V|E E E L D/R/A Q E R(L)		139.35	576.6347	1727.892	-0.0027	-1.6	4.25	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
7634	dirMS_041712_NAR_60mM_minus.18971.18971.3	3	11.41	1	2.48E+05		(R)DSIVAEL	(R)D S|I/V/A E/L/D R E M S R(S)		168.02	507.5858	1520.737	0.0055	3.6	4.32	34709.6	4.98	HUMAN	O14579	Coatomer subunit epsilon
7635	dirMS_041712_NAR_120mM_plus.6260.6260.3	3	11.41	1	5.04E+05		(R)ARSDEG	(R)A R S D E G Q|L|S|P A/T/R(G)		86.7	463.2395	1387.692	0.0115	8.3	6.12	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
7636	dirMS_041712_NAR_20mM_plus.18132.18132.2	2	11.41	0	1.31E+05	M153m	(K)VVTYGm	(K)V V T|Y|G/m A N L L T G P K(R)	m:Oxidized methionine	196.32	740.3997	1463.793	15.9995	3.1	8.56	28454.5	6.24	HUMAN	B0AZP7	Synaptic vesicle membrane protein VAT-1 homolog
7637	dirMS_041712_NAR_20mM_plus.18762.18762.3	3	11.41	0	1.31E+05		(K)IYVDDGI	(K)I Y V D D G\L/I/S L Q V/K(Q)		200.6	488.2764	1462.815	-0.0005	-0.4	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
7638	dirMS_041712_NAR_20mM_plus.7919.7919.2	2	11.41	0	9.11E+04	M21m	(K)ATAVmF	(K)A T/A\V|m/P D G Q F K(D)	m:Oxidized methionine	124.52	590.7861	1164.572	15.9932	-1.5	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
7639	dirMS_041712_NAR_20mM_plus.8648.8648.2	2	11.41	0	2.99E+05		(K)DVNQQI	(K)D V|N/Q/Q E F/V/R(A)		129.47	567.7865	1134.554	0.0119	10.5	4.37	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
7640	dirMS_041712_NAR_30mM_plus2.10625.10714.2	2	11.41	0	8.67E+05		(K)IGALEGY	(K)I/G|A|L/E/G Y/R(G)		109.57	439.7397	878.473	-0.0009	-1	6	20203.8	9.79	HUMAN	B4DG16	Asparagine--tRNA ligase, cytoplasmic
7641	dirMS_041712_NAR_30mM_plus2.12032.12075.2	2	11.41	0	6.57E+05		(K)GCGTVL	(K)G C|G/T|V/L/L/S/G/P R(K)	C:Carbamidomethylation	116.2	558.7944	1116.583	-0.0015	-1.3	9.75	14643	11.93	HUMAN	F8VUA6	60S ribosomal protein L18 (Fragment)
7642	dirMS_041712_NAR_30mM_plus2.21538.21538.2	2	11.41	0	1.58E+05		(R)VFIGNLI	(R)V/F/I/G/N/L N T L V V K(K)		167.38	658.8983	1316.794	-0.0043	-3.3	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
7643	dirMS_041712_NAR_30mM_plus2.7721.7721.2	2	11.41	0	3.29E+05		(K)NIGVDN	(K)N I|G/V/D N/P A A K(V)		94.6	499.7668	998.527	-0.0002	-0.2	5.84	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
7644	dirMS_041712_NAR_40mM_plus2.12793.12813.2	2	11.41	0	1.31E+05		(K)YMACCL	(K)Y/M|A|C C/L L/Y/R(G)	C:Carbamidomethylation	141.83	625.28	1249.553	0.0001	0.1	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
7645	dirMS_041712_NAR_40mM_plus2.19769.19769.3	3	11.41	0	3.68E+05		(R)DLLDTVI	(R)D L|L/D T V L/P H L Y N E T K(V)		185.23	590.9774	1770.927	-0.0096	-5.4	4.54	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
7646	dirMS_041712_NAR_50mM_plus2.10667.10667.3	3	11.41	1	9.71E+04		(K)GLESTTL	(K)G L/E/S/T T L A D K D G E/I Y C K(G)	C:Carbamidomethylation	123.6	633.9707	1899.9	-0.0029	-1.5	4.32	16685.6	9.7	HUMAN	E9PND2	Cysteine and glycine-rich protein 1 (Fragment)
7647	dirMS_041712_NAR_60mM_plus.15720.15720.3	3	11.41	0	4.13E+04		(R)VWYVSN	(R)V W/Y/V/S/N I/D/G T H I A K(T)		138.42	534.9464	1602.828	-0.0028	-1.8	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
7648	dirMS_041712_NAR_60mM_plus.17742.17782.3	3	11.41	0	3.72E+05		(R)SLESLHS	(R)S L|E/S L/H/S F V/A A A T K(E)		149.9	487.5963	1460.774	0	0	6.47	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
7649	dirMS_041712_NAR_20mM_minus.11546.11546.2	2	11.4	0	1.40E+05	M98m	(R)TLTIVDT	(R)T/L|T\I|V/D T G/I G/m T K(A)	m:Oxidized methionine	163.17	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
7650	dirMS_041712_NAR_30mM_minus2.10486.10486.2	2	11.4	0	1.47E+06		(R)GLTSVIN	(R)G L/T/S V/I/N Q/K(L)		111.3	480.2794	959.552	-0.0005	-0.5	8.75	36923.1	5.71	HUMAN	P07195	L-lactate dehydrogenase B chain
7651	dirMS_041712_NAR_30mM_minus2.16426.16426.2	2	11.4	0	5.06E+05	M185m	(K)LAVNm\	(K)L/A|V/N/m|V P/F P R(L)	m:Oxidized methionine	142.53	580.3178	1143.634	15.994	-0.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
7652	dirMS_041712_NAR_30mM_minus2.19565.19568.2	2	11.4	0	4.72E+05		(R)ASLSLW	(R)A S/L|S|L/W Q/A/M E K(G)		162.75	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
7653	dirMS_041712_NAR_50mM_minus2.15963.15963.3	3	11.4	0	5.46E+05		(K)GSDHSA	(K)G S D H S A S L\E|P G E|L/A/E L/V R(S)		159.35	622.978	1866.919	0.0003	0.1	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
7654	dirMS_041712_NAR_60mM_minus.17249.17249.3	3	11.4	1	1.10E+05		(R)CRVDLP	(R)C R V D\L|P/L/A V L/S K(M)	C:Carbamidomethylation	156	457.5982	1370.782	-0.0024	-1.7	8.75	7765.6	8.23	HUMAN	H3BSA6	dCTP pyrophosphatase 1
7655	dirMS_041712_NAR_30mM_plus2.12151.12151.2	2	11.4	0	1.44E+06		(K)GIYAVGI	(K)G I/Y|A/V|G D V C/G K(A)	C:Carbamidomethylation	117.63	569.7798	1138.556	-0.0038	-3.3	5.83	56826.6	9.16	HUMAN	P00390	Glutathione reductase, mitochondrial
7656	dirMS_041712_NAR_30mM_plus2.12247.12335.2	2	11.4	0	6.53E+05		(R)IATGSFL	(R)I/A|T/G S F/L/K(R)		117.15	418.7442	836.488	-0.0065	-7.8	8.75	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
7657	dirMS_041712_NAR_30mM_plus2.5617.5752.2	2	11.4	0	2.73E+05	M283m	(R)DYDDm:	(R)D/Y|D|D m/S/P R(R)	m:Oxidized methionine	84.23	507.6956	998.388	15.9955	0.6	3.93	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
7658	dirMS_041712_NAR_40mM_plus2.19263.19263.3	3	11.4	0	1.61E+06		(R)AGKPVI(	(R)A G K\P V I\C\A|T/Q|M L E S M I/K(K)	C:Carbamidomethylation	180.63	626.3273	1876.969	-0.002	-1.1	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
7659	dirMS_041712_NAR_50mM_plus2.12637.12637.3	3	11.4	1	8.84E+05		(R)ELISNSSI	(R)E\L/I/S N/S/S D/A\L D K I R(Y)		134.15	520.9473	1560.823	0.0046	2.9	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
7660	dirMS_041712_NAR_50mM_plus2.18039.18039.3	3	11.4	0	7.94E+04		(K)LILPHVD	(K)L/I|L/P/H V D I Q L K(Y)		163.23	430.2706	1288.799	-0.0015	-1.2	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
7661	dirMS_041712_NAR_60mM_plus.15485.15485.3	3	11.4	0	3.36E+05		(K)SKPGAA	(K)S K/P G A A M V E M|A/D/G Y|A/V D R(A)		137.83	623.2943	1867.868	0.0007	0.3	4.56	64759.2	8.88	HUMAN	P14866	Heterogeneous nuclear ribonucleoprotein L
7662	dirMS_041712_NAR_120mM_minus.19021.19021.4	4	11.39	1	3.58E+05		(R)HATALEI	(R)H A T A\L\E|E/L/S E Q L E Q A K R(F)		158.55	489.0065	1953.004	0.0006	0.3	4.91	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
7663	dirMS_041712_NAR_120mM_minus.7981.7981.3	3	11.39	1	2.26E+05		(R)AEERAEI	(R)A/E/E R A/E\L\S/E/G Q V/R(Q)		97.93	491.9127	1473.729	-0.0057	-3.8	4.49	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
7664	dirMS_041712_NAR_30mM_minus2.15716.15716.2	2	11.39	0	9.77E+04		(R)GSTDNL	(R)G/S T/D/N L/M/D D I E R(A)		138.77	683.3009	1365.595	-0.0006	-0.4	3.84	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
7665	dirMS_041712_NAR_30mM_minus2.8452.8514.2	2	11.39	0	3.72E+06		(R)QLEEQLI	(R)Q|L|E/E/Q/L/R(I)		101.02	458.2488	915.489	0.0009	1	4.53	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
7666	dirMS_041712_NAR_40mM_minus2.15577.15577.3	3	11.39	1	6.82E+05		(K)LLPLVSD	(K)L L|P L/V/S/D E V F I R D V A K(V)		180.33	605.3511	1814.042	-0.0035	-1.9	4.56	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
7667	dirMS_041712_NAR_50mM_minus2.14708.14708.3	3	11.39	1	1.82E+05		(K)ELKIDIIP	(K)E L K I D I\I|P/N/P Q E R(T)		151.52	522.2945	1564.869	-0.0004	-0.2	4.68	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
7668	dirMS_041712_NAR_50mM_minus2.16761.16761.3	3	11.39	0	2.59E+05		(K)ALVSHN	(K)A L/V S H N G S L\I/N/V|G S L/L/Q R(A)		163.72	626.6879	1878.056	-0.0064	-3.4	9.8	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
7669	dirMS_041712_NAR_50mM_minus2.4955.4955.3	3	11.39	1	2.84E+05	M137m	(R)mQNDT.	(R)m Q\N D T/A/E N E T T/E/K/E/E K(S)	m:Oxidized methionine	83	638.2738	1896.813	15.9941	-0.4	4.14	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
7670	dirMS_041712_NAR_20mM_plus.17076.17076.2	2	11.39	0	1.91E+05		(K)VQIAVA	(K)V Q|I\A/V/A/N A Q E L\L Q R(M)		188.3	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
7671	dirMS_041712_NAR_20mM_plus.18604.18604.2	2	11.39	0	2.69E+05		(K)LAVEAL:	(K)L A\V E/A|L\S/S/L/D G D L A G R(Y)		200.43	793.9214	1586.838	-0.0029	-1.8	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
7672	dirMS_041712_NAR_20mM_plus.6018.6018.3	3	11.39	0	1.02E+06	M295m M2	(R)mGQmA	(R)m\G\Q\m A m G G\A|m|G|I/N N R(G)	m:Oxidized methionine	100.27	534.8861	1538.67	63.9743	-3.4	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
7673	dirMS_041712_NAR_30mM_plus2.13725.13725.2	2	11.39	0	1.97E+05		(K)VANVEL	(K)V A|N|V/E/L Y/Y/R(A)		124.78	563.7923	1126.589	-0.0118	-10.5	5.97	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
7674	dirMS_041712_NAR_30mM_plus2.15339.15339.2	2	11.39	0	5.45E+05		(R)YPVNSV	(R)Y/P/V/N/S/V N/I\L K(A)		133.18	573.8278	1146.652	-0.0034	-3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
7675	dirMS_041712_NAR_30mM_plus2.17658.17789.2	2	11.39	0	1.03E+06		(R)NILGGT\	(R)N I|L|G/G\T V F/R(E)		145.63	488.7809	976.557	-0.0029	-3	9.75	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
7676	dirMS_041712_NAR_30mM_plus2.19908.19908.3	3	11.39	0	2.45E+05		(R)IIPGFMC	(R)I I/P G F M C/Q/G/G D/F T R(H)	C:Carbamidomethylation	157.77	533.5865	1598.745	-0.0004	-0.3	5.84	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
7677	dirMS_041712_NAR_30mM_plus2.9609.9610.2	2	11.39	0	7.52E+05		(K)AELDDTI	(K)A E|L/D/D/T/P M/R(G)		104.78	524.2438	1047.478	0.0028	2.7	4.03	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
7678	dirMS_041712_NAR_50mM_plus2.7128.7128.3	3	11.39	0	2.50E+04		(R)LLEATAK	(R)L L\E/A T A K/P/E/P E E K(S)		103.13	485.5983	1454.774	0.0066	4.6	4.49	64224	8.98	HUMAN	Q96KC8	DnaJ homolog subfamily C member 1
7679	dirMS_041712_NAR_60mM_plus.7153.7225.3	3	11.39	1	4.98E+05		(K)TIIQNPT	(K)T I|I Q/N/P/T D Q Q K K(D)		95.72	471.9324	1413.77	0.013	9.2	8.26	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
7680	dirMS_041712_NAR_30mM_minus2.17756.17797.2	2	11.38	0	2.08E+05		(R)TEMDW	(R)T/E|M/D/W V/L K(H)		151.1	511.2565	1021.502	0.0034	3.4	4.37	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
7681	dirMS_041712_NAR_50mM_minus2.12100.12100.3	3	11.38	1	1.96E+05		(R)LATALQI	(R)L/A|T/A/L Q K L E E/A E K(A)		137.05	481.9385	1443.805	-0.0044	-3	4.79	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
7682	dirMS_041712_NAR_50mM_minus2.5880.5880.3	3	11.38	0	5.84E+03		(R)ITPPAAK	(R)I T|P P A/A K/P G\S P Q A K(S)		95.57	454.9324	1362.774	0.0087	6.4	10	214357.5	7.19	HUMAN	P35658	Nuclear pore complex protein Nup214
7683	dirMS_041712_NAR_50mM_minus2.6782.6782.3	3	11.38	0	5.92E+05		(R)EATNPP'	(R)E A T N/P/P V I Q/E/E K/P K(K)		105.52	527.2846	1579.833	0.0066	4.2	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
7684	dirMS_041712_NAR_20mM_plus.10815.10815.2	2	11.38	0	8.63E+04		(R)FLEQQN	(R)F/L/E Q Q\N Q/V/L Q|T\K(W)		146.73	738.3942	1475.785	-0.0041	-2.8	6	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
7685	dirMS_041712_NAR_30mM_plus2.10718.11023.2	2	11.38	0	1.66E+06		(R)SLVNLG(	(R)S L|V/N/L/G G/S K(S)		110.57	437.7532	874.499	-0.0001	-0.2	8.47	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
7686	dirMS_041712_NAR_30mM_plus2.12227.12486.2	2	11.38	0	8.56E+05		(K)TYAICGA	(K)T Y|A|I/C/G A/I/R(R)	C:Carbamidomethylation	117.75	512.7674	1024.524	0.0031	3	8.41	9225.3	9.16	HUMAN	P63220	40S ribosomal protein S21
7687	dirMS_041712_NAR_40mM_plus2.14334.14334.3	3	11.38	1	1.83E+05		(K)IMASSPI	(K)I M/A S S/P D M/D L A T V S A L R K(M)		151.13	635.9975	1905.977	0.0007	0.4	5.96	36208.1	7.21	HUMAN	B4DMU0	Pyrroline-5-carboxylate reductase
7688	dirMS_041712_NAR_50mM_plus2.12311.12311.3	3	11.38	1	4.91E+05		(K)ILDSVGII	(K)I/L|D S/V/G I E/A D D D R L N K(V)		132.85	591.6385	1772.902	-0.0015	-0.9	4.04	11664.7	4.42	HUMAN	P05387	60S acidic ribosomal protein P2
7689	dirMS_041712_NAR_50mM_plus2.15030.15030.3	3	11.38	0	6.83E+05		(R)QIFHPE(	(R)Q I F H/P E\Q L/I/T/G/K(E)		147.28	470.9293	1410.774	-0.0006	-0.4	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
7690	dirMS_041712_NAR_60mM_plus.11869.11869.3	3	11.38	1	7.13E+05	M239m	(R)MSMKE'	(R)M/S M K E V\D\E\Q/m/L/N V\Q N K(N)	m:Oxidized methionine	119.38	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
7691	dirMS_041712_NAR_60mM_plus.5660.5660.3	3	11.38	0	3.20E+04		(R)AEAEAG	(R)A E|A E/A G S/P R\P D/P\R(E)		87.72	451.5555	1352.655	-0.0034	-2.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
7692	dirMS_041712_NAR_60mM_plus.6734.6734.3	3	11.38	1	1.14E+05		(R)GTDDSP	(R)G T/D D S/P K D S/Q/E/D/L\Q E/R(H)		93.75	607.2705	1819.794	0.0029	1.6	3.96	23420.8	4.74	HUMAN	Q5H9L2	Transcription elongation factor A protein-like 5
7693	dirMS_041712_NAR_30mM_minus2.18552.18552.2	2	11.37	0	4.01E+05		(R)QAQEYE	(R)Q A\Q/E/Y E/A L/L/N/I K(V)		154.8	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
7694	dirMS_041712_NAR_30mM_minus2.5974.5974.2	2	11.37	0	1.16E+05		(K)MAGAM	(K)M/A|G/A M/S T T A K(T)		86.95	484.7299	968.454	-0.0014	-1.5	8.5	23963.2	8.9	HUMAN	Q9UQN3	Charged multivesicular body protein 2b
7695	dirMS_041712_NAR_40mM_minus2.14933.14933.3	3	11.37	0	1.07E+05		(R)EAVELPI	(R)E A/V E/L/P L/T H F E L Y/K(Q)		173.08	563.6324	1688.889	-0.0068	-4	4.75	47479.5	5.09	HUMAN	P43686	26S protease regulatory subunit 6B
7696	dirMS_041712_NAR_50mM_minus2.9229.9229.3	3	11.37	1	7.89E+04		(R)LAEFSSC	(R)L/A|E/F/S S Q/A A/E E E E K V K(S)		120.68	598.964	1794.876	0.0018	1	4.32	232239.1	5.52	HUMAN	F2Z2U8	Myosin-14
7697	dirMS_041712_NAR_120mM_plus.10404.10404.3	3	11.37	1	2.55E+05		(R)LRQLAEI	(R)L R Q L A E\E D|L/A/Q Q/R(A)		107.03	523.949	1569.834	-0.0019	-1.2	4.68	533778	5.74	HUMAN	Q15149	Plectin
7698	dirMS_041712_NAR_20mM_plus.14380.14380.2	2	11.37	0	6.21E+04		(K)GAVEIIF	(K)G A|V|E/I/I F|K(G)		170.95	438.7639	876.519	0.0016	1.8	6	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
7699	dirMS_041712_NAR_20mM_plus.14754.14754.2	2	11.37	0	1.14E+05		(K)FANPFP/	(K)F A/N|P/F/P A A V R(G)		173.75	545.2958	1089.584	0.0003	0.3	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
7700	dirMS_041712_NAR_20mM_plus.15457.15457.3	3	11.37	0	8.25E+04		(R)AITIAGV	(R)A I T\I A G V/P/Q S/V T/E C V K(Q)	C:Carbamidomethylation	178.52	558.303	1672.894	0.0006	0.4	6.05	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
7701	dirMS_041712_NAR_30mM_plus2.17675.17675.2	2	11.37	0	2.11E+05		(K)LFDFPGI	(K)L/F|D|F/P G R(G)		146.22	426.2291	851.441	0.0099	11.6	5.84	56825.2	9.49	HUMAN	Q9P258	Protein RCC2
7702	dirMS_041712_NAR_30mM_plus2.21078.21334.2	2	11.37	0	6.89E+05		(K)IPDWFLI	(K)I/P/D|W/F/L N R(Q)		165.78	530.785	1060.557	0.0053	5	5.84	9767.1	11.41	HUMAN	J3JS69	40S ribosomal protein S18
7703	dirMS_041712_NAR_40mM_plus2.13570.13570.3	3	11.37	0	1.89E+05		(R)LSAMLV	(R)L S|A/M L V|P\V|T/P E V K P K(R)		145.9	536.9848	1608.939	0.0005	0.3	8.59	31524.1	4.5	HUMAN	P82970	High mobility group nucleosome-binding domain-containing protein 5
7704	dirMS_041712_NAR_50mM_plus2.14697.14697.3	3	11.37	1	9.20E+05		(K)MQSAAI	(K)M/Q|S A A F/S\I A/A D V K D/V K(A)		145.55	560.9581	1680.863	-0.0028	-1.7	5.72	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
7705	dirMS_041712_NAR_50mM_plus2.8328.8328.3	3	11.37	0	2.33E+05		(K)VQQAEL	(K)V Q|Q/A E L/H/T G S L P\R(I)		110.33	479.2607	1435.765	0.0023	1.6	6.72	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
7706	dirMS_041712_NAR_50mM_plus2.9889.9890.3	3	11.37	1	4.79E+05		(K)TAVCDIF	(K)T/A|V/C/D I/P P R/G L K(M)	C:Carbamidomethylation	119.47	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
7707	dirMS_041712_NAR_60mM_plus.17577.17577.3	3	11.37	1	1.76E+05		(R)RTVQSLI	(R)R T V Q S L|E\I/D/L/D/S M R(N)		148.8	554.954	1662.848	-0.0005	-0.3	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
7708	dirMS_041712_NAR_60mM_plus.18854.18854.3	3	11.37	1	2.24E+05		(K)GPREEIV	(K)G P R E E I\V|Y\L|P/C I Y\R(N)	C:Carbamidomethylation	156.1	588.9744	1764.91	-0.0015	-0.9	6.14	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
7709	dirMS_041712_NAR_120mM_minus.14881.14881.3	3	11.36	1	2.69E+05		(K)KKELEEI'	(K)K K E L E E I|V|Q/P I/I S K(L)		135.13	551.9968	1653.978	-0.0027	-1.6	6.23	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
7710	dirMS_041712_NAR_120mM_minus.7674.7843.3	3	11.36	1	2.74E+06	M281m	(R)SRAEAE:	(R)S R A E\A\E|S/m/Y Q/I/K(Y)	m:Oxidized methionine	96.75	476.8951	1412.684	15.9869	-5.6	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
7711	dirMS_041712_NAR_20mM_minus.7052.7052.2	2	11.36	0	4.77E+05	M281m	(R)AEAESm	(R)A E|A/E/S m/Y/Q I/K(Y)	m:Oxidized methionine	117.9	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
7712	dirMS_041712_NAR_50mM_minus2.10570.10570.3	3	11.36	0	1.92E+05		(K)VFEGNR	(K)V/F|E|G N R P T N S I V F/T/K(L)		128.82	570.3032	1708.902	-0.0066	-3.9	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
7713	dirMS_041712_NAR_50mM_minus2.5190.5190.3	3	11.36	1	8.82E+04		(R)MQNDT	(R)M Q|N D T/A\E N/E T T E K E/E K(S)		86.63	632.9425	1896.813	0.0002	0.1	4.14	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
7714	dirMS_041712_NAR_60mM_minus.17377.17377.3	3	11.36	1	4.29E+06		(R)VSFELFA	(R)V/S/F E L F/A/D/K V P K(T)		157.62	460.5911	1379.757	0.0018	1.3	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
7715	dirMS_041712_NAR_60mM_minus.19385.19393.3	3	11.36	1	6.95E+05		(K)LASDLLE	(K)L/A|S D/L L E/W I R/R(T)		172.9	457.9288	1371.774	-0.0025	-1.8	6.07	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
7716	dirMS_041712_NAR_120mM_plus.9983.10314.3	3	11.36	1	1.24E+06		(R)QYFEEIC	(R)Q/Y/F/E/E/I Q R/R(F)		106.33	423.5524	1268.638	0.0044	3.5	6.14	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
7717	dirMS_041712_NAR_20mM_plus.10697.10697.3	3	11.36	0	2.82E+04		(K)SQLLAPI	(K)S Q\L L A/P|P/P/P S A P/P G N K(T)		146.3	524.2902	1570.859	-0.0027	-1.7	8.47	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
7718	dirMS_041712_NAR_20mM_plus.18864.18864.3	3	11.36	0	1.19E+05		(K)IYVDDGI	(K)I Y V D D G\L|I/S L/Q V K(Q)		200.72	488.2764	1462.815	-0.0005	-0.4	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
7719	dirMS_041712_NAR_30mM_plus2.10298.10298.2	2	11.36	0	2.98E+04		(K)TAVCDIF	(K)T A|V|C D/I/P|P/R(G)	C:Carbamidomethylation	106.05	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
7720	dirMS_041712_NAR_30mM_plus2.14892.15040.2	2	11.36	0	7.43E+05		(R)LSLYQAI	(R)L/S|L/Y/Q/A M/R(Q)		131.28	491.2638	981.519	0.0017	1.7	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
7721	dirMS_041712_NAR_30mM_plus2.20380.20380.2	2	11.36	0	8.58E+05		(R)ILVATNL	(R)I L|V/A T/N\L/F G R(G)		161.72	552.331	1103.657	-0.0024	-2.2	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
7722	dirMS_041712_NAR_30mM_plus2.6035.6037.2	2	11.36	0	1.61E+05		(K)SPEYPE(	(K)S/P|E|Y|P E/G R(D)		85.98	467.7183	934.427	0.0028	3	4.53	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
7723	dirMS_041712_NAR_40mM_plus2.12297.12356.3	3	11.36	1	1.90E+05		(K)IINADSE	(K)I I|N/A D/S E D|P K Y I I N V/K(Q)		138.92	611.3255	1831.98	-0.0181	-9.9	4.56	14693.3	4.69	HUMAN	C9JLS9	26S protease regulatory subunit 7 (Fragment)
7724	dirMS_041712_NAR_40mM_plus2.13093.13093.3	3	11.36	0	5.11E+04		(R)IVATKPL	(R)I V|A/T K/P L Y|V A L/A Q R(K)		143.25	514.9835	1542.937	-0.0007	-0.4	9.99	65918.2	9.74	HUMAN	E7EQV3	Polyadenylate-binding protein 1
7725	dirMS_041712_NAR_40mM_plus2.17361.17361.3	3	11.36	1	2.00E+05		(R)GDSVIV\	(R)G D\S/V/I/V V/L/R N P L I/A G K(-)		168.75	551.0007	1650.99	-0.0026	-1.6	8.75	6144.3	10.23	HUMAN	K7EJB5	Small nuclear ribonucleoprotein Sm D2
7726	dirMS_041712_NAR_40mM_plus2.6846.6846.2	2	11.36	0	4.44E+04		(K)SFQQSSI	(K)S F/Q/Q/S S L/S/R(D)		100.17	520.2619	1039.517	-0.0002	-0.2	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
7727	dirMS_041712_NAR_50mM_plus2.12641.12641.3	3	11.36	1	3.83E+05		(K)LPGGELI	(K)L/P/G G E L N/P G E D/E V E G L K R(L)		134.28	636.9936	1908.966	0.0001	0.1	4.25	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
7728	dirMS_041712_NAR_50mM_plus2.19427.19427.3	3	11.36	1	2.22E+05		(K)SGGIVIS	(K)S G G I/V|I/S P\F R L E E\L T N R(L)		170.42	630.0135	1888.029	-0.0027	-1.5	5.87	53461.2	6.87	HUMAN	Q16204	Coiled-coil domain-containing protein 6
7729	dirMS_041712_NAR_60mM_plus.10612.10612.3	3	11.36	1	3.21E+04		(R)LRQLAEI	(R)L R Q L A/E/E|D\L/A|Q Q R(A)		112.7	523.9486	1569.834	-0.0031	-2	4.68	533778	5.74	HUMAN	Q15149	Plectin
7730	dirMS_041712_NAR_60mM_plus.15523.15560.2	2	11.36	1	5.83E+05		(R)ADLIAYL	(R)A/D|L|I/A/Y L/K K(-)		137.95	517.8155	1034.624	-0.0007	-0.7	8.54	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
7731	dirMS_041712_NAR_60mM_plus.15736.15736.3	3	11.36	1	1.98E+05		(R)DLEEKLE	(R)D/L/E/E K/L E T L R(L)		138.4	415.8936	1245.669	-0.0023	-1.8	4.41	141626	5.5	HUMAN	A8MY36	Dynactin subunit 1
7732	dirMS_041712_NAR_60mM_plus.17744.17744.3	3	11.36	0	1.33E+05		(R)FQSGDF	(R)F Q|S\G\D F H/V I/N G V L R(T)		149.73	530.2831	1588.823	0.0117	7.4	6.74	104619	5.75	HUMAN	F8W904	Exportin-2
7733	dirMS_041712_NAR_60mM_plus.6516.6516.2	2	11.36	0	1.48E+05		(K)TVEAEA/	(K)T/V/E|A/E A A H G T V T R(H)		92.68	671.3399	1341.676	-0.0032	-2.4	5.37	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
7734	dirMS_041712_NAR_120mM_minus.4755.4755.3	3	11.35	1	4.06E+05		(K)AGADEE	(K)A/G\A|D/E E R A E/T A R(L)		76.82	425.8687	1275.592	-0.0008	-0.7	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta

7735	dirMS_041712_NAR_40mM_minus2.11305.11305.3	3	11.35	0	4.39E+05		(R)TIQVEN	(R)T I|Q/V/E N S H L I/L T/G A/G A L/N K(V)		150.5	660.3663	1979.092	-0.0077	-3.9	6.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
7736	dirMS_041712_NAR_50mM_minus2.11346.11346.3	3	11.35	1	1.29E+05		(K)NQVALN	(K)N\Q|V|A L/N|P\Q N T V/F D A K R(L)		132.68	605.6545	1814.951	-0.0018	-1	8.75	70336.2	5.48	HUMAN	P08107	Heat shock 70 kDa protein 1A/1B
7737	dirMS_041712_NAR_50mM_minus2.15639.15884.3	3	11.35	1	6.66E+05		(K)SIYGEKF	(K)S I|Y/G/E K F E D E N F I/L/K(H)		158	611.3086	1831.911	0	0	4.41	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
7738	dirMS_041712_NAR_50mM_minus2.8758.8758.3	3	11.35	0	1.19E+06		(R)EIVHIQA	(R)E/I/V H I Q\A\G Q/C/G N Q\I/G A K(F)	C:Carbamidomethylation	117.03	608.3087	1822.923	-0.0113	-6.2	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
7739	dirMS_041712_NAR_60mM_minus.15387.15555.3	3	11.35	0	1.06E+06		(R)LSDQFH	(R)L/S|D Q/F H/D/I/L I/R(K)		145.62	452.9148	1356.727	0.0028	2.1	5.21	12284.6	4.89	HUMAN	H0Y9X3	Programmed cell death protein 6 (Fragment)
7740	dirMS_041712_NAR_60mM_minus.9078.9145.3	3	11.35	1	1.02E+06		(R)ETAEAD	(R)E T/A/E A D/V/A S L N R R(I)		111.37	477.9107	1431.719	-0.0011	-0.8	4.68	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
7741	dirMS_041712_NAR_20mM_plus.18332.18416.2	2	11.35	1	1.35E+05		(K)DIGFIKLI	(K)D/I|G|F/I/K L\D(-)		198.13	460.7578	920.509	-0.0004	-0.5	4.53	6904.9	11.35	HUMAN	P62273	40S ribosomal protein S29
7742	dirMS_041712_NAR_30mM_plus2.13083.13136.2	2	11.35	0	1.23E+06		(R)TIGISVD	(R)T I|G|I|S V D|P/R(R)		121	479.2725	957.536	0.0014	1.4	5.5	14749.1	12.2	HUMAN	J3QSB4	60S ribosomal protein L13 (Fragment)
7743	dirMS_041712_NAR_30mM_plus2.15120.15323.2	2	11.35	0	1.41E+06		(K)VYFDLR	(K)V/Y|F D/L/R(I)		132.23	406.7191	812.43	0.0008	1	5.8	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
7744	dirMS_041712_NAR_30mM_plus2.16092.16092.2	2	11.35	0	5.18E+05		(K)GVLFYGI	(K)G V L|F/Y/G/P P/G C G K(T)	C:Carbamidomethylation	137.57	626.3175	1251.619	0.0087	6.9	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
7745	dirMS_041712_NAR_30mM_plus2.23509.23509.2	2	11.35	0	1.80E+05		(R)IAIYELLF	(R)I/A|I/Y/E\L L F K(E)		190.25	555.3331	1109.661	-0.0016	-1.4	6	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
7746	dirMS_041712_NAR_30mM_plus2.8634.8634.2	2	11.35	0	1.02E+05		(R)YNYIEGT	(R)Y/N|Y/I/E/G T K(M)		99.03	494.2448	987.478	0.0041	4.2	6	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
7747	dirMS_041712_NAR_40mM_plus2.18112.18112.2	2	11.35	0	8.61E+04		(R)SLDMDS	(R)S L/D|M/D\S I I/A E V K(A)		173.07	660.8385	1320.671	-0.0018	-1.4	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
7748	dirMS_041712_NAR_50mM_plus2.10678.10678.3	3	11.35	1	6.61E+05		(K)GCGVVK	(K)G C/G V/V K F E/S|P/E V A E R(A)	C:Carbamidomethylation	123.88	555.2753	1663.811	0.0005	0.3	4.79	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
7749	dirMS_041712_NAR_50mM_plus2.7265.7265.3	3	11.35	0	1.63E+05		(R)EATNPP	(R)E A/T N/P/P V I/Q E E K/P K(K)		104.22	527.282	1579.833	-0.0012	-0.7	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
7750	dirMS_041712_NAR_50mM_plus2.8626.8626.3	3	11.35	0	6.11E+04		(R)VGMVE	(R)V/G|M/V/E/T N S Q D/R P V D D|V K(I)		112.28	630.3068	1888.907	-0.0011	-0.6	4.23	18350.6	7.96	HUMAN	Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1
7751	dirMS_041712_NAR_30mM_minus2.7160.7160.2	2	11.34	0	4.82E+05		(K)DAQGQI	(K)D A/Q|G\Q|P G\L E R(A)		92.98	535.762	1070.523	-0.0058	-5.4	4.37	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
7752	dirMS_041712_NAR_40mM_minus2.11219.11219.3	3	11.34	0	4.48E+04		(R)EALAEA	(R)E A|L|A/E|A A/L E S P R P A L V R(S)		149.25	598.3347	1792.992	-0.002	-1.1	4.79	22148.2	5.87	HUMAN	B3KY21	Na(+)/H(+) exchange regulatory cofactor NHE-RF1
7753	dirMS_041712_NAR_50mM_minus2.12386.12458.3	3	11.34	1	1.67E+05		(K)IINADSE	(K)I/I\N|A/D/S E D/P K Y I I N V K(Q)		139.08	611.3243	1831.98	-0.0217	-11.8	4.56	14693.3	4.69	HUMAN	C9JLS9	26S protease regulatory subunit 7 (Fragment)
7754	dirMS_041712_NAR_60mM_minus.15180.15180.2	2	11.34	0	4.20E+05		(R)EHALLA	(R)E H|A|L\L|A/Y/T L G V\K(Q)		144.65	657.873	1314.742	-0.0029	-2.2	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
7755	dirMS_041712_NAR_120mM_plus.11005.11005.4	4	11.34	1	5.61E+05		(K)AVEHINI	(K)A V\E H I N K T I A/P\A\L/V\S/K(K)		110.72	423.5016	1690.985	-0.0005	-0.3	8.64	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
7756	dirMS_041712_NAR_120mM_plus.11544.11544.3	3	11.34	2	3.74E+05		(K)KGEKDIF	(K)K\G E K D I\P G L|T/D T|T/V/P R(R)		113.53	576.3192	1726.933	0.0097	5.6	6.12	25082	11.29	HUMAN	A2A3R5	40S ribosomal protein S6
7757	dirMS_041712_NAR_120mM_plus.16322.16322.4	4	11.34	1	9.26E+05		(R)ALEHFTI	(R)A/L E H/F T D L Y/D/I K R(A)		138.4	405.9647	1620.838	-0.0011	-0.7	5.38	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
7758	dirMS_041712_NAR_120mM_plus.20755.20755.3	3	11.34	0	3.47E+05		(K)VHLVGII	(K)V H L V G\I/D\I/F/T/G/K(K)		161.67	433.5874	1298.747	0.0009	0.7	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
7759	dirMS_041712_NAR_120mM_plus.9433.9573.3	3	11.34	1	1.66E+06		(R)GKLDGN	(R)G K\L D\G N Q|D/L/I/R(F)		103.23	410.2263	1228.664	-0.0001	-0.1	5.96	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
7760	dirMS_041712_NAR_20mM_plus.10912.11100.2	2	11.34	0	1.28E+05		(K)TIVFVET	(K)T I|V/F V/E/T/K(R)		148.33	468.7674	936.54	-0.0125	-13.4	5.66	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
7761	dirMS_041712_NAR_20mM_plus.6016.6016.3	3	11.34	0	1.02E+06	M295m M2	(R)mGQmA	(R)m G Q\m A m G G|A|m/G/I/N N R(G)	m:Oxidized methionine	100.27	534.8861	1538.67	63.9743	-3.4	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
7762	dirMS_041712_NAR_20mM_plus.7750.7750.2	2	11.34	0	5.41E+04		(K)LAAIGEA	(K)L/A|A/I|G/E A T R(L)		123.2	451.2557	901.51	-0.006	-6.7	6	533778	5.74	HUMAN	Q15149	Plectin
7763	dirMS_041712_NAR_30mM_plus2.19636.19636.2	2	11.34	0	3.65E+05		(K)SNNVEN	(K)S N|N/V|E M D\W V L/K(H)		156.72	667.8205	1334.641	-0.0072	-5.4	4.37	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
7764	dirMS_041712_NAR_50mM_plus2.16184.16184.3	3	11.34	1	1.35E+06		(K)CEFQDA	(K)C E F\Q D A/Y V|L|L\S E/K K(I)	C:Carbamidomethylation	152.35	577.2866	1729.847	-0.0013	-0.8	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
7765	dirMS_041712_NAR_50mM_plus2.18613.18613.3	3	11.34	1	9.79E+05		(R)LKLPSIPI	(R)L K L P S I P L/V/P V S A Q K(R)		166.8	530.6702	1589.999	-0.0028	-1.8	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
7766	dirMS_041712_NAR_50mM_plus2.20533.20533.3	3	11.34	1	1.87E+05		(K)SYLNMD	(K)S Y/L/N M/D A I/M E A I/K K(T)		176.7	542.9473	1626.823	0.0044	2.7	5.79	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
7767	dirMS_041712_NAR_60mM_plus.4794.4794.3	3	11.34	1	3.22E+05		(K)AGADEE	(K)A/G/A/D/E E R A/E T A\R(L)		79.42	425.868	1275.592	-0.0029	-2.3	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
7768	dirMS_041712_NAR_20mM_minus.11758.11758.2	2	11.33	0	8.32E+04		(R)GGIVDE	(R)G G I|V/D/E G A L L R(A)		166.5	550.3071	1099.611	-0.0037	-3.3	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
7769	dirMS_041712_NAR_20mM_minus.14683.14683.2	2	11.33	0	9.62E+04		(K)IYVDDGI	(K)I Y|V/D D G L|I/S L Q V/K(Q)		201.6	731.9104	1462.815	-0.0016	-1.1	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
7770	dirMS_041712_NAR_30mM_minus2.14395.14395.2	2	11.33	0	2.02E+05		(R)ELAFQIS	(R)E L/A/F/Q/I S K(E)		131.83	468.2614	935.52	-0.0041	-4.4	6.1	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
7771	dirMS_041712_NAR_30mM_minus2.17869.17869.2	2	11.33	0	8.07E+04		(R)ILFQEFR	(R)I/L|F/Q|E F\R(Q)		151.47	476.7657	952.525	-0.001	-1	6	232239.1	5.52	HUMAN	F2Z2U8	Myosin-14
7772	dirMS_041712_NAR_30mM_minus2.9521.9731.2	2	11.33	1	3.10E+06	S190s M19	(K)LRSFsm(	(K)L/R|S|F/s m(-)	s:N-acetylglucosamine (S) m:	106.32	480.2405	740.376	219.0978	24.5	9.75	22086.5	10.19	HUMAN	H0YAC5	Receptor expression-enhancing protein 2 (Fragment)
7773	dirMS_041712_NAR_50mM_minus2.15742.15742.3	3	11.33	0	9.11E+04		(K)SLLSSAS	(K)S L|L|S S/A S A/T V G H G L T A V K(E)		158.02	566.9809	1698.939	-0.0103	-6.1	8.49	61083	4.61	HUMAN	Q8IWE2	Protein NOXP20
7774	dirMS_041712_NAR_60mM_minus.17254.17338.3	3	11.33	0	3.22E+05		(K)GSDHSA	(K)G S D H S A S\L\E|P G\E\L|A E L/V R(S)		156.83	622.9764	1866.919	-0.0045	-2.4	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
7775	dirMS_041712_NAR_120mM_plus.16099.16159.3	3	11.33	1	1.91E+05		(R)KSEIEYY	(R)K\S E I\E|Y|Y/A/M L/A K(T)		138.35	482.5826	1445.735	-0.0012	-0.9	6.14	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
7776	dirMS_041712_NAR_120mM_plus.6678.6680.3	3	11.33	1	8.63E+05		(R)SKEQAE	(R)S K E Q\A|E|L/E/A A/R(Q)		88.25	411.2137	1231.628	-0.0012	-0.9	4.78	533778	5.74	HUMAN	Q15149	Plectin
7777	dirMS_041712_NAR_20mM_plus.14829.14829.2	2	11.33	0	1.13E+05		(K)LLGELLQ	(K)L/L|G E/L/L Q|D N A K(L)		173.7	607.3421	1213.679	-0.0018	-1.4	4.37	35556.4	9.3	HUMAN	F2Z393	Transaldolase
7778	dirMS_041712_NAR_20mM_plus.19050.19050.3	3	11.33	0	2.07E+05		(K)TLETQS	(K)T L E\T Q S A L/G/P/A/L Q A A F K(L)		202.57	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
7779	dirMS_041712_NAR_30mM_plus2.11316.11316.2	2	11.33	0	6.71E+05		(K)LTVDSAI	(K)L T|V/D|S A I A R(D)		113.02	473.2687	945.536	-0.0062	-6.6	5.84	334221.3	6.44	HUMAN	P15924	Desmoplakin
7780	dirMS_041712_NAR_30mM_plus2.13550.13550.2	2	11.33	0	2.02E+05		(R)LIIAGTS	(R)L I|I/A/G T S A Y A/R(L)		124.3	568.322	1135.647	-0.0103	-9	8.75	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
7781	dirMS_041712_NAR_30mM_plus2.14588.14878.2	2	11.33	0	6.45E+05		(R)TFEDFVI	(R)T/F|E/D F V/R(I)		130.13	457.225	913.441	0.0013	1.4	4.37	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
7782	dirMS_041712_NAR_30mM_plus2.19469.19469.2	2	11.33	0	2.67E+05		(K)TVDNFV	(K)T V|D N F/V/A/L A T G E K(G)		155.35	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
7783	dirMS_041712_NAR_30mM_plus2.20744.20744.2	2	11.33	0	2.60E+05		(R)ASLSLW	(R)A S/L/S|L/W/Q/A/M E/K(G)		162.9	632.3231	1263.64	-0.0013	-1	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
7784	dirMS_041712_NAR_30mM_plus2.21138.21138.2	2	11.33	0	3.35E+05		(R)GVVQEL	(R)G V/V/Q E/L/Q\Q A/I/S K(L)		165.75	650.3632	1299.727	-0.0076	-5.8	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
7785	dirMS_041712_NAR_30mM_plus2.6370.6370.2	2	11.33	0	2.23E+05		(R)SPDNPN	(R)S/P/D|N|P M N Q R(A)		88.22	529.7357	1058.468	-0.0042	-4	5.55	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
7786	dirMS_041712_NAR_30mM_plus2.7253.7253.2	2	11.33	0	1.34E+05		(K)AAAAAA	(K)A A|A|A|A|A/A L Q A K(S)		92.78	478.7844	956.552	0.0092	9.6	8.8	37884.5	11.27	HUMAN	H3BM89	60S ribosomal protein L4
7787	dirMS_041712_NAR_120mM_minus.10449.10449.3	3	11.32	1	2.31E+05		(R)RQQEQ	(R)R/Q Q|E\Q\Q\V/P I L E/K(F)		111.02	499.2772	1495.823	-0.0057	-3.8	6.14	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
7788	dirMS_041712_NAR_120mM_minus.7297.7297.3	3	11.32	1	1.49E+06		(R)CREMDI	(R)C R E\M/D|E|Q I/R(L)	C:Carbamidomethylation	93.97	412.8591	1236.546	0.0168	13.6	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
7789	dirMS_041712_NAR_30mM_minus2.19589.19589.2	2	11.32	0	2.93E+05		(R)YLTVAA	(R)Y L|T/V/A/A/V F R(G)		162.75	520.2998	1039.593	-0.0012	-1.1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
7790	dirMS_041712_NAR_40mM_minus2.13493.13493.3	3	11.32	1	3.72E+04		(K)VTLVVG	(K)V T/L/V/V/G/A S Q D I I/P Q L K K(K)		163.58	603.696	1809.084	-0.011	-6.1	8.56	25180.2	5.34	HUMAN	E7EMS6	Catechol O-methyltransferase (Fragment)
7791	dirMS_041712_NAR_40mM_minus2.14278.14278.3	3	11.32	1	1.76E+05		(K)ITSDEPL	(K)I/T|S/D|E/P L T K D D\I/P V F L R(H)		168.4	653.6833	1959.043	-0.008	-4.1	4.23	22313.1	4.9	HUMAN	B1AHE4	Ataxin 10 (Fragment)
7792	dirMS_041712_NAR_40mM_minus2.6945.6945.2	2	11.32	0	5.85E+05		(R)GYSFTT	(R)G Y/S|F/T|T T|A E R(E)		111.95	566.7661	1132.527	-0.002	-1.8	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
7793	dirMS_041712_NAR_60mM_minus.10852.10852.3	3	11.32	1	2.63E+05		(R)QSVEAD	(R)Q S/V/E/A/D/I N G\L R R(V)		120.58	453.2461	1357.718	0.0055	4	6.07	19213.2	4.66	HUMAN	K7EMD9	Keratin, type I cytoskeletal 13 (Fragment)
7794	dirMS_041712_NAR_60mM_minus.15537.15537.3	3	11.32	0	3.64E+05		(K)THLPGF	(K)T H/L\P G F\V|E/Q/A E A L K(A)		146.38	513.947	1539.817	0.0099	6.4	5.37	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
7795	dirMS_041712_NAR_60mM_minus.15540.15540.3	3	11.32	1	1.97E+05		(R)ASLISAV	(R)A S|L/I/S A/V S\D K L R(W)		146.18	420.5811	1259.732	-0.003	-2.4	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
7796	dirMS_041712_NAR_60mM_minus.15801.15801.3	3	11.32	1	2.33E+05		(K)ELKIDIIP	(K)E L/K\I D I\I/P N/P Q E R(T)		148.62	522.2935	1564.869	-0.0034	-2.2	4.68	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
7797	dirMS_041712_NAR_60mM_minus.9386.9387.3	3	11.32	0	1.30E+05	M151m	(R)AYADSY	(R)A Y|A D/S/Y/Y|Y E/D G G m K P R(V)	m:Oxidized methionine	112.08	634.6041	1885.806	15.9916	-1.7	4.56	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
7798	dirMS_041712_NAR_120mM_plus.9029.9029.3	3	11.32	0	1.41E+06		(K)HTGPNS	(K)H T G P\N\S P D|T\A|N/D/G F V R(L)		100.03	562.26	1684.767	-0.0019	-1.2	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
7799	dirMS_041712_NAR_20mM_plus.8311.8311.2	2	11.32	0	2.60E+04		(K)SPVESTT	(K)S/P V|E\S T T E\P/P A V/R(A)		127.48	685.3502	1369.696	-0.0027	-1.9	4.53	38808	7.85	HUMAN	B4DZT4	Protein transport protein Sec24C
7800	dirMS_041712_NAR_30mM_plus2.21825.21825.2	2	11.32	0	3.83E+05		(R)FSWNV	(R)F S/W|N|V W/P\S/S R(L)		169.53	633.3085	1265.606	0.0035	2.8	9.75	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
7801	dirMS_041712_NAR_30mM_plus2.22153.22153.2	2	11.32	0	2.52E+05		(K)LISLFQA	(K)L I|S L/F Q A M K(K)		171.13	525.8042	1050.602	-0.0005	-0.5	8.75	533778	5.74	HUMAN	Q15149	Plectin
7802	dirMS_041712_NAR_40mM_plus2.6823.6944.2	2	11.32	0	4.64E+05		(K)QYGFCK	(K)Q/Y/G/F/C/K(A)	C:Carbamidomethylation	100.4	401.6809	802.355	-0.0007	-0.9	8.59	40209.9	5.43	HUMAN	C9JV77	Alpha-2-HS-glycoprotein
7803	dirMS_041712_NAR_50mM_plus2.12302.12302.3	3	11.32	1	1.20E+06		(K)ASLENSL	(K)A S|L/E/N S L R/E V E/A R(Y)		132.27	491.9313	1473.766	0.0138	9.3	4.79	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
7804	dirMS_041712_NAR_50mM_plus2.14690.14690.3	3	11.32	0	1.17E+06		(R)EHALLA	(R)E H A\L\L\A/Y/T/L/G/V/K(Q)		145.75	438.9176	1314.742	-0.0034	-2.6	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
7805	dirMS_041712_NAR_50mM_plus2.20238.20238.3	3	11.32	1	3.86E+05		(R)FLDKALE	(R)F L/D K A L E\L/N/M/L/S L K(G)		174.82	545.6431	1634.919	-0.0038	-2.4	6.07	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
7806	dirMS_041712_NAR_50mM_plus2.8513.8513.3	3	11.32	0	5.51E+04		(K)EAAYHP	(K)E/A A Y/H/P E V/A/P D/V R(L)		111.45	485.2423	1453.707	0.0053	3.7	4.65	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
7807	dirMS_041712_NAR_120mM_minus.20522.20540.3	3	11.31	1	3.46E+05		(R)LDLAGR	(R)L/D|L/A/G R D L/T D/Y\L M/K(I)		169.02	541.9508	1623.841	-0.0032	-2	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
7808	dirMS_041712_NAR_120mM_minus.4459.4590.2	2	11.31	0	2.84E+06	M46m M4	(R)HQGVm	(R)H/Q|G V|m/V/G m\G Q|K(D)	m:Oxidized methionine	73.83	602.2834	1171.571	31.9885	-1.1	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
7809	dirMS_041712_NAR_20mM_minus.13145.13145.2	2	11.31	0	2.34E+05		(R)GVVDSE	(R)G V/V\D\S\E D I/P/L N/L S\R(E)		183.02	757.3944	1513.786	-0.0041	-2.7	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
7810	dirMS_041712_NAR_30mM_minus2.15334.15334.2	2	11.31	0	6.01E+05		(R)YPVNSV	(R)Y/P V|N S V N I/L K(A)		136.9	573.8282	1146.652	-0.0026	-2.3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
7811	dirMS_041712_NAR_40mM_minus2.14868.14868.3	3	11.31	1	1.04E+06	M116m	(R)ELAILLG	(R)E L/A I/L L/G m L D/P A E K D E/K(G)	m:Oxidized methionine	171.45	634.338	1884.999	16.0008	3.1	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
7812	dirMS_041712_NAR_50mM_minus2.11538.11539.3	3	11.31	1	5.31E+04		(K)ILDSVGI	(K)I/L/D/S V/G I E/A D D D R L N K(V)		133.65	591.6389	1772.902	-0.0003	-0.2	4.04	11664.7	4.42	HUMAN	P05387	60S acidic ribosomal protein P2
7813	dirMS_041712_NAR_50mM_minus2.12904.12904.3	3	11.31	1	1.79E+05		(K)GGELVY	(K)G G E/L|V|Y/T D S E A R D V F E K(A)		141.53	638.9739	1914.908	-0.0008	-0.4	4.18	533778	5.74	HUMAN	Q15149	Plectin
7814	dirMS_041712_NAR_20mM_plus.12863.12863.2	2	11.31	0	1.41E+05		(R)LVVPAS	(R)L V|V/P A S Q/C G S L I/G K(G)	C:Carbamidomethylation	161.55	714.8991	1428.788	0.003	2.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
7815	dirMS_041712_NAR_20mM_plus.15140.15140.2	2	11.31	0	2.46E+05		(K)LLCGLLA	(K)L/L|C/G/L L/A E R(L)	C:Carbamidomethylation	176.63	522.7971	1044.587	-0.0001	-0.1	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
7816	dirMS_041712_NAR_20mM_plus.17831.17831.2	2	11.31	0	8.88E+04		(K)VDFPQD	(K)V/D/F/P Q\D/Q/L T/A L T G R(I)		194.77	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
7817	dirMS_041712_NAR_30mM_plus2.8870.8946.2	2	11.31	0	3.99E+05		(R)LLEAAS	(R)L/L|E|A/A/S V/S\S K(G)		100.32	502.7831	1004.562	-0.0033	-3.3	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
7818	dirMS_041712_NAR_50mM_plus2.17236.17320.3	3	11.31	1	1.17E+06		(K)DNNGVI	(K)D N/N/G V/I/G L/L/E/P M K K(S)		158.73	509.9448	1527.82	-0.0001	-0.1	6.07	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
7819	dirMS_041712_NAR_50mM_plus2.21651.21651.3	3	11.31	1	2.38E+05		(K)LGFAGL	(K)L/G|F\A/G L V/Q E I S F G T T K D K(M)		184.83	637.6781	1911.022	-0.0025	-1.3	6.07	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
7820	dirMS_041712_NAR_60mM_plus.12182.12182.3	3	11.31	1	1.01E+06	M232m	(R)MSmKE	(R)M S m K E V D\E Q|M|L/N V/Q N K(N)	m:Oxidized methionine	120.57	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
7821	dirMS_041712_NAR_40mM_minus2.14684.14684.3	3	11.3	0	1.70E+05	M159m	(R)SVAAIHI	(R)S V/A A I H P S L E/I\P m/L I/P K(E)	m:Oxidized methionine	171.33	611.3477	1816.04	15.9884	-3.5	6.47	31606.3	6.72	HUMAN	B4E329	Phosphoribosyl pyrophosphate synthase-associated protein 2
7822	dirMS_041712_NAR_50mM_minus2.5893.5893.3	3	11.3	0	8.40E+04		(K)ANESSPI	(K)A N/E|S S/P K P V G/P/P|P E R(D)		95.83	521.2695	1561.797	-0.0029	-1.9	6.19	10501.2	5.81	HUMAN	A6PVM9	Allograft inflammatory factor 1-like
7823	dirMS_041712_NAR_50mM_minus2.5914.5914.3	3	11.3	0	8.40E+04		(K)ANESSPI	(K)A N|E/S/S/P/K/P V G P/P P E R(D)		95.83	521.2695	1561.797	-0.0029	-1.9	6.19	10501.2	5.81	HUMAN	A6PVM9	Allograft inflammatory factor 1-like
7824	dirMS_041712_NAR_60mM_minus.11922.11922.2	2	11.3	1	3.16E+05		(K)TIDDLED	(K)T I|D/D\L/E D K L/K(C)		126.35	595.3185	1189.631	-0.0013	-1.1	4.22	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
7825	dirMS_041712_NAR_60mM_minus.17203.17203.3	3	11.3	0	9.52E+04		(R)GFGHIG	(R)G F G H I G I A V|P D/V Y S A C K(R)	C:Carbamidomethylation	156.02	597.6347	1790.889	0.0001	0.1	6.74	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
7826	dirMS_041712_NAR_60mM_minus.4987.4987.3	3	11.3	1	1.11E+05		(K)DSYVGD	(K)D S/Y/V/G D E A Q S K/R(G)		82.27	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
7827	dirMS_041712_NAR_120mM_plus.22833.23004.3	3	11.3	1	4.87E+05		(K)GLAPDLI	(K)G L|A\P/D/L/P E/D L/Y H L I K K(A)		174.02	608.0076	1822.011	-0.0027	-1.5	5.38	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
7828	dirMS_041712_NAR_20mM_plus.16628.16628.2	2	11.3	0	1.99E+05		(K)VQIAVA	(K)V Q/I/A/V/A/N A Q E L/L Q/R(M)		186.25	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
7829	dirMS_041712_NAR_20mM_plus.17095.17095.2	2	11.3	0	9.29E+04		(R)AVLVDLI	(R)A V\L\V D L/E/P/G T M D S V R(S)		189.42	801.414	1601.82	0.0004	0.2	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
7830	dirMS_041712_NAR_20mM_plus.19061.19061.3	3	11.3	0	2.07E+05		(K)TLETQS	(K)T L E T Q S A|L/G/P/A L Q A A/F K(L)		202.57	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
7831	dirMS_041712_NAR_20mM_plus.19114.19114.2	2	11.3	0	2.26E+05		(K)ILTFDQL	(K)I L|T|F D Q L A|L D S P K(G)		203.22	730.9063	1460.8	0.0058	4	4.21	14643	11.93	HUMAN	F8VUA6	60S ribosomal protein L18 (Fragment)
7832	dirMS_041712_NAR_20mM_plus.7920.7920.2	2	11.3	0	9.11E+04	M21m	(K)ATAVmF	(K)A T/A V/m/P D G Q F K(D)	m:Oxidized methionine	124.52	590.7861	1164.572	15.9932	-1.5	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
7833	dirMS_041712_NAR_30mM_plus2.14602.14602.3	3	11.3	0	7.47E+04		(K)VNQIGS	(K)V N\Q I\G S\V T/E/S/I/Q/A C/K(L)	C:Carbamidomethylation	129.65	545.28	1633.821	0.0041	2.5	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
7834	dirMS_041712_NAR_30mM_plus2.21533.21533.2	2	11.3	0	3.35E+05		(R)NSYLEVI	(R)N S|Y|L/E V L L K(L)		167.92	539.8092	1078.614	-0.0032	-2.9	6	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
7835	dirMS_041712_NAR_30mM_plus2.6309.6309.2	2	11.3	0	1.43E+05		(R)FGGSGS	(R)F/G/G\S/G S Q/V/D S A R(M)		87.52	584.2731	1167.539	0	0	5.84	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
7836	dirMS_041712_NAR_30mM_plus2.8472.8472.2	2	11.3	0	7.92E+05		(K)TAVCDIF	(K)T A|V/C D/I|P\P/R(G)	C:Carbamidomethylation	99.28	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
7837	dirMS_041712_NAR_40mM_plus2.10268.10268.2	2	11.3	0	6.93E+04		(R)EYQELM	(R)E/Y|Q/E/L/M N/V K(L)		125.03	577.2823	1153.556	0.0015	1.3	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
7838	dirMS_041712_NAR_40mM_plus2.13287.13287.3	3	11.3	0	6.01E+05		(R)QVSASE	(R)Q V/S A S/E L H T S/G I|L/G P E T L R(D)		145.08	665.6807	1995.051	-0.023	-11.5	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
7839	dirMS_041712_NAR_40mM_plus2.16740.16740.3	3	11.3	0	3.49E+04	M64m	(R)GFGFITF	(R)G F/G\F|I/T/F T N P E H A S V A m R(A)	m:Oxidized methionine	164.88	666.6524	1981.959	15.9838	-5.6	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
7840	dirMS_041712_NAR_40mM_plus2.19783.19783.3	3	11.3	1	4.44E+05		(R)ILDDDTI	(R)I/L|D/D D T\I I/T T L E/N L K R(E)		185.12	625.0111	1873.028	-0.0089	-4.8	4.23	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
7841	dirMS_041712_NAR_50mM_plus2.18583.18583.3	3	11.3	0	4.06E+05		(R)AVSILPL	(R)A V/S|I/L/P L/L/G H G\V/P R(L)		165.87	476.9615	1428.869	0.0014	1	9.8	66841.7	7.74	HUMAN	F5H721	WW domain-binding protein 11
7842	dirMS_041712_NAR_50mM_plus2.19115.19115.3	3	11.3	0	2.29E+05		(K)LAKPLSS	(K)L A\K P L S S L T/P/L/I M A/A K(E)		168.37	552.004	1653.997	0.0003	0.2	10	24711.4	5.19	HUMAN	H7C1X3	PAK-2p34 (Fragment)
7843	dirMS_041712_NAR_50mM_plus2.19811.19811.3	3	11.3	1	1.48E+04		(K)AKINEA	(K)A K I N E A|V/E C|L/L|S L/K(A)	C:Carbamidomethylation	172.07	529.9621	1587.878	-0.0057	-3.6	6.18	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase

7844	dirMS_041712_NAR_50mM_plus2.8902.8902.3	3	11.3	0	1.53E+06		(R)LESGM	(R)L E|S G M Q N M/S I H/T/K(T)		113.25	492.5704	1475.698	-0.0015	-1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
7845	dirMS_041712_NAR_60mM_plus.21133.21133.3	3	11.3	1	1.05E+05		(K)AKINEA	(K)A/K I N E A\V E|C/L L/S/L K(A)	C:Carbamidomethylation	173.75	529.9643	1587.878	0.0009	0.6	6.18	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
7846	dirMS_041712_NAR_60mM_plus.7204.7204.2	2	11.3	0	5.06E+05		(R)IGKPAP	(R)I/G K/P/A/P D/F/K(A)		95.78	486.7793	972.551	0	0	8.59	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
7847	dirMS_041712_NAR_60mM_plus.7597.7620.3	3	11.3	1	9.64E+05		(R)YLAEVA	(R)Y/L/A E/V/A A/G D D/K K(G)		97.83	427.2226	1279.653	0.0004	0.3	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
7848	dirMS_041712_NAR_30mM_minus2.10102.10102.2	2	11.29	0	6.04E+04		(R)MYAAL	(R)M/Y|A A L/G/D/P/K(A)		109.15	483.2423	965.476	0.0012	1.3	5.59	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
7849	dirMS_041712_NAR_30mM_minus2.18162.18162.2	2	11.29	0	2.92E+05		(K)LLCGLLA	(K)L L|C/G L/L/A E R(L)	C:Carbamidomethylation	152.05	522.7963	1044.587	-0.0017	-1.6	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
7850	dirMS_041712_NAR_30mM_minus2.6108.6108.2	2	11.29	0	1.56E+05		(R)AQAEQ	(R)A Q|A/E/Q A A/L/R(Q)		87.63	479.2592	957.511	-0.0001	-0.1	6.05	533778	5.74	HUMAN	Q15149	Plectin
7851	dirMS_041712_NAR_40mM_minus2.14105.14105.3	3	11.29	0	6.49E+05		(R)IHFPLAT	(R)I H F/P L A\T Y|A|P/V I S A E K(A)		167.75	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
7852	dirMS_041712_NAR_50mM_minus2.8650.8650.3	3	11.29	0	1.58E+06		(R)EIVHIQA	(R)E/I V H\I Q A\G|Q/C/G N Q/I/G/A K(F)	C:Carbamidomethylation	116.8	608.3087	1822.923	-0.0113	-6.2	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
7853	dirMS_041712_NAR_120mM_plus.6689.6689.2	2	11.29	0	5.08E+05		(R)HLTGEF	(R)H/L/T G E F E/K(K)		88.68	480.743	960.479	0.0002	0.2	5.4	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
7854	dirMS_041712_NAR_120mM_plus.7124.7183.3	3	11.29	1	1.73E+06		(R)RQLETL	(R)R\Q\L E|T|L/G Q E K(L)		91.05	401.2207	1201.653	-0.006	-5	6.14	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
7855	dirMS_041712_NAR_20mM_plus.13852.13852.2	2	11.29	0	1.73E+05		(K)APILIAT	(K)A/P I|L|I/A/T D V A S/R(G)		166.88	613.8559	1226.71	-0.0058	-4.7	5.88	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
7856	dirMS_041712_NAR_20mM_plus.17840.17840.2	2	11.29	0	1.54E+05		(R)TVQSLEI	(R)T V|Q|S\L E/I D L D/S M R(N)		194.82	753.8776	1506.747	0.0011	0.7	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
7857	dirMS_041712_NAR_30mM_plus2.10228.10246.2	2	11.29	0	8.95E+05		(R)GLDVED	(R)G L|D|V/E D/V K(F)		108.02	437.7293	874.452	-0.0003	-0.4	4.03	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
7858	dirMS_041712_NAR_30mM_plus2.10272.10272.2	2	11.29	0	4.82E+05		(R)LGAPAL	(R)L G|A/P A/L T S R(Q)		107.23	443.2607	885.515	-0.0011	-1.3	9.75	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
7859	dirMS_041712_NAR_30mM_plus2.10673.10760.2	2	11.29	0	7.29E+05		(R)GGDLM	(R)G G\D|L|M|A/Y D/R(R)		110	499.2257	997.441	0.0034	3.4	4.21	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
7860	dirMS_041712_NAR_30mM_plus2.5940.5967.2	2	11.29	0	4.28E+05		(K)MIYASS	(K)M/I/Y A/S/S/K(D)		85.65	400.2035	799.402	-0.0021	-2.7	8.34	22956	8.8	HUMAN	E9PK25	Cofilin-1
7861	dirMS_041712_NAR_40mM_plus2.16569.16569.3	3	11.29	0	1.92E+05		(R)VAAGLP	(R)V A|A G L/P P I\L V H T D A A Q A L/G K(Q)		164.08	648.041	1942.112	-0.0036	-1.8	6.71	17974.2	4.97	HUMAN	C9JNL5	Selenocysteine lyase (Fragment)
7862	dirMS_041712_NAR_50mM_plus2.14233.14233.3	3	11.29	0	1.02E+05		(R)VWYVSN	(R)V/W|Y/V/S/N I/D G T H I A/K(T)		142.87	534.9466	1602.828	-0.0022	-1.4	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
7863	dirMS_041712_NAR_50mM_plus2.20074.20074.3	3	11.29	0	2.78E+05		(R)LQSLPF	(R)L Q|S L/P F A L/T/H L N L K(A)		173.85	532.3178	1594.931	0.0073	4.6	8.76	175851.7	5.01	HUMAN	Q14160	Protein scribble homolog
7864	dirMS_041712_NAR_60mM_plus.10162.10162.3	3	11.29	1	1.48E+06		(K)IFRDGEE	(K)I/F\R D G E E\A\G/A/Y/D G/P R(T)		111.47	551.593	1652.766	-0.0019	-1.1	4.32	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
7865	dirMS_041712_NAR_60mM_plus.16235.16235.3	3	11.29	0	5.41E+05		(K)WIGLDL	(K)W I|G/L D L/S/N G K/P R(D)		141.97	452.5864	1355.743	0.0016	1.2	8.75	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
7866	dirMS_041712_NAR_120mM_minus.11948.11948.4	4	11.28	2	6.11E+05		(R)YESLTD	(R)Y E/S L/T D/P S K L D/S G K E/L K(I)		119.2	478.2478	1909.975	-0.0059	-3.1	4.78	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
7867	dirMS_041712_NAR_120mM_minus.15875.16039.4	4	11.28	1	1.70E+06		(K)QLEAID	(K)Q\L E A/I/D Q/L/H/L/E/Y A K R(A)		140.95	457.499	1826.976	-0.0018	-1	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
7868	dirMS_041712_NAR_120mM_minus.7962.7970.2	2	11.28	1	1.29E+05		(K)MKGDY	(K)M/K|G|D/Y F/R(Y)		97.72	458.7226	916.434	0.0034	3.7	8.34	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
7869	dirMS_041712_NAR_20mM_minus.12344.12344.3	3	11.28	0	7.45E+05	M73m	(R)AVLVDL	(R)A V|L V D\L\E/P G T\m/D S V R(S)	m:Oxidized methionine	172.42	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
7870	dirMS_041712_NAR_20mM_minus.8230.8337.2	2	11.28	0	1.66E+05	M161m	(K)LLIEmE	(K)L/L|I/E/m/E Q/R(L)	m:Oxidized methionine	132.15	524.2783	1031.555	15.9939	-0.9	4.53	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
7871	dirMS_041712_NAR_40mM_minus2.12388.12388.3	3	11.28	0	6.96E+04		(R)VYALPE	(R)V Y A L/P E D L/V/E V K/P K(M)		156.27	533.9726	1599.899	0.004	2.5	4.68	69862.6	5.58	HUMAN	B4DGB4	Plastin-3
7872	dirMS_041712_NAR_40mM_minus2.14667.14667.3	3	11.28	0	1.69E+05	M159m	(R)SVAAIH	(R)S V/A\A I/H P S L E I/P m L I P K(E)	m:Oxidized methionine	171.32	611.3477	1816.04	15.9884	-3.5	6.47	31606.3	6.72	HUMAN	B4E329	Phosphoribosyl pyrophosphate synthase-associated protein 2
7873	dirMS_041712_NAR_50mM_minus2.11368.11368.3	3	11.28	1	9.59E+04		(R)LLIVSTT	(R)L L|I/V|S T/T P Y/S E/K D/T K(Q)		133.12	565.6428	1694.921	-0.0072	-4.3	6.07	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
7874	dirMS_041712_NAR_50mM_minus2.11772.11772.3	3	11.28	0	1.97E+05	M221m	(K)mLDAE	(K)m/L\D\A/E/D/I/V G T A R P D/E K(A)	m:Oxidized methionine	134.93	592.6214	1759.853	15.9966	0.9	4.1	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
7875	dirMS_041712_NAR_50mM_minus2.12438.12438.3	3	11.28	0	2.71E+05		(K)AASDIA	(K)A A/S/D I/A M\T E L/P/P T H P I R(L)		139.15	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
7876	dirMS_041712_NAR_60mM_minus.8317.8458.3	3	11.28	0	4.60E+05	M148m	(R)AHSSmV	(R)A H S S\m\V/G\V|N/L/P Q K(A)	m:Oxidized methionine	106.77	461.9064	1367.71	15.9947	-0.2	8.8	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
7877	dirMS_041712_NAR_60mM_minus.9784.9801.3	3	11.28	1	3.78E+05		(R)YLAEFA	(R)Y/L|A E/F A/T G N D/R K(E)		114.65	462.2282	1384.686	-0.0155	-11.2	6.07	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
7878	dirMS_041712_NAR_120mM_plus.20607.20607.4	4	11.28	1	2.15E+05		(K)AAIDWF	(K)A A/I/D W/F D G K E/F H/G N I I K(V)		161.23	491.0027	1960.992	-0.0026	-1.3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
7879	dirMS_041712_NAR_20mM_plus.16754.16754.2	2	11.28	0	1.25E+05		(R)LLEAQIA	(R)L L\E A Q I|A\T G G I I/D|P|K(E)		185.92	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
7880	dirMS_041712_NAR_30mM_plus2.11384.11384.2	2	11.28	0	1.33E+05		(R)LVDMM	(R)L/V|D/M M/E R(G)		112.3	447.2119	893.422	-0.0054	-6.1	4.37	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
7881	dirMS_041712_NAR_30mM_plus2.17233.17233.2	2	11.28	0	2.55E+05		(R)LIVNVN	(R)L I|V|N/V N D/L R(R)		143.57	528.3113	1055.621	-0.0054	-5.2	5.84	91606.8	5.53	HUMAN	P25205	DNA replication licensing factor MCM3
7882	dirMS_041712_NAR_40mM_plus2.10330.10330.2	2	11.28	0	9.40E+04		(K)IGGIGTV	(K)I/G G\I/G/T/V\P V\G\R(V)		125.75	513.3081	1025.61	-0.0013	-1.2	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
7883	dirMS_041712_NAR_60mM_plus.12628.12648.3	3	11.28	0	1.29E+06		(K)ADDGR	(K)A/D|D/G R P/F/P Q V I/K(S)		121.67	448.2414	1342.711	-0.0017	-1.3	6	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
7884	dirMS_041712_NAR_60mM_plus.15880.15880.3	3	11.28	0	2.66E+05		(K)NFDLRP	(K)N/F/D/L R/P G V I V/R(-)		139.93	429.248	1285.738	-0.0081	-6.3	9.6	33192.3	6.77	HUMAN	B4DN45	S-adenosylmethionine synthase
7885	dirMS_041712_NAR_60mM_plus.16542.16542.3	3	11.28	1	5.15E+05		(R)TDGKVF	(R)T/D|G K/V F/Q/F L N/A K(C)		143.5	456.5782	1367.732	-0.0117	-8.6	8.26	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
7886	dirMS_041712_NAR_60mM_plus.16807.16807.3	3	11.28	1	2.02E+05		(K)IKDLSTV	(K)I K\D L S T V/E|A/L Q N L/K(N)		144.67	524.6388	1571.9	0.0015	1	6.07	13242.4	4.17	HUMAN	E9PPH5	Acidic leucine-rich nuclear phosphoprotein 32 family member E (Fragment)
7887	dirMS_041712_NAR_120mM_minus.12350.12350.3	3	11.27	0	1.03E+06		(K)TFTAWC	(K)T/F|T/A/W|C N S H L R(K)	C:Carbamidomethylation	121.72	464.8871	1392.648	-0.001	-0.7	9.44	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
7888	dirMS_041712_NAR_30mM_minus2.13080.13080.2	2	11.27	0	2.84E+05		(K)LSELEPG	(K)L S|E/L|E|P G T G D L R(F)		124.53	643.8325	1286.659	-0.0009	-0.7	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
7889	dirMS_041712_NAR_30mM_minus2.14842.14842.2	2	11.27	0	2.59E+04		(R)LSLYQA	(R)L/S|L/Y Q/A/M R(Q)		134.33	491.2611	981.519	-0.0037	-3.8	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
7890	dirMS_041712_NAR_30mM_minus2.16973.17191.2	2	11.27	0	5.12E+05		(K)NSLESY	(K)N S|L|E/S/Y|A F/N M K(A)		146.62	652.3031	1303.599	0.0002	0.2	6	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
7891	dirMS_041712_NAR_30mM_minus2.9259.9355.2	2	11.27	0	5.64E+05		(R)TVIDYN	(R)T V|I|D/Y/N G E R(T)		105.1	533.7595	1066.516	-0.0046	-4.4	4.37	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
7892	dirMS_041712_NAR_40mM_minus2.14315.14315.3	3	11.27	1	1.61E+05		(K)TGISDVF	(K)T G I/S D\V/F A K N/D L/A/V/V D V R(I)		168.48	640.3454	1919.023	-0.0016	-0.8	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
7893	dirMS_041712_NAR_60mM_minus.10771.10771.3	3	11.27	0	1.99E+05		(K)TGNLGN	(K)T G\N L/G N/V/V/H I E/R(F)		120.1	436.9057	1308.702	0.0007	0.5	6.41	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
7894	dirMS_041712_NAR_120mM_plus.5397.5397.3	3	11.27	1	7.24E+05	M117m	(K)EmQLR	(K)E m/Q/L/R Q E E/E R(R)	m:Oxidized methionine	80.92	455.2145	1347.632	15.9968	1.4	4.49	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
7895	dirMS_041712_NAR_20mM_plus.14238.14238.2	2	11.27	0	3.41E+04		(R)IALTDN	(R)I/A|L/T/D N/A L I/A R(S)		170.65	585.8432	1170.684	-0.005	-4.2	5.84	24489.6	10.74	HUMAN	A8MUD9	60S ribosomal protein L7
7896	dirMS_041712_NAR_30mM_plus2.19583.19583.2	2	11.27	0	2.61E+05		(K)APDFVF	(K)A/P/D F/V/F Y/A P R(L)		156.63	591.8008	1182.594	0.0001	0.1	5.88	71218.8	6.3	HUMAN	A7YIJ8	Radixin
7897	dirMS_041712_NAR_40mM_plus2.6363.6378.2	2	11.27	0	4.41E+05		(K)NAGFTP	(K)N A|G|F/T/P Q E/R(Q)		96.23	510.2487	1019.491	-0.0004	-0.4	6	29474.8	6.94	HUMAN	G3V3M6	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
7898	dirMS_041712_NAR_50mM_plus2.16351.16351.3	3	11.27	1	4.20E+06		(K)LLQDFF	(K)L L|Q|D/F F/N G K E L N K(S)		154.6	522.6137	1565.832	-0.0057	-3.6	6.07	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
7899	dirMS_041712_NAR_60mM_plus.9771.9877.3	3	11.27	1	1.92E+05		(K)VLIANR	(K)V/L|I/A/N R G E I A C R(V)	C:Carbamidomethylation	109.6	457.9222	1371.753	-0.0005	-0.4	9.57	12879.9	10.9	HUMAN	F8WDI3	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial
7900	dirMS_041712_NAR_20mM_minus.12348.12348.2	2	11.26	0	1.25E+05		(K)LVSIGAE	(K)L V|S|I/G A|E/E I V/D G/N A K(M)		171.77	757.9044	1514.806	-0.0045	-3	4.14	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
7901	dirMS_041712_NAR_30mM_minus2.12825.13290.2	2	11.26	0	8.55E+05		(R)GGEPQ	(R)G G\E/P Q/G|P P F I|K(Y)		125.33	563.7964	1126.589	-0.0036	-3.2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
7902	dirMS_041712_NAR_30mM_minus2.15533.15533.2	2	11.26	0	3.29E+04		(K)FLMAN	(K)F L|M|A/N G Q L V K(M)		138.07	560.8108	1120.618	-0.004	-3.6	8.75	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
7903	dirMS_041712_NAR_30mM_minus2.18132.18132.2	2	11.26	0	1.96E+05		(K)VADIGL	(K)V A/D\I/G/L\A/A W/G R(K)		152.82	564.8076	1128.616	-0.0081	-7.2	5.81	48285.8	5.93	HUMAN	P23526	Adenosylhomocysteinase
7904	dirMS_041712_NAR_50mM_minus2.12840.12840.3	3	11.26	0	1.53E+05		(K)ASLASLP	(K)A S\L\A S L/P/P L H V A K(L)		141.37	435.2622	1303.773	-0.0012	-0.9	8.8	141626	5.5	HUMAN	A8MY36	Dynactin subunit 1
7905	dirMS_041712_NAR_50mM_minus2.13496.13496.3	3	11.26	1	1.35E+05		(K)IDSRLEQ	(K)I D/S R L E Q Y/T/S/A\I E G T K(S)		144.65	604.3145	1810.918	0.0108	6	4.68	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
7906	dirMS_041712_NAR_60mM_minus.15254.15254.3	3	11.26	1	3.23E+05		(R)LLDAQL	(R)L L/D/A/Q/L|A T G G L V C P A R R(L)	C:Carbamidomethylation	145.55	604.3344	1810.996	-0.007	-3.8	9.6	266161	5.68	HUMAN	E9PPU0	Epiplakin
7907	dirMS_041712_NAR_120mM_plus.7126.7149.3	3	11.26	1	3.79E+05		(K)IYEDGD	(K)I/Y/E/D/G D/D D M K/R(T)		90.88	452.8635	1356.574	0.0023	1.7	4.03	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
7908	dirMS_041712_NAR_20mM_plus.13589.13682.2	2	11.26	0	2.13E+05	M98m	(R)TLTIVDT	(R)T L|T|I/V|D/T G I G m T K(A)	m:Oxidized methionine	166.47	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
7909	dirMS_041712_NAR_20mM_plus.7146.7146.2	2	11.26	0	6.83E+04		(R)VLANPG	(R)V/L/A N|P G N S/Q V A R(V)		116.42	613.3355	1225.665	-0.001	-0.8	9.72	16598.6	5.48	HUMAN	J3QR48	Importin subunit beta-1 (Fragment)
7910	dirMS_041712_NAR_20mM_plus.7930.7930.2	2	11.26	0	3.83E+05	M239m	(K)EVDEQ	(K)E V/D E/Q|m L|N V/Q|N K(N)	m:Oxidized methionine	125	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
7911	dirMS_041712_NAR_30mM_plus2.16063.16063.2	2	11.26	0	1.60E+06		(R)MGAG	(R)M/G\A/G M/G F/G\L E R(M)		137.5	563.2636	1125.518	0.002	1.7	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
7912	dirMS_041712_NAR_30mM_plus2.18805.18805.2	2	11.26	0	1.47E+05		(K)GLIPWE	(K)G L I|P/W/E/Q A A R(L)		152.75	570.8113	1140.616	-0.0007	-0.6	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
7913	dirMS_041712_NAR_50mM_plus2.13058.13058.3	3	11.26	1	1.56E+06	M356m	(K)VGEVIV	(K)V/G E|V/I/V T K D/D A m L L/K(G)	m:Oxidized methionine	137.15	549.6381	1630.908	15.9913	-2.2	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
7914	dirMS_041712_NAR_50mM_plus2.20711.20711.3	3	11.26	1	1.70E+05		(R)VNSKFD	(R)V N S K F D/T|I/Y/Q/I L/L/K(K)		177.62	561.3209	1681.952	-0.0042	-2.5	8.47	72626.7	9.13	HUMAN	Q14258	E3 ubiquitin/ISG15 ligase TRIM25
7915	dirMS_041712_NAR_60mM_plus.17946.18078.3	3	11.26	0	2.48E+05		(R)FHQLDI	(R)F H\Q\L D\I|D/D|L/Q/S I/R(A)		151.47	533.9414	1599.813	-0.0029	-1.8	4.41	24897.7	9.84	HUMAN	A8MTM1	Carbonyl reductase [NADPH] 1
7916	dirMS_041712_NAR_60mM_plus.6256.6256.3	3	11.26	1	5.10E+05		(K)SVQATT	(K)S V|Q|A/T T E N/K E L K(T)		91.72	449.9085	1347.711	-0.0005	-0.4	5.86	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
7917	dirMS_041712_NAR_60mM_plus.6465.6465.3	3	11.26	0	2.48E+05		(R)CGETGH	(R)C/G E T/G H\V/A|I/N C S/K(T)	C:Carbamidomethylation	92.37	478.2118	1432.631	-0.0099	-6.9	6.75	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
7918	dirMS_041712_NAR_60mM_plus.6738.6738.2	2	11.26	1	4.77E+05		(K)GPSSVE	(K)G P|S/S|V/E/D I/K A/K(M)		93.85	565.8054	1130.605	-0.0017	-1.5	6.07	32745.6	4.64	HUMAN	P06748	Nucleophosmin
7919	dirMS_041712_NAR_120mM_minus.13791.13791.3	3	11.25	1	1.12E+05		(R)KYEMFA	(R)K\Y E M F\A Q/T|L/Q/Q S R(G)		129.37	543.9428	1629.805	0.0085	5.2	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
7920	dirMS_041712_NAR_30mM_minus2.14000.14000.2	2	11.25	0	3.07E+05		(K)TIVMGA	(K)T I|V|M|G A S F R(N)		129.1	491.2611	981.519	-0.0037	-3.8	9.41	35556.4	9.3	HUMAN	F2Z393	Transaldolase
7921	dirMS_041712_NAR_40mM_minus2.14291.14291.3	3	11.25	0	1.23E+05		(R)GTEDITS	(R)G T|E/D/I/T S/P/H G I/P L/D\L\L D R(V)		168.55	650.3366	1948.997	-0.0022	-1.1	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
7922	dirMS_041712_NAR_50mM_minus2.14895.14895.3	3	11.25	0	4.05E+05		(K)QLEAID	(K)Q L/E/A/I/D Q L/H L E Y A/K(R)		152.45	557.6327	1670.875	0.0087	5.2	4.65	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
7923	dirMS_041712_NAR_60mM_minus.7133.7133.3	3	11.25	1	1.70E+05		(K)AADIDQ	(K)A A/D/I/D/Q E V K E/R(A)		99.03	425.2172	1273.638	-0.0012	-1	4.32	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
7924	dirMS_041712_NAR_60mM_minus.8320.8320.3	3	11.25	0	7.55E+04		(K)HTGPNS	(K)H T\G\P N S P D/T A|N/D/G/F V R(L)		106.42	562.2608	1684.767	0.0005	0.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
7925	dirMS_041712_NAR_120mM_plus.20224.20224.3	3	11.25	1	3.26E+05		(R)AKFEEL	(R)A/K F E E L|N|M|D/L F/R(S)		159.17	504.9201	1512.752	-0.0058	-3.8	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
7926	dirMS_041712_NAR_120mM_plus.9579.9579.3	3	11.25	0	1.07E+05		(K)STAGDT	(K)S/T|A/G D/T H/L/G G E D F D N R(M)		103.08	564.579	1691.726	-0.0031	-1.9	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
7927	dirMS_041712_NAR_30mM_plus2.12084.12192.2	2	11.25	0	3.33E+05		(R)NLQDA	(R)N L|Q|D/A|M/Q/V/C R(N)	C:Carbamidomethylation	116.67	617.791	1234.567	0.008	6.5	5.84	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
7928	dirMS_041712_NAR_30mM_plus2.7140.7140.2	2	11.25	0	1.83E+04		(R)SGGGG	(R)S G G G\G/G/G G/L/G S/G G S I R(S)		92.03	616.8023	1232.598	-0.0005	-0.4	9.47	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
7929	dirMS_041712_NAR_40mM_plus2.12718.13154.3	3	11.25	0	4.16E+05		(K)NLPPSG	(K)N L|P/P S\G A V P V/T G I/P P H V V K(V)		143.25	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
7930	dirMS_041712_NAR_40mM_plus2.8094.8094.3	3	11.25	0	3.12E+04		(R)SSQSSS	(R)S S\Q S S S Q Q F/S G/I G/R(S)		107.58	485.8998	1455.682	0.0026	1.8	9.47	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
7931	dirMS_041712_NAR_50mM_plus2.10661.10724.3	3	11.25	1	5.66E+05		(R)ELLTLDE	(R)E L/L/T/L D E K D/P|R(R)		123.8	443.5761	1328.706	0.0081	6.1	4.32	9591.1	10.94	HUMAN	A8MXK4	40S ribosomal protein S9
7932	dirMS_041712_NAR_50mM_plus2.12002.12002.3	3	11.25	1	4.97E+05	M327m	(R)VAGGP	(R)V/A/G G/P Q m/I/Q/L S L D G K/R(L)	m:Oxidized methionine	131.13	562.6377	1669.905	15.9931	-1	8.72	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
7933	dirMS_041712_NAR_50mM_plus2.13253.13253.3	3	11.25	0	2.27E+06		(R)SCTVNI	(R)S C|T V/N/I/M/F G T/P Q E H R(N)	C:Carbamidomethylation	138.43	592.9438	1776.816	0.0012	0.7	6.47	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
7934	dirMS_041712_NAR_50mM_plus2.14175.14175.3	3	11.25	0	5.08E+05		(K)VTHAVV	(K)V T H A V V\T V/P/A/Y/F N D/A Q R(Q)		142.7	629.9955	1887.971	0.0008	0.4	6.71	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
7935	dirMS_041712_NAR_50mM_plus2.14304.14305.3	3	11.25	0	4.78E+05		(K)VVEIAP	(K)V V/E I/A/P/A A H L/D/P Q L/R(T)		143.6	543.6378	1628.912	-0.013	-8	5.32	58266.4	9.46	HUMAN	B4DN00	Pyruvate carboxylase, mitochondrial
7936	dirMS_041712_NAR_50mM_plus2.18692.18743.3	3	11.25	0	1.81E+05		(K)ASVITQ	(K)A/S|V I|T Q V F H\V/P L E/E R(K)		166.42	575.6533	1724.933	0.0124	7.2	5.4	24511.6	6.62	HUMAN	C9J5E5	Vigilin (Fragment)
7937	dirMS_041712_NAR_50mM_plus2.21552.21552.3	3	11.25	1	1.85E+05		(K)LKVNFL	(K)L K V N F\L|P E I I|T L S K(E)		184.25	539.0011	1614.983	0.0058	3.6	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
7938	dirMS_041712_NAR_60mM_plus.16304.16327.3	3	11.25	0	3.26E+05		(R)FVFDRP	(R)F/V/F D/R/P L/P V S R(L)		142.5	444.917	1332.742	-0.0058	-4.4	9.6	18685.5	9.45	HUMAN	B4DEV8	Proteasome subunit alpha type
7939	dirMS_041712_NAR_60mM_plus.16463.16463.3	3	11.25	1	5.15E+05		(R)TDGKVF	(R)T/D/G K V/F Q/F L N A/K(C)		143.5	456.5782	1367.732	-0.0117	-8.6	8.26	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
7940	dirMS_041712_NAR_60mM_plus.18268.18268.3	3	11.25	1	3.15E+05	N97n	(R)LLQDIKE	(R)L/L/Q/D/I/K E T F n R(C)	n:N-acetylglucosamine (N)	152.63	527.2793	1376.753	203.0701	-5.9	6.07	21818.4	6.99	HUMAN	D6REK2	E3 ubiquitin-protein ligase TRIM41 (Fragment)
7941	dirMS_041712_NAR_120mM_minus.10551.10679.3	3	11.24	1	6.68E+05		(R)RGVVG	(R)R G V\V G|P|E\L/Y\G/R(L)		113.2	401.559	1202.664	-0.0016	-1.3	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
7942	dirMS_041712_NAR_20mM_minus.6171.6171.2	2	11.24	0	3.70E+06		(K)DSYVGD	(K)D/S/Y|V|G/D E A\Q S K(R)		103.85	599.7642	1198.522	-0.0011	-0.9	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
7943	dirMS_041712_NAR_30mM_minus2.12519.12519.2	2	11.24	0	7.59E+05		(R)GVVGPE	(R)G V|V/G/P E L/Y/G R(L)		122.5	523.7834	1046.563	-0.0034	-3.2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
7944	dirMS_041712_NAR_30mM_minus2.19515.19528.2	2	11.24	0	2.81E+05		(R)ILVATNL	(R)I L|V/A/T/N/L F G R(G)		162.03	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
7945	dirMS_041712_NAR_30mM_minus2.7140.7140.2	2	11.24	0	4.82E+05		(K)DAQGQ	(K)D A\Q/G Q|P G/L E R(A)		92.98	535.762	1070.523	-0.0058	-5.4	4.37	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
7946	dirMS_041712_NAR_60mM_minus.10917.10917.3	3	11.24	1	2.24E+05		(K)VTVAGL	(K)V T|V/A/G/L/A G K D P V Q C S R(D)	C:Carbamidomethylation	121.03	553.2923	1657.869	-0.0067	-4	8.72	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
7947	dirMS_041712_NAR_60mM_minus.8079.8079.3	3	11.24	1	7.06E+04		(R)ELYDKG	(R)E L/Y/D K G G E Q/A I/K(E)		105.07	450.9003	1350.69	-0.0036	-2.7	4.68	45609.1	6.66	HUMAN	P31689	DnaJ homolog subfamily A member 1
7948	dirMS_041712_NAR_120mM_plus.6823.6823.3	3	11.24	1	6.52E+05		(R)NKQTYS	(R)N K Q T Y\S/T/E/P N N L K(A)		88.83	512.9261	1536.765	-0.0015	-1	8.5	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
7949	dirMS_041712_NAR_20mM_plus.13380.13380.2	2	11.24	0	9.84E+04	M98m	(R)TLTIVDT	(R)T L/T I/V/D/T/G I G m T K(A)	m:Oxidized methionine	165.03	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
7950	dirMS_041712_NAR_20mM_plus.13672.13743.3	3	11.24	0	3.85E+05		(R)GALQNI	(R)G A\L Q N\I\I|P A/S T/G A A/K(A)		167.25	471.2683	1411.79	0	0	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
7951	dirMS_041712_NAR_20mM_plus.14194.14194.3	3	11.24	0	7.24E+03		(R)VPTANV	(R)V P T A N V S|V|V/D L/T C R(L)	C:Carbamidomethylation	169.75	510.9348	1530.795	-0.0046	-3	5.81	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
7952	dirMS_041712_NAR_30mM_plus2.12547.12547.2	2	11.24	0	2.91E+05		(R)ELAEDG	(R)E L/A/E/D G Y/S/G V/E V R(V)		119.03	712.3382	1423.67	-0.0008	-0.6	4	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3

7953	dirMS_041712_NAR_30mM_plus2.18548.18628.3	3	11.24	0	3.37E+05		(R)GVVDSE	(R)G V\V D S E D I|P/L/N/L/S R(E)		150.87	505.2679	1513.786	0.0035	2.3	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
7954	dirMS_041712_NAR_30mM_plus2.19367.19449.2	2	11.24	0	2.36E+05		(K)NFSGAE	(K)N F|S/G/A/E/L|E G L V R(A)		155.45	646.3361	1291.664	0.0008	0.6	4.53	71924.9	6.25	HUMAN	B4DFA2	Vesicle-fusing ATPase
7955	dirMS_041712_NAR_30mM_plus2.6643.6643.2	2	11.24	0	2.92E+05		(R)EAGEQ	(R)E A/G E/Q/G D/I E/P R(R)		89.77	600.7772	1200.549	-0.002	-1.7	4	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
7956	dirMS_041712_NAR_50mM_plus2.12462.12462.3	3	11.24	1	2.64E+05		(R)SVELNP	(R)S V|E/L N/P T Q K/D L V/L K(I)		133.58	528.6368	1583.9	-0.0045	-2.8	5.79	198852.6	5.95	HUMAN	A6NKT7	RanBP2-like and GRIP domain-containing protein 3
7957	dirMS_041712_NAR_50mM_plus2.15688.15750.3	3	11.24	1	1.23E+05		(K)ELKIDIIP	(K)E L K I D I\I/P/N/P Q E/R(T)		150.97	522.2931	1564.869	-0.0046	-2.9	4.68	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
7958	dirMS_041712_NAR_60mM_plus.12889.12889.3	3	11.24	0	3.71E+06		(R)ITLRPDP	(R)I/T/L R P D\P\L/P E/R(S)		123.6	436.2506	1306.748	-0.0105	-8	6.07	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
7959	dirMS_041712_NAR_60mM_plus.17956.18039.3	3	11.24	1	3.47E+05		(K)YAVLYQ	(K)Y/A|V/L/Y Q/P L/F D/K R(F)		151.38	504.9379	1512.821	-0.0218	-14.4	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
7960	dirMS_041712_NAR_60mM_plus.21213.21213.3	3	11.24	0	2.16E+05		(K)ALESPEF	(K)A L/E/S/P\E/R P/F L A I/L G G A/K(V)		174.75	590.3367	1768.996	0	0	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
7961	dirMS_041712_NAR_60mM_plus.7188.7305.3	3	11.24	0	7.57E+05		(K)LMELHG	(K)L/M/E/L/H/G E G S S S G/K(A)		95.93	444.5486	1331.626	0.0053	3.9	5.4	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
7962	dirMS_041712_NAR_20mM_minus.10616.10616.2	2	11.23	0	1.03E+05		(K)FLIPNAS	(K)F L|I|P/N A S Q A E S K(V)		154.5	652.8447	1304.685	-0.0024	-1.8	6	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
7963	dirMS_041712_NAR_30mM_minus2.17194.17194.2	2	11.23	0	1.03E+05		(R)NGGQIL	(R)N G\G\Q|I|L I/A D/L R(G)		147.92	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
7964	dirMS_041712_NAR_40mM_minus2.12837.12837.3	3	11.23	0	1.33E+05		(K)GVTIIGP	(K)G V\T I|I/G P A T V/G G/I K/P G C F K(I)	C:Carbamidomethylation	159.27	624.6828	1872.041	-0.0073	-3.9	10	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
7965	dirMS_041712_NAR_50mM_minus2.14330.14330.3	3	11.23	0	4.31E+05		(R)QIFHPE	(R)Q I F/H/P E\Q/L/I/T G K(E)		149.72	470.9286	1410.774	-0.0027	-1.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
7966	dirMS_041712_NAR_50mM_minus2.15633.15633.3	3	11.23	1	4.82E+05		(K)QGGLGF	(K)Q G G L|G P M|N I/P L V S D/P K R(T)		157.48	593.6566	1778.958	-0.0029	-1.6	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
7967	dirMS_041712_NAR_20mM_plus.14960.14960.2	2	11.23	0	1.45E+05		(K)VLEQLT	(K)V L\E Q L/T/G Q T|P\V/F/S K(A)		174.65	773.9244	1546.848	-0.006	-3.9	5.97	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
7968	dirMS_041712_NAR_20mM_plus.15873.15873.2	2	11.23	0	2.44E+05		(R)GVVDSE	(R)G V V/D|S E/D I|P L N/L/S R(E)		179.95	757.3956	1513.786	-0.0017	-1.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
7969	dirMS_041712_NAR_20mM_plus.16622.16622.2	2	11.23	0	1.71E+05		(K)IAFAITAI	(K)I/A|F\A/I T A/I K(G)		185.5	474.2987	947.592	-0.0023	-2.4	8.75	17718.4	10.99	HUMAN	P62269	40S ribosomal protein S18
7970	dirMS_041712_NAR_20mM_plus.18974.18974.3	3	11.23	0	1.87E+05		(K)TLETQS	(K)T L E T Q S A L|G|P/A L Q A A F/K(L)		202.45	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
7971	dirMS_041712_NAR_30mM_plus2.12925.12925.2	2	11.23	0	5.62E+05		(R)YSGSYNI	(R)Y/S|G/S Y/N D Y L R(A)		120.42	619.2776	1237.548	-0.0005	-0.4	5.83	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
7972	dirMS_041712_NAR_30mM_plus2.15999.16060.2	2	11.23	0	2.92E+06		(R)INEILSN	(R)I/N|E|I|L\S N A L/K(R)		137.87	557.8307	1114.647	0.0075	6.7	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
7973	dirMS_041712_NAR_30mM_plus2.18462.18462.2	2	11.23	0	7.81E+04		(R)VVNVSS	(R)V V/N|V|S/S I/M S V R(A)		149.77	595.8347	1190.656	0.006	5	9.72	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
7974	dirMS_041712_NAR_30mM_plus2.19110.19110.2	2	11.23	0	3.59E+04		(K)DAGTIA	(K)D A G T|I/A/G L N V L/R(I)		153.85	600.3411	1199.674	0.0007	0.6	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
7975	dirMS_041712_NAR_40mM_plus2.6132.6132.2	2	11.23	0	5.66E+04		(R)QAFPNT	(R)Q A|F/P/N/T N/R(W)		94.88	474.2383	947.469	0	0	9.75	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
7976	dirMS_041712_NAR_50mM_plus2.13065.13065.3	3	11.23	1	2.49E+05		(K)NSVTPD	(K)N/S/V/T/P/D/M M E E M/Y K K(A)		137.03	568.2557	1702.748	0.0041	2.4	4.68	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
7977	dirMS_041712_NAR_50mM_plus2.15692.15692.3	3	11.23	1	2.25E+05		(R)AEGAIA	(R)A/E|G A I/A/G F R D/P F S G K(Q)		150.13	508.2614	1522.765	0.0048	3.1	6.12	266161	5.68	HUMAN	E9PPU0	Epiplakin
7978	dirMS_041712_NAR_50mM_plus2.7140.7202.3	3	11.23	0	1.04E+06		(R)EATNPP	(R)E A|T/N/P/P V I Q/E E K/P K(K)		103.55	527.282	1579.833	-0.0012	-0.7	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
7979	dirMS_041712_NAR_50mM_plus2.8312.8312.3	3	11.23	0	2.33E+05		(K)VQQAEL	(K)V/Q|Q/A/E L/H T G S/L P R(I)		110.33	479.2607	1435.765	0.0023	1.6	6.72	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
7980	dirMS_041712_NAR_60mM_plus.21664.21664.3	3	11.23	1	6.91E+05		(K)EIIDLVLI	(K)E I\I/D/L V L D R I/R(K)		180.78	452.2733	1354.805	0.0001	0.1	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
7981	dirMS_041712_NAR_60mM_plus.6919.6919.3	3	11.23	1	5.17E+05	M281m	(R)SRAEAE	(R)S R A E\A\E|S m/Y Q I/K(Y)	m:Oxidized methionine	94.65	476.8976	1412.684	15.9944	-0.4	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
7982	dirMS_041712_NAR_120mM_minus.11349.11349.3	3	11.22	0	2.31E+05		(R)GFCLPP	(R)G F/C/L|P/P/H C S R(G)	C:Carbamidomethylation	116.42	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
7983	dirMS_041712_NAR_120mM_minus.11928.11928.4	4	11.22	2	6.11E+05		(R)YESLTDF	(R)Y E|S\L/T/D/P S K L/D S G K E L K(I)		119.2	478.2478	1909.975	-0.0059	-3.1	4.78	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
7984	dirMS_041712_NAR_20mM_minus.9451.9451.2	2	11.22	0	1.04E+05		(K)LVPVLS	(K)L V/P/V L/S/A K(A)		145.03	413.7734	826.54	-0.0001	-0.2	8.75	37710.6	6.36	HUMAN	P37837	Transaldolase
7985	dirMS_041712_NAR_30mM_minus2.12293.12293.2	2	11.22	0	5.26E+05		(R)EYQELM	(R)E Y|Q/E/L/M/N/V K(L)		119.63	577.2825	1153.556	0.0019	1.7	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
7986	dirMS_041712_NAR_30mM_minus2.6211.6211.2	2	11.22	0	1.72E+05		(R)AQAEQ	(R)A/Q|A/E/Q/A A/L/R(Q)		88.18	479.2592	957.511	-0.0001	-0.1	6.05	533778	5.74	HUMAN	Q15149	Plectin
7987	dirMS_041712_NAR_40mM_minus2.11797.11797.3	3	11.22	0	2.24E+05		(R)LASTLV	(R)L/A|S/T L V H L G/E Y\Q A/A|V D G A R(K)		153.02	657.6842	1971.029	0.0086	4.4	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
7988	dirMS_041712_NAR_50mM_minus2.9261.9261.3	3	11.22	1	3.64E+04		(K)IQVLQQ	(K)I Q|V/L\Q Q Q/A/D/D A E E R A E R(L)		120.93	666.9985	1998.984	-0.003	-1.5	4.18	26611.3	4.47	HUMAN	A6NL28	Putative tropomyosin alpha-3 chain-like protein
7989	dirMS_041712_NAR_120mM_plus.9552.9552.3	3	11.22	1	1.66E+06		(R)GKLDGN	(R)G K L D G N\Q|D/L/I/R(F)		103.23	410.2263	1228.664	-0.0001	-0.1	5.96	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
7990	dirMS_041712_NAR_20mM_plus.14676.14676.2	2	11.22	0	1.03E+05		(R)FIDTTLA	(R)F I/D T/T/L/A I T S R(F)		172.25	619.3413	1237.679	-0.0034	-2.7	5.84	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
7991	dirMS_041712_NAR_30mM_plus2.14574.14574.2	2	11.22	0	3.18E+06		(R)FPGQLN	(R)F/P/G/Q/L/N A D|L R(K)		130.15	565.801	1130.595	-0.0006	-0.5	5.84	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
7992	dirMS_041712_NAR_30mM_plus2.19941.19941.2	2	11.22	0	5.04E+04		(K)TFESLVD	(K)T F|E/S L/V D/F S K(A)		158.22	586.793	1172.583	-0.0047	-4	4.37	35407.1	6.73	HUMAN	E9PF18	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial
7993	dirMS_041712_NAR_30mM_plus2.20979.20979.2	2	11.22	0	2.95E+05		(K)IPDWFLI	(K)I/P/D/W/F/L/N\R(Q)		165.05	530.785	1060.557	0.0053	5	5.84	9767.1	11.41	HUMAN	J3JS69	40S ribosomal protein S18
7994	dirMS_041712_NAR_40mM_plus2.14341.14341.3	3	11.22	1	5.33E+05		(R)IINEPTA	(R)I/I/N E/P T A\A A\I/A/Y G L D K K(V)		150.48	596.6671	1787.99	-0.0034	-1.9	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
7995	dirMS_041712_NAR_40mM_plus2.17504.17504.3	3	11.22	0	2.09E+04		(R)IHFPLAT	(R)I H F\P L\A T Y/A/P V/I S A E K(A)		169.42	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
7996	dirMS_041712_NAR_50mM_plus2.11498.11498.3	3	11.22	1	1.25E+06		(K)NQVAM	(K)N\Q|V|A/M/N P T\N T/V F D/A K R(L)		127.8	602.6354	1805.896	-0.0046	-2.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
7997	dirMS_041712_NAR_50mM_plus2.16166.16166.3	3	11.22	1	1.41E+06		(K)CEFQDA	(K)C E/F Q/D/A Y/V/L L/S E K K(I)	C:Carbamidomethylation	152.32	577.2866	1729.847	-0.0013	-0.8	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
7998	dirMS_041712_NAR_60mM_plus.14667.14845.3	3	11.22	1	6.12E+05		(R)ELAVQI	(R)E L/A V/Q I/Y/E/E\A R K(F)		133.45	483.5949	1448.774	-0.0042	-2.9	4.79	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
7999	dirMS_041712_NAR_60mM_plus.16900.16900.3	3	11.22	0	8.89E+05		(K)TTISVAH	(K)T T|I/S V A/H L|L A A/R(Q)		144.63	418.2478	1252.737	-0.0083	-6.7	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
8000	dirMS_041712_NAR_60mM_plus.17574.17574.3	3	11.22	1	8.23E+05		(R)DKLNNL	(R)D K\L N N|L/V/L F/D/K(A)		148.43	440.2499	1318.737	-0.0014	-1	5.96	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
8001	dirMS_041712_NAR_120mM_minus.9096.9096.3	3	11.21	0	8.47E+05		(K)HTGPNS	(K)H T G P/N S P D T|A/N/D/G F V R(L)		103.3	562.2599	1684.767	-0.0022	-1.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
8002	dirMS_041712_NAR_30mM_minus2.5920.5920.2	2	11.21	0	1.90E+05		(K)TSEVNC	(K)T S|E/V/N C/Y R(C)	C:Carbamidomethylation	86.62	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
8003	dirMS_041712_NAR_40mM_minus2.13116.13116.3	3	11.21	1	9.20E+04		(K)VLDSGA	(K)V L|D\S G/A|P I K I|P V G P E T L G R(I)		160.87	640.3618	1919.096	-0.0252	-13.1	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
8004	dirMS_041712_NAR_40mM_minus2.14699.14699.3	3	11.21	1	1.42E+05		(R)EQIPAG	(R)E\Q\I/P A G T L L L/A V/E D/P E K R(V)		170.82	660.3663	1979.081	0.0036	1.8	4.41	19773.1	4.48	HUMAN	B4DEU5	L-fucose kinase
8005	dirMS_041712_NAR_40mM_minus2.16103.16103.3	3	11.21	1	6.73E+05		(R)ELAILLG	(R)E L/A I|L/L G M/L/D P A E K D E K(G)		189.58	629.0034	1884.999	-0.003	-1.6	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
8006	dirMS_041712_NAR_50mM_minus2.11450.11495.3	3	11.21	1	2.41E+04		(R)ESDVPL	(R)E S D V/P/L/K|T E/E/F E V\T K(T)		133.62	584.3049	1750.874	0.0256	14.6	4.25	18909	6.21	HUMAN	Q969H8	UPF0556 protein C19orf10
8007	dirMS_041712_NAR_50mM_minus2.17493.17493.3	3	11.21	0	2.60E+05		(R)LLLDGA	(R)L L L\D G A/P/L/I/A I H K(A)		168.5	458.6218	1373.852	-0.0007	-0.5	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
8008	dirMS_041712_NAR_60mM_minus.10016.10016.3	3	11.21	1	1.25E+05		(R)AGTGVD	(R)A G/T/G/V/D N V/D L E/A/A T R K(G)		115.55	539.6117	1616.824	-0.0033	-2	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
8009	dirMS_041712_NAR_60mM_minus.9177.9177.3	3	11.21	1	5.12E+04		(R)QLEEAEI	(R)Q L|E E/A/E/E E/A Q R/A N A S R(R)		110.88	610.9566	1830.858	-0.0024	-1.3	4.33	227783.5	5.5	HUMAN	P35579	Myosin-9
8010	dirMS_041712_NAR_20mM_plus.14504.14504.2	2	11.21	0	1.39E+05		(R)FIDTTLA	(R)F/I|D|T/T L/A I T/S R(F)		171.63	619.3413	1237.679	-0.0034	-2.7	5.84	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
8011	dirMS_041712_NAR_20mM_plus.15654.15654.3	3	11.21	0	2.11E+05		(R)GVVDSE	(R)G V\V D S E D/I/P L N L/S R(E)		179.38	505.2667	1513.786	-0.0001	-0.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
8012	dirMS_041712_NAR_20mM_plus.18646.18646.2	2	11.21	0	2.93E+05		(K)TAVETA	(K)T A|V/E/T/A/V L\L/L R(I)		199.9	593.3625	1185.72	-0.0024	-2	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
8013	dirMS_041712_NAR_30mM_plus2.12083.12083.2	2	11.21	0	1.39E+05		(R)INGWA	(R)I N|G W/A/V/E/C/R(V)	C:Carbamidomethylation	116.55	552.7679	1104.526	0.003	2.7	6	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
8014	dirMS_041712_NAR_30mM_plus2.7815.7833.2	2	11.21	0	4.12E+05		(K)CNLLAE	(K)C/N|L|L/A E/K(Q)	C:Carbamidomethylation	94.87	424.2213	847.434	0.0011	1.3	6	40209.9	5.43	HUMAN	C9JV77	Alpha-2-HS-glycoprotein
8015	dirMS_041712_NAR_40mM_plus2.14799.14812.3	3	11.21	1	2.18E+05		(R)VVVDAL	(R)V/V|V/D A L/S/G L K G D\L A G/R(Y)		154.27	523.9701	1569.896	-0.0001	-0.1	5.93	26949.2	7.99	HUMAN	C9JSQ1	Creatine kinase U-type, mitochondrial (Fragment)
8016	dirMS_041712_NAR_40mM_plus2.6471.6471.2	2	11.21	0	6.37E+04		(R)SDYDGI	(R)S D/Y/D/G I/G S R(G)		97.52	485.2217	969.427	0.0089	9.2	4.21	15031.5	6.72	HUMAN	B4DLA0	ATP-dependent RNA helicase DDX3X
8017	dirMS_041712_NAR_40mM_plus2.8193.8193.2	2	11.21	0	4.70E+04		(R)LASYLDF	(R)L/A|S/Y L D/R(V)		108.52	419.2273	837.447	0.0008	1	5.83	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
8018	dirMS_041712_NAR_50mM_plus2.12242.12242.3	3	11.21	0	3.98E+05		(K)IVLEDGT	(K)I V|L/E D G T L/H/V/T E G S G R(Y)		132.23	561.6272	1682.871	-0.0037	-2.2	4.65	62748.9	5.95	HUMAN	Q16555	Dihydropyrimidinase-related protein 2
8019	dirMS_041712_NAR_50mM_plus2.16109.16109.3	3	11.21	1	4.91E+05		(K)YAVLYQ	(K)Y/A|V\L Y Q/P L F D/K R(F)		152.48	504.9436	1512.821	-0.0047	-3.1	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
8020	dirMS_041712_NAR_50mM_plus2.7565.7565.3	3	11.21	1	2.58E+05		(K)SEETLDE	(K)S E|E/T/L D/E/G/P P K Y T K(S)		105.8	531.9261	1593.764	-0.0005	-0.3	4.41	25233.4	9.34	HUMAN	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3
8021	dirMS_041712_NAR_60mM_plus.18376.18376.3	3	11.21	0	2.08E+05		(K)DHGLEV	(K)D H G L\E\V/L/G L V/R(V)		153.55	403.2318	1207.679	0.0015	1.2	5.32	17732.8	5.85	HUMAN	F5GYJ1	U8 snoRNA-decapping enzyme
8022	dirMS_041712_NAR_120mM_minus.6798.6798.2	2	11.2	0	4.89E+05		(K)HQPTAII	(K)H/Q|P T A|I/I A K(T)		91.83	489.7898	978.573	-0.0008	-0.8	8.76	63448.4	7.29	HUMAN	B4E022	Transketolase
8023	dirMS_041712_NAR_30mM_minus2.8855.8855.2	2	11.2	0	4.90E+05		(K)SDPVVS	(K)S D|P/V/V/S Y R(E)		102.62	461.7315	922.463	-0.0071	-7.7	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
8024	dirMS_041712_NAR_50mM_minus2.15651.15873.3	3	11.2	1	4.93E+05		(K)QGGLGF	(K)Q G/G L/G/P M/N I|P L V S D/P K R(T)		157.5	593.6566	1778.958	-0.0029	-1.6	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
8025	dirMS_041712_NAR_60mM_minus.19077.19077.3	3	11.2	0	5.77E+05		(R)LGFHLPI	(R)L G F H\L/P L/E|V/A/Y Q/R(G)		168.65	514.9512	1542.843	-0.0037	-2.4	6.75	533778	5.74	HUMAN	Q15149	Plectin
8026	dirMS_041712_NAR_60mM_minus.9931.9931.3	3	11.2	1	5.63E+05	M230m M2	(R)mSmKE	(R)m S m K E V D E Q\M|L/N\V Q|N/K(N)	m:Oxidized methionine	114.97	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
8027	dirMS_041712_NAR_120mM_plus.6710.6807.2	2	11.2	0	5.08E+05		(R)HLTGEF	(R)H/L|T G E/F\E|K(K)		88.68	480.743	960.479	0.0002	0.2	5.4	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
8028	dirMS_041712_NAR_20mM_plus.8981.8981.2	2	11.2	0	2.13E+05		(K)VTADVI	(K)V T/A\D/V/I/N A/A E K(L)		132.6	565.806	1130.605	-0.0005	-0.4	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
8029	dirMS_041712_NAR_50mM_plus2.16869.16869.3	3	11.2	0	7.72E+05		(R)QYYTLL	(R)Q Y Y/T|L L\N Q A/P/D|M L H R(K)		156.92	621.6447	1862.922	-0.0022	-1.2	6.74	4335.1	9.82	HUMAN	E5RH00	Ras GTPase-activating protein-binding protein 1
8030	dirMS_041712_NAR_60mM_plus.11128.11128.3	3	11.2	1	6.41E+06		(R)QQEGFK	(R)Q Q E G F/K G T/F/P D/A R(E)		115.52	494.2424	1480.718	-0.0053	-3.6	6.07	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
8031	dirMS_041712_NAR_60mM_plus.13031.13070.3	3	11.2	1	3.99E+05		(K)LAEQAE	(K)L/A|E/Q/A/E/R Y D D M A A A M K(A)		124.77	604.9452	1812.825	-0.0044	-2.5	4.32	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
8032	dirMS_041712_NAR_60mM_plus.7140.7140.2	2	11.2	0	3.11E+05		(K)TIEAEAA	(K)T\I|E/A/E/A/A H/G T V T R(H)		95.57	678.3494	1355.691	0.0002	0.1	5.37	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
8033	dirMS_041712_NAR_120mM_minus.10074.10074.3	3	11.19	1	9.65E+04		(K)LLKDAE	(K)L L/K D A\E|A\L/S/Q/R(L)		109.18	415.2365	1243.7	-0.0055	-4.4	6.07	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
8034	dirMS_041712_NAR_30mM_minus2.11040.11040.2	2	11.19	0	1.13E+06		(R)TSASIILR	(R)T/S/A/S|I/I L R(G)		113.52	430.7619	860.52	-0.0035	-4	9.41	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
8035	dirMS_041712_NAR_30mM_minus2.11078.11078.2	2	11.19	0	6.20E+05		(K)VAGQD	(K)V/A|G\Q|D\G S/V V/Q\F K(I)		113.9	617.824	1234.643	-0.0019	-1.5	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
8036	dirMS_041712_NAR_30mM_minus2.15602.15602.2	2	11.19	0	2.02E+05		(K)ALELDS	(K)A L|E/L/D S/N L/Y R(I)		138.85	597.3118	1193.616	0.0002	0.2	4.37	227783.5	5.5	HUMAN	P35579	Myosin-9
8037	dirMS_041712_NAR_40mM_minus2.11129.11129.3	3	11.19	0	4.11E+05		(R)DAGEGL	(R)D A|G\E/G L/L A/V/Q I T D Q E G K/P K(R)		148.25	657.0157	1969.024	0.0089	4.5	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
8038	dirMS_041712_NAR_50mM_minus2.14817.14817.3	3	11.19	1	2.80E+05		(K)NIYVLQE	(K)N/I|Y/V/L Q E L D N P G A K/R(I)		152.6	577.3116	1729.923	-0.0029	-1.7	6.07	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
8039	dirMS_041712_NAR_50mM_minus2.7482.7482.3	3	11.19	1	3.43E+04		(K)ATQPET	(K)A T\Q/P E/T T/E E V T D\L K R(Q)		109.37	573.2875	1717.86	-0.0123	-7.2	4.41	72152.1	5.27	HUMAN	A0MZ66	Shootin-1
8040	dirMS_041712_NAR_20mM_plus.13693.13693.2	2	11.19	0	6.65E+04		(K)ADSLLA	(K)A/D/S/L/L A/V V\K(R)		166.17	458.2789	915.551	-0.0004	-0.5	5.88	103309.5	5.34	HUMAN	A0AV56	SAFB protein
8041	dirMS_041712_NAR_20mM_plus.8722.8722.2	2	11.19	0	2.41E+05		(R)VPPPPPI	(R)V/P|P/P P P I A R(A)		130.6	472.2851	943.572	-0.0094	-10	9.72	32085.2	8.93	HUMAN	B4DY08	Heterogeneous nuclear ribonucleoproteins C1/C2
8042	dirMS_041712_NAR_30mM_plus2.12043.12086.2	2	11.19	0	5.36E+05		(R)AGGLLG	(R)A G G L|L/G/A/G|P D|P R(G)		116.18	540.7921	1080.58	-0.0027	-2.5	5.88	51390.4	12.42	HUMAN	P0CG12	Chromosome transmission fidelity protein 8 homolog isoform 2
8043	dirMS_041712_NAR_30mM_plus2.7095.7434.2	2	11.19	0	1.27E+06	M157m	(R)MGYmD	(R)M/G/Y m D|P/R(E)	m:Oxidized methionine	92.6	443.1849	869.364	15.9981	3.6	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
8044	dirMS_041712_NAR_40mM_plus2.13286.13327.3	3	11.19	1	1.32E+05		(R)DLPGALI	(R)D L|P/G A/L/D/E/K E L I E/K(M)		144.48	523.9493	1569.837	-0.0037	-2.3	4.18	21643.7	7.87	HUMAN	Q96BM9	ADP-ribosylation factor-like protein 8A
8045	dirMS_041712_NAR_40mM_plus2.17365.17365.3	3	11.19	0	2.47E+04		(R)GTEDITS	(R)G T/E/D|I|T/S P H G I/P L D|L\L D R(V)		169.42	650.3372	1948.997	-0.0004	-0.2	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
8046	dirMS_041712_NAR_50mM_plus2.12979.12979.3	3	11.19	1	3.89E+05		(K)LAEIGAF	(K)L A|E/I/G A/P I Q G N R E E L V E/R(L)		135.98	665.3593	1994.066	-0.0032	-1.6	4.49	38572.2	6.31	HUMAN	E9PJ04	Splicing factor 3B subunit 2 (Fragment)
8047	dirMS_041712_NAR_50mM_plus2.9344.9344.3	3	11.19	1	3.84E+05	S306s	(R)DHHMS	(R)D H H M S G W|s|Y/K R V E K(S)	s:N-acetylglucosamine (S)	116.45	654.9726	1759.833	203.0699	-4.8	8.51	51648.4	5.55	HUMAN	B7XGB9	Protein phosphatase 1M
8048	dirMS_041712_NAR_60mM_plus.14429.14429.3	3	11.19	1	7.29E+05		(K)KAEEIAN	(K)K\A E E\I\A|N/E/M/I/E/A A K(A)		132	516.2635	1546.778	-0.0022	-1.4	4.49	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
8049	dirMS_041712_NAR_60mM_plus.16665.16665.3	3	11.19	1	4.37E+05		(R)VTPTRTI	(R)V/T/P T R\T E I I I/L A T/R(T)		143.27	528.653	1583.948	-0.0035	-2.2	9.57	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
8050	dirMS_041712_NAR_60mM_plus.9933.10126.3	3	11.19	1	1.59E+06	M142m	(K)VKEGM	(K)V K E G M N\I|V/E/A m E/R(F)	m:Oxidized methionine	110.08	507.9187	1505.745	15.9965	1	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
8051	dirMS_041712_NAR_120mM_minus.8724.8724.2	2	11.18	1	1.51E+06	M174m	(R)VKYETEL	(R)V K|Y|E T/E/L/A m/R(Q)	m:Oxidized methionine	101.97	628.3209	1239.64	15.9943	-0.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
8052	dirMS_041712_NAR_20mM_minus.14701.14701.2	2	11.18	0	1.38E+05		(R)IITLAGP	(R)I I/T\L/A/G/P/T N A I F K(A)		202.15	679.9047	1358.804	-0.0021	-1.5	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
8053	dirMS_041712_NAR_30mM_minus2.17976.17976.2	2	11.18	0	5.56E+04		(K)NLDENG	(K)N L|D/E\N/G L/D L L|S K(M)		152.6	665.846	1330.685	-0.0002	-0.1	4.03	34151.9	8.46	HUMAN	P06493	Cyclin-dependent kinase 1
8054	dirMS_041712_NAR_40mM_minus2.15007.15007.3	3	11.18	1	7.94E+04		(R)VLEALLP	(R)V L/E A L L/P L K G L E/E/R(V)		173.35	527.317	1579.942	-0.0053	-3.4	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
8055	dirMS_041712_NAR_50mM_minus2.14484.14484.3	3	11.18	0	6.18E+04		(K)VALLLLD	(K)V A/L L|L|L/D Q G A/S P H A A A K(N)		150.53	558.9883	1674.954	-0.0034	-2	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
8056	dirMS_041712_NAR_60mM_minus.11677.11703.3	3	11.18	1	2.27E+05		(K)KLEEEQI	(K)K\L E E\E Q\I|I|L/E/D Q N C K(L)	C:Carbamidomethylation	125.35	630.3154	1888.932	-0.0004	-0.2	4.25	227783.5	5.5	HUMAN	P35579	Myosin-9
8057	dirMS_041712_NAR_20mM_plus.11595.11595.2	2	11.18	0	1.32E+05		(R)ANTFVA	(R)A N/T|F/V A E/L/K(G)		152.93	496.7735	992.541	-0.0014	-1.4	6.05	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
8058	dirMS_041712_NAR_20mM_plus.15479.15653.2	2	11.18	0	3.47E+05		(K)VGINYQ	(K)V G I N\Y/Q|P\P T V|V|P G G D L\A K(V)		179.05	912.9952	1824.985	-0.0023	-1.3	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
8059	dirMS_041712_NAR_30mM_plus2.13551.13673.2	2	11.18	0	7.56E+05		(R)SSMTFL	(R)S S|M/T|F/L/T\R(Q)		124.75	471.7412	942.471	0.0038	4	9.47	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
8060	dirMS_041712_NAR_30mM_plus2.17037.17060.2	2	11.18	0	2.20E+05		(R)GLGLDD	(R)G L|G L/D/D/A/L/E/P R(Q)		142.2	578.3042	1155.6	0.0007	0.6	4.03	51326.8	5.49	HUMAN	Q9Y230	RuvB-like 2
8061	dirMS_041712_NAR_30mM_plus2.5758.5758.2	2	11.18	0	2.39E+05		(K)TSEVNC	(K)T S|E V/N\C Y/R(C)	C:Carbamidomethylation	85	514.7261	1028.447	-0.0016	-1.6	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein

8062	dirMS_041712_NAR_50mM_plus2.5410.5410.3	3	11.18	1	5.11E+04		(R)DASTLQ	(R)D A|S T L Q S Q K/A E/G T G D A K(-)		89.17	569.61	1706.819	-0.0037	-2.2	4.56	9538.7	10.48	HUMAN	O00479	High mobility group nucleosome-binding domain-containing protein 4
8063	dirMS_041712_NAR_60mM_plus.12080.12080.3	3	11.18	1	2.47E+05		(K)IDKTDY	(K)I D K T D Y\M|V/G/S Y/G P R(A)		120.28	534.5906	1601.763	-0.0056	-3.5	5.96	21671	5.37	HUMAN	J3KTF8	Rho GDP-dissociation inhibitor 1 (Fragment)
8064	dirMS_041712_NAR_30mM_minus2.19584.19593.2	2	11.17	0	2.93E+05		(R)YLTVAA	(R)Y L|T|V/A/A V F/R(G)		162.75	520.2998	1039.593	-0.0012	-1.1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
8065	dirMS_041712_NAR_50mM_minus2.14216.14216.3	3	11.17	0	1.56E+05	M13m	(R)DLISHDE	(R)D L/I/S/H D E m F S D I/Y K(I)	m:Oxidized methionine	149.13	576.9343	1712.784	16.0047	5.7	4.22	19709.1	4.83	HUMAN	P13693	Translationally-controlled tumor protein
8066	dirMS_041712_NAR_50mM_minus2.16061.16153.3	3	11.17	1	1.58E+05		(K)ISMPDI	(K)I/S|M/P D/I/D L/N L K G P K(V)		160.03	514.2852	1540.84	0.0007	0.5	5.96	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
8067	dirMS_041712_NAR_50mM_minus2.17894.17894.3	3	11.17	1	9.75E+03		(K)TFVNITP	(K)T F|V|N\I/T/P A E V G V L V G K D R(S)		170.58	639.0247	1915.065	-0.0052	-2.7	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
8068	dirMS_041712_NAR_50mM_minus2.18328.18328.3	3	11.17	1	8.35E+05		(R)KAIIIFVP	(R)K A I I I F\V/P/V P/Q/L K(S)		173.97	489.3206	1465.95	-0.0032	-2.2	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
8069	dirMS_041712_NAR_60mM_minus.8373.8373.3	3	11.17	1	2.41E+05		(K)MIYASS	(K)M I/Y A/S/S K D/A I K(K)		106.4	409.5576	1226.645	0.0133	10.9	8.26	22956	8.8	HUMAN	E9PK25	Cofilin-1
8070	dirMS_041712_NAR_120mM_plus.15319.15319.4	4	11.17	2	7.82E+05		(R)AGEVER	(R)A/G/E V/E R D L D K/A/D/S M I R(L)		133.22	451.9773	1804.886	0.0016	0.9	4.44	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
8071	dirMS_041712_NAR_120mM_plus.9939.10383.4	4	11.17	2	2.14E+06		(K)MQASIE	(K)M Q\A/S I E/K/G G S L/P K V E/A K(F)		105.85	443.9944	1772.958	-0.0017	-1	8.25	32745.6	4.64	HUMAN	P06748	Nucleophosmin
8072	dirMS_041712_NAR_20mM_plus.8192.8192.2	2	11.17	0	1.06E+05		(K)VTEDTS	(K)V T/E/D/T S S V L R(S)		126.02	553.7889	1106.569	0.0017	1.6	4.37	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
8073	dirMS_041712_NAR_30mM_plus2.7927.7927.2	2	11.17	0	2.20E+05		(K)IAVAAQ	(K)I A|V|A A/Q N C Y K(V)	C:Carbamidomethylation	96.05	569.2905	1137.572	0.0016	1.4	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
8074	dirMS_041712_NAR_40mM_plus2.12078.12078.3	3	11.17	1	2.00E+04	M467m	(R)DmTLPP	(R)D m\T/L/P P E T/N/V/I L T K D K(A)	m:Oxidized methionine	137.58	610.9868	1814.957	15.989	-3.2	4.56	246695.2	5.91	HUMAN	E7EVA0	Microtubule-associated protein
8075	dirMS_041712_NAR_40mM_plus2.12822.12822.2	2	11.17	0	2.97E+04		(R)FGLNVS	(R)F G L/N/V/S S I S\R(K)		141.92	540.2954	1079.584	-0.0009	-0.8	9.75	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
8076	dirMS_041712_NAR_50mM_plus2.11260.11260.3	3	11.17	0	2.13E+05		(K)NAQLNI	(K)N A\Q\L/N I E/L/E A A/H H(-)		127	487.2488	1459.729	0.003	2.1	5.23	13452	8.89	HUMAN	F5H246	Protein NAMPTL
8077	dirMS_041712_NAR_50mM_plus2.19043.19043.3	3	11.17	0	1.35E+06		(R)LGFHLP	(R)L G F H L|P\L E|V/A|Y Q R(G)		167.77	514.9522	1542.843	-0.0007	-0.4	6.75	533778	5.74	HUMAN	Q15149	Plectin
8078	dirMS_041712_NAR_60mM_plus.20126.20384.3	3	11.17	0	2.10E+06		(K)VHLVGI	(K)V H\L\V\G\I|D|I/F/T/G K(K)		166.1	433.5839	1298.747	-0.0096	-7.4	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
8079	dirMS_041712_NAR_120mM_minus.7474.7474.3	3	11.16	1	1.11E+05		(K)AQLEPV	(K)A Q|L/E/P V A S P A K K/P K(V)		94.93	488.6239	1463.858	-0.0009	-0.6	9.7	533778	5.74	HUMAN	Q15149	Plectin
8080	dirMS_041712_NAR_30mM_minus2.17924.17924.2	2	11.16	0	1.60E+05		(R)VPFSLLR	(R)V/P/F|S/L L R(G)		151.43	416.2578	831.509	-0.0004	-0.5	9.72	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
8081	dirMS_041712_NAR_30mM_minus2.19181.19181.2	2	11.16	0	1.04E+05		(K)TVALW	(K)T V|A/L W D/L R(N)		159.22	487.2765	973.547	-0.0008	-0.8	5.5	19598	4.45	HUMAN	B4DRT0	Histone-binding protein RBBP4
8082	dirMS_041712_NAR_40mM_minus2.11611.11712.3	3	11.16	1	1.36E+05		(K)TVGVEP	(K)T V|G V/E|P A A D G K/G V V V V I K(R)		152.03	580.008	1738.011	-0.0015	-0.8	5.73	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
8083	dirMS_041712_NAR_50mM_minus2.16500.16500.3	3	11.16	0	8.97E+04		(R)LLLDIPL	(R)L L|L D I/P L/Q T P H K(L)		162.35	463.2805	1387.831	-0.0038	-2.7	6.74	198852.6	5.95	HUMAN	A6NKT7	RanBP2-like and GRIP domain-containing protein 3
8084	dirMS_041712_NAR_20mM_plus.17550.17550.2	2	11.16	0	3.20E+04		(K)LFVTND	(K)L F|V|T/N D A A T/I L R(E)		192.63	667.3752	1333.747	-0.0043	-3.2	5.84	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
8085	dirMS_041712_NAR_20mM_plus.19095.19095.2	2	11.16	0	2.04E+05		(R)VCTLAII	(R)V C/T|L A I|I/D P G D S D I I/R(S)	C:Carbamidomethylation	202.77	879.4578	1757.91	-0.0019	-1.1	3.93	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
8086	dirMS_041712_NAR_30mM_plus2.13594.13595.2	2	11.16	0	5.45E+05		(K)VGLQVV	(K)V/G|L|Q/V/V/A V K(A)		124.17	456.7974	912.588	-0.0002	-0.2	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
8087	dirMS_041712_NAR_30mM_plus2.6162.6173.2	2	11.16	0	2.28E+05		(K)FIDTTSK	(K)F/I|D/T/T/S K(F)		86.52	406.2102	811.42	-0.0065	-8	5.84	40551.6	10.15	HUMAN	G5E9G0	60S ribosomal protein L3
8088	dirMS_041712_NAR_50mM_plus2.13258.13258.3	3	11.16	0	3.85E+05		(K)VQASLA	(K)V Q|A|S/L A A N T/F T\I T G H A E T K(Q)		137.68	654.0087	1960.013	-0.0019	-1	6.72	11802.2	5.6	HUMAN	D6RDG3	Transcription factor BTF3 (Fragment)
8089	dirMS_041712_NAR_60mM_plus.11180.11180.3	3	11.16	0	2.87E+05		(K)MQEHS	(K)M Q E/H S D Q\V|P\V G N I P R(S)		115.93	569.6188	1706.828	0.014	8.2	5.3	20991.8	10.19	HUMAN	C9J8M6	DNA replication licensing factor MCM7 (Fragment)
8090	dirMS_041712_NAR_60mM_plus.15852.15852.3	3	11.16	0	4.48E+05		(R)VWYVS	(R)V W/Y/V/S N I D/G T/H I A/K(T)		139.77	534.9464	1602.828	-0.0028	-1.8	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
8091	dirMS_041712_NAR_60mM_plus.16005.16005.3	3	11.16	0	5.11E+05		(R)VWYVS	(R)V W|Y/V S N I D G T H I\A K(T)		140.07	534.9464	1602.828	-0.0028	-1.8	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
8092	dirMS_041712_NAR_60mM_plus.6814.6814.2	2	11.16	1	2.58E+05		(K)SLDEME	(K)S L/D/E/M/E/K|Q Q R(E)		94.13	632.3035	1263.6	-0.0001	0	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
8093	dirMS_041712_NAR_120mM_minus.8159.8159.3	3	11.15	2	1.08E+06		(K)KGAVAE	(K)K|G A\V/A E D G D/E L R T\E\P E|A K(K)		99.27	638.9836	1914.94	-0.0041	-2.1	4.36	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
8094	dirMS_041712_NAR_120mM_minus.8585.8626.3	3	11.15	1	1.40E+05		(R)SEGFDT	(R)S/E|G/F/D/T Y R C D/R(N)	C:Carbamidomethylation	101.1	469.1998	1405.58	0.0047	3.4	4.56	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
8095	dirMS_041712_NAR_120mM_minus.9401.9401.4	4	11.15	2	2.08E+05		(K)NKQGLE	(K)N K Q G L/E/T/D N K/E L\A/C E/V/K(V)	C:Carbamidomethylation	105.85	494.7536	1975.975	0.0172	8.7	4.87	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
8096	dirMS_041712_NAR_30mM_minus2.7678.7678.2	2	11.15	0	3.46E+05	M67m	(R)QmVETE	(R)Q m|V/E T E/L/K(L)	m:Oxidized methionine	96.17	497.2476	977.497	15.9907	-4.2	4.53	12818.9	8.18	HUMAN	K7EIT4	14-3-3 protein epsilon (Fragment)
8097	dirMS_041712_NAR_50mM_minus2.7318.7353.3	3	11.15	1	1.43E+05		(R)VLVNDA	(R)V L|V/N D A Q K/V T/E/G Q Q E R(L)		108.8	605.3171	1813.94	-0.0035	-1.9	4.68	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
8098	dirMS_041712_NAR_60mM_minus.18270.18270.3	3	11.15	1	1.37E+05		(R)SELELTL	(R)S E|L/E L/T L|G/K L E Q V R(S)		163.05	538.9724	1614.906	-0.0035	-2.1	4.78	533778	5.74	HUMAN	Q15149	Plectin
8099	dirMS_041712_NAR_120mM_plus.14409.14953.4	4	11.15	1	4.09E+06		(K)LDKSQI	(K)L/D K S Q I H\D\I\V\L\V/G/G/S/T R(I)		130.45	460.2603	1838.013	0.0063	3.4	6.75	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
8100	dirMS_041712_NAR_120mM_plus.15912.15912.4	4	11.15	1	8.06E+05		(K)THLPGF	(K)T\H\L\P G\F/V/E/Q A/E/A L K/A K(G)		137.05	435.4926	1738.949	-0.0001	0	6.42	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
8101	dirMS_041712_NAR_20mM_plus.11479.11479.2	2	11.15	0	2.08E+05		(K)VGLQVV	(K)V/G/L/Q V V\A V/K(A)		151.53	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
8102	dirMS_041712_NAR_20mM_plus.16891.16891.2	2	11.15	0	3.17E+05		(K)VQIAVA	(K)V Q\I\A V|A/N\A/Q E/L L Q R(M)		187.73	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
8103	dirMS_041712_NAR_20mM_plus.17191.17191.2	2	11.15	0	9.03E+04		(K)VLDIIATI	(K)V L/D\I|I A/T I/N\K(G)		189.97	550.3381	1099.672	-0.0032	-2.9	5.81	19639	5.52	HUMAN	H0YA83	Beta-hexosaminidase subunit beta (Fragment)
8104	dirMS_041712_NAR_20mM_plus.18597.18597.2	2	11.15	0	1.98E+05		(R)VFIGNL	(R)V F/I/G\N L N T L V\V/K(K)		200.12	658.8999	1316.794	-0.0011	-0.9	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
8105	dirMS_041712_NAR_20mM_plus.18936.18936.2	2	11.15	0	1.05E+05		(K)DTSYLF	(K)D T S Y\L/F|I/T/G P D V V/K(S)		201.92	777.9049	1554.805	-0.0025	-1.6	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
8106	dirMS_041712_NAR_20mM_plus.7283.7283.2	2	11.15	0	3.85E+05	M532m M	(R)mVPAG	(R)m V|P A/G m G A G/L E R(M)	m:Oxidized methionine	117.88	610.7907	1188.586	31.9877	-1.7	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
8107	dirMS_041712_NAR_30mM_plus2.16392.16392.2	2	11.15	0	2.54E+05		(K)ELPELLQ	(K)E L/P|E/L/L/Q R(N)		138.87	499.2973	997.568	0.0197	19.7	4.53	96649	6.13	HUMAN	Q8WUM4	Programmed cell death 6-interacting protein
8108	dirMS_041712_NAR_30mM_plus2.21482.21482.2	2	11.15	0	3.90E+05		(R)VNQAI	(R)V/N\Q|A|I/W L|L C\T G A R(E)	C:Carbamidomethylation	166.88	751.3976	1501.794	-0.0065	-4.3	9.72	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
8109	dirMS_041712_NAR_30mM_plus2.5671.5671.2	2	11.15	0	6.92E+04		(R)AYGGS	(R)A/Y/G/G/S M C/A K(C)	C:Carbamidomethylation	83.82	472.7087	944.396	0.0137	14.5	8.63	13520.9	11.92	HUMAN	P49207	60S ribosomal protein L34
8110	dirMS_041712_NAR_30mM_plus2.7598.7599.2	2	11.15	0	8.52E+05		(R)LTEGCS	(R)L/T|E/G/C/S F/R(R)	C:Carbamidomethylation	94.1	485.2288	969.446	0.0045	4.6	6	5988.9	10.55	HUMAN	C9J1C5	40S ribosomal protein S27
8111	dirMS_041712_NAR_50mM_plus2.10117.10117.3	3	11.15	0	7.46E+05		(R)GISEETT	(R)G I|S E|E T T/T G/V/H N L Y K(M)		120.05	550.2759	1648.818	-0.0045	-2.8	5.4	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
8112	dirMS_041712_NAR_50mM_plus2.9818.9844.3	3	11.15	1	1.03E+06		(R)VAIEPG	(R)V/A|I|E|P G A P R E N D E F C K(M)	C:Carbamidomethylation	119.12	611.296	1831.864	0.0091	5	4.41	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
8113	dirMS_041712_NAR_60mM_plus.7222.7222.2	2	11.15	0	5.06E+05		(R)IGKPAP	(R)I/G K/P A/P D|F K(A)		95.78	486.7793	972.551	0	0	8.59	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
8114	dirMS_041712_NAR_60mM_plus.8327.8327.3	3	11.15	1	4.18E+04	M185m	(K)ALIEmE	(K)A L|I|E/m/E K Q Q Q D/Q V D R(N)	m:Oxidized methionine	101.47	616.3117	1830.901	16.0191	13.1	4.32	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)
8115	dirMS_041712_NAR_120mM_minus.11476.11476.2	2	11.14	1	4.01E+05		(R)KLTVEE	(R)K|L|T/V E E A/F\K(A)		116.75	532.8007	1064.599	-0.0045	-4.2	6.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
8116	dirMS_041712_NAR_20mM_minus.11093.11093.2	2	11.14	0	8.46E+04		(K)VIDPAT	(K)V I/D|P A T/A T S V D L R(D)		158.43	679.3706	1357.732	0.0018	1.3	4.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
8117	dirMS_041712_NAR_20mM_minus.8514.8652.2	2	11.14	0	2.54E+05		(K)TIAPALV	(K)T I|A|P A L V S K(K)		135.52	450.2808	899.556	-0.0017	-1.9	8.41	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
8118	dirMS_041712_NAR_30mM_minus2.15558.15558.2	2	11.14	0	9.61E+04		(K)TLAAEM	(K)T L|A|A/E M\Q/E L/R(V)		137.87	581.3003	1161.593	0.0001	0.1	4.53	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
8119	dirMS_041712_NAR_30mM_minus2.18319.18319.3	3	11.14	0	5.00E+05		(R)QAQEYE	(R)Q/A Q E Y E\A/L/L N/I/K(V)		154.63	473.9196	1419.748	-0.0036	-2.5	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
8120	dirMS_041712_NAR_40mM_minus2.12318.12318.3	3	11.14	1	2.92E+05		(K)DVAIKE	(K)D/V|A I K E/P L\V|D V/V D/P K(Q)		156.1	546.3068	1636.916	-0.0098	-6	4.23	24376.8	6.08	HUMAN	E9PIX6	Protein arginine N-methyltransferase 1 (Fragment)
8121	dirMS_041712_NAR_40mM_minus2.8238.8238.3	3	11.14	0	2.47E+05	M35m	(K)AASDIA	(K)A A S D I\A/m T\E/L P P T H P I R(L)	m:Oxidized methionine	128.65	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
8122	dirMS_041712_NAR_60mM_minus.7929.7929.3	3	11.14	1	1.80E+05		(K)EASKQA	(K)E A S K Q\A D/V/N/L/V/N/A K(L)		104.17	496.2639	1486.786	-0.0089	-6	6.17	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
8123	dirMS_041712_NAR_120mM_plus.10247.10308.2	2	11.14	1	2.02E+06		(R)VKYETE	(R)V/K|Y|E T E/L/A M/R(Q)		107.43	620.3237	1239.64	-0.0001	0	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
8124	dirMS_041712_NAR_120mM_plus.6256.6256.3	3	11.14	0	7.62E+05		(K)QRPQAT	(K)Q R P Q\A|T/A/E/Q/I/R(L)		86.03	433.2367	1297.697	-0.0016	-1.2	9.6	113668.7	6.2	HUMAN	F8W726	Ubiquitin-associated protein 2-like
8125	dirMS_041712_NAR_20mM_plus.10929.10929.2	2	11.14	0	2.19E+05	M33m	(K)VAGmD	(K)V/A/G m/D V E/L|T/V E/E R(N)	m:Oxidized methionine	147.28	732.3555	1447.71	15.994	-0.6	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
8126	dirMS_041712_NAR_20mM_plus.14482.14705.2	2	11.14	0	2.39E+05		(K)VSTLPAI	(K)V/S|T/L/P A I T L K(L)		172.37	521.8283	1042.651	-0.0013	-1.3	8.72	20599.3	9.19	HUMAN	H7C1V0	Cathepsin D light chain (Fragment)
8127	dirMS_041712_NAR_30mM_plus2.6093.6133.2	2	11.14	0	2.31E+05		(K)AMEAV	(K)A M|E|A|V|A|A\Q/G K(A)		86.4	488.2554	975.493	0.0107	11	6.05	28936.8	9.22	HUMAN	P15259	Phosphoglycerate mutase 2
8128	dirMS_041712_NAR_30mM_plus2.6614.6615.2	2	11.14	0	1.98E+05		(K)TLNAGA	(K)T/L|N|A G A/Y S K(V)		89.15	462.7408	924.479	-0.0042	-4.5	8.26	30197.4	7.91	HUMAN	E9PMG2	Palmitoyl-protein thioesterase 1 (Fragment)
8129	dirMS_041712_NAR_30mM_plus2.8513.8513.2	2	11.14	0	2.28E+05		(K)DVDEAY	(K)D V/D E/A/Y/M/N K(V)		98.55	542.7341	1084.462	-0.0006	-0.6	4.03	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
8130	dirMS_041712_NAR_50mM_plus2.10891.10891.3	3	11.14	1	2.35E+06		(R)MQKEIT	(R)M Q K E I T/A|L/A/P S T/M K(I)		124.07	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
8131	dirMS_041712_NAR_50mM_plus2.13185.13185.3	3	11.14	1	1.00E+06		(K)ASLAET	(K)A/S/L/A/E/T D K I T/L E V/A K(L)		137.4	530.2925	1588.879	-0.0163	-10.2	4.68	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
8132	dirMS_041712_NAR_50mM_plus2.13215.13306.3	3	11.14	1	2.24E+06		(R)DGRGAL	(R)D G R G A L Q\N\I|I|P/A S T G A A K(A)		138.1	580.6491	1739.94	-0.0071	-4.1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
8133	dirMS_041712_NAR_50mM_plus2.17200.17200.3	3	11.14	1	8.40E+05		(R)VYAEDP	(R)V Y/A E D/P Y K S F/G L|P S I G R(L)		159.15	633.6509	1898.965	-0.0265	-14	6.04	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
8134	dirMS_041712_NAR_50mM_plus2.17802.17802.3	3	11.14	0	6.69E+05		(K)ALVSHN	(K)A/L V S H N G S L I|N\V|G S L L/Q R(A)		161.37	626.6872	1878.056	-0.0085	-4.5	9.8	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
8135	dirMS_041712_NAR_120mM_minus.14226.14226.3	3	11.13	1	1.09E+06		(R)RLEAAY	(R)R L E A\A|Y\L/D\L Q R(I)		131.78	449.9126	1347.738	-0.0147	-10.9	6.07	15962.5	9.61	HUMAN	B4DT30	Tubulin-specific chaperone A
8136	dirMS_041712_NAR_120mM_minus.9882.9882.3	3	11.13	1	2.01E+05		(R)SRSGEG	(R)S R S G E\G E\V|S/G L M/R(K)		108.07	455.559	1364.659	0.0038	2.8	5.87	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
8137	dirMS_041712_NAR_50mM_minus2.16180.16325.3	3	11.13	1	4.86E+05		(K)LFTAESL	(K)L F|T/A/E S L I G L K/N/P E K(S)		160.7	553.9759	1659.932	-0.0185	-11.1	6.14	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
8138	dirMS_041712_NAR_60mM_minus.19322.19322.3	3	11.13	0	1.03E+06		(R)SLHDAL	(R)S L/H D A L\C/V/L/A/Q T V K(D)	C:Carbamidomethylation	171.23	518.9484	1554.831	-0.0002	-0.1	6.46	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
8139	dirMS_041712_NAR_120mM_plus.10898.10898.3	3	11.13	0	1.18E+06		(R)GSAVHC	(R)G S/A|V/H/Q L/S/E/E/L/R(C)		110.8	442.5657	1325.681	0.0017	1.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
8140	dirMS_041712_NAR_20mM_plus.13900.13900.2	2	11.13	0	1.84E+04		(R)GLCAIA	(R)G L/C/A|I/A|Q/A E\S L R(Y)	C:Carbamidomethylation	167.55	644.8389	1288.668	0.0027	2.1	6	18529.2	9.98	HUMAN	E9PL45	40S ribosomal protein S3
8141	dirMS_041712_NAR_20mM_plus.8131.8131.2	2	11.13	0	8.42E+04		(R)AAPGAE	(R)A A/P|G\A E/F A P N K(R)		125.68	536.7749	1072.542	0.0003	0.3	6.05	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
8142	dirMS_041712_NAR_30mM_plus2.19478.19478.2	2	11.13	0	1.18E+05		(K)VQIAVA	(K)V Q\I/A|V|A|N\A/Q E/L/L Q R(M)		155.73	776.9425	1552.881	-0.0028	-1.8	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
8143	dirMS_041712_NAR_40mM_plus2.15914.15914.3	3	11.13	0	2.77E+05		(K)VAIVKP	(K)V/A|I\V/K P G V/P M/E/I V L N K(E)		160.87	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
8144	dirMS_041712_NAR_40mM_plus2.6264.6346.2	2	11.13	0	4.41E+05		(K)NAGFTP	(K)N/A|G|F/T/P Q E R(Q)		96.23	510.2487	1019.491	-0.0004	-0.4	6	29474.8	6.94	HUMAN	G3V3M6	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
8145	dirMS_041712_NAR_50mM_plus2.16891.17035.3	3	11.13	1	5.56E+05		(K)TLNDM	(K)T/L|N D/M R Q E Y/E\Q\L I/A/K(N)		156.75	617.98	1851.927	-0.0015	-0.8	4.68	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
8146	dirMS_041712_NAR_50mM_plus2.22157.22202.3	3	11.13	1	5.40E+05		(R)ELAILLG	(R)E L/A I/L/L G/M L D/P A E/K D/E K(G)		190.32	629.004	1884.999	-0.0012	-0.7	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
8147	dirMS_041712_NAR_60mM_plus.16279.16298.3	3	11.13	0	2.04E+05		(R)EHALLA	(R)E H A\L\L|A\Y|T/L/G V/K(Q)		141.97	438.9179	1314.742	-0.0025	-1.9	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
8148	dirMS_041712_NAR_60mM_plus.16947.16947.3	3	11.13	0	8.01E+05		(K)TTISVAH	(K)T\T/I/S V/A/H/L/L A A/R(Q)		144.73	418.2478	1252.737	-0.0083	-6.7	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
8149	dirMS_041712_NAR_30mM_minus2.6150.6150.2	2	11.12	0	2.70E+05		(K)TSEVNC	(K)T|S|E/V/N C Y/R(C)	C:Carbamidomethylation	87.72	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
8150	dirMS_041712_NAR_50mM_minus2.18097.18097.3	3	11.12	1	1.52E+05		(R)GDLGIE	(R)G D L/G/I/E I/P A E K V F L A Q K(M)		172.1	610.0112	1828.022	-0.0024	-1.3	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
8151	dirMS_041712_NAR_60mM_minus.10622.10622.3	3	11.12	0	2.57E+05		(R)SVIHSLA	(R)S V I H S\L/A/S|V/E A Q K(S)		119.02	456.9195	1368.748	-0.0042	-3.1	6.47	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
8152	dirMS_041712_NAR_60mM_minus.12026.12026.3	3	11.12	1	5.65E+05		(R)ISVYYNE	(R)I/S/V/Y/Y N E A T G G K Y V/P R(A)		127.47	606.3103	1816.923	-0.0065	-3.6	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
8153	dirMS_041712_NAR_60mM_minus.17883.17963.3	3	11.12	1	3.70E+05		(K)NLRDID	(K)N L R D I D\E\V/S/S/L/L R(T)		160.93	510.6099	1529.828	-0.013	-8.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
8154	dirMS_041712_NAR_120mM_plus.18218.18233.4	4	11.12	1	1.39E+06		(K)YYITIIDA	(K)Y Y\I\T\I/I/D/A/P G H R D F I K(N)		148.93	481.2587	1922.017	-0.0041	-2.1	6.75	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
8155	dirMS_041712_NAR_20mM_plus.15830.15905.2	2	11.12	0	1.31E+05		(R)GTPLISP	(R)G T/P|L/I/S P L/I K(W)		181	519.8306	1038.656	-0.0018	-1.8	8.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
8156	dirMS_041712_NAR_30mM_plus2.11199.11199.2	2	11.12	0	4.82E+05		(K)TVSPALI	(K)T V|S/P A/L I/S R(F)		111.48	472.2823	943.557	0.0002	0.2	9.41	50425	5.53	HUMAN	H0YH27	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
8157	dirMS_041712_NAR_50mM_plus2.14582.14689.3	3	11.12	0	3.94E+05		(K)ILMDKP	(K)I/L|M/D K/P/E M N V\V L/K(N)		144.9	510.6214	1529.843	0.0067	4.4	6.07	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
8158	dirMS_041712_NAR_50mM_plus2.21230.21230.3	3	11.12	0	2.09E+06		(R)AGKPVI	(R)A G K\P V\I\C A\T Q/M/L E S M I/K(K)	C:Carbamidomethylation	180.65	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
8159	dirMS_041712_NAR_50mM_plus2.8226.8226.3	3	11.12	1	3.09E+05		(R)NTVSQS	(R)N T/V/S/Q S I/S G D/P E I D K/K(I)		110.27	573.2915	1717.86	-0.0003	-0.2	4.56	58392.6	9.36	HUMAN	B4DF96	Eukaryotic translation initiation factor 2A
8160	dirMS_041712_NAR_50mM_plus2.9076.9076.3	3	11.12	1	2.37E+05		(K)LLDGPS	(K)L/L|D/G P S T/E K D L D/E/K(K)		115.12	520.5958	1559.78	-0.0071	-4.5	4.11	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
8161	dirMS_041712_NAR_60mM_plus.11204.11204.3	3	11.12	1	2.81E+05	M61m	(K)NQVAm	(K)N Q|V|A m N\P T/N/T V/F D/A K/R(L)	m:Oxidized methionine	116.13	607.9666	1805.896	15.989	-3.3	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
8162	dirMS_041712_NAR_60mM_plus.13192.13192.2	2	11.12	1	5.31E+05		(R)SVETLKE	(R)S V/E/T L K/E M I\K(S)		125.77	589.3278	1177.65	-0.0014	-1.2	5.86	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
8163	dirMS_041712_NAR_30mM_minus2.16982.16982.2	2	11.11	0	1.97E+05		(R)SIQEEL	(R)S I|Q/E/E\L Q Q/L/R(Q)		146.5	622.3359	1243.664	0.0004	0.3	4.53	533778	5.74	HUMAN	Q15149	Plectin
8164	dirMS_041712_NAR_30mM_minus2.19116.19116.3	3	11.11	0	1.79E+05		(K)SYELPD	(K)S/Y\E\L P D G Q/V/I/T/I/G N E R(F)		158.88	597.6343	1790.892	-0.0036	-2	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
8165	dirMS_041712_NAR_50mM_minus2.6757.6757.3	3	11.11	0	3.88E+04	M144m	(R)VGmVE	(R)V/G/m|V E/T N S Q D R\P V D D/V K(I)	m:Oxidized methionine	105.02	635.6378	1888.907	15.9919	-1.6	4.23	18350.6	7.96	HUMAN	Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1
8166	dirMS_041712_NAR_50mM_minus2.7892.7934.3	3	11.11	0	1.36E+05	M1969m	(R)FVPQE	(R)F V|P Q/E m G V/H T V/S V/K(Y)	m:Oxidized methionine	112.15	525.2727	1557.809	15.9942	-0.5	6.75	258215.9	5.48	HUMAN	E7EN95	Filamin-B
8167	dirMS_041712_NAR_60mM_minus.13946.13946.3	3	11.11	1	2.41E+04		(K)VKEGM	(K)V K\E G M N I|V/E/A M/E R(F)		137.6	502.5858	1505.745	-0.0022	-1.5	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
8168	dirMS_041712_NAR_60mM_minus.18442.18442.3	3	11.11	0	1.18E+06		(R)IHFPLAT	(R)I H F P L A T\Y|A|P V/I S A E K(A)		165.17	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
8169	dirMS_041712_NAR_120mM_plus.10738.10738.4	4	11.11	2	5.03E+05		(K)SKGCGV	(K)S K G C G V V K F E S|P E|V/A/E R(A)	C:Carbamidomethylation	109.53	470.4895	1878.938	-0.0017	-0.9	5.95	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
8170	dirMS_041712_NAR_20mM_plus.7556.7654.2	2	11.11	0	2.49E+05		(K)VLTPTQ	(K)V L|T|P T/Q V/K(N)		121.73	443.2734	885.54	-0.0009	-1	8.72	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1

8171	dirMS_041712_NAR_30mM_plus2.6449.6449.2	2	11.11	0	1.26E+05		(K)SGYLSSE	(K)S G/Y|L/S/S E R(L)		87.8	449.7152	898.427	-0.0034	-3.7	5.72	65692.2	5.7	HUMAN	E7EQR4	Ezrin
8172	dirMS_041712_NAR_30mM_plus2.7630.7631.2	2	11.11	0	4.16E+05		(K)IDDVVN	(K)I/D|D|V/V/N T/R(-)		94.37	466.2425	931.484	-0.0066	-7.1	4.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
8173	dirMS_041712_NAR_30mM_plus2.9114.9655.2	2	11.11	0	2.63E+06		(K)VGVNGF	(K)V/G|V/N/G F G|R(I)		103.97	403.2192	805.432	-0.0004	-0.5	9.72	36223.7	8.79	HUMAN	P04406	Glyceraldehyde-3-phosphate dehydrogenase
8174	dirMS_041712_NAR_40mM_plus2.18132.18132.2	2	11.11	0	8.61E+04		(R)SLDMDS	(R)S L|D|M|D/S I I A/E V K(A)		173.07	660.8385	1320.671	-0.0018	-1.4	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
8175	dirMS_041712_NAR_50mM_plus2.13564.13580.3	3	11.11	0	2.25E+06		(K)AGVVGF	(K)A/G V|V/G/P E/L/H E Q L L/S A E K(A)		138.68	592.986	1776.949	-0.0056	-3.1	4.75	533778	5.74	HUMAN	Q15149	Plectin
8176	dirMS_041712_NAR_50mM_plus2.15207.15376.3	3	11.11	1	7.51E+05		(K)TVGVEP	(K)T V|G V E/P A A D/G K G V V V V I K(R)		147.78	580.0056	1738.011	-0.0087	-5	5.73	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
8177	dirMS_041712_NAR_50mM_plus2.16779.16779.3	3	11.11	1	1.87E+05	M132m	(R)TLAEIAK	(R)T L|A|E/I A K V/E L D/N m P L R(G)	m:Oxidized methionine	155.92	610.3302	1812.989	15.9873	-4.2	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
8178	dirMS_041712_NAR_50mM_plus2.20752.20752.3	3	11.11	1	1.70E+05		(R)VNSKFD	(R)V/N/S K F D/T|I/Y/Q I L/L K(K)		177.62	561.3209	1681.952	-0.0042	-2.5	8.47	72626.7	9.13	HUMAN	Q14258	E3 ubiquitin/ISG15 ligase TRIM25
8179	dirMS_041712_NAR_60mM_plus.20483.20483.3	3	11.11	1	3.02E+05		(R)AQFEGI	(R)A Q|F/E G I/V T D L I R R(T)		167.4	506.6178	1517.843	-0.0046	-3	6.12	18505.2	10.14	HUMAN	H0YBG6	Stress-70 protein, mitochondrial (Fragment)
8180	dirMS_041712_NAR_40mM_minus2.12851.12851.3	3	11.1	0	4.66E+05		(K)FTISDHP	(K)F T/I/S D H/P Q/P I D/P/L L\K(N)		159.58	574.3124	1720.927	-0.0042	-2.4	5.21	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
8181	dirMS_041712_NAR_50mM_minus2.10703.10703.3	3	11.1	1	3.25E+05		(K)NQVAM	(K)N\Q|V/A\M/N/P/T N T V F D/A K R(L)		128.88	602.6379	1805.896	0.0029	1.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
8182	dirMS_041712_NAR_50mM_minus2.13591.13591.3	3	11.1	1	5.31E+05		(K)LTEDKAI	(K)L T/E D K/A D V/Q/S I|I/G L Q R(F)		144.8	595.9939	1785.97	-0.0034	-1.9	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
8183	dirMS_041712_NAR_60mM_minus.11298.11298.3	3	11.1	1	9.28E+05	M232m	(R)MSmKE	(R)M S\m K E V\D\E Q/M|L/N V Q N\K(N)	m:Oxidized methionine	122.78	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
8184	dirMS_041712_NAR_20mM_plus.15949.15949.2	2	11.1	0	1.33E+05		(K)SILFVPT	(K)S I|L/F|V|P T S A P R(G)		181.2	594.3403	1187.678	-0.005	-4.2	9.47	92752.5	4.76	HUMAN	P14625	Endoplasmin
8185	dirMS_041712_NAR_20mM_plus.18139.18139.2	2	11.1	0	1.70E+05		(R)LTGQLFI	(R)L/T|G Q/L/F/L/G G S I V/K(G)		197.02	666.8962	1332.789	-0.0034	-2.6	8.75	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
8186	dirMS_041712_NAR_20mM_plus.18454.18454.3	3	11.1	0	3.15E+05		(R)AAVEEG	(R)A A V E E G I\V/L/G G G C A/L L R(C)	C:Carbamidomethylation	198.02	562.3058	1684.905	-0.0022	-1.3	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
8187	dirMS_041712_NAR_30mM_plus2.10442.10585.2	2	11.1	0	5.44E+05		(K)ACQIFVF	(K)A/C|Q|I|F/V|R(N)	C:Carbamidomethylation	108.75	447.2386	893.466	0.0037	4.2	9.79	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
8188	dirMS_041712_NAR_30mM_plus2.19604.19604.2	2	11.1	0	1.08E+05		(K)VQIAVA	(K)V Q I|A\V/A/N A/Q E\L L Q\R(M)		155.87	776.9425	1552.881	-0.0028	-1.8	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
8189	dirMS_041712_NAR_30mM_plus2.7007.7007.2	2	11.1	0	8.26E+04		(K)ITITNDQ	(K)I T|I|T/N D/Q N R(L)		91.1	537.7813	1074.554	0.0015	1.4	5.84	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
8190	dirMS_041712_NAR_40mM_plus2.15039.15039.3	3	11.1	0	5.93E+05		(K)IEVIKPG	(K)I/E|V/I K/P G D\L G V D L T S K(L)		155.93	561.9876	1683.953	-0.0045	-2.7	4.56	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
8191	dirMS_041712_NAR_40mM_plus2.18650.18650.3	3	11.1	1	3.71E+05		(R)TLAEIAK	(R)T/L|A/E I A/K/V/E L D N M/P L R(G)		176.5	604.9967	1812.989	-0.0132	-7.3	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
8192	dirMS_041712_NAR_40mM_plus2.19727.19763.3	3	11.1	0	3.68E+05		(R)DLLDTVI	(R)D L|L/D/T V/L P H L Y N E/T K(V)		185.23	590.9774	1770.927	-0.0096	-5.4	4.54	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
8193	dirMS_041712_NAR_50mM_plus2.15339.15339.3	3	11.1	1	7.54E+05		(K)EAFSLFD	(K)E A|F/S/L/F D/K D G D\G T I/T T K(E)		149.33	615.6348	1844.891	-0.0014	-0.8	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
8194	dirMS_041712_NAR_120mM_minus.13870.13870.4	4	11.09	1	1.62E+06		(K)ASIHEA	(K)A S|I/H E A W/T D/G K E A/M L/K(H)		129.97	447.476	1786.879	0.0029	1.6	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
8195	dirMS_041712_NAR_20mM_minus.7530.7530.2	2	11.09	0	6.69E+05	M239m	(K)EVDEQm	(K)E V|D E/Q|m L N V|Q N/K(N)	m:Oxidized methionine	123.7	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
8196	dirMS_041712_NAR_30mM_minus2.18824.18865.2	2	11.09	0	1.61E+05		(K)GWPLYL	(K)G W|P/L/Y L S T K(N)		157.23	532.7918	1064.578	-0.0012	-1.1	8.59	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
8197	dirMS_041712_NAR_40mM_minus2.12769.12769.3	3	11.09	0	3.62E+05	M460m	(R)ISIEmN	(R)I/S/I/E/m/N G T L E D Q L S H/L K(Q)	m:Oxidized methionine	158.97	648.6649	1927.979	16.0008	3	4.65	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
8198	dirMS_041712_NAR_60mM_minus.5547.5566.3	3	11.09	1	2.78E+05		(K)EAEGAP	(K)E A/E/G/A P Q/V/E A G K R(L)		87.38	447.8959	1341.676	-0.0026	-1.9	4.79	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
8199	dirMS_041712_NAR_120mM_plus.17844.17844.3	3	11.09	0	7.30E+05		(R)HLLQAP	(R)H L|L Q\A/P V/D D A\Q/E I/L/H S R(F)		146.82	648.0088	1942.014	-0.0023	-1.2	5.21	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
8200	dirMS_041712_NAR_20mM_plus.11353.11353.2	2	11.09	0	3.00E+05		(K)LITPAVV	(K)L I/T|P/A/V V S E R(L)		150.6	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
8201	dirMS_041712_NAR_20mM_plus.8111.8111.2	2	11.09	0	1.06E+05		(K)VTEDTS	(K)V/T|E/D/T S S V L/R(S)		126.02	553.7889	1106.569	0.0017	1.6	4.37	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
8202	dirMS_041712_NAR_30mM_plus2.11220.11220.2	2	11.09	0	4.73E+05		(K)TVSPALI	(K)T V|S/P/A/L I S R(F)		111.5	472.2823	943.557	0.0002	0.2	9.41	50425	5.53	HUMAN	H0YH27	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
8203	dirMS_041712_NAR_30mM_plus2.16046.16046.2	2	11.09	0	1.77E+06		(K)ICSWNV	(K)I/C|S/W/N V D G L R(A)	C:Carbamidomethylation	137.82	610.3003	1219.589	0.0045	3.7	5.84	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
8204	dirMS_041712_NAR_30mM_plus2.22665.22665.3	3	11.09	0	5.00E+05		(R)ALTVPEI	(R)A L T\V/P E L T Q/Q/V F D A/K(N)		175.77	553.9697	1659.895	-0.0007	-0.4	4.37	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
8205	dirMS_041712_NAR_30mM_plus2.8538.8538.2	2	11.09	0	8.93E+05		(R)LGLGEG	(R)L G/L/G E/G A E/E K(S)		98.92	501.7639	1002.51	0.0103	10.3	4.25	40096.8	9.24	HUMAN	C9JW69	Regulator of chromosome condensation (Fragment)
8206	dirMS_041712_NAR_50mM_plus2.10380.10380.3	3	11.09	0	1.39E+05		(R)LIAHAG	(R)L/I/A/H\A\G S\L/T N\L|A K(Y)		122	436.9248	1308.763	-0.0036	-2.7	8.76	24485.6	9.74	HUMAN	H0Y653	Nucleolar protein 56 (Fragment)
8207	dirMS_041712_NAR_50mM_plus2.15118.15118.3	3	11.09	0	8.61E+05		(K)LHIIEVG	(K)L H I\I\E V\G\T|P/P T G N Q P F/P K(K)		147.2	649.0216	1945.054	-0.0039	-2	6.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
8208	dirMS_041712_NAR_50mM_plus2.20177.20177.3	3	11.09	0	5.36E+05		(R)QARPTY	(R)Q/A R P T Y\A\T A|M/L|Q S L L/K(-)		174.55	597.9962	1791.979	-0.0045	-2.5	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
8209	dirMS_041712_NAR_50mM_plus2.7779.7779.3	3	11.09	1	1.02E+05		(K)ELQAAG	(K)E L Q|A/A G K/S P/E/D L E R(L)		106.55	514.9321	1542.776	0.0059	3.8	4.41	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
8210	dirMS_041712_NAR_60mM_plus.15442.15442.3	3	11.09	1	3.77E+05		(R)SLIANLA	(R)S L|I/A/N/L|A A/A N C Y K K(E)	C:Carbamidomethylation	137.45	512.9411	1536.82	-0.0115	-7.5	9.7	36978.6	6.33	HUMAN	B7Z800	Adenosine kinase
8211	dirMS_041712_NAR_60mM_plus.15915.15915.3	3	11.09	1	2.52E+05		(R)TSFLDD	(R)T/S F/L/D/D/A F R K(N)		139.92	400.5399	1199.605	-0.0004	-0.3	5.62	21195.7	6.97	HUMAN	H0YJ21	Cytoplasmic dynein 1 heavy chain 1 (Fragment)
8212	dirMS_041712_NAR_120mM_minus.19468.19468.3	3	11.08	1	1.87E+05		(K)RSIQFVD	(K)R S I Q\F|V/D\W/C/P T G F K(V)	C:Carbamidomethylation	161.45	580.9561	1740.853	0.0011	0.6	8.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
8213	dirMS_041712_NAR_20mM_minus.11058.11058.2	2	11.08	0	1.31E+05	M92m	(R)ImNTFS	(R)I m|N\T/F/S V/V/P/S P K(V)	m:Oxidized methionine	158.32	668.3513	1319.703	15.9925	-1.8	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
8214	dirMS_041712_NAR_30mM_minus2.13855.14021.2	2	11.08	0	3.87E+05		(R)LAGLFNI	(R)L/A|G|L|F/N E Q R(K)		129.18	524.2789	1047.558	-0.0076	-7.3	6	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
8215	dirMS_041712_NAR_50mM_minus2.14736.14878.3	3	11.08	1	3.05E+05		(R)EAVTEIL	(R)E A|V/T E/I/L/G I E/P D R E K(G)		152.27	566.9683	1698.891	-0.0005	-0.3	4.25	25685.9	6.4	HUMAN	E9PGT1	Translin
8216	dirMS_041712_NAR_50mM_minus2.18091.18091.3	3	11.08	1	1.52E+05		(R)GDLGIEI	(R)G D L/G|I\E/I/P A E K V F L A Q K(M)		172.1	610.0112	1828.022	-0.0024	-1.3	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
8217	dirMS_041712_NAR_50mM_minus2.8642.8738.3	3	11.08	1	9.59E+04		(K)ALDLDS	(K)A L|D|L/D/S/S C K E A A D G Y Q/R(C)	C:Carbamidomethylation	117.47	633.6221	1898.855	-0.0031	-1.7	4.23	60404.6	6.4	HUMAN	F5H0T1	Stress-induced-phosphoprotein 1
8218	dirMS_041712_NAR_60mM_minus.11068.11132.3	3	11.08	1	1.26E+05		(R)LRSILEVI	(R)L/R S/I/L E V/H Q R(I)		121.03	417.5881	1250.733	0.017	13.6	9.61	83058.5	9.6	HUMAN	F5H141	Zinc finger protein 607
8219	dirMS_041712_NAR_60mM_minus.17109.17109.3	3	11.08	0	1.14E+04	M365m	(R)VLGFSHI	(R)V/L/G F S/H E E I/I S m L R(M)	m:Oxidized methionine	155.37	549.6245	1630.862	15.9968	1.1	5.4	232239.1	5.52	HUMAN	F2Z2U8	Myosin-14
8220	dirMS_041712_NAR_60mM_minus.19736.19736.3	3	11.08	0	4.58E+06		(R)LHFFMP	(R)L H F F M\P G|F|A/P|L/T S R(G)		179.22	540.9491	1620.835	-0.0028	-1.7	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
8221	dirMS_041712_NAR_20mM_plus.15554.15554.3	3	11.08	0	1.93E+04		(R)IIDVVYN	(R)I I D V V Y N/A/S N/N/E L V R(T)		179.13	573.6388	1718.907	-0.0053	-3.1	4.37	24490	10.56	HUMAN	P62241	40S ribosomal protein S8
8222	dirMS_041712_NAR_20mM_plus.17669.17669.2	2	11.08	0	8.56E+04		(R)GDGPICI	(R)G/D/G P I|C/L/V/L/A/P T R(E)	C:Carbamidomethylation	193.13	684.8681	1368.73	-0.0015	-1.1	5.84	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
8223	dirMS_041712_NAR_30mM_plus2.19308.19308.2	2	11.08	0	2.30E+04		(K)NQALFP	(K)N Q|A|L/F/P A C V L K(N)	C:Carbamidomethylation	155.17	630.8399	1260.677	-0.0044	-3.5	8.75	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
8224	dirMS_041712_NAR_30mM_plus2.20627.20627.2	2	11.08	0	3.52E+05		(K)GGIVGN	(K)G G I|V|G M|T/L\P I A R(D)		161.93	592.8453	1184.682	0.0013	1.1	9.75	27150.8	7.95	HUMAN	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2
8225	dirMS_041712_NAR_30mM_plus2.4189.4235.2	2	11.08	0	1.21E+06	M299m M	(K)NmmAA	(K)N m|m/A/A C D|P R(H)	C:Carbamidomethylation m:Oxid	69.58	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
8226	dirMS_041712_NAR_30mM_plus2.5552.5667.2	2	11.08	0	7.09E+05		(R)QQEEMI	(R)Q|Q/E/E/M/M/R(R)		84.08	476.2056	951.402	0.0017	1.7	4.53	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
8227	dirMS_041712_NAR_30mM_plus2.7710.7710.2	2	11.08	0	8.85E+05		(K)FAEQTL	(K)F/A|E/Q T L/R(Q)		94.45	432.7306	864.457	-0.0035	-4	6	533778	5.74	HUMAN	Q15149	Plectin
8228	dirMS_041712_NAR_30mM_plus2.8076.8491.2	2	11.08	0	8.24E+05		(K)LAAIGE	(K)L/A|A|I/G E/A T/R(L)		97.72	451.2545	901.51	-0.0084	-9.4	6	533778	5.74	HUMAN	Q15149	Plectin
8229	dirMS_041712_NAR_50mM_plus2.15180.15180.3	3	11.08	1	1.02E+06		(R)GDVVPK	(R)G D\V/V/P/K D V/N A|A I A T I/K(T)		147.9	537.6393	1610.911	-0.0079	-4.9	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
8230	dirMS_041712_NAR_50mM_plus2.9409.9409.3	3	11.08	0	2.40E+05	M389m	(K)MIVDPV	(K)M I|V/D/P\V E/P H G/E m K(F)	m:Oxidized methionine	116.62	499.9106	1481.713	16.0045	6.4	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
8231	dirMS_041712_NAR_60mM_plus.11221.11267.3	3	11.08	1	5.14E+05		(K)SFEEKVE	(K)S/F/E E/K/V E N L/K(S)		116.17	408.2176	1222.631	0.0069	5.6	4.78	25978.5	4.91	HUMAN	C9J502	Prostate leucine zipper variant 2
8232	dirMS_041712_NAR_120mM_minus.10977.10977.3	3	11.07	0	6.08E+05		(R)ISNRPAF	(R)I/S|N\R/P A F\M|P/S E G K(M)		113.93	478.5776	1433.721	-0.0023	-1.6	8.75	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
8233	dirMS_041712_NAR_120mM_minus.17387.17420.3	3	11.07	1	5.23E+05		(R)KVNNAD	(R)K\V N N A D D|F|P/N/L F R(Q)		150.12	517.2634	1549.776	-0.0001	-0.1	5.96	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
8234	dirMS_041712_NAR_30mM_minus2.11631.11668.2	2	11.07	0	5.59E+05	M64m	(K)VmYGF	(K)V/m|Y|G F/C S V/K(D)	C:Carbamidomethylation m:Oxid	117.33	553.7611	1090.506	16.0089	12.7	8.56	76925.9	4.46	HUMAN	A8MV58	Drebrin
8235	dirMS_041712_NAR_50mM_minus2.19062.19062.3	3	11.07	1	1.34E+06		(R)KEGGLG	(R)K|E G G L G\P L N\I|P L/L A D V T R(R)		187.5	621.6941	1863.07	-0.0021	-1.1	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
8236	dirMS_041712_NAR_50mM_minus2.8001.8001.3	3	11.07	1	1.21E+05		(K)TAVCDII	(K)T A V/C D I/P/P R/G L K(M)	C:Carbamidomethylation	112.2	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
8237	dirMS_041712_NAR_60mM_minus.15310.15310.2	2	11.07	0	4.13E+05		(R)EHALLA	(R)E/H|A/L|L/A Y T L G V/K(Q)		144.67	657.873	1314.742	-0.0029	-2.2	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
8238	dirMS_041712_NAR_60mM_minus.15768.15768.3	3	11.07	1	2.90E+05		(R)GFPTIYF	(R)G F/P T I/Y F S/P/A/N K\K(L)		147.25	490.5972	1469.779	-0.0017	-1.1	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
8239	dirMS_041712_NAR_60mM_minus.18895.18895.3	3	11.07	1	2.67E+05		(K)NAAGAL	(K)N/A|A/G A/L D L L K E L K(N)		166.87	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
8240	dirMS_041712_NAR_60mM_minus.5773.5773.2	2	11.07	1	1.44E+06		(K)DSYVGD	(K)D/S/Y\V|G/D/E A Q S K R(G)		88.92	677.8144	1354.623	-0.0018	-1.3	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
8241	dirMS_041712_NAR_120mM_plus.11517.11533.4	4	11.07	2	5.81E+05		(K)KGEKDIF	(K)K\G E K D I P G\L T D\T/T/V/P/R(R)		113.53	432.4918	1726.933	0.012	6.9	6.12	25082	11.29	HUMAN	A2A3R5	40S ribosomal protein S6
8242	dirMS_041712_NAR_120mM_plus.12676.12676.4	4	11.07	2	8.69E+05		(K)KGTVEG	(K)K G T V E/G\F E/P/A D/N K C L L/R(A)	C:Carbamidomethylation	118.95	484.2468	1933.98	-0.0147	-7.6	6.18	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
8243	dirMS_041712_NAR_120mM_plus.6660.6660.3	3	11.07	1	7.19E+05		(R)AEKAQD	(R)A/E K A/Q/D T E L A A Y L\E N R(Q)		88.27	607.9762	1821.898	0.0163	9	4.41	102170	8.79	HUMAN	A8MVN1	Diacylglycerol kinase zeta
8244	dirMS_041712_NAR_20mM_plus.14258.14258.2	2	11.07	0	3.41E+04		(R)IALTDN	(R)I/A|L/T/D/N/A|L I A R(S)		170.65	585.8432	1170.684	-0.005	-4.2	5.84	24489.6	10.74	HUMAN	A8MUD9	60S ribosomal protein L7
8245	dirMS_041712_NAR_20mM_plus.18333.18333.2	2	11.07	0	1.22E+05		(R)GVVQEL	(R)G V|V/Q E/L/Q/Q A/I/S K(L)		198.05	650.3656	1299.727	-0.0028	-2.1	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
8246	dirMS_041712_NAR_30mM_plus2.16005.16005.2	2	11.07	0	2.97E+05		(R)YSVDIPL	(R)Y/S|V/D/I/P/L/D K(T)		136.27	525.2819	1049.551	0.0052	4.9	4.21	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
8247	dirMS_041712_NAR_30mM_plus2.16820.16820.2	2	11.07	0	4.12E+05		(K)GCSFLPI	(K)G C|S F/L|P D/P Y\Q/K(Q)	C:Carbamidomethylation	140.93	656.306	1311.604	0.0009	0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
8248	dirMS_041712_NAR_30mM_plus2.9001.9001.2	2	11.07	0	6.03E+05		(R)LATNTS	(R)L A/T/N/T/S A P D/L K(N)		100.52	565.801	1130.605	-0.0105	-9.2	5.84	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
8249	dirMS_041712_NAR_40mM_plus2.10451.10451.3	3	11.07	0	7.46E+03		(R)AEGPVA	(R)A E|G\P/V/A/V/V V N G H T E G P A P A R(S)		125.88	643.3403	1927.998	0.0079	4.1	5.4	100461	9.46	HUMAN	Q86UK7	Zinc finger protein 598
8250	dirMS_041712_NAR_40mM_plus2.15675.15675.3	3	11.07	0	1.01E+04		(R)LQVIVCS	(R)L Q|V/I/V/C S A T L H S F D/V K(K)	C:Carbamidomethylation	158.6	606.3237	1816.963	-0.006	-3.3	6.74	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
8251	dirMS_041712_NAR_50mM_plus2.13290.13291.3	3	11.07	1	4.30E+05		(K)ILQEYIT	(K)I/L|Q/E/Y/I/T Q Q S N K L E/T G K(S)		138.07	665.0231	1993.06	-0.0053	-2.7	6.14	28001.7	5.46	HUMAN	K7EJJ1	AP-1 complex subunit mu-2 (Fragment)
8252	dirMS_041712_NAR_50mM_plus2.6459.6459.3	3	11.07	1	1.31E+05	M365m	(R)IVEQDT	(R)I V|E/Q/D T m/P P K G V R(H)	m:Oxidized methionine	98.88	495.9283	1469.778	15.9923	-1.8	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
8253	dirMS_041712_NAR_60mM_plus.12209.12209.3	3	11.07	1	1.23E+06		(R)LNDSILC	(R)L/N/D/S/I L Q A T E Q R/R(R)		120.47	515.2771	1543.819	-0.0019	-1.3	6.07	334221.3	6.44	HUMAN	P15924	Desmoplakin
8254	dirMS_041712_NAR_60mM_plus.9768.9768.3	3	11.07	1	2.90E+05		(K)SEEQLKE	(K)S/E|E Q\L/K E E/G I E/Y K(V)		109.28	527.9264	1581.764	0.0004	0.2	4.32	43928.7	6.58	HUMAN	B4DHG0	Dihydrolipoyl dehydrogenase, mitochondrial
8255	dirMS_041712_NAR_20mM_minus.12170.12170.2	2	11.06	0	5.04E+05	M185m	(K)LAVNm	(K)L A|V/N m|V/P F P R(L)	m:Oxidized methionine	171.05	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
8256	dirMS_041712_NAR_30mM_minus2.11425.11425.2	2	11.06	0	1.21E+05	M39m	(K)mFLYAD	(K)m F|L|Y/A D/N E D R(A)	m:Oxidized methionine	115.58	645.2795	1273.552	16	3.9	4.03	24724.1	5.17	HUMAN	E7ETQ7	Vacuolar protein sorting-associated protein VTA1 homolog
8257	dirMS_041712_NAR_30mM_minus2.18251.18251.2	2	11.06	0	1.22E+04		(R)LIDFLES	(R)L/I/D/F L E|S G/K(T)		153.68	511.2832	1021.556	0.0027	2.6	4.37	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
8258	dirMS_041712_NAR_30mM_minus2.7226.7226.2	2	11.06	0	1.45E+05	M88m	(K)DVDEAY	(K)D V|D|E A/Y/m N K(V)	m:Oxidized methionine	92.98	550.7326	1084.462	15.9964	1.3	4.03	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
8259	dirMS_041712_NAR_30mM_minus2.7819.8054.2	2	11.06	0	4.61E+05		(K)IYSSEAIK	(K)I/Y|S/S/E A I/K(S)		97.85	455.7458	910.488	-0.0037	-4.1	6	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
8260	dirMS_041712_NAR_50mM_minus2.18291.18291.3	3	11.06	0	3.68E+05		(K)ALIEVLQ	(K)A L|I/E/V L/Q P L I A E/H Q A R(R)		175.27	601.0139	1801.033	-0.0059	-3.3	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
8261	dirMS_041712_NAR_50mM_minus2.6641.6641.3	3	11.06	1	6.22E+04		(R)EGVLTG	(R)E G\V/L/T/G S/P E Q K E E A A K(A)		104.1	558.2834	1672.839	-0.0032	-1.9	4.49	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
8262	dirMS_041712_NAR_60mM_minus.11024.11024.3	3	11.06	0	2.68E+05		(R)ALPESLC	(R)A L/P/E/S L/G Q H A L/R(S)		121.42	431.2376	1291.712	-0.0135	-10.4	6.79	31463.6	5.53	HUMAN	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1
8263	dirMS_041712_NAR_60mM_minus.8444.8444.3	3	11.06	0	1.10E+05		(K)VDNDEN	(K)V/D|N/D E N E H Q/L S L R(T)		107.02	523.5817	1568.73	0.0006	0.4	4.31	6862.5	4.32	HUMAN	E5RGW4	Nucleophosmin (Fragment)
8264	dirMS_041712_NAR_60mM_minus.9262.9262.3	3	11.06	1	4.82E+04		(R)VLVNDA	(R)V/L|V/N/D A Q K\V T E G Q Q E R(L)		111.38	605.316	1813.94	-0.0068	-3.8	4.68	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
8265	dirMS_041712_NAR_120mM_plus.15509.15509.4	4	11.06	2	5.39E+05		(R)KTVGVE	(R)K\T V G V\E/P/A A/D G K G V V V V I/K(R)		134.93	467.2783	1866.106	-0.0145	-7.8	8.5	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
8266	dirMS_041712_NAR_120mM_plus.15983.16012.4	4	11.06	1	3.61E+05	M108m	(K)FLSDVYF	(K)F L\S D/V|Y/P D G F K/G H m L/T K(S)	m:Oxidized methionine	137.13	493.498	1954.973	15.997	1.1	6.74	15838.9	7.03	HUMAN	H0Y5U0	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
8267	dirMS_041712_NAR_20mM_plus.16296.16296.2	2	11.06	0	6.43E+04		(R)LSNIFVI	(R)L/S|N I/F V I/G K(G)		183.62	495.8022	990.598	-0.0011	-1.1	8.75	29825.4	10.37	HUMAN	P62701	40S ribosomal protein S4, X isoform
8268	dirMS_041712_NAR_20mM_plus.7867.7867.2	2	11.06	0	1.21E+05		(K)VEIIAND	(K)V/E|I|I/A/N D Q G N R(T)		124.5	614.8177	1228.628	0.0001	0.1	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
8269	dirMS_041712_NAR_30mM_plus2.13180.13180.2	2	11.06	0	2.92E+05		(R)GGAEQF	(R)G G A/E|Q/F/M|E E/T E R(S)		122.27	692.2951	1383.584	-0.0016	-1.2	4.09	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
8270	dirMS_041712_NAR_30mM_plus2.9399.9399.2	2	11.06	0	4.79E+05		(R)GGGQII	(R)G G G Q|I|I/P/T A R(R)		103.9	485.2772	969.548	-0.0005	-0.5	9.75	15036.9	7.16	HUMAN	K7EJ74	116 kDa U5 small nuclear ribonucleoprotein component (Fragment)
8271	dirMS_041712_NAR_40mM_plus2.17952.17952.3	3	11.06	1	4.73E+04		(K)TFVNITP	(K)T F|V/N/I/T P/A E V G V L/V/G K D/R(S)		172.23	639.0251	1915.065	-0.004	-2.1	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
8272	dirMS_041712_NAR_60mM_plus.8421.8441.2	2	11.06	1	4.35E+05		(K)EAIEGTY	(K)E/A|I/E/G T Y I D/K K(C)		102.33	633.8318	1266.658	-0.0013	-1	4.68	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
8273	dirMS_041712_NAR_20mM_minus.13955.13955.2	2	11.05	0	6.38E+05		(R)VLITTDL	(R)V L|I|T/T D L L A R(G)		192.17	557.8438	1114.683	-0.0027	-2.4	5.81	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
8274	dirMS_041712_NAR_40mM_minus2.10785.10785.3	3	11.05	0	1.27E+05	M56m	(K)VAIVKP	(K)V/A|I/V/K P G V|P/m E I V L N K(E)	m:Oxidized methionine	146.87	575.0112	1707.024	15.9953	0.2	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
8275	dirMS_041712_NAR_40mM_minus2.15255.15255.3	3	11.05	0	7.22E+05		(K)ALIEVLQ	(K)A L|I/E/V/L/Q P/L I A E H Q A R(R)		175.35	601.0146	1801.033	-0.0038	-2.1	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
8276	dirMS_041712_NAR_50mM_minus2.10426.10426.3	3	11.05	1	1.84E+04		(R)TEMEDL	(R)T/E/M E/D L/M/S S K D D/V/G K(S)		127.38	562.2507	1684.74	-0.0029	-1.7	4.1	227783.5	5.5	HUMAN	P35579	Myosin-9
8277	dirMS_041712_NAR_50mM_minus2.11881.11916.3	3	11.05	1	1.49E+05		(R)LIEDGR	(R)L/I/E/D/G R G C E/V I Q E I K(S)	C:Carbamidomethylation	135.83	586.9724	1758.906	-0.0028	-1.6	4.41	22452.9	9.82	HUMAN	H0Y9N5	60 kDa SS-A/Ro ribonucleoprotein (Fragment)
8278	dirMS_041712_NAR_50mM_minus2.12847.12847.3	3	11.05	0	1.04E+05		(R)NFDLTA	(R)N F|D/L T/A I/P C A N H K(M)	C:Carbamidomethylation	141.1	500.914	1500.726	0.0011	0.7	6.74	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
8279	dirMS_041712_NAR_50mM_minus2.13551.13551.3	3	11.05	0	3.38E+05		(R)AVAIDLI	(R)A V A I D/L/P/G L G H S K(E)		144.6	426.5785	1277.721	-0.0003	-0.2	6.79	19983.6	8.14	HUMAN	B4DQI4	Alpha/beta hydrolase domain-containing protein 14B

8280	dirMS_041712_NAR_50mM_minus2.13572.13572.3	3	11.05	0	4.59E+04		(K)MLDAEL	(K)M L/D\A E/D/I V N/T A/R\P D E K(A)		144.98	606.2965	1816.875	0.0004	0.2	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
8281	dirMS_041712_NAR_50mM_minus2.15948.15948.3	3	11.05	0	3.52E+05		(K)LYGPTNI	(K)L/Y/G\P T N/F S/P I/I N/H V A R(F)		158.25	600.3221	1798.96	-0.0081	-4.5	8.75	60985.3	5.6	HUMAN	O75131	Copine-3
8282	dirMS_041712_NAR_50mM_minus2.19096.19096.3	3	11.05	1	1.34E+06		(R)KEGGLG	(R)K\E G G L G\P L N\I|P L/L/A/D V T R(R)		187.5	621.6941	1863.07	-0.0021	-1.1	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
8283	dirMS_041712_NAR_120mM_plus.15488.15781.4	4	11.05	2	7.62E+05		(R)KTVGVE	(R)K\T V G\V\E|P/A/A D/G K G V V V V I/K(R)		135.38	467.2783	1866.106	-0.0145	-7.8	8.5	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
8284	dirMS_041712_NAR_20mM_plus.15854.15854.2	2	11.05	0	6.04E+05	M73m	(R)AILVDLE	(R)A I/L/V/D/L|E|P G/T\m D S V R(S)	m:Oxidized methionine	179.72	816.4181	1615.836	15.9929	-1.2	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
8285	dirMS_041712_NAR_30mM_plus2.15982.15982.2	2	11.05	0	4.68E+05		(R)MGPNIY	(R)M/G|P/N/I/Y/E L/R(T)		136.68	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
8286	dirMS_041712_NAR_30mM_plus2.16682.16843.2	2	11.05	0	4.19E+05		(R)LWDLTT	(R)L/W|D|L/T/T/G/T T T R(R)		140.43	632.8304	1264.653	0.0003	0.3	5.84	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
8287	dirMS_041712_NAR_30mM_plus2.19646.19865.3	3	11.05	0	2.45E+05		(R)IIPGFMC	(R)I I|P G F M C/Q/G/G D/F T R(H)	C:Carbamidomethylation	157.77	533.5865	1598.745	-0.0004	-0.3	5.84	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
8288	dirMS_041712_NAR_30mM_plus2.20268.20326.2	2	11.05	0	3.95E+05		(R)FLIQNVL	(R)F/L|I/Q N V\L/R(L)		161.17	501.8112	1002.61	0.0056	5.6	9.75	132902.3	5.82	HUMAN	J3KR24	Isoleucine--tRNA ligase, cytoplasmic
8289	dirMS_041712_NAR_40mM_plus2.11930.11930.3	3	11.05	0	7.59E+04	M26m	(R)LSAmLV	(R)L S A m\L V\P V T/P E V/K P K(R)	m:Oxidized methionine	136.4	542.3146	1608.939	15.9899	-3.1	8.59	31524.1	4.5	HUMAN	P82970	High mobility group nucleosome-binding domain-containing protein 5
8290	dirMS_041712_NAR_40mM_plus2.18087.18087.3	3	11.05	0	1.19E+05		(K)LVLIGSN	(K)L V|L/I/G S N H S L/P F L K(F)		172.83	513.3081	1537.91	-0.0003	-0.2	8.76	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
8291	dirMS_041712_NAR_50mM_plus2.18741.18741.3	3	11.05	0	7.92E+05		(R)CRPDQL	(R)C R P D Q L\T|G\L/S/L/L/P\L S E K(A)	C:Carbamidomethylation	167.32	643.0148	1927.032	-0.0019	-1	6.07	533778	5.74	HUMAN	Q15149	Plectin
8292	dirMS_041712_NAR_50mM_plus2.8273.8273.3	3	11.05	1	7.95E+04		(R)DTGEKL	(R)D/T|G E K L T V/A/E/N E A/E T K(L)		109.95	578.9478	1734.839	-0.0104	-6	4.25	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
8293	dirMS_041712_NAR_120mM_minus.11433.11466.4	4	11.04	2	1.39E+06	M105m	(R)AQKDEE	(R)A Q\K D E E K m E\I|Q/E/I Q/L K(E)	m:Oxidized methionine	116.63	494.7536	1960.006	15.987	-4	4.58	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
8294	dirMS_041712_NAR_120mM_minus.17143.17143.4	4	11.04	1	5.17E+05		(K)YYVTIID	(K)Y Y\V/T I|I/D/A/P G H R D F I/K(N)		147.97	477.7556	1908.001	-0.0008	-0.4	6.75	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
8295	dirMS_041712_NAR_120mM_minus.4853.4853.3	3	11.04	1	5.63E+05		(K)AGADEE	(K)A/G/A/D/E/E R A/E T A R(L)		77.42	425.8687	1275.592	-0.0008	-0.7	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
8296	dirMS_041712_NAR_30mM_minus2.15743.15743.2	2	11.04	0	4.68E+04		(R)INEILSN	(R)I/N/E|I/L S N A L K(R)		139.15	557.8242	1114.647	-0.0055	-5	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
8297	dirMS_041712_NAR_40mM_minus2.12798.12798.3	3	11.04	0	1.29E+05		(K)GVTIIGP	(K)G V T\I/I/G/P A/T V/G G I K/P G C F K(I)	C:Carbamidomethylation	159.23	624.6828	1872.041	-0.0073	-3.9	10	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
8298	dirMS_041712_NAR_50mM_minus2.12748.12748.3	3	11.04	0	3.41E+06	M84m	(K)YPIEHGI	(K)Y/P I/E H G I I\T|N/W/D D m E\K(I)	m:Oxidized methionine	141.47	659.6398	1960.911	15.9939	-0.5	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
8299	dirMS_041712_NAR_60mM_minus.10361.10361.3	3	11.04	1	3.29E+04	M88m	(K)DVDEAY	(K)D V/D E/A/Y m N K/V/E L E S/R(L)	m:Oxidized methionine	116.62	605.2791	1797.832	15.9904	-2.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
8300	dirMS_041712_NAR_60mM_minus.10789.10789.3	3	11.04	1	5.44E+05	M239m	(R)MSMKE	(R)M/S M K E V\D E\Q|m|L N V\Q/N K(N)	m:Oxidized methionine	119.9	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
8301	dirMS_041712_NAR_120mM_plus.16321.16352.4	4	11.04	1	9.26E+05		(R)ALEHFT	(R)A L E H/F/T/D L/Y/D I K/R(A)		138.4	405.9647	1620.838	-0.0011	-0.7	5.38	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
8302	dirMS_041712_NAR_120mM_plus.17867.17867.4	4	11.04	0	3.77E+05		(R)HLLQAP	(R)H L\L Q\A|P/V/D D A Q E I L/H S R(F)		146.78	486.2589	1942.014	-0.0003	-0.2	5.21	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
8303	dirMS_041712_NAR_20mM_plus.15869.15869.3	3	11.04	0	3.34E+04	M73m	(R)AILVDLE	(R)A I L V D L E|P/G/T m D S V R(S)	m:Oxidized methionine	180.95	544.6139	1615.836	15.9912	-2.3	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
8304	dirMS_041712_NAR_20mM_plus.17877.17877.2	2	11.04	0	1.93E+05		(K)GADFLV	(K)G A D F/L|V|T E|V/E N G G S L G S K(K)		195.13	890.4414	1779.876	-0.0004	-0.2	4.14	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
8305	dirMS_041712_NAR_30mM_plus2.4251.4251.2	2	11.04	0	9.19E+05	M299m M	(K)NmmAA	(K)N m\m/A/A C D|P/R(H)	C:Carbamidomethylation m:Oxid	69.88	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
8306	dirMS_041712_NAR_30mM_plus2.8809.8809.2	2	11.04	0	6.99E+05		(R)AAPGAE	(R)A A|P/G A/E F A P N/K(R)		100.33	536.7755	1072.542	0.0015	1.4	6.05	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
8307	dirMS_041712_NAR_40mM_plus2.18011.18011.3	3	11.04	0	2.73E+05		(K)LLYDLAD	(K)L L/Y/D/L\A D Q/L H A A V\G A S R(A)		171.4	604.9967	1812.96	0.0153	8.4	5.21	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
8308	dirMS_041712_NAR_40mM_plus2.6958.6958.2	2	11.04	0	1.41E+05		(R)MGPVM	(R)M/G|P/V/M\D/R(M)		100.52	403.1892	805.37	0.0016	2	5.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
8309	dirMS_041712_NAR_50mM_plus2.20101.20101.3	3	11.04	1	1.08E+05		(K)SVISGGL	(K)S V/I|S G G L/D A/L/E F I G K K(T)		174.18	545.3096	1633.916	-0.0017	-1	5.79	22133.2	4.82	HUMAN	E5RGF9	Protein FAM114A2 (Fragment)
8310	dirMS_041712_NAR_50mM_plus2.7834.7834.3	3	11.04	1	6.95E+04	M227m M	(R)mQKEIT	(R)m Q K E I T\A|L/A/P S T/m K(I)	m:Oxidized methionine	106.93	527.6045	1548.812	31.9865	-2.1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
8311	dirMS_041712_NAR_60mM_plus.9769.9769.3	3	11.04	1	2.90E+05		(K)SEEQLKE	(K)S E|E/Q\L K E E|G I E/Y/K(V)		109.28	527.9264	1581.764	0.0004	0.2	4.32	43928.7	6.58	HUMAN	B4DHG0	Dihydrolipoyl dehydrogenase, mitochondrial
8312	dirMS_041712_NAR_120mM_minus.6946.6946.2	2	11.03	0	4.18E+05		(K)HNAAFC	(K)H/N|A\A/F C|Y/K(L)	C:Carbamidomethylation	92.42	505.7282	1010.451	-0.0021	-2.1	8.6	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
8313	dirMS_041712_NAR_120mM_minus.8191.8191.3	3	11.03	1	2.76E+04		(K)SSGGREI	(K)S/S/G G R E D\L|E|S|S G L Q\R(R)		98.9	526.5882	1577.751	-0.0014	-0.9	4.68	11625.5	8.01	HUMAN	B8ZZT7	Hematological and neurological-expressed 1 protein
8314	dirMS_041712_NAR_20mM_minus.10408.10408.2	2	11.03	0	5.15E+04		(K)VLIANN	(K)V L|I|A/N/N/G I A A V/K(C)		152.82	591.863	1182.72	-0.0018	-1.5	8.72	269989.9	5.92	HUMAN	F8W8T8	Acetyl-CoA carboxylase 2
8315	dirMS_041712_NAR_30mM_minus2.16894.16894.2	2	11.03	0	4.71E+05		(K)NSLESYA	(K)N S|L|E/S Y/A/F N M K(A)		146.57	652.3031	1303.599	0.0002	0.2	6	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
8316	dirMS_041712_NAR_50mM_minus2.12481.12481.3	3	11.03	1	3.32E+05		(K)LYEQILA	(K)L/Y|E Q\I/L/A\E N E K L K(A)		139.12	530.9592	1590.874	-0.0107	-6.7	4.79	22046.7	5.8	HUMAN	H0YIM2	Protein phosphatase 1 regulatory subunit 12A (Fragment)
8317	dirMS_041712_NAR_50mM_minus2.18386.18393.3	3	11.03	0	3.39E+06		(K)ALESPER	(K)A/L|E|S/P E R P/F L A I/L\G G A K(V)		175.03	590.3356	1768.996	-0.0033	-1.9	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
8318	dirMS_041712_NAR_120mM_plus.22434.22434.4	4	11.03	2	3.40E+05		(R)TKIDPSA	(R)T K I D\P S A|L/V Q/K/L E L D/V R(S)		171.28	482.0309	1925.107	-0.0048	-2.5	5.79	22331.4	11.18	HUMAN	C9JJU7	Protein FAM207A (Fragment)
8319	dirMS_041712_NAR_20mM_plus.10257.10257.2	2	11.03	0	9.56E+04		(K)LEAEIAT	(K)L/E|A/E/I A T Y R(R)		143.43	533.2797	1065.557	-0.0054	-5	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
8320	dirMS_041712_NAR_20mM_plus.11107.11107.2	2	11.03	0	2.58E+03		(R)TAAALA	(R)T A A\A/L|A|P A S L T S A R(M)		148.3	650.862	1300.722	-0.0052	-4	9.41	300351.7	12.1	HUMAN	Q9UQ35	Serine/arginine repetitive matrix protein 2
8321	dirMS_041712_NAR_20mM_plus.13616.13890.3	3	11.03	0	3.85E+05		(R)GALQNI	(R)G A L\Q N\I\I/P/A/S T G\A A K(A)		167.25	471.2683	1411.79	0	0	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
8322	dirMS_041712_NAR_20mM_plus.17115.17115.2	2	11.03	0	1.22E+05		(K)FATEAAI	(K)F/A|T\E A/A/I/T\I L/R(I)		188.93	603.3442	1205.689	-0.0077	-6.4	6	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
8323	dirMS_041712_NAR_20mM_plus.17870.17887.2	2	11.03	0	1.96E+05		(R)SLVPAAI	(R)S L|V|P/A A E/L L E S R(V)		194.82	642.8613	1284.716	-0.0005	-0.4	4.53	533778	5.74	HUMAN	Q15149	Plectin
8324	dirMS_041712_NAR_30mM_plus2.12004.12004.2	2	11.03	0	1.12E+05		(K)TFITQQ	(K)T F|I/T/Q Q G/I/K(S)		116	518.2927	1035.583	-0.0052	-5	8.41	22338.2	9.61	HUMAN	C9JGT8	AP-2 complex subunit mu (Fragment)
8325	dirMS_041712_NAR_30mM_plus2.16722.16806.2	2	11.03	0	3.94E+05		(R)LWDLTT	(R)L W|D|L|T/T/G T T T R(R)		140.47	632.8304	1264.653	0.0003	0.3	5.84	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
8326	dirMS_041712_NAR_30mM_plus2.19070.19070.2	2	11.03	0	2.47E+05		(R)SWSLAT	(R)S W|S|L/A/T F R(T)		152.93	484.2579	967.5	0.0089	9.2	9.47	533778	5.74	HUMAN	Q15149	Plectin
8327	dirMS_041712_NAR_30mM_plus2.4142.4240.2	2	11.03	0	1.40E+06	M299m M	(K)NmmAA	(K)N/m|m|A|A C D|P R(H)	C:Carbamidomethylation m:Oxid	69.35	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
8328	dirMS_041712_NAR_40mM_plus2.7035.7056.2	2	11.03	0	1.61E+05		(R)QLETLG	(R)Q L|E|T/L/G Q/E K(L)		101.52	523.282	1045.552	0.0043	4.1	4.53	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
8329	dirMS_041712_NAR_50mM_plus2.11214.11214.3	3	11.03	1	4.13E+05		(R)MLFKDD	(R)M L/F K D D Y|P S S/P P K(C)		127.05	508.9188	1524.74	0.0016	1	5.71	20685.4	9.18	HUMAN	B0QYN7	SUMO-conjugating enzyme UBC9
8330	dirMS_041712_NAR_50mM_plus2.11400.11400.3	3	11.03	0	4.52E+05		(R)LLELGPK	(R)L/L|E/L/G P K/P E V A/Q Q T/R(K)		128.07	560.3195	1678.949	-0.0047	-2.8	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
8331	dirMS_041712_NAR_50mM_plus2.16528.16528.3	3	11.03	1	1.22E+05		(K)VIGNQS	(K)V/I|G|N\Q S L V\N E L A F T A R K(M)		154.88	620.6788	1860.034	-0.0119	-6.4	8.72	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
8332	dirMS_041712_NAR_50mM_plus2.6718.6718.3	3	11.03	0	1.60E+05		(K)IGEEEIQ	(K)I/G E E E I Q/K/P E E/K(V)		100.35	476.9126	1428.722	0.0016	1.1	4.32	81733.5	5.24	HUMAN	E9PAW1	Splicing factor 3A subunit 1
8333	dirMS_041712_NAR_50mM_plus2.8806.8806.3	3	11.03	0	2.04E+05		(K)VVQVSA	(K)V V/Q|V|S A G D S H T A/A/L/T D D G R(V)		113.45	633.6509	1898.92	0.0179	9.4	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
8334	dirMS_041712_NAR_60mM_plus.13951.14048.3	3	11.03	0	1.79E+06		(K)GIHPTIIS	(K)G I|H\P T I\I|S E/S F Q/K(A)		130.6	486.2646	1456.78	-0.0002	-0.1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
8335	dirMS_041712_NAR_30mM_minus2.13666.13704.2	2	11.02	0	2.35E+05		(K)LTVEEAF	(K)L/T|V/E/E A F/K(A)		127.65	468.7559	936.504	0.0008	0.9	4.53	266161	5.68	HUMAN	E9PPU0	Epiplakin
8336	dirMS_041712_NAR_30mM_minus2.14351.14351.2	2	11.02	0	4.27E+05		(K)QLFDQV	(K)Q L/F/D|Q/V V/K(T)		132.33	488.7803	976.546	0.0071	7.3	5.84	71218.8	6.3	HUMAN	A7YIJ8	Radixin
8337	dirMS_041712_NAR_50mM_minus2.15466.15466.3	3	11.02	1	2.25E+04		(K)CEFQDA	(K)C/E|F Q/D A|Y V L/L S E/K K(I)	C:Carbamidomethylation	156.05	577.2917	1729.847	0.014	8.1	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
8338	dirMS_041712_NAR_60mM_minus.7577.7577.3	3	11.02	1	1.79E+05		(K)DSIKLDD	(K)D S|I K/L/D/D/D S/E R(K)		101.45	431.5388	1292.597	0.0054	4.2	4.04	6116.1	5.2	HUMAN	F5H6I6	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
8339	dirMS_041712_NAR_20mM_plus.10434.10434.2	2	11.02	0	1.88E+05	M592m M	(R)mGPAm	(R)m G/P/A|m/G|P A\L/G|A G I E R(M)	m:Oxidized methionine	144.65	730.3568	1427.713	31.993	2.1	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
8340	dirMS_041712_NAR_20mM_plus.15491.15491.2	2	11.02	0	2.97E+04		(R)VLELVSI	(R)V L|E|L/V|S I T|A N K(N)		178.48	593.8535	1186.704	-0.0044	-3.7	5.97	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
8341	dirMS_041712_NAR_20mM_plus.17011.17011.2	2	11.02	0	1.83E+05		(K)LFLVQLC	(K)L F|L\V/Q L Q/E K(A)		189.33	559.3342	1117.662	-0.0004	-0.4	6	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
8342	dirMS_041712_NAR_20mM_plus.18208.18208.3	3	11.02	0	1.36E+05		(R)AILVDLE	(R)A I L/V D L E|P G T/M/D S V R(S)		196.55	539.2833	1615.836	-0.0006	-0.4	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
8343	dirMS_041712_NAR_30mM_plus2.12123.12123.2	2	11.02	0	7.10E+05		(K)EQFAWI	(K)E Q/F/A/W/R(H)		116.93	418.7093	836.405	0.0064	7.6	6.1	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
8344	dirMS_041712_NAR_30mM_plus2.22351.22351.3	3	11.02	0	5.16E+05		(R)VGNLGL	(R)V G\N L\G L/A/T/S F/F N/E/R(N)		172.82	508.9306	1524.781	-0.0033	-2.1	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
8345	dirMS_041712_NAR_30mM_plus2.7448.7448.2	2	11.02	0	7.14E+04		(R)IYHQNR	(R)I/Y|H Q N/R(K)		93.52	415.7147	830.427	-0.0046	-5.6	8.75	103324.6	8.72	HUMAN	E9PBP6	Microsomal triglyceride transfer protein large subunit
8346	dirMS_041712_NAR_40mM_plus2.11225.11225.3	3	11.02	0	1.03E+05		(R)VLVASS	(R)V L|V/A/S S V V A/G E S Q K/P E L K(A)		132.08	614.3443	1841.038	-0.0195	-10.6	6.11	61441.6	5.93	HUMAN	G8JLE9	Fragile X mental retardation protein 1
8347	dirMS_041712_NAR_40mM_plus2.11806.11806.3	3	11.02	1	2.71E+05		(R)IVAPGK	(R)I/V/A/P/G K G I L A A/D/E/S T G S I A K(R)		135.43	633.3568	1898.059	-0.0035	-1.8	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
8348	dirMS_041712_NAR_50mM_plus2.15239.15239.3	3	11.02	1	5.28E+05		(K)TKDGQII	(K)T K D G Q I\L|P|V|P N V\V V/R(D)		148.55	545.6573	1634.959	-0.0015	-0.9	8.41	56825.2	9.49	HUMAN	Q9P258	Protein RCC2
8349	dirMS_041712_NAR_50mM_plus2.8270.8270.3	3	11.02	0	1.40E+05		(R)IYDLNKF	(R)I/Y/D/L N K P E A E P K(E)		110.27	472.917	1416.737	-0.0005	-0.3	4.68	28733.7	4.82	HUMAN	B0AZV0	Serine-threonine kinase receptor-associated protein
8350	dirMS_041712_NAR_60mM_plus.16337.16356.3	3	11.02	0	6.18E+05		(K)MTHLPE	(K)M T H L P E\L/D|T|L/S/S E R(A)		142.28	543.6023	1628.795	-0.0025	-1.5	4.65	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
8351	dirMS_041712_NAR_30mM_minus2.17144.17187.2	2	11.01	0	2.44E+05		(K)FEDENFI	(K)F/E|D E/N F/I/L/K(H)		147.58	577.7894	1154.573	-0.0013	-1.1	4.14	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
8352	dirMS_041712_NAR_50mM_minus2.10493.10493.3	3	11.01	0	3.38E+04		(R)GITINAA	(R)G I/T/I/N/A A H V E Y S T A A R(H)		127.28	558.6229	1673.861	-0.0064	-3.8	6.75	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
8353	dirMS_041712_NAR_50mM_minus2.11158.11158.3	3	11.01	1	1.86E+05		(R)DNKQA	(R)D N/K Q A|G\V/F/E|P T I V K(V)		132.05	515.9485	1545.827	0.0038	2.5	6.07	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
8354	dirMS_041712_NAR_50mM_minus2.6234.6234.3	3	11.01	0	2.41E+05	M434m	(R)LESGmC	(R)L E|S/G m Q N M/S I H/T K(T)	m:Oxidized methionine	98.83	497.9018	1475.698	15.9927	-1.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
8355	dirMS_041712_NAR_120mM_plus.10458.10458.3	3	11.01	1	2.54E+06		(R)LQAEIEG	(R)L Q|A/E/I/E/G L K G Q R(A)		106.97	447.9207	1341.748	-0.0009	-0.7	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
8356	dirMS_041712_NAR_120mM_plus.4138.4138.3	3	11.01	1	1.70E+06	M54m	(K)SLDEmE	(K)S L/D/E/m/E K/Q/Q R(E)	m:Oxidized methionine	69.92	427.2032	1263.6	15.9953	0.3	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
8357	dirMS_041712_NAR_20mM_plus.13189.13189.2	2	11.01	0	6.48E+04		(R)ILGADTS	(R)I/L|G/A D\T S V/D L E E T G R(V)		163.12	788.3928	1575.786	-0.0077	-4.9	3.91	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
8358	dirMS_041712_NAR_20mM_plus.18650.18650.3	3	11.01	0	1.88E+04		(R)APVPAS	(R)A P V P A S E\L\L|A/S/G V L S/R(A)		199.92	522.9655	1566.885	-0.003	-1.9	6.05	533778	5.74	HUMAN	Q15149	Plectin
8359	dirMS_041712_NAR_20mM_plus.19060.19060.3	3	11.01	0	2.51E+05		(R)VCTLAII	(R)V C T L A\I\I/D/P/G D S D/I I R(S)	C:Carbamidomethylation	202.67	586.641	1757.91	-0.0018	-1	3.93	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
8360	dirMS_041712_NAR_20mM_plus.7021.7081.2	2	11.01	0	4.35E+05		(R)IQEAGTI	(R)I/Q|E|A/G T E/V V K(A)		115.37	537.2946	1073.584	-0.0018	-1.7	4.53	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
8361	dirMS_041712_NAR_40mM_plus2.11734.11734.2	2	11.01	0	2.68E+05		(R)NLLSVA	(R)N L|L/S V A/Y K(N)		135.18	454.2649	907.525	-0.0022	-2.4	8.59	18789.1	6.77	HUMAN	A2IDB2	14-3-3 protein eta (Fragment)
8362	dirMS_041712_NAR_50mM_plus2.11709.11709.3	3	11.01	1	4.13E+05		(R)ISVYYNE	(R)I/S V|Y/Y N/E/A T G G K Y V P R(A)		130.3	606.3123	1816.923	-0.0005	-0.3	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
8363	dirMS_041712_NAR_50mM_plus2.12809.12932.3	3	11.01	1	3.89E+05		(K)LAEIGAF	(K)L/A|E|I/G/A/P I Q G N R E E L V E R(L)		135.98	665.3593	1994.066	-0.0032	-1.6	4.49	38572.2	6.31	HUMAN	E9PJ04	Splicing factor 3B subunit 2 (Fragment)
8364	dirMS_041712_NAR_50mM_plus2.15461.15461.3	3	11.01	1	6.87E+05		(R)GFPTIYF	(R)G F/P T I/Y F/S/P A N K/K(L)		149.05	490.5973	1469.779	-0.0014	-0.9	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
8365	dirMS_041712_NAR_60mM_plus.12347.12370.3	3	11.01	0	1.51E+06		(K)RPGAAL	(K)R\P G A\A\L|D|P G C V L A/K(M)	C:Carbamidomethylation	121.18	475.5976	1424.768	0.0104	7.3	8.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
8366	dirMS_041712_NAR_60mM_plus.17109.17109.3	3	11.01	1	6.74E+06		(K)LKVPEW	(K)L K\V P E|W/V/D T V/K(L)		145.8	438.5872	1313.746	0.0007	0.5	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
8367	dirMS_041712_NAR_60mM_plus.6857.6857.2	2	11.01	0	2.45E+05		(R)MEELHN	(R)M/E|E/L|H N Q E\M Q/K(R)		94.28	708.8155	1416.625	-0.0009	-0.6	4.75	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
8368	dirMS_041712_NAR_120mM_minus.11748.11764.3	3	11	0	6.01E+05		(R)STYYWP	(R)S|T|Y/Y/W/P R P R(R)		118.07	409.2126	1225.611	0.012	9.8	9.98	13152.8	4.23	HUMAN	A1L429	G antigen 12B/C/D/E
8369	dirMS_041712_NAR_30mM_minus2.15985.16005.2	2	11	0	3.45E+05		(R)FGLNVS	(R)F/G\L/N|V/S S\I|S R(K)		140.08	540.2895	1079.584	-0.0127	-11.7	9.75	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
8370	dirMS_041712_NAR_30mM_minus2.18166.18166.2	2	11	0	1.57E+05		(K)FGAYIVD	(K)F G\A|Y/I/V D/G/L/R(Q)		153.6	555.7984	1110.594	-0.0047	-4.2	5.83	269989.9	5.92	HUMAN	F8W8T8	Acetyl-CoA carboxylase 2
8371	dirMS_041712_NAR_40mM_minus2.10880.10880.3	3	11	0	1.15E+05	M56m	(K)VAIVKP	(K)V/A/I/V K/P G V/P/m E/I V L N K(E)	m:Oxidized methionine	147	575.0112	1707.024	15.9953	0.2	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
8372	dirMS_041712_NAR_40mM_minus2.13872.13872.3	3	11	1	4.48E+04		(K)FGEVVD	(K)F G E|V|V\D C T L/K L D/P I T G R(S)	C:Carbamidomethylation	165.3	640.6656	1919.989	-0.0073	-3.8	4.56	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
8373	dirMS_041712_NAR_40mM_minus2.14546.14546.3	3	11	0	2.20E+04		(K)SLCIPFKI	(K)S L/C|I/P F K/P L C E L Q/P G A K(C)	C:Carbamidomethylation	169.72	653.3446	1958.024	-0.0046	-2.3	8.31	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
8374	dirMS_041712_NAR_40mM_minus2.14979.14979.3	3	11	1	7.94E+04		(R)VLEALLP	(R)V/L|E/A/L L/P L K G L E E R(V)		173.35	527.317	1579.942	-0.0053	-3.4	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
8375	dirMS_041712_NAR_50mM_minus2.12095.12095.3	3	11	1	7.12E+04		(R)LADLEAI	(R)L/A|D L E/A L K V A D/S K(T)		137.23	458.2586	1372.768	-0.007	-5.1	4.56	33736.6	5.14	HUMAN	O75792	Ribonuclease H2 subunit A
8376	dirMS_041712_NAR_50mM_minus2.14819.14819.3	3	11	1	2.45E+05		(K)IIVDELK	(K)I I\V/D/E/L/K Q E V I S T S S K(A)		152.52	597.0016	1788.995	-0.0051	-2.8	4.68	30149.5	5.96	HUMAN	D6RAC2	Guanine nucleotide-binding protein subunit beta-2-like 1
8377	dirMS_041712_NAR_50mM_minus2.18877.18877.3	3	11	1	2.12E+06		(R)LIALLEVI	(R)L/I|A L L/E/V/L S Q K R(M)		183.8	461.6289	1382.873	-0.0008	-0.6	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
8378	dirMS_041712_NAR_120mM_plus.7888.7907.3	3	11	1	9.65E+04		(R)VLIGENE	(R)V L|I/G E N E/K A E/R(M)		95.07	419.8978	1257.68	-0.0009	-0.7	4.79	142137.5	9.17	HUMAN	E7ENU4	Double-stranded RNA-specific adenosine deaminase
8379	dirMS_041712_NAR_20mM_plus.14956.14956.2	2	11	0	2.17E+05		(K)GLAITFV	(K)G L A\I|T\F/V|S/D E N D A/K(I)		175.3	740.3693	1479.733	-0.0012	-0.8	4.03	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
8380	dirMS_041712_NAR_20mM_plus.16313.16313.2	2	11	0	8.43E+04		(R)AYILNLV	(R)A Y|I/L/N L/V/K(Q)		183.77	467.2905	933.577	-0.0031	-3.3	8.63	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
8381	dirMS_041712_NAR_20mM_plus.17056.17154.2	2	11	0	8.68E+04		(K)VNIIPIIA	(K)V/N|I|I/P/I/I A K(A)		189.28	490.8283	980.65	-0.001	-1	8.72	51212	5.84	HUMAN	A6NFQ9	Septin-8
8382	dirMS_041712_NAR_30mM_plus2.14187.14187.3	3	11	0	2.76E+05		(R)LNDSILC	(R)L N D S I L/Q/A/T E/Q R(R)		127.3	463.2439	1387.718	-0.0004	-0.3	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
8383	dirMS_041712_NAR_30mM_plus2.21604.21604.2	2	11	0	1.79E+05		(R)TTNFAG	(R)T T|N F A/G/I L\S/Q/G L R(I)		169.17	689.3749	1377.748	-0.006	-4.3	9.41	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
8384	dirMS_041712_NAR_30mM_plus2.6810.6810.2	2	11	0	9.23E+04		(R)GAEQLA	(R)G A/E|Q/L A E|G G R(M)		90.18	494.2448	987.485	-0.0031	-3.1	4.53	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b
8385	dirMS_041712_NAR_50mM_plus2.13420.13420.3	3	11	0	8.41E+05		(R)VLVVHD	(R)V L/V/V/H/D G F E G L/A K(G)		139.35	461.9229	1383.763	-0.0089	-6.5	5.32	18719.9	6.91	HUMAN	F8VP00	6-phosphofructokinase, muscle type (Fragment)
8386	dirMS_041712_NAR_50mM_plus2.8956.8956.3	3	11	1	2.37E+04		(R)GGSDDS	(R)G G S D/D|S\S K D/P|I|D/V N Y E K(L)		114.08	609.2765	1825.809	0.0063	3.5	4.03	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
8387	dirMS_041712_NAR_120mM_minus.11323.11323.3	3	10.99	1	4.36E+05		(K)SFEEKVE	(K)S/F/E E K/V/E N L K(S)		116.57	408.2147	1222.631	-0.0018	-1.5	4.78	25978.5	4.91	HUMAN	C9J502	Prostate leucine zipper variant 2
8388	dirMS_041712_NAR_120mM_minus.20828.20828.4	4	10.99	1	5.83E+05		(R)SLHDAL	(R)S L\H D A L C\V/L/A Q/T/V K/D/S R(T)	C:Carbamidomethylation	173.1	479.0049	1912.991	0.0068	3.6	6.47	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta

<table>
<tr><td>8389</td><td>dirMS_041712_NAR_20mM_minus.12250.12250.2</td><td>2</td><td>10.99</td><td>0</td><td>3.47E+05</td><td>M73m</td><td>(R)AVLVDLI</td><td>(R)A V/L\V/D\L/E/P G/T\m/D S V/R(S)</td><td>m:Oxidized methionine</td><td>171.95</td><td>809.4088</td><td>1601.82</td><td>15.99</td><td>-3</td><td>4.03</td><td>13112.4</td><td>5.23</td><td>HUMAN</td><td>F8W813</td><td>Tubulin beta-8 chain</td></tr>
<tr><td>8390</td><td>dirMS_041712_NAR_20mM_minus.9945.9945.3</td><td>3</td><td>10.99</td><td>0</td><td>6.58E+04</td><td>M526m</td><td>(R)AmLAQ(</td><td>(R)A m L\A Q\Q\Y Q/E/G T L S V E K(L)</td><td>m:Oxidized methionine</td><td>149.72</td><td>604.632</td><td>1795.89</td><td>15.992</td><td>-1.6</td><td>4.53</td><td>266161</td><td>5.68</td><td>HUMAN</td><td>E9PPU0</td><td>Epiplakin</td></tr>
<tr><td>8391</td><td>dirMS_041712_NAR_30mM_minus2.15859.15859.2</td><td>2</td><td>10.99</td><td>2</td><td>2.72E+05</td><td></td><td>(K)LTLGGR\</td><td>(K)L T|L/G/G\R V K E/T(-)</td><td></td><td>139.5</td><td>537.313</td><td>1073.631</td><td>-0.0126</td><td>-11.7</td><td>8.75</td><td>21427</td><td>6.05</td><td>HUMAN</td><td>Q9BXU8</td><td>Ferritin heavy polypeptide-like 17</td></tr>
<tr><td>8392</td><td>dirMS_041712_NAR_40mM_minus2.9339.9339.3</td><td>3</td><td>10.99</td><td>0</td><td>1.31E+05</td><td></td><td>(K)VQASLA</td><td>(K)V Q/A/S L/A/A N T F/T I T\G H A E/T K(Q)</td><td></td><td>137.35</td><td>654.0087</td><td>1960.013</td><td>-0.0019</td><td>-1</td><td>6.72</td><td>11802.2</td><td>5.6</td><td>HUMAN</td><td>D6RDG3</td><td>Transcription factor BTF3 (Fragment)</td></tr>
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<tr><td>8394</td><td>dirMS_041712_NAR_50mM_minus2.18838.18838.3</td><td>3</td><td>10.99</td><td>1</td><td>2.24E+06</td><td></td><td>(R)LIALLEVI</td><td>(R)L I|A/L/L E V/L/S Q K/R(M)</td><td></td><td>183.72</td><td>461.6289</td><td>1382.873</td><td>-0.0008</td><td>-0.6</td><td>8.75</td><td>280326.9</td><td>5.48</td><td>HUMAN</td><td>O75369</td><td>Filamin-B</td></tr>
<tr><td>8395</td><td>dirMS_041712_NAR_50mM_minus2.9033.9033.3</td><td>3</td><td>10.99</td><td>1</td><td>1.70E+05</td><td></td><td>(K)ITIKNDP</td><td>(K)I/T|I/K N D/P S/L P E/P K(C)</td><td></td><td>119.82</td><td>484.6056</td><td>1451.81</td><td>-0.0082</td><td>-5.6</td><td>6.07</td><td>20203.8</td><td>9.79</td><td>HUMAN</td><td>B4DG16</td><td>Asparagine--tRNA ligase, cytoplasmic</td></tr>
<tr><td>8396</td><td>dirMS_041712_NAR_60mM_minus.11586.11587.3</td><td>3</td><td>10.99</td><td>0</td><td>2.25E+05</td><td></td><td>(K)ADDGRF</td><td>(K)A/D|D/G R P F/P/Q V/I K(S)</td><td></td><td>124.53</td><td>448.2371</td><td>1342.711</td><td>-0.0146</td><td>-10.9</td><td>6</td><td>15633.5</td><td>9.15</td><td>HUMAN</td><td>H3BMQ8</td><td>Fructose-bisphosphate aldolase A (Fragment)</td></tr>
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<tr><td>8399</td><td>dirMS_041712_NAR_120mM_plus.14208.14208.4</td><td>4</td><td>10.99</td><td>1</td><td>7.09E+05</td><td></td><td>(R)ETNLDSI</td><td>(R)E T N L D S\L/P L/V D/T H S K/R(T)</td><td></td><td>127.72</td><td>456.9906</td><td>1824.945</td><td>-0.0044</td><td>-2.4</td><td>5.38</td><td>53707.8</td><td>5.06</td><td>HUMAN</td><td>P08670</td><td>Vimentin</td></tr>
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<tr><td>8401</td><td>dirMS_041712_NAR_120mM_plus.6957.6957.3</td><td>3</td><td>10.99</td><td>0</td><td>4.69E+05</td><td></td><td>(K)SQFSDKI</td><td>(K)S Q|F\S D/K/P V/Q/D/R(G)</td><td></td><td>89.9</td><td>436.2209</td><td>1306.639</td><td>0.0095</td><td>7.3</td><td>5.68</td><td>13194</td><td>9.99</td><td>HUMAN</td><td>E9PI70</td><td>Chitinase domain-containing protein 1 (Fragment)</td></tr>
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<tr><td>8403</td><td>dirMS_041712_NAR_20mM_plus.16710.16710.2</td><td>2</td><td>10.99</td><td>0</td><td>2.59E+05</td><td></td><td>(K)VQIAVA</td><td>(K)V Q|I\A\V/A|N A/Q E\L L/Q R(M)</td><td></td><td>186.67</td><td>776.9419</td><td>1552.881</td><td>-0.004</td><td>-2.6</td><td>5.97</td><td>10728.1</td><td>9.15</td><td>HUMAN</td><td>Q9Y5L4</td><td>Mitochondrial import inner membrane translocase subunit Tim13</td></tr>
<tr><td>8404</td><td>dirMS_041712_NAR_20mM_plus.16893.16893.2</td><td>2</td><td>10.99</td><td>0</td><td>3.17E+05</td><td></td><td>(K)VQIAVA</td><td>(K)V Q\I|A/V/A/N A|Q E L L Q R(M)</td><td></td><td>187.73</td><td>776.9419</td><td>1552.881</td><td>-0.004</td><td>-2.6</td><td>5.97</td><td>10728.1</td><td>9.15</td><td>HUMAN</td><td>Q9Y5L4</td><td>Mitochondrial import inner membrane translocase subunit Tim13</td></tr>
<tr><td>8405</td><td>dirMS_041712_NAR_30mM_plus2.11825.11825.2</td><td>2</td><td>10.99</td><td>0</td><td>1.26E+06</td><td></td><td>(R)GGGGNI</td><td>(R)G G G G/N/F/G/P G P/G\S N F R(G)</td><td></td><td>114.42</td><td>689.3175</td><td>1377.629</td><td>-0.0017</td><td>-1.2</td><td>9.75</td><td>37486.1</td><td>9.03</td><td>HUMAN</td><td>P22626</td><td>Heterogeneous nuclear ribonucleoproteins A2/B1</td></tr>
<tr><td>8406</td><td>dirMS_041712_NAR_30mM_plus2.16409.16487.2</td><td>2</td><td>10.99</td><td>0</td><td>3.38E+05</td><td></td><td>(K)SFVPFPF</td><td>(K)S F|V|P F/P R(V)</td><td></td><td>138.97</td><td>425.239</td><td>849.462</td><td>0.009</td><td>10.6</td><td>9.47</td><td>51390.4</td><td>12.42</td><td>HUMAN</td><td>P0CG12</td><td>Chromosome transmission fidelity protein 8 homolog isoform 2</td></tr>
<tr><td>8407</td><td>dirMS_041712_NAR_30mM_plus2.9923.9957.2</td><td>2</td><td>10.99</td><td>0</td><td>1.79E+05</td><td></td><td>(R)EMVECF</td><td>(R)E M/V/E/C/F|N/K(I)</td><td>C:Carbamidomethylation</td><td>105.62</td><td>528.7288</td><td>1056.449</td><td>0.0014</td><td>1.4</td><td>4.53</td><td>36157.9</td><td>8.65</td><td>HUMAN</td><td>Q13011</td><td>Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial</td></tr>
<tr><td>8408</td><td>dirMS_041712_NAR_50mM_plus2.14760.14832.3</td><td>3</td><td>10.99</td><td>0</td><td>8.13E+05</td><td></td><td>(K)SIEIPRP\</td><td>(K)S I|E|I|P R P V D G V/E/V/P G C G K(I)</td><td>C:Carbamidomethylation</td><td>145.65</td><td>636.9936</td><td>1908.985</td><td>-0.0185</td><td>-9.7</td><td>4.68</td><td>34243.5</td><td>4.88</td><td>HUMAN</td><td>K7ENG2</td><td>Splicing factor U2AF 65 kDa subunit</td></tr>
<tr><td>8409</td><td>dirMS_041712_NAR_50mM_plus2.18512.18512.3</td><td>3</td><td>10.99</td><td>1</td><td>4.01E+05</td><td></td><td>(R)IAKEEIF(</td><td>(R)I A K E E I/F/G|P/V Q/P L F K(F)</td><td></td><td>165.08</td><td>572.6586</td><td>1715.973</td><td>-0.0118</td><td>-6.9</td><td>6.14</td><td>57661.7</td><td>6.36</td><td>HUMAN</td><td>P30837</td><td>Aldehyde dehydrogenase X, mitochondrial</td></tr>
<tr><td>8410</td><td>dirMS_041712_NAR_50mM_plus2.5920.5920.3</td><td>3</td><td>10.99</td><td>0</td><td>3.28E+05</td><td></td><td>(K)TVEAEA/</td><td>(K)T V|E/A E/A/A H G T V T/R(H)</td><td></td><td>94.9</td><td>447.8962</td><td>1341.676</td><td>-0.0017</td><td>-1.2</td><td>5.37</td><td>46943.7</td><td>6.54</td><td>HUMAN</td><td>O75874</td><td>Isocitrate dehydrogenase [NADP] cytoplasmic</td></tr>
<tr><td>8411</td><td>dirMS_041712_NAR_50mM_plus2.7813.7813.3</td><td>3</td><td>10.99</td><td>0</td><td>1.21E+05</td><td></td><td>(K)EAPPME</td><td>(K)E\A/P/P/M/E K/P E V V K(T)</td><td></td><td>106.95</td><td>451.9073</td><td>1353.708</td><td>-0.0009</td><td>-0.7</td><td>4.79</td><td>14798.1</td><td>10.35</td><td>HUMAN</td><td>K7EJ78</td><td>40S ribosomal protein S15 (Fragment)</td></tr>
<tr><td>8412</td><td>dirMS_041712_NAR_60mM_plus.13089.13374.3</td><td>3</td><td>10.99</td><td>1</td><td>1.02E+06</td><td></td><td>(R)ISVYYNE</td><td>(R)I/S|V/Y/Y N E A T G G K/Y V/P R(A)</td><td></td><td>125.95</td><td>606.3113</td><td>1816.923</td><td>-0.0035</td><td>-1.9</td><td>8.43</td><td>27549.9</td><td>4.39</td><td>HUMAN</td><td>E9PBJ4</td><td>Tubulin beta chain</td></tr>
<tr><td>8413</td><td>dirMS_041712_NAR_60mM_plus.16649.16649.2</td><td>2</td><td>10.99</td><td>0</td><td>7.99E+05</td><td></td><td>(R)EHALLA\</td><td>(R)E/H|A L/L|A Y T L/G V K(Q)</td><td></td><td>143.85</td><td>657.8735</td><td>1314.742</td><td>-0.0019</td><td>-1.4</td><td>6.85</td><td>50482.3</td><td>9.31</td><td>HUMAN</td><td>P68104</td><td>Elongation factor 1-alpha 1</td></tr>
<tr><td>8414</td><td>dirMS_041712_NAR_120mM_minus.11684.11684.3</td><td>3</td><td>10.98</td><td>2</td><td>3.38E+05</td><td></td><td>(R)SGKYDLI</td><td>(R)S G K/Y\D L D F/K/S|P D D|P S R(Y)</td><td></td><td>117.87</td><td>609.6226</td><td>1826.855</td><td>-0.0023</td><td>-1.3</td><td>4.58</td><td>47510.4</td><td>7.04</td><td>HUMAN</td><td>P06733</td><td>Alpha-enolase</td></tr>
<tr><td>8415</td><td>dirMS_041712_NAR_120mM_minus.12074.12074.3</td><td>3</td><td>10.98</td><td>1</td><td>2.38E+06</td><td></td><td>(K)MKEIAE/</td><td>(K)M K E I A E/A/Y/L/G K(T)</td><td></td><td>119.63</td><td>418.2252</td><td>1252.661</td><td>0.0005</td><td>0.4</td><td>5.9</td><td>17973</td><td>5.16</td><td>HUMAN</td><td>E9PI65</td><td>Heat shock cognate 71 kDa protein (Fragment)</td></tr>
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<tr><td>8417</td><td>dirMS_041712_NAR_30mM_minus2.13879.14063.2</td><td>2</td><td>10.98</td><td>0</td><td>2.29E+05</td><td></td><td>(K)LVPVGY(</td><td>(K)L V/P/V/G Y G I/R(K)</td><td></td><td>129.62</td><td>487.2949</td><td>973.583</td><td>-0.0004</td><td>-0.4</td><td>8.75</td><td>29184.1</td><td>4.91</td><td>HUMAN</td><td>E9PBQ9</td><td>Elongation factor 1-delta</td></tr>
<tr><td>8418</td><td>dirMS_041712_NAR_30mM_minus2.14657.14657.2</td><td>2</td><td>10.98</td><td>0</td><td>1.45E+04</td><td></td><td>(R)YLLGDM</td><td>(R)Y L|L/G D/M E/G R(L)</td><td></td><td>133.25</td><td>527.2613</td><td>1053.503</td><td>0.012</td><td>11.4</td><td>4.37</td><td>122967</td><td>5.33</td><td>HUMAN</td><td>F5GY55</td><td>DNA damage-binding protein 1</td></tr>
<tr><td>8419</td><td>dirMS_041712_NAR_50mM_minus2.10702.10702.3</td><td>3</td><td>10.98</td><td>1</td><td>3.25E+05</td><td></td><td>(K)NQVAM</td><td>(K)N Q|V|A\M/N\P/T N T V F D A\K R(L)</td><td></td><td>128.88</td><td>602.6379</td><td>1805.896</td><td>0.0029</td><td>1.6</td><td>8.75</td><td>20069.4</td><td>6.74</td><td>HUMAN</td><td>E9PK54</td><td>Heat shock cognate 71 kDa protein (Fragment)</td></tr>
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<tr><td>8422</td><td>dirMS_041712_NAR_30mM_plus2.13776.13798.2</td><td>2</td><td>10.98</td><td>0</td><td>4.07E+05</td><td></td><td>(K)LSSLPFQ</td><td>(K)L/S|S/L/P F Q/K(I)</td><td></td><td>125.47</td><td>460.2648</td><td>919.525</td><td>-0.0024</td><td>-2.6</td><td>8.75</td><td>12272.7</td><td>5.08</td><td>HUMAN</td><td>H3BRV9</td><td>Nuclear transport factor 2 (Fragment)</td></tr>
<tr><td>8423</td><td>dirMS_041712_NAR_30mM_plus2.14252.14252.2</td><td>2</td><td>10.98</td><td>0</td><td>2.88E+05</td><td></td><td>(K)ASEGPA</td><td>(K)A S/E G|P/A/F/F P G R(C)</td><td></td><td>127.82</td><td>568.2831</td><td>1135.553</td><td>0.0058</td><td>5.1</td><td>6.05</td><td>55373.1</td><td>7.25</td><td>HUMAN</td><td>F5H6Y1</td><td>Phenylalanine--tRNA ligase beta subunit</td></tr>
<tr><td>8424</td><td>dirMS_041712_NAR_30mM_plus2.14268.14268.2</td><td>2</td><td>10.98</td><td>0</td><td>2.89E+05</td><td></td><td>(K)ASEGPA</td><td>(K)A S\E/G/P A/F F/P/G R(C)</td><td></td><td>127.87</td><td>568.2831</td><td>1135.553</td><td>0.0058</td><td>5.1</td><td>6.05</td><td>55373.1</td><td>7.25</td><td>HUMAN</td><td>F5H6Y1</td><td>Phenylalanine--tRNA ligase beta subunit</td></tr>
<tr><td>8425</td><td>dirMS_041712_NAR_30mM_plus2.19940.19940.2</td><td>2</td><td>10.98</td><td>0</td><td>1.19E+05</td><td></td><td>(K)SLNNQF</td><td>(K)S L/N/N|Q F A/S F I/D K(V)</td><td></td><td>158.13</td><td>692.3489</td><td>1383.69</td><td>0.0002</td><td>0.2</td><td>5.55</td><td>66208.7</td><td>8.32</td><td>HUMAN</td><td>P04264</td><td>Keratin, type II cytoskeletal 1</td></tr>
<tr><td>8426</td><td>dirMS_041712_NAR_30mM_plus2.20017.20265.2</td><td>2</td><td>10.98</td><td>0</td><td>2.43E+05</td><td></td><td>(K)LYNLFLK</td><td>(K)L/Y|N|L F/L/K(I)</td><td></td><td>159.32</td><td>455.7738</td><td>910.54</td><td>0.0007</td><td>0.7</td><td>8.59</td><td>41666</td><td>7.73</td><td>HUMAN</td><td>E9PDQ8</td><td>Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial</td></tr>
<tr><td>8427</td><td>dirMS_041712_NAR_30mM_plus2.21936.21936.2</td><td>2</td><td>10.98</td><td>0</td><td>9.31E+03</td><td></td><td>(R)ALLSAP\</td><td>(R)A L|L/S/A/P W Y L N R(I)</td><td></td><td>170.53</td><td>652.3617</td><td>1303.716</td><td>0.0004</td><td>0.3</td><td>8.79</td><td>34763.8</td><td>4.71</td><td>HUMAN</td><td>E9PGL4</td><td>Beta-hexosaminidase subunit alpha</td></tr>
<tr><td>8428</td><td>dirMS_041712_NAR_30mM_plus2.6962.7079.2</td><td>2</td><td>10.98</td><td>0</td><td>2.58E+05</td><td></td><td>(K)MAQFD/</td><td>(K)M/A|Q|F D/A K(K)</td><td></td><td>91.35</td><td>405.6961</td><td>810.381</td><td>0.0035</td><td>4.3</td><td>5.59</td><td>56491.1</td><td>7.78</td><td>HUMAN</td><td>B4DTG2</td><td>Elongation factor 1-gamma</td></tr>
<tr><td>8429</td><td>dirMS_041712_NAR_50mM_plus2.5173.5264.3</td><td>3</td><td>10.98</td><td>0</td><td>1.37E+06</td><td></td><td>(K)TATPQQ</td><td>(K)T A|T/P Q Q A Q/E/V/H E K(L)</td><td></td><td>86.38</td><td>489.5774</td><td>1466.723</td><td>-0.0057</td><td>-3.9</td><td>5.37</td><td>31075.7</td><td>5.65</td><td>HUMAN</td><td>P60174</td><td>Triosephosphate isomerase</td></tr>
<tr><td>8430</td><td>dirMS_041712_NAR_50mM_plus2.7330.7330.3</td><td>3</td><td>10.98</td><td>0</td><td>1.63E+05</td><td></td><td>(R)EATNPP'</td><td>(R)E A T/N/P/P/V I Q E E K P K(K)</td><td></td><td>104.22</td><td>527.282</td><td>1579.833</td><td>-0.0012</td><td>-0.7</td><td>4.79</td><td>55361.8</td><td>6.42</td><td>HUMAN</td><td>G5EA52</td><td>Protein disulfide isomerase family A, member 3, isoform CRA_b</td></tr>
<tr><td>8431</td><td>dirMS_041712_NAR_120mM_minus.8246.8325.2</td><td>2</td><td>10.97</td><td>1</td><td>1.04E+06</td><td></td><td>(R)KVIDDTI</td><td>(R)K|V|I/D|D/T N I T/R(L)</td><td></td><td>99.52</td><td>587.8241</td><td>1174.643</td><td>-0.0017</td><td>-1.5</td><td>5.96</td><td>43773.3</td><td>5.26</td><td>HUMAN</td><td>F8VZY9</td><td>Keratin, type I cytoskeletal 18</td></tr>
<tr><td>8432</td><td>dirMS_041712_NAR_20mM_minus.10599.10599.2</td><td>2</td><td>10.97</td><td>0</td><td>2.00E+05</td><td></td><td>(R)TTPSYV/</td><td>(R)T T/P S\Y/V/A/F T D T E/R(L)</td><td></td><td>154.63</td><td>744.3547</td><td>1487.701</td><td>0.0009</td><td>0.6</td><td>4.37</td><td>58502.6</td><td>6.09</td><td>HUMAN</td><td>B4DXY3</td><td>Heat shock 70 kDa protein 1-like</td></tr>
<tr><td>8433</td><td>dirMS_041712_NAR_30mM_minus2.14331.14331.2</td><td>2</td><td>10.97</td><td>0</td><td>2.40E+05</td><td></td><td>(K)CCSGAII'</td><td>(K)C C|S/G A I/I/V L T K(S)</td><td>C:Carbamidomethylation</td><td>131.97</td><td>611.3188</td><td>1221.633</td><td>-0.0027</td><td>-2.2</td><td>8.75</td><td>58506.4</td><td>8.38</td><td>HUMAN</td><td>P14618</td><td>Pyruvate kinase isozymes M1/M2</td></tr>
<tr><td>8434</td><td>dirMS_041712_NAR_30mM_minus2.16472.16472.2</td><td>2</td><td>10.97</td><td>0</td><td>2.09E+05</td><td></td><td>(R)LLGWIQ</td><td>(R)L L|G/W/I Q/N\K(L)</td><td></td><td>142.77</td><td>486.2861</td><td>971.567</td><td>-0.0024</td><td>-2.4</td><td>8.75</td><td>67046.8</td><td>9.38</td><td>HUMAN</td><td>F8WE98</td><td>Filamin-A (Fragment)</td></tr>
<tr><td>8435</td><td>dirMS_041712_NAR_40mM_minus2.11883.11883.3</td><td>3</td><td>10.97</td><td>0</td><td>2.40E+05</td><td></td><td>(K)DAGEGL</td><td>(K)D A|G|E G L L A V Q/I T D|P E\G K\P K(K)</td><td></td><td>153.83</td><td>646.6785</td><td>1938.018</td><td>0.0031</td><td>1.6</td><td>4.32</td><td>283472.4</td><td>5.71</td><td>HUMAN</td><td>P21333</td><td>Filamin-A</td></tr>
<tr><td>8436</td><td>dirMS_041712_NAR_50mM_minus2.11653.11653.3</td><td>3</td><td>10.97</td><td>0</td><td>1.08E+05</td><td></td><td>(R)VTCPNH</td><td>(R)V/T|C/P N H/P D A I L|V/E D Y/R(A)</td><td>C:Carbamidomethylation</td><td>134.73</td><td>633.641</td><td>1898.907</td><td>0.0019</td><td>1</td><td>4.54</td><td>25558.6</td><td>9.3</td><td>HUMAN</td><td>B1APE1</td><td>General transcription factor IIB (Fragment)</td></tr>
<tr><td>8437</td><td>dirMS_041712_NAR_50mM_minus2.12580.12580.3</td><td>3</td><td>10.97</td><td>0</td><td>1.06E+06</td><td>M114m M:</td><td>(R)AGKPVI(</td><td>(R)A G/K|P V I|C A T/Q|m/L\E/S m I K(K)</td><td>C:Carbamidomethylation m:Oxid</td><td>139.83</td><td>636.9917</td><td>1876.969</td><td>31.9912</td><td>0.7</td><td>8.64</td><td>18466.1</td><td>5.78</td><td>HUMAN</td><td>H3BSU3</td><td>Pyruvate kinase (Fragment)</td></tr>
<tr><td>8438</td><td>dirMS_041712_NAR_50mM_minus2.14146.14146.3</td><td>3</td><td>10.97</td><td>0</td><td>1.50E+05</td><td></td><td>(K)SIEIPRP\</td><td>(K)S I|E/I|P R P V D G V E/V/P G C G K(I)</td><td>C:Carbamidomethylation</td><td>148.28</td><td>636.9917</td><td>1908.985</td><td>-0.0242</td><td>-12.7</td><td>4.68</td><td>34243.5</td><td>4.88</td><td>HUMAN</td><td>K7ENG2</td><td>Splicing factor U2AF 65 kDa subunit</td></tr>
<tr><td>8439</td><td>dirMS_041712_NAR_60mM_minus.15515.15515.3</td><td>3</td><td>10.97</td><td>1</td><td>5.92E+05</td><td>M81m</td><td>(K)EVNKFQ</td><td>(K)E V/N K F Q m/A/Y/S/N/L L R(A)</td><td>m:Oxidized methionine</td><td>146.73</td><td>576.9619</td><td>1712.879</td><td>15.9923</td><td>-1.5</td><td>8.69</td><td>14683.8</td><td>10.19</td><td>HUMAN</td><td>P37108</td><td>Signal recognition particle 14 kDa protein</td></tr>
<tr><td>8440</td><td>dirMS_041712_NAR_60mM_minus.18780.18796.3</td><td>3</td><td>10.97</td><td>0</td><td>2.66E+05</td><td></td><td>(K)LHDNLII:</td><td>(K)L H\D N\L\I|I/S/D/L\E\N T V K(K)</td><td></td><td>166.12</td><td>575.3117</td><td>1723.922</td><td>-0.0019</td><td>-1.1</td><td>4.54</td><td>88624.6</td><td>5.09</td><td>HUMAN</td><td>C9J8U1</td><td>Cytospin-A (Fragment)</td></tr>
<tr><td>8441</td><td>dirMS_041712_NAR_60mM_minus.4979.4985.3</td><td>3</td><td>10.97</td><td>1</td><td>8.21E+04</td><td></td><td>(K)VSSAEG/</td><td>(K)V/S|S/A E/G A A K E/E/P K(R)</td><td></td><td>82.42</td><td>434.8904</td><td>1302.654</td><td>0.0031</td><td>2.3</td><td>4.79</td><td>4801.6</td><td>11.17</td><td>HUMAN</td><td>F2Z2W6</td><td>Non-histone chromosomal protein HMG-14</td></tr>
<tr><td>8442</td><td>dirMS_041712_NAR_20mM_plus.11077.11078.2</td><td>2</td><td>10.97</td><td>0</td><td>1.28E+05</td><td></td><td>(K)TIVFVET</td><td>(K)T I|V/F V E/T K(R)</td><td></td><td>148.33</td><td>468.7674</td><td>936.54</td><td>-0.0125</td><td>-13.4</td><td>5.66</td><td>61018.6</td><td>9.44</td><td>HUMAN</td><td>B4DLW8</td><td>Probable ATP-dependent RNA helicase DDX5</td></tr>
<tr><td>8443</td><td>dirMS_041712_NAR_20mM_plus.7747.7747.2</td><td>2</td><td>10.97</td><td>0</td><td>1.91E+05</td><td></td><td>(R)ALANSL/</td><td>(R)A L|A/N|S/L A/C Q G K(Y)</td><td>C:Carbamidomethylation</td><td>123.77</td><td>566.7967</td><td>1132.578</td><td>0.0082</td><td>7.2</td><td>8.8</td><td>13951.6</td><td>9.48</td><td>HUMAN</td><td>H3BR68</td><td>Fructose-bisphosphate aldolase A (Fragment)</td></tr>
<tr><td>8444</td><td>dirMS_041712_NAR_20mM_plus.8264.8264.2</td><td>2</td><td>10.97</td><td>0</td><td>5.19E+04</td><td></td><td>(R)AVVIVDI</td><td>(R)A V/V|I V/D/D/R(G)</td><td></td><td>127.05</td><td>443.7527</td><td>886.499</td><td>-0.0011</td><td>-1.3</td><td>4.21</td><td>23729.5</td><td>9.89</td><td>HUMAN</td><td>C9IZL7</td><td>Non-POU domain-containing octamer-binding protein (Fragment)</td></tr>
<tr><td>8445</td><td>dirMS_041712_NAR_20mM_plus.9340.9340.2</td><td>2</td><td>10.97</td><td>0</td><td>6.69E+04</td><td></td><td>(K)TGQEIP\</td><td>(K)T G Q/E/I|P V N V R(F)</td><td></td><td>135.92</td><td>556.8027</td><td>1112.606</td><td>-0.0077</td><td>-6.9</td><td>5.66</td><td>28051.5</td><td>4.98</td><td>HUMAN</td><td>J3QKT2</td><td>Cytosolic non-specific dipeptidase (Fragment)</td></tr>
<tr><td>8446</td><td>dirMS_041712_NAR_30mM_plus2.12264.12264.3</td><td>3</td><td>10.97</td><td>0</td><td>1.23E+06</td><td></td><td>(K)EVDEQN</td><td>(K)E V D E Q M|L/N/V Q/N K(N)</td><td></td><td>116.97</td><td>482.9009</td><td>1446.689</td><td>-0.0012</td><td>-0.8</td><td>4.14</td><td>40069.4</td><td>4.83</td><td>HUMAN</td><td>E7EWR1</td><td>Tubulin beta chain</td></tr>
<tr><td>8447</td><td>dirMS_041712_NAR_30mM_plus2.13886.14008.2</td><td>2</td><td>10.97</td><td>0</td><td>3.55E+05</td><td>M81m</td><td>(K)mIFVGIK</td><td>(K)m/I|F/V/G I/K(K)</td><td>m:Oxidized methionine</td><td>125.95</td><td>412.2409</td><td>807.48</td><td>15.9948</td><td>-0.1</td><td>8.5</td><td>11447.2</td><td>9.81</td><td>HUMAN</td><td>C9JFR7</td><td>Cytochrome c (Fragment)</td></tr>
<tr><td>8448</td><td>dirMS_041712_NAR_40mM_plus2.16313.16313.3</td><td>3</td><td>10.97</td><td>0</td><td>4.11E+04</td><td></td><td>(K)VLISSLQ</td><td>(K)V L|I/S S/L/Q D C L H G I E/S K(S)</td><td>C:Carbamidomethylation</td><td>161.47</td><td>600.3172</td><td>1798.937</td><td>0.0003</td><td>0.2</td><td>5.32</td><td>52440.1</td><td>6</td><td>HUMAN</td><td>F8WJN3</td><td>Cleavage and polyadenylation-specificity factor subunit 6</td></tr>
<tr><td>8449</td><td>dirMS_041712_NAR_40mM_plus2.8527.8527.2</td><td>2</td><td>10.97</td><td>0</td><td>8.22E+04</td><td></td><td>(K)DVNQQI</td><td>(K)D V|N|Q/Q E F V/R(A)</td><td></td><td>110.82</td><td>567.78</td><td>1134.554</td><td>-0.0011</td><td>-1</td><td>4.37</td><td>16060.2</td><td>10.31</td><td>HUMAN</td><td>P39019</td><td>40S ribosomal protein S19</td></tr>
<tr><td>8450</td><td>dirMS_041712_NAR_50mM_plus2.19594.19594.3</td><td>3</td><td>10.97</td><td>1</td><td>9.25E+04</td><td></td><td>(K)TFVNITP</td><td>(K)T F|V|N/I/T/P A E V G V L V G K D R(S)</td><td></td><td>171.23</td><td>639.0247</td><td>1915.065</td><td>-0.0052</td><td>-2.7</td><td>5.74</td><td>17630.6</td><td>11.62</td><td>HUMAN</td><td>I3L3D5</td><td>Profilin-1 (Fragment)</td></tr>
<tr><td>8451</td><td>dirMS_041712_NAR_50mM_plus2.20006.20006.3</td><td>3</td><td>10.97</td><td>1</td><td>5.31E+05</td><td></td><td>(-)MDELQL</td><td>(-)M/D|E\L Q L/F R G D/T V L L K(G)</td><td></td><td>173.25</td><td>593.3209</td><td>1777.952</td><td>-0.0035</td><td>-2</td><td>4.56</td><td>18601</td><td>5.1</td><td>HUMAN</td><td>C9IZA5</td><td>Transitional endoplasmic reticulum ATPase (Fragment)</td></tr>
<tr><td>8452</td><td>dirMS_041712_NAR_50mM_plus2.6027.6027.3</td><td>3</td><td>10.97</td><td>0</td><td>8.84E+04</td><td></td><td>(R)ITPPAAK</td><td>(R)I T/P/P A A K P G S P Q/A K(S)</td><td></td><td>95.85</td><td>454.9298</td><td>1362.774</td><td>0.0009</td><td>0.6</td><td>10</td><td>214357.5</td><td>7.19</td><td>HUMAN</td><td>P35658</td><td>Nuclear pore complex protein Nup214</td></tr>
<tr><td>8453</td><td>dirMS_041712_NAR_60mM_plus.12914.12914.3</td><td>3</td><td>10.97</td><td>1</td><td>8.37E+05</td><td></td><td>(R)EFEVYGI</td><td>(R)E F E/V/Y/G/P I K R(I)</td><td></td><td>124.55</td><td>413.2246</td><td>1237.658</td><td>0.0017</td><td>1.4</td><td>6.24</td><td>51612.9</td><td>9.98</td><td>HUMAN</td><td>P08621</td><td>U1 small nuclear ribonucleoprotein 70 kDa</td></tr>
<tr><td>8454</td><td>dirMS_041712_NAR_60mM_plus.17895.17895.3</td><td>3</td><td>10.97</td><td>1</td><td>1.90E+05</td><td></td><td>(K)LKEVFSN</td><td>(K)L K E V F S\M/A/G V/V V R(A)</td><td></td><td>150.6</td><td>478.9419</td><td>1434.814</td><td>-0.0026</td><td>-1.8</td><td>8.75</td><td>77799.7</td><td>9.09</td><td>HUMAN</td><td>P52272</td><td>Heterogeneous nuclear ribonucleoprotein M</td></tr>
<tr><td>8455</td><td>dirMS_041712_NAR_60mM_plus.7443.7443.3</td><td>3</td><td>10.97</td><td>1</td><td>5.05E+05</td><td></td><td>(K)SSGGREI</td><td>(K)S/S/G G R E D\L|E|S/S G L Q\R(R)</td><td></td><td>97.3</td><td>526.5897</td><td>1577.751</td><td>0.0031</td><td>2</td><td>4.68</td><td>11625.5</td><td>8.01</td><td>HUMAN</td><td>B8ZZT7</td><td>Hematological and neurological-expressed 1 protein</td></tr>
<tr><td>8456</td><td>dirMS_041712_NAR_120mM_minus.11029.11264.4</td><td>4</td><td>10.96</td><td>0</td><td>1.61E+06</td><td></td><td>(K)SAKPTKI</td><td>(K)S A\K P T K\P A A/S D\L\P\V|P A/E G V R(N)</td><td></td><td>114.97</td><td>498.5274</td><td>1991.092</td><td>-0.0042</td><td>-2.1</td><td>8.31</td><td>54214.9</td><td>5.66</td><td>HUMAN</td><td>C9J813</td><td>Caldesmon (Fragment)</td></tr>
<tr><td>8457</td><td>dirMS_041712_NAR_120mM_minus.14856.14856.4</td><td>4</td><td>10.96</td><td>1</td><td>4.81E+05</td><td></td><td>(K)KKELEEI'</td><td>(K)K K E L E E I\V\Q\P I/I S/K(L)</td><td></td><td>135.12</td><td>414.2486</td><td>1653.978</td><td>-0.006</td><td>-3.6</td><td>6.23</td><td>72445.7</td><td>5.07</td><td>HUMAN</td><td>P11021</td><td>78 kDa glucose-regulated protein</td></tr>
<tr><td>8458</td><td>dirMS_041712_NAR_120mM_minus.19910.20005.3</td><td>3</td><td>10.96</td><td>1</td><td>2.47E+05</td><td></td><td>(R)AKFEELN</td><td>(R)A K\F E E\L|N|M/D/L/F R(S)</td><td></td><td>164.85</td><td>504.9216</td><td>1512.752</td><td>-0.0013</td><td>-0.8</td><td>4.68</td><td>72445.7</td><td>5.07</td><td>HUMAN</td><td>P11021</td><td>78 kDa glucose-regulated protein</td></tr>
<tr><td>8459</td><td>dirMS_041712_NAR_20mM_minus.12268.12353.2</td><td>2</td><td>10.96</td><td>0</td><td>5.36E+05</td><td>M73m</td><td>(R)AVLVDLI</td><td>(R)A V/L|V D/L|E|P G/T m D S V R(S)</td><td>m:Oxidized methionine</td><td>172.4</td><td>809.4088</td><td>1601.82</td><td>15.99</td><td>-3</td><td>4.03</td><td>13112.4</td><td>5.23</td><td>HUMAN</td><td>F8W813</td><td>Tubulin beta-8 chain</td></tr>
<tr><td>8460</td><td>dirMS_041712_NAR_50mM_minus2.12499.12499.3</td><td>3</td><td>10.96</td><td>0</td><td>1.00E+06</td><td>M114m M:</td><td>(R)AGKPVI(</td><td>(R)A G K\P V I/C\A T|Q m|L E/S m I K(K)</td><td>C:Carbamidomethylation m:Oxid</td><td>139.77</td><td>636.9917</td><td>1876.969</td><td>31.9912</td><td>0.7</td><td>8.64</td><td>18466.1</td><td>5.78</td><td>HUMAN</td><td>H3BSU3</td><td>Pyruvate kinase (Fragment)</td></tr>
<tr><td>8461</td><td>dirMS_041712_NAR_50mM_minus2.14164.14164.3</td><td>3</td><td>10.96</td><td>1</td><td>1.56E+05</td><td></td><td>(K)KGVNLP</td><td>(K)K G V N L P G\A\A\V/D|L/P A V S E K(D)</td><td></td><td>148.73</td><td>588.9987</td><td>1764.985</td><td>-0.0039</td><td>-2.2</td><td>6.07</td><td>30947.9</td><td>6.47</td><td>HUMAN</td><td>H3BQ34</td><td>Pyruvate kinase</td></tr>
<tr><td>8462</td><td>dirMS_041712_NAR_60mM_minus.9345.9345.3</td><td>3</td><td>10.96</td><td>0</td><td>1.02E+06</td><td></td><td>(K)QEYDES(</td><td>(K)Q E/Y/D E S/G/P/S I/V H R(K)</td><td></td><td>111.27</td><td>506.2391</td><td>1516.703</td><td>0.0001</td><td>0.1</td><td>4.65</td><td>123097.1</td><td>5.83</td><td>HUMAN</td><td>A5A3E0</td><td>POTE ankyrin domain family member F</td></tr>
<tr><td>8463</td><td>dirMS_041712_NAR_120mM_plus.5548.5548.3</td><td>3</td><td>10.96</td><td>1</td><td>3.76E+05</td><td></td><td>(K)TCEESSF</td><td>(K)T|C|E E S S F/C K/R(Q)</td><td>C:Carbamidomethylation</td><td>82.18</td><td>435.1877</td><td>1303.541</td><td>0.008</td><td>6.1</td><td>5.81</td><td>10576.1</td><td>11.44</td><td>HUMAN</td><td>E9PRF8</td><td>Neutral alpha-glucosidase AB</td></tr>
<tr><td>8464</td><td>dirMS_041712_NAR_20mM_plus.15798.15798.3</td><td>3</td><td>10.96</td><td>0</td><td>1.71E+05</td><td></td><td>(R)GVVDSE</td><td>(R)G V\V D S E D\I/P L N L S R(E)</td><td></td><td>179.57</td><td>505.2667</td><td>1513.786</td><td>-0.0001</td><td>-0.1</td><td>4.03</td><td>74494.3</td><td>7.79</td><td>HUMAN</td><td>F5H897</td><td>Heat shock protein 75 kDa, mitochondrial</td></tr>
<tr><td>8465</td><td>dirMS_041712_NAR_20mM_plus.19186.19186.2</td><td>2</td><td>10.96</td><td>0</td><td>1.75E+05</td><td></td><td>(R)VCTLAII(</td><td>(R)V C\T L A/I/I|D\P G D S D I I/R(S)</td><td>C:Carbamidomethylation</td><td>202.9</td><td>879.4578</td><td>1757.91</td><td>-0.0019</td><td>-1.1</td><td>3.93</td><td>12826.8</td><td>9.82</td><td>HUMAN</td><td>E5RI99</td><td>60S ribosomal protein L30 (Fragment)</td></tr>
<tr><td>8466</td><td>dirMS_041712_NAR_30mM_plus2.10533.10533.2</td><td>2</td><td>10.96</td><td>0</td><td>2.12E+05</td><td></td><td>(R)TEEGPTI</td><td>(R)T E|E/G/P T L S Y G\R(D)</td><td></td><td>108.83</td><td>605.2924</td><td>1209.575</td><td>0.0029</td><td>2.4</td><td>4.53</td><td>100478.9</td><td>5.71</td><td>HUMAN</td><td>A8MXP9</td><td>Matrin-3</td></tr>
<tr><td>8467</td><td>dirMS_041712_NAR_50mM_plus2.17321.17321.3</td><td>3</td><td>10.96</td><td>0</td><td>1.24E+05</td><td></td><td>(R)FGVPVI/</td><td>(R)F G\V/P/V/I A D G G I Q N V/G H I A K(A)</td><td></td><td>159.7</td><td>631.3464</td><td>1892.039</td><td>-0.0142</td><td>-7.5</td><td>6.74</td><td>51583.4</td><td>8.8</td><td>HUMAN</td><td>H0Y4R1</td><td>Inosine-5'-monophosphate dehydrogenase 2 (Fragment)</td></tr>
<tr><td>8468</td><td>dirMS_041712_NAR_60mM_plus.12725.12725.3</td><td>3</td><td>10.96</td><td>1</td><td>1.28E+06</td><td></td><td>(K)DLFPYEE</td><td>(K)D/L\F/P/Y/E E S K E K(F)</td><td></td><td>123.67</td><td>462.2281</td><td>1384.663</td><td>0.0067</td><td>4.8</td><td>4.41</td><td>23020.5</td><td>4.53</td><td>HUMAN</td><td>A8K8G0</td><td>Hepatoma-derived growth factor</td></tr>
<tr><td>8469</td><td>dirMS_041712_NAR_60mM_plus.17896.17896.3</td><td>3</td><td>10.96</td><td>0</td><td>2.66E+05</td><td></td><td>(R)LLIHQSL</td><td>(R)L L I/H Q\S\L|A/G G I/I/G V K(G)</td><td></td><td>150.48</td><td>506.9815</td><td>1518.937</td><td>-0.0067</td><td>-4.4</td><td>8.76</td><td>51260.6</td><td>5.39</td><td>HUMAN</td><td>P61978</td><td>Heterogeneous nuclear ribonucleoprotein K</td></tr>
<tr><td>8470</td><td>dirMS_041712_NAR_60mM_plus.7810.7831.3</td><td>3</td><td>10.96</td><td>0</td><td>1.06E+06</td><td></td><td>(R)SAHATA</td><td>(R)S A H\A|T A\P\V/N|I|A G S R(T)</td><td></td><td>99.03</td><td>451.2397</td><td>1351.708</td><td>-0.0031</td><td>-2.3</td><td>9.49</td><td>300351.7</td><td>12.1</td><td>HUMAN</td><td>Q9UQ35</td><td>Serine/arginine repetitive matrix protein 2</td></tr>
<tr><td>8471</td><td>dirMS_041712_NAR_120mM_minus.15043.15043.3</td><td>3</td><td>10.95</td><td>1</td><td>1.12E+06</td><td></td><td>(K)VKEGMI</td><td>(K)V K E G M N\I|V/E/A/M/E R(F)</td><td></td><td>136.7</td><td>502.5853</td><td>1505.745</td><td>-0.0037</td><td>-2.5</td><td>4.79</td><td>18240.4</td><td>7.96</td><td>HUMAN</td><td>P62937</td><td>Peptidyl-prolyl cis-trans isomerase A</td></tr>
<tr><td>8472</td><td>dirMS_041712_NAR_40mM_minus2.14538.14538.3</td><td>3</td><td>10.95</td><td>1</td><td>1.45E+05</td><td></td><td>(K)GTVPDD</td><td>(K)G T/V/P D D A V E A/L/A D S L G K K(E)</td><td></td><td>170.3</td><td>595.9791</td><td>1785.923</td><td>-0.0001</td><td>-0.1</td><td>4.23</td><td>81397.3</td><td>4.99</td><td>HUMAN</td><td>B7Z468</td><td>Calpastatin</td></tr>
<tr><td>8473</td><td>dirMS_041712_NAR_40mM_minus2.9867.9867.2</td><td>2</td><td>10.95</td><td>0</td><td>2.03E+06</td><td></td><td>(R)VAPEEH</td><td>(R)V A/P E\E/H|P V L L T E A|P L\N/P/K(A)</td><td></td><td>140.5</td><td>977.5343</td><td>1954.064</td><td>-0.0031</td><td>-1.6</td><td>4.75</td><td>18032.2</td><td>5.25</td><td>HUMAN</td><td>E7EVS6</td><td>Actin, cytoplasmic 1 (Fragment)</td></tr>
<tr><td>8474</td><td>dirMS_041712_NAR_50mM_minus2.13321.13467.3</td><td>3</td><td>10.95</td><td>0</td><td>5.21E+05</td><td></td><td>(K)SLTNDW</td><td>(K)S L|T/N/D/W/E D H L A V/K(H)</td><td></td><td>144.18</td><td>509.9192</td><td>1527.744</td><td>-0.0008</td><td>-0.5</td><td>4.53</td><td>85057.6</td><td>4.94</td><td>HUMAN</td><td>P07900</td><td>Heat shock protein HSP 90-alpha</td></tr>
<tr><td>8475</td><td>dirMS_041712_NAR_50mM_minus2.13656.13656.3</td><td>3</td><td>10.95</td><td>0</td><td>4.59E+04</td><td></td><td>(K)MLDAEE</td><td>(K)M/L/D/A E D I V/N T A R P D/E K(A)</td><td></td><td>144.98</td><td>606.2965</td><td>1816.875</td><td>0.0004</td><td>0.2</td><td>4.1</td><td>105308.6</td><td>5.27</td><td>HUMAN</td><td>O43707</td><td>Alpha-actinin-4</td></tr>
<tr><td>8476</td><td>dirMS_041712_NAR_50mM_minus2.16205.16205.3</td><td>3</td><td>10.95</td><td>0</td><td>1.46E+05</td><td></td><td>(K)LDPHLVI</td><td>(K)L D|P/H L|V|L D Q L R(C)</td><td></td><td>160.2</td><td>440.2533</td><td>1318.748</td><td>-0.0024</td><td>-1.8</td><td>5.21</td><td>233493.8</td><td>5.45</td><td>HUMAN</td><td>F8VTL3</td><td>Myosin-10</td></tr>
<tr><td>8477</td><td>dirMS_041712_NAR_60mM_minus.9127.9127.2</td><td>2</td><td>10.95</td><td>0</td><td>9.67E+05</td><td></td><td>(K)QEYDES(</td><td>(K)Q E|Y/D E/S/G P S I/V H/R(K)</td><td></td><td>110.35</td><td>758.8539</td><td>1516.703</td><td>-0.0021</td><td>-1.4</td><td>4.65</td><td>123097.1</td><td>5.83</td><td>HUMAN</td><td>A5A3E0</td><td>POTE ankyrin domain family member F</td></tr>
<tr><td>8478</td><td>dirMS_041712_NAR_120mM_plus.18592.18592.4</td><td>4</td><td>10.95</td><td>1</td><td>4.75E+05</td><td></td><td>(R)SKDVVE</td><td>(R)S K/D V V/E/P L/L/R/P Q W Y V R(C)</td><td></td><td>150.35</td><td>497.0291</td><td>1985.097</td><td>-0.0021</td><td>-1.1</td><td>8.31</td><td>141718.6</td><td>7.8</td><td>HUMAN</td><td>B0V043</td><td>Valine--tRNA ligase</td></tr>
<tr><td>8479</td><td>dirMS_041712_NAR_20mM_plus.6938.6938.2</td><td>2</td><td>10.95</td><td>0</td><td>9.56E+04</td><td></td><td>(K)AAAAAA</td><td>(K)A A|A\A|A/A|A L Q A K(S)</td><td></td><td>114.28</td><td>478.7792</td><td>956.552</td><td>-0.0012</td><td>-1.3</td><td>8.8</td><td>37884.5</td><td>11.27</td><td>HUMAN</td><td>H3BM89</td><td>60S ribosomal protein L4</td></tr>
<tr><td>8480</td><td>dirMS_041712_NAR_20mM_plus.9951.9951.2</td><td>2</td><td>10.95</td><td>0</td><td>2.47E+05</td><td></td><td>(K)VASGCLI</td><td>(K)V A|S|G\C/L/D I N S S V K(G)</td><td>C:Carbamidomethylation</td><td>139.8</td><td>675.3376</td><td>1349.673</td><td>-0.005</td><td>-3.7</td><td>5.81</td><td>56837</td><td>7.19</td><td>HUMAN</td><td>E7ETT1</td><td>Propionyl-CoA carboxylase beta chain, mitochondrial</td></tr>
<tr><td>8481</td><td>dirMS_041712_NAR_30mM_plus2.10898.11065.2</td><td>2</td><td>10.95</td><td>0</td><td>1.36E+06</td><td></td><td>(R)GGNFGI</td><td>(R)G G\N|F|G/F/G D/S/R(G)</td><td></td><td>110.93</td><td>507.2274</td><td>1013.444</td><td>0.004</td><td>3.9</td><td>5.84</td><td>37486.1</td><td>9.03</td><td>HUMAN</td><td>P22626</td><td>Heterogeneous nuclear ribonucleoproteins A2/B1</td></tr>
<tr><td>8482</td><td>dirMS_041712_NAR_30mM_plus2.16349.16349.2</td><td>2</td><td>10.95</td><td>0</td><td>6.18E+05</td><td></td><td>(R)GALQNI</td><td>(R)G A/L\Q/N/I|I\P A S T G A A K(A)</td><td></td><td>137.7</td><td>706.3979</td><td>1411.79</td><td>-0.0018</td><td>-1.3</td><td>8.75</td><td>31718.5</td><td>7.17</td><td>HUMAN</td><td>E7EUT4</td><td>Glyceraldehyde-3-phosphate dehydrogenase</td></tr>
<tr><td>8483</td><td>dirMS_041712_NAR_30mM_plus2.19700.19700.2</td><td>2</td><td>10.95</td><td>0</td><td>2.35E+05</td><td></td><td>(K)APDFVF'</td><td>(K)A/P/D\F/V/F Y A P R(L)</td><td></td><td>156.72</td><td>591.8008</td><td>1182.594</td><td>0.0001</td><td>0.1</td><td>5.88</td><td>71218.8</td><td>6.3</td><td>HUMAN</td><td>A7YIJ8</td><td>Radixin</td></tr>
<tr><td>8484</td><td>dirMS_041712_NAR_30mM_plus2.21536.21536.2</td><td>2</td><td>10.95</td><td>0</td><td>2.79E+05</td><td></td><td>(R)EADDIVI</td><td>(R)E A|D D I/V/N/W L/K(K)</td><td></td><td>167.58</td><td>601.81</td><td>1202.605</td><td>0.0075</td><td>6.3</td><td>4.03</td><td>26363.4</td><td>4.91</td><td>HUMAN</td><td>I3L312</td><td>Protein disulfide-isomerase (Fragment)</td></tr>
<tr><td>8485</td><td>dirMS_041712_NAR_40mM_plus2.14456.14456.3</td><td>3</td><td>10.95</td><td>1</td><td>1.51E+05</td><td></td><td>(K)IMASSPI</td><td>(K)I/M|A/S/S/P\D/M D L A T V S A L R K(M)</td><td></td><td>151.42</td><td>635.9975</td><td>1905.977</td><td>0.0007</td><td>0.4</td><td>5.96</td><td>36208.1</td><td>7.21</td><td>HUMAN</td><td>B4DMU0</td><td>Pyrroline-5-carboxylate reductase</td></tr>
<tr><td>8486</td><td>dirMS_041712_NAR_50mM_plus2.10744.10744.3</td><td>3</td><td>10.95</td><td>1</td><td>5.66E+05</td><td></td><td>(R)ELLTLDE</td><td>(R)E L L T/L D E/K D/P/R(R)</td><td></td><td>123.8</td><td>443.5761</td><td>1328.706</td><td>0.0081</td><td>6.1</td><td>4.32</td><td>9591.1</td><td>10.94</td><td>HUMAN</td><td>A8MXK4</td><td>40S ribosomal protein S9</td></tr>
<tr><td>8487</td><td>dirMS_041712_NAR_60mM_plus.16192.16192.3</td><td>3</td><td>10.95</td><td>1</td><td>6.05E+05</td><td></td><td>(R)IKIGDPL</td><td>(R)I K I G D\P L|L/E/D/T/R(M)</td><td></td><td>141.57</td><td>457.2595</td><td>1369.769</td><td>-0.0046</td><td>-3.4</td><td>4.56</td><td>47309.6</td><td>5.42</td><td>HUMAN</td><td>B4DXY7</td><td>4-trimethylaminobutyraldehyde dehydrogenase</td></tr>
<tr><td>8488</td><td>dirMS_041712_NAR_60mM_plus.16594.16594.3</td><td>3</td><td>10.95</td><td>1</td><td>5.78E+05</td><td></td><td>(K)AAVEWI</td><td>(K)A A/V/E/W F D G K/D F Q G S K(L)</td><td></td><td>143.15</td><td>562.2762</td><td>1684.797</td><td>0.0175</td><td>10.4</td><td>4.56</td><td>65213.5</td><td>9.57</td><td>HUMAN</td><td>B0QYK0</td><td>Ewing sarcoma breakpoint region 1</td></tr>
<tr><td>8489</td><td>dirMS_041712_NAR_60mM_plus.17195.17195.3</td><td>3</td><td>10.95</td><td>1</td><td>4.64E+05</td><td></td><td>(R)GPIKFN\</td><td>(R)G P\I K F\N\V|W/D|T|A G\Q E K(F)</td><td></td><td>146.65</td><td>563.9572</td><td>1689.86</td><td>-0.0024</td><td>-1.4</td><td>6.07</td><td>26394.9</td><td>6.5</td><td>HUMAN</td><td>B5MDF5</td><td>GTP-binding nuclear protein Ran</td></tr>
<tr><td>8490</td><td>dirMS_041712_NAR_60mM_plus.8220.8220.2</td><td>2</td><td>10.95</td><td>1</td><td>4.67E+05</td><td>M174m</td><td>(R)VKYETEI</td><td>(R)V/K|Y|E/T/E L A m R(Q)</td><td>m:Oxidized methionine</td><td>101.53</td><td>628.3208</td><td>1239.64</td><td>15.9941</td><td>-0.6</td><td>6.11</td><td>43773.3</td><td>5.26</td><td>HUMAN</td><td>F8VZY9</td><td>Keratin, type I cytoskeletal 18</td></tr>
<tr><td>8491</td><td>dirMS_041712_NAR_120mM_minus.11724.11786.3</td><td>3</td><td>10.94</td><td>0</td><td>6.21E+05</td><td></td><td>(R)STYYWP</td><td>(R)S/T|Y/Y/W/P R P/R(R)</td><td></td><td>118.07</td><td>409.2126</td><td>1225.611</td><td>0.012</td><td>9.8</td><td>9.98</td><td>13152.8</td><td>4.23</td><td>HUMAN</td><td>A1L429</td><td>G antigen 12B/C/D/E</td></tr>
<tr><td>8492</td><td>dirMS_041712_NAR_30mM_minus2.16092.16092.2</td><td>2</td><td>10.94</td><td>0</td><td>1.41E+05</td><td></td><td>(K)GCSFLPI</td><td>(K)G C\S|F/L/P D/P Y\Q/K(Q)</td><td>C:Carbamidomethylation</td><td>141.02</td><td>656.3051</td><td>1311.604</td><td>-0.0009</td><td>-0.7</td><td>5.83</td><td>63688.6</td><td>5.11</td><td>HUMAN</td><td>B1AVU8</td><td>Prosaposin</td></tr>
<tr><td>8493</td><td>dirMS_041712_NAR_50mM_minus2.15283.15283.3</td><td>3</td><td>10.94</td><td>1</td><td>3.99E+05</td><td></td><td>(R)VCENIPI'</td><td>(R)V/C|E N I/P\I V\L C G\N K V D\I K(D)</td><td>C:Carbamidomethylation</td><td>155.53</td><td>657.6803</td><td>1971.04</td><td>-0.0138</td><td>-7</td><td>6.04</td><td>14844.8</td><td>5.89</td><td>HUMAN</td><td>B4DV51</td><td>GTP-binding nuclear protein Ran</td></tr>
<tr><td>8494</td><td>dirMS_041712_NAR_50mM_minus2.18209.18209.3</td><td>3</td><td>10.94</td><td>0</td><td>2.31E+05</td><td></td><td>(K)ILFIFIDSI</td><td>(K)I L|F/I/F I D/S D H T D N Q R(I)</td><td></td><td>172.78</td><td>611.9745</td><td>1833.913</td><td>-0.004</td><td>-2.2</td><td>4.41</td><td>51524.1</td><td>4.82</td><td>HUMAN</td><td>F5H8J2</td><td>Protein disulfide-isomerase</td></tr>
<tr><td>8495</td><td>dirMS_041712_NAR_60mM_minus.11852.12025.3</td><td>3</td><td>10.94</td><td>0</td><td>1.71E+06</td><td></td><td>(K)SQIHDIV</td><td>(K)S Q I H D\I\V|L|V/G/G S T R(I)</td><td></td><td>126.72</td><td>494.6084</td><td>1481.807</td><td>0.0036</td><td>2.4</td><td>6.46</td><td>45508.6</td><td>5.5</td><td>HUMAN</td><td>A8K7Q2</td><td>Heat shock cognate 71 kDa protein</td></tr>
<tr><td>8496</td><td>dirMS_041712_NAR_60mM_minus.18897.18897.3</td><td>3</td><td>10.94</td><td>0</td><td>1.29E+06</td><td></td><td>(R)IHFPLAT</td><td>(R)I H F P L A|T\Y|A|P V/I S A E K(A)</td><td></td><td>166.27</td><td>586.3248</td><td>1756.963</td><td>-0.0034</td><td>-1.9</td><td>6.75</td><td>49012.3</td><td>4.9</td><td>HUMAN</td><td>A8MUB1</td><td>Tubulin alpha-4A chain</td></tr>
<tr><td>8497</td><td>dirMS_041712_NAR_60mM_minus.6413.6413.3</td><td>3</td><td>10.94</td><td>1</td><td>6.33E+04</td><td></td><td>(R)GTDDSP</td><td>(R)G T|D/D/S/P K D S Q/E/D/L Q E R(H)</td><td></td><td>94.48</td><td>607.2707</td><td>1819.794</td><td>0.0035</td><td>1.9</td><td>3.96</td><td>23420.8</td><td>4.74</td><td>HUMAN</td><td>Q5H9L2</td><td>Transcription elongation factor A protein-like 5</td></tr>
</table>

8498	dirMS_041712_NAR_20mM_plus.11130.11130.2	2	10.94	0	1.49E+05		(K)YGVSGY	(K)Y/G|V/S/G Y P/T L/K(I)		149.72	542.7869	1084.567	-0.0008	-0.8	8.5	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
8499	dirMS_041712_NAR_20mM_plus.14422.14422.2	2	10.94	0	1.29E+05		(R)FIDTTLA	(R)F I|D/T/T|L/A I T S R(F)		171.38	619.3413	1237.679	-0.0034	-2.7	5.84	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
8500	dirMS_041712_NAR_20mM_plus.18795.18795.2	2	10.94	0	1.04E+05		(K)LTVYTTL	(K)L T/V Y/T/T L/I/D V T/K(G)		200.83	683.8948	1366.783	-0.0005	-0.4	5.83	42194.9	8.75	HUMAN	E7EMM4	Acid ceramidase
8501	dirMS_041712_NAR_30mM_plus2.10295.10295.2	2	10.94	0	2.97E+05		(R)LNQDQL	(R)L N\Q/D/Q/L D/A V S/K(Y)		107.28	615.819	1230.632	-0.0017	-1.4	4.21	20235.4	6.77	HUMAN	E9PLA9	Caprin-1 (Fragment)
8502	dirMS_041712_NAR_30mM_plus2.17733.17983.2	2	10.94	0	1.02E+06		(R)SMVEDI	(R)S M|V|E/D I T/G L/R(L)		146.43	560.7925	1120.567	0.011	9.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
8503	dirMS_041712_NAR_30mM_plus2.21868.21868.2	2	10.94	0	2.25E+05		(R)TTNFAG	(R)T T/N\F/A|G I L/S Q G L/R(I)		169.58	689.3749	1377.748	-0.006	-4.3	9.41	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
8504	dirMS_041712_NAR_30mM_plus2.5516.5535.2	2	10.94	0	5.53E+04		(K)YIDENQ	(K)Y/I|D/E/N Q\D/R(Y)		83.07	526.7354	1052.464	-0.0008	-0.8	4.03	6412.4	9.52	HUMAN	J3KSS4	Cytosolic non-specific dipeptidase (Fragment)
8505	dirMS_041712_NAR_50mM_plus2.19246.19246.3	3	10.94	1	1.15E+05		(K)GLKVNL	(K)G L K V N L\F|P|G L S/P S A L/K(A)		169.47	547.6608	1640.973	-0.0056	-3.4	10	182819.3	4.77	HUMAN	Q9C0C2	182 kDa tankyrase-1-binding protein
8506	dirMS_041712_NAR_50mM_plus2.9449.9492.3	3	10.94	0	7.71E+05		(R)DNIQGI	(R)D N|I|Q G I/T/K/P A I R(R)		117.22	442.5902	1325.754	0.0025	1.9	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
8507	dirMS_041712_NAR_60mM_plus.8737.8737.3	3	10.94	0	6.39E+05		(K)GQVCV	(K)G Q/V/C V/M/I/H S G S R(G)	C:Carbamidomethylation	103.08	444.2219	1330.636	0.0157	11.8	9.75	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
8508	dirMS_041712_NAR_60mM_plus.9613.9613.2	2	10.94	0	2.23E+05		(R)FATHAA	(R)F/A/T/H/A A\A L/S V R(N)		108.87	572.3143	1143.627	-0.0056	-4.9	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
8509	dirMS_041712_NAR_120mM_minus.20525.20536.3	3	10.93	1	3.46E+05		(R)LDLAGR	(R)L D|L/A/G R\D L T/D/Y L M/K(I)		169.02	541.9508	1623.841	-0.0032	-2	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
8510	dirMS_041712_NAR_20mM_minus.6901.6901.2	2	10.93	0	1.34E+05	M453m	(K)ImATPE	(K)I/m|A/T|P E Q V/G K(M)	m:Oxidized methionine	115.42	545.2807	1073.566	15.9882	-6.2	6	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
8511	dirMS_041712_NAR_30mM_minus2.13221.13221.2	2	10.93	0	2.97E+05		(R)GATQQI	(R)G A/T\Q/Q/I/L/D\E A E/R(S)		125.18	665.833	1330.66	-0.001	-0.8	4.14	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
8512	dirMS_041712_NAR_40mM_minus2.8151.8151.3	3	10.93	0	1.18E+04	M33m	(R)VLTEDE	(R)V/L/T/E D E m/G H P E/I G D A I A R(L)	m:Oxidized methionine	127.97	656.9824	1952.938	15.9944	-0.2	4.17	40874	5.06	HUMAN	E9PCI9	Farnesyl pyrophosphate synthase
8513	dirMS_041712_NAR_50mM_minus2.18178.18178.3	3	10.93	0	2.31E+05		(K)ILFIFIDS	(K)I|L/F I/F I/D S D H T D N Q R(I)		172.78	611.9745	1833.913	-0.004	-2.2	4.41	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
8514	dirMS_041712_NAR_50mM_minus2.9301.9301.3	3	10.93	0	1.54E+05		(R)TPVIDA	(R)T P|V/I/D A D K/P/V S S Q L/R(V)		121.28	542.6354	1625.886	0.0059	3.7	5.62	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
8515	dirMS_041712_NAR_60mM_minus.11537.11537.3	3	10.93	0	6.83E+04	M186m	(K)NmQNV	(K)N m/Q\N V E H V/P L S/L D/R(A)	m:Oxidized methionine	124.27	556.6111	1651.822	15.9967	1.1	5.32	26717.1	8.65	HUMAN	P20618	Proteasome subunit beta type-1
8516	dirMS_041712_NAR_60mM_minus.11683.11683.3	3	10.93	1	1.91E+05		(R)MLFKD	(R)M/L/F/K D D Y/P S/S/P/P K(C)		125.58	508.9172	1524.74	-0.0032	-2.1	5.71	20685.4	9.18	HUMAN	B0QYN7	SUMO-conjugating enzyme UBC9
8517	dirMS_041712_NAR_60mM_minus.13511.13511.3	3	10.93	1	1.95E+05		(R)KFNALF	(R)K F N A L F\A\Q|G N/Y/S E A A K(V)		134.8	586.9642	1758.881	-0.0029	-1.7	8.5	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
8518	dirMS_041712_NAR_60mM_minus.9304.9304.3	3	10.93	0	9.34E+04		(K)GHENVE	(K)G H\E N V\E\A\A/Q/A|E Y/I E/K(F)		111.78	563.2673	1687.792	-0.0049	-2.9	4.48	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
8519	dirMS_041712_NAR_120mM_plus.8905.8905.2	2	10.93	0	5.81E+05		(R)NGVMP	(R)N G\V|M/P S H\F S R(G)		99.88	566.274	1131.536	0.0043	3.8	9.75	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
8520	dirMS_041712_NAR_30mM_plus2.21809.21809.2	2	10.93	0	1.94E+05		(K)ALELNM	(K)A L|E/L/N M\L/S L K(G)		169.67	566.3204	1131.644	-0.0107	-9.4	6.05	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
8521	dirMS_041712_NAR_30mM_plus2.23645.23645.2	2	10.93	0	2.77E+04		(R)IAIYELLF	(R)I/A/I/Y/E/L\L F K(E)		192.48	555.3331	1109.661	-0.0016	-1.4	6	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
8522	dirMS_041712_NAR_50mM_plus2.20943.20943.3	3	10.93	0	3.47E+05		(K)HSQFIG	(K)H S Q F I/G\Y|P I\T L/F V E/K(E)		179.4	593.6536	1778.948	-0.0013	-0.8	6.75	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
8523	dirMS_041712_NAR_120mM_minus.6645.6666.2	2	10.92	1	4.24E+06		(K)IREEYPD	(K)I R|E/E|Y|P D|R(I)		90.72	539.2683	1077.532	-0.003	-2.8	4.68	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
8524	dirMS_041712_NAR_20mM_minus.10470.10470.2	2	10.92	0	1.44E+05		(R)IYVVDV	(R)I Y|V|V|D/V G/S E/P R(A)		152.93	617.3216	1233.647	-0.0115	-9.3	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
8525	dirMS_041712_NAR_30mM_minus2.10290.10290.2	2	10.92	0	6.09E+05	M239m	(K)EITALAP	(K)E I\T/A/L/A/P S T/m/K(I)	m:Oxidized methionine	109.48	589.3092	1161.618	15.9927	-1.8	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
8526	dirMS_041712_NAR_40mM_minus2.12869.13016.3	3	10.92	0	3.35E+05		(R)DVQIGD	(R)D V\Q|I|G/D I/V/T V/G E C R P L S K(T)	C:Carbamidomethylation	159.67	662.684	1986.033	0.005	2.5	4.56	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
8527	dirMS_041712_NAR_50mM_minus2.13297.13297.3	3	10.92	0	4.15E+05		(R)EQTLSP	(R)E Q/T/L/S/P T I/T S G L H N\I A R(S)		143.5	613.3274	1837.977	-0.009	-4.9	6.85	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
8528	dirMS_041712_NAR_60mM_minus.9531.9531.3	3	10.92	1	4.47E+05		(K)TAVCDI	(K)T A|V/C/D\I/P P/R G L K(M)	C:Carbamidomethylation	112.42	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
8529	dirMS_041712_NAR_120mM_plus.8609.8609.3	3	10.92	0	2.03E+06		(K)HTGPNS	(K)H T\G P N\S\P D T/A/N/D/G F V R(L)		98.93	562.26	1684.767	-0.0019	-1.2	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
8530	dirMS_041712_NAR_20mM_plus.12319.12319.2	2	10.92	0	1.17E+05		(K)VNQIGS	(K)V N\Q\I|G S V/T/E S I Q A C K(L)	C:Carbamidomethylation	157.67	817.4114	1633.821	-0.0059	-3.6	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
8531	dirMS_041712_NAR_20mM_plus.18396.18396.2	2	10.92	0	1.22E+05		(R)GVVQEL	(R)G V V Q/E|L/Q Q/A I/S K(L)		198.05	650.3656	1299.727	-0.0028	-2.1	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
8532	dirMS_041712_NAR_20mM_plus.6945.6945.2	2	10.92	0	9.56E+04		(K)AAAAAA	(K)A A|A\A/A|A/A L Q A K(S)		114.28	478.7792	956.552	-0.0012	-1.3	8.8	37884.5	11.27	HUMAN	H3BM89	60S ribosomal protein L4
8533	dirMS_041712_NAR_20mM_plus.7843.7843.3	3	10.92	0	1.06E+05		(K)AQAAA	(K)A Q A A/A\P\A S/V/P A Q/A\P K(R)		123.6	459.9204	1377.748	-0.0018	-1.3	8.8	17808.8	11.77	HUMAN	P47914	60S ribosomal protein L29
8534	dirMS_041712_NAR_20mM_plus.9938.9938.2	2	10.92	0	2.45E+05		(K)VASGCL	(K)V/A|S/G C L/D I N/S S V K(G)	C:Carbamidomethylation	139.77	675.3376	1349.673	-0.005	-3.7	5.81	56837	7.19	HUMAN	E7ETT1	Propionyl-CoA carboxylase beta chain, mitochondrial
8535	dirMS_041712_NAR_40mM_plus2.15301.15301.3	3	10.92	1	8.47E+03		(K)QGGLG	(K)Q/G G L/G P M|N I/P/L V S D/P K R(T)		156.17	593.6623	1778.958	0.0142	8	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
8536	dirMS_041712_NAR_40mM_plus2.16371.16371.3	3	10.92	1	3.74E+05		(R)CITDPQ	(R)C I|T/D/P Q T G L C L/L P L K E K(K)	C:Carbamidomethylation	163.12	662.6815	1986.04	-0.0099	-5	6.07	533778	5.74	HUMAN	Q15149	Plectin
8537	dirMS_041712_NAR_40mM_plus2.8897.8897.2	2	10.92	0	1.06E+05		(K)TEWLD	(K)T/E|W/L D/G K(H)		114.47	424.7133	848.415	0.0045	5.3	4.37	18393.6	9.55	HUMAN	A2BFH1	Peptidyl-prolyl cis-trans isomerase A-like 4G
8538	dirMS_041712_NAR_50mM_plus2.11717.11717.3	3	10.92	1	1.31E+05		(K)IGRIEDV	(K)I G R\I E\D\V\T|P I/P S D S T R(R)		128.73	585.9784	1755.924	-0.0029	-1.7	4.56	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
8539	dirMS_041712_NAR_50mM_plus2.19196.19196.3	3	10.92	0	1.09E+06		(K)LVLIGSN	(K)L/V|L/I/G S N H S/L P F L K(F)		169.83	513.3073	1537.91	-0.0027	-1.8	8.76	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
8540	dirMS_041712_NAR_60mM_plus.11033.11075.3	3	10.92	0	6.44E+05		(K)GSYVSIH	(K)G S/Y/V/S/I/H/S S G F R(D)		115.62	432.8835	1296.633	0.0028	2.2	8.75	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
8541	dirMS_041712_NAR_60mM_plus.7048.7048.2	2	10.92	1	4.51E+05		(K)IVSGKD	(K)I V/S|G/K/D Y/N V/T A\N\S/K(L)		95.18	748.3906	1495.775	-0.0012	-0.8	8.5	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
8542	dirMS_041712_NAR_20mM_minus.12010.12010.2	2	10.91	0	4.88E+05	M313m	(R)TVQSLE	(R)T V/Q S L/E/I D L D/S\m R(N)	m:Oxidized methionine	169.88	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
8543	dirMS_041712_NAR_30mM_minus2.17741.17741.2	2	10.91	0	6.65E+04		(K)IFFAGDT	(K)I/F\F|A G D/T I P K(S)		151.17	554.8038	1108.604	-0.0034	-3.1	5.84	258215.9	5.48	HUMAN	E7EN95	Filamin-B
8544	dirMS_041712_NAR_40mM_minus2.8306.8306.3	3	10.91	0	1.94E+05	M35m	(K)AASDIA	(K)A A/S D|I/A m T E L/P P T\H P I R(L)	m:Oxidized methionine	128.9	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
8545	dirMS_041712_NAR_50mM_minus2.13933.13933.3	3	10.91	1	4.53E+05	M85m	(K)TVTAm	(K)T V|T/A/m/D V V/Y A L K R(Q)	m:Oxidized methionine	148.15	494.9385	1466.804	15.9974	1.7	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
8546	dirMS_041712_NAR_50mM_minus2.13976.14142.3	3	10.91	1	5.56E+05	M85m	(K)TVTAm	(K)T V|T/A/m/D V/V/Y A L K R(Q)	m:Oxidized methionine	148.35	494.9385	1466.804	15.9974	1.7	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
8547	dirMS_041712_NAR_50mM_minus2.14295.14295.3	3	10.91	1	1.58E+04		(R)VLGTPV	(R)V/L|G T/P V E T I E L T E D R R(A)		149.13	609.9954	1827.981	-0.0094	-5.2	4.41	238243.7	6.1	HUMAN	F8VPD4	CAD protein
8548	dirMS_041712_NAR_60mM_minus.14861.14861.3	3	10.91	1	5.73E+05		(K)TDKTLV	(K)T/D K T L|V L/L/M G/K(E)		142.62	406.9088	1218.713	-0.0008	-0.6	8.26	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
8549	dirMS_041712_NAR_60mM_minus.16759.16759.3	3	10.91	0	1.02E+05		(K)ICDQWD	(K)I/C/D Q/W D A/L/G S L T H S R(R)	C:Carbamidomethylation	153.88	586.9446	1758.823	-0.0035	-2	5.21	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
8550	dirMS_041712_NAR_60mM_minus.18786.18786.3	3	10.91	0	1.43E+05		(K)VAHALA	(K)V A H A L\A E G\L|G V|I/A C I G E K(L)	C:Carbamidomethylation	166.95	603.3262	1807.974	-0.0094	-5.2	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
8551	dirMS_041712_NAR_120mM_plus.5732.5752.3	3	10.91	1	3.76E+05		(R)AAQDRD	(R)A/A|Q|D/R D Q\I Y/R(R)		83.3	412.5446	1235.613	0.0065	5.3	6	12660.6	10.51	HUMAN	H7C2L4	Transformer-2 protein homolog beta (Fragment)
8552	dirMS_041712_NAR_20mM_plus.12701.12701.2	2	10.91	0	4.99E+04	M17m M2	(K)GAEEmE	(K)G A/E E m/E/T|V\I|P V/D V m R(R)	m:Oxidized methionine	160.18	854.3998	1675.803	31.9894	-0.3	4	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
8553	dirMS_041712_NAR_20mM_plus.14769.14769.2	2	10.91	0	1.03E+05		(K)LVILANN	(K)L V|I\L/A/N N C|P A L R(K)	C:Carbamidomethylation	172.93	677.3851	1353.767	-0.0042	-3.1	9.75	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
8554	dirMS_041712_NAR_30mM_plus2.20553.20553.2	2	10.91	0	1.57E+05		(K)GSFSEQ	(K)G S F/S\E/Q/G I|N E F L/R(E)		161.13	742.362	1483.718	-0.0009	-0.6	4.53	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
8555	dirMS_041712_NAR_40mM_plus2.17715.17715.3	3	10.91	1	1.96E+05		(R)LKLPSIP	(R)L K L/P S I|P L\V|P V S A Q K(R)		170.73	530.671	1589.999	-0.0004	-0.3	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
8556	dirMS_041712_NAR_40mM_plus2.8723.8737.2	2	10.91	0	4.09E+05		(K)VCADLI	(K)V/C|A/D L/I/R(G)	C:Carbamidomethylation	113.22	423.7286	846.45	-0.0003	-0.3	5.81	6885.1	10.56	HUMAN	E5RJX2	40S ribosomal protein S20
8557	dirMS_041712_NAR_50mM_plus2.11969.11969.3	3	10.91	1	8.28E+05		(R)INVYYN	(R)I N|V/Y/Y\N E A T G G K Y V P R(A)		130.53	615.3151	1843.934	-0.003	-1.6	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
8558	dirMS_041712_NAR_50mM_plus2.9126.9126.3	3	10.91	0	1.50E+05		(R)NDIASH	(R)N D|I|A/S H/P P V E G S Y|A P/R(R)		114.92	570.6114	1709.824	-0.0045	-2.6	5.32	26398.4	5.21	HUMAN	H7C597	Staphylococcal nuclease domain-containing protein 1 (Fragment)
8559	dirMS_041712_NAR_60mM_plus.16693.16693.2	2	10.91	0	8.01E+05		(R)EHALLAY	(R)E/H|A\L\L|A/Y T L G V/K(Q)		143.92	657.8735	1314.742	-0.0019	-1.4	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
8560	dirMS_041712_NAR_60mM_plus.17998.17998.3	3	10.91	1	4.10E+05		(K)ESQAKD	(K)E S/Q/A K D V|I/E/E/Y/F K(C)		151.17	529.2635	1585.774	0.0015	1	4.41	14914.1	6.84	HUMAN	P25398	40S ribosomal protein S12
8561	dirMS_041712_NAR_60mM_plus.9881.9881.2	2	10.91	0	4.34E+05		(R)QSVEND	(R)Q/S/V/E|N D/I/H\G L R(K)		109.77	634.3217	1267.639	-0.0028	-2.2	5.32	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
8562	dirMS_041712_NAR_120mM_minus.19977.19977.3	3	10.9	0	7.83E+04		(R)INLWHL	(R)I/N L W H/L/E\I T D R(S)		165.22	470.5897	1409.754	0.001	0.7	5.32	52204.6	5.82	HUMAN	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
8563	dirMS_041712_NAR_120mM_minus.5058.5058.3	3	10.9	1	4.89E+05		(R)AAEEED	(R)A/A|E|E E D/E/A D/P K R(Q)		79.55	453.8716	1359.602	-0.002	-1.5	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
8564	dirMS_041712_NAR_120mM_minus.8653.8653.3	3	10.9	1	2.00E+05		(R)KQSTDE	(R)K Q S T D E/E|V/T/S L A K(S)		101.68	479.2478	1435.728	0.0014	1	4.68	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
8565	dirMS_041712_NAR_20mM_minus.7848.7848.2	2	10.9	0	1.69E+05		(K)SVEAAA	(K)S V|E|A/A|A E\L/S A K(D)		128.45	538.2838	1075.563	-0.0027	-2.5	4.53	12131.5	11.14	HUMAN	F5GXR3	Parathymosin
8566	dirMS_041712_NAR_30mM_minus2.14232.14232.2	2	10.9	0	1.84E+05		(K)ALELTGL	(K)A/L|E/L T/G L K(V)		130.63	422.7649	844.514	0.0087	10.3	6.05	76670.1	4.6	HUMAN	P19338	Nucleolin
8567	dirMS_041712_NAR_30mM_minus2.7308.7384.2	2	10.9	0	5.49E+05		(R)QIDNPD	(R)Q I/D/N/P/D/Y/K(G)		94.5	496.7354	992.468	-0.0048	-4.9	4.21	28545.1	4.5	HUMAN	K7EJB9	Calreticulin (Fragment)
8568	dirMS_041712_NAR_40mM_minus2.14965.14965.3	3	10.9	1	7.94E+04		(R)VLEALLP	(R)V/L/E\A\L L/P L K G L E E R(V)		173.35	527.317	1579.942	-0.0053	-3.4	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
8569	dirMS_041712_NAR_50mM_minus2.10956.10956.3	3	10.9	1	4.01E+05		(R)INVYYN	(R)I/N|V\Y/Y\N E A T G G K Y/V/P R(A)		131.28	615.3184	1843.934	0.0069	3.8	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
8570	dirMS_041712_NAR_50mM_minus2.8301.8301.3	3	10.9	1	2.13E+05		(K)GILAADE	(K)G I|L/A/A D E S/T/G S I A K R(L)		114.9	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
8571	dirMS_041712_NAR_60mM_minus.11299.11299.3	3	10.9	1	9.28E+05	M232m	(R)MSmKE	(R)M/S m K E V\D\E\Q|M/L/N V Q N K(N)	m:Oxidized methionine	122.78	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
8572	dirMS_041712_NAR_60mM_minus.14934.14934.3	3	10.9	1	1.25E+05		(K)ESLKELS	(K)E S L K E L S L\A G N/E|L|G D/E G A R(L)		143.02	663.341	1987.993	0.0154	7.7	4.25	31761.7	6.01	HUMAN	H0YCR7	Ribonuclease inhibitor (Fragment)
8573	dirMS_041712_NAR_60mM_minus.9733.9733.3	3	10.9	0	3.05E+05		(R)KPLLESG	(R)K P L\L\E/S/G T/L/G/T K(G)		114.13	415.25	1243.726	0.0098	7.9	8.59	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
8574	dirMS_041712_NAR_30mM_plus2.4885.4885.2	2	10.9	0	1.93E+05		(K)NCSETQ	(K)N/C|S/E|T/Q Y\E S K(V)	C:Carbamidomethylation	76.95	623.256	1245.505	-0.0005	-0.4	4.53	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
8575	dirMS_041712_NAR_60mM_plus.9536.9536.3	3	10.9	0	1.08E+06		(R)IQFKPD	(R)I Q/F K|P D D\G\T T/P E R(I)		107.58	501.923	1503.744	0.0106	7.1	4.56	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
8576	dirMS_041712_NAR_20mM_minus.11200.11284.2	2	10.89	0	1.03E+05	M148m	(R)DLTDYL	(R)D L|T|D Y/L/m/K(I)	m:Oxidized methionine	160.13	507.7443	998.486	15.995	0.1	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
8577	dirMS_041712_NAR_40mM_minus2.8373.8373.3	3	10.89	1	4.74E+03		(R)IAEFTTN	(R)I/A/E/F/T/T N L/T E E E E K S K(S)		129.48	623.6417	1868.912	-0.0018	-1	4.32	227783.5	5.5	HUMAN	P35579	Myosin-9
8578	dirMS_041712_NAR_50mM_minus2.14134.14134.3	3	10.89	1	1.53E+05		(K)YMACCL	(K)Y/M|A C C L L/Y R G D V V/P K(E)	C:Carbamidomethylation	149.08	615.6336	1844.886	0.0007	0.4	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
8579	dirMS_041712_NAR_50mM_minus2.14692.14692.3	3	10.89	1	3.52E+06		(R)IINEPTA	(R)I I/N/E/P T A A A I A Y G/L D K K(V)		151.02	596.6655	1787.99	-0.0082	-4.6	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
8580	dirMS_041712_NAR_50mM_minus2.14840.14896.3	3	10.89	0	4.48E+05		(R)LQQELD	(R)L/Q\Q/E/L/D D L/T V D/L D H Q R(Q)		153.03	646.6559	1937.956	-0.0032	-1.6	4.03	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
8581	dirMS_041712_NAR_120mM_plus.20527.20527.3	3	10.89	1	1.03E+06		(K)AAIDWF	(K)A A|I/D/W F D G K E F/H G N I I K(V)		160.12	654.3334	1960.992	-0.0059	-3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
8582	dirMS_041712_NAR_120mM_plus.5505.5505.3	3	10.89	1	7.14E+05		(R)QREEEIE	(R)Q R E E\E|I|E/A Q/E K(A)		81.97	463.5595	1388.665	-0.0013	-0.9	4.33	29841.1	9.04	HUMAN	O75937	DnaJ homolog subfamily C member 8
8583	dirMS_041712_NAR_20mM_plus.10393.10393.3	3	10.89	0	1.35E+05	M592m M5	(R)mGPAm	(R)m G P A m\G\P/A|L/G/A G I E R(M)	m:Oxidized methionine	144.65	487.2418	1427.713	31.9975	5.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
8584	dirMS_041712_NAR_20mM_plus.16711.16711.2	2	10.89	0	1.90E+05		(R)ELLIIGG	(R)E L|L\I/I|G/G V A A R(D)		186.3	556.3437	1111.683	-0.0032	-2.9	6.1	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
8585	dirMS_041712_NAR_30mM_plus2.16662.16802.2	2	10.89	0	4.84E+05		(K)GCSFLP	(K)G C|S\F/L|P D/P Y\Q\K(Q)	C:Carbamidomethylation	140.68	656.306	1311.604	0.0009	0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
8586	dirMS_041712_NAR_50mM_plus2.10037.10037.3	3	10.89	0	2.40E+04	M457m M4	(R)mGPLGL	(R)m/G/P L/G L/D H/m A/S S I E R(M)	m:Oxidized methionine	119.67	549.2613	1613.777	31.9919	1.3	5.3	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
8587	dirMS_041712_NAR_50mM_plus2.8099.8099.3	3	10.89	1	2.64E+05	M227m M2	(R)mQKEIT	(R)m Q|K E I T A\L|A|P S T m K(I)	m:Oxidized methionine	108.98	527.6045	1548.812	31.9865	-2.1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
8588	dirMS_041712_NAR_60mM_plus.11470.11470.3	3	10.89	0	1.67E+06		(K)AQVARP	(K)A/Q|V/A/R P G G D T/I F G K(I)		116.72	472.9241	1416.759	-0.0016	-1.2	8.79	7323.5	9.4	HUMAN	D6RC06	Histidine triad nucleotide-binding protein 1
8589	dirMS_041712_NAR_60mM_plus.12322.12322.3	3	10.89	1	1.09E+06		(R)VCEEIAI	(R)V C E E I|A|I/I/P S K K(L)	C:Carbamidomethylation	121.32	462.9253	1386.766	-0.0048	-3.4	6.11	21927.8	9.55	HUMAN	H0YK46	40S ribosomal protein S17 (Fragment)
8590	dirMS_041712_NAR_60mM_plus.18761.18845.3	3	10.89	1	3.96E+06		(R)VSFELFA	(R)V/S F/E L/F A D K V/P K(T)		155.83	460.5914	1379.757	0.0027	2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
8591	dirMS_041712_NAR_30mM_minus2.15866.15866.2	2	10.88	0	1.25E+05		(R)TINEVEN	(R)T I|N E/V/E N Q I/L T R(D)		139.6	715.3834	1429.765	-0.005	-3.5	4.53	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
8592	dirMS_041712_NAR_30mM_minus2.16059.16059.2	2	10.88	0	1.16E+05		(K)EQFLDG	(K)E/Q|F L/D/G D/G W/T S R(W)		141.08	705.8174	1410.628	-0.0009	-0.6	4.03	28545.1	4.5	HUMAN	K7EJB9	Calreticulin (Fragment)
8593	dirMS_041712_NAR_30mM_minus2.5943.5943.2	2	10.88	0	1.98E+05		(K)TSEVNC	(K)T\S|E/V/N C/Y R(C)	C:Carbamidomethylation	86.7	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
8594	dirMS_041712_NAR_40mM_minus2.11010.11010.3	3	10.88	0	1.74E+05		(R)DLSHIG	(R)D L S H I G D A\V|V/I/S/C A K(D)	C:Carbamidomethylation	147.45	528.9384	1584.805	-0.0044	-2.8	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
8595	dirMS_041712_NAR_50mM_minus2.16686.16791.3	3	10.88	1	2.99E+05		(R)SELELTL	(R)S E|L/E/L T/L G K L E Q V/R(S)		163.72	538.9725	1614.906	-0.0032	-2	4.78	533778	5.74	HUMAN	Q15149	Plectin
8596	dirMS_041712_NAR_50mM_minus2.16726.16726.3	3	10.88	1	9.23E+04		(R)DSEQVA	(R)D S/E Q V/A E/L K Q E L A T L/K(S)		163.05	601.3217	1801.954	-0.0036	-2	4.41	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
8597	dirMS_041712_NAR_50mM_minus2.8590.8590.3	3	10.88	1	1.16E+05		(K)LTSDDV	(K)L/T|S D D/V K/E Q I Y K(L)		116.18	480.252	1438.742	-0.001	-0.7	4.56	12573.5	10.39	HUMAN	E9PS50	40S ribosomal protein S13 (Fragment)
8598	dirMS_041712_NAR_60mM_minus.18179.18179.3	3	10.88	1	1.56E+05		(R)IRVESLL	(R)I R V E S\L|L|V|T\A I S K(A)		162.58	476.9628	1428.878	-0.0046	-3.2	8.75	91730	7.16	HUMAN	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15
8599	dirMS_041712_NAR_20mM_plus.10986.10986.2	2	10.88	0	3.80E+04		(K)IGGIGTV	(K)I/G/G/I|G/T V/P V G R(V)		148.1	513.3057	1025.61	-0.0061	-5.9	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
8600	dirMS_041712_NAR_20mM_plus.12368.12368.2	2	10.88	0	1.73E+05		(R)GVEICIA	(R)G V/E\I/C/I\A/T/P G R(L)	C:Carbamidomethylation	158.5	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
8601	dirMS_041712_NAR_20mM_plus.7913.8106.3	3	10.88	0	4.57E+05	M239m	(K)EVDEQm	(K)E V D E Q m|L/N V/Q/N/K(N)	m:Oxidized methionine	125.12	488.2328	1446.689	15.9945	-0.3	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
8602	dirMS_041712_NAR_30mM_plus2.12588.12775.2	2	10.88	0	3.73E+05		(K)IGVTVLS	(K)I/G|V/T/V L/S/R(I)		119.82	422.7657	844.525	-0.001	-1.1	9.75	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
8603	dirMS_041712_NAR_30mM_plus2.15041.15068.2	2	10.88	0	7.43E+05		(R)LSLYQA	(R)L/S|L/Y/Q/A M R(Q)		131.28	491.2638	981.519	0.0017	1.7	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
8604	dirMS_041712_NAR_40mM_plus2.12041.12041.3	3	10.88	1	2.33E+05		(R)VVDALG	(R)V/V/D A L/G N A I D/G K G P I G S K(T)		137.12	570.9838	1710.939	-0.0016	-1	5.93	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
8605	dirMS_041712_NAR_40mM_plus2.13780.13780.3	3	10.88	1	3.43E+05		(R)QVFGEA	(R)Q V/F G E A T K Q|P G I/T/F I A A K(F)		147.45	636.0176	1906.043	-0.005	-2.6	8.59	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
8606	dirMS_041712_NAR_50mM_plus2.12294.12294.3	3	10.88	0	2.88E+05		(R)LIAEQPP	(R)L I|A E/Q/P P H L T/P G I R(E)		132.35	514.631	1541.88	-0.0014	-0.9	6.75	20915.7	6.45	HUMAN	C9JBI3	Phosphoserine phosphatase (Fragment)

8607	dirMS_041712_NAR_60mM_plus.9804.9804.3	3	10.88	1	1.29E+06		(K)EAALST	(K)E A/A L/S/T/A L/S E/K R(T)		109.78	425.898	1275.69	-0.0109	-8.5	6.24	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
8608	dirMS_041712_NAR_40mM_minus2.11389.11389.3	3	10.87	0	1.98E+05		(K)LVTSIGD	(K)L V|T S/I/G D V V N/H D P V V/G D R(L)		150.33	631.3335	1891.987	-0.0013	-0.7	4.41	27786.2	5.93	HUMAN	H0Y4Z6	Phosphorylase (Fragment)
8609	dirMS_041712_NAR_60mM_minus.4694.4694.3	3	10.87	1	9.42E+04		(K)AGADEE	(K)A/G|A/D/E E R/A E T A/R(L)		77.88	425.8679	1275.592	-0.0032	-2.5	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
8610	dirMS_041712_NAR_120mM_plus.10647.10753.3	3	10.87	0	1.23E+06		(R)GLHQSI	(R)G L/H Q S\I/E/E/F/R(A)		109.27	405.8796	1215.612	0.0126	10.4	5.4	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
8611	dirMS_041712_NAR_120mM_plus.17569.17569.3	3	10.87	1	1.05E+06		(R)RAPFDLI	(R)R A P F/D|L|F E/N R(K)		146.12	422.22	1264.643	0.0022	1.7	6.07	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
8612	dirMS_041712_NAR_20mM_plus.10358.10358.2	2	10.87	0	8.23E+04		(K)AVYTQD	(K)A V|Y/T/Q/D\C P L A A/A K(A)	C:Carbamidomethylation	144.03	704.3502	1407.694	-0.0006	-0.4	5.88	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
8613	dirMS_041712_NAR_20mM_plus.12617.12617.2	2	10.87	0	9.34E+04	M91m	(R)AITGASL	(R)A I|T/G A\S\L|A\D I m A K(R)	m:Oxidized methionine	159.93	639.3398	1261.682	15.9903	-3.6	5.88	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
8614	dirMS_041712_NAR_20mM_plus.19035.19035.2	2	10.87	0	5.75E+04		(K)ILTFDQL	(K)I L|T|F/D Q L/A/L D S P K(G)		202.35	730.9063	1460.8	0.0058	4	4.21	14643	11.93	HUMAN	F8VUA6	60S ribosomal protein L18 (Fragment)
8615	dirMS_041712_NAR_30mM_plus2.15109.15109.2	2	10.87	0	1.91E+05		(K)GFFEGTI	(K)G/F/F/E/G T I A S K(G)		131.67	528.7748	1056.536	0.0063	5.9	6	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
8616	dirMS_041712_NAR_30mM_plus2.20466.20466.2	2	10.87	0	2.16E+04		(R)ILLLGLDI	(R)I/L|L/L/G L|D N A G/K(T)		161.85	563.8448	1126.683	-0.0007	-0.6	5.84	20626.3	6.76	HUMAN	P36405	ADP-ribosylation factor-like protein 3
8617	dirMS_041712_NAR_30mM_plus2.7229.7229.2	2	10.87	0	2.41E+05		(R)FVDPNT	(R)F/V/D|P N T Q E K(V)		91.7	539.2643	1077.521	0.0002	0.2	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
8618	dirMS_041712_NAR_50mM_plus2.13874.13874.3	3	10.87	1	1.05E+07		(R)TEMENE	(R)T E|M E N E|F/V/L I K K(D)		141.17	494.262	1480.772	-0.0001	-0.1	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
8619	dirMS_041712_NAR_50mM_plus2.9282.9302.3	3	10.87	1	4.02E+05		(R)IEDVTPI	(R)I/E|D\V/T P/I/P S D S T R R(K)		116.25	529.2768	1585.818	-0.0022	-1.4	4.56	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
8620	dirMS_041712_NAR_60mM_plus.14287.14287.3	3	10.87	0	6.17E+04		(R)MSCFSR	(R)M/S/C F/S R P S\M S/P T P L D R(C)	C:Carbamidomethylation	131.22	623.6198	1868.845	-0.0003	-0.2	9.35	300351.7	12.1	HUMAN	Q9UQ35	Serine/arginine repetitive matrix protein 2
8621	dirMS_041712_NAR_60mM_plus.19263.19263.3	3	10.87	1	4.43E+05		(R)TRIEGLL	(R)T R I E G\L|L/A|A/F/P K(L)		159.32	439.262	1315.773	-0.0018	-1.4	8.41	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
8622	dirMS_041712_NAR_120mM_minus.9374.9495.2	2	10.86	0	5.89E+05		(K)HVVFIA	(K)H|V|V/F I/A Q/R(R)		105.95	485.2837	969.563	-0.0027	-2.8	9.75	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
8623	dirMS_041712_NAR_30mM_minus2.11374.11374.2	2	10.86	0	5.00E+05		(K)TWTVV	(K)T W|T/V/V D/A/K(T)		115.73	460.2501	919.488	0.0046	5	5.5	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
8624	dirMS_041712_NAR_30mM_minus2.7691.7691.2	2	10.86	0	1.15E+05		(K)GEEKPSI	(K)G E|E|K/P S/M|Y(-)		96.3	470.7096	940.408	0.0039	4.1	4.53	26181.8	5.67	HUMAN	H0YM70	Proteasome activator complex subunit 2
8625	dirMS_041712_NAR_40mM_minus2.14261.14261.3	3	10.86	0	3.15E+04		(K)GVTIAS	(K)G V/T I/A/S G G V L/P N I H P E L L A K(K)		168.03	662.715	1986.138	-0.0078	-3.9	6.75	17631.5	10.76	HUMAN	D6RCF2	Histone H2A
8626	dirMS_041712_NAR_50mM_minus2.10105.10105.3	3	10.86	1	1.05E+05		(R)ALRETL	(R)A L R E T\L|P/A/E\Q/D L/T T K(N)		125.52	562.6354	1685.907	-0.0152	-9	4.68	26790	6.25	HUMAN	F5GX11	Proteasome subunit alpha type-1
8627	dirMS_041712_NAR_50mM_minus2.18799.18829.3	3	10.86	1	2.24E+06		(R)LIALLEVI	(R)L I|A L/L E/V L/S Q K R(M)		183.72	461.6289	1382.873	-0.0008	-0.6	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
8628	dirMS_041712_NAR_60mM_minus.17119.17119.3	3	10.86	1	3.51E+04	M833m M8	(K)mmALDI	(K)m/m/A/L D R E V Q/Y L L/N/K(A)	m:Oxidized methionine	155.48	585.9628	1723.887	31.9869	-1.7	5.82	105005	5.57	HUMAN	E9PL22	Hypoxia up-regulated protein 1
8629	dirMS_041712_NAR_20mM_plus.14953.14953.2	2	10.86	0	1.19E+05		(R)ILNVPQ	(R)I L|N|V|P Q/E L Y E K(G)		174.55	673.3693	1345.736	-0.0049	-3.6	4.53	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
8630	dirMS_041712_NAR_20mM_plus.17983.17983.2	2	10.86	0	1.38E+05		(R)LFDQAF	(R)L F|D/Q|A/F/G L P R(L)		195.5	582.3166	1163.621	0.0052	4.4	5.84	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
8631	dirMS_041712_NAR_30mM_plus2.15980.15980.2	2	10.86	0	4.68E+05		(R)MGPNIY	(R)M/G/P N/I/Y/E L R(T)		136.68	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
8632	dirMS_041712_NAR_30mM_plus2.18913.18913.2	2	10.86	0	5.13E+04		(R)MGPGI	(R)M/G/P/G/I|G A I L E R(S)		152.52	557.3091	1113.609	0.0024	2.2	5.75	14175.1	9.89	HUMAN	H0YKS1	Myelin expression factor 2 (Fragment)
8633	dirMS_041712_NAR_30mM_plus2.19780.19780.2	2	10.86	0	6.87E+05		(K)SLLQAL	(K)S/L\L/Q|A/L N E/V K(G)		157.95	557.8307	1114.647	0.0075	6.7	5.72	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
8634	dirMS_041712_NAR_40mM_plus2.5898.5898.2	2	10.86	0	6.04E+04		(K)SGYLSSE	(K)S G/Y|L|S/S E R(L)		92.52	449.7162	898.427	-0.0014	-1.5	5.72	65692.2	5.7	HUMAN	E7EQR4	Ezrin
8635	dirMS_041712_NAR_50mM_plus2.16706.16718.3	3	10.86	0	1.14E+05		(K)AQDGS	(K)A Q|D/G S/H/P L S L Q D L I E K(V)		155.92	584.2981	1750.897	-0.0173	-9.9	4.54	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
8636	dirMS_041712_NAR_50mM_plus2.6529.6529.3	3	10.86	1	3.80E+05		(R)IVDGKV	(R)I/V|D/G K V V S E T/N/D T K(V)		100.3	502.2651	1504.785	-0.0046	-3	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
8637	dirMS_041712_NAR_50mM_plus2.9915.9915.3	3	10.86	1	4.84E+05		(K)TAVCDI	(K)T/A/V/C D/I/P P R G L K(M)	C:Carbamidomethylation	119.48	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
8638	dirMS_041712_NAR_60mM_plus.18848.18848.3	3	10.86	1	2.18E+05		(R)TKEEALE	(R)T K E E A L E\L\I/N/G Y I/Q K(I)		155.85	583.6498	1748.943	-0.008	-4.6	4.78	16245.7	9.47	HUMAN	K7EMU7	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1
8639	dirMS_041712_NAR_60mM_plus.8959.8959.2	2	10.86	0	1.94E+05		(R)VLIAAH	(R)V/L|I/A/A H/G N S L R(G)		105.23	575.8377	1150.669	-0.001	-0.9	9.73	28936.8	9.22	HUMAN	P15259	Phosphoglycerate mutase 2
8640	dirMS_041712_NAR_120mM_minus.12244.12244.3	3	10.85	0	7.30E+05		(K)TFTAWC	(K)T F|T/A W/C/N S H/L R(K)	C:Carbamidomethylation	121.4	464.8871	1392.648	-0.001	-0.7	9.44	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
8641	dirMS_041712_NAR_120mM_minus.18332.18332.3	3	10.85	1	1.16E+04		(R)IRGETL	(R)I R G E T L G\L|I/G/F G R(T)		155.07	463.6046	1388.801	-0.0016	-1.2	9.6	49457.5	6.47	HUMAN	P56545	C-terminal-binding protein 2
8642	dirMS_041712_NAR_30mM_minus2.14471.14533.2	2	10.85	0	4.21E+06		(R)NLLSVA	(R)N L|L|S/V/A/Y|K(N)		133.32	454.2604	907.525	-0.0112	-12.4	8.59	18789.1	6.77	HUMAN	A2IDB2	14-3-3 protein eta (Fragment)
8643	dirMS_041712_NAR_30mM_minus2.19400.19400.2	2	10.85	0	2.32E+05		(R)FEELNA	(R)F/E|E L/N A D/L F R(G)		160.93	627.3141	1253.616	0.0048	3.9	4.14	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
8644	dirMS_041712_NAR_30mM_minus2.7400.7400.2	2	10.85	0	2.79E+04		(K)FQGPD	(K)F/Q|G|P/D\N G Q G P K(Y)		94.62	572.7726	1144.538	-0.0002	-0.2	5.84	19162.1	4.62	HUMAN	G3V1K0	Thioredoxin-like 1, isoform CRA_b
8645	dirMS_041712_NAR_30mM_minus2.7722.7739.2	2	10.85	0	4.76E+05		(R)EVIINSR	(R)E V|I|I/N S/R(F)		96.58	415.7421	830.473	0.0039	4.7	6.1	15838.9	7.03	HUMAN	H0Y5U0	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
8646	dirMS_041712_NAR_40mM_minus2.15817.15817.3	3	10.85	0	6.91E+05		(K)GLAPDLI	(K)G L|A/P D L/P E D L Y/H L/I K(K)		184.53	565.3111	1693.916	0.0028	1.7	4.54	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
8647	dirMS_041712_NAR_40mM_minus2.6465.6465.3	3	10.85	1	1.94E+05		(K)GAVAED	(K)G A/V/A|E/D/G D/E L R T E P E A K(K)		104.53	596.2893	1786.845	0.008	4.5	4.08	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
8648	dirMS_041712_NAR_60mM_minus.12091.12157.3	3	10.85	1	3.97E+05		(K)QQEAAL	(K)Q Q/E A/A/L/E/L/E E\L\K K(K)		127.52	510.2782	1528.822	-0.0017	-1.1	4.49	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
8649	dirMS_041712_NAR_120mM_plus.17160.17347.4	4	10.85	1	1.28E+06		(K)FLSDVY	(K)F L S D V/Y/P/D/G F K G H M L T K(S)		143.43	489.4962	1954.973	-0.0102	-5.2	6.74	15838.9	7.03	HUMAN	H0Y5U0	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
8650	dirMS_041712_NAR_120mM_plus.9259.9259.3	3	10.85	0	1.03E+06		(K)EFHLNE	(K)E F H L N\E/S/G D/P/S/S K(S)		102.32	482.8884	1446.65	0.0011	0.7	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
8651	dirMS_041712_NAR_20mM_plus.16383.16383.2	2	10.85	0	3.12E+05		(K)LGGSAV	(K)L/G/G S A V/I/S L E G\K|P L(-)		185.25	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
8652	dirMS_041712_NAR_30mM_plus2.6902.7010.2	2	10.85	0	5.05E+05		(K)ISDSEGF	(K)I/S|D|S E G/F/K(A)		91.13	441.7168	882.42	0.006	6.8	4.37	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
8653	dirMS_041712_NAR_40mM_plus2.16267.16267.3	3	10.85	0	4.11E+04		(K)VLISSLQ	(K)V/L|I S S/L Q D C L H G I E/S K(S)	C:Carbamidomethylation	161.47	600.3172	1798.937	0.0003	0.2	5.32	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
8654	dirMS_041712_NAR_40mM_plus2.16774.16774.3	3	10.85	0	3.49E+04	M64m	(R)GFGFITF	(R)G F/G|F/I/T F/T N P E H A/S V A m R(A)	m:Oxidized methionine	164.88	666.6524	1981.959	15.9838	-5.6	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
8655	dirMS_041712_NAR_50mM_plus2.6099.6099.3	3	10.85	0	1.25E+05		(R)SGSMDF	(R)S G S M/D/P/S G A H P S V R(Q)		96.5	462.214	1384.627	0.0001	0	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
8656	dirMS_041712_NAR_60mM_plus.12104.12357.3	3	10.85	1	1.55E+06		(R)ELLTLDE	(R)E L/L/T L\D E K D/P|R(R)		120.77	443.5754	1328.706	0.006	4.5	4.32	9591.1	10.94	HUMAN	A8MXK4	40S ribosomal protein S9
8657	dirMS_041712_NAR_60mM_plus.12706.12706.3	3	10.85	1	8.88E+05		(K)NKTGAA	(K)N K T G\A A|P/I|I/D V V R(S)		122.72	451.9377	1353.785	0.0137	10.1	8.75	10240.9	10.46	HUMAN	E9PJD9	60S ribosomal protein L27a
8658	dirMS_041712_NAR_60mM_plus.13269.13269.3	3	10.85	0	7.61E+05	M1m	(-)mVNHFI	(-)m V/N H F\I/A E/F|K(R)	m:Oxidized methionine	125.98	417.8778	1235.624	15.9947	-0.2	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
8659	dirMS_041712_NAR_60mM_plus.7854.7879.3	3	10.85	1	5.18E+05		(K)FAAKGE	(K)F/A|A/K G E G Q|L/G P/A E R(A)		99.2	477.5865	1430.739	0.0063	4.4	6.14	96306.4	6.41	HUMAN	P13639	Elongation factor 2
8660	dirMS_041712_NAR_30mM_minus2.13101.13101.2	2	10.84	0	2.97E+05		(R)GATQQI	(R)G A\T Q/Q|I/L/D E/A/E R(S)		125.18	665.833	1330.66	-0.001	-0.8	4.14	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
8661	dirMS_041712_NAR_30mM_minus2.16637.16637.2	2	10.84	0	2.66E+05	M2243m	(K)mSIYQA	(K)m S/I|Y/Q A M/W/K(G)	m:Oxidized methionine	144.22	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
8662	dirMS_041712_NAR_30mM_minus2.16683.16830.2	2	10.84	0	1.86E+05		(K)NLYIISV	(K)N L|Y|I|I/S/V/K(G)		144.78	475.2872	949.572	-0.0046	-4.8	8.59	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
8663	dirMS_041712_NAR_50mM_minus2.13675.13675.3	3	10.84	0	7.43E+04		(K)MLDAED	(K)M/L|D A\E D I V\N/T A R P D/E K(A)		146.2	606.2965	1816.875	0.0004	0.2	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
8664	dirMS_041712_NAR_50mM_minus2.15693.15693.3	3	10.84	0	1.29E+05		(K)FTISDHP	(K)F/T|I/S D H P Q\P I D|P L L/K(N)		157.77	574.3122	1720.927	-0.0048	-2.8	5.21	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
8665	dirMS_041712_NAR_50mM_minus2.7193.7193.3	3	10.84	1	2.32E+04		(K)AAAAAS	(K)A A|A|A/A S A/A G P G G L V A G K E E/K(K)		107.67	575.9781	1725.913	0.0068	3.9	6.18	28364.3	5.45	HUMAN	A6NIH7	Protein unc-119 homolog B
8666	dirMS_041712_NAR_60mM_minus.6168.6168.3	3	10.84	1	7.20E+05		(K)DSYVGD	(K)D S Y|V/G D/E/A Q S K R(G)		92.6	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
8667	dirMS_041712_NAR_120mM_plus.6795.6795.3	3	10.84	1	1.77E+05		(R)RYPSSIS	(R)R Y P S S\I/S/S/S/P Q K(D)		88.95	446.2323	1336.686	-0.0032	-2.4	9.99	113668.7	6.2	HUMAN	F8W726	Ubiquitin-associated protein 2-like
8668	dirMS_041712_NAR_120mM_plus.6809.7083.3	3	10.84	0	5.49E+05		(K)SQFSDKI	(K)S\Q|F|S D/K|P V Q D R(G)		89.72	436.2209	1306.639	0.0095	7.3	5.68	13194	9.99	HUMAN	E9PI70	Chitinase domain-containing protein 1 (Fragment)
8669	dirMS_041712_NAR_120mM_plus.9282.9282.3	3	10.84	0	5.51E+05		(K)SPQYCQ	(K)S/P Q\Y/C/Q/V I H/R(L)	C:Carbamidomethylation	102.12	429.8865	1287.626	0.0187	14.5	8.49	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
8670	dirMS_041712_NAR_20mM_plus.13015.13015.2	2	10.84	0	4.84E+05	M1m N6n	(-)mPLFPnL	(-)m P|L F/P n L/P/R(L)	m:Oxidized methionine n:N-	162.1	652.3439	1084.597	219.0833	6.9	9.5	39133.5	4.5	HUMAN	Q8TD91-2	Isoform 2 of Melanoma-associated antigen C3
8671	dirMS_041712_NAR_20mM_plus.13997.13997.2	2	10.84	0	1.74E+05	M98m	(R)TLTIVDT	(R)T L|T|I V|D T G I G m T K(A)	m:Oxidized methionine	167.73	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
8672	dirMS_041712_NAR_20mM_plus.8066.8066.2	2	10.84	0	4.21E+05	M239m	(K)EVDEQm	(K)E V D E/Q|m L\N/V|Q/N\K(N)	m:Oxidized methionine	125.1	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
8673	dirMS_041712_NAR_30mM_plus2.7910.7910.2	2	10.84	0	3.63E+05		(K)SDPVVS	(K)S D/P V/V|S Y R(E)		94.63	461.7327	922.463	-0.0047	-5.1	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
8674	dirMS_041712_NAR_40mM_plus2.5701.5701.2	2	10.84	0	1.15E+05		(R)NQGGY	(R)N Q|G/G|Y/G G S S S S/S S Y G S G R(R)		90.67	847.8525	1694.7	-0.0024	-1.4	8.59	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
8675	dirMS_041712_NAR_60mM_plus.15876.15876.3	3	10.84	0	5.74E+05		(R)VWYVS	(R)V W|Y/V/S N I/D G/T H I A K(T)		139.5	534.9464	1602.828	-0.0028	-1.8	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
8676	dirMS_041712_NAR_20mM_minus.10369.10369.2	2	10.83	0	9.30E+04		(R)NTGIICT	(R)N T|G\I|I/C T|I/G P A S R(S)	C:Carbamidomethylation	152.63	680.3561	1359.705	0	0	9.75	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
8677	dirMS_041712_NAR_30mM_minus2.7019.7110.2	2	10.83	0	3.48E+05		(R)TYDETY	(R)T Y|D|E/T/Y Q/R(Y)		92.97	538.2398	1075.469	0.0032	3	4.37	40616.6	9.46	HUMAN	H0YHI8	Protein phosphatase 1 regulatory subunit 12A (Fragment)
8678	dirMS_041712_NAR_30mM_minus2.9452.9452.2	2	10.83	0	1.01E+06		(K)QADVNL	(K)Q A/D/V/N/L V/N/A/K(L)		105.43	536.2917	1071.579	-0.0032	-3	5.84	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
8679	dirMS_041712_NAR_60mM_minus.9098.9098.3	3	10.83	0	2.82E+05		(K)SVIHSGF	(K)S V/I H/S G P/F|T/E/S Q K(S)		111.08	472.9099	1416.712	0.0034	2.4	6.47	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
8680	dirMS_041712_NAR_20mM_plus.11429.11429.2	2	10.83	0	1.43E+05		(K)STGGAP	(K)S T/G G/A|P T F N V/T V T K(T)		150.88	690.3592	1379.717	-0.0054	-3.9	8.47	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
8681	dirMS_041712_NAR_20mM_plus.17532.17532.2	2	10.83	0	1.13E+05	M90m	(R)LFVGNLI	(R)L F/V/G N\L|P\P D I T E E E m/R(K)	m:Oxidized methionine	192.65	938.4602	1859.921	15.9923	-1.4	4	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
8682	dirMS_041712_NAR_20mM_plus.17948.17948.2	2	10.83	0	1.64E+05		(R)YISPDQL	(R)Y I/S/P D Q L/A D L Y K(S)		194.4	713.3667	1425.726	0.0001	0.1	4.21	47510.4	7.04	HUMAN	P06733	Alpha-enolase
8683	dirMS_041712_NAR_20mM_plus.18863.18863.3	3	10.83	0	1.19E+05		(K)IYVDDGI	(K)I/Y\V D D G\L/I/S L Q/V K(Q)		200.72	488.2764	1462.815	-0.0005	-0.4	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
8684	dirMS_041712_NAR_30mM_plus2.12089.12089.2	2	10.83	0	6.09E+05		(R)LVGIISS	(R)L V|G\I|I/S S R(D)		116.17	422.7657	844.525	-0.001	-1.1	9.75	30838.7	4.9	HUMAN	E7ETK5	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
8685	dirMS_041712_NAR_30mM_plus2.19766.20009.2	2	10.83	0	7.35E+05		(K)SLLQAL	(K)S L|L|Q/A/L N E/V K(G)		158.03	557.8307	1114.647	0.0075	6.7	5.72	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
8686	dirMS_041712_NAR_30mM_plus2.9037.9037.2	2	10.83	0	5.49E+05		(R)LATNTS	(R)L A|T N/T/S A P D|L K(N)		100.63	565.801	1130.605	-0.0105	-9.2	5.84	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
8687	dirMS_041712_NAR_30mM_plus2.9561.9561.2	2	10.83	0	2.82E+05		(R)SQMLLS	(R)S/Q|M/L/L/S/R(R)		103.93	417.7282	834.45	-0.0011	-1.3	9.47	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
8688	dirMS_041712_NAR_50mM_plus2.12017.12017.3	3	10.83	1	4.97E+05	M327m	(R)VAGGP	(R)V/A|G/G/P Q m I Q L/S L/D G K R(L)	m:Oxidized methionine	131.13	562.6377	1669.905	15.9931	-1	8.72	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
8689	dirMS_041712_NAR_50mM_plus2.13017.13017.3	3	10.83	1	1.53E+06	M356m	(K)VGEVIV	(K)V/G|E|V I/V/T K D D/A m L L K(G)	m:Oxidized methionine	137.12	549.6381	1630.908	15.9913	-2.2	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
8690	dirMS_041712_NAR_50mM_plus2.19013.19299.3	3	10.83	1	3.50E+05		(K)GVPTGF	(K)G V|P/T G/F/I L/P I\R D/I R(A)		169.55	518.6453	1553.916	0.0051	3.3	9.6	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
8691	dirMS_041712_NAR_120mM_minus.7758.7779.2	2	10.82	1	1.08E+06		(R)AQYDEL	(R)A/Q|Y/D/E L A R K(N)		96.87	547.2876	1093.564	0.0043	3.9	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
8692	dirMS_041712_NAR_30mM_minus2.17737.17737.2	2	10.82	0	1.59E+04		(R)SLAALS	(R)S L A/A/L/S Q\I|A/Y/Q R(N)		150.98	660.8642	1320.727	-0.0059	-4.5	8.46	64225	6.66	HUMAN	E7EX44	Caldesmon
8693	dirMS_041712_NAR_30mM_minus2.5485.5582.2	2	10.82	0	1.12E+06	M139m	(R)LmDQNI	(R)L/m|D/Q N/L K(C)	m:Oxidized methionine	84.92	439.2266	861.45	15.9961	1.3	5.84	26611.3	4.47	HUMAN	A6NL28	Putative tropomyosin alpha-3 chain-like protein
8694	dirMS_041712_NAR_40mM_minus2.13709.13709.3	3	10.82	0	1.22E+05		(R)VAAGLP	(R)V A|A G L/P P I L V H T D A A Q A L/G K(Q)		164.83	648.0401	1942.112	-0.0063	-3.2	6.71	17974.2	4.97	HUMAN	C9JNL5	Selenocysteine lyase (Fragment)
8695	dirMS_041712_NAR_50mM_minus2.13571.13571.3	3	10.82	0	4.59E+04		(K)MLDAED	(K)M/L|D A E|D I/V N T A R P D E K(A)		144.98	606.2965	1816.875	0.0004	0.2	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
8696	dirMS_041712_NAR_50mM_minus2.17386.17386.3	3	10.82	0	1.23E+05		(K)VHLVGI	(K)V H L\V G\I|D\I/F T/G/K(K)		167.63	433.5856	1298.747	-0.0045	-3.4	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
8697	dirMS_041712_NAR_50mM_minus2.17873.17873.3	3	10.82	1	2.28E+05	M116m	(R)ELAILLG	(R)E L/A/I/L\L/G m L D P A E K D/E K(G)	m:Oxidized methionine	170.82	634.3353	1884.999	15.9927	-1.2	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
8698	dirMS_041712_NAR_60mM_minus.6096.6096.3	3	10.82	1	9.65E+04		(K)DSYVGD	(K)D S/Y|V/G/D/E/A Q S K R(G)		93.18	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
8699	dirMS_041712_NAR_120mM_plus.4347.4347.3	3	10.82	1	3.08E+05		(K)AGADEE	(K)A/G/A/D/E E R A/E\T A R(L)		71.55	425.869	1275.592	0.0001	0.1	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
8700	dirMS_041712_NAR_120mM_plus.8163.8163.3	3	10.82	1	1.23E+06		(K)MVQFEE	(K)M/V/Q\F E/E/N G R K(E)		96.97	413.2074	1237.599	0.0083	6.7	5.9	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
8701	dirMS_041712_NAR_20mM_plus.7351.7394.2	2	10.82	0	2.86E+05		(K)TGQAPG	(K)T G Q|A|P\G Y/S Y T/A A N K(N)		119.52	714.8394	1428.675	-0.0039	-2.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
8702	dirMS_041712_NAR_30mM_plus2.10185.10185.2	2	10.82	0	5.39E+04		(R)GVNVSA	(R)G V|N\V/S A L S R(D)		106.67	451.7509	902.505	-0.0109	-12.1	9.75	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
8703	dirMS_041712_NAR_30mM_plus2.17262.17262.2	2	10.82	0	5.16E+05		(K)NAAGAL	(K)N A|A|G A/L D L L K(E)		143.33	493.2867	985.568	-0.0015	-1.6	5.84	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
8704	dirMS_041712_NAR_30mM_plus2.9604.9604.2	2	10.82	0	5.06E+05		(K)QTTCWI	(K)Q T/T|C/W/D|G V|R(N)	C:Carbamidomethylation	104.53	561.7585	1122.5	0.0101	9	5.84	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1
8705	dirMS_041712_NAR_40mM_plus2.14433.14433.3	3	10.82	1	5.88E+05		(K)IIVDELK	(K)I I|V D E L K/Q/E V/I/S T S S K(A)		152.5	597.0023	1788.995	-0.003	-1.7	4.68	30149.5	5.96	HUMAN	D6RAC2	Guanine nucleotide-binding protein subunit beta-2-like 1
8706	dirMS_041712_NAR_50mM_plus2.10621.10621.3	3	10.82	0	4.86E+05		(K)MIVDPV	(K)M I|V\D/P V/E/P H G E/M K(F)		123.28	494.5783	1481.713	0.0076	5.2	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
8707	dirMS_041712_NAR_50mM_plus2.6009.6009.3	3	10.82	1	2.40E+04		(R)GTDDSP	(R)G T|D/D S P/K D S Q E D\L/Q E R(H)		95.62	607.2766	1819.794	0.0212	11.6	3.96	23420.8	4.74	HUMAN	Q5H9L2	Transcription elongation factor A protein-like 5
8708	dirMS_041712_NAR_60mM_plus.16680.16680.3	3	10.82	1	3.08E+05		(K)ARLEIEP	(K)A R L E\I\E|P E/W/A/Y G K(K)		144.35	521.2734	1561.801	0.0047	3	4.79	25233.4	9.34	HUMAN	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3
8709	dirMS_041712_NAR_60mM_plus.8661.8661.3	3	10.82	1	5.57E+05		(R)SSGGSYI	(R)S/S G/G\S Y R D S/Y/D/S\Y/A T H/N E(-)		103.95	665.9403	1995.795	0.0112	5.6	4.81	18647.7	9.51	HUMAN	Q14011	Cold-inducible RNA-binding protein
8710	dirMS_041712_NAR_120mM_minus.12052.12052.3	3	10.81	1	2.38E+06		(K)MKEIAE	(K)M K E I A/E A|Y/L/G K(T)		119.63	418.2252	1252.661	0.0005	0.4	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
8711	dirMS_041712_NAR_30mM_minus2.9313.9314.2	2	10.81	0	1.81E+05		(K)YADEEIP	(K)Y/A|D/E/E I/P/R(S)		105	496.7354	992.468	-0.0048	-4.9	4.14	258215.9	5.48	HUMAN	E7EN95	Filamin-B
8712	dirMS_041712_NAR_40mM_minus2.14421.14421.3	3	10.81	0	2.72E+05		(R)DVCTELI	(R)D V/C/T/E L L/P L I K P Q\G R(V)	C:Carbamidomethylation	168.95	580.3211	1738.952	-0.0033	-1.9	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
8713	dirMS_041712_NAR_50mM_minus2.13896.13896.3	3	10.81	0	3.00E+04		(K)TGEEIFG	(K)T G|E/E I/F/G T I/G M R P N\A K(N)		146.93	574.2947	1720.869	0.0009	0.5	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
8714	dirMS_041712_NAR_60mM_minus.12058.12112.3	3	10.81	0	2.17E+05		(K)LSLGTYA	(K)L/S|L/G T\Y/A/S L H G R(I)		127.42	425.5679	1274.685	0.004	3.1	8.75	67446.5	5.63	HUMAN	F8VQE1	LIM domain and actin-binding protein 1
8715	dirMS_041712_NAR_120mM_plus.11392.11393.3	3	10.81	1	8.84E+05		(R)ARSEQF	(R)A R S E\Q|F|I/N/L/R(E)		112.93	411.8988	1233.67	0.012	9.7	9.64	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit

8716	dirMS_041712_NAR_20mM_plus.10963.10963.2	2	10.81	0	3.80E+04		(K)IGGIGTV	(K)I/G/G I/G T/V/P V G R(V)		148.1	513.3057	1025.61	-0.0061	-5.9	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
8717	dirMS_041712_NAR_20mM_plus.12660.12660.2	2	10.81	0	9.94E+04		(R)LAVEAL	(R)L/A|V/E/A L V/R(T)		160.48	435.7739	870.541	-0.0002	-0.2	6	65558.6	9.87	HUMAN	G3V1S7	Hyaluronan synthase 1
8718	dirMS_041712_NAR_30mM_plus2.12503.12503.2	2	10.81	0	4.53E+05		(R)QGVDA	(R)Q/G V|D/A/D I/N G L R(Q)		118.13	579.2997	1157.591	0.0012	1	4.21	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
8719	dirMS_041712_NAR_30mM_plus2.16927.16947.3	3	10.81	0	5.02E+05	M313m	(R)TVQSLEI	(R)T V\Q S L/E\I/D/L/D/S m R(N)	m:Oxidized methionine	142.1	508.2535	1506.747	15.9991	2.8	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
8720	dirMS_041712_NAR_30mM_plus2.16979.16979.2	2	10.81	0	3.26E+05		(K)SNQQLV	(K)S N/Q Q/L/V/D/I I E/K(V)		141.43	643.8504	1286.695	-0.0015	-1.2	4.37	22568.6	6.35	HUMAN	B3KQ25	Proteasome activator complex subunit 3
8721	dirMS_041712_NAR_30mM_plus2.18826.18826.2	2	10.81	0	1.53E+05		(K)FGAYIV	(K)F G\A|Y|I/V/D/G L R(Q)		152.32	555.8011	1110.594	0.0007	0.6	5.83	269989.9	5.92	HUMAN	F8W8T8	Acetyl-CoA carboxylase 2
8722	dirMS_041712_NAR_30mM_plus2.7111.7306.2	2	10.81	0	1.72E+06		(R)AQVIYT	(R)A Q|V|I/Y T/R(N)		92.9	425.7397	850.478	-0.006	-7.1	8.79	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
8723	dirMS_041712_NAR_50mM_plus2.9359.9359.3	3	10.81	0	2.91E+05		(K)GLSSDN	(K)G L/S/S D N K/P M V N\L D K(L)		116.17	506.5928	1517.763	0.001	0.7	5.96	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
8724	dirMS_041712_NAR_60mM_plus.11919.11952.3	3	10.81	0	9.36E+05		(R)ALPESL	(R)A L|P E/S L/G Q H|A L R(S)		119.38	431.2397	1291.712	-0.0072	-5.5	6.79	31463.6	5.53	HUMAN	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1
8725	dirMS_041712_NAR_60mM_plus.13740.13740.3	3	10.81	1	8.88E+05		(K)SLEKVC	(K)S L/E/K/V C/A D/L I/R(G)	C:Carbamidomethylation	128.38	435.2389	1303.704	-0.0017	-1.3	5.79	6885.1	10.56	HUMAN	E5RJX2	40S ribosomal protein S20
8726	dirMS_041712_NAR_60mM_plus.17841.17841.3	3	10.81	1	1.90E+05		(K)LKEVFS	(K)L K E V F S\M|A/G V|V V/R(A)		150.6	478.9419	1434.814	-0.0026	-1.8	8.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
8727	dirMS_041712_NAR_60mM_plus.8484.8713.3	3	10.81	1	1.56E+06		(K)MQASIE	(K)M/Q/A/S I E/K/G G S L/P K(V)		103.4	449.2449	1345.714	0.0057	4.3	8.35	32745.6	4.64	HUMAN	P06748	Nucleophosmin
8728	dirMS_041712_NAR_120mM_minus.7595.7595.3	3	10.8	1	1.88E+05	M42m	(R)SRNTDE	(R)S R N T D E|m/V/E/L/R(I)	m:Oxidized methionine	95.92	455.8866	1349.648	15.9975	1.9	4.68	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
8729	dirMS_041712_NAR_30mM_minus2.12094.12617.2	2	10.8	0	5.20E+05		(K)DISLSDY	(K)D I|S|L/S D/Y/K(G)		120.53	470.7357	940.462	0.0019	2	4.21	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
8730	dirMS_041712_NAR_30mM_minus2.17333.17333.2	2	10.8	0	1.15E+04		(K)VIVPNM	(K)V I|V/P N M E F R(A)		147.4	552.7932	1104.587	-0.0079	-7.2	5.97	86098.8	5.31	HUMAN	B4DUC5	Exportin-2
8731	dirMS_041712_NAR_50mM_minus2.15008.15048.3	3	10.8	0	2.21E+05		(R)GAPPSS	(R)G A|P|P S S/N I E D F H G L L/P K(G)		153.2	593.6417	1778.907	0.0034	1.9	5.32	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
8732	dirMS_041712_NAR_60mM_minus.11204.11204.3	3	10.8	1	6.58E+04		(K)IDKTDY	(K)I D K T D\Y/M/V/G/S/Y G P R(A)		122.35	534.591	1601.763	-0.0044	-2.7	5.96	21671	5.37	HUMAN	J3KTF8	Rho GDP-dissociation inhibitor 1 (Fragment)
8733	dirMS_041712_NAR_60mM_minus.12117.12117.3	3	10.8	1	3.77E+05		(K)AAAGKA	(K)A A/A G/K/A E L E|L E|L G R(I)		127.53	476.5974	1427.785	-0.0076	-5.3	4.79	533778	5.74	HUMAN	Q15149	Plectin
8734	dirMS_041712_NAR_60mM_minus.8693.8693.3	3	10.8	0	7.20E+05		(K)QEYDES	(K)Q E/Y/D E S G/P/S I/V/H R(K)		108.87	506.2391	1516.703	0.0001	0.1	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
8735	dirMS_041712_NAR_60mM_minus.8753.8753.3	3	10.8	1	1.14E+05		(K)YAGKDG	(K)Y/A/G/K/D G Y N Y T L/S/K(T)		109.12	493.9126	1479.711	0.0118	8	8.38	11854.4	6.57	HUMAN	P31949	Protein S100-A11
8736	dirMS_041712_NAR_120mM_plus.12993.12993.3	3	10.8	0	3.53E+05		(K)HVTSECI	(K)H V T S E\C|L/G/W/M/R(Q)	C:Carbamidomethylation	121.52	459.2138	1375.625	0.0023	1.7	6.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
8737	dirMS_041712_NAR_120mM_plus.16808.16849.4	4	10.8	1	9.68E+05		(K)FSHEEIA	(K)F S H E E\I/A/M/A/T/V T A L\R/R(T)		141.43	458.7454	1831.948	0.0114	6.2	6.76	39795.8	9.08	HUMAN	H3BQN4	Fructose-bisphosphate aldolase
8738	dirMS_041712_NAR_20mM_plus.14282.14282.3	3	10.8	0	7.24E+03		(R)VPTANV	(R)V P T A N/V S\V V/D/L/T C/R(L)	C:Carbamidomethylation	169.75	510.9348	1530.795	-0.0046	-3	5.81	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
8739	dirMS_041712_NAR_20mM_plus.15465.15465.2	2	10.8	0	7.27E+04		(R)AVLNPL	(R)A V|L\N|P/L C Q V D/Y R(A)	C:Carbamidomethylation	178.62	724.3735	1447.736	0.0035	2.4	5.88	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
8740	dirMS_041712_NAR_20mM_plus.7695.7695.2	2	10.8	0	2.07E+05	M328m	(K)ALmDEV	(K)A/L|m/D\E|V V/K(A)	m:Oxidized methionine	122.63	460.741	904.481	15.9939	-1.1	4.37	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
8741	dirMS_041712_NAR_30mM_plus2.16904.16904.2	2	10.8	0	3.66E+05		(K)SNQQLV	(K)S N Q/Q|L|V/D I I E K(V)		141.3	643.8504	1286.695	-0.0015	-1.2	4.37	22568.6	6.35	HUMAN	B3KQ25	Proteasome activator complex subunit 3
8742	dirMS_041712_NAR_40mM_plus2.19360.19360.3	3	10.8	1	4.09E+05		(K)ALFEEV	(K)A L/F/E E/V/P E L L/T E A/E K K(E)		181.65	615.9991	1845.984	-0.0017	-0.9	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
8743	dirMS_041712_NAR_50mM_plus2.20237.20237.3	3	10.8	0	5.12E+05		(R)QARPTY	(R)Q/A R P T Y\A|T/A|M/L/Q S L L K(-)		174.62	597.9962	1791.979	-0.0045	-2.5	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
8744	dirMS_041712_NAR_50mM_plus2.9417.9417.3	3	10.8	0	1.45E+04		(K)ILNSDE	(K)I/L/N S D E H/A V V I/S S/A K(T)		116.68	528.2865	1582.843	0.0014	0.9	5.32	102513.4	5.36	HUMAN	F5GYP2	Diacylglycerol kinase eta
8745	dirMS_041712_NAR_60mM_plus.15542.15542.3	3	10.8	0	4.04E+05		(R)TPLHEIA	(R)T/P|L/H/E I A L S I/K(L)		137.92	407.9112	1221.72	-0.0011	-0.9	6.41	142268.2	6.41	HUMAN	Q08211	ATP-dependent RNA helicase A
8746	dirMS_041712_NAR_60mM_plus.20909.20909.3	3	10.8	1	1.36E+05		(K)TFVNITP	(K)T F|V/N I|T/P A E V G V/L V G K D R(S)		170.58	639.0248	1915.065	-0.0049	-2.6	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
8747	dirMS_041712_NAR_120mM_minus.4366.4527.3	3	10.79	1	1.50E+07	M310m	(R)TKTEISE	(R)T\K\T E\I|S/E/m/N R(N)	m:Oxidized methionine	72.87	408.8693	1208.594	15.9994	3.7	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
8748	dirMS_041712_NAR_20mM_minus.7304.7304.2	2	10.79	0	3.99E+04		(K)AVTEQG	(K)A V/T\E|Q/G/A/E L/S N E E R(N)		120.98	766.8612	1532.719	-0.0036	-2.3	4.09	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
8749	dirMS_041712_NAR_30mM_minus2.6442.6442.2	2	10.79	0	1.91E+04		(K)EVEEDE	(K)E V/E/E/D/E/Y/K(A)		89.48	520.7257	1040.442	0.0023	2.2	3.91	92752.5	4.76	HUMAN	P14625	Endoplasmin
8750	dirMS_041712_NAR_40mM_minus2.11864.12007.3	3	10.79	0	2.78E+05		(K)DAGEGL	(K)D/A|G|E/G L/L A/V Q I T D/P E G K\P K(K)		154.02	646.6785	1938.018	0.0031	1.6	4.32	283472.4	5.71	HUMAN	P21333	Filamin-A
8751	dirMS_041712_NAR_50mM_minus2.10397.10397.3	3	10.79	0	2.78E+05	M35m	(K)AASDIA	(K)A A/S D|I/A/m T E L/P P T|H P I R(L)	m:Oxidized methionine	127.6	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
8752	dirMS_041712_NAR_50mM_minus2.14292.14292.3	3	10.79	1	9.64E+04		(R)TIPWLE	(R)T I/P/W L/E D R V P Q/K(T)		149.27	494.6068	1481.811	-0.0052	-3.5	5.74	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
8753	dirMS_041712_NAR_50mM_minus2.6784.6784.3	3	10.79	1	2.55E+04		(K)LAQYEPI	(K)L/A|Q/Y/E/P/P Q E E/K R A E(-)		104.98	563.2743	1687.829	-0.0202	-12	4.69	11966.5	5.71	HUMAN	Q99417	C-Myc-binding protein
8754	dirMS_041712_NAR_60mM_minus.10044.10044.3	3	10.79	0	1.13E+05		(K)YQYGGL	(K)Y/Q|Y/G G L N S G R P V T P P/R(T)		115.72	587.9726	1761.903	0.0002	0.1	9.99	37984.9	5.84	HUMAN	P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit
8755	dirMS_041712_NAR_60mM_minus.15099.15099.3	3	10.79	1	1.80E+05		(K)IKDLSTV	(K)I K D L S T\V/E|A/L/Q/N L K(N)		144.25	524.6378	1571.9	-0.0015	-0.9	6.07	13242.4	4.17	HUMAN	E9PPH5	Acidic leucine-rich nuclear phosphoprotein 32 family member E (Fragment)
8756	dirMS_041712_NAR_60mM_minus.16752.16752.3	3	10.79	1	3.08E+05		(R)LKLPAV	(R)L K L P A V|V/T A/D/L R(L)		153.88	432.6056	1295.805	-0.0023	-1.8	8.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
8757	dirMS_041712_NAR_60mM_minus.9142.9148.3	3	10.79	1	5.12E+04		(R)QLEEAE	(R)Q L|E/E A/E/E E A Q/R A/N A S R(R)		110.88	610.9566	1830.858	-0.0024	-1.3	4.33	227783.5	5.5	HUMAN	P35579	Myosin-9
8758	dirMS_041712_NAR_120mM_plus.5946.5946.4	4	10.79	2	5.78E+05		(R)KTGQAP	(R)K T G Q A|P/G/Y S/Y T A A|N K N/K(G)		83.85	450.4826	1798.908	0.0003	0.2	9.83	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
8759	dirMS_041712_NAR_20mM_plus.10485.10485.3	3	10.79	0	2.60E+05		(R)AQIFAN	(R)A Q\I\F\A N T/V/D/N A/R(I)		145.25	440.5608	1319.67	-0.0024	-1.8	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
8760	dirMS_041712_NAR_20mM_plus.13978.14355.3	3	10.79	0	3.57E+06	M313m	(R)TVQSLEI	(R)T V\Q S L E\I/D|L/D/S m R(N)	m:Oxidized methionine	170.13	508.2519	1506.747	15.9943	-0.4	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
8761	dirMS_041712_NAR_20mM_plus.14137.14137.2	2	10.79	0	2.12E+05		(R)AALQEL	(R)A A|L\Q/E/L L S K(G)		168.92	486.789	972.572	-0.0017	-1.7	6.05	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
8762	dirMS_041712_NAR_20mM_plus.16838.16838.2	2	10.79	0	2.77E+05		(K)LGGSAV	(K)L G G S A/V|I|S L|E G K|P L(-)		186.28	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
8763	dirMS_041712_NAR_30mM_plus2.9442.9442.2	2	10.79	0	5.41E+05		(R)GGGQII	(R)G G G Q/I|I/P T A R(R)		103.97	485.2772	969.548	-0.0005	-0.5	9.75	15036.9	7.16	HUMAN	K7EJ74	116 kDa U5 small nuclear ribonucleoprotein component (Fragment)
8764	dirMS_041712_NAR_40mM_plus2.14033.14243.3	3	10.79	0	1.20E+05		(R)LVLEVA	(R)L/V|L/E V/A Q/H L/G E S T V R(T)		149.27	550.9762	1650.917	-0.0033	-2	5.4	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
8765	dirMS_041712_NAR_50mM_plus2.16640.16640.3	3	10.79	1	3.33E+05		(K)LLTGELL	(K)L L/T/G E L L/P T D G M I R K(H)		155.22	552.9815	1656.935	-0.0054	-3.2	6.07	73070	7.16	HUMAN	Q75MJ1	ATP-binding cassette sub-family F member 2
8766	dirMS_041712_NAR_50mM_plus2.17807.17807.3	3	10.79	0	4.45E+05	M64m	(R)GFGFITF	(R)G F|G\F|I/T F T N/P E H A S V A m R(A)	m:Oxidized methionine	161.67	666.658	1981.959	16.0006	2.8	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
8767	dirMS_041712_NAR_50mM_plus2.9354.9354.3	3	10.79	0	2.40E+05	M378m	(K)mIVDPV	(K)m I|V D P/V E/P H G E/M K(F)	m:Oxidized methionine	116.62	499.9106	1481.713	16.0045	6.4	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
8768	dirMS_041712_NAR_60mM_plus.7917.7917.3	3	10.79	0	7.33E+05		(K)YKPESEE	(K)Y K\P E S E E|L/T/A E R(I)		99.3	484.5717	1451.701	-0.0007	-0.5	4.5	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
8769	dirMS_041712_NAR_120mM_minus.13273.13273.4	4	10.78	1	7.94E+05		(K)SVHSSV	(K)S V H\S S V|P\L/L/N S K D/P I D R(I)		127	466.7525	1863.992	-0.0041	-2.2	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
8770	dirMS_041712_NAR_30mM_minus2.12506.12506.2	2	10.78	0	7.31E+05		(R)GVVGPE	(R)G V|V/G/P E L Y G/R(L)		122.47	523.7834	1046.563	-0.0034	-3.2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
8771	dirMS_041712_NAR_30mM_minus2.16816.16816.2	2	10.78	0	1.53E+05		(K)NLYIISV	(K)N/L|Y/I/I S V K(G)		145.12	475.2872	949.572	-0.0046	-4.8	8.59	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
8772	dirMS_041712_NAR_50mM_minus2.13464.13464.3	3	10.78	1	5.31E+05		(K)LTEDKA	(K)L T/E D K A D V Q/S\I/I/G L Q R(F)		144.8	595.9939	1785.97	-0.0034	-1.9	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
8773	dirMS_041712_NAR_50mM_minus2.17980.17980.3	3	10.78	1	1.42E+04		(K)GVPTGF	(K)G V/P T/G F/I L P I\R D/I/R(A)		171.02	518.6444	1553.916	0.0024	1.6	9.6	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
8774	dirMS_041712_NAR_50mM_minus2.5836.5836.3	3	10.78	0	1.31E+05		(R)AGAAG	(R)A G|A|A/G G P E E E A E/K/P V K(T)		95.32	513.9233	1539.765	-0.0096	-6.2	4.49	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
8775	dirMS_041712_NAR_50mM_minus2.7214.7214.3	3	10.78	1	4.43E+04		(R)LGTPELS	(R)L/G/T/P E/L S/T A E R K(E)		107.93	434.572	1301.706	-0.0045	-3.5	6.14	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
8776	dirMS_041712_NAR_120mM_plus.11640.11680.4	4	10.78	1	8.44E+05		(R)KVSQPIE	(R)K\V S Q|P/I/E G H A A S F/A Q F K(M)		113.75	461.9971	1844.965	0.0012	0.7	8.6	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
8777	dirMS_041712_NAR_20mM_plus.13448.13448.2	2	10.78	0	1.18E+05	M98m	(R)TLTIVDT	(R)T L\T I/V D\T/G I G m/T K(A)	m:Oxidized methionine	165.38	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
8778	dirMS_041712_NAR_20mM_plus.15871.15871.2	2	10.78	0	4.78E+05	M73m	(R)AILVDLE	(R)A I\L\V/D L|E|P G T m D S V R(S)	m:Oxidized methionine	179.88	816.4181	1615.836	15.9929	-1.2	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
8779	dirMS_041712_NAR_20mM_plus.17623.17647.3	3	10.78	0	8.98E+04	M215m	(K)TLNDEL	(K)T\L N\D\E\L/E|I/I/E G m K(F)	m:Oxidized methionine	193.08	507.5886	1504.756	15.9949	0	4	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
8780	dirMS_041712_NAR_30mM_plus2.11075.11075.2	2	10.78	0	2.25E+05		(R)INVSGLT	(R)I/N|V/S/G\L T T K(N)		111.23	466.7724	932.541	-0.0036	-3.9	8.75	44431.6	8.52	HUMAN	B7Z7E9	Aspartate aminotransferase
8781	dirMS_041712_NAR_30mM_plus2.14824.14824.2	2	10.78	0	6.63E+05		(R)NLLSVA	(R)N L|L/S/V A Y/K(N)		131.4	454.2621	907.525	-0.0078	-8.6	8.59	18789.1	6.77	HUMAN	A2IDB2	14-3-3 protein eta (Fragment)
8782	dirMS_041712_NAR_30mM_plus2.18457.18457.2	2	10.78	0	2.36E+05		(K)GNFNYI	(K)G N/F|N/Y/I E F T/R(I)		150.27	630.8035	1260.601	-0.001	-0.8	6	20513.6	4.62	HUMAN	J3QRS3	Myosin regulatory light chain 12A
8783	dirMS_041712_NAR_30mM_plus2.21884.21884.2	2	10.78	0	3.21E+05		(R)SFITWL	(R)S/F|I/T/W L/R(D)		170.53	461.7608	922.515	-0.0002	-0.2	9.47	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
8784	dirMS_041712_NAR_40mM_plus2.13931.13931.2	2	10.78	0	5.54E+04		(K)AILFVPR	(K)A I/L|F V/P R(R)		147.92	408.2603	815.514	-0.0005	-0.6	9.79	57660.2	6.38	HUMAN	Q9NQH7	Probable Xaa-Pro aminopeptidase 3
8785	dirMS_041712_NAR_40mM_plus2.16897.16995.3	3	10.78	1	3.08E+05		(R)LFVGNL	(R)L F\V/G N/L|P T D I/T E E D F K R(L)		166.38	665.3502	1994.023	0.0131	6.6	4.32	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
8786	dirMS_041712_NAR_50mM_plus2.11800.11929.3	3	10.78	1	4.35E+05		(K)QIDLSTV	(K)Q I/D L/S T/V/D L/K/K(L)		130.47	420.5781	1259.72	-0.0008	-0.6	5.96	21156.2	9.41	HUMAN	P55145	Mesencephalic astrocyte-derived neurotrophic factor
8787	dirMS_041712_NAR_50mM_plus2.14158.14158.3	3	10.78	1	6.91E+04		(K)VVSSSIV	(K)V/V|S S S I V D K Y/I/G E S A\R(L)		142.2	570.6392	1709.907	-0.0038	-2.2	6.04	29938.9	6.07	HUMAN	H0YJC0	26S protease regulatory subunit 10B (Fragment)
8788	dirMS_041712_NAR_50mM_plus2.20058.20058.3	3	10.78	0	5.36E+05		(R)QARPTY	(R)Q/A R P T Y A\T/A|M/L/Q S L L K(-)		174.55	597.9962	1791.979	-0.0045	-2.5	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
8789	dirMS_041712_NAR_50mM_plus2.21407.21407.3	3	10.78	0	8.95E+04		(K)GAEILEV	(K)G A/E/I|L/E V L H S L P A V R(Q)		183.4	535.3092	1603.917	-0.0036	-2.2	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
8790	dirMS_041712_NAR_60mM_plus.18785.18785.3	3	10.78	0	1.99E+05		(K)GSDHSA	(K)G S D H S A S L E|P G E|L|A/E L/V R(S)		155.43	622.9778	1866.919	-0.0003	-0.2	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
8791	dirMS_041712_NAR_120mM_minus.15914.15914.4	4	10.77	1	1.70E+06		(K)QLEAID	(K)Q L E/A/I/D Q/L H L/E Y A K/R(A)		140.95	457.499	1826.976	-0.0018	-1	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
8792	dirMS_041712_NAR_40mM_minus2.8310.8310.3	3	10.77	1	4.63E+04		(K)VAVVAG	(K)V A\V|V/A/G Y G\D/V G K G C A Q/A L R(G)	C:Carbamidomethylation	129.1	630.9989	1890.985	-0.0033	-1.7	8.56	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
8793	dirMS_041712_NAR_50mM_minus2.11552.11552.3	3	10.77	0	2.88E+05	M291m	(K)TGEEIFG	(K)T/G\E/E/I/F/G T I G m R/P N A/K(N)	m:Oxidized methionine	134.13	579.6239	1720.869	15.9885	-3.7	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
8794	dirMS_041712_NAR_50mM_minus2.18070.18070.3	3	10.77	0	2.72E+05		(K)ISSIQSIV	(K)I/S|S I/Q S I V/P A L E I A/N/A H R(K)		171.43	640.361	1919.071	-0.0024	-1.3	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
8795	dirMS_041712_NAR_120mM_plus.18064.18064.3	3	10.77	1	3.70E+05		(R)ARFEEL	(R)A R F E\E\L/N/A/D/L F R(G)		147.85	494.2571	1480.754	0.0024	1.7	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
8796	dirMS_041712_NAR_120mM_plus.8496.8496.3	3	10.77	1	2.94E+05		(R)ASGNYA	(R)A/S|G N|Y/A T V/I S H N P E T K K(T)		97.62	606.3102	1816.919	-0.0028	-1.5	8.55	24115.6	11.59	HUMAN	E9PIZ3	60S ribosomal protein L8
8797	dirMS_041712_NAR_20mM_plus.12230.12588.2	2	10.77	0	4.54E+05		(K)VLLGVG	(K)V L/L G|V|G/D P/K(I)		158.47	449.2728	897.54	-0.0021	-2.3	5.81	66448.1	9.42	HUMAN	O00567	Nucleolar protein 56
8798	dirMS_041712_NAR_20mM_plus.15059.15059.2	2	10.77	0	1.22E+05		(R)LLDAQL	(R)L L D A/Q|L/S/T G/G I V/D/P S K(S)		174.7	807.4389	1613.874	-0.004	-2.5	4.21	533778	5.74	HUMAN	Q15149	Plectin
8799	dirMS_041712_NAR_20mM_plus.17542.17542.3	3	10.77	0	2.21E+05	M90m	(R)LFVGNL	(R)L F\V G N L/P/P\D I/T/E/E E m R(K)	m:Oxidized methionine	192.63	625.9762	1859.921	15.9933	-0.9	4	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
8800	dirMS_041712_NAR_30mM_plus2.22072.22072.3	3	10.77	0	2.33E+05		(K)NSSYFVE	(K)N S S Y F\V E|W/I/P N N V K(V)		171.73	566.2872	1696.833	0.0141	8.3	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
8801	dirMS_041712_NAR_30mM_plus2.5991.5991.2	2	10.77	0	9.97E+04		(R)QLAEED	(R)Q L/A/E/E/D A A/R(Q)		85.77	501.7464	1002.485	0.0005	0.5	4.14	533778	5.74	HUMAN	Q15149	Plectin
8802	dirMS_041712_NAR_40mM_plus2.11014.11014.3	3	10.77	0	6.44E+04		(K)SLYVAEY	(K)S L|Y|V|A E Y H S E/P V E D E K P(-)		130.75	664.6419	1991.923	-0.0121	-6.1	4.25	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
8803	dirMS_041712_NAR_50mM_plus2.15285.15285.3	3	10.77	1	5.21E+05		(K)TKDGQII	(K)T K D G Q I|L|P/V/P\N V/V V R(D)		148.62	545.6573	1634.959	-0.0015	-0.9	8.41	56825.2	9.49	HUMAN	Q9P258	Protein RCC2
8804	dirMS_041712_NAR_50mM_plus2.8905.8905.3	3	10.77	0	5.34E+04		(K)GIVEFS	(K)G I/V/E F/S/G K/P A A/R(K)		113.88	411.2309	1231.679	-0.0012	-1	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
8805	dirMS_041712_NAR_60mM_plus.15645.15645.3	3	10.77	0	1.71E+05		(R)ILHGLGF	(R)I L H G L\G\F\T/P/A/M Q R(K)		138.35	480.9305	1440.778	-0.0011	-0.7	9.75	27043.5	6.34	HUMAN	C9JHK9	ATP-binding cassette sub-family F member 2 (Fragment)
8806	dirMS_041712_NAR_40mM_minus2.11042.11042.3	3	10.76	0	4.70E+05		(R)DAGEGL	(R)D A|G E/G/L/L A V Q I/T D Q E G K P K(R)		148.08	657.0157	1969.024	0.0089	4.5	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
8807	dirMS_041712_NAR_50mM_minus2.17679.17679.3	3	10.76	0	3.67E+05		(K)VAHALA	(K)V A H A L A E G\L|G\V/I/A/C I G E K(L)	C:Carbamidomethylation	168.9	603.3247	1807.974	-0.0139	-7.7	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
8808	dirMS_041712_NAR_50mM_minus2.9704.9704.3	3	10.76	0	2.51E+05		(K)TSEVDL	(K)T/S|E/V/D L A K/P L/V/K(F)		123.18	433.9205	1299.752	-0.0049	-3.8	5.73	17178.3	5.63	HUMAN	C9IZF9	Programmed cell death 6-interacting protein (Fragment)
8809	dirMS_041712_NAR_60mM_minus.13381.13381.3	3	10.76	1	2.62E+04		(R)TVENIK	(R)T\V|E N I/K D/P/L/F R(F)		134.57	444.5792	1331.732	-0.0087	-6.6	5.74	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
8810	dirMS_041712_NAR_60mM_minus.14324.14324.3	3	10.76	1	3.35E+05		(K)KSDIDE	(K)K S D I D E I V|L|V/G G S T R(I)		139.68	530.2846	1588.854	-0.0148	-9.3	4.56	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
8811	dirMS_041712_NAR_60mM_minus.15681.15681.3	3	10.76	1	6.80E+05		(R)FLQDYF	(R)F/L/Q D Y/F D/G N L K R(Y)		147.7	505.924	1515.759	-0.0016	-1.1	5.96	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
8812	dirMS_041712_NAR_60mM_minus.17968.17968.3	3	10.76	1	1.25E+04		(K)RSIQFV	(K)R S I Q\F\V/D/W/C/P T G F K(V)	C:Carbamidomethylation	161.33	580.9568	1740.853	0.0032	1.8	8.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
8813	dirMS_041712_NAR_120mM_plus.7980.7980.2	2	10.76	0	4.64E+05		(K)STTTGH	(K)S T|T/T/G/H L I/Y/K(C)		95.25	560.8014	1120.6	-0.0042	-3.7	8.34	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
8814	dirMS_041712_NAR_20mM_plus.14614.14614.2	2	10.76	0	7.57E+04	M73m	(R)AVLVDL	(R)A V L\V|D L|E|P G T m\D/S V R(S)	m:Oxidized methionine	172.83	809.4082	1601.82	15.9888	-3.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
8815	dirMS_041712_NAR_30mM_plus2.17454.17454.2	2	10.76	0	3.94E+05		(K)SFNLSAL	(K)S F/N L|S A L E K(H)		144.37	504.7726	1008.536	0.0019	1.9	5.72	82756.6	5.34	HUMAN	C9JIF9	Acylamino-acid-releasing enzyme
8816	dirMS_041712_NAR_40mM_plus2.6959.6959.2	2	10.76	0	1.41E+05		(R)MGPVM	(R)M/G|P|V/M D/R(M)		100.52	403.1892	805.37	0.0016	2	5.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
8817	dirMS_041712_NAR_50mM_plus2.12568.12568.3	3	10.76	0	1.02E+05		(K)TYSTSFT	(K)T Y/S T S F T/P/M Y H A V T K(R)		134.05	578.611	1733.82	-0.0019	-1.1	8.2	56826.6	9.16	HUMAN	P00390	Glutathione reductase, mitochondrial
8818	dirMS_041712_NAR_50mM_plus2.13682.13682.3	3	10.76	0	4.46E+05		(K)FLSDPQ	(K)F L|S/D/P Q V/H T V L V E R(S)		140.13	547.2984	1639.88	0.0004	0.3	5.32	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
8819	dirMS_041712_NAR_60mM_plus.17678.17678.3	3	10.76	0	4.55E+05		(R)FDASFF	(R)F/D/A S F\F/G V/H/P/K(Q)		149.22	417.8778	1251.616	0.0032	2.5	6.74	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
8820	dirMS_041712_NAR_60mM_plus.6351.6363.3	3	10.76	1	2.06E+05	M1m	(-)mDSETD	(-)m/D|S|E T/D M V R Q I R(A)	m:Oxidized methionine	91.9	499.5719	1480.688	16.0129	12	4.56	28693	5.27	HUMAN	E9PJ36	Vacuolar protein sorting-associated protein 51 homolog (Fragment)
8821	dirMS_041712_NAR_120mM_minus.11439.11439.2	2	10.75	0	7.46E+05		(R)GSAVH	(R)G S A V/H|Q/L\S/E E L R(C)		116.68	663.3434	1325.681	-0.0013	-1	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
8822	dirMS_041712_NAR_120mM_minus.13770.13770.4	4	10.75	2	7.92E+05	M100m	(K)KQGGLG	(K)K Q G G L G/P m/N\I/P L/V S D/P K R(T)	m:Oxidized methionine	128.6	481.5173	1907.053	15.9942	-0.3	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
8823	dirMS_041712_NAR_120mM_minus.7491.7491.3	3	10.75	1	1.25E+05		(R)SSFREE	(R)S/S|F R\E\E D/N/T Y\R(C)		95.05	468.5448	1403.619	0.0012	0.9	4.68	95051	6.63	HUMAN	B3KXW5	AP-1 complex subunit gamma-1
8824	dirMS_041712_NAR_20mM_minus.14412.14412.2	2	10.75	0	2.52E+05		(R)APGSGL	(R)A/P/G/S G L/A L L/P L/K(I)		198.32	568.8551	1136.704	-0.0008	-0.7	8.8	266161	5.68	HUMAN	E9PPU0	Epiplakin

8825	dirMS_041712_NAR_30mM_minus2.14039.14039.2	2	10.75	0	2.72E+05		(K)CDFPIM	(K)C D|F/P I/M/K(F)	C:Carbamidomethylation	129.67	455.7144	910.416	0.0054	5.9	5.84	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
8826	dirMS_041712_NAR_30mM_minus2.16749.16749.2	2	10.75	0	1.85E+05		(K)FANPFP	(K)F A/N|P F/P/A A V\R(G)		145.35	545.2937	1089.584	-0.0039	-3.5	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
8827	dirMS_041712_NAR_30mM_minus2.19045.19098.2	2	10.75	0	2.12E+05		(K)MAILQI	(K)M/A|I|L/Q I/M K(E)		158.38	474.2745	947.542	0.0001	0.1	8.5	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
8828	dirMS_041712_NAR_50mM_minus2.14476.14476.3	3	10.75	1	4.84E+05		(R)VEKIPG	(R)V E K I/P G G\I\I/E/D/S C V\L R(G)	C:Carbamidomethylation	149.27	595.6534	1784.958	-0.0118	-6.6	4.68	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
8829	dirMS_041712_NAR_50mM_minus2.6118.6118.3	3	10.75	0	4.44E+05	M437m	(R)LESGMC	(R)L E|S/G M\Q|N m/S I/H T K(T)	m:Oxidized methionine	97.77	497.9018	1475.698	15.9927	-1.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
8830	dirMS_041712_NAR_50mM_minus2.9043.9043.3	3	10.75	0	7.04E+04		(R)EANALA	(R)E A N A/L/A A G/H/P A/Q/A V A I N A R(L)		119.77	615.6611	1844.973	-0.0038	-2.1	6.85	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
8831	dirMS_041712_NAR_60mM_minus.6513.6513.3	3	10.75	1	8.87E+04		(K)SESPKEP	(K)S E|S/P K E/P E Q L R(K)		94.9	433.8887	1299.654	-0.0024	-1.8	4.78	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
8832	dirMS_041712_NAR_30mM_plus2.6302.6320.2	2	10.75	0	2.56E+05		(K)SAVLQE	(K)S A|V|L|Q E/A/R(I)		87.2	437.2414	873.479	-0.0033	-3.8	5.72	28218.2	9.35	HUMAN	F6X838	Coatomer subunit gamma-2
8833	dirMS_041712_NAR_30mM_plus2.9688.9703.2	2	10.75	0	3.55E+05		(R)TSLGPN	(R)T/S|L/G|P N G L D K(M)		104.43	501.2717	1001.526	0.0099	9.9	5.5	55804.4	5.33	HUMAN	B7ZAR1	T-complex protein 1 subunit epsilon
8834	dirMS_041712_NAR_40mM_plus2.7674.7674.2	2	10.75	0	2.04E+04		(R)INISEGN	(R)I/N/I/S/E/G N/C P E R(I)	C:Carbamidomethylation	105.07	644.7998	1288.595	-0.0027	-2.1	4.53	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
8835	dirMS_041712_NAR_50mM_plus2.10123.10123.3	3	10.75	1	5.30E+05		(K)STGGAP	(K)S T/G/G A/P/T F N\V T V T K\T D K(T)		120.03	575.303	1723.886	0.0083	4.8	8.31	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
8836	dirMS_041712_NAR_50mM_plus2.13584.13584.3	3	10.75	0	4.67E+05		(R)LVVVLC	(R)L V/V\V/L C/N L K P Q K(M)	C:Carbamidomethylation	139.48	470.9516	1410.85	-0.0099	-7	10	59484.7	6.61	HUMAN	P54577	Tyrosine--tRNA ligase, cytoplasmic
8837	dirMS_041712_NAR_50mM_plus2.8101.8101.3	3	10.75	1	3.71E+05		(R)VLVNDA	(R)V L/V|N D A Q K V/T/E/G Q Q E R(L)		109.88	605.3151	1813.94	-0.0095	-5.2	4.68	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
8838	dirMS_041712_NAR_60mM_plus.12042.12042.2	2	10.75	1	7.93E+05		(K)MKEIAE	(K)M K|E/I|A/E/A Y L/G K(T)		120.2	626.8335	1252.661	-0.0009	-0.7	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
8839	dirMS_041712_NAR_60mM_plus.14280.14280.3	3	10.75	1	6.49E+05		(K)WKDSD	(K)W K D|S D E/A|D L|V L/A K(E)		131.03	497.2559	1489.753	-0.0002	-0.1	4.23	20982.2	5.23	HUMAN	Q13185	Chromobox protein homolog 3
8840	dirMS_041712_NAR_120mM_minus.12096.12096.3	3	10.74	1	2.45E+05		(R)MQKEIT	(R)M Q K E I T/A\L|A/P S T/M/K(I)		119.85	516.9425	1548.812	0.0005	0.3	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
8841	dirMS_041712_NAR_120mM_minus.18450.18450.3	3	10.74	0	1.63E+05		(R)FHQLDI	(R)F H|Q L D\I\D/D\L|Q/S I R(A)		155.4	533.9425	1599.813	0.0004	0.3	4.41	24897.7	9.84	HUMAN	A8MTM1	Carbonyl reductase [NADPH] 1
8842	dirMS_041712_NAR_20mM_minus.13569.13569.2	2	10.74	0	1.36E+05		(R)QAQEYE	(R)Q A\Q/E/Y/E/A L/L N I K(V)		186.8	710.3754	1419.748	-0.0043	-3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
8843	dirMS_041712_NAR_30mM_minus2.18230.18230.2	2	10.74	0	8.12E+04		(K)SCDFLSS	(K)S C/D|F/L/S/S F R(D)	C:Carbamidomethylation	153.88	559.7501	1118.494	-0.0006	-0.5	5.55	42963.5	5.19	HUMAN	P35237	Serpin B6
8844	dirMS_041712_NAR_40mM_minus2.7815.7815.3	3	10.74	0	7.49E+04	M44m M5	(K)SGTGIA	(K)S G T/G I/A/A/m\S V M/R/P E Q I m K(S)	m:Oxidized methionine	125.22	646.9867	1906.955	31.9908	0.5	8.46	8797.3	9.3	HUMAN	H3BR50	V-type proton ATPase 16 kDa proteolipid subunit
8845	dirMS_041712_NAR_50mM_minus2.15451.15451.3	3	10.74	0	7.78E+04		(R)DLTPEHI	(R)D L|T/P E H L P/L L R(N)		155.98	435.2497	1303.737	-0.0023	-1.8	5.32	38779.2	5.93	HUMAN	Q96C86	m7GpppX diphosphatase
8846	dirMS_041712_NAR_50mM_minus2.16537.16537.3	3	10.74	1	1.87E+04		(R)EVQLEEI	(R)E V/Q/L E E/L/E/A A R D L V/S K(E)		161.82	610.3273	1828.965	0.0023	1.2	4.25	45984.6	6.24	HUMAN	B4E1G6	Galactokinase
8847	dirMS_041712_NAR_60mM_minus.14422.14422.3	3	10.74	1	2.87E+05		(K)KSDIDEI	(K)K S D I D E I\V\L|V/G G/S T/R(I)		139.9	530.2846	1588.854	-0.0148	-9.3	4.56	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
8848	dirMS_041712_NAR_60mM_minus.18507.18645.3	3	10.74	0	2.58E+05		(R)DFLLKPE	(R)D F|L/L/K/P E L/L R(A)		165.43	415.25	1243.741	-0.0054	-4.4	6.07	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
8849	dirMS_041712_NAR_120mM_plus.15262.15263.3	3	10.74	1	9.12E+05		(R)VKPAPD	(R)V K|P A/P D E T/S F S/E A|L L K R(N)		133	630.011	1888.017	0.001	0.5	6.15	43289.6	5.19	HUMAN	Q12905	Interleukin enhancer-binding factor 2
8850	dirMS_041712_NAR_20mM_plus.14965.14965.2	2	10.74	0	2.17E+05		(K)GLAITFV	(K)G L A I|T/F/V/S D E N D A\K(I)		175.3	740.3693	1479.733	-0.0012	-0.8	4.03	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
8851	dirMS_041712_NAR_30mM_plus2.19300.19300.2	2	10.74	0	2.93E+05		(K)TVDNFV	(K)T V|D|N F/V/A L/A T G E K(G)		154.93	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
8852	dirMS_041712_NAR_30mM_plus2.21466.21466.2	2	10.74	0	3.90E+05		(R)VNQAIW	(R)V N\Q\A|I\W/L|L/C/T G A R(E)	C:Carbamidomethylation	166.88	751.3976	1501.794	-0.0065	-4.3	9.72	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
8853	dirMS_041712_NAR_30mM_plus2.21681.21681.2	2	10.74	0	2.82E+05		(R)NSYLEVL	(R)N S/Y|L/E V L/L K(L)		168.22	539.8092	1078.614	-0.0032	-2.9	6	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
8854	dirMS_041712_NAR_30mM_plus2.8427.8427.2	2	10.74	0	5.88E+05		(R)LGLGEG	(R)L/G|L/G E/G A E E/K(S)		98.35	501.7639	1002.51	0.0103	10.3	4.25	40096.8	9.24	HUMAN	C9JW69	Regulator of chromosome condensation (Fragment)
8855	dirMS_041712_NAR_40mM_plus2.6996.6998.2	2	10.74	0	2.31E+05		(K)NMMAA	(K)N M|M|A|A|C D/P R(H)	C:Carbamidomethylation	101.42	533.2182	1065.427	0.0017	1.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
8856	dirMS_041712_NAR_50mM_plus2.21601.21601.3	3	10.74	1	1.93E+05		(K)LKVNFLF	(K)L K/V N F\L|P E/I I/T L S K(E)		184.3	539.0011	1614.983	0.0058	3.6	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
8857	dirMS_041712_NAR_50mM_plus2.6113.6113.3	3	10.74	1	6.55E+04		(R)NTDVAC	(R)N T/D V/A/Q S/P E/A/P K Q E A P A K(K)		96.33	627.6463	1880.935	-0.0105	-5.6	4.68	152868.9	8.79	HUMAN	Q9P2E9	Ribosome-binding protein 1
8858	dirMS_041712_NAR_50mM_plus2.9537.9537.3	3	10.74	1	1.35E+05		(K)NVSEELD	(K)N V|S/E E/L D R T P\P E/V S K(K)		117.42	567.2893	1699.85	0.0036	2.1	4.41	136658.9	5.13	HUMAN	Q15393	Splicing factor 3B subunit 3
8859	dirMS_041712_NAR_50mM_plus2.9577.9577.3	3	10.74	0	7.71E+05		(R)DNIQGIT	(R)D N|I/Q G|I/T K/P A I R(R)		117.22	442.5902	1325.754	0.0025	1.9	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
8860	dirMS_041712_NAR_60mM_plus.16694.16694.3	3	10.74	1	1.13E+06		(R)ELISNAS	(R)E L|I/S/N/A/S D A L/D K I R(L)		144.67	515.6144	1544.828	0.0008	0.5	4.56	5582.4	4.81	HUMAN	F8W026	Endoplasmin (Fragment)
8861	dirMS_041712_NAR_60mM_plus.7985.7985.3	3	10.74	1	4.32E+05		(R)QLQLEA	(R)Q\L/Q/L E|A/E E Q R K(Q)		99.82	457.9111	1371.723	-0.0039	-2.9	4.79	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
8862	dirMS_041712_NAR_120mM_minus.11931.11931.3	3	10.73	2	2.05E+05		(R)YESLTDF	(R)Y/E/S L/T D|P S K L D S G K E L K(I)		119.27	637.325	1909.975	-0.0149	-7.8	4.78	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
8863	dirMS_041712_NAR_30mM_minus2.8249.8249.2	2	10.73	0	1.96E+04		(R)QLEEAEI	(R)Q/L/E E/A|E/E/E/A/Q R(A)		99.67	666.3076	1331.607	0.0006	0.4	3.98	227783.5	5.5	HUMAN	P35579	Myosin-9
8864	dirMS_041712_NAR_30mM_minus2.9986.9986.2	2	10.73	0	3.52E+05		(K)LAEQFPI	(K)L/A|E/Q F/P R(Q)		108.9	430.7364	860.462	0.003	3.5	6	15778.8	9.12	HUMAN	E9PL10	Transcription factor BTF3 homolog 4
8865	dirMS_041712_NAR_40mM_minus2.8158.8158.3	3	10.73	1	3.18E+05		(R)DGKLVS	(R)D G K L V\S E/S/S D V L/P/K(-)		128.2	491.9311	1473.78	-0.0008	-0.5	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
8866	dirMS_041712_NAR_50mM_minus2.10455.10455.3	3	10.73	1	1.84E+04		(R)TEMEDL	(R)T\E|M E D|L/M/S S K/D D V/G K(S)		127.38	562.2507	1684.74	-0.0029	-1.7	4.1	227783.5	5.5	HUMAN	P35579	Myosin-9
8867	dirMS_041712_NAR_50mM_minus2.10955.11139.3	3	10.73	1	4.01E+05		(R)INVYYNE	(R)I/N|V|Y/Y|N E/A T G G K Y V P R(A)		131.28	615.3184	1843.934	0.0069	3.8	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
8868	dirMS_041712_NAR_50mM_minus2.16933.16933.3	3	10.73	0	1.44E+05		(K)TVSGVN	(K)T V|S/G V/N G P L V I L D/H V K(V)		164.98	549.9835	1647.943	-0.0069	-4.2	6.41	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
8869	dirMS_041712_NAR_60mM_minus.14262.14374.3	3	10.73	1	2.95E+05		(K)ALQQGL	(K)A L|Q/Q/G L V/G L/E L K E K(L)		139.65	509.2999	1525.895	-0.0097	-6.3	6.18	266161	5.68	HUMAN	E9PPU0	Epiplakin
8870	dirMS_041712_NAR_60mM_minus.16712.16712.3	3	10.73	1	2.40E+05		(R)KGFSEGI	(R)K G F S E G L\W E|I/E/N/N/P\T V/K(A)		153.72	649.9986	1947.981	0.0002	0.1	4.79	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
8871	dirMS_041712_NAR_60mM_minus.6479.6479.3	3	10.73	1	1.99E+05		(R)AIEAAPC	(R)A I|E A\A/P Q/E P E Q K R(S)		95.33	489.5907	1466.76	-0.0022	-1.5	4.79	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
8872	dirMS_041712_NAR_120mM_plus.7622.7622.3	3	10.73	1	2.02E+06	M281m	(R)SRAEAES	(R)S R A E\A\E|S/m/Y/Q\I/K(Y)	m:Oxidized methionine	93.02	476.8977	1412.684	15.9947	-0.1	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
8873	dirMS_041712_NAR_20mM_plus.13658.13889.2	2	10.73	0	6.17E+05		(R)GALQNI	(R)G A L|Q/N|I|I\P A S T G A A K(A)		167.23	706.3975	1411.79	-0.0026	-1.9	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
8874	dirMS_041712_NAR_30mM_plus2.16025.16068.2	2	10.73	0	6.98E+05		(R)YLCGLG	(R)Y L/C/G\L/G/A V/G G V R(L)	C:Carbamidomethylation	137.42	611.3189	1221.641	-0.0103	-8.5	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
8875	dirMS_041712_NAR_30mM_plus2.21664.21664.2	2	10.73	0	1.33E+05		(R)IITLAGP	(R)I I/T\L/A/G/P T N A I/F K(A)		168.33	679.9016	1358.804	-0.0083	-6.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
8876	dirMS_041712_NAR_30mM_plus2.22596.22596.3	3	10.73	0	5.00E+05		(R)ALTVPEL	(R)A L\T V/P E L T/Q Q V/F D A K(N)		175.77	553.9697	1659.895	-0.0007	-0.4	4.37	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
8877	dirMS_041712_NAR_50mM_plus2.11140.11142.3	3	10.73	0	9.67E+05		(R)TFIAIKPI	(R)T/F|I|A I/K/P D/G V Q R(G)		126.28	448.9241	1344.763	-0.0057	-4.2	8.41	6640.6	8.25	HUMAN	C9K028	Nucleoside diphosphate kinase A (Fragment)
8878	dirMS_041712_NAR_50mM_plus2.12872.12872.3	3	10.73	1	3.49E+05		(R)ELAVQIY	(R)E L A/V/Q/I/Y E E A R K(F)		135.48	483.5916	1448.774	-0.0141	-9.7	4.79	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
8879	dirMS_041712_NAR_60mM_plus.14833.14833.3	3	10.73	1	3.95E+05		(K)NKDQGT	(K)N K D Q G T/Y|E/D|Y/V/E/G L R(V)		134.12	596.2816	1786.824	0.006	3.4	4.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
8880	dirMS_041712_NAR_60mM_plus.15791.15791.3	3	10.73	0	2.54E+05		(K)QQGVLA	(K)Q Q/G/V/L A/L R P/Y L Q/K(Q)		138.85	505.2982	1513.885	-0.0049	-3.2	9.99	62841.3	5.15	HUMAN	B3KVK7	Methionine--tRNA ligase, cytoplasmic
8881	dirMS_041712_NAR_20mM_minus.10841.10841.2	2	10.72	0	2.18E+04	M92m	(R)ImNTFSV	(R)I m|N\T F/S/V/V/P S P K(V)	m:Oxidized methionine	155.92	668.3513	1319.703	15.9925	-1.8	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
8882	dirMS_041712_NAR_40mM_minus2.14219.14219.3	3	10.72	0	3.15E+04		(K)GVTIASG	(K)G V T\I/A/S G/G V L/P/N I H P E L L A K(K)		168.03	662.715	1986.138	-0.0078	-3.9	6.75	17631.5	10.76	HUMAN	D6RCF2	Histone H2A
8883	dirMS_041712_NAR_60mM_minus.17159.17159.3	3	10.72	1	7.39E+05		(K)QLDDLK	(K)Q/L/D D/L K V/E L/S Q L/R(V)		156.18	519.6267	1556.864	0.0013	0.8	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
8884	dirMS_041712_NAR_60mM_minus.9128.9128.2	2	10.72	0	9.67E+05		(K)QEYDESG	(K)Q E/Y\D/E/S/G P S I/V/H/R(K)		110.35	758.8539	1516.703	-0.0021	-1.4	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
8885	dirMS_041712_NAR_120mM_plus.13003.13003.4	4	10.72	1	1.55E+06		(K)GVIVDKI	(K)G V/I V/D K D/F S H/P Q/M P K(K)		121.9	425.2229	1697.868	0.0018	1.1	6.75	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
8886	dirMS_041712_NAR_20mM_plus.10140.10140.2	2	10.72	0	4.14E+04		(K)LVSESSD	(K)L V|S|E/S S D V/L/P K(-)		142.18	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
8887	dirMS_041712_NAR_20mM_plus.10636.10653.2	2	10.72	0	3.45E+04		(R)LLVVTDF	(R)L L|V|V/T D/P R(A)		146	456.7796	912.551	0.0006	0.7	5.84	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
8888	dirMS_041712_NAR_20mM_plus.15514.15514.3	3	10.72	0	1.81E+05		(R)GVVDSE	(R)G V V D S E/D/I/P\L N\L S R(E)		179.22	505.2667	1513.786	-0.0001	-0.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
8889	dirMS_041712_NAR_30mM_plus2.16616.16616.2	2	10.72	0	3.72E+05		(K)QLQEMI	(K)Q L/Q/E/M L/G L S K(V)		140.13	573.8112	1146.619	-0.0036	-3.1	6	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
8890	dirMS_041712_NAR_40mM_plus2.13207.13285.3	3	10.72	1	1.32E+05		(R)DLPGALI	(R)D L|P G/A|L D/E K/E L I E K(M)		144.48	523.9493	1569.837	-0.0037	-2.3	4.18	21643.7	7.87	HUMAN	Q96BM9	ADP-ribosylation factor-like protein 8A
8891	dirMS_041712_NAR_40mM_plus2.19589.19589.3	3	10.72	0	1.06E+06		(R)GLAPVQ	(R)G L|A|P V/Q A Y L H I P D I I K(V)		183.65	583.3378	1748.011	-0.0117	-6.7	6.74	58266.4	9.46	HUMAN	B4DN00	Pyruvate carboxylase, mitochondrial
8892	dirMS_041712_NAR_50mM_plus2.19127.19127.3	3	10.72	0	5.12E+05		(R)GFGFITF	(R)G F|G|F/I/T F/T N/P E H A S V A M R(A)		168.95	661.3258	1981.959	0.004	2	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
8893	dirMS_041712_NAR_50mM_plus2.19382.19382.3	3	10.72	1	4.32E+05		(R)LKVPPAI	(R)L K|V|P P A I N/Q|F/T Q A L D R(Q)		169.82	604.3351	1811.017	-0.0266	-14.7	8.75	30166.2	10.79	HUMAN	P62424	60S ribosomal protein L7a
8894	dirMS_041712_NAR_50mM_plus2.20998.20998.3	3	10.72	0	4.35E+06		(R)AGKPVIC	(R)A G K\P V I|C A/T\Q/M/L/E S M I K(K)	C:Carbamidomethylation	179.62	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
8895	dirMS_041712_NAR_60mM_plus.16620.16620.3	3	10.72	1	2.17E+04	M557m	(K)mFGIDR	(K)m F/G/I/D R D/A I/A Q A/V/R(G)	m:Oxidized methionine	143.9	526.9346	1562.811	15.9785	-10.4	5.71	63448.4	7.29	HUMAN	B4E022	Transketolase
8896	dirMS_041712_NAR_60mM_plus.18895.18895.3	3	10.72	1	2.03E+05		(R)ANTFVA	(R)A N|T/F/V A E L K G L D/P A R(V)		155.83	534.6306	1601.865	0.0127	7.9	6.12	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
8897	dirMS_041712_NAR_120mM_minus.11876.11876.3	3	10.71	1	3.78E+05		(R)QSVEAD	(R)Q/S/V/E/A/D I N G\L R R(V)		118.77	453.244	1357.718	-0.0008	-0.6	6.07	19213.2	4.66	HUMAN	K7EMD9	Keratin, type I cytoskeletal 13 (Fragment)
8898	dirMS_041712_NAR_120mM_minus.6048.6048.3	3	10.71	1	2.07E+04		(K)NVICDKC	(K)N V/I/C D/K/C/E G R(G)	C:Carbamidomethylation	86.4	417.525	1250.562	-0.0012	-0.9	6.07	45609.1	6.66	HUMAN	P31689	DnaJ homolog subfamily A member 1
8899	dirMS_041712_NAR_120mM_minus.7144.7177.2	2	10.71	0	2.68E+05		(R)HLTGEFI	(R)H|L|T G E\F E|K(K)		93.38	480.7433	960.479	0.0008	0.8	5.4	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
8900	dirMS_041712_NAR_30mM_minus2.14336.14336.2	2	10.71	0	4.05E+05		(K)QLFDQV	(K)Q L/F|D/Q V/V/K(T)		132.3	488.7803	976.546	0.0071	7.3	5.84	71218.8	6.3	HUMAN	A7YIJ8	Radixin
8901	dirMS_041712_NAR_30mM_minus2.8379.8379.2	2	10.71	0	2.70E+04	M496m	(R)YmDLAE	(R)Y/m/D|L/A E N A R(F)	m:Oxidized methionine	100.4	549.7514	1082.494	16.002	6.5	4.37	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
8902	dirMS_041712_NAR_40mM_minus2.14345.14345.3	3	10.71	0	6.01E+05		(R)IHFPLAT	(R)I/H F P L A\T Y|A|P V I/S A E K(A)		167.95	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
8903	dirMS_041712_NAR_50mM_minus2.11287.11287.3	3	10.71	1	1.14E+05		(K)AVAFSPV	(K)A V|A/F/S/P V T E L/K K(D)		132.35	430.585	1289.746	-0.0059	-4.6	8.64	85815.7	7.35	HUMAN	P17858	6-phosphofructokinase, liver type
8904	dirMS_041712_NAR_50mM_minus2.13722.13722.3	3	10.71	0	4.70E+05		(K)LQMEAP	(K)L Q|M E/A/P H/I I/V G T P G R(V)		145.85	540.2947	1618.873	-0.0038	-2.4	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
8905	dirMS_041712_NAR_120mM_plus.9304.9304.3	3	10.71	0	1.03E+06		(K)EFHLNES	(K)E F H L N\E|S/G D/P/S S/K(S)		102.32	482.8884	1446.65	0.0011	0.7	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
8906	dirMS_041712_NAR_30mM_plus2.15376.15376.2	2	10.71	0	3.95E+05		(R)MAGAIA	(R)M/A/G|A|I/A/Q G\L I R(A)		133.27	550.816	1100.624	0.0002	0.2	9.5	4449.1	11.42	HUMAN	F8WEI0	Pyrroline-5-carboxylate reductase 3
8907	dirMS_041712_NAR_30mM_plus2.17093.17093.2	2	10.71	0	7.46E+05		(R)MNVLAD	(R)M/N|V|L/A D A L K(S)		142.93	487.7743	974.534	0.0074	7.6	5.59	27396	9.9	HUMAN	H3BN98	Uncharacterized protein (Fragment)
8908	dirMS_041712_NAR_30mM_plus2.18766.18780.2	2	10.71	0	3.63E+05		(R)NLVCTD	(R)N L|V|C/T D L F/T R(G)	C:Carbamidomethylation	152.18	619.8128	1238.62	-0.0015	-1.2	5.84	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
8909	dirMS_041712_NAR_30mM_plus2.19599.19599.2	2	10.71	0	3.67E+05		(K)SNNVEM	(K)S N|N V|E/M D/W V L K(H)		156.63	667.8205	1334.641	-0.0072	-5.4	4.37	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
8910	dirMS_041712_NAR_30mM_plus2.20182.20182.2	2	10.71	0	1.40E+05		(R)MLDMG	(R)M L|D/M/G F/E P Q I\R(K)		159.13	668.8241	1336.639	0.0021	1.6	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
8911	dirMS_041712_NAR_40mM_plus2.14830.14873.3	3	10.71	1	2.18E+05		(R)VVVDAL	(R)V/V\V/D/A L S/G L/K/G D L A G R(Y)		154.27	523.9701	1569.896	-0.0001	-0.1	5.93	26949.2	7.99	HUMAN	C9JSQ1	Creatine kinase U-type, mitochondrial (Fragment)
8912	dirMS_041712_NAR_40mM_plus2.9755.9755.2	2	10.71	0	3.20E+05		(K)SCNCLLL	(K)S/C|N C L L/L/K(V)	C:Carbamidomethylation	120.88	504.2542	1007.501	-0.0001	-0.1	8.47	47510.4	7.04	HUMAN	P06733	Alpha-enolase
8913	dirMS_041712_NAR_50mM_plus2.13276.13276.3	3	10.71	0	3.85E+05		(K)VQASLA	(K)V Q|A/S\L/A A N T/F T\I T G H A E T K(Q)		137.68	654.0087	1960.013	-0.0019	-1	6.72	11802.2	5.6	HUMAN	D6RDG3	Transcription factor BTF3 (Fragment)
8914	dirMS_041712_NAR_50mM_plus2.15970.15970.3	3	10.71	1	1.91E+05		(R)GLIVYQL	(R)G L/I|V/Y/Q L/E N Q P S E F R R(I)		151.77	650.3463	1949.024	0.0004	0.2	6.14	24460.2	5.69	HUMAN	E9PPG9	mRNA export factor
8915	dirMS_041712_NAR_50mM_plus2.16639.16641.3	3	10.71	1	3.33E+05		(K)LLTGELL	(K)L/L/T|G E\L L/P T D/G M I/R K(H)		155.22	552.9815	1656.935	-0.0054	-3.2	6.07	73070	7.16	HUMAN	Q75MJ1	ATP-binding cassette sub-family F member 2
8916	dirMS_041712_NAR_50mM_plus2.7402.7402.3	3	10.71	1	2.78E+05		(R)IVEQDTI	(R)I/V|E/Q D T/M/P/P K G V R(H)		105.25	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
8917	dirMS_041712_NAR_60mM_plus.17833.17833.3	3	10.71	0	2.66E+05		(R)LLIHQSL	(R)L L/I H/Q S L|A/G G I I G V K(G)		150.48	506.9815	1518.937	-0.0067	-4.4	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
8918	dirMS_041712_NAR_60mM_plus.8546.8546.3	3	10.71	0	2.30E+05		(K)ISSDLDG	(K)I/S\S/D L/D G H P/V P/K(Q)		103.22	422.2223	1264.653	-0.0008	-0.7	5.21	63448.4	7.29	HUMAN	B4E022	Transketolase
8919	dirMS_041712_NAR_60mM_plus.9473.9473.3	3	10.71	0	4.80E+05		(K)QADNPH	(K)Q A/D\N/P H V/A L/Y/Q A R(F)		107.52	494.9186	1482.745	-0.0036	-2.4	6.74	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
8920	dirMS_041712_NAR_120mM_minus.17661.17661.3	3	10.7	2	1.87E+05		(R)GYSFTTT	(R)G Y/S/F/T/T T A E R E I V R D|I K(E)		150.65	662.6807	1986.029	-0.0015	-0.8	6.18	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
8921	dirMS_041712_NAR_20mM_minus.14120.14120.3	3	10.7	0	1.02E+06		(K)SYELPDG	(K)S Y E|L P D G Q\V\I/T/I/G N E/R(F)		194.17	597.6345	1790.892	-0.003	-1.7	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
8922	dirMS_041712_NAR_20mM_minus.7926.7926.3	3	10.7	0	4.94E+04		(R)EGQGEG	(R)E G Q G E G E T Q E|A/A/A|A T/A A A R(R)		128.8	606.6126	1817.826	-0.0028	-1.5	4.09	558007.1	5.44	HUMAN	P58107	Epiplakin
8923	dirMS_041712_NAR_50mM_minus2.11602.11602.3	3	10.7	1	1.92E+05		(K)IEVEKPF	(K)I/E/V E/K/P F A I A/K E(-)		134.38	458.5927	1373.767	-0.0039	-2.9	5.01	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
8924	dirMS_041712_NAR_50mM_minus2.12405.12405.3	3	10.7	1	3.20E+05		(K)LYEQILA	(K)L/Y|E/Q\I/L/A\E/N E K L K(A)		139.03	530.9592	1590.874	-0.0107	-6.7	4.79	22046.7	5.8	HUMAN	H0YIM2	Protein phosphatase 1 regulatory subunit 12A (Fragment)
8925	dirMS_041712_NAR_60mM_minus.10612.10612.3	3	10.7	0	1.44E+05	M271m	(R)DLNYCFS	(R)D L|N\Y|C/F S/G m S D H R(Y)	C:Carbamidomethylation m:Oxid	119.2	539.8863	1601.647	15.9972	1.4	5.21	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
8926	dirMS_041712_NAR_60mM_minus.13404.13404.3	3	10.7	1	2.62E+04		(R)TVENIKD	(R)T/V/E/N I K D/P/L/F R(F)		134.57	444.5792	1331.732	-0.0087	-6.6	5.74	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
8927	dirMS_041712_NAR_60mM_minus.17470.17470.3	3	10.7	0	2.90E+05		(K)GSDHSA	(K)G S/D H S A S L\E|P\G E L/A E/L V R(S)		156.97	622.9764	1866.919	-0.0045	-2.4	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
8928	dirMS_041712_NAR_60mM_minus.9953.9953.3	3	10.7	1	5.63E+05	M230m M2	(R)mSmKEV	(R)m S m K E V\D|E Q|M/L/N V Q N/K(N)	m:Oxidized methionine	114.97	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
8929	dirMS_041712_NAR_120mM_plus.13246.13539.2	2	10.7	1	1.54E+06		(K)DKGFGF	(K)D/K|G/F/G F I/R(L)		123.33	470.2551	939.505	-0.0018	-1.9	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
8930	dirMS_041712_NAR_20mM_plus.10354.10354.2	2	10.7	0	1.88E+05	M592m M5	(R)mGPAm	(R)m G/P A m/G/P A L/G A/G I E R(M)	m:Oxidized methionine	144.65	730.3568	1427.713	31.993	2.1	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
8931	dirMS_041712_NAR_20mM_plus.10607.10630.2	2	10.7	0	4.51E+04	M222m	(K)VVPEmT	(K)V V|P/E/m T E I L/K(K)	m:Oxidized methionine	145.88	587.8225	1158.644	15.9939	-0.9	4.53	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
8932	dirMS_041712_NAR_20mM_plus.12793.12793.2	2	10.7	0	1.23E+05		(R)LVVPASC	(R)L V|V|P/A S Q C G S L I G K(G)	C:Carbamidomethylation	161.42	714.8991	1428.788	0.003	2.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
8933	dirMS_041712_NAR_20mM_plus.14343.14343.3	3	10.7	0	7.24E+03		(R)VPTANV	(R)V P T A N V\S\V|V/D/L/T/C R(L)	C:Carbamidomethylation	169.75	510.9348	1530.795	-0.0046	-3	5.81	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase

8934	dirMS_041712_NAR_20mM_plus.16438.16438.3	3	10.7	0	1.35E+05		(R)QAQEYE	(R)Q A\Q\E\Y\E/A/L/L/N I K(V)		184.45	473.9191	1419.748	-0.0051	-3.6	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
8935	dirMS_041712_NAR_30mM_plus2.20837.20837.2	2	10.7	0	1.83E+05		(K)EGLLLW	(K)E G L/L|L/W/C Q R(K)	C:Carbamidomethylation	163.22	587.8038	1174.604	-0.0034	-2.9	6.1	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
8936	dirMS_041712_NAR_50mM_plus2.12895.12895.3	3	10.7	1	1.35E+06		(K)LIADVAF	(K)L I|A/D/V A P S A I R E N D/I/K(S)		136.52	575.6533	1724.954	-0.0088	-5.1	4.56	18388.8	6.85	HUMAN	F5H1Y3	Flap endonuclease 1 (Fragment)
8937	dirMS_041712_NAR_50mM_plus2.6363.6363.3	3	10.7	0	6.07E+05	M437m	(R)LESGMC	(R)L/E|S G M Q N m/S I/H/T K(T)	m:Oxidized methionine	98.85	497.9026	1475.698	15.9951	0.1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
8938	dirMS_041712_NAR_120mM_minus.10846.10846.3	3	10.69	1	2.09E+06		(R)LQAEIEG	(R)L/Q|A E/I/E G L K/G Q R(A)		112.88	447.9206	1341.748	-0.0012	-0.9	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
8939	dirMS_041712_NAR_30mM_minus2.15845.15871.2	2	10.69	0	2.33E+04		(K)MLLYTE	(K)M/L|L|Y/T/E V T/R(Y)		139.67	563.2971	1125.597	-0.0103	-9.2	5.75	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
8940	dirMS_041712_NAR_40mM_minus2.10542.10542.3	3	10.69	1	1.70E+06		(K)TITLEVEI	(K)T\I|T|L E/V E/P S D T I E N V K A K(I)		145.28	663.0226	1987.059	-0.0061	-3.1	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
8941	dirMS_041712_NAR_60mM_minus.11426.11426.3	3	10.69	0	1.65E+05		(R)ELTLEKP	(R)E\L/T/L/E K P E/L/K(A)		123.82	400.5662	1199.688	-0.0041	-3.4	4.79	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
8942	dirMS_041712_NAR_120mM_plus.6367.6367.2	2	10.69	1	3.44E+05		(K)DSYVGD	(K)D/S Y\V|G D E/A Q/S K R(G)		86.3	677.815	1354.623	-0.0006	-0.5	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
8943	dirMS_041712_NAR_20mM_plus.11425.11425.2	2	10.69	0	2.15E+05		(R)YALYDA	(R)Y A|L|Y/D A T Y/E T K(E)		151.13	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
8944	dirMS_041712_NAR_20mM_plus.18826.18826.2	2	10.69	0	2.00E+05		(K)TAVETA	(K)T A|V/E/T/A/V L|L/L R(I)		200.32	593.3625	1185.72	-0.0024	-2	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
8945	dirMS_041712_NAR_20mM_plus.8987.8987.2	2	10.69	0	2.15E+05		(K)VTADVII	(K)V|T|A/D V|I\N A A E K(L)		132.62	565.806	1130.605	-0.0005	-0.4	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
8946	dirMS_041712_NAR_30mM_plus2.6813.6813.2	2	10.69	0	1.50E+05		(K)VPLTQA	(K)V/P|L/T Q A T R(G)		90.48	443.2607	885.515	-0.0011	-1.3	9.72	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
8947	dirMS_041712_NAR_40mM_plus2.15125.15375.3	3	10.69	0	4.85E+05		(K)FTISDHP	(K)F/T\I/S D H/P Q/P I D/P L/L K(N)		156.65	574.3118	1720.927	-0.006	-3.5	5.21	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
8948	dirMS_041712_NAR_40mM_plus2.19224.19224.3	3	10.69	0	1.61E+06		(R)AGKPVI	(R)A G K P V I/C A/T|Q M/L/E/S M I K(K)	C:Carbamidomethylation	180.63	626.3273	1876.969	-0.002	-1.1	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
8949	dirMS_041712_NAR_50mM_plus2.13694.13694.3	3	10.69	0	4.46E+05		(K)FLSDPQ	(K)F L|S D/P Q V/H T/V L V E R(S)		140.13	547.2984	1639.88	0.0004	0.3	5.32	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
8950	dirMS_041712_NAR_50mM_plus2.18526.18526.3	3	10.69	0	4.12E+05		(R)VYAILTH	(R)V/Y|A/I/L T H/G I F S G P A I S R(I)		165.83	601.3347	1801.996	-0.0064	-3.5	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
8951	dirMS_041712_NAR_50mM_plus2.6434.6434.3	3	10.69	1	1.31E+05	M365m	(R)IVEQDT	(R)I V/E Q D/T m/P/P K/G V|R(H)	m:Oxidized methionine	98.88	495.9283	1469.778	15.9923	-1.8	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
8952	dirMS_041712_NAR_60mM_plus.7430.7430.3	3	10.69	1	1.93E+06		(R)SEEKISD	(R)S E/E K I/S/D S E/G F/K(A)		96.8	452.5501	1355.632	0.0032	2.4	4.41	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
8953	dirMS_041712_NAR_60mM_plus.9203.9203.3	3	10.69	1	9.40E+05		(K)YAGKDG	(K)Y/A|G K/D G Y\N/Y T\L S K(T)		106.28	493.9098	1479.711	0.0034	2.3	8.38	11854.4	6.57	HUMAN	P31949	Protein S100-A11
8954	dirMS_041712_NAR_120mM_minus.18580.18580.3	3	10.68	1	3.30E+05		(R)ARFEEL	(R)A R F E E\L|C/S/D/L/F R(S)	C:Carbamidomethylation	156.88	514.9175	1542.737	0.001	0.7	4.68	25598.3	6.45	HUMAN	E7EP11	Heat shock 70 kDa protein 1A/1B
8955	dirMS_041712_NAR_120mM_minus.9536.9640.3	3	10.68	0	1.70E+06		(K)EFHLNES	(K)E F H\L N\E/S/G D/P/S S K(S)		106.18	482.8881	1446.65	0.0002	0.1	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
8956	dirMS_041712_NAR_30mM_minus2.13386.13386.2	2	10.68	0	2.45E+05		(K)QYGNEV	(K)Q Y/G/N E V/F/L/A/K(L)		126.23	584.7961	1168.6	-0.0148	-12.6	6	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
8957	dirMS_041712_NAR_30mM_minus2.13437.13437.2	2	10.68	0	2.45E+05		(K)QYGNEV	(K)Q Y|G/N E V F L/A|K(L)		126.23	584.7961	1168.6	-0.0148	-12.6	6	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
8958	dirMS_041712_NAR_30mM_minus2.18944.18944.2	2	10.68	0	1.92E+05		(K)SYELPDC	(K)S Y E L/P D/G Q V/I|T\I/G N E R(F)		158.62	895.9492	1790.892	-0.0008	-0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
8959	dirMS_041712_NAR_30mM_minus2.19743.19743.2	2	10.68	0	3.53E+04		(K)EGLLLW	(K)E G L L|L/W/C Q/R(K)	C:Carbamidomethylation	164.27	587.8058	1174.604	0.0006	0.5	6.1	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
8960	dirMS_041712_NAR_30mM_minus2.7031.7031.2	2	10.68	0	3.20E+05		(R)TYDETY	(R)T Y|D/E/T/Y Q R(Y)		92.85	538.2398	1075.469	0.0032	3	4.37	40616.6	9.46	HUMAN	H0YHI8	Protein phosphatase 1 regulatory subunit 12A (Fragment)
8961	dirMS_041712_NAR_50mM_minus2.11578.11578.3	3	10.68	1	5.14E+05		(K)ILIANTG	(K)I/L/I\A/N/T G M D T D/K I K(I)		133.45	511.6179	1532.835	0.0039	2.5	5.96	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
8962	dirMS_041712_NAR_50mM_minus2.14737.14737.3	3	10.68	1	1.84E+05		(K)EILDKFT	(K)E I/L D/K F T|E/E V V/K(Q)		152.1	483.932	1449.784	-0.0021	-1.4	4.41	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
8963	dirMS_041712_NAR_50mM_minus2.6953.6953.3	3	10.68	1	3.77E+04		(R)IQAGEV	(R)I/Q|A/G E V S Q/P S K E Q L E K(L)		106.17	590.9708	1770.923	-0.0254	-14.3	4.79	22655.1	9.45	HUMAN	Q9BRP8	Partner of Y14 and mago
8964	dirMS_041712_NAR_60mM_minus.13182.13208.3	3	10.68	0	5.10E+05		(K)GIHPTIIS	(K)G I H\P T\I\I|S/E/S F Q K(A)		133.38	486.2642	1456.78	-0.0014	-1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
8965	dirMS_041712_NAR_60mM_minus.8533.8533.3	3	10.68	1	5.78E+04		(K)GAVAED	(K)G A/V|A/E/D G D E L R T E P E A K(K)		107.4	596.2923	1786.845	0.017	9.5	4.08	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
8966	dirMS_041712_NAR_120mM_plus.15238.15677.3	3	10.68	1	1.81E+06		(K)VKEGMI	(K)V K E G\M N\I|V|E/A/M E/R(F)		133.88	502.5857	1505.745	-0.0025	-1.7	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
8967	dirMS_041712_NAR_120mM_plus.18611.18611.4	4	10.68	1	4.71E+05		(R)SKDVVE	(R)S K D V V E/P L/L\R/P Q W Y V R(C)		150.38	497.0291	1985.097	-0.0021	-1.1	8.31	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
8968	dirMS_041712_NAR_120mM_plus.7412.7412.3	3	10.68	1	1.14E+06		(R)EKVPGG	(R)E K/V/P G G L/Q/G/S Q D R(G)		92.32	457.5737	1370.702	0.0043	3.1	6.17	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
8969	dirMS_041712_NAR_120mM_plus.8510.8510.3	3	10.68	0	1.29E+04		(K)MADHW	(K)M/A D/H W E/T A/P/R(H)		97.3	405.188	1213.542	0.0076	6.2	5.3	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
8970	dirMS_041712_NAR_120mM_plus.9595.9595.3	3	10.68	0	6.06E+05		(K)STAGDT	(K)S T|A/G D/T H L/G G E D F/D/N/R(M)		104.03	564.579	1691.726	-0.0031	-1.9	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
8971	dirMS_041712_NAR_20mM_plus.13975.13975.2	2	10.68	0	1.85E+05	M98m	(R)TLTIVDT	(R)T L\T|I/V|D/T/G I G m T K(A)	m:Oxidized methionine	167.67	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
8972	dirMS_041712_NAR_20mM_plus.8869.8869.3	3	10.68	0	1.55E+04		(K)VLEEAN	(K)V L\E E\A\N|Q/A/I/N/P K(L)		131.57	442.5729	1325.706	-0.0018	-1.4	4.53	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
8973	dirMS_041712_NAR_30mM_plus2.17632.17632.2	2	10.68	0	3.10E+05		(K)SLEDQV	(K)S L|E/D/Q/V/E/M L R(T)		145.7	610.3003	1219.599	-0.0054	-4.4	4.14	61161.1	4.34	HUMAN	K7ELL7	Glucosidase 2 subunit beta
8974	dirMS_041712_NAR_30mM_plus2.7223.7369.2	2	10.68	0	1.31E+06		(R)VTDALN	(R)V/T|D/A/L/N A T/R(A)		92.9	480.759	960.511	-0.0002	-0.2	5.81	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
8975	dirMS_041712_NAR_30mM_plus2.7377.7395.2	2	10.68	0	1.03E+06	M154m	(R)mGYMD	(R)m/G\Y|M/D|P/R(E)	m:Oxidized methionine	92.92	443.1849	869.364	15.9981	3.6	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
8976	dirMS_041712_NAR_30mM_plus2.8897.8897.2	2	10.68	0	1.86E+05		(R)QPLGAT	(R)Q/P/L/G A/T S\G A S L K(T)		100.28	565.3227	1129.621	0.017	15	8.75	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
8977	dirMS_041712_NAR_40mM_plus2.12837.12837.3	3	10.68	0	4.88E+03		(R)EQTLSPT	(R)E Q/T L/S/P/T I/T S G L H N I A R(S)		142.85	613.3236	1837.977	-0.0204	-11.1	6.85	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
8978	dirMS_041712_NAR_40mM_plus2.13466.13466.3	3	10.68	0	6.01E+05		(R)QVSASE	(R)Q V/S A S E L H T/S G I/L/G P E T L R(D)		145.08	665.6807	1995.051	-0.023	-11.5	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
8979	dirMS_041712_NAR_40mM_plus2.8044.8044.2	2	10.68	0	2.13E+05		(R)AVVIVDI	(R)A V|V\I/V/D D/R(G)		108.22	443.7528	886.499	-0.0009	-1.1	4.21	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
8980	dirMS_041712_NAR_50mM_plus2.13566.13566.3	3	10.68	1	1.88E+06		(R)QATKDA	(R)Q/A/T K D A G T I/A/G L N V L/R(I)		140	543.3085	1627.913	-0.0016	-1	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
8981	dirMS_041712_NAR_50mM_plus2.15505.15505.3	3	10.68	1	7.67E+05		(K)VQGGAI	(K)V Q|G G/A L E D S Q\L V A G/V/A F K K(T)		150.35	639.6848	1917.044	-0.0042	-2.2	6.04	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
8982	dirMS_041712_NAR_50mM_plus2.9011.9011.3	3	10.68	1	3.60E+05		(K)TAVCDIF	(K)T/A\V/C D/I/P P R G L/K(M)	C:Carbamidomethylation	114.93	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
8983	dirMS_041712_NAR_60mM_plus.18596.18596.3	3	10.68	1	6.82E+05		(R)IRIDSLSA	(R)I R/I D S L\S\A Q/L/S Q L/Q/K(Q)		154.38	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
8984	dirMS_041712_NAR_120mM_minus.18069.18069.3	3	10.67	1	2.86E+05		(R)ARFEELN	(R)A R F\E E\L|N|A/D/L F R(G)		153.08	494.2561	1480.754	-0.0006	-0.4	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
8985	dirMS_041712_NAR_30mM_minus2.12503.12761.2	2	10.67	0	5.07E+05		(R)GQVVSL	(R)G Q|V|V/S/L I/R(M)		122.25	436.2706	871.536	-0.0021	-2.4	9.75	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
8986	dirMS_041712_NAR_30mM_minus2.6523.6523.2	2	10.67	0	2.34E+05		(R)QQYESV	(R)Q Q/Y/E/S V/A A/K(N)		89.95	512.2534	1023.511	-0.011	-10.8	6	49709.6	5.19	HUMAN	B0YJC4	Vimentin
8987	dirMS_041712_NAR_50mM_minus2.10422.10422.3	3	10.67	0	2.62E+05		(R)TFIAIKPI	(R)T F/I A I/K/P D G V Q R(G)		126.87	448.923	1344.763	-0.009	-6.7	8.41	6640.6	8.25	HUMAN	C9K028	Nucleoside diphosphate kinase A (Fragment)
8988	dirMS_041712_NAR_60mM_minus.10812.10812.3	3	10.67	1	1.60E+05		(K)GITEQQI	(K)G I|T E/Q Q K E G L/E I V/K(M)		120.13	524.623	1571.864	-0.0095	-6	4.79	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
8989	dirMS_041712_NAR_60mM_minus.14110.14110.3	3	10.67	0	3.65E+05		(K)QLPLVKI	(K)Q L/P L/V K/P Y L R(S)		138.22	409.59	1226.762	-0.0065	-5.3	9.99	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
8990	dirMS_041712_NAR_120mM_plus.8219.8219.3	3	10.67	1	7.73E+05		(R)SQYEQL	(R)S Q|Y/E Q L/A E Q N R K(D)		96.67	498.5821	1493.734	-0.0025	-1.7	5.86	59054.3	5.14	HUMAN	P13645	Keratin, type I cytoskeletal 10
8991	dirMS_041712_NAR_20mM_plus.18614.18614.2	2	10.67	0	1.68E+05	M332m	(R)IVSQLLT	(R)I V/S Q\L/L/T/L/m D G L/K(Q)	m:Oxidized methionine	199.43	723.9145	1430.829	15.993	-1.3	5.84	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
8992	dirMS_041712_NAR_20mM_plus.8132.8132.2	2	10.67	0	8.20E+04		(R)AAPGAE	(R)A A/P/G A/E F A|P N/K(R)		125.72	536.7749	1072.542	0.0003	0.3	6.05	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
8993	dirMS_041712_NAR_30mM_plus2.20156.20156.2	2	10.67	0	1.46E+05		(K)TVALWD	(K)T V|A|L W/D/L R(N)		159.07	487.2769	973.547	0	0	5.5	19598	4.45	HUMAN	B4DRT0	Histone-binding protein RBBP4
8994	dirMS_041712_NAR_30mM_plus2.8447.8447.2	2	10.67	0	9.63E+05		(K)LYEQLSG	(K)L/Y|E\Q L S/G/K(-)		99.03	469.2488	937.499	-0.0086	-9.2	6	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
8995	dirMS_041712_NAR_40mM_plus2.11055.11055.3	3	10.67	0	6.82E+04		(R)LLELGPK	(R)L/L/E/L/G P\K P E V\A Q Q T R(K)		131.02	560.318	1678.949	-0.0092	-5.5	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
8996	dirMS_041712_NAR_40mM_plus2.18970.18970.3	3	10.67	0	3.71E+05		(R)DYLHLPI	(R)D Y L H L\P P E\I|V|P A/T L R(R)		177.78	578.6565	1733.959	-0.0035	-2	5.32	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
8997	dirMS_041712_NAR_50mM_plus2.16923.16923.3	3	10.67	1	3.41E+05		(K)QLDDLK	(K)Q L/D/D/L K/V E/L S Q L R(V)		156.88	519.6261	1556.864	-0.0005	-0.3	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
8998	dirMS_041712_NAR_50mM_plus2.9450.9471.3	3	10.67	0	7.71E+05		(R)DNIQGIT	(R)D N/I/Q/G I/T/K/P A I R(R)		117.22	442.5902	1325.754	0.0025	1.9	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
8999	dirMS_041712_NAR_60mM_plus.12215.12215.3	3	10.67	0	2.53E+05		(R)ITADGAI	(R)I/T/A D G/A H/F E/L R(L)		120.72	410.553	1229.627	0.0171	13.9	5.32	105388.1	9.49	HUMAN	J3QK89	Calcium homeostasis endoplasmic reticulum protein
9000	dirMS_041712_NAR_60mM_plus.14490.14490.3	3	10.67	1	9.50E+05		(K)TKEVYEL	(K)T|K E V Y E\L|L/D/S/P G K(V)		131.9	493.5959	1478.774	-0.0006	-0.4	4.68	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
9001	dirMS_041712_NAR_60mM_plus.19107.19107.3	3	10.67	1	3.50E+04		(K)SELVAM	(K)S E/L/V/A M/L E E E E/L R K(A)		158.07	559.288	1675.857	-0.0077	-4.6	4.32	18679.2	5.61	HUMAN	B4DWW1	ADP-ribosylation factor-like protein 1
9002	dirMS_041712_NAR_60mM_plus.4783.4783.3	3	10.67	1	1.78E+06		(R)AAEEED	(R)A A|E/E/E D/E A/D/P K/R(Q)		80	453.872	1359.602	-0.0008	-0.6	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
9003	dirMS_041712_NAR_60mM_plus.6566.6566.3	3	10.67	0	2.19E+05		(R)CPPGVV	(R)C P/P\G V\V|P A/C/H N S K(D)	C:Carbamidomethylation	92.8	474.8947	1422.662	0.0079	5.5	8.76	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
9004	dirMS_041712_NAR_120mM_minus.11041.11041.3	3	10.66	0	6.08E+05		(R)ISNRPAF	(R)I/S/N R P A F M|P/S E G K(M)		113.93	478.5776	1433.721	-0.0023	-1.6	8.75	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
9005	dirMS_041712_NAR_20mM_minus.13746.13746.2	2	10.66	0	3.96E+05		(K)LGGSAV	(K)L G G S/A/V|I/S L E G K|P L(-)		188.67	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
9006	dirMS_041712_NAR_30mM_minus2.18759.18802.2	2	10.66	0	9.20E+04		(K)GFGGIG	(K)G F|G/G\I/G G I L/R(Y)		156.77	473.7762	946.547	-0.0018	-1.9	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
9007	dirMS_041712_NAR_50mM_minus2.10646.10646.3	3	10.66	0	1.27E+05		(R)IMLFTNI	(R)I M|L|F/T/N E D N/P/H G N D S A K(A)		129.08	634.9586	1902.865	-0.0038	-2	4.54	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
9008	dirMS_041712_NAR_60mM_minus.19072.19072.3	3	10.66	0	5.77E+05		(R)LGFHLPI	(R)L G F H L P\L|E|V/A/Y Q R(G)		168.63	514.9512	1542.843	-0.0037	-2.4	6.75	533778	5.74	HUMAN	Q15149	Plectin
9009	dirMS_041712_NAR_20mM_plus.10709.10709.3	3	10.66	0	7.11E+04	M175m	(R)LEQGQA	(R)L E Q G Q A\I/D/D/L/m/P A Q K(-)	m:Oxidized methionine	146.07	558.2795	1656.826	15.9978	1.7	4.03	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
9010	dirMS_041712_NAR_20mM_plus.12827.12827.2	2	10.66	0	1.24E+05	M137m	(K)IEVIEImT	(K)I E|V|I/E/I m T D R(G)	m:Oxidized methionine	160.98	617.8225	1218.64	15.9979	2.4	4.14	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
9011	dirMS_041712_NAR_30mM_plus2.14818.14964.2	2	10.66	0	7.38E+05		(K)APAMFN	(K)A/P|A|M/F N I/R(N)		131.03	460.2391	919.482	-0.0109	-11.9	9.79	25835.7	9.86	HUMAN	D6RG13	40S ribosomal protein S3a (Fragment)
9012	dirMS_041712_NAR_30mM_plus2.16905.16905.2	2	10.66	0	2.05E+05		(R)VFSGLVS	(R)V/F|S/G L\V S\T G L K(V)		141.95	554.322	1107.641	-0.0041	-3.7	8.72	96306.4	6.41	HUMAN	P13639	Elongation factor 2
9013	dirMS_041712_NAR_30mM_plus2.19830.19830.2	2	10.66	0	4.57E+05		(K)NLIDAG	(K)N L|I|D/A/G V/D\A L R(V)		156.82	578.8183	1156.632	-0.0027	-2.4	4.21	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
9014	dirMS_041712_NAR_50mM_plus2.18441.18458.3	3	10.66	1	3.49E+05		(R)GDSVIV	(R)G D/S/V/I/V V L R N P L I A\G/K(-)		165.37	550.9999	1650.99	-0.005	-3	8.75	6144.3	10.23	HUMAN	K7EJB5	Small nuclear ribonucleoprotein Sm D2
9015	dirMS_041712_NAR_50mM_plus2.6451.6451.3	3	10.66	1	3.43E+04		(K)AEAGPE	(K)A E|A/G\P E G V/A P A/P E G E K K(Q)		98.62	546.2803	1636.818	0.0087	5.3	4.49	105005	5.57	HUMAN	E9PL22	Hypoxia up-regulated protein 1
9016	dirMS_041712_NAR_60mM_plus.11413.11413.3	3	10.66	1	4.52E+05		(K)TCVFEKE	(K)T C|V/F E/K E N D|P S/V/M R(S)	C:Carbamidomethylation	117.33	571.2635	1711.778	-0.0019	-1.1	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
9017	dirMS_041712_NAR_60mM_plus.13352.13457.3	3	10.66	1	6.19E+06		(R)VVDLMA	(R)V/V|D/L M/A|H M A S K E(-)		127.22	444.2219	1330.649	0.0018	1.3	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
9018	dirMS_041712_NAR_60mM_plus.16378.16378.3	3	10.66	0	9.05E+05		(K)MTHLPE	(K)M T H L\P E\L/D|T|L/S/S E R(A)		142.02	543.6023	1628.795	-0.0025	-1.5	4.65	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
9019	dirMS_041712_NAR_60mM_plus.17215.17215.3	3	10.66	0	1.05E+06		(R)QIFHPE	(R)Q I F H P/E\Q/L I/T/G K(E)		146.92	470.9225	1410.774	-0.021	-14.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
9020	dirMS_041712_NAR_60mM_plus.9120.9120.2	2	10.66	1	4.14E+05		(R)ALSTGEI	(R)A L/S/T G E K\G/F G Y/K(G)		105.68	629.3259	1257.647	-0.0029	-2.3	8.54	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
9021	dirMS_041712_NAR_30mM_minus2.6989.6989.2	2	10.65	0	1.47E+05		(K)ISTVVSS	(K)I/S\T V/V/S/S/K(E)		92.48	410.7405	820.477	-0.0037	-4.6	8.75	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
9022	dirMS_041712_NAR_30mM_minus2.8606.8606.2	2	10.65	0	4.89E+05	M281m	(R)AEAESm	(R)A E|A/E|S m/Y Q I K(Y)	m:Oxidized methionine	101.12	593.2765	1169.551	15.995	0.1	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
9023	dirMS_041712_NAR_50mM_minus2.15512.15512.3	3	10.65	1	3.81E+05		(K)GADFLV	(K)G A/D F/L/V/T E/V E N G G S L G S K K(G)		155.77	636.662	1907.971	0.0005	0.3	4.68	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
9024	dirMS_041712_NAR_50mM_minus2.16057.16057.3	3	10.65	0	2.36E+05		(K)AQDGSH	(K)A Q|D/G S H/P L S L Q D L I E/K(V)		159.08	584.3049	1750.897	0.0031	1.8	4.54	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
9025	dirMS_041712_NAR_20mM_plus.17494.17536.2	2	10.65	0	1.59E+05		(K)DVDLEFI	(K)D V|D|L|E/F L A K(M)		192.67	525.2795	1049.551	0.0004	0.4	4.03	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
9026	dirMS_041712_NAR_20mM_plus.7902.7902.2	2	10.65	0	1.23E+05		(K)VEIIAND	(K)V E\I\I|A/N D/Q G N R(T)		124.53	614.8177	1228.628	0.0001	0.1	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
9027	dirMS_041712_NAR_30mM_plus2.11162.11162.2	2	10.65	0	2.60E+05		(K)IINNTEN	(K)I/I|N N/T/E N L/V R(E)		111.5	593.3333	1185.659	0.0007	0.6	6	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
9028	dirMS_041712_NAR_30mM_plus2.13787.13807.2	2	10.65	0	9.40E+05		(R)LPLQDV	(R)L/P|L/Q D V Y/K(I)		125.37	488.28	975.551	0.0018	1.8	5.83	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
9029	dirMS_041712_NAR_30mM_plus2.13866.13890.2	2	10.65	0	4.24E+05		(K)SPAQILII	(K)S/P|A|Q|I/L I/R(F)		125.53	449.2784	897.552	-0.0021	-2.3	9.47	23434.6	5.78	HUMAN	G3V1C1	1,5-anhydro-D-fructose reductase
9030	dirMS_041712_NAR_40mM_plus2.11800.11800.3	3	10.65	1	2.71E+05		(R)IVAPGK	(R)I V|A P G K G I/L A/A/D E S T/G S I/A K(R)		135.43	633.3568	1898.059	-0.0035	-1.8	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
9031	dirMS_041712_NAR_40mM_plus2.18553.18553.3	3	10.65	0	4.72E+04		(R)NEVSFVI	(R)N E/V/S/F/V I H N L/P\V L A K(M)		175.93	560.6533	1679.948	-0.0026	-1.5	6.75	35663.7	5.91	HUMAN	B4DWK0	Selenide, water dikinase 1
9032	dirMS_041712_NAR_50mM_plus2.13098.13246.3	3	10.65	0	7.93E+05		(R)VLHVSEI	(R)V L H V\S\E\N\P\V|P/L T V R(V)		137.38	520.6339	1559.89	-0.0033	-2.1	6.72	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
9033	dirMS_041712_NAR_50mM_plus2.15434.15435.3	3	10.65	1	7.09E+05		(R)GFPTIYF	(R)G F|P T I/Y/F S/P A N K K(L)		149.02	490.5973	1469.779	-0.0014	-0.9	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
9034	dirMS_041712_NAR_50mM_plus2.9914.9914.3	3	10.65	1	1.41E+05		(K)TCVFEKE	(K)T C|V|F E K E N D/P/S V M R(S)	C:Carbamidomethylation	119.48	571.2629	1711.778	-0.0037	-2.1	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
9035	dirMS_041712_NAR_60mM_plus.14270.14270.3	3	10.65	1	6.64E+05		(K)WKDSDI	(K)W K D S D E|A|D|L/V/L/A/K(E)		131	497.2559	1489.753	-0.0002	-0.1	4.23	20982.2	5.23	HUMAN	Q13185	Chromobox protein homolog 3
9036	dirMS_041712_NAR_60mM_plus.16321.16321.3	3	10.65	1	6.56E+05		(R)IKIGDPL	(R)I K I G D P\L/L/E D/T R(M)		141.82	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
9037	dirMS_041712_NAR_60mM_plus.18811.18811.3	3	10.65	0	7.04E+04		(R)LYDLNH	(R)L/Y/D/L N H/N E/I G E L I R(M)		155.95	566.9611	1698.881	-0.0122	-7.2	4.65	246157.8	5.73	HUMAN	O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase
9038	dirMS_041712_NAR_20mM_minus.13577.13577.2	2	10.64	0	1.38E+05		(K)DIYALISI	(K)D I|Y A/L/I/S D Q/K(H)		186.58	583.3076	1165.61	-0.002	-1.7	4.21	266161	5.68	HUMAN	E9PPU0	Epiplakin
9039	dirMS_041712_NAR_30mM_minus2.7262.7262.2	2	10.64	0	2.75E+05		(K)SAVLQE	(K)S A/V|L/Q E A R(I)		94.43	437.2408	873.479	-0.0045	-5.2	5.72	28218.2	9.35	HUMAN	F6X838	Coatomer subunit gamma-2
9040	dirMS_041712_NAR_30mM_minus2.9379.9451.2	2	10.64	0	4.42E+05		(K)SETDTSL	(K)S E|T|D/T S/L I/R(G)		105.57	511.2565	1021.516	-0.0103	-10.1	4.37	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
9041	dirMS_041712_NAR_50mM_minus2.12284.12284.3	3	10.64	0	1.00E+05		(K)IVLDNS	(K)I V/L D N/S/V/F S/E/H/R(N)		138.13	472.5813	1415.728	0.0016	1.1	5.32	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
9042	dirMS_041712_NAR_50mM_minus2.16658.16658.3	3	10.64	1	1.61E+05		(K)TVTAMI	(K)T/V|T A M/D V/V Y A L K R(Q)		162.78	489.6051	1466.804	-0.0028	-1.9	8.25	11367.1	11.36	HUMAN	P62805	Histone H4

9043	dirMS_041712_NAR_50mM_minus2.8601.8601.3	3	10.64	0	1.65E+05	M180m	(R)VVVLmG	(R)V V/V/L/m G S/T S D/L G H C E K(I)	C:Carbamidomethylation m:Oxid	117.55	583.2829	1731.84	15.9937	-0.7	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
9044	dirMS_041712_NAR_60mM_minus.17607.17607.3	3	10.64	1	4.27E+06		(R)VSFELFA	(R)V/S|F/E L\F A D K V/P K(T)		157.75	460.5911	1379.757	0.0018	1.3	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
9045	dirMS_041712_NAR_120mM_plus.12730.12730.2	2	10.64	0	6.79E+05		(K)HLSVND	(K)H/L|S V/N D/L|P V G R(S)		119.32	603.8321	1206.659	-0.002	-1.7	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
9046	dirMS_041712_NAR_120mM_plus.6810.6924.3	3	10.64	0	5.07E+05		(K)SQFSDKI	(K)S Q|F S D/K/P V/Q D R(G)		89.58	436.2209	1306.639	0.0095	7.3	5.68	13194	9.99	HUMAN	E9PI70	Chitinase domain-containing protein 1 (Fragment)
9047	dirMS_041712_NAR_20mM_plus.15841.15859.2	2	10.64	0	1.24E+05		(R)GTPLISP	(R)G T|P\L|I/S P L I K(W)		180.95	519.8306	1038.656	-0.0018	-1.8	8.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
9048	dirMS_041712_NAR_20mM_plus.18659.18659.2	2	10.64	0	2.88E+05		(K)TAVETA	(K)T A V|E/T\A/V L|L L R(I)		199.92	593.3625	1185.72	-0.0024	-2	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
9049	dirMS_041712_NAR_30mM_plus2.10300.10300.2	2	10.64	0	2.69E+05		(K)LVIEEAE	(K)L/V|I/E E A E R(S)		107.23	479.7648	958.52	0.0019	2	4.25	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
9050	dirMS_041712_NAR_30mM_plus2.6120.6120.2	2	10.64	0	4.34E+05	M29m	(K)ELGTVm	(K)E L/G/T/V m/R(M)	m:Oxidized methionine	86.22	411.2138	805.424	15.9967	2.1	6.1	16439	4.08	HUMAN	C9J7T9	Troponin C type 2 (Fast), isoform CRA_a
9051	dirMS_041712_NAR_40mM_plus2.19051.19051.3	3	10.64	0	2.96E+05		(R)DYLHLPI	(R)D Y L H\L\P\P E\I|V|P/A T L R(R)		178.12	578.6565	1733.959	-0.0035	-2	5.32	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
9052	dirMS_041712_NAR_50mM_plus2.12522.12522.3	3	10.64	1	2.64E+05		(R)SVELNPT	(R)S V/E/L/N/P T Q K D L V L K(I)		133.58	528.6368	1583.9	-0.0045	-2.8	5.79	198852.6	5.95	HUMAN	A6NKT7	RanBP2-like and GRIP domain-containing protein 3
9053	dirMS_041712_NAR_50mM_plus2.22262.22262.3	3	10.64	1	1.35E+06		(K)EGGLGP	(K)E G G L/G|P/L N/I P L L A D V T R R(L)		191	631.029	1891.076	-0.0035	-1.9	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
9054	dirMS_041712_NAR_50mM_plus2.9585.9622.3	3	10.64	0	7.85E+05		(K)YIQQTKI	(K)Y/I/Q/Q T K/P L/T L E R(T)		117.05	497.2822	1489.837	-0.0053	-3.5	8.59	26283.8	8.96	HUMAN	O43809	Cleavage and polyadenylation specificity factor subunit 5
9055	dirMS_041712_NAR_60mM_plus.7692.7692.3	3	10.64	0	9.11E+05		(K)LFQECCI	(K)L/F|Q/E C C/P/H S T D R(V)	C:Carbamidomethylation	98.37	517.2234	1549.652	0.0034	2.2	5.32	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
9056	dirMS_041712_NAR_120mM_minus.17087.17087.3	3	10.63	1	7.58E+04		(R)IRGETLG	(R)I R G E T\L G\I|I|G L G R(V)		148.32	452.2751	1354.816	-0.0058	-4.3	9.6	20631.5	6.98	HUMAN	D6RAX2	C-terminal-binding protein 1 (Fragment)
9057	dirMS_041712_NAR_30mM_minus2.14846.14905.2	2	10.63	0	7.08E+04		(R)MSIPEAI	(R)M/S/I/P E A L/R(R)		134.48	458.753	916.492	0.0067	7.3	5.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
9058	dirMS_041712_NAR_30mM_minus2.15969.15969.2	2	10.63	0	3.18E+04		(K)NLILVVR	(K)N L|I/L/V V/R(G)		139.73	413.7746	826.551	-0.009	-10.9	9.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
9059	dirMS_041712_NAR_50mM_minus2.15315.15315.3	3	10.63	0	5.45E+05		(R)DGLAFN	(R)D G L|A F/N A/L/I/H R(H)		155.45	409.5594	1226.664	-0.0004	-0.3	6.74	146974	5.55	HUMAN	C9JRP8	Spectrin beta chain, non-erythrocytic 4
9060	dirMS_041712_NAR_60mM_minus.8748.8749.3	3	10.63	1	2.00E+06	M227m M	(R)mQKEIT.	(R)m Q K E I\T\A\L|A|P S T m K(I)	m:Oxidized methionine	109.63	527.6044	1548.812	31.9862	-2.3	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
9061	dirMS_041712_NAR_120mM_plus.4076.4305.3	3	10.63	1	1.73E+07	M310m	(R)TKTEISE	(R)T K\T E\I|S|E/m/N R(N)	m:Oxidized methionine	69.83	408.8687	1208.594	15.9976	2.2	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
9062	dirMS_041712_NAR_20mM_plus.13192.13192.2	2	10.63	0	5.96E+04		(R)LAPDYD.	(R)L A/P D/Y/D A L D\V A N/K(I)		162.93	702.8524	1404.7	-0.003	-2.1	3.93	22029.9	10.62	HUMAN	A8MUS3	60S ribosomal protein L23a
9063	dirMS_041712_NAR_20mM_plus.14940.14940.2	2	10.63	0	1.26E+05		(R)LLDAQLS	(R)L L\D/A/Q|L|S\T G G I/V/D|P S K(S)		174.67	807.4389	1613.874	-0.004	-2.5	4.21	533778	5.74	HUMAN	Q15149	Plectin
9064	dirMS_041712_NAR_20mM_plus.17518.17518.2	2	10.63	0	3.36E+04		(R)YLTVAA	(R)Y/L|T V/A A\V F R(G)		192.65	520.3009	1039.593	0.001	1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
9065	dirMS_041712_NAR_20mM_plus.17824.17824.2	2	10.63	0	1.51E+05		(R)TVQSLEI	(R)T V|Q\S/L/E/I D L/D/S M R(N)		194.8	753.8776	1506.747	0.0011	0.7	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9066	dirMS_041712_NAR_20mM_plus.7006.7006.2	2	10.63	0	4.30E+05		(R)IQEAGTI	(R)I Q|E|A G T/E V V K(A)		115.35	537.2946	1073.584	-0.0018	-1.7	4.53	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
9067	dirMS_041712_NAR_20mM_plus.7391.7391.2	2	10.63	0	2.86E+05		(K)TGQAPG	(K)T G Q\A|P G Y/S/Y/T A A N K(N)		119.52	714.8394	1428.675	-0.0039	-2.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
9068	dirMS_041712_NAR_20mM_plus.9868.9868.2	2	10.63	0	5.34E+05		(R)ISVYYNE	(R)I/S\V/Y|Y/N E\A T G G K(Y)		138.6	651.3211	1301.637	-0.0023	-1.8	6	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
9069	dirMS_041712_NAR_30mM_plus2.19983.20242.2	2	10.63	0	2.43E+05		(K)LYNLFLK	(K)L/Y|N L/F/L K(I)		159.32	455.7738	910.54	0.0007	0.7	8.59	41666	7.73	HUMAN	E9PDQ8	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial
9070	dirMS_041712_NAR_30mM_plus2.8451.8573.2	2	10.63	0	8.32E+05		(R)FSELTAE	(R)F/S|E\L/T A/E K(L)		99.32	462.7408	924.467	0.007	7.6	4.53	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
9071	dirMS_041712_NAR_30mM_plus2.9127.9127.2	2	10.63	0	6.30E+05		(R)SSQSSS	(R)S S Q/S S/S Q/Q/F S G|I/G R(S)		101.03	728.345	1455.682	0.0005	0.3	9.47	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
9072	dirMS_041712_NAR_50mM_plus2.18008.18008.3	3	10.63	0	7.29E+05		(K)TVSGVN	(K)T V|S/G V/N G P L V/I/L D H V K(V)		161.93	549.9834	1647.943	-0.0072	-4.4	6.41	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
9073	dirMS_041712_NAR_60mM_plus.14724.14724.3	3	10.63	1	5.53E+05		(R)ELAVQIY	(R)E L A/V/Q I/Y E E/A R K(F)		133.62	483.5949	1448.774	-0.0042	-2.9	4.79	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
9074	dirMS_041712_NAR_60mM_plus.19917.19917.3	3	10.63	1	1.53E+05		(R)GMLRED	(R)G M/L/R E D/A\V|L/E Y L K(I)		163.87	512.9411	1536.809	-0.0003	-0.2	4.68	67933	6.08	HUMAN	P26038	Moesin
9075	dirMS_041712_NAR_60mM_plus.7182.7182.3	3	10.63	1	4.98E+05		(K)TIIQNPT	(K)T I|I/Q/N P T/D/Q Q K K(D)		95.72	471.9324	1413.77	0.013	9.2	8.26	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
9076	dirMS_041712_NAR_120mM_minus.4517.4517.2	2	10.62	0	7.35E+05		(R)HSDGNL	(R)H/S|D|G N L\C\V K(V)	C:Carbamidomethylation	73.95	515.2423	1029.478	-0.0009	-0.9	6.74	7781.8	6.82	HUMAN	E9PE20	Signal recognition particle 9 kDa protein
9077	dirMS_041712_NAR_30mM_minus2.11343.11399.2	2	10.62	0	2.19E+05		(K)ATAVMI	(K)A T\A|V|M/P D/G Q F K(D)		115.47	582.7922	1164.572	0.0054	4.6	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
9078	dirMS_041712_NAR_30mM_minus2.15791.15791.2	2	10.62	0	1.25E+05		(R)TINEVEN	(R)T I/N\E|V/E N Q I L/T R(D)		139.6	715.3834	1429.765	-0.005	-3.5	4.53	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
9079	dirMS_041712_NAR_30mM_minus2.17616.17616.2	2	10.62	0	1.71E+05		(K)GFLIDGY	(K)G F/L|I/D G Y P R(E)		150.27	519.2752	1037.542	0.0017	1.6	5.83	15567.5	8.13	HUMAN	H0Y4J6	Adenylate kinase isoenzyme 1 (Fragment)
9080	dirMS_041712_NAR_40mM_minus2.14053.14053.3	3	10.62	0	5.38E+05		(R)IHFPLAT	(R)I H F P L\A\T|Y A/P V I S A/E K(A)		167.63	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
9081	dirMS_041712_NAR_50mM_minus2.8335.8335.3	3	10.62	1	7.12E+04		(K)NVSEELI	(K)N V|S/E E L D R T/P P E V S K(K)		115.6	567.289	1699.85	0.0027	1.6	4.41	136658.9	5.13	HUMAN	Q15393	Splicing factor 3B subunit 3
9082	dirMS_041712_NAR_60mM_minus.10138.10138.3	3	10.62	1	5.93E+03		(R)VEVGKD	(R)V/E/V/G K D Q E F/T V D T R(G)		116.62	541.6051	1622.802	-0.0013	-0.8	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
9083	dirMS_041712_NAR_60mM_minus.14432.14432.3	3	10.62	0	1.71E+05		(R)GEAHLA	(R)G E A\H L A V N/D F/E/L/A/R(A)		139.9	514.591	1541.771	-0.0122	-7.9	4.65	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
9084	dirMS_041712_NAR_120mM_plus.13258.13325.2	2	10.62	0	8.76E+04		(R)DYLHYIR	(R)D Y|L/H/Y/I/R(K)		122.77	490.2536	979.5	0.0003	0.3	6.74	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
9085	dirMS_041712_NAR_120mM_plus.7040.7040.3	3	10.62	0	4.26E+05		(K)SQFSDKI	(K)S\Q|F S D/K/P V/Q D R(G)		90.13	436.2209	1306.639	0.0095	7.3	5.68	13194	9.99	HUMAN	E9PI70	Chitinase domain-containing protein 1 (Fragment)
9086	dirMS_041712_NAR_120mM_plus.7923.7923.4	4	10.62	0	6.18E+04		(K)AVVTHS	(K)A V|V/T/H/S\S G N H G Q A L T Y A A/K(L)		95.07	478.7463	1911.967	-0.0038	-2	8.65	11029.5	9.89	HUMAN	I3L3N0	Serine racemase (Fragment)
9087	dirMS_041712_NAR_20mM_plus.17448.17448.3	3	10.62	0	2.34E+05	M90m	(R)LFVGNLI	(R)L F V G N L/P\P D|I/T E/E\E m R(K)	m:Oxidized methionine	192.3	625.9762	1859.921	15.9933	-0.9	4	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
9088	dirMS_041712_NAR_20mM_plus.18174.18174.2	2	10.62	0	1.70E+05		(R)LTGQLFI	(R)L T/G/Q|L/F/L G G S I V K(G)		197.02	666.8962	1332.789	-0.0034	-2.6	8.75	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
9089	dirMS_041712_NAR_20mM_plus.18615.18615.2	2	10.62	0	2.69E+05		(K)LAVEALS	(K)L A\V E A\L/S S/L/D/G D L A/G R(Y)		200.43	793.9214	1586.838	-0.0029	-1.8	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
9090	dirMS_041712_NAR_50mM_plus2.11445.11481.3	3	10.62	0	3.42E+05		(K)YTVQDE	(K)Y/T|V/Q/D E S H S E W/V/S C V R(F)	C:Carbamidomethylation	127.98	661.2946	1981.871	-0.0016	-0.8	4.65	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
9091	dirMS_041712_NAR_50mM_plus2.19855.19855.3	3	10.62	0	5.26E+04		(K)GLCLLEC	(K)G L/C/L/L/E Q I D S F K/P P Q R(S)	C:Carbamidomethylation	172.9	634.3344	1900.995	-0.0063	-3.3	6.07	45536.8	9.03	HUMAN	B7Z1K2	HBS1-like protein
9092	dirMS_041712_NAR_50mM_plus2.20075.20075.3	3	10.62	0	2.78E+05		(R)LQSLPFA	(R)L Q|S L/P F A L T H L/N L K(A)		173.85	532.3178	1594.931	0.0073	4.6	8.76	175851.7	5.01	HUMAN	Q14160	Protein scribble homolog
9093	dirMS_041712_NAR_20mM_minus.8339.8339.2	2	10.61	0	5.90E+04	M1015m	(R)LDQPmT	(R)L D/Q/P/m T E I/V/S R(V)	m:Oxidized methionine	133	652.8286	1288.657	15.9934	-1.2	4.37	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
9094	dirMS_041712_NAR_30mM_minus2.11251.11251.2	2	10.61	0	3.89E+05		(R)NTDEM	(R)N T|D/E|M V/E/L R(I)		115.05	553.7611	1106.515	0.0003	0.2	4.14	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
9095	dirMS_041712_NAR_30mM_minus2.11326.11390.2	2	10.61	0	5.95E+05		(R)ELVALCI	(R)E L|V/A/L/C R(S)	C:Carbamidomethylation	115.38	430.7364	860.466	-0.0003	-0.4	6.1	266161	5.68	HUMAN	E9PPU0	Epiplakin
9096	dirMS_041712_NAR_30mM_minus2.16658.16658.2	2	10.61	0	2.71E+05	M2243m	(K)mSIYQA	(K)m/S|I|Y Q/A M W|K(G)	m:Oxidized methionine	144.3	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
9097	dirMS_041712_NAR_30mM_minus2.7461.7553.2	2	10.61	0	8.37E+05		(R)QAFPNT	(R)Q A|F|P N/T N/R(W)		95.65	474.2403	947.469	0.004	4.2	9.75	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
9098	dirMS_041712_NAR_30mM_minus2.7935.7935.2	2	10.61	0	2.38E+06	M189m	(K)LTGmAF	(K)L/T/G/m A F R(V)	m:Oxidized methionine	97.77	406.2108	795.418	15.9962	1.5	9.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
9099	dirMS_041712_NAR_60mM_minus.17318.17318.3	3	10.61	0	3.22E+05		(K)GSDHSA	(K)G S D H\S A S L\E|P G\E/L/A/E L V R(S)		156.83	622.9764	1866.919	-0.0045	-2.4	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
9100	dirMS_041712_NAR_60mM_minus.9092.9092.3	3	10.61	1	1.62E+05	M232m M	(R)MSmKE	(R)M S m K E V/D\E\Q|m|L/N V Q/N K(N)	m:Oxidized methionine	110.57	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
9101	dirMS_041712_NAR_20mM_plus.18959.18959.3	3	10.61	0	1.74E+05		(K)TLETQS	(K)T L E T Q S A\L|G/P/A L Q/A A F K(L)		202.38	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
9102	dirMS_041712_NAR_30mM_plus2.13721.13760.2	2	10.61	0	2.55E+05		(K)GGKPEP	(K)G G K\P E\P P A\M|P Q|P\V|P T\A(-)		125.03	787.4049	1573.804	-0.0018	-1.1	6	25541.5	9.92	HUMAN	E9PL09	40S ribosomal protein S3
9103	dirMS_041712_NAR_30mM_plus2.14350.14350.2	2	10.61	0	2.16E+05		(K)ASEGPA	(K)A S\E/G/P A F/F/P G/R(C)		127.95	568.2831	1135.553	0.0058	5.1	6.05	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
9104	dirMS_041712_NAR_30mM_plus2.16109.16109.2	2	10.61	0	3.24E+05		(R)MGPNIY	(R)M/G|P N/I/Y E/L/R(T)		136.63	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
9105	dirMS_041712_NAR_30mM_plus2.7178.7178.2	2	10.61	0	2.83E+05		(K)ALLQSS	(K)A L/L/Q/S S/A/S R(K)		91.82	466.7618	932.516	0.0004	0.4	9.79	44128.4	6.13	HUMAN	Q9UQ80	Proliferation-associated protein 2G4
9106	dirMS_041712_NAR_40mM_plus2.17422.17422.3	3	10.61	0	3.97E+05		(R)DVCTELI	(R)D V|C/T/E L L/P L I K P Q G R(V)	C:Carbamidomethylation	169.52	580.3213	1738.952	-0.0027	-1.5	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
9107	dirMS_041712_NAR_40mM_plus2.18197.18197.3	3	10.61	0	1.04E+05		(K)VLSLPKP	(K)V L/S\L/P K P T I\I|L/S/A Y Q R(K)		173.45	600.3613	1799.079	-0.0096	-5.3	9.99	80080.5	5.54	HUMAN	J3KMX1	Nuclear pore complex protein Nup88 (Fragment)
9108	dirMS_041712_NAR_60mM_plus.15206.15206.3	3	10.61	1	2.48E+05		(-)MKVELC	(-)M K V E\L\C/S/F/S/G/Y/K(I)	C:Carbamidomethylation	136.28	483.5686	1448.691	0	0	8.26	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
9109	dirMS_041712_NAR_60mM_plus.6401.6401.2	2	10.61	1	1.56E+06		(K)DSYVGD	(K)D/S Y/V|G/D\E A Q/S K R(G)		91.98	677.8149	1354.623	-0.0008	-0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
9110	dirMS_041712_NAR_120mM_minus.11725.11785.3	3	10.6	0	6.15E+05		(R)STYYWP	(R)S/T/Y/Y/W/P R P R(R)		118.05	409.2126	1225.611	0.012	9.8	9.98	13152.8	4.23	HUMAN	A1L429	G antigen 12B/C/D/E
9111	dirMS_041712_NAR_120mM_minus.16683.16683.3	3	10.6	0	5.65E+05		(R)EHALLA	(R)E H\A\L L|A/Y/T/L/G V/K(Q)		145.5	438.9186	1314.742	-0.0004	-0.3	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
9112	dirMS_041712_NAR_20mM_minus.11859.11859.2	2	10.6	0	1.25E+05	M98m	(R)TLTIVDT	(R)T L/T I/V/D/T/G I G m T K(A)	m:Oxidized methionine	167.03	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
9113	dirMS_041712_NAR_30mM_minus2.14883.14883.2	2	10.6	0	2.44E+05		(K)IDIIPNP	(K)I D I|I|P/N P Q E R(T)		134.87	597.8249	1194.648	-0.0052	-4.3	4.37	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
9114	dirMS_041712_NAR_50mM_minus2.10309.10309.3	3	10.6	0	1.46E+05		(K)VGSLDN	(K)V/G|S L/D N V/G H/L/P/A G G A V K(I)		126.9	530.9592	1590.86	0.0032	2	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
9115	dirMS_041712_NAR_50mM_minus2.17235.17235.3	3	10.6	0	1.30E+05	M195m	(R)LHFFmP	(R)L H F F m\P G/F/A/P L T/S/R(G)	m:Oxidized methionine	165.65	546.2872	1620.835	16.0115	10.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
9116	dirMS_041712_NAR_50mM_minus2.8957.8957.3	3	10.6	1	1.16E+05	M88m	(K)DVDEAY	(K)D V|D/E A Y/m N K V\E L E/S R(L)	m:Oxidized methionine	118.62	605.2817	1797.832	15.9982	1.8	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
9117	dirMS_041712_NAR_120mM_plus.8883.8883.2	2	10.6	0	6.76E+05		(K)HFVALS	(K)H|F|V|A L/S T/N T T K(V)		99.33	609.8311	1218.648	0.0072	5.9	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
9118	dirMS_041712_NAR_20mM_plus.8669.8669.2	2	10.6	0	2.94E+05		(K)DVNQQI	(K)D V|N\Q|Q E F V/R(A)		129.48	567.7865	1134.554	0.0119	10.5	4.37	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
9119	dirMS_041712_NAR_30mM_plus2.12435.12435.2	2	10.6	0	4.70E+05		(R)QGVDAI	(R)Q G V|D/A/D I/N/G L/R(Q)		118.08	579.2997	1157.591	0.0012	1	4.21	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
9120	dirMS_041712_NAR_30mM_plus2.19280.19280.2	2	10.6	0	2.85E+05		(K)TVDNFV	(K)T V|D N F|V/A L/A T G\E K(G)		154.87	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
9121	dirMS_041712_NAR_30mM_plus2.5778.5778.2	2	10.6	0	1.37E+05		(R)TVQCLSI	(R)T/V/Q/C\L S R(E)	C:Carbamidomethylation	85.03	432.2218	863.44	-0.004	-4.7	9.41	14357.1	4.94	HUMAN	H0Y4B9	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
9122	dirMS_041712_NAR_30mM_plus2.6100.6100.2	2	10.6	0	9.08E+04		(K)VTEGGE	(K)V/T/E/G/G/E/P Y R(L)		86.25	504.2397	1007.479	-0.0071	-7.1	4.53	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
9123	dirMS_041712_NAR_50mM_plus2.6088.6088.3	3	10.6	1	2.74E+04		(R)AQLGGI	(R)A Q/L/G G P E/A A/K/S D E T A A K(-)		96.15	548.6114	1643.824	-0.0039	-2.3	4.68	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
9124	dirMS_041712_NAR_50mM_plus2.8767.8767.3	3	10.6	1	2.21E+05		(K)TTSPPE	(K)T T/S|P/P/E/V S G/Y S Y E K T E R(S)		113.33	644.3093	1930.903	0.0105	5.4	4.78	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
9125	dirMS_041712_NAR_60mM_plus.10378.10378.3	3	10.6	1	6.69E+05	M86m	(K)mKEIAE	(K)m K\E I\A/E/A|Y/L/G K(T)	m:Oxidized methionine	112.17	423.5533	1252.661	15.9848	-8	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
9126	dirMS_041712_NAR_60mM_plus.12696.12696.3	3	10.6	0	5.74E+05		(K)GSYSLSH	(K)G S/Y/S L S H V|Y/T/P N D/V R(M)		123.12	565.6098	1694.813	0.0016	0.9	6.74	63566.6	6.3	HUMAN	P07686	Beta-hexosaminidase subunit beta
9127	dirMS_041712_NAR_60mM_plus.14455.14536.3	3	10.6	1	4.30E+05		(R)KMNVSI	(R)K\M N V S\P D\V/N|Y/E/E/L A/R(C)		132.12	588.9576	1764.859	-0.0003	-0.1	4.68	44608.2	4.94	HUMAN	E9PM69	26S protease regulatory subunit 6A
9128	dirMS_041712_NAR_60mM_plus.6815.6815.2	2	10.6	1	2.58E+05		(K)SLDEME	(K)S L/D/E/M E/K/Q Q/R(E)		94.13	632.3035	1263.6	-0.0001	0	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
9129	dirMS_041712_NAR_20mM_minus.9788.9788.2	2	10.59	0	3.36E+05		(K)IGGIGTV	(K)I/G|G I|G|T V/P V/G R(V)		147.47	513.3075	1025.61	-0.0025	-2.4	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
9130	dirMS_041712_NAR_30mM_minus2.20036.20036.2	2	10.59	0	1.29E+04		(K)EIIDLVLI	(K)E I/I/D/L/V L D/R(I)		168.95	543.3132	1085.62	-0.001	-0.9	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
9131	dirMS_041712_NAR_30mM_minus2.7051.7083.2	2	10.59	0	2.02E+05	M88m	(K)DVDEAY	(K)D V|D|E/A/Y m/N K(V)	m:Oxidized methionine	92.73	550.7326	1084.462	15.9964	1.3	4.03	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
9132	dirMS_041712_NAR_30mM_minus2.7858.7858.2	2	10.59	0	5.46E+05		(K)TQLAVC	(K)T Q|L|A/V C/Q Q R(I)	C:Carbamidomethylation	96.65	552.2842	1103.563	-0.0015	-1.3	9.41	9740.1	10.08	HUMAN	H0YFG2	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed (Fragment)
9133	dirMS_041712_NAR_40mM_minus2.14055.14055.3	3	10.59	0	4.48E+04		(K)LQAVEV	(K)L Q|A|V/E V/V I T/H L A P/G T K(H)		166.73	559.3273	1675.974	-0.0068	-4	6.75	16120	9.05	HUMAN	Q9Y2V2	Calcium-regulated heat stable protein 1
9134	dirMS_041712_NAR_40mM_minus2.15508.15508.3	3	10.59	1	6.58E+05		(K)LLPLVSD	(K)L L/P L/V S/D E V F/I R D V A K(V)		180.23	605.3511	1814.042	-0.0035	-1.9	4.56	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
9135	dirMS_041712_NAR_50mM_minus2.7867.7867.3	3	10.59	1	1.10E+05		(K)VLLQSKI	(K)V/L|L/Q|S K D Q I T A/G N A A R(K)		111.77	562.3158	1684.934	-0.0012	-0.7	8.72	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
9136	dirMS_041712_NAR_60mM_minus.13487.13487.3	3	10.59	2	1.16E+05		(K)DVYSKQ	(K)D V/Y S K\Q R/N/L Y E L N/R(L)		135.43	599.9744	1797.924	-0.0156	-8.7	8.5	384118.5	5.99	HUMAN	A4UGR9	Xin actin-binding repeat-containing protein 2
9137	dirMS_041712_NAR_60mM_minus.15556.15556.3	3	10.59	1	1.13E+06		(R)TIPWLEI	(R)T I/P W L/E D R V P Q K(T)		145.77	494.6084	1481.811	-0.0004	-0.3	5.74	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
9138	dirMS_041712_NAR_60mM_minus.16100.16158.3	3	10.59	1	3.83E+05		(K)NIYVLQE	(K)N I/Y|V/L/Q E L D N P G A K R(I)		150.42	577.3128	1729.923	0.0007	0.4	6.07	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
9139	dirMS_041712_NAR_60mM_minus.8980.8980.2	2	10.59	0	9.67E+05		(K)QEYDES	(K)Q\E\Y\D|E/S G P S I/V/H|R(K)		110.35	758.8539	1516.703	-0.0021	-1.4	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
9140	dirMS_041712_NAR_20mM_plus.10660.10660.2	2	10.59	0	5.11E+04	M175m	(R)LEQGQA	(R)L E Q/G Q/A/I|D D L m/P A Q K(-)	m:Oxidized methionine	146.23	836.9105	1656.826	15.9876	-4.4	4.03	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
9141	dirMS_041712_NAR_20mM_plus.13817.13817.2	2	10.59	0	5.65E+04	M33m	(R)LVQSPN	(R)L V/Q|S|P N S Y F m D V|K(C)	m:Oxidized methionine	167.07	772.3772	1527.751	15.9959	0.7	5.83	11227.9	9.22	HUMAN	C9JLI6	40S ribosomal protein S27
9142	dirMS_041712_NAR_30mM_plus2.9588.9588.2	2	10.59	0	5.53E+05		(K)EAESSPI	(K)E A|E/S/S/P F/V/E/R(L)		104.9	575.7726	1150.537	0.0004	0.4	4.25	92752.5	4.76	HUMAN	P14625	Endoplasmin
9143	dirMS_041712_NAR_40mM_plus2.17518.17518.3	3	10.59	0	2.47E+04		(R)GTEDITS	(R)G T|E/D\I/T S/P/H G I P L D\L L D R(V)		169.42	650.3372	1948.997	-0.0004	-0.2	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
9144	dirMS_041712_NAR_40mM_plus2.9103.9103.2	2	10.59	0	8.93E+04		(K)GSDFDC	(K)G S/D/F/D/C/E L R(L)	C:Carbamidomethylation	115.47	549.7296	1098.452	-0.0001	-0.1	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
9145	dirMS_041712_NAR_50mM_plus2.10435.10435.3	3	10.59	0	1.42E+05		(R)ILSKPIEV	(R)I L/S K|P I E V/Q\V/G G R(S)		122.35	465.9487	1395.832	-0.0003	-0.2	8.75	117873.5	9.45	HUMAN	Q7L014	Probable ATP-dependent RNA helicase DDX46
9146	dirMS_041712_NAR_50mM_plus2.10918.10918.3	3	10.59	1	4.68E+05		(R)ALRETLF	(R)A L R E T L|P/A/E Q D/L/T T K(N)		125.08	562.6377	1685.907	-0.0083	-4.9	4.68	26790	6.25	HUMAN	F5GX11	Proteasome subunit alpha type-1
9147	dirMS_041712_NAR_50mM_plus2.17216.17216.3	3	10.59	1	1.09E+06		(K)DNNGVI	(K)D N|N G V/I G L/L\E/P M K/K(S)		158.6	509.9448	1527.82	-0.0001	-0.1	6.07	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
9148	dirMS_041712_NAR_60mM_plus.13759.13759.3	3	10.59	1	4.71E+05		(R)KYEMFA	(R)K Y E M\F\A\Q T|L/Q Q/S R(G)		128.72	543.9389	1629.805	-0.0032	-2	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
9149	dirMS_041712_NAR_60mM_plus.18637.18637.3	3	10.59	1	6.36E+05		(R)IRIDSLS	(R)I R I D S\L S\A|Q|L S/Q L Q K(Q)		154.55	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
9150	dirMS_041712_NAR_20mM_minus.14563.14563.2	2	10.58	0	6.88E+03		(K)LAVEALS	(K)L A V E/A/L/S S L/D G\D L/A G R(Y)		200	793.922	1586.838	-0.0017	-1.1	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
9151	dirMS_041712_NAR_30mM_minus2.10161.10184.2	2	10.58	0	9.67E+05		(R)VQEVLLI	(R)V/Q|E/V/L/L|K(A)		109.13	414.7625	828.519	-0.0012	-1.5	5.97	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1

9152	dirMS_041712_NAR_30mM_minus2.13810.13810.2	2	10.58	0	2.26E+05		(K)TYSVEYL	(K)T Y/S\V|E Y L/P K(V)		128.3	550.2855	1099.567	-0.0033	-3	5.66	258215.9	5.48	HUMAN	E7EN95	Filamin-B
9153	dirMS_041712_NAR_30mM_minus2.14416.14416.2	2	10.58	0	2.40E+05		(K)CCSGAII	(K)C C|S/G/A I\I/V L/T K(S)	C:Carbamidomethylation	131.97	611.3188	1221.633	-0.0027	-2.2	8.75	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
9154	dirMS_041712_NAR_30mM_minus2.18967.18967.2	2	10.58	0	9.01E+05		(K)LAVNM	(K)L/A|V/N/M V/P F/P R(L)		158.83	572.3143	1143.634	-0.013	-11.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
9155	dirMS_041712_NAR_50mM_minus2.10501.10501.3	3	10.58	0	1.12E+05	M271m	(R)DLSYCLS	(R)D L|S Y/C/L S/G m/Y D H R(Y)	C:Carbamidomethylation m:Oxid	128.07	544.8966	1616.683	15.9921	-1.7	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
9156	dirMS_041712_NAR_50mM_minus2.12278.12278.3	3	10.58	1	1.37E+05		(R)VFDKDG	(R)V F D K\D G N/G Y/I/S/A/A E L R(H)		137.82	585.6286	1754.871	0.0005	0.3	4.56	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
9157	dirMS_041712_NAR_50mM_minus2.12884.12884.3	3	10.58	0	1.53E+05		(K)ASLASLP	(K)A S L\A S L/P P/L H V A K(L)		141.37	435.2622	1303.773	-0.0012	-0.9	8.8	141626	5.5	HUMAN	A8MY36	Dynactin subunit 1
9158	dirMS_041712_NAR_50mM_minus2.17734.17734.3	3	10.58	1	3.97E+05		(R)LKLPSIPI	(R)L K L P S I P|L\V/P V S A Q K(R)		169.73	530.669	1589.999	-0.0064	-4.1	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
9159	dirMS_041712_NAR_60mM_minus.13955.13978.3	3	10.58	1	3.86E+05		(R)SLIANLA	(R)S L|I/A N/L|A/A A N C Y K K(E)	C:Carbamidomethylation	138.28	512.9419	1536.82	-0.0091	-5.9	9.7	36978.6	6.33	HUMAN	B7Z800	Adenosine kinase
9160	dirMS_041712_NAR_60mM_minus.14948.14948.3	3	10.58	1	3.27E+05	M557m	(K)mFGIDR	(K)m/F/G I D R D A\I/A Q/A/V R(G)	m:Oxidized methionine	143.58	526.9353	1562.811	15.9806	-9.1	5.71	63448.4	7.29	HUMAN	B4E022	Transketolase
9161	dirMS_041712_NAR_120mM_plus.16053.16371.4	4	10.58	2	1.70E+06		(K)SIYGERF	(K)S I\Y/G/E R F P D E/N F K/L K(H)		138.32	461.4898	1842.939	-0.0011	-0.6	5.9	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
9162	dirMS_041712_NAR_20mM_plus.10431.10431.2	2	10.58	0	5.59E+04		(K)EVDEQM	(K)E/V/D E\Q M L/N V Q/N/K(N)		144.95	723.8487	1446.689	0.0008	0.6	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
9163	dirMS_041712_NAR_20mM_plus.11505.11505.2	2	10.58	0	1.69E+05		(R)YALYDA	(R)Y/A|L|Y/D/A T Y E/T K(E)		151.57	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
9164	dirMS_041712_NAR_20mM_plus.12315.12315.3	3	10.58	0	2.90E+05		(K)VNQIGS	(K)V N Q I G S V T E/S/I|Q A C K(L)	C:Carbamidomethylation	157.67	545.2781	1633.821	-0.0016	-1	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
9165	dirMS_041712_NAR_20mM_plus.17105.17105.3	3	10.58	2	1.42E+05	M95m	(K)LRSHmV	(K)L R S H m V|E/R L C E/R(K)	C:Carbamidomethylation m:Oxid	189.42	534.6105	1585.805	16.012	10.6	9.52	15412.9	8.93	HUMAN	H7C129	Zinc finger protein 709 (Fragment)
9166	dirMS_041712_NAR_40mM_plus2.13304.13304.3	3	10.58	0	3.27E+05		(K)LQMEAF	(K)L/Q/M E A/P H/I I V/G T P G R(V)		144.08	540.2954	1618.873	-0.0017	-1.1	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
9167	dirMS_041712_NAR_40mM_plus2.19765.19772.3	3	10.58	1	4.44E+05		(R)ILDDDTI	(R)I/L|D D D T I|I/T T L E N L K R(E)		185.12	625.0111	1873.028	-0.0089	-4.8	4.23	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
9168	dirMS_041712_NAR_50mM_plus2.13728.13728.3	3	10.58	1	8.77E+06		(R)TEMENE	(R)T E|M/E N E\F/V/L I K/K(D)		140.98	494.262	1480.772	-0.0001	-0.1	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
9169	dirMS_041712_NAR_50mM_plus2.14405.14429.3	3	10.58	1	4.03E+05		(R)AIKNDS	(R)A I K N D S V\V/A/G G G A/I/E/M E L S K(Y)		143.95	663.6812	1989.032	-0.0031	-1.5	4.68	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
9170	dirMS_041712_NAR_50mM_plus2.20228.20228.3	3	10.58	0	2.66E+05		(R)DYLHLP	(R)D Y L H L\P P E\I\V/P/A/T L R(R)		173.98	578.658	1733.959	0.001	0.6	5.32	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
9171	dirMS_041712_NAR_50mM_plus2.6791.6791.3	3	10.58	1	1.75E+05		(R)EGVLTG	(R)E/G V|L/T|G S/P E Q K E E A A K(A)		100.88	558.2837	1672.839	-0.0023	-1.4	4.49	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
9172	dirMS_041712_NAR_50mM_plus2.7271.7271.3	3	10.58	1	9.48E+03	M625m	(K)AQALRD	(K)A Q/A\L/R D N S T/m/G Y M/A/A K(K)	m:Oxidized methionine	104.12	581.944	1727.82	15.9971	1.3	8.63	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
9173	dirMS_041712_NAR_60mM_plus.12169.12169.3	3	10.58	0	1.36E+06		(K)VYNYNH	(K)V/Y|N Y/N H L M/P T R(Y)		120.25	469.8993	1407.684	-0.0004	-0.3	8.57	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
9174	dirMS_041712_NAR_60mM_plus.16440.16440.3	3	10.58	1	6.53E+05		(K)AAVEWI	(K)A/A/V/E/W F D G K D F Q G S K(L)		142.82	562.2762	1684.797	0.0175	10.4	4.56	65213.5	9.57	HUMAN	B0QYK0	Ewing sarcoma breakpoint region 1
9175	dirMS_041712_NAR_30mM_minus2.13912.13912.2	2	10.57	0	1.66E+05		(K)NVIGLQI	(K)N V|I/G L\Q|M/G\T N R(G)		129.38	601.8183	1202.631	-0.0017	-1.4	9.75	22562.2	8.8	HUMAN	P37802	Transgelin-2
9176	dirMS_041712_NAR_50mM_minus2.10964.10964.3	3	10.57	1	3.04E+06	M72m	(R)TEmENE	(R)T/E/m E N E\F V\L I/K K(D)	m:Oxidized methionine	129.87	499.5937	1480.772	15.995	0	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
9177	dirMS_041712_NAR_50mM_minus2.11847.11847.3	3	10.57	1	1.19E+05		(K)DVDEAY	(K)D V/D/E/A Y M N K V/E L E/S R(L)		135.67	599.9481	1797.832	-0.0026	-1.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
9178	dirMS_041712_NAR_50mM_minus2.14585.14585.3	3	10.57	1	1.93E+05		(R)AEGAIA	(R)A E|G A/I/A G F R D P F S G/K(Q)		151.2	508.2599	1522.765	0.0003	0.2	6.12	266161	5.68	HUMAN	E9PPU0	Epiplakin
9179	dirMS_041712_NAR_50mM_minus2.18803.18803.3	3	10.57	1	2.15E+06		(R)LIALLEVI	(R)L I|A L|L/E V/L/S Q/K R(M)		183.68	461.6289	1382.873	-0.0008	-0.6	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
9180	dirMS_041712_NAR_60mM_minus.16350.16350.3	3	10.57	1	1.27E+05	M84m	(K)ETmQSL	(K)E T/m Q/S/L N D R L A/S Y L D/R(V)	m:Oxidized methionine	150.62	643.3097	1911.923	15.9916	-1.7	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9181	dirMS_041712_NAR_60mM_minus.7283.7283.3	3	10.57	0	2.51E+06	M434m	(R)LESGmC	(R)L E|S/G m/Q N/M S I H T K(T)	m:Oxidized methionine	98.97	497.9023	1475.698	15.9942	-0.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
9182	dirMS_041712_NAR_20mM_plus.17684.17684.2	2	10.57	0	1.88E+05		(R)YISPDQL	(R)Y I|S/P D/Q L A D L Y K(S)		194.17	713.3667	1425.726	0.0001	0.1	4.21	47510.4	7.04	HUMAN	P06733	Alpha-enolase
9183	dirMS_041712_NAR_20mM_plus.7273.7273.2	2	10.57	0	2.85E+04		(R)VLEEGS	(R)V/L|E/E/G/S V E/A R(T)		118.03	544.7829	1088.558	0.0003	0.3	4.25	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
9184	dirMS_041712_NAR_30mM_plus2.16839.16839.2	2	10.57	0	4.02E+05		(K)GCSFLP	(K)G C/S/F/L/P D/P Y Q K(Q)	C:Carbamidomethylation	140.97	656.306	1311.604	0.0009	0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
9185	dirMS_041712_NAR_30mM_plus2.18848.18848.2	2	10.57	0	2.59E+05		(K)AITGFD	(K)A I|T/G F/D D P F S G K(T)		151.77	627.8052	1254.6	0.003	2.4	4.21	334221.3	6.44	HUMAN	P15924	Desmoplakin
9186	dirMS_041712_NAR_30mM_plus2.21591.21591.2	2	10.57	0	1.46E+05		(R)IITLAGP	(R)I I/T\L/A/G/P T N\A I/F K(A)		168.2	679.9016	1358.804	-0.0083	-6.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
9187	dirMS_041712_NAR_40mM_plus2.18636.18636.3	3	10.57	0	4.72E+04		(R)NEVSFV	(R)N\E|V/S/F V I/H N L P\V/L A K(M)		175.93	560.6533	1679.948	-0.0026	-1.5	6.75	35663.7	5.91	HUMAN	B4DWK0	Selenide, water dikinase 1
9188	dirMS_041712_NAR_50mM_plus2.10969.10969.3	3	10.57	1	1.34E+05		(R)LGGEVS	(R)L/G/G\E/V/S C L V/A G T K C D K(V)	C:Carbamidomethylation	125.42	565.2794	1693.825	-0.0011	-0.7	6.07	30619.5	9.34	HUMAN	H0YKF0	Electron transfer flavoprotein subunit alpha, mitochondrial (Fragment)
9189	dirMS_041712_NAR_50mM_plus2.17460.17460.3	3	10.57	0	6.06E+05		(R)IMEVID	(R)I/M/E/V/I D A I T T T A Q S H Q R(T)		160.3	638.6636	1913.975	0.0013	0.7	5.32	85815.7	7.35	HUMAN	P17858	6-phosphofructokinase, liver type
9190	dirMS_041712_NAR_60mM_plus.12032.12032.2	2	10.57	1	1.52E+06		(R)DGKLVS	(R)D/G K\L|V|S/E/S S/D V L/P K(-)		120.25	737.3869	1473.78	-0.013	-8.8	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
9191	dirMS_041712_NAR_60mM_plus.14247.14492.3	3	10.57	1	1.22E+06		(K)AVLFCLS	(K)A V|L/F/C L/S E D K/K(N)	C:Carbamidomethylation	131.62	437.2332	1309.682	0.003	2.3	6.11	22956	8.8	HUMAN	E9PK25	Cofilin-1
9192	dirMS_041712_NAR_60mM_plus.14620.14620.3	3	10.57	1	5.07E+05		(K)NKDQG	(K)N K D Q G T Y E\D/Y/V/E/G L R(V)		133.13	596.2816	1786.824	0.006	3.4	4.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
9193	dirMS_041712_NAR_60mM_plus.15361.15361.3	3	10.57	1	6.65E+04		(K)SKLTFSC	(K)S K/L T F S|C L/G/G S D N/F K(H)	C:Carbamidomethylation	137.6	554.2751	1660.8	0.0108	6.5	8.31	15014.9	3.9	HUMAN	B4DHP2	Prostaglandin E synthase 3
9194	dirMS_041712_NAR_60mM_plus.19956.19956.3	3	10.57	1	1.46E+05		(R)SELELTL	(R)S E|L/E/L/T/L G K L/E Q\V R(S)		163.83	538.9738	1614.906	0.0007	0.5	4.78	533778	5.74	HUMAN	Q15149	Plectin
9195	dirMS_041712_NAR_120mM_minus.8392.8392.3	3	10.56	1	6.76E+05		(R)LKQIEEC	(R)L/K Q/I E/E/Q/T/I/K(A)		100.15	410.5736	1229.71	-0.0037	-3	6.14	71218.8	6.3	HUMAN	A7YIJ8	Radixin
9196	dirMS_041712_NAR_50mM_minus2.10390.10390.3	3	10.56	0	1.66E+05		(K)LQAEAP	(K)L Q|A|E A P H\I/V V G T/P G R(V)		127.08	515.6179	1544.854	-0.0152	-9.8	6.75	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
9197	dirMS_041712_NAR_50mM_minus2.14464.14464.3	3	10.56	0	6.18E+04		(K)VALLLLD	(K)V A|L\L/L L D/Q G A S P H A A A K(N)		150.53	558.9883	1674.954	-0.0034	-2	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
9198	dirMS_041712_NAR_50mM_minus2.6783.6783.3	3	10.56	0	5.92E+05		(R)EATNPP	(R)E A T N/P/P/V I Q E/E K P K(K)		105.52	527.2846	1579.833	0.0066	4.2	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
9199	dirMS_041712_NAR_120mM_plus.13276.13276.4	4	10.56	1	1.43E+06		(K)SVHSSV	(K)S V H S S V/P/L/L/N S\K D/P I/D R(I)		123.27	466.7533	1863.992	-0.0009	-0.5	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
9200	dirMS_041712_NAR_20mM_plus.13983.13983.2	2	10.56	0	2.82E+05		(R)INEILSN	(R)I/N|E|I|L/S N\A L K(R)		167.63	557.8267	1114.647	-0.0005	-0.5	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
9201	dirMS_041712_NAR_20mM_plus.18226.18226.2	2	10.56	0	1.14E+04		(K)AIDLFTD	(K)A/I|D|L|F T D A I/K(L)		197.1	553.8073	1106.609	-0.0019	-1.7	4.21	18141.9	4.7	HUMAN	F6VDH7	Hsc70-interacting protein (Fragment)
9202	dirMS_041712_NAR_20mM_plus.9889.9889.2	2	10.56	0	2.36E+05		(K)VASGCLI	(K)V A/S/G/C/L\D I N S S V K(G)	C:Carbamidomethylation	139.62	675.3376	1349.673	-0.005	-3.7	5.81	56837	7.19	HUMAN	E7ETT1	Propionyl-CoA carboxylase beta chain, mitochondrial
9203	dirMS_041712_NAR_30mM_plus2.11512.11512.2	2	10.56	0	5.15E+05		(R)SGEGEV	(R)S G E|G E|V S/G L M/R(K)		114.07	561.2662	1121.526	-0.0004	-0.4	4.53	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
9204	dirMS_041712_NAR_30mM_plus2.16393.16393.2	2	10.56	0	2.71E+04		(R)GDLGIEI	(R)G D/L/G I/E/I|P A E K(V)		138.85	571.3087	1141.61	0.0002	0.2	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
9205	dirMS_041712_NAR_30mM_plus2.7038.7038.2	2	10.56	0	2.98E+05		(K)ALLQSS	(K)A L|L/Q|S S/A S/R(K)		91.87	466.7618	932.516	0.0004	0.4	9.79	44128.4	6.13	HUMAN	Q9UQ80	Proliferation-associated protein 2G4
9206	dirMS_041712_NAR_30mM_plus2.8128.8128.2	2	10.56	0	1.36E+06		(K)QGGGG	(K)Q G G/G/G/G G G/S/V/P G I E R(M)		97.17	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
9207	dirMS_041712_NAR_40mM_plus2.12015.12015.3	3	10.56	0	1.14E+04		(R)TVVSGS	(R)T V|V/S/G S C A A H S L L/I T T E G K(L)	C:Carbamidomethylation	137.22	644.3327	1930.99	-0.0067	-3.5	6.41	56825.2	9.49	HUMAN	Q9P258	Protein RCC2
9208	dirMS_041712_NAR_40mM_plus2.6086.6086.2	2	10.56	0	1.72E+04		(R)ENPYYD	(R)E N|P Y Y D/S R(V)		94.68	522.2253	1043.443	0.0005	0.4	4.37	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
9209	dirMS_041712_NAR_50mM_plus2.10743.10743.3	3	10.56	1	2.46E+06		(R)MQKEIT	(R)M Q|K E I T A|L|A/P/S T M K(I)		124.03	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
9210	dirMS_041712_NAR_50mM_plus2.20750.20750.3	3	10.56	0	2.17E+05		(K)GLEHVT	(K)G L\E H V T V D D\L|V/A E/I T/P K(G)		178.28	612.6632	1835.975	0.0001	0.1	4.31	11429.2	9.63	HUMAN	E5RHX8	Enhancer of yellow 2 transcription factor homolog
9211	dirMS_041712_NAR_50mM_plus2.5622.5622.3	3	10.56	0	2.03E+05		(K)SVSSASE	(K)S V/S/S A S E H S T|T E/P S/P/A\A/R(R)		91.42	600.9498	1800.836	-0.001	-0.6	5.38	133030.9	10.9	HUMAN	F5H1R7	Protein FLJ22184
9212	dirMS_041712_NAR_60mM_plus.15411.15411.3	3	10.56	1	5.97E+05		(R)FVNVVP	(R)F V|N\V/V/P T F/G K K(K)		137.58	412.5761	1235.715	-0.0009	-0.7	10	10904.6	11.56	HUMAN	E9PR30	40S ribosomal protein S30
9213	dirMS_041712_NAR_60mM_plus.20635.20635.3	3	10.56	0	4.44E+05		(R)CRPDQL	(R)C R P D\Q\L T|G\L S L\L/P L/S E K(A)	C:Carbamidomethylation	168.32	643.0146	1927.032	-0.0025	-1.3	6.07	533778	5.74	HUMAN	Q15149	Plectin
9214	dirMS_041712_NAR_60mM_plus.21428.21428.3	3	10.56	1	3.68E+05		(R)ARDDLI	(R)A R D D\L\I|T/D|L|L/N E A K(Q)		177.42	529.6165	1586.838	-0.0035	-2.2	4.23	23653.1	9.28	HUMAN	C9J8H1	V-type proton ATPase subunit E 1 (Fragment)
9215	dirMS_041712_NAR_60mM_plus.7308.7498.3	3	10.56	1	9.36E+05		(R)AVTGYK	(R)A V|T/G Y K/D/P Y/S G K(L)		96.6	429.2193	1285.642	0.0011	0.8	8.47	533778	5.74	HUMAN	Q15149	Plectin
9216	dirMS_041712_NAR_60mM_plus.8608.8608.3	3	10.56	1	1.39E+06		(K)MQASIE	(K)M/Q|A/S I/E/K G G S L/P K(V)		103.22	449.2449	1345.714	0.0057	4.3	8.35	32745.6	4.64	HUMAN	P06748	Nucleophosmin
9217	dirMS_041712_NAR_120mM_minus.15117.15172.3	3	10.55	1	2.52E+05		(R)IQLVEEE	(R)I/Q\L|V/E E E L D/R A Q E R(L)		136.88	576.6344	1727.892	-0.0036	-2.1	4.25	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
9218	dirMS_041712_NAR_120mM_minus.5798.5798.3	3	10.55	1	3.11E+05		(R)QREEEIE	(R)Q R E E\E|I/E/A Q/E K(A)		85.25	463.5589	1388.665	-0.0031	-2.2	4.33	29841.1	9.04	HUMAN	O75937	DnaJ homolog subfamily C member 8
9219	dirMS_041712_NAR_30mM_minus2.17472.17472.2	2	10.55	0	3.93E+05		(R)EQLAIAE	(R)E Q\L/A/I/A/E F A/R(S)		150.17	574.3084	1147.611	-0.0011	-0.9	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
9220	dirMS_041712_NAR_30mM_minus2.18336.18336.2	2	10.55	0	5.54E+03		(R)LTAEDLF	(R)L/T|A/E/D|L F/E A R(I)		153.52	582.7922	1164.59	-0.0124	-10.7	4.14	533778	5.74	HUMAN	Q15149	Plectin
9221	dirMS_041712_NAR_40mM_minus2.14106.14106.3	3	10.55	0	3.46E+05		(R)LLEVLSG	(R)L L|E/V L/S G E I/L P K P T/K(G)		166.62	546.333	1636.988	-0.0039	-2.4	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
9222	dirMS_041712_NAR_50mM_minus2.11897.11897.3	3	10.55	1	1.19E+05		(K)DVDEAY	(K)D V|D|E/A/Y M N K V E L E S R(L)		135.67	599.9481	1797.832	-0.0026	-1.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
9223	dirMS_041712_NAR_50mM_minus2.9511.9511.3	3	10.55	1	2.04E+05	M183m	(R)VEVERD	(R)V/E/V E R D N\L/A/E/D I m R(L)	m:Oxidized methionine	122.12	568.9459	1688.827	15.9959	0.6	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
9224	dirMS_041712_NAR_60mM_minus.11542.11542.3	3	10.55	1	2.94E+05		(R)VFDKEG	(R)V/F\D K E G\N G T|V/M/G/A E/I R(H)		124.35	574.9539	1722.848	-0.0008	-0.5	4.68	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
9225	dirMS_041712_NAR_60mM_minus.17048.17048.3	3	10.55	1	4.37E+04		(R)FSFSPEP	(R)F/S|F/S/P E P T L E/D I R/R(L)		155.08	565.2904	1693.854	0.0022	1.3	4.68	18794.6	4.93	HUMAN	Q9H773	dCTP pyrophosphatase 1
9226	dirMS_041712_NAR_120mM_plus.5648.5648.3	3	10.55	1	1.36E+05		(R)ALCDYK	(R)A L/C D/Y K Q D/Q K(I)	C:Carbamidomethylation	82.62	423.5365	1268.594	0.001	0.8	6.01	334221.3	6.44	HUMAN	P15924	Desmoplakin
9227	dirMS_041712_NAR_20mM_plus.15707.15707.3	3	10.55	0	7.37E+05		(K)VGINYQ	(K)V G I N Y\Q/P P/T V V/P G G D L/A K(V)		179.22	608.9991	1824.985	-0.0027	-1.5	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
9228	dirMS_041712_NAR_20mM_plus.16224.16224.3	3	10.55	0	1.12E+06	M221m	(R)ALTVPEL	(R)A L\T\V/P E L T/Q/Q m F/D A/K(N)	m:Oxidized methionine	184.32	569.9583	1691.867	15.9931	-1.1	4.37	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
9229	dirMS_041712_NAR_20mM_plus.19102.19102.3	3	10.55	0	2.37E+05		(R)VCTLAII	(R)V C T L A I\I/D/P/G D S D I I/R(S)	C:Carbamidomethylation	202.77	586.641	1757.91	-0.0018	-1	3.93	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
9230	dirMS_041712_NAR_30mM_plus2.19621.19621.2	2	10.55	0	3.67E+05		(K)SNNVEM	(K)S N|N|V/E|M D W/V L K(H)		156.67	667.8205	1334.641	-0.0072	-5.4	4.37	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
9231	dirMS_041712_NAR_30mM_plus2.21340.21340.2	2	10.55	0	3.13E+05		(K)FDGILG	(K)F D\G|I/L/G M/A Y P/R(I)		167.3	620.3199	1239.619	0.0135	10.9	5.83	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
9232	dirMS_041712_NAR_40mM_plus2.7030.7030.2	2	10.55	0	2.07E+04		(K)STCIYGG	(K)S T/C/I/Y/G G A/P K(G)	C:Carbamidomethylation	101.43	527.2536	1053.503	-0.0034	-3.3	8.31	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
9233	dirMS_041712_NAR_50mM_plus2.13605.13605.3	3	10.55	1	9.86E+05		(R)LAIYRAE	(R)L/A/I|Y R A E T E E/G P D V L R(W)		138.95	611.3256	1831.955	0.0074	4	4.41	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
9234	dirMS_041712_NAR_50mM_plus2.13687.13687.3	3	10.55	1	7.51E+05		(K)LIQEIVD	(K)L/I/Q E I/V D K/S G/V V/R(V)		140.07	485.9552	1455.853	-0.0019	-1.3	6.07	66105.7	7.3	HUMAN	A8MQB8	Fragile X mental retardation protein 1
9235	dirMS_041712_NAR_50mM_plus2.20651.20651.3	3	10.55	1	1.70E+05		(R)VNSKFD	(R)V/N S\K F D T\I/Y/Q/I L L K(K)		177.62	561.3209	1681.952	-0.0042	-2.5	8.47	72626.7	9.13	HUMAN	Q14258	E3 ubiquitin/ISG15 ligase TRIM25
9236	dirMS_041712_NAR_50mM_plus2.9512.9512.3	3	10.55	0	5.99E+05		(K)GAVDG	(K)G A|V/D/G G L/S\I/P H/S T K(R)		117.25	446.9057	1338.701	0.0013	1	6.74	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
9237	dirMS_041712_NAR_60mM_plus.9898.9898.3	3	10.55	0	2.35E+05		(R)ASGNYA	(R)A/S|G/N Y\A T V I/S H/N P E/T K(K)		109.37	563.613	1688.824	0.0006	0.4	6.79	24115.6	11.59	HUMAN	E9PIZ3	60S ribosomal protein L8
9238	dirMS_041712_NAR_20mM_minus.14685.14685.2	2	10.54	0	1.34E+05		(R)IITLAGP	(R)I I/T\L/A|G|P T N A I F K(A)		202.13	679.9047	1358.804	-0.0021	-1.5	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
9239	dirMS_041712_NAR_20mM_minus.7043.7043.2	2	10.54	0	4.77E+05	M281m	(R)AEAESm	(R)A E|A|E/S m/Y Q I K(Y)	m:Oxidized methionine	117.9	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
9240	dirMS_041712_NAR_30mM_minus2.16010.16026.2	2	10.54	0	4.92E+05		(K)LIINSLY	(K)L/I|I/N\S L Y/K(N)		141.22	482.2955	963.587	-0.0036	-3.8	8.59	5582.4	4.81	HUMAN	F8W026	Endoplasmin (Fragment)
9241	dirMS_041712_NAR_50mM_minus2.16242.16242.3	3	10.54	0	1.99E+05		(R)DEPIHIL	(R)D E|P/I H I L N/V\A I K(T)		160.45	454.5974	1361.779	-0.0011	-0.8	5.32	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
9242	dirMS_041712_NAR_50mM_minus2.16843.16843.3	3	10.54	0	4.60E+05		(K)NILFVIT	(K)N I/L/F V I/T/K P D V Y/K(S)		164.12	517.2991	1549.899	-0.0161	-10.4	8.5	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
9243	dirMS_041712_NAR_60mM_minus.13435.13435.3	3	10.54	1	1.40E+06		(R)QLREYQ	(R)Q/L R E Y\Q/E|L/M N V K(L)		135.27	517.6033	1550.8	-0.0042	-2.7	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
9244	dirMS_041712_NAR_60mM_minus.19278.19278.3	3	10.54	0	1.04E+06		(R)SLHDAL	(R)S L H D\A L\C|V|L/A Q T V K(D)	C:Carbamidomethylation	171.22	518.9484	1554.831	-0.0002	-0.1	6.46	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
9245	dirMS_041712_NAR_60mM_minus.7439.7460.3	3	10.54	2	6.13E+05		(K)QSVDKV	(K)Q S/V D K V T/S/P T/K\V(-)		100.82	430.241	1288.711	-0.0023	-1.8	8.59	64225	6.66	HUMAN	E7EX44	Caldesmon
9246	dirMS_041712_NAR_20mM_plus.12407.12407.2	2	10.54	0	1.87E+05		(R)GVEICIA	(R)G V\E\I/C/I/A|T P G R(L)	C:Carbamidomethylation	158.58	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
9247	dirMS_041712_NAR_20mM_plus.14116.14116.2	2	10.54	0	7.05E+04	M313m	(R)TVQSLEI	(R)T V|Q/S L/E I\D L D/S m R(N)	m:Oxidized methionine	169.18	761.8738	1506.747	15.9935	-0.9	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9248	dirMS_041712_NAR_20mM_plus.14304.14304.2	2	10.54	0	8.58E+04		(R)VFSGLV	(R)V/F|S|G/L V/S T G L K(V)		170.27	554.3224	1107.641	-0.0033	-3	8.72	96306.4	6.41	HUMAN	P13639	Elongation factor 2
9249	dirMS_041712_NAR_20mM_plus.18549.18549.3	3	10.54	0	2.04E+05		(R)LSVEEA	(R)L S V E E A V A A|G\V|V|G/G E I Q E/K(L)		198.6	629.0001	1884.991	-0.0056	-2.9	4.09	266161	5.68	HUMAN	E9PPU0	Epiplakin
9250	dirMS_041712_NAR_20mM_plus.7261.7261.2	2	10.54	0	2.87E+05	M281m	(R)AEAESm	(R)A E/A/E/S m|Y Q I K(Y)	m:Oxidized methionine	118.4	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
9251	dirMS_041712_NAR_30mM_plus2.16621.16621.2	2	10.54	0	2.99E+05		(R)SIQADG	(R)S I|Q/A/D\G/L V/W/G S S K(L)		140.23	674.3475	1347.69	-0.0026	-1.9	5.55	24934.4	4.5	HUMAN	P24534	Elongation factor 1-beta
9252	dirMS_041712_NAR_40mM_plus2.18233.18233.3	3	10.54	0	1.04E+05		(K)VLSLPKP	(K)V L|S L P K P T\I\I|L/S|A/Y Q R(K)		173.45	600.3613	1799.079	-0.0096	-5.3	9.99	80080.5	5.54	HUMAN	J3KMX1	Nuclear pore complex protein Nup88 (Fragment)
9253	dirMS_041712_NAR_40mM_plus2.18502.18955.3	3	10.54	0	8.75E+05		(R)DYLHLP	(R)D Y L H\L\P P E\I|V/P/A T L R(R)		176.45	578.6565	1733.959	-0.0035	-2	5.32	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
9254	dirMS_041712_NAR_50mM_plus2.20348.20367.3	3	10.54	1	1.87E+04		(K)SSVLEN	(K)S S/V/L/E/N/F\V G R D F L/P\R(G)		176.38	579.3128	1735.913	0.0113	6.5	5.79	73288.1	8.96	HUMAN	E5RHK8	Dynamin-3
9255	dirMS_041712_NAR_60mM_plus.14136.14136.3	3	10.54	1	8.21E+05		(K)TTVKDL	(K)T\T V K D L S E|L/G S/V/R(T)		130.38	468.9268	1404.769	-0.0034	-2.4	5.74	533778	5.74	HUMAN	Q15149	Plectin
9256	dirMS_041712_NAR_60mM_plus.17959.17959.3	3	10.54	1	1.75E+05		(K)FNADEF	(K)F N|A/D/E F E D/M V A E/K R(L)		150.68	567.5906	1700.758	-0.0012	-0.7	4.18	18819.6	10.31	HUMAN	F8W7C6	60S ribosomal protein L10
9257	dirMS_041712_NAR_60mM_plus.6668.6668.3	3	10.54	1	3.85E+05		(R)GPPPPP	(R)G P|P/P/P P T A S E P T R R(S)		93.8	487.2585	1459.765	-0.0043	-2.9	9.6	124127.1	8.81	HUMAN	O14776	Transcription elongation regulator 1
9258	dirMS_041712_NAR_30mM_minus2.5849.5849.2	2	10.53	0	1.32E+05		(K)TSEVNC	(K)T S|E|V/N C Y R(C)	C:Carbamidomethylation	86.63	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
9259	dirMS_041712_NAR_40mM_minus2.11849.11849.3	3	10.53	0	2.32E+05		(K)DAGEGL	(K)D/A/G E/G L/L A V Q I/T D P E G\K/P/K(K)		153.8	646.6785	1938.018	0.0031	1.6	4.32	283472.4	5.71	HUMAN	P21333	Filamin-A
9260	dirMS_041712_NAR_50mM_minus2.14822.14822.3	3	10.53	1	6.81E+04	M84m	(K)ETmQSL	(K)E T m/Q/S/L N D R L A/S/Y L D R(V)	m:Oxidized methionine	152.25	643.3122	1911.923	15.9991	2.2	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18

9261	dirMS_041712_NAR_50mM_minus2.15300.15300.3	3	10.53	1	4.51E+05		(K)GADFLV	(K)G A|D\F L|V|T E V E N G G S L G S K K(G)		155.55	636.662	1907.971	0.0005	0.3	4.68	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
9262	dirMS_041712_NAR_50mM_minus2.9600.9600.3	3	10.53	0	1.82E+05		(R)AIGSASE	(R)A I|G S A S E/G A Q S S L/Q E V Y/H K(S)		122.55	654.6559	1961.956	-0.0032	-1.6	5.4	20148.5	4.65	HUMAN	B4E2V4	Proteasome (Prosome, macropain) subunit, alpha type, 5, isoform CRA_c
9263	dirMS_041712_NAR_60mM_minus.5120.5120.3	3	10.53	1	4.16E+04		(K)VSQGVE	(K)V/S|Q|G V E/D G P D T K/R(A)		83.18	463.2294	1387.681	-0.0076	-5.4	4.56	33726	7.84	HUMAN	B3KNJ4	SUMO-1 activating enzyme subunit 1, isoform CRA_a
9264	dirMS_041712_NAR_20mM_plus.18422.18422.3	3	10.53	0	8.65E+04	M36m	(K)NIPmTL	(K)N I/P m/T L E/L\L/Q S T R(I)	m:Oxidized methionine	197.88	511.28	1515.82	16.0055	6.9	6	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
9265	dirMS_041712_NAR_20mM_plus.9940.9940.2	2	10.53	0	1.34E+05		(K)GEATVS	(K)G E|A T V|S/F D/D/P P S A K(A)		140.2	710.8324	1420.659	-0.0015	-1.1	4.03	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
9266	dirMS_041712_NAR_30mM_plus2.14897.15001.2	2	10.53	0	1.06E+06		(K)SLDLVT	(K)S/L|D|L/V/T M/K(K)		131.83	453.7487	906.496	-0.0064	-7	5.55	51212	5.84	HUMAN	A6NFQ9	Septin-8
9267	dirMS_041712_NAR_30mM_plus2.17094.17094.2	2	10.53	0	3.76E+04	M185m	(K)LAVNm	(K)L A/V/N m/V|P/F/P R(L)	m:Oxidized methionine	142.12	580.3176	1143.634	15.9936	-1.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
9268	dirMS_041712_NAR_30mM_plus2.22034.22034.2	2	10.53	0	1.97E+05		(K)QSLGELI	(K)Q S\L G/E|L/I/G T L N A A K(V)		170.3	707.8889	1414.79	-0.0195	-13.8	6	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
9269	dirMS_041712_NAR_30mM_plus2.6874.6874.2	2	10.53	0	7.31E+04		(R)ENPYYD	(R)E N|P/Y Y D/S R(V)		90.4	522.2255	1043.443	0.0009	0.8	4.37	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
9270	dirMS_041712_NAR_30mM_plus2.8871.8972.2	2	10.53	0	1.69E+05		(R)AYEFAE	(R)A/Y|E/F/A E/R(C)		99.37	443.2095	885.41	0.0016	1.8	4.53	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
9271	dirMS_041712_NAR_50mM_plus2.21474.21474.3	3	10.53	0	8.95E+04		(K)GAEILEV	(K)G A|E|I/L E/V\L H S L/P/A V R(Q)		183.4	535.3092	1603.917	-0.0036	-2.2	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
9272	dirMS_041712_NAR_60mM_plus.9460.9460.2	2	10.53	0	4.97E+05		(K)SYCAEIA	(K)S Y/C|A E/I/A/H/N V S S K(N)	C:Carbamidomethylation	107.47	733.3425	1465.674	0.0037	2.5	6.47	15730.4	11.67	HUMAN	D3YTB1	60S ribosomal protein L32 (Fragment)
9273	dirMS_041712_NAR_120mM_minus.6182.6206.3	3	10.52	1	1.20E+05		(K)AQQELE	(K)A Q|Q/E/L/E/E Q T R/R(A)		87.68	463.2365	1387.692	0.0025	1.8	4.79	67933	6.08	HUMAN	P26038	Moesin
9274	dirMS_041712_NAR_40mM_minus2.13913.13913.3	3	10.52	1	2.77E+04		(R)LQISTPD	(R)L Q|I\S/T P D/I K/D N I V A Q L K(Q)		166.05	632.6978	1896.08	-0.0012	-0.6	5.96	42442.7	4.65	HUMAN	F5GWX8	Interferon regulatory factor 6
9275	dirMS_041712_NAR_40mM_minus2.9514.9514.3	3	10.52	1	5.83E+04		(K)VLCGGD	(K)V L/C G G D I\Y|V/P E D P K L K(D)	C:Carbamidomethylation	138.65	601.6499	1802.936	-0.0006	-0.3	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
9276	dirMS_041712_NAR_60mM_minus.15473.15473.3	3	10.52	1	4.63E+05		(K)YQLDKD	(K)Y/Q/L/D/K D G V/V L/F K(K)		146.32	475.5992	1424.778	0.0047	3.3	5.96	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
9277	dirMS_041712_NAR_20mM_plus.8791.8791.2	2	10.52	0	3.69E+03		(R)AVLIAG	(R)A V\L|I/A|G Q/P G T G K(T)		131.15	556.3256	1111.647	-0.0031	-2.8	8.8	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
9278	dirMS_041712_NAR_30mM_plus2.11203.11203.3	3	10.52	0	2.44E+05	M304m	(R)MGQM	(R)M/G Q M\A M/G G A/m/G I/N N R(G)	m:Oxidized methionine	112.5	518.8921	1538.67	15.9923	-1.7	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
9279	dirMS_041712_NAR_30mM_plus2.21905.21905.2	2	10.52	0	2.21E+05		(R)NSILAQ	(R)N S\I/L/A/Q|V\L|D Q S A R(A)		170.18	707.8889	1414.765	0.0057	4	5.84	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
9280	dirMS_041712_NAR_30mM_plus2.7582.7582.2	2	10.52	0	1.94E+06		(R)GTLDPV	(R)G T|L/D/P V/E K(A)		94.1	429.7312	858.457	-0.0016	-1.9	4.37	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
9281	dirMS_041712_NAR_30mM_plus2.9284.9284.2	2	10.52	0	2.55E+05		(K)SVEAAA	(K)S V|E/A/A/A E L/S/A K(D)		103.17	538.2855	1075.563	0.0007	0.7	4.53	12131.5	11.14	HUMAN	F5GXR3	Parathymosin
9282	dirMS_041712_NAR_30mM_plus2.9405.9510.2	2	10.52	0	8.41E+06		(R)LASYLD	(R)L/A|S|Y L D/R(V)		104.42	419.2286	837.447	0.0034	4.1	5.83	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9283	dirMS_041712_NAR_40mM_plus2.17404.17404.3	3	10.52	1	3.02E+05		(K)TGISDV	(K)T G/I/S/D V F A K\N D\L/A V/V D/V R(I)		169.28	640.3451	1919.023	-0.0025	-1.3	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
9284	dirMS_041712_NAR_50mM_plus2.15399.15399.3	3	10.52	1	3.32E+05		(K)TVGVEP	(K)T V|G\V E/P A A D G K G V V V V I K(R)		148.63	580.0056	1738.011	-0.0087	-5	5.73	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
9285	dirMS_041712_NAR_50mM_plus2.16659.16659.3	3	10.52	1	3.33E+05		(K)LLTGELL	(K)L L|T G E\L L/P T D G M I R K(H)		155.22	552.9815	1656.935	-0.0054	-3.2	6.07	73070	7.16	HUMAN	Q75MJ1	ATP-binding cassette sub-family F member 2
9286	dirMS_041712_NAR_120mM_minus.13197.13197.4	4	10.51	1	5.13E+05		(K)SVHSSV	(K)S V H S\S V|P L/L N/S K D P I D/R(I)		126.43	466.7525	1863.992	-0.0041	-2.2	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
9287	dirMS_041712_NAR_40mM_minus2.12196.12196.3	3	10.51	1	4.38E+05		(R)IIAFVGS	(R)I I|A\F/V/G\S P/V E D N E K D L V K(L)		155.88	658.3553	1973.059	-0.0076	-3.9	4.32	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
9288	dirMS_041712_NAR_50mM_minus2.11121.11121.3	3	10.51	0	1.29E+05		(R)IELGDV	(R)I E|L/G D V/T/P H/N I K(Q)		131.2	445.912	1335.727	-0.0052	-3.9	5.32	14942.8	8.71	HUMAN	C9J5D1	N-alpha-acetyltransferase 50
9289	dirMS_041712_NAR_50mM_minus2.14818.14818.3	3	10.51	1	2.80E+05		(K)NIYVLQ	(K)N I|Y/V/L/Q E L/D/N P G A K R(I)		152.6	577.3116	1729.923	-0.0029	-1.7	6.07	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
9290	dirMS_041712_NAR_50mM_minus2.6969.6969.3	3	10.51	0	1.74E+05		(R)SAEEEA	(R)S/A|E|E/E A A/D L/P T K P T K(I)		106.92	529.6012	1586.791	-0.0018	-1.1	4.41	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
9291	dirMS_041712_NAR_50mM_minus2.7827.7827.3	3	10.51	1	1.10E+05		(K)VLLQSK	(K)V/L|L Q|S K D Q I/T A G/N A A R(K)		111.77	562.3158	1684.934	-0.0012	-0.7	8.72	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
9292	dirMS_041712_NAR_60mM_minus.12794.12794.3	3	10.51	1	1.97E+05		(K)LSAEKV	(K)L/S/A E/K V/E\I A T L T R(E)		131.02	477.6112	1430.821	-0.0023	-1.6	6.14	26661.1	7.81	HUMAN	H0YL69	Proteasome subunit alpha type (Fragment)
9293	dirMS_041712_NAR_120mM_plus.18677.18677.4	4	10.51	1	4.35E+05		(R)SKDVVE	(R)S K D V\V\E/P/L/L R P Q W Y V R(C)		150.58	497.0291	1985.097	-0.0021	-1.1	8.31	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
9294	dirMS_041712_NAR_20mM_plus.10435.10435.2	2	10.51	0	1.88E+05	M592m M	(R)mGPAm	(R)m G/P A\m|G P A\L|G A G I/E/R(M)	m:Oxidized methionine	144.65	730.3568	1427.713	31.993	2.1	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
9295	dirMS_041712_NAR_20mM_plus.13706.13706.2	2	10.51	0	2.16E+05	M98m	(R)TLTIVDT	(R)T L/T|I/V\D T/G I/G m T K(A)	m:Oxidized methionine	166.85	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
9296	dirMS_041712_NAR_20mM_plus.18215.18215.2	2	10.51	0	1.00E+05		(R)AILVDLE	(R)A I\L V|D\L|E|P G T M D S V R(S)		196.67	808.419	1615.836	-0.0053	-3.3	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
9297	dirMS_041712_NAR_30mM_plus2.13929.13955.2	2	10.51	0	5.96E+05		(K)ALDFIAS	(K)A L|D|F/I/A/S K(G)		126	432.7483	864.482	0.0068	7.8	5.88	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
9298	dirMS_041712_NAR_30mM_plus2.18577.18634.2	2	10.51	0	1.93E+05		(K)ELEFYLR	(K)E L|E|F/Y/L/R(K)		150.95	485.2559	969.504	0.0005	0.5	4.53	24490	10.56	HUMAN	P62241	40S ribosomal protein S8
9299	dirMS_041712_NAR_40mM_plus2.10686.10686.3	3	10.51	0	6.79E+04	M35m	(K)AASDIA	(K)A A/S/D I/A/m T E/L/P/P/T H P I R(L)	m:Oxidized methionine	128.38	612.652	1819.937	16.0044	5.1	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
9300	dirMS_041712_NAR_40mM_plus2.8349.8349.2	2	10.51	0	2.86E+05		(R)FGSGM	(R)F/G/S\G/M N M G R(I)		109.45	478.706	956.408	-0.003	-3.1	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
9301	dirMS_041712_NAR_50mM_plus2.17151.17151.3	3	10.51	1	1.02E+06		(K)DNNGVI	(K)D N/N|G V/I/G L L E P M K K(S)		158.53	509.9448	1527.82	-0.0001	-0.1	6.07	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
9302	dirMS_041712_NAR_50mM_plus2.5192.5192.3	3	10.51	0	1.37E+06		(K)TATPQQ	(K)T\A|T|P Q Q/A Q E V H E K(L)		86.38	489.5774	1466.723	-0.0057	-3.9	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
9303	dirMS_041712_NAR_60mM_plus.12185.12185.3	3	10.51	1	1.01E+06	M232m	(R)MSmKE	(R)M/S\m K E V\D E/Q|M|L/N V/Q N K(N)	m:Oxidized methionine	120.57	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
9304	dirMS_041712_NAR_60mM_plus.14896.14896.3	3	10.51	1	1.99E+05		(K)LVKELE	(K)L V/K/E L\E/G\V I/T K(A)		134.62	410.254	1228.751	-0.0037	-3	6.14	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
9305	dirMS_041712_NAR_60mM_plus.16296.16296.3	3	10.51	1	3.69E+05	S177s	(K)DIDISsP	(K)D I D I S s|P/E/F K I K(I)	s:N-acetylglucosamine (S)	142.85	532.2733	1391.742	203.0637	-9.8	4.56	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
9306	dirMS_041712_NAR_120mM_minus.10339.10339.3	3	10.5	1	6.18E+04		(R)KEEELQ	(R)K E E E L|Q/A/A/L/A/R(A)		111.02	419.8975	1257.68	-0.0018	-1.4	4.79	232239.1	5.52	HUMAN	F2Z2U8	Myosin-14
9307	dirMS_041712_NAR_120mM_minus.10623.10640.3	3	10.5	1	1.97E+06		(R)VKYETE	(R)V K Y E T E/L/A/M/R(Q)		111.73	413.885	1239.64	0.0003	0.2	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9308	dirMS_041712_NAR_30mM_minus2.16793.16793.2	2	10.5	0	1.47E+05		(R)NPSAAF	(R)N/P|S/A A|F F C V A R(L)	C:Carbamidomethylation	144.82	620.3013	1239.594	0.0014	1.1	9.75	18626.5	5.64	HUMAN	B8ZZK2	Gamma-glutamylcyclotransferase
9309	dirMS_041712_NAR_30mM_minus2.17470.17470.2	2	10.5	0	2.34E+05		(R)NGGQIL	(R)N G/G\Q/I|L I/A D/L R(G)		149.18	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
9310	dirMS_041712_NAR_40mM_minus2.11319.11319.3	3	10.5	0	4.83E+05		(R)TIQVEN	(R)T/I|Q/V E N S H L I/L T/G/A G A L N K(V)		150.57	660.3663	1979.092	-0.0077	-3.9	6.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
9311	dirMS_041712_NAR_50mM_minus2.13401.13570.3	3	10.5	1	5.31E+05		(K)LTEDKA	(K)L/T/E D K A D V\Q\S|I/I/G L Q R(F)		144.8	595.9939	1785.97	-0.0034	-1.9	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
9312	dirMS_041712_NAR_50mM_minus2.14837.14837.3	3	10.5	1	4.12E+05		(K)GCLELIK	(K)G C L/E L I K/E T G V/P/I/A G R(H)	C:Carbamidomethylation	151.83	571.6494	1712.936	-0.0027	-1.6	6.14	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
9313	dirMS_041712_NAR_50mM_minus2.15133.15133.3	3	10.5	0	1.83E+05		(K)AETLASS	(K)A E/T/L/A|S S L Q E/D L A H T R(N)		154.87	581.2998	1741.872	0.0133	7.7	4.65	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
9314	dirMS_041712_NAR_60mM_minus.11947.11947.3	3	10.5	0	1.77E+05	M271m	(R)DLSYCLS	(R)D L/S/Y/C\L/S G m|Y D H R(Y)	C:Carbamidomethylation m:Oxid	126.72	544.8984	1616.683	15.9975	1.6	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
9315	dirMS_041712_NAR_60mM_minus.18421.18421.3	3	10.5	0	1.13E+04		(R)HLEPAL	(R)H L E P A L A\F\Q/L/E/L N R(M)		163.17	550.9705	1650.896	0.0007	0.4	5.4	97883.4	6.02	HUMAN	F6QQI9	Acetyl-CoA carboxylase 2
9316	dirMS_041712_NAR_60mM_minus.6575.6575.3	3	10.5	1	2.18E+05		(R)KTGQAP	(R)K\T G\Q A/P G Y/S/Y T/A A N K(N)		95.27	519.5963	1556.77	0.004	2.6	9.53	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
9317	dirMS_041712_NAR_60mM_minus.6870.6870.3	3	10.5	1	1.33E+05		(R)LCAGAS	(R)L C/A/G/A S E/D I/R E K(L)	C:Carbamidomethylation	97.07	450.2225	1348.652	0.0004	0.3	4.68	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
9318	dirMS_041712_NAR_120mM_plus.18283.18367.3	3	10.5	1	6.47E+05		(R)RFDAM	(R)R F D A\M|P/F/T L/R(A)		149.22	418.5539	1253.646	0.0012	1	9.6	42088	5.39	HUMAN	F8VTY8	Proliferation-associated protein 2G4
9319	dirMS_041712_NAR_20mM_plus.18661.18661.3	3	10.5	0	1.88E+04		(R)APVPAS	(R)A P V P A S E L\L|A/S/G V\L S/R(A)		199.92	522.9655	1566.885	-0.003	-1.9	6.05	533778	5.74	HUMAN	Q15149	Plectin
9320	dirMS_041712_NAR_30mM_plus2.17017.17017.2	2	10.5	0	2.05E+05		(R)VFSGLV	(R)V/F/S|G L/V\S T G L/K(V)		141.95	554.322	1107.641	-0.0041	-3.7	8.72	96306.4	6.41	HUMAN	P13639	Elongation factor 2
9321	dirMS_041712_NAR_30mM_plus2.17268.17268.2	2	10.5	0	6.98E+04		(K)WPLYM	(K)W/P/L/Y M/S T K(N)		144.88	513.2647	1025.513	0.0097	9.4	8.59	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
9322	dirMS_041712_NAR_30mM_plus2.8249.8249.2	2	10.5	0	1.36E+06		(K)QGGGG	(K)Q G G\G G|G/G/G/S V/P G I E R(M)		97.17	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
9323	dirMS_041712_NAR_30mM_plus2.8576.8576.2	2	10.5	0	1.03E+06		(K)TAVCDI	(K)T A|V/C/D/I|P\P R(G)	C:Carbamidomethylation	99.43	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
9324	dirMS_041712_NAR_30mM_plus2.9185.9185.2	2	10.5	0	3.86E+05		(K)ATFDAIS	(K)A T|F/D A/I\S/K(T)		101.92	426.7266	852.446	-0.0002	-0.3	5.88	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
9325	dirMS_041712_NAR_30mM_plus2.9687.9687.2	2	10.5	0	3.55E+05		(R)TSLGPN	(R)T S|L/G/P\N G L D/K(M)		104.43	501.2717	1001.526	0.0099	9.9	5.5	55804.4	5.33	HUMAN	B7ZAR1	T-complex protein 1 subunit epsilon
9326	dirMS_041712_NAR_40mM_plus2.16120.16260.3	3	10.5	0	5.99E+05		(R)FGVPVI	(R)F G\V P V/I/A D G G I Q N V/G/H I/A/K(A)		162.45	631.3436	1892.039	-0.0226	-12	6.74	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
9327	dirMS_041712_NAR_40mM_plus2.9501.9501.2	2	10.5	0	7.31E+04		(R)GGGGN	(R)G G/G G N F/G/P G|P G S N F R(G)		119.27	689.3182	1377.629	-0.0003	-0.2	9.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
9328	dirMS_041712_NAR_50mM_plus2.10942.10942.3	3	10.5	0	6.36E+04		(K)MVMIQ	(K)M V|M/I/Q/D G/P Q N T G A D K P L R(I)		125.3	657.663	1970.979	-0.0042	-2.1	5.71	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
9329	dirMS_041712_NAR_50mM_plus2.13622.13622.3	3	10.5	1	1.04E+06		(R)IQLVEEE	(R)I Q|L/V/E E E L D R A/Q/E R(L)		140.12	576.6349	1727.892	-0.0021	-1.2	4.25	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
9330	dirMS_041712_NAR_60mM_plus.10816.10816.3	3	10.5	1	2.08E+06		(R)KLDPGS	(R)K L D\P G S|E\E T Q/T/L/V/R(E)		114.88	524.9456	1572.823	-0.0005	-0.3	4.68	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
9331	dirMS_041712_NAR_60mM_plus.20512.20512.3	3	10.5	1	3.09E+05		(K)ITQDIFQ	(K)I T/Q/D I/F Q/Q L L K R(G)		167.93	501.626	1502.869	-0.0055	-3.7	8.75	72796.9	6.75	HUMAN	A6NC17	Methionine--tRNA ligase, cytoplasmic
9332	dirMS_041712_NAR_60mM_plus.6534.6559.2	2	10.5	1	3.07E+05		(R)TKTEISE	(R)T/K|T|E|I/S E M N R(N)		92.77	604.8004	1208.594	-0.0004	-0.4	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
9333	dirMS_041712_NAR_20mM_minus.14726.14892.2	2	10.49	0	3.01E+06		(K)EIIDLVL	(K)E I|I/D|L/V L/D/R(I)		203.67	543.3133	1085.62	-0.0008	-0.7	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
9334	dirMS_041712_NAR_40mM_minus2.14383.14383.3	3	10.49	1	1.61E+05		(K)TGISDV	(K)T G|I S D V/F A/K N D\L A/V/V D/V R(I)		168.48	640.3454	1919.023	-0.0016	-0.8	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
9335	dirMS_041712_NAR_40mM_minus2.8377.8377.3	3	10.49	0	2.03E+05	M35m	(K)AASDIA	(K)A A S/D I/A m/T E L/P P T H P I R(L)	m:Oxidized methionine	129.82	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
9336	dirMS_041712_NAR_50mM_minus2.11000.11000.3	3	10.49	0	1.29E+05		(R)IELGDV	(R)I/E|L/G D V/T/P H N I K(Q)		131.2	445.912	1335.727	-0.0052	-3.9	5.32	14942.8	8.71	HUMAN	C9J5D1	N-alpha-acetyltransferase 50
9337	dirMS_041712_NAR_50mM_minus2.11188.11188.3	3	10.49	0	5.57E+03		(R)ISLGMP	(R)I S|L/G M/P V/G P N A H/K(V)		132.17	440.9072	1320.709	-0.0022	-1.7	8.76	98282.7	5.49	HUMAN	E9PPJ0	Splicing factor 3B subunit 2
9338	dirMS_041712_NAR_50mM_minus2.12555.12555.3	3	10.49	0	2.96E+05		(K)AASDIA	(K)A A/S/D I/A M|T E L/P/P T H P I R(L)		139.5	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
9339	dirMS_041712_NAR_50mM_minus2.15819.15819.3	3	10.49	0	3.64E+05		(K)LYGPTN	(K)L Y/G|P T/N F/S P\I/I/N H/V A R(F)		158.22	600.3221	1798.96	-0.0081	-4.5	8.75	60985.3	5.6	HUMAN	O75131	Copine-3
9340	dirMS_041712_NAR_50mM_minus2.16346.16346.3	3	10.49	1	1.69E+05		(R)EGDVLT	(R)E G|D V/L/T/L/L E S E R E/A R(R)		160.53	572.9609	1716.876	-0.0081	-4.7	4.25	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
9341	dirMS_041712_NAR_50mM_minus2.16895.16895.3	3	10.49	0	1.44E+05		(K)TVSGVN	(K)T V|S/G V N G/P L/V/I L D H V K(V)		164.98	549.9835	1647.943	-0.0069	-4.2	6.41	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
9342	dirMS_041712_NAR_60mM_minus.7217.7217.3	3	10.49	1	1.75E+05		(K)AADIDQ	(K)A/A/D\I/D Q E/V K E R(A)		99.07	425.2172	1273.638	-0.0012	-1	4.32	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
9343	dirMS_041712_NAR_120mM_plus.21619.21619.4	4	10.49	2	4.07E+05	M145m	(R)RGVmL	(R)R G V\m\L\A/V D A V/I A E L K K(Q)	m:Oxidized methionine	166.32	433.0059	1713.009	15.9926	-1.3	8.59	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
9344	dirMS_041712_NAR_120mM_plus.8478.8478.3	3	10.49	1	2.94E+05		(R)ASGNYA	(R)A/S/G N Y/A/T V I S H N P E T K K(T)		97.62	606.3102	1816.919	-0.0028	-1.5	8.55	24115.6	11.59	HUMAN	E9PIZ3	60S ribosomal protein L8
9345	dirMS_041712_NAR_20mM_plus.15216.15216.2	2	10.49	0	6.89E+04		(K)DVLSVA	(K)D V/L/S V/A|F/S/S D N R(Q)		175.98	655.3293	1309.638	0.0131	10	4.21	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
9346	dirMS_041712_NAR_20mM_plus.17864.17864.2	2	10.49	0	9.78E+04		(K)VDFPQD	(K)V D/F/P Q\D Q L T A/L/T|G R(I)		194.95	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
9347	dirMS_041712_NAR_20mM_plus.7964.7964.2	2	10.49	0	1.33E+05		(K)VEIIAND	(K)V E|I/I|A/N D Q G N R(T)		124.62	614.8177	1228.628	0.0001	0.1	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
9348	dirMS_041712_NAR_20mM_plus.8109.8109.2	2	10.49	0	1.33E+05		(R)LLEAAS	(R)L L|E/A A/S/V S\S K(G)		126.02	502.7839	1004.562	-0.0017	-1.7	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
9349	dirMS_041712_NAR_30mM_plus2.16909.16909.2	2	10.49	1	2.65E+05		(R)FVLSQA	(R)F V|L/S/Q A K D E\L(-)		141.43	575.3104	1149.615	-0.0015	-1.3	4.37	41053.3	5.58	HUMAN	Q86UY0	TXNDC5 protein
9350	dirMS_041712_NAR_30mM_plus2.9434.9434.2	2	10.49	0	8.52E+04		(K)VCNPIIT	(K)V/C|N|P I I T/K(L)	C:Carbamidomethylation	104.22	472.7711	944.523	0.0116	12.2	8.72	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
9351	dirMS_041712_NAR_40mM_plus2.19142.19156.3	3	10.49	0	3.19E+05		(K)AIEPPPL	(K)A I|E|P/P/P L D A/V I E A E H/T L R(E)		179.85	657.6841	1971.055	-0.0168	-8.5	4.4	142268.2	6.41	HUMAN	Q08211	ATP-dependent RNA helicase A
9352	dirMS_041712_NAR_50mM_plus2.6525.6525.3	3	10.49	1	3.51E+05		(R)IVDGKV	(R)I V/D/G\K V/V/S/E T\N D T K(V)		100.28	502.2651	1504.785	-0.0046	-3	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
9353	dirMS_041712_NAR_50mM_plus2.9092.9092.3	3	10.49	1	7.17E+04		(R)LQAEIE	(R)L/Q|A E/I/E/G L K G Q R(A)		114.8	447.921	1341.748	0	0	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
9354	dirMS_041712_NAR_50mM_plus2.9980.9980.3	3	10.49	0	2.40E+04	M457m M	(R)mGPLG	(R)m G|P L/G L/D H m A S S I E R(M)	m:Oxidized methionine	119.67	549.2613	1613.777	31.9919	1.3	5.3	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
9355	dirMS_041712_NAR_60mM_plus.12167.12167.3	3	10.49	1	1.01E+06	M232m	(R)MSmKE	(R)M S m K E V D E/Q|M|L/N V Q\N K(N)	m:Oxidized methionine	120.57	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
9356	dirMS_041712_NAR_60mM_plus.14281.14281.3	3	10.49	1	6.49E+05		(K)WKDSD	(K)W K D\S D\E A/D|L/V/L/A K(E)		131.03	497.2559	1489.753	-0.0002	-0.1	4.23	20982.2	5.23	HUMAN	Q13185	Chromobox protein homolog 3
9357	dirMS_041712_NAR_60mM_plus.16630.16630.2	2	10.49	0	7.97E+05		(R)EHALLA	(R)E/H\A|L/L/A/Y T L G V/K(Q)		143.82	657.8735	1314.742	-0.0019	-1.4	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
9358	dirMS_041712_NAR_20mM_minus.14720.14720.2	2	10.48	0	1.66E+05		(K)TAVETA	(K)T A/V/E/T A/V/L\L L/R(I)		201.42	593.3613	1185.72	-0.0048	-4.1	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
9359	dirMS_041712_NAR_20mM_minus.7978.7978.2	2	10.48	0	4.16E+04		(K)VVTDTD	(K)V V|T D|T/D E T E L A R(Q)		129.38	674.8314	1348.659	-0.0035	-2.6	3.91	36396.8	5.02	HUMAN	P05198	Eukaryotic translation initiation factor 2 subunit 1
9360	dirMS_041712_NAR_20mM_minus.8851.8851.2	2	10.48	0	2.33E+05		(R)ALGQN	(R)A L|G Q|N/P T N/A E V L K(V)		138.65	677.871	1354.733	0.0022	1.6	6.05	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
9361	dirMS_041712_NAR_30mM_minus2.19017.19017.2	2	10.48	0	2.39E+05		(K)SYELPD	(K)S Y E\L|P D G Q V I/T/I G N E R(F)		158.78	895.9492	1790.892	-0.0008	-0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
9362	dirMS_041712_NAR_30mM_minus2.19134.19134.3	3	10.48	0	1.77E+05		(K)SYELPD	(K)S Y E\L/P D G/Q\V I/T/I/G N E R(F)		158.88	597.6343	1790.892	-0.0036	-2	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
9363	dirMS_041712_NAR_40mM_minus2.9799.9799.2	2	10.48	0	2.04E+06		(R)VAPEEH	(R)V A/P E E/H/P V L L\T\E/A/P L N P K(A)		140.28	977.5343	1954.064	-0.0031	-1.6	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
9364	dirMS_041712_NAR_50mM_minus2.7454.7454.3	3	10.48	1	8.03E+04		(R)VAVEAK	(R)V/A|V E/A K/N P A D L P K(L)		109.27	451.2571	1351.758	-0.0012	-0.9	6.04	96306.4	6.41	HUMAN	P13639	Elongation factor 2
9365	dirMS_041712_NAR_120mM_plus.4575.4575.3	3	10.48	0	8.60E+05		(R)YINTEH	(R)Y/I|N T/E/H G G S Q A R(F)		74.2	444.8857	1332.629	0.0134	10.1	6.75	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
9366	dirMS_041712_NAR_20mM_plus.12826.12826.2	2	10.48	0	2.85E+04	M92m	(R)ImNTFS	(R)I/m/N T|F S V V/P S/P K(V)	m:Oxidized methionine	160.95	668.3516	1319.703	15.9931	-1.3	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
9367	dirMS_041712_NAR_20mM_plus.15615.15615.2	2	10.48	0	5.93E+03		(R)SSFYVN	(R)S S F Y/V/N G L T/L G/G Q K(C)		178.63	735.8818	1470.759	-0.0024	-1.6	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
9368	dirMS_041712_NAR_20mM_plus.16965.17305.2	2	10.48	0	6.93E+05		(K)VLTPELY	(K)V L|T|P/E/L Y A E L R(A)		189.62	652.3664	1303.726	-0.0001	-0.1	4.53	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
9369	dirMS_041712_NAR_20mM_plus.7533.7533.2	2	10.48	0	2.93E+04		(K)VTLTSEE	(K)V/T L/T/S/E E E A/R(L)		120.93	567.7865	1134.564	0.002	1.8	4.25	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase

9370	dirMS_041712_NAR_30mM_plus2.10296.10296.2	2	10.48	0	2.97E+05		(R)LNQDQI	(R)L N|Q/D Q/L D/A/V S K(Y)		107.28	615.819	1230.632	-0.0017	-1.4	4.21	20235.4	6.77	HUMAN	E9PLA9	Caprin-1 (Fragment)
9371	dirMS_041712_NAR_30mM_plus2.13095.13147.2	2	10.48	0	2.48E+05		(R)YTSLMLI	(R)Y/T|S/L M/L/R(D)		122.1	442.2411	883.471	0.0043	4.9	8.75	66876.9	6.17	HUMAN	O75083	WD repeat-containing protein 1
9372	dirMS_041712_NAR_30mM_plus2.16758.16758.2	2	10.48	0	3.63E+05		(K)QLQEMI	(K)Q L/Q E/M L/G/L/S K(V)		140.63	573.8112	1146.619	-0.0036	-3.1	6	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
9373	dirMS_041712_NAR_30mM_plus2.18736.18736.2	2	10.48	0	3.13E+05		(R)ESLEALL	(R)E/S\L|E/A L/L/Q/R(A)		152	529.8026	1058.584	0.0139	13.1	4.53	107721.8	8.85	HUMAN	O94906	Pre-mRNA-processing factor 6
9374	dirMS_041712_NAR_30mM_plus2.19897.19897.2	2	10.48	0	5.50E+05		(-)MDELQL	(-)M/D/E|L/Q/L F\R(G)		157.03	526.2726	1051.524	0.0138	13.2	4.37	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
9375	dirMS_041712_NAR_40mM_plus2.11204.11204.3	3	10.48	1	7.92E+04		(K)AVEEED	(K)A V|E/E E D K M\T\P/E Q L A\I K(N)		131.97	610.9764	1830.915	-0.0007	-0.4	4.25	34747.6	6.06	HUMAN	O00487	26S proteasome non-ATPase regulatory subunit 14
9376	dirMS_041712_NAR_50mM_plus2.10554.10554.3	3	10.48	0	5.29E+04		(R)LQAQQI	(R)L Q/A/Q Q D A\V N I V C H S K(T)	C:Carbamidomethylation	123.17	570.9571	1710.859	-0.0024	-1.4	6.74	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
9377	dirMS_041712_NAR_50mM_plus2.14602.14602.3	3	10.48	1	5.76E+05		(R)SEGVVA	(R)S E|G V V/A/V L L/T K K(S)		144.37	415.2585	1243.762	-0.0011	-0.9	8.31	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
9378	dirMS_041712_NAR_50mM_plus2.18928.18928.3	3	10.48	1	2.23E+05		(K)IGEEFLT	(K)I/G|E/E/F L T D|L S Q L K K(L)		167.02	540.965	1620.884	-0.0039	-2.4	4.68	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
9379	dirMS_041712_NAR_50mM_plus2.19937.19937.3	3	10.48	0	5.26E+04		(K)GLCLLEC	(K)G L|C L L/E Q/I D/S F/K/P P Q R(S)	C:Carbamidomethylation	172.9	634.3344	1900.995	-0.0063	-3.3	6.07	45536.8	9.03	HUMAN	B7Z1K2	HBS1-like protein
9380	dirMS_041712_NAR_50mM_plus2.9922.9922.3	3	10.48	1	9.24E+05	M227m	(R)mQKEIT.	(R)m Q\K E\I T/A\L/A/P S T|M K(I)	m:Oxidized methionine	119.38	522.2726	1548.812	15.9908	-2.6	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
9381	dirMS_041712_NAR_60mM_plus.11842.11842.2	2	10.48	0	3.70E+05		(K)TGNLGN	(K)T G/N\L/G N/V V/H/I\E R(F)		119.1	654.8542	1308.702	-0.0008	-0.6	6.41	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
9382	dirMS_041712_NAR_60mM_plus.14051.14154.3	3	10.48	0	1.99E+06		(K)GIHPTIIS	(K)G I H\P T I\I/S/E/S F/Q/K(A)		130.72	486.2646	1456.78	-0.0002	-0.1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
9383	dirMS_041712_NAR_60mM_plus.9127.9127.3	3	10.48	1	2.08E+05		(K)YYDDTYI	(K)Y/Y/D/D T Y/P S V K E Q K(A)		105.92	545.9214	1635.754	-0.004	-2.5	4.56	18430.9	4.79	HUMAN	F8VS17	Coatomer subunit zeta-1
9384	dirMS_041712_NAR_20mM_minus.10609.10609.2	2	10.47	0	2.00E+05		(R)TTPSYVA	(R)T T/P S Y/V A/F\T D T E R(L)		154.63	744.3547	1487.701	0.0009	0.6	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
9385	dirMS_041712_NAR_20mM_minus.10758.10758.2	2	10.47	0	4.16E+05		(K)DVNAAI	(K)D V|N/A/A/I A A I/K(T)		155.97	493.287	985.568	-0.0009	-1	5.84	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
9386	dirMS_041712_NAR_30mM_minus2.15494.15635.2	2	10.47	0	4.79E+03		(K)FLMANG	(K)F/L|M|A/N G Q L V/K(M)		139.85	560.8108	1120.618	-0.004	-3.6	8.75	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
9387	dirMS_041712_NAR_30mM_minus2.6522.6648.2	2	10.47	0	5.02E+05		(K)SPEDLEF	(K)S/P|E|D\L E/R(L)		90.07	423.2044	845.4	0.0016	1.9	4.14	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
9388	dirMS_041712_NAR_40mM_minus2.8070.8070.3	3	10.47	1	3.15E+05		(R)DGKLVS	(R)D G K L V\S E/S/S/D V L/P K(-)		128.18	491.9311	1473.78	-0.0008	-0.5	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
9389	dirMS_041712_NAR_50mM_minus2.14853.14853.3	3	10.47	0	4.24E+05		(K)YPIEHGI	(K)Y/P/I E H G I I/T/N|W|D D\M E K(I)		152.52	654.3084	1960.911	-0.0003	-0.1	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
9390	dirMS_041712_NAR_50mM_minus2.16594.16594.3	3	10.47	1	1.60E+05		(K)VVSSVLC	(K)V V|S/S V/L Q F G N I S F K K(E)		162	551.6488	1652.937	-0.0052	-3.1	10	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
9391	dirMS_041712_NAR_50mM_minus2.7767.7767.3	3	10.47	1	5.68E+04		(R)LGAAPE	(R)L G|A A|P/E/E/E S A/Y V A G E K R(Q)		111.32	592.9614	1776.876	-0.0066	-3.7	4.5	30276.7	5	HUMAN	F2Z2K0	NSFL1 cofactor p47
9392	dirMS_041712_NAR_60mM_minus.15429.15429.3	3	10.47	0	2.06E+06		(R)QIFHPEC	(R)Q I\F H/P E Q L/I/T/G K(E)		146.53	470.9285	1410.774	-0.003	-2.1	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
9393	dirMS_041712_NAR_60mM_minus.6541.6541.3	3	10.47	1	2.18E+05		(R)KTGQAP	(R)K T G Q A|P G\Y|S|Y T A/A N K(N)		95.27	519.5963	1556.77	0.004	2.6	9.53	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
9394	dirMS_041712_NAR_120mM_plus.13688.13688.3	3	10.47	1	2.85E+05		(K)SLEKVCA	(K)S L/E/K V/C/A D L I/R(G)	C:Carbamidomethylation	124.72	435.2407	1303.704	0.0037	2.8	5.79	6885.1	10.56	HUMAN	E5RJX2	40S ribosomal protein S20
9395	dirMS_041712_NAR_20mM_plus.14990.14990.2	2	10.47	0	2.17E+05		(K)GLAITFV	(K)G L/A I|T/F\V/S/D E|N D A\K(I)		175.3	740.3693	1479.733	-0.0012	-0.8	4.03	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
9396	dirMS_041712_NAR_20mM_plus.17646.17646.2	2	10.47	0	1.28E+05		(K)LATQSN	(K)L A T Q S/N E|I/T I|P V T F\E S R(A)		193.23	953.4986	1905.992	-0.0017	-0.9	4.53	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
9397	dirMS_041712_NAR_20mM_plus.7452.7452.2	2	10.47	0	1.17E+05		(K)AQYEDIA	(K)A Q|Y/E/D/I A N R(S)		120.42	540.2601	1079.512	0.0013	1.2	4.37	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
9398	dirMS_041712_NAR_30mM_plus2.16000.16000.2	2	10.47	0	4.81E+05		(R)MGPNIY	(R)M/G|P N/I/Y/E L R(T)		136.78	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
9399	dirMS_041712_NAR_30mM_plus2.17690.17690.2	2	10.47	0	1.45E+05		(K)AILFVPR	(K)A I|L/F V/P/R(R)		145.63	408.2604	815.514	-0.0003	-0.3	9.79	57660.2	6.38	HUMAN	Q9NQH7	Probable Xaa-Pro aminopeptidase 3
9400	dirMS_041712_NAR_30mM_plus2.19320.19860.2	2	10.47	0	4.11E+06		(K)TLGILGL	(K)T L|G|I|L|G L/G R(I)		156.62	450.2857	899.567	-0.0032	-3.5	9.41	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
9401	dirMS_041712_NAR_30mM_plus2.19809.19809.2	2	10.47	0	1.27E+05		(R)NTWLYC	(R)N T\W/L|Y/Q A L R(E)		157.13	582.8112	1164.616	-0.0009	-0.8	8.75	49457.5	6.47	HUMAN	P56545	C-terminal-binding protein 2
9402	dirMS_041712_NAR_40mM_plus2.12107.12107.3	3	10.47	1	2.39E+05		(R)VVDALG	(R)V/V/D/A\L/G/N A I/D/G K G P I G S K(T)		137.15	570.9838	1710.939	-0.0016	-1	5.93	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
9403	dirMS_041712_NAR_40mM_plus2.17586.17586.3	3	10.47	1	2.99E+05		(K)TGISDVF	(K)T G I/S/D V F A K N D\L/A/V V D/V R(I)		169.4	640.3451	1919.023	-0.0025	-1.3	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
9404	dirMS_041712_NAR_40mM_plus2.19006.19006.3	3	10.47	1	6.36E+03		(R)VISGVLC	(R)V/I|S/G V|L Q L G N I V F K K(E)		178.52	539.0014	1614.994	-0.0045	-2.8	10	227783.5	5.5	HUMAN	P35579	Myosin-9
9405	dirMS_041712_NAR_50mM_plus2.10028.10028.3	3	10.47	1	3.09E+05		(R)LGLPGD	(R)L/G L/P/G D E/V/D N K V K(G)		120.28	461.9229	1383.748	0.0063	4.6	4.56	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
9406	dirMS_041712_NAR_50mM_plus2.11290.11331.3	3	10.47	0	5.44E+05		(R)LLEAQAC	(R)L L|E|A/Q/A/C T G G I I H/P T T G Q K(L)	C:Carbamidomethylation	127.32	665.6855	1995.033	0.0092	4.6	6.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
9407	dirMS_041712_NAR_50mM_plus2.12845.12845.3	3	10.47	0	5.97E+05		(R)FDAERP	(R)F D/A/E/R P V D C/S V/I V/V/N K(Q)	C:Carbamidomethylation	135.82	616.6476	1847.932	-0.0038	-2	4.56	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
9408	dirMS_041712_NAR_50mM_plus2.15648.15648.3	3	10.47	0	1.49E+06		(R)LASTLVH	(R)L/A/S T L V H L G E Y Q A/A/V D G A R(K)		149.7	657.6802	1971.029	-0.0034	-1.7	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
9409	dirMS_041712_NAR_60mM_plus.12859.12859.3	3	10.47	1	8.89E+05	M232m	(R)MSmKEV	(R)M S m K E V D E\Q|M|L/N V Q N K(N)	m:Oxidized methionine	123.58	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
9410	dirMS_041712_NAR_60mM_plus.13009.13171.3	3	10.47	1	5.76E+05		(R)VVNGKV	(R)V/V/N/G K/V/E/Y F L K(W)		124.92	432.5826	1295.736	-0.0026	-2	8.47	11857.8	9.63	HUMAN	B8ZZ43	Chromobox homolog 3 (HP1 gamma homolog, Drosophila), isoform CRA_b
9411	dirMS_041712_NAR_60mM_plus.16702.16702.3	3	10.47	1	4.68E+04		(K)VGEVIVT	(K)V/G/E/V/I/V/T K D D A M L/L K(G)		144.18	544.3059	1630.908	-0.0053	-3.2	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
9412	dirMS_041712_NAR_60mM_plus.17432.17432.3	3	10.47	1	3.55E+05		(R)LAAELNI	(R)L/A/A E/L/N K F\M L E/K(V)		147.63	469.5946	1406.771	-0.002	-1.4	6.14	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
9413	dirMS_041712_NAR_60mM_plus.9446.9446.3	3	10.47	1	1.94E+06		(K)VVWVEE	(K)V V|W V/E E/S D/K R(S)		107.43	416.221	1246.643	0.0058	4.7	4.68	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
9414	dirMS_041712_NAR_30mM_minus2.16946.16946.2	2	10.46	0	1.31E+05		(R)IMNTFS	(R)I/M|N T|F|S/V V/P S P K(V)		146.03	660.3534	1319.703	-0.0033	-2.5	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
9415	dirMS_041712_NAR_30mM_minus2.19537.19537.2	2	10.46	0	2.76E+05		(R)ILVATNL	(R)I L|V/A/T N L/F G R(G)		162.08	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
9416	dirMS_041712_NAR_30mM_minus2.5291.5291.2	2	10.46	0	5.86E+05		(R)TDTGEP	(R)T D|T/G E\P M G R(G)		82.5	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
9417	dirMS_041712_NAR_40mM_minus2.13510.13510.3	3	10.46	0	3.00E+04		(K)YVDTPFC	(K)Y/V|D T|P F G K P S D A L/I L G K(I)		163.33	607.6637	1820.979	-0.0027	-1.5	5.96	33699.1	7.18	HUMAN	B4DUC8	S-methyl-5'-thioadenosine phosphorylase
9418	dirMS_041712_NAR_60mM_minus.12188.12188.3	3	10.46	1	5.65E+05		(R)ISVYYNE	(R)I/S|V/Y/Y N E A/T G G K Y V P R(A)		127.47	606.3103	1816.923	-0.0065	-3.6	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
9419	dirMS_041712_NAR_60mM_minus.16646.16646.3	3	10.46	1	8.10E+04		(R)RDDGTC	(R)R D D G T G Q\L/L\L|P L S D/A R(K)		152.85	576.307	1726.908	-0.0018	-1	4.43	533778	5.74	HUMAN	Q15149	Plectin
9420	dirMS_041712_NAR_60mM_minus.16801.16801.3	3	10.46	1	2.16E+05		(K)YAVLYQ	(K)Y/A|V/L/Y Q/P L F D K R(F)		154.38	504.9409	1512.821	-0.0128	-8.4	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
9421	dirMS_041712_NAR_60mM_minus.9845.9845.3	3	10.46	1	2.35E+05	M145m	(K)IDKTDYm	(K)I/D/K T D Y m/V|G S Y G P R(A)	m:Oxidized methionine	115.05	539.9245	1601.763	15.9961	0.8	5.96	21671	5.37	HUMAN	J3KTF8	Rho GDP-dissociation inhibitor 1 (Fragment)
9422	dirMS_041712_NAR_20mM_plus.11019.11019.2	2	10.46	0	1.17E+05		(K)EITALAP	(K)E I/T A/L/A P S/T M K(I)		148.15	581.3129	1161.618	0.0001	0.1	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
9423	dirMS_041712_NAR_20mM_plus.16708.16708.2	2	10.46	0	2.48E+05		(K)VQIAVA	(K)V Q I/A/V/A/N A/Q/E L\L/Q R(M)		186.6	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
9424	dirMS_041712_NAR_30mM_plus2.15320.15320.2	2	10.46	0	3.76E+05		(R)MAGAIA	(R)M A|G A|I/A|Q/G\L/I R(A)		133.05	550.816	1100.624	0.0002	0.2	9.5	4449.1	11.42	HUMAN	F8WEI0	Pyrroline-5-carboxylate reductase 3
9425	dirMS_041712_NAR_30mM_plus2.17988.17988.3	3	10.46	0	1.41E+05		(R)VNPALA	(R)V N/P/A\L/A/E|L N L R(S)		147.58	403.9019	1209.695	-0.0039	-3.2	5.97	20026.6	4.67	HUMAN	E9PIK5	Ribonuclease inhibitor (Fragment)
9426	dirMS_041712_NAR_30mM_plus2.6997.6997.2	2	10.46	0	4.61E+05		(R)GPGPLQ	(R)G P|G/P L Q E/R(S)		90.55	427.2296	853.453	-0.0007	-0.8	6	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
9427	dirMS_041712_NAR_50mM_plus2.14910.14910.3	3	10.46	0	8.03E+05		(R)TIQVENS	(R)T I/Q|V E/N\S H L I\L/T/G A G A L N K(V)		146.07	660.3668	1979.092	-0.0062	-3.1	6.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
9428	dirMS_041712_NAR_60mM_plus.7598.7601.3	3	10.46	1	9.64E+05		(R)YLAEVA	(R)Y/L|A E/V/A/A G D D/K K(G)		97.83	427.2226	1279.653	0.0004	0.3	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
9429	dirMS_041712_NAR_20mM_minus.14379.14379.2	2	10.45	0	2.52E+05		(R)APGSGL	(R)A/P/G S G L/A L\L/P L K(I)		198.32	568.8551	1136.704	-0.0008	-0.7	8.8	266161	5.68	HUMAN	E9PPU0	Epiplakin
9430	dirMS_041712_NAR_30mM_minus2.11461.11461.2	2	10.45	0	3.32E+05		(R)VQELPL	(R)V Q|E|L\P/L A/R(I)		115.82	463.2738	925.547	-0.0062	-6.7	5.97	16202.4	6.61	HUMAN	E9PI99	Nuclear transcription factor Y subunit gamma (Fragment)
9431	dirMS_041712_NAR_60mM_minus.12172.12172.3	3	10.45	1	9.57E+05		(R)VVDLMA	(R)V/V/D L M/A/H M A/S K/E(-)		127.78	444.2256	1330.649	0.0129	9.7	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
9432	dirMS_041712_NAR_60mM_minus.12300.12612.3	3	10.45	0	7.53E+05		(K)QADLYIS	(K)Q\A D L/Y/I/S E/G L/H/P R(I)		128.07	500.2603	1498.765	0.0015	1	5.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
9433	dirMS_041712_NAR_20mM_plus.11298.11298.3	3	10.45	0	1.11E+05		(R)GCITIIGC	(R)G C I T I I/G|G G D/T/A/T C C A/K(W)	C:Carbamidomethylation	150.27	585.5999	1754.787	-0.0019	-1.1	5.84	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
9434	dirMS_041712_NAR_30mM_plus2.10524.10524.2	2	10.45	0	8.39E+05		(R)LTVEEA	(R)L/T|V/E/E/A V/R(H)		109.25	458.7641	916.51	0.0111	12.1	4.53	862169.3	5.27	HUMAN	H3BPE1	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5
9435	dirMS_041712_NAR_30mM_plus2.13010.13150.2	2	10.45	0	2.49E+05		(K)FGPALS	(K)F/G|P/A L/S V K(V)		122.13	409.7432	818.477	0.0021	2.5	8.75	65918.2	9.74	HUMAN	E7EQV3	Polyadenylate-binding protein 1
9436	dirMS_041712_NAR_30mM_plus2.19937.19937.2	2	10.45	0	1.48E+05		(K)SNSVEM	(K)S N|S\V/E/M D W/V L K(H)		157.97	654.3191	1307.63	0.0009	0.7	4.37	49548	5.89	HUMAN	P55795	Heterogeneous nuclear ribonucleoprotein H2
9437	dirMS_041712_NAR_40mM_plus2.9850.9850.3	3	10.45	0	1.23E+05		(R)VMLGET	(R)V M|L|G E/T N P A D S K/P G T I R(G)		122.05	595.9778	1785.916	0.0025	1.4	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
9438	dirMS_041712_NAR_50mM_plus2.13151.13151.3	3	10.45	0	3.85E+05		(K)VQASLA	(K)V Q/A S/L A A N T F T I/T G H/A/E T K(Q)		137.68	654.0087	1960.013	-0.0019	-1	6.72	11802.2	5.6	HUMAN	D6RDG3	Transcription factor BTF3 (Fragment)
9439	dirMS_041712_NAR_50mM_plus2.18501.18501.3	3	10.45	0	9.87E+05		(K)VAHALA	(K)V A H A L A E G\L|G\V/I|A C I G E K(L)	C:Carbamidomethylation	166.15	603.3265	1807.974	-0.0085	-4.7	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
9440	dirMS_041712_NAR_50mM_plus2.20762.20762.3	3	10.45	1	1.54E+05		(R)GGGNQ	(R)G G G/N Q/V/S L/L|N/V/V M/D L K K(C)		178.55	591.3291	1771.974	-0.0007	-0.4	8.59	218583	5.58	HUMAN	F5GWX5	Chromodomain-helicase-DNA-binding protein 4
9441	dirMS_041712_NAR_50mM_plus2.7427.7427.3	3	10.45	1	2.93E+05		(R)IVEQDTI	(R)I V|E/Q D/T/M/P P K G V R(H)		105.32	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
9442	dirMS_041712_NAR_60mM_plus.11784.11784.3	3	10.45	1	1.10E+06		(K)QSSSSRI	(K)Q/S/S/S S R D D N M/F Q I/G\K(M)		119.07	567.2609	1699.77	-0.0023	-1.3	5.96	14395.1	9.6	HUMAN	P53999	Activated RNA polymerase II transcriptional coactivator p15
9443	dirMS_041712_NAR_60mM_plus.15399.15399.3	3	10.45	0	3.46E+05		(K)DCGATV	(K)D C|G|A/T W V/V/L/G H S E R(R)	C:Carbamidomethylation	137.57	529.5842	1586.738	0	0	5.32	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
9444	dirMS_041712_NAR_60mM_plus.16406.16427.3	3	10.45	0	4.31E+05		(R)FVFDRPI	(R)F/V|F D R/P L|P V S R(L)		142.5	444.917	1332.742	-0.0058	-4.4	9.6	18685.5	9.45	HUMAN	B4DEV8	Proteasome subunit alpha type
9445	dirMS_041712_NAR_60mM_plus.21232.21232.3	3	10.45	0	2.16E+05		(K)ALESPEF	(K)A L/E S/P/E R P F L A I L/G G A K(V)		174.75	590.3367	1768.996	0	0	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
9446	dirMS_041712_NAR_120mM_minus.7013.7013.2	2	10.44	1	1.40E+05		(K)IIAPPERI	(K)I/I/A/P/P E R K(Y)		92.63	462.2871	923.567	-0.0004	-0.4	8.75	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
9447	dirMS_041712_NAR_30mM_minus2.10409.10598.2	2	10.44	0	1.29E+06		(K)TFEINPR	(K)T/F|E/I/N/P/R(H)		111.37	438.7375	876.457	0.0103	11.8	5.66	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
9448	dirMS_041712_NAR_30mM_minus2.12493.12493.2	2	10.44	0	1.27E+05		(K)IGVTVLS	(K)I/G|V/T/V L S/R(I)		121.38	422.7649	844.525	-0.0026	-3	9.75	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
9449	dirMS_041712_NAR_30mM_minus2.18822.18822.2	2	10.44	0	9.16E+04		(K)NYLIDFK	(K)N/Y|L/I\D F K(H)		157.13	456.7503	912.482	0.0108	11.8	5.83	49548.2	9.34	HUMAN	B7Z9D5	Testis-expressed sequence 10 protein
9450	dirMS_041712_NAR_40mM_minus2.6980.6980.2	2	10.44	0	5.85E+05		(R)GYSFTTT	(R)G Y|S|F/T\T\T A E R(E)		111.95	566.7661	1132.527	-0.002	-1.8	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
9451	dirMS_041712_NAR_50mM_minus2.12727.12727.3	3	10.44	0	3.18E+06	M84m	(K)YPIEHGI	(K)Y/P/I E H G I I|T|N/W/D D m E K(I)	m:Oxidized methionine	141.42	659.6398	1960.911	15.9939	-0.5	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
9452	dirMS_041712_NAR_50mM_minus2.9131.9131.3	3	10.44	1	7.92E+05		(K)ATAVVD	(K)A T|A/V/V/D/G A F/K E V K(L)		119.97	445.5821	1334.731	0.0003	0.2	6.11	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
9453	dirMS_041712_NAR_60mM_minus.4643.4643.3	3	10.44	1	6.72E+04		(R)AAEEED	(R)A A/E E/E/D E A/D/P K/R(Q)		77.55	453.872	1359.602	-0.0008	-0.6	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
9454	dirMS_041712_NAR_60mM_minus.7302.7302.3	3	10.44	0	2.48E+06	M434m	(R)LESGmC	(R)L E|S/G m Q N/M/S I H T K(T)	m:Oxidized methionine	98.97	497.9023	1475.698	15.9942	-0.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
9455	dirMS_041712_NAR_120mM_plus.20263.20263.3	3	10.44	0	2.78E+05		(R)INLWHL	(R)I/N|L/W H L/E I T D/R(S)		159.48	470.5889	1409.754	-0.0014	-1	5.32	52204.6	5.82	HUMAN	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
9456	dirMS_041712_NAR_120mM_plus.4607.4607.3	3	10.44	0	6.19E+05		(R)THSQGC	(R)T H\S\Q G G|Y/G/S Q/G/Y K(Y)		74.07	457.2092	1369.613	-0.0001	-0.1	8.2	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
9457	dirMS_041712_NAR_30mM_plus2.12457.12457.2	2	10.44	0	7.27E+05		(K)LGITQLR	(K)L/G/I/T Q L/R(F)		117.73	400.7516	800.499	-0.0029	-3.7	9.75	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
9458	dirMS_041712_NAR_30mM_plus2.13117.13117.2	2	10.44	0	6.36E+05		(K)GDYPLEA	(K)G D|Y/P/L E/A V R(M)		121.95	510.2633	1019.516	0.0037	3.6	4.37	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
9459	dirMS_041712_NAR_30mM_plus2.13471.13538.2	2	10.44	0	1.91E+06		(K)IYFMAG	(K)I/Y|F|M/A/G/S S/R(K)		125.05	516.2597	1031.498	0.0142	13.8	8.75	92752.5	4.76	HUMAN	P14625	Endoplasmin
9460	dirMS_041712_NAR_30mM_plus2.18416.18416.2	2	10.44	0	3.65E+05		(R)SQVEEEI	(R)S Q|V|E/E|E/L F/S V/R(V)		149.58	661.8302	1322.659	-0.0055	-4.2	4.25	533778	5.74	HUMAN	Q15149	Plectin
9461	dirMS_041712_NAR_30mM_plus2.4284.4284.2	2	10.44	0	1.80E+05		(R)SMPEQT	(R)S M/P E Q/T/G E K(-)		71.28	503.7289	1006.451	-0.0005	-0.5	4.53	12955	9.87	HUMAN	P62888	60S ribosomal protein L30
9462	dirMS_041712_NAR_40mM_plus2.5522.5523.2	2	10.44	0	2.45E+05	M299m	(K)NmMAA	(K)N m|M|A|A/C D|P R(H)	C:Carbamidomethylation m:Oxid	89.2	541.2145	1065.427	15.9943	-0.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
9463	dirMS_041712_NAR_40mM_plus2.5532.5532.2	2	10.44	0	2.45E+05	M299m	(K)NmMAA	(K)N/m|M/A/A C D/P R(H)	C:Carbamidomethylation m:Oxid	89.2	541.2145	1065.427	15.9943	-0.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
9464	dirMS_041712_NAR_50mM_plus2.15327.15327.3	3	10.44	1	8.32E+05		(R)GFPTIYF	(R)G F/P T I Y/F S/P A N K K(L)		148.8	490.5973	1469.779	-0.0014	-0.9	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
9465	dirMS_041712_NAR_50mM_plus2.5314.5314.3	3	10.44	0	3.81E+05	M116m	(R)ATAPQT	(R)A T|A/P/Q/T Q H V S P m R(Q)	m:Oxidized methionine	87.6	480.5727	1423.711	15.9925	-1.7	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
9466	dirMS_041712_NAR_60mM_plus.18660.18660.3	3	10.44	1	2.26E+05		(R)RGDINLI	(R)R G D I N L\L/M|L/G D/P G T A/K(S)		154.7	557.6331	1670.889	-0.0047	-2.8	5.96	78390.7	9.27	HUMAN	B1AHB1	DNA replication licensing factor MCM5
9467	dirMS_041712_NAR_60mM_plus.18857.18857.3	3	10.44	1	2.12E+05		(R)ANTFVA	(R)A N/T/F/V A E L/K/G L D P A R(V)		155.78	534.6306	1601.865	0.0127	7.9	6.12	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
9468	dirMS_041712_NAR_60mM_plus.18908.18908.3	3	10.44	0	3.09E+05		(R)GGHVVE	(R)G G H\V V E G\L\A|G E|L E/Q L R(A)		156.17	555.2949	1663.876	-0.0061	-3.6	4.75	106088.3	5.78	HUMAN	P10275	Androgen receptor
9469	dirMS_041712_NAR_120mM_minus.6882.6899.3	3	10.43	1	2.11E+07		(R)TKTEISEI	(R)T\K T E/I/S/E/M N R(N)		92.55	403.5363	1208.594	0.0004	0.3	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
9470	dirMS_041712_NAR_40mM_minus2.8616.8616.3	3	10.43	0	2.84E+05		(R)SVIDPVF	(R)S V\I/D P V/P A/P V G D S H V D G A A K(S)		132.52	644.3329	1930.987	-0.0027	-1.4	4.41	58326.8	5.7	HUMAN	Q13177	Serine/threonine-protein kinase PAK 2
9471	dirMS_041712_NAR_40mM_minus2.9174.9174.3	3	10.43	0	1.57E+05	M26m	(R)LSAmLV	(R)L/S/A/m L/V\P V T/P E V\K P K(R)	m:Oxidized methionine	136.37	542.315	1608.939	15.9911	-2.3	8.59	31524.1	4.5	HUMAN	P82970	High mobility group nucleosome-binding domain-containing protein 5
9472	dirMS_041712_NAR_50mM_minus2.11851.11851.3	3	10.43	1	1.57E+05		(K)TVNVVC	(K)T V|N V/V/Q F E/P S K G A I G K(A)		135.88	558.6442	1673.922	-0.004	-2.4	8.26	83905.8	6.62	HUMAN	P41250	Glycine--tRNA ligase
9473	dirMS_041712_NAR_50mM_minus2.14187.14187.3	3	10.43	1	1.31E+05		(R)QFVPIKV	(R)Q F V|P I/K\V E Q I/E/A G/T/P G R(L)		148.68	623.6775	1869.023	-0.0049	-2.6	6.14	55287.2	6.08	HUMAN	B2R5P6	Thioredoxin reductase 1, cytoplasmic
9474	dirMS_041712_NAR_50mM_minus2.17829.17829.3	3	10.43	0	4.30E+04		(R)IHFPLAT	(R)I H F P L A T\Y|A/P V I S A E K(A)		169.93	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
9475	dirMS_041712_NAR_60mM_minus.15683.15683.3	3	10.43	1	3.07E+05		(R)GFPTIYF	(R)G F/P T/I Y|F S P A N/K K(L)		147.2	490.5972	1469.779	-0.0017	-1.1	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
9476	dirMS_041712_NAR_60mM_minus.8223.8223.3	3	10.43	0	1.91E+05		(R)QYDISDI	(R)Q Y|D/I/S D/P Q/R/P R(L)		105.63	458.8971	1374.676	0.0007	0.5	5.96	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
9477	dirMS_041712_NAR_120mM_plus.5679.5679.3	3	10.43	1	3.76E+05		(R)AAQDRI	(R)A/A|Q|D\R D Q I Y R(R)		83.3	412.5446	1235.613	0.0065	5.3	6	12660.6	10.51	HUMAN	H7C2L4	Transformer-2 protein homolog beta (Fragment)
9478	dirMS_041712_NAR_20mM_plus.14713.14713.3	3	10.43	0	5.44E+04	M174m	(K)AmGAAC	(K)A m G A A Q\V|V/V/T/D L S A T R(L)	m:Oxidized methionine	173.1	535.9457	1589.832	15.991	-2.5	5.88	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase

9479	dirMS_041712_NAR_20mM_plus.17792.17792.2	2	10.43	0	9.19E+04	M148m	(K)TFAPEEI	(K)T F/A/P/E E\I S A m V L T K(M)	m:Oxidized methionine	193.65	776.8996	1536.798	15.9941	-0.5	4.53	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
9480	dirMS_041712_NAR_20mM_plus.18159.18159.2	2	10.43	0	1.02E+05		(R)AILVDLE	(R)A I\L|V/D L/E|P G T M D/S V R(S)		196.63	808.419	1615.836	-0.0053	-3.3	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
9481	dirMS_041712_NAR_30mM_plus2.7461.7500.2	2	10.43	0	7.62E+05	M1006m	(K)FmNAH	(K)F/m N/A H/N A L/K(T)	m:Oxidized methionine	93.58	531.266	1045.525	16	4.8	8.76	121034.8	9.43	HUMAN	P15918	V(D)J recombination-activating protein 1
9482	dirMS_041712_NAR_30mM_plus2.8320.8370.2	2	10.43	0	2.24E+05		(R)VAIEPG	(R)V/A|I|E|P G A P\R(E)		97.73	455.2602	909.515	-0.0021	-2.3	5.97	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
9483	dirMS_041712_NAR_40mM_plus2.11208.11208.3	3	10.43	0	1.02E+05		(R)VLVASS	(R)V L/V/A|S S/V/V/A/G E S Q K P E L K(A)		132.05	614.3443	1841.038	-0.0195	-10.6	6.11	61441.6	5.93	HUMAN	G8JLE9	Fragile X mental retardation protein 1
9484	dirMS_041712_NAR_40mM_plus2.13528.13528.3	3	10.43	0	2.60E+05		(R)VAPDEH	(R)V A|P/D E H P I L L T\E A/P L N/P K(I)		145.53	652.0252	1954.064	-0.0034	-1.7	4.65	42344.8	5.39	HUMAN	Q562R1	Beta-actin-like protein 2
9485	dirMS_041712_NAR_40mM_plus2.9279.9279.2	2	10.43	0	5.48E+04		(K)TIAPALV	(K)T I/A|P A L V S/K(K)		116.88	450.2765	899.556	-0.0103	-11.5	8.41	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
9486	dirMS_041712_NAR_40mM_plus2.9542.9542.2	2	10.43	0	7.31E+04		(R)GGGGN	(R)G G G G N\F/G|P G/P G S/N F/R(G)		119.27	689.3182	1377.629	-0.0003	-0.2	9.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
9487	dirMS_041712_NAR_50mM_plus2.12033.12033.3	3	10.43	1	5.06E+05		(R)DNKQA	(R)D N K Q A\G\V/F/E/P T I/V K(V)		131.38	515.9483	1545.827	0.0032	2.1	6.07	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
9488	dirMS_041712_NAR_50mM_plus2.19960.19960.3	3	10.43	0	5.26E+04		(K)GLCLLE	(K)G L/C L/L/E/Q I D S F K/P P\Q R(S)	C:Carbamidomethylation	172.9	634.3344	1900.995	-0.0063	-3.3	6.07	45536.8	9.03	HUMAN	B7Z1K2	HBS1-like protein
9489	dirMS_041712_NAR_60mM_plus.8202.8202.3	3	10.43	1	6.15E+05		(R)KQSTDE	(R)K\Q S T D E|E|V/T/S L A K(S)		100.87	479.2461	1435.728	-0.0037	-2.6	4.68	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
9490	dirMS_041712_NAR_20mM_minus.14477.14477.3	3	10.42	0	2.19E+05		(K)LAAELS	(K)L A\A E\L S A T/L|E|Q A/A/A/T A R(V)		198.9	562.9713	1686.902	-0.0027	-1.6	4.53	558007.1	5.44	HUMAN	P58107	Epiplakin
9491	dirMS_041712_NAR_50mM_minus2.16105.16244.3	3	10.42	0	1.46E+05		(K)LDPHLV	(K)L D|P/H/L/V\L D/Q L R(C)		160.2	440.2533	1318.748	-0.0024	-1.8	5.21	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
9492	dirMS_041712_NAR_60mM_minus.12077.12077.3	3	10.42	1	4.75E+05		(R)INVYYN	(R)I N|V|Y/Y\N E/A/T G G K Y/V P R(A)		127.67	615.3145	1843.934	-0.0048	-2.6	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
9493	dirMS_041712_NAR_120mM_plus.11119.11119.4	4	10.42	1	3.46E+04		(R)IFHTVTT	(R)I F H T V T/T/T D D/P V/I R K(L)		111.6	436.4888	1742.944	-0.0102	-5.8	6.75	31956.7	9.73	HUMAN	B0QYA5	Eukaryotic translation initiation factor 3 subunit D (Fragment)
9494	dirMS_041712_NAR_120mM_plus.16302.16302.4	4	10.42	1	9.60E+05		(R)ALEHFT	(R)A L\E H F T/D L Y/D/I|K R(A)		138.37	405.9647	1620.838	-0.0011	-0.7	5.38	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
9495	dirMS_041712_NAR_120mM_plus.16964.16964.3	3	10.42	2	5.20E+05		(R)ALAEIAK	(R)A L|A E I/A K/A\E L D/D|T\P M R G R(Q)		142	653.0096	1957.017	-0.0029	-1.5	4.78	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
9496	dirMS_041712_NAR_120mM_plus.20205.20205.3	3	10.42	1	3.71E+06		(K)AAIDWF	(K)A A/I/D/W F D G K E/F H\G N I I\K(V)		158.78	654.3334	1960.992	-0.0059	-3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
9497	dirMS_041712_NAR_120mM_plus.5556.5556.4	4	10.42	1	4.14E+05		(K)VGGTSD	(K)V G\G T S D\V/E/V/N E K/K D/R(V)		82.25	408.9601	1632.819	-0.0002	-0.1	4.78	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
9498	dirMS_041712_NAR_20mM_plus.17730.17730.2	2	10.42	0	9.69E+04	M148m	(K)TFAPEEI	(K)T F/A/P/E E\I S A m V L T K(M)	m:Oxidized methionine	193.58	776.8996	1536.798	15.9941	-0.5	4.53	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
9499	dirMS_041712_NAR_30mM_plus2.19388.19388.2	2	10.42	0	1.85E+04		(K)MNEFLE	(K)M/N|E/F/L/E/N F E K(N)		155.87	650.7974	1300.588	-0.0003	-0.2	4.25	28580.2	9.35	HUMAN	Q9UFN0	Protein NipSnap homolog 3A
9500	dirMS_041712_NAR_30mM_plus2.19580.19580.2	2	10.42	0	2.14E+05		(K)TVDNFV	(K)T V|D N/F|V/A/L/A T G E/K(G)		155.58	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
9501	dirMS_041712_NAR_30mM_plus2.22195.22195.2	2	10.42	0	1.82E+05		(K)GLSSLLC	(K)G L/S/S L|L/C N F/T/K(S)	C:Carbamidomethylation	171.9	620.3199	1239.64	-0.0077	-6.2	8.75	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
9502	dirMS_041712_NAR_30mM_plus2.8307.8307.2	2	10.42	0	2.73E+05		(K)EIAENAL	(K)E I/A\E/N A/L G/K(H)		96.92	472.755	944.505	-0.002	-2.1	4.53	36982.9	6.37	HUMAN	P31942	Heterogeneous nuclear ribonucleoprotein H3
9503	dirMS_041712_NAR_40mM_plus2.8348.8348.2	2	10.42	0	2.86E+05		(R)FGSGM	(R)F/G/S/G/M N M/G R(I)		109.45	478.706	956.408	-0.003	-3.1	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
9504	dirMS_041712_NAR_50mM_plus2.22108.22108.3	3	10.42	1	5.71E+05		(K)AGFLDL	(K)A/G/F/L D/L/K D\F L/P K(E)		188.93	455.2587	1363.762	-0.0005	-0.3	6	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
9505	dirMS_041712_NAR_60mM_plus.13796.13796.3	3	10.42	0	7.04E+05		(K)VLSLNFS	(K)V L/S L/N F/S\E C/H T/K(I)	C:Carbamidomethylation	129.08	478.9108	1434.705	0.0133	9.3	6.72	16092.9	6.43	HUMAN	D6RAC7	Ras GTPase-activating protein-binding protein 2 (Fragment)
9506	dirMS_041712_NAR_60mM_plus.14402.14402.3	3	10.42	1	1.02E+06		(R)SGKAPIL	(R)S G K A P I\L\I/A/T/D/V/A S\R(G)		131.57	500.2895	1498.859	-0.0048	-3.2	8.46	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
9507	dirMS_041712_NAR_30mM_minus2.11352.11459.2	2	10.41	0	5.93E+05		(K)TWTVV	(K)T W|T/V/V/D/A K(T)		115.98	460.2501	919.488	0.0046	5	5.5	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
9508	dirMS_041712_NAR_40mM_minus2.9349.9349.3	3	10.41	1	6.96E+05	M356m	(K)VGEVIV	(K)V/G\E|V\I V T K/D D A m L L K(G)	m:Oxidized methionine	136.93	549.6354	1630.908	15.9832	-7.1	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
9509	dirMS_041712_NAR_50mM_minus2.10593.10593.3	3	10.41	1	7.44E+03		(K)VAVVAG	(K)V/A/V/V/A/G Y G/D/V G K G C A Q A L/R(G)	C:Carbamidomethylation	129.78	630.9952	1890.985	-0.0144	-7.6	8.56	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
9510	dirMS_041712_NAR_60mM_minus.17898.17898.3	3	10.41	0	1.19E+06		(K)VSHLLGI	(K)V S H L\L G I\N|V/T/D F T R(G)		161.52	524.623	1571.854	0.0004	0.3	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
9511	dirMS_041712_NAR_60mM_minus.9990.9990.3	3	10.41	1	1.25E+05		(R)AGTGVD	(R)A G/T/G/V/D N V/D/L E/A A T R\K(G)		115.55	539.6117	1616.824	-0.0033	-2	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
9512	dirMS_041712_NAR_20mM_plus.12794.12794.2	2	10.41	0	1.23E+05		(R)LVVPAS	(R)L V|V/P A/S Q C G S L I/G K(G)	C:Carbamidomethylation	161.42	714.8991	1428.788	0.003	2.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
9513	dirMS_041712_NAR_20mM_plus.13410.13410.2	2	10.41	0	9.69E+04		(R)AELIVQ	(R)A E|L|I/V\Q P E/L/K(Y)		164.3	570.3361	1139.667	-0.0021	-1.9	4.53	334221.3	6.44	HUMAN	P15924	Desmoplakin
9514	dirMS_041712_NAR_20mM_plus.13697.13713.2	2	10.41	0	9.86E+04		(R)LVVPAT	(R)L V|V|P A T Q C G S L I/G K(G)	C:Carbamidomethylation	166.88	721.9033	1442.804	-0.0042	-2.9	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
9515	dirMS_041712_NAR_20mM_plus.19241.19241.2	2	10.41	0	1.63E+05		(R)TGAIVD	(R)T G A\I V/D\V|P\V/G E E L L G R(V)		204.47	812.9497	1624.891	0.0017	1	4.14	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
9516	dirMS_041712_NAR_20mM_plus.8177.8177.2	2	10.41	0	1.06E+05		(K)VTEDTS	(K)V/T/E/D T S S V/L R(S)		126.02	553.7889	1106.569	0.0017	1.6	4.37	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
9517	dirMS_041712_NAR_30mM_plus2.18250.18250.2	2	10.41	0	2.50E+05		(K)TTFEDL	(K)T/T|F/E D/L/I Q/R(C)		148.95	561.7934	1122.579	0.0006	0.5	4.37	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
9518	dirMS_041712_NAR_30mM_plus2.8404.8404.2	2	10.41	0	8.89E+05		(R)TLLEGEE	(R)T L|L/E/G E E/S R(M)		98.47	517.2613	1033.516	-0.0007	-0.7	4.25	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
9519	dirMS_041712_NAR_40mM_plus2.11718.11718.2	2	10.41	0	7.03E+04		(K)IAWALS	(K)I/A|W/A L/S R(K)		135.1	408.7393	816.473	-0.0013	-1.6	9.75	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
9520	dirMS_041712_NAR_50mM_plus2.11465.11465.3	3	10.41	1	2.61E+05		(K)CATITP	(K)C A|T\I/T P D E A R/V E E/F K(L)	C:Carbamidomethylation	127.75	589.2842	1765.843	-0.0045	-2.5	4.41	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
9521	dirMS_041712_NAR_50mM_plus2.14516.14516.3	3	10.41	1	4.49E+05		(R)ETFEKT	(R)E T/F E K T/P V/E/V/P V G G F K(G)		144.3	588.644	1763.921	-0.004	-2.3	4.79	533778	5.74	HUMAN	Q15149	Plectin
9522	dirMS_041712_NAR_50mM_plus2.15671.15671.3	3	10.41	1	1.24E+06		(K)VQGGAL	(K)V Q|G/G/A L E D S Q L V A G V A F K/K(T)		150.85	639.6848	1917.044	-0.0042	-2.2	6.04	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
9523	dirMS_041712_NAR_50mM_plus2.21829.21829.3	3	10.41	1	2.08E+05		(R)KVPELM	(R)K\V P/E\L M E M/F L/P A T K(N)		185.52	545.2925	1633.869	-0.0063	-3.8	6.14	95051	6.63	HUMAN	B3KXW5	AP-1 complex subunit gamma-1
9524	dirMS_041712_NAR_120mM_minus.7048.7048.2	2	10.4	0	4.18E+05		(K)HNAAFC	(K)H/N|A\A F\C\Y/K(L)	C:Carbamidomethylation	92.42	505.7282	1010.451	-0.0021	-2.1	8.6	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
9525	dirMS_041712_NAR_20mM_minus.7044.7044.2	2	10.4	0	4.77E+05	M281m	(R)AEAESm	(R)A E|A/E/S m Y\Q I K(Y)	m:Oxidized methionine	117.9	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
9526	dirMS_041712_NAR_20mM_minus.9914.9914.2	2	10.4	0	7.44E+04		(K)DVNAA	(K)D V|N|A|A/I A T I K(T)		149.2	508.2919	1015.578	-0.0017	-1.7	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
9527	dirMS_041712_NAR_30mM_minus2.17143.17143.2	2	10.4	0	1.84E+05		(R)SIQEEL	(R)S I/Q/E/E L/Q Q L R(Q)		146.58	622.3359	1243.664	0.0004	0.3	4.53	533778	5.74	HUMAN	Q15149	Plectin
9528	dirMS_041712_NAR_50mM_minus2.12557.12557.3	3	10.4	0	2.96E+05		(K)AASDIA	(K)A A|S/D I|A M/T E L/P P T H P I R(L)		139.5	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
9529	dirMS_041712_NAR_50mM_minus2.13044.13044.3	3	10.4	1	7.44E+05		(K)VLAGDK	(K)V L|A G D K N F I|T/A E E L R(R)		142.85	559.3044	1675.901	-0.0027	-1.6	4.68	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
9530	dirMS_041712_NAR_60mM_minus.19786.19786.3	3	10.4	1	1.54E+06		(K)EIIDLVL	(K)E I/I/D/L V L D R I/R(K)		179.68	452.2739	1354.805	0.0019	1.4	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
9531	dirMS_041712_NAR_120mM_plus.10575.10772.3	3	10.4	0	1.23E+06		(R)GLHQSI	(R)G L/H Q S\I/E/E/F/R(A)		109.27	405.8796	1215.612	0.0126	10.4	5.4	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
9532	dirMS_041712_NAR_120mM_plus.17216.17216.3	3	10.4	1	3.01E+05		(K)NKYQEL	(K)N K Y Q E\L|I|N/D/I A R(D)		143.02	492.9299	1476.781	-0.0054	-3.6	6.07	125076	8.92	HUMAN	H0YLE8	Ras GTPase-activating-like protein IQGAP1
9533	dirMS_041712_NAR_120mM_plus.20758.20886.4	4	10.4	1	5.00E+05		(R)GIEKPP	(R)G I|E K/P/P F E L/P D/F I K R(T)		162.38	447.2518	1785.99	-0.0044	-2.5	6.18	98282.7	5.49	HUMAN	E9PPJ0	Splicing factor 3B subunit 2
9534	dirMS_041712_NAR_120mM_plus.23940.23940.4	4	10.4	2	2.64E+05		(R)RGVML	(R)R G V\M|L/A\V D A V/I/A E L K/K(Q)		179.85	429.0075	1713.009	-0.001	-0.6	8.59	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
9535	dirMS_041712_NAR_20mM_plus.16448.16448.2	2	10.4	0	1.66E+05		(R)LLEAQIA	(R)L L E A Q I|A|T/G G/I/I\D|P K(E)		185.07	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
9536	dirMS_041712_NAR_20mM_plus.19126.19126.3	3	10.4	0	2.32E+05		(R)VCTLAII	(R)V C T/L\A I\I/D/P G D S D I I R(S)	C:Carbamidomethylation	202.78	586.641	1757.91	-0.0018	-1	3.93	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
9537	dirMS_041712_NAR_40mM_plus2.10643.10739.3	3	10.4	0	1.77E+05		(K)MAPVPL	(K)M/A|P V|P L D D S N/R P A S L T K(D)		128.32	604.6467	1811.932	-0.0065	-3.6	5.71	53030.7	11.3	HUMAN	E9PJA7	Bcl-2-associated transcription factor 1
9538	dirMS_041712_NAR_40mM_plus2.14486.14833.3	3	10.4	0	5.22E+05		(R)GAPPSS	(R)G A|P|P/S S N I E D/F H G L L/P\K(G)		153.5	593.6385	1778.907	-0.0062	-3.5	5.32	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
9539	dirMS_041712_NAR_40mM_plus2.17391.17391.3	3	10.4	1	2.93E+05		(K)TGISDV	(K)T G I/S/D V F\A K N D L|A|V/V D/V R(I)		169.25	640.3451	1919.023	-0.0025	-1.3	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
9540	dirMS_041712_NAR_50mM_plus2.12345.12345.3	3	10.4	1	4.91E+05		(K)ILDSVG	(K)I/L/D/S V/G/I/E A D D D R L N/K(V)		132.85	591.6385	1772.902	-0.0015	-0.9	4.04	11664.7	4.42	HUMAN	P05387	60S acidic ribosomal protein P2
9541	dirMS_041712_NAR_50mM_plus2.17537.17537.3	3	10.4	1	7.25E+05		(K)SELVAM	(K)S E|L/V/A/M L E E E E L R K(A)		159.73	559.2899	1675.857	-0.002	-1.2	4.32	18679.2	5.61	HUMAN	B4DWW1	ADP-ribosylation factor-like protein 1
9542	dirMS_041712_NAR_60mM_plus.16614.16614.3	3	10.4	0	1.92E+05		(R)LSQYQE	(R)L/S/Q/Y/Q E/P L H L/P G V R(V)		143.7	546.297	1636.881	-0.0041	-2.5	6.75	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
9543	dirMS_041712_NAR_120mM_minus.4523.4528.2	2	10.39	0	7.45E+05		(R)HSDGNL	(R)H/S/D|G N L C|V K(V)	C:Carbamidomethylation	73.97	515.2423	1029.478	-0.0009	-0.9	6.74	7781.8	6.82	HUMAN	E9PE20	Signal recognition particle 9 kDa protein
9544	dirMS_041712_NAR_50mM_minus2.7895.7895.3	3	10.39	0	4.58E+04		(R)QLSQAG	(R)Q L/S\Q/A G/S F/S D/G T H/G G L R(Y)		111.92	573.2875	1717.825	0.0227	13.2	6.74	266161	5.68	HUMAN	E9PPU0	Epiplakin
9545	dirMS_041712_NAR_120mM_plus.5256.5256.3	3	10.39	0	9.66E+03		(R)YIDTEH	(R)Y/I/D T E/H G G S Q A R(F)		80.57	445.2109	1333.613	0.005	3.8	5.32	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
9546	dirMS_041712_NAR_20mM_plus.8960.8960.2	2	10.39	0	3.80E+05	M161m	(K)LLIEmE	(K)L L|I|E m E/Q R(L)	m:Oxidized methionine	132.62	524.278	1031.555	15.9933	-1.5	4.53	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
9547	dirMS_041712_NAR_30mM_plus2.18422.18422.2	2	10.39	0	2.36E+05		(K)GNFNYI	(K)G N\F|N/Y/I/E F T R(I)		150.27	630.8035	1260.601	-0.001	-0.8	6	20513.6	4.62	HUMAN	J3QRS3	Myosin regulatory light chain 12A
9548	dirMS_041712_NAR_30mM_plus2.21770.21939.2	2	10.39	0	6.86E+05		(K)NGFLLD	(K)N G|F|L|L/D/G F/P R(T)		170.28	568.3022	1135.59	0.0077	6.7	5.84	21283.1	6.45	HUMAN	F8VY04	Adenylate kinase 2, mitochondrial
9549	dirMS_041712_NAR_40mM_plus2.11332.11332.3	3	10.39	0	3.11E+04		(K)LQALAN	(K)L Q|A L/A/N E Q/A\A A A H/E L E K(M)		132.83	602.981	1806.935	-0.006	-3.3	4.75	156557.7	5.52	HUMAN	Q86UP2	Kinectin
9550	dirMS_041712_NAR_40mM_plus2.6277.6277.2	2	10.39	1	2.84E+05		(R)YSGGNY	(R)Y/S|G G N/Y R D N|Y|D/N(-)		95.58	719.2857	1437.567	-0.0024	-1.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
9551	dirMS_041712_NAR_50mM_plus2.6068.6068.3	3	10.39	0	3.54E+04		(K)QPPTAA	(K)Q P/P T/A/A/G R P V D/A S P R(V)		95.98	507.2698	1519.798	-0.0027	-1.8	9.6	43421.2	6.21	HUMAN	E9PHI6	Cytoplasmic dynein 1 light intermediate chain 1
9552	dirMS_041712_NAR_50mM_plus2.8143.8143.3	3	10.39	1	2.57E+05	M227m M2	(R)mQKEIT	(R)m Q K/E I T A|L/A|P S/T m K(I)	m:Oxidized methionine	109.02	527.6045	1548.812	31.9865	-2.1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
9553	dirMS_041712_NAR_60mM_plus.12206.12206.3	3	10.39	0	5.63E+05		(R)ILDEIEE	(R)I/L|D/E I/E\E H/N I K(I)		120.53	451.5717	1352.706	-0.0051	-3.8	4.4	37167.8	5.8	HUMAN	B5MCX3	Septin-2
9554	dirMS_041712_NAR_60mM_plus.15282.15387.3	3	10.39	0	2.64E+06		(R)LIDLHSP	(R)L/I D/L H/S/P S E I/V/K(Q)		137.42	450.9323	1350.763	0.0196	14.5	5.32	7304.3	9.39	HUMAN	G3XAN0	40S ribosomal protein S20
9555	dirMS_041712_NAR_120mM_minus.13891.13891.4	4	10.38	1	1.62E+06		(K)ASIHEA	(K)A/S I/H E A W T D/G K E A/M L K(H)		129.97	447.476	1786.879	0.0029	1.6	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
9556	dirMS_041712_NAR_30mM_minus2.6216.6216.2	2	10.38	0	9.08E+04		(R)EAEEVY	(R)E A|E/E V/Y/R(N)		88.12	448.2136	895.416	0.0043	4.8	4.25	54793.4	10.51	HUMAN	B7Z4Q3	Putative RNA-binding protein Luc7-like 2
9557	dirMS_041712_NAR_40mM_minus2.15617.15617.3	3	10.38	1	4.96E+05		(K)ALFEEV	(K)A L|F/E/E V/P E L L T E A E K K(E)		181.8	615.9988	1845.984	-0.0026	-1.4	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
9558	dirMS_041712_NAR_50mM_minus2.10078.10078.3	3	10.38	0	2.79E+05		(R)EALLSSA	(R)E/A|L|L/S S A|V D H G S D E V K(F)		125.1	552.9403	1656.807	-0.0012	-0.7	4.31	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
9559	dirMS_041712_NAR_50mM_minus2.10949.10949.3	3	10.38	1	1.10E+04		(K)ALELDP	(K)A L|E|L/D/P D N E T Y K S N L K(I)		130.67	617.3102	1849.918	-0.0018	-0.9	4.32	34290.7	4.81	HUMAN	O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha
9560	dirMS_041712_NAR_50mM_minus2.7675.7675.3	3	10.38	1	3.42E+04		(K)EAVAPV	(K)E A/V/A/P V Q E E S D L/E/K K(R)		110.72	557.9594	1671.844	0.0201	12	4.25	70939.9	5.17	HUMAN	B7ZA04	Cytoplasmic dynein 1 intermediate chain 2
9561	dirMS_041712_NAR_20mM_plus.10152.10152.2	2	10.38	0	1.61E+05		(K)GEATVS	(K)G E/A/T|V|S/F D D/P P S A K(A)		142.05	710.8324	1420.659	-0.0015	-1.1	4.03	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
9562	dirMS_041712_NAR_20mM_plus.10245.10245.3	3	10.38	0	1.31E+05	M281m M2	(R)NmPQA	(R)N m/P Q A D\A m|V|L/V/A/R(N)	m:Oxidized methionine	143.42	483.2393	1415.713	31.99	0.1	5.84	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
9563	dirMS_041712_NAR_20mM_plus.11248.11248.2	2	10.38	0	1.28E+05		(R)YALYDA	(R)Y A|L/Y/D/A/T/Y E T K(E)		150.22	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
9564	dirMS_041712_NAR_20mM_plus.14992.14992.2	2	10.38	0	5.86E+04		(R)NTGTEA	(R)N T\G T E|A/P D Y L/A T V/D/V D P K(S)		174.47	953.4536	1905.908	-0.0077	-4	3.84	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
9565	dirMS_041712_NAR_20mM_plus.15412.15412.2	2	10.38	0	7.36E+05		(K)LLCGLLA	(K)L/L/C/G L L A E R(L)	C:Carbamidomethylation	177.8	522.7971	1044.587	-0.0001	-0.1	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
9566	dirMS_041712_NAR_20mM_plus.8911.8911.2	2	10.38	0	1.30E+05		(K)VLEEAN	(K)V L/E|E/A/N Q\A\I/N\P K(L)		131.6	663.353	1325.706	-0.0072	-5.5	4.53	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
9567	dirMS_041712_NAR_30mM_plus2.11684.11684.2	2	10.38	0	6.20E+05		(R)AMGEQ	(R)A M|G E/Q/A/V/A L/A/R(A)		114.52	558.7944	1116.583	-0.0015	-1.3	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
9568	dirMS_041712_NAR_30mM_plus2.7231.7338.2	2	10.38	0	1.84E+05		(K)AAAAAA	(K)A A|A|A|A|A/A L Q/A K(S)		92.88	478.7844	956.552	0.0092	9.6	8.8	37884.5	11.27	HUMAN	H3BM89	60S ribosomal protein L4
9569	dirMS_041712_NAR_50mM_plus2.12349.12349.3	3	10.38	0	3.51E+05		(K)TVPEEL	(K)T V/P E/E L/V K/P E E/L S/K(Y)		132.6	533.2917	1597.868	-0.0078	-4.9	4.49	27945.7	6.25	HUMAN	F5GY56	Pre-mRNA-processing factor 19 (Fragment)
9570	dirMS_041712_NAR_50mM_plus2.13784.13784.3	3	10.38	1	3.88E+05		(K)ALELDS	(K)A L|E|L/D S N N/E\K G L/F R(R)		140.25	535.9422	1605.823	-0.0111	-6.9	4.68	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
9571	dirMS_041712_NAR_50mM_plus2.16720.16831.3	3	10.38	1	5.45E+05	M137m	(K)LKEAELL	(K)L/K|E A E L\L\E|P L/m/P A I R(A)	m:Oxidized methionine	156.03	580.3229	1722.982	15.9719	-13.2	4.79	56164.6	6.01	HUMAN	E9PP73	Coatomer subunit beta (Fragment)
9572	dirMS_041712_NAR_60mM_plus.6324.6340.3	3	10.38	1	4.98E+05		(R)TAQEVE	(R)T|A|Q/E V E T Y R/R(S)		91.87	418.2158	1252.628	0.0048	3.8	5.81	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
9573	dirMS_041712_NAR_120mM_minus.11617.11830.3	3	10.37	1	6.27E+05		(R)ARSEQF	(R)A R\S\E\Q|F|I/N L/R(E)		117.93	411.8945	1233.67	-0.0009	-0.7	9.64	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
9574	dirMS_041712_NAR_30mM_minus2.12028.12422.2	2	10.37	0	2.65E+05		(R)IFYDMK	(R)I/F|Y D/M/K(V)		119.18	408.702	816.396	0.0007	0.8	5.83	15739.2	9.3	HUMAN	F6RFD5	Destrin
9575	dirMS_041712_NAR_30mM_minus2.7543.7543.2	2	10.37	0	1.19E+05		(R)GGGEQE	(R)G G G E Q/E/T Q/E|L/A S/K(R)		95.42	667.3161	1333.623	0.0019	1.4	4.25	33411.4	5.35	HUMAN	Q96QR8	Transcriptional activator protein Pur-beta
9576	dirMS_041712_NAR_30mM_minus2.9932.9968.2	2	10.37	0	3.68E+04		(R)YVLCTA	(R)Y V|L/C/T/A/P R(A)	C:Carbamidomethylation	106.85	490.2513	979.503	-0.0076	-7.8	8.75	86292.1	5.81	HUMAN	J3KQ69	DNA replication licensing factor MCM3
9577	dirMS_041712_NAR_40mM_minus2.11983.11983.3	3	10.37	0	2.73E+05		(K)DAGEGL	(K)D A|G/E/G L/L A V Q I T D/P E G K\P K(K)		154	646.6785	1938.018	0.0031	1.6	4.32	283472.4	5.71	HUMAN	P21333	Filamin-A
9578	dirMS_041712_NAR_40mM_minus2.15043.15043.3	3	10.37	0	1.44E+05		(K)LFLFHTS	(K)L F\L F H T S L/P|I/A E\A/P G/K(L)		173.92	580.9924	1740.968	-0.0057	-3.3	6.75	108105.4	6.57	HUMAN	E7EP00	Protein transport protein Sec24C
9579	dirMS_041712_NAR_50mM_minus2.12437.12437.3	3	10.37	0	2.71E+05		(K)AASDIA	(K)A A|S/D/I|A M/T E L/P P T H P I R(L)		139.15	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
9580	dirMS_041712_NAR_50mM_minus2.12877.12877.3	3	10.37	0	4.17E+06	M84m	(K)YPIEHGI	(K)Y/P/I E H G I I|T N|W/D D m E K(I)	m:Oxidized methionine	141.65	659.6398	1960.911	15.9939	-0.5	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
9581	dirMS_041712_NAR_50mM_minus2.7446.7446.3	3	10.37	0	1.91E+04		(R)AVEVQG	(R)A V|E/V Q/G P S L/E/S G D/H/G K(I)		109.23	537.2631	1609.782	-0.0069	-4.3	4.65	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
9582	dirMS_041712_NAR_60mM_minus.9547.9629.3	3	10.37	1	3.49E+05	M64m	(K)LmDQLE	(K)L m|D Q\L/E/A L/K K(Q)	m:Oxidized methionine	113.47	402.2246	1188.666	15.9936	-1.1	6.07	34163.9	5.87	HUMAN	Q9NP79	Vacuolar protein sorting-associated protein VTA1 homolog
9583	dirMS_041712_NAR_120mM_plus.12663.12663.3	3	10.37	1	1.02E+06		(K)VKLEAEI	(K)V K L E A E\I|A/T/Y R(R)		120.2	431.5774	1292.721	-0.0032	-2.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9584	dirMS_041712_NAR_120mM_plus.25688.25688.3	3	10.37	1	4.77E+05		(R)GVMLA	(R)G V/M/L/A V D A/V/I A E L K/K(Q)		193.27	519.6402	1556.908	-0.002	-1.3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
9585	dirMS_041712_NAR_120mM_plus.5711.5711.3	3	10.37	1	3.76E+05		(R)AAQDRD	(R)A/A|Q/D\R D Q I Y/R(R)		83.3	412.5446	1235.613	0.0065	5.3	6	12660.6	10.51	HUMAN	H7C2L4	Transformer-2 protein homolog beta (Fragment)
9586	dirMS_041712_NAR_20mM_plus.9336.9336.2	2	10.37	0	1.61E+05	M209m	(K)AGAGSA	(K)A G A G S/A\T/L/S m A/Y A/G A R(F)	m:Oxidized methionine	135.33	735.851	1454.706	15.9891	-4	8.79	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
9587	dirMS_041712_NAR_30mM_plus2.12927.12945.2	2	10.37	0	2.82E+05		(K)DISLSDY	(K)D I|S|L/S D/Y/K(G)		121.2	470.7391	940.462	0.0087	9.3	4.21	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1

9588	dirMS_041712_NAR_30mM_plus2.14787.15028.2	2	10.37	0	1.28E+06		(R)LCFEGLF	(R)L/C|F/E/G L/R(S)	C:Carbamidomethylation	130.85	447.7285	894.45	-0.0005	-0.5	6	533778	5.74	HUMAN	Q15149	Plectin
9589	dirMS_041712_NAR_30mM_plus2.18257.18257.2	2	10.37	0	2.20E+05		(K)GVEGLIC	(K)G V/E G\L/I/D/I/E/N/P N R(V)		149.4	713.3669	1425.733	-0.0067	-4.7	4.14	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
9590	dirMS_041712_NAR_40mM_plus2.16018.16018.2	2	10.37	0	1.03E+05		(R)YLTVAA\	(R)Y L|T/V/A/A V F/R(G)		161.77	520.2997	1039.593	-0.0014	-1.3	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
9591	dirMS_041712_NAR_40mM_plus2.5544.5544.2	2	10.37	0	2.45E+05	M299m	(K)NmMAA	(K)N m|M/A|A C D/P R(H)	C:Carbamidomethylation m:Oxid	89.2	541.2145	1065.427	15.9943	-0.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
9592	dirMS_041712_NAR_50mM_plus2.18966.18966.3	3	10.37	1	2.89E+05		(K)LALFQAI	(K)L/A|L/F Q/A I G|K E V V D R(A)		168	520.3019	1558.895	-0.004	-2.6	6.07	266161	5.68	HUMAN	E9PPU0	Epiplakin
9593	dirMS_041712_NAR_50mM_plus2.21431.21431.3	3	10.37	1	1.55E+05		(K)ALFEEVF	(K)A L|F\E E/V/P E L L T E A E K K(E)		182.65	615.9987	1845.984	-0.0029	-1.6	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
9594	dirMS_041712_NAR_60mM_plus.5716.5716.3	3	10.37	1	1.53E+05	M131m	(R)QmGQP	(R)Q m/G\Q/P C/D\A/Y Q K R(L)	C:Carbamidomethylation m:Oxid	87.98	499.8898	1481.662	15.9925	-1.6	8.59	334221.3	6.44	HUMAN	P15924	Desmoplakin
9595	dirMS_041712_NAR_40mM_minus2.10900.10985.3	3	10.36	0	1.98E+05		(R)DLSHIGI	(R)D L S H I\G D\A\V|V|I/S/C A K(D)	C:Carbamidomethylation	147.28	528.9384	1584.805	-0.0044	-2.8	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
9596	dirMS_041712_NAR_50mM_minus2.13091.13091.3	3	10.36	1	2.73E+04		(K)VVSSSIV	(K)V V|S S/S I V D K Y I/G E/S A R(L)		142.6	570.6413	1709.907	0.0025	1.5	6.04	29938.9	6.07	HUMAN	H0YJC0	26S protease regulatory subunit 10B (Fragment)
9597	dirMS_041712_NAR_50mM_minus2.7911.7911.3	3	10.36	1	1.26E+05		(K)LLDGPST	(K)L L|D/G P S/T\E K D L D E K(K)		112	520.5968	1559.78	-0.0041	-2.6	4.11	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
9598	dirMS_041712_NAR_60mM_minus.7554.7554.3	3	10.36	0	4.90E+04		(R)QSLGHP	(R)Q S L G H\P|P P E/P/G P D R(V)		101.33	495.2483	1483.729	0.0015	1	5.32	12758.7	4.21	HUMAN	C9J830	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
9599	dirMS_041712_NAR_60mM_minus.8986.8986.3	3	10.36	1	3.60E+05	M230m M:	(R)mSMKE\	(R)m S M K E\V\D E\Q/m/L|N/V|Q N K(N)	m:Oxidized methionine	110.3	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
9600	dirMS_041712_NAR_60mM_minus.9340.9340.3	3	10.36	1	1.60E+05		(R)TPGKEA'	(R)T/P G K E A V/A/M/E S Y/A K(A)		111.93	494.5814	1481.73	-0.0008	-0.5	5.81	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
9601	dirMS_041712_NAR_120mM_plus.4851.4851.3	3	10.36	1	3.66E+05		(R)LRAETE(	(R)L R A E T E|Q|G/E/Q/Q R(Q)		76.6	482.2449	1444.714	0.0063	4.3	4.79	533778	5.74	HUMAN	Q15149	Plectin
9602	dirMS_041712_NAR_20mM_plus.14592.14592.2	2	10.36	0	4.50E+04	M256m	(R)SLDmDS	(R)S L/D|m/D|S I I A E V K(A)	m:Oxidized methionine	171.72	668.8371	1320.671	15.9954	0.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
9603	dirMS_041712_NAR_20mM_plus.19073.19073.3	3	10.36	0	2.07E+05		(K)TLETQS/	(K)T L E T Q S A\L/G/P/A L Q A A/F K(L)		202.57	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
9604	dirMS_041712_NAR_30mM_plus2.11776.11776.2	2	10.36	0	2.78E+06		(K)LSDGVA'	(K)L/S|D/G/V A V L K(V)		115.52	451.2712	901.535	-0.0002	-0.2	5.84	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
9605	dirMS_041712_NAR_30mM_plus2.12819.12819.2	2	10.36	0	2.25E+05		(K)SKPVFSE	(K)S K|P V/F\S E S|L|S D(-)		120.3	598.2946	1195.584	-0.0022	-1.8	4.67	11226.4	5.09	HUMAN	O60220	Mitochondrial import inner membrane translocase subunit Tim8 A
9606	dirMS_041712_NAR_30mM_plus2.18174.18174.2	2	10.36	0	2.80E+05		(R)VNPALA	(R)V N/P A\L A E/L N L R(S)		147.88	605.3509	1209.695	-0.0005	-0.4	5.97	20026.6	4.67	HUMAN	E9PIK5	Ribonuclease inhibitor (Fragment)
9607	dirMS_041712_NAR_30mM_plus2.19132.19132.2	2	10.36	0	3.59E+04		(K)DAGTIA(	(K)D A G|T|I/A/G L N V L R(I)		153.85	600.3411	1199.674	0.0007	0.6	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
9608	dirMS_041712_NAR_40mM_plus2.16370.16370.3	3	10.36	1	3.74E+05		(R)CITDPQ1	(R)C I/T|D/P Q T G L C L L/P/L K E K(K)	C:Carbamidomethylation	163.12	662.6815	1986.04	-0.0099	-5	6.07	533778	5.74	HUMAN	Q15149	Plectin
9609	dirMS_041712_NAR_40mM_plus2.20065.20065.3	3	10.36	1	5.88E+05		(K)EGGLGP	(K)E/G G L|G/P/L N I P L L A D V T R R(L)		189.8	631.0288	1891.076	-0.0041	-2.2	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
9610	dirMS_041712_NAR_50mM_plus2.11708.11708.3	3	10.36	1	5.26E+05		(K)LIPDSIGI	(K)L/I|P/D S I/G K D I\E K(A)		128.77	443.2514	1327.747	-0.0071	-5.4	4.56	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
9611	dirMS_041712_NAR_60mM_plus.5373.5373.2	2	10.36	1	8.14E+04		(K)CDSSPD!	(K)C D|S/S/P/D S A E D/V R K(V)	C:Carbamidomethylation	85.72	733.3133	1465.622	-0.003	-2.1	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
9612	dirMS_041712_NAR_120mM_minus.12116.12116.2	2	10.35	0	2.74E+05		(R)HEIVQTI	(R)H|E|I/V Q T L S/L/K(D)		120	584.3388	1167.673	-0.0029	-2.5	6.75	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
9613	dirMS_041712_NAR_20mM_minus.10483.10483.2	2	10.35	0	1.42E+05		(R)IYVVDV(	(R)I Y|V|V/D V/G S E P R(A)		152.95	617.3216	1233.647	-0.0115	-9.3	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
9614	dirMS_041712_NAR_30mM_minus2.12568.12654.2	2	10.35	0	2.85E+05		(R)NLGLYVI	(R)N/L|G L/Y/V K(T)		122.08	403.7423	806.477	0.0003	0.3	8.59	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
9615	dirMS_041712_NAR_30mM_minus2.17849.17849.2	2	10.35	0	7.98E+04		(R)ILFQEFR	(R)I/L|F Q/E/F/R(Q)		151.38	476.7657	952.525	-0.001	-1	6	232239.1	5.52	HUMAN	F2Z2U8	Myosin-14
9616	dirMS_041712_NAR_30mM_minus2.9653.9653.2	2	10.35	0	5.10E+04		(R)VTVVDV	(R)V T|V|V|D/V/N E S R(I)		106.58	559.2986	1117.585	0.0051	4.6	4.37	6026	6.52	HUMAN	D6RHF4	UDP-glucose 6-dehydrogenase (Fragment)
9617	dirMS_041712_NAR_50mM_minus2.9050.9050.3	3	10.35	1	1.91E+05		(R)VLTVIN(	(R)V L|T/V/I N Q T Q K E N L\R(K)		119.83	552.6528	1655.944	0	0	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
9618	dirMS_041712_NAR_60mM_minus.17839.17839.3	3	10.35	1	3.41E+05		(K)YGKLEV/	(K)Y/G K L E V A\N|L/L/L Q/K(S)		159.68	496.9631	1488.878	-0.0037	-2.5	8.5	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
9619	dirMS_041712_NAR_60mM_minus.7881.7881.3	3	10.35	1	4.85E+05		(R)YLAEVA'	(R)Y L/A E\V/A T/G E/K R(A)		104.22	412.8902	1236.658	-0.0022	-1.8	6.14	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
9620	dirMS_041712_NAR_120mM_plus.8842.8842.2	2	10.35	0	7.48E+05		(K)HFVALST	(K)H/F|V A L/S T N T T K(V)		99.23	609.8311	1218.648	0.0072	5.9	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
9621	dirMS_041712_NAR_20mM_plus.12978.12978.2	2	10.35	0	2.33E+04		(K)AVDSLVI	(K)A V/D/S/L/V/P I G R(G)		162.43	513.8007	1026.594	-0.0001	-0.1	5.88	48851.3	9.2	HUMAN	K7EK63	ATP synthase subunit alpha, mitochondrial
9622	dirMS_041712_NAR_20mM_plus.15641.15641.2	2	10.35	0	4.98E+03		(R)SSFYVN(	(R)S S/F\Y\V/N/G L\T\L/G G Q K(C)		180.83	735.8818	1470.759	-0.0024	-1.6	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
9623	dirMS_041712_NAR_20mM_plus.18723.18723.3	3	10.35	0	1.13E+05		(K)VIGNQS	(K)V I G N Q S L\V/N E/L\A/F\T A R(K)		200.63	577.9842	1731.939	-0.0008	-0.4	5.97	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
9624	dirMS_041712_NAR_20mM_plus.19144.19144.2	2	10.35	0	1.44E+05		(R)EGDVLT	(R)E G D\V/L\T/L/L E S E R(E)		203.47	680.8536	1360.696	0.0045	3.3	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
9625	dirMS_041712_NAR_20mM_plus.19350.19350.3	3	10.35	0	9.30E+04		(R)ALIAGG(	(R)A L|I|A G G G A|P E I/E L A/L/R(L)		205.05	517.6345	1550.89	-0.0011	-0.7	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
9626	dirMS_041712_NAR_20mM_plus.6982.6995.2	2	10.35	0	1.09E+05		(K)AGFAGD	(K)A G|F|A|G D D/A/P R(A)		114.77	488.7307	976.448	0.0058	6	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
9627	dirMS_041712_NAR_20mM_plus.7436.7436.2	2	10.35	0	2.40E+05		(K)VTLTSEE	(K)V T/L T/S/E/E E/A R(L)		119.92	567.7865	1134.564	0.002	1.8	4.25	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
9628	dirMS_041712_NAR_30mM_plus2.12713.12713.2	2	10.35	0	6.43E+04		(R)YLDGLT/	(R)Y/L/D/G L/T A/E R(T)		118.67	519.2668	1037.526	0.0001	0.1	4.37	65717	8.32	HUMAN	P35908	Keratin, type II cytoskeletal 2 epidermal
9629	dirMS_041712_NAR_30mM_plus2.22469.22469.2	2	10.35	0	1.02E+05		(R)SLDMDS	(R)S L|D/M/D S/I I/A E V K(A)		173.67	660.8437	1320.671	0.0086	6.5	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
9630	dirMS_041712_NAR_30mM_plus2.5398.5398.2	2	10.35	0	4.63E+05		(K)VSSFEEK	(K)V/S/S/F E/E K(M)		81.78	413.203	825.399	-0.0002	-0.2	4.53	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
9631	dirMS_041712_NAR_40mM_plus2.7108.7108.2	2	10.35	0	4.55E+04		(R)SSYLESP	(R)S S|Y/L/E/S P\R(G)		101.58	469.7347	938.458	0.0043	4.6	5.72	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
9632	dirMS_041712_NAR_50mM_plus2.17608.17608.3	3	10.35	1	2.09E+05		(R)EVQLEEI	(R)E V|Q/L/E/E L E/A A R D L V\S K(E)		160.73	610.3302	1828.965	0.011	6	4.25	45984.6	6.24	HUMAN	B4E1G6	Galactokinase
9633	dirMS_041712_NAR_60mM_plus.16195.16195.3	3	10.35	0	4.88E+05		(K)TTITMAI	(K)T T/I/T/M A/H L L A A R(E)		141.72	433.5839	1298.725	0.0122	9.4	9.44	37589.6	5.96	HUMAN	Q52LJ0	Protein FAM98B
9634	dirMS_041712_NAR_60mM_plus.6811.6827.3	3	10.35	1	6.59E+05		(R)EKVPGG	(R)E K V\P G G\L/Q/G/S Q D/R(G)		94.18	457.576	1370.702	0.0112	8.2	6.17	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
9635	dirMS_041712_NAR_120mM_minus.9983.9983.3	3	10.34	1	6.70E+05		(R)SRNTDE	(R)S\R N T D\E\M/V/E/L R(I)		108.62	450.5556	1349.648	0.0045	3.3	4.68	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
9636	dirMS_041712_NAR_50mM_minus2.10681.10826.3	3	10.34	1	3.29E+05		(K)NQVAM	(K)N Q|V/A M/N/P T N/T V/F/D A K R(L)		128.87	602.6379	1805.896	0.0029	1.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
9637	dirMS_041712_NAR_50mM_minus2.12634.12634.3	3	10.34	0	2.14E+05		(R)VLVVHD	(R)V/L/V/V/H D G F E G L A K(G)		139.9	461.9238	1383.763	-0.0062	-4.5	5.32	18719.9	6.91	HUMAN	F8VP00	6-phosphofructokinase, muscle type (Fragment)
9638	dirMS_041712_NAR_50mM_minus2.8356.8356.3	3	10.34	1	8.27E+04	M61m	(K)NQVAm	(K)N Q|V/A|m N/P T N T V F D/A K R(L)	m:Oxidized methionine	114.92	607.968	1805.896	15.9932	-1	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
9639	dirMS_041712_NAR_120mM_plus.7125.7289.3	3	10.34	1	1.73E+06		(R)RQLETL(	(R)R Q\L E|T|L/G Q/E K(L)		91.05	401.2207	1201.653	-0.006	-5	6.14	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
9640	dirMS_041712_NAR_20mM_plus.10439.10439.2	2	10.34	0	2.32E+05		(R)AQIFAN'	(R)A Q|I/F|A/N\T V D/N A R(I)		145.25	660.3343	1319.67	-0.0089	-6.8	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9641	dirMS_041712_NAR_20mM_plus.15451.15451.2	2	10.34	0	5.10E+04		(R)AITIAGV	(R)A I T/I/A|G V|P/Q/S V T E C V K(Q)	C:Carbamidomethylation	178.55	836.9443	1672.894	-0.0125	-7.5	6.05	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
9642	dirMS_041712_NAR_20mM_plus.15488.15488.3	3	10.34	0	1.92E+05		(K)TITLEVEI	(K)T\I\T L E V/E/P S/D T I E N V K(A)		178.98	596.6463	1787.927	-0.003	-1.7	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
9643	dirMS_041712_NAR_30mM_plus2.17143.17143.2	2	10.34	0	3.37E+05		(R)GLVGIEF	(R)G L/V|G|I E F/K(E)		143.3	431.7495	862.503	-0.0116	-13.4	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
9644	dirMS_041712_NAR_30mM_plus2.21264.21283.2	2	10.34	0	8.25E+03		(R)GAFQNL	(R)G A F|Q|N/L F/Q/S V/R(E)		164.77	633.8315	1266.659	-0.0032	-2.5	9.75	68629.9	5.59	HUMAN	E7EVX6	Androgen receptor
9645	dirMS_041712_NAR_30mM_plus2.7497.7555.2	2	10.34	0	1.76E+06		(R)FFSDCK(	(R)F/F|S D/C/K(I)	C:Carbamidomethylation	93.83	402.1754	803.339	0.0043	5.3	5.84	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
9646	dirMS_041712_NAR_30mM_plus2.8759.8759.3	3	10.34	0	1.43E+06		(R)FGQGG/	(R)F G/Q G G A G|P|V/G/G Q G P R(G)		99.68	447.893	1341.666	-0.0014	-1	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
9647	dirMS_041712_NAR_40mM_plus2.15231.15231.3	3	10.34	0	1.28E+05		(R)IETMLGI	(R)I E\T M L G/D V/A/V|A V H P K(D)		156.15	527.286	1579.851	-0.0078	-4.9	5.32	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
9648	dirMS_041712_NAR_40mM_plus2.7937.7937.2	2	10.34	0	1.43E+05		(R)ELNITAA	(R)E L|N/I/T/A/A/K(E)		106.88	430.2474	859.488	-0.0008	-1	6.1	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
9649	dirMS_041712_NAR_40mM_plus2.9064.9258.2	2	10.34	0	6.07E+05		(K)SSFFSDR	(K)S S|F|F/S D\R(G)		116.33	423.1935	845.379	0.0009	1.1	5.55	15031.5	6.72	HUMAN	B4DLA0	ATP-dependent RNA helicase DDX3X
9650	dirMS_041712_NAR_40mM_plus2.9117.9117.2	2	10.34	0	8.93E+04		(K)GSDFDC	(K)G S|D/F/D C/E|L/R(L)	C:Carbamidomethylation	115.47	549.7296	1098.452	-0.0001	-0.1	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
9651	dirMS_041712_NAR_60mM_plus.11360.11360.3	3	10.34	0	3.70E+05		(R)SLGTAD'	(R)S L|G T A/D V/H/F E/R(K)		116.88	411.2075	1231.607	0.0014	1.1	5.3	27557.2	11.05	HUMAN	E9PB61	THO complex subunit 4
9652	dirMS_041712_NAR_60mM_plus.12337.12337.2	2	10.34	0	4.51E+05		(R)HVFGES	(R)H/V|F/G E/S/D/E L|I/G Q K(V)		121.58	729.8644	1458.722	-0.0008	-0.6	4.65	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
9653	dirMS_041712_NAR_60mM_plus.13953.13953.3	3	10.34	0	1.56E+06		(K)LAQANG	(K)L/A\Q A\N/G W G V M\V S/H R(S)		129.07	509.2606	1525.769	-0.002	-1.3	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
9654	dirMS_041712_NAR_60mM_plus.16749.16749.3	3	10.34	1	4.68E+04		(K)VGEVIV1	(K)V/G/E\V/I V T K D D A M L L/K(G)		144.18	544.3059	1630.908	-0.0053	-3.2	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
9655	dirMS_041712_NAR_60mM_plus.19824.19824.3	3	10.34	1	1.46E+05		(R)SELELTL(	(R)S E L E/L/T\L/G K L\E/Q/V/R(S)		163.83	538.9738	1614.906	0.0007	0.5	4.78	533778	5.74	HUMAN	Q15149	Plectin
9656	dirMS_041712_NAR_30mM_minus2.18073.18073.2	2	10.33	0	3.67E+05		(R)EPGGVV	(R)E P G/G V V D G L I G K(H)		153.38	570.8106	1140.626	-0.012	-10.5	4.37	17657.6	9.02	HUMAN	Q5JZB7	Spindlin family, member 2B
9657	dirMS_041712_NAR_50mM_minus2.7456.7456.3	3	10.33	0	1.51E+05		(K)IVIGYQS	(K)I V|I/G Y Q/S H A D T A T K(S)		109.52	501.9321	1503.78	0.0016	1	6.74	28739.8	8.54	HUMAN	D6RBW1	Eukaryotic translation initiation factor 4E
9658	dirMS_041712_NAR_60mM_minus.13919.13919.3	3	10.33	0	1.94E+05		(K)ADFCIIH	(K)A/D/F C/I I H/Y/A G\K(V)	C:Carbamidomethylation	137.33	432.2132	1294.625	0.0002	0.1	6.79	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
9659	dirMS_041712_NAR_60mM_minus.15409.15409.3	3	10.33	0	1.03E+06		(R)LSDQFH	(R)L/S D Q/F/H/D I L I R(K)		145.65	452.9148	1356.727	0.0028	2.1	5.21	12284.6	4.89	HUMAN	H0Y9X3	Programmed cell death protein 6 (Fragment)
9660	dirMS_041712_NAR_60mM_minus.17273.17273.3	3	10.33	1	1.10E+05		(R)CRVDLP	(R)C R V D\L|P\L/A V L/S K(M)	C:Carbamidomethylation	156	457.5982	1370.782	-0.0024	-1.7	8.75	7765.6	8.23	HUMAN	H3BSA6	dCTP pyrophosphatase 1
9661	dirMS_041712_NAR_60mM_minus.18660.18660.3	3	10.33	0	2.93E+05		(K)TFLVWV	(K)T F|L|V W V/N E E D H L R(V)		165.78	553.2818	1657.833	-0.0024	-1.5	4.65	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
9662	dirMS_041712_NAR_20mM_plus.15414.15414.2	2	10.33	0	3.88E+04	M73m	(R)AILVDLE	(R)A I L/V/D|L|E|P/G T m D S V/R(S)	m:Oxidized methionine	178.07	816.4181	1615.836	15.9929	-1.2	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
9663	dirMS_041712_NAR_30mM_plus2.19281.19281.2	2	10.33	0	2.85E+05		(K)TVDNFV	(K)T V/D\N/F/V/A L\A T G E K(G)		154.87	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
9664	dirMS_041712_NAR_40mM_plus2.10999.10999.2	2	10.33	0	7.20E+03		(R)GDFCIQ'	(R)G D/F/C/I/Q/V G R(-)	C:Carbamidomethylation	131.12	526.2539	1051.499	0.0016	1.5	5.84	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
9665	dirMS_041712_NAR_40mM_plus2.17060.17060.3	3	10.33	0	6.64E+04		(R)IHFPLAT	(R)I H\F\P L A T\Y|A/P V/I/S A E/K(A)		166.77	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
9666	dirMS_041712_NAR_40mM_plus2.19949.19949.3	3	10.33	1	9.72E+05		(R)ELAILLG	(R)E L/A/I L/L G M L/D/P A E K D/E K(G)		188.8	629.003	1884.999	-0.0042	-2.3	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
9667	dirMS_041712_NAR_40mM_plus2.7211.7289.2	2	10.33	0	2.96E+05		(K)VIDDTNI	(K)V/I|D/D/T/N I/T R(L)		103.5	523.7788	1046.548	0.0027	2.5	4.21	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9668	dirMS_041712_NAR_50mM_plus2.10049.10049.3	3	10.33	1	3.09E+05		(R)LGLPGD	(R)L/G\L/P/G D/E V D N K V K(G)		120.28	461.9229	1383.748	0.0063	4.6	4.56	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
9669	dirMS_041712_NAR_50mM_plus2.11276.11276.3	3	10.33	1	3.31E+05		(K)DLFPYEE	(K)D/L|F/P/Y E E S K E K(F)		127.05	462.2257	1384.663	-0.0005	-0.4	4.41	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
9670	dirMS_041712_NAR_50mM_plus2.18442.18442.3	3	10.33	1	4.02E+05		(R)IAKEEIF(	(R)I/A K E E I\F|G/P/V Q/P L F K(F)		164.95	572.6586	1715.973	-0.0118	-6.9	6.14	57661.7	6.36	HUMAN	P30837	Aldehyde dehydrogenase X, mitochondrial
9671	dirMS_041712_NAR_50mM_plus2.21582.21582.3	3	10.33	1	1.88E+05		(K)LKVNFLF	(K)L K V N F L|P/E I|I T L/S K(E)		184.27	539.0011	1614.983	0.0058	3.6	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
9672	dirMS_041712_NAR_60mM_plus.12010.12162.3	3	10.33	1	4.22E+06		(K)MKEIAE/	(K)M/K E I A/E/A/Y/L/G/K(T)		120.2	418.2255	1252.661	0.0014	1.1	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
9673	dirMS_041712_NAR_60mM_plus.14414.14414.3	3	10.33	1	7.29E+05		(K)KAEEIAN	(K)K\A E E\I\A/N/E|M/I/E A/A K(A)		132	516.2635	1546.778	-0.0022	-1.4	4.49	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
9674	dirMS_041712_NAR_60mM_plus.17172.17172.3	3	10.33	1	3.54E+05		(K)YQLDKD	(K)Y Q/L D/K/D G V V\L/F K(K)		146.65	475.5976	1424.778	-0.0001	-0.1	5.96	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
9675	dirMS_041712_NAR_60mM_plus.20170.20170.3	3	10.33	1	6.74E+04		(K)KSVEEV/	(K)K S V E E V A|S E|I\Q/P/F L R(G)		165.4	577.9775	1731.928	-0.0096	-5.6	4.79	334221.3	6.44	HUMAN	P15924	Desmoplakin
9676	dirMS_041712_NAR_120mM_minus.5185.5185.3	3	10.32	1	3.17E+05		(R)LRAETE(	(R)L R A E T\E\Q/G/E/Q Q R(Q)		81.13	482.2432	1444.714	0.0012	0.8	4.79	533778	5.74	HUMAN	Q15149	Plectin
9677	dirMS_041712_NAR_20mM_minus.9772.9772.2	2	10.32	0	1.57E+05		(K)LSELEPG	(K)L S|E L/E|P G T\G D L R(F)		147.78	643.8318	1286.659	-0.0023	-1.8	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
9678	dirMS_041712_NAR_30mM_minus2.19414.19503.2	2	10.32	0	2.44E+05		(R)ILVATNL	(R)I/L|V|A|T N L F/G R(G)		162.07	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
9679	dirMS_041712_NAR_30mM_minus2.6840.6841.2	2	10.32	0	1.71E+05		(R)GCLDEE'	(R)G/C|L|D|E/E/T S R(A)	C:Carbamidomethylation	91.75	533.7297	1066.447	0.0052	4.8	4.14	533778	5.74	HUMAN	Q15149	Plectin
9680	dirMS_041712_NAR_40mM_minus2.12874.12874.3	3	10.32	0	3.58E+05	M460m	(R)ISIEmNG	(R)I/S|I/E m N G T L E/D Q/L S H L K(Q)	m:Oxidized methionine	158.97	648.6649	1927.979	16.0008	3	4.65	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
9681	dirMS_041712_NAR_50mM_minus2.15838.15838.3	3	10.32	0	1.67E+05		(R)VSLDVN	(R)V/S|L/D V N H F|A P D E L T V K(T)		158.53	595.3104	1783.922	-0.0058	-3.3	4.54	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
9682	dirMS_041712_NAR_50mM_minus2.17588.17588.3	3	10.32	0	2.60E+05		(R)LLLDGAI	(R)L/L\L/D G A/P L I A I H K(A)		168.5	458.6218	1373.852	-0.0007	-0.5	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
9683	dirMS_041712_NAR_60mM_minus.10112.10112.3	3	10.32	0	8.26E+04		(R)EIVHIQA	(R)E/I V H\I Q A G/Q/C/G N Q I/G A K(F)	C:Carbamidomethylation	116.48	608.3099	1822.923	-0.0077	-4.2	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
9684	dirMS_041712_NAR_60mM_minus.11444.11444.3	3	10.32	1	5.59E+05	M136m	(K)VKEGmN	(K)V K\E G m N\I/V/E A/M/E R(F)	m:Oxidized methionine	122.9	507.9181	1505.745	15.9947	-0.1	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
9685	dirMS_041712_NAR_20mM_plus.15031.15031.2	2	10.32	0	2.00E+04		(R)LSIPTYG	(R)L S I/P T/Y G L/Q/C T R(G)	C:Carbamidomethylation	175.1	704.8627	1408.725	-0.0072	-5.1	8.75	8533.6	12.23	HUMAN	J3KTF0	Enoyl-[acyl-carrier-protein] reductase (Fragment)
9686	dirMS_041712_NAR_30mM_plus2.11932.11932.2	2	10.32	0	6.61E+05		(K)FSASGEI	(K)F S\A/S/G/E/L/G N/G N I/K(L)		115.27	647.3242	1293.643	-0.0022	-1.7	6	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
9687	dirMS_041712_NAR_30mM_plus2.19447.19447.2	2	10.32	0	2.77E+05		(K)TVDNFV	(K)T/V|D N F/V/A L\A T/G E K(G)		155.3	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
9688	dirMS_041712_NAR_30mM_plus2.21034.21166.2	2	10.32	0	3.66E+05		(K)TIFAYFT(	(K)T I|F|A/Y F T G S K(D)		165.25	567.7949	1134.583	-0.0005	-0.4	8.26	8599.5	5.51	HUMAN	I3L0K2	Thioredoxin domain-containing protein 17
9689	dirMS_041712_NAR_40mM_plus2.16483.16483.3	3	10.32	0	2.33E+05		(R)VEGRPG	(R)V E G R P/G A S L|P|P L D L Q A L E K(E)		163.68	664.0298	1990.097	-0.0219	-11	4.68	32787.4	5.89	HUMAN	E9PS68	Pyruvate carboxylase, mitochondrial
9690	dirMS_041712_NAR_40mM_plus2.6306.6306.2	2	10.32	0	1.94E+05		(K)TEISEMI	(K)T E|I/S/E/M/N R(N)		96.27	490.2292	979.451	-0.0002	-0.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
9691	dirMS_041712_NAR_40mM_plus2.6443.6443.2	2	10.32	0	2.00E+05	M154m	(R)mGYMD	(R)m/G/Y|M D|P R(E)	m:Oxidized methionine	96.93	443.1854	869.364	15.9991	4.7	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
9692	dirMS_041712_NAR_50mM_plus2.15105.15223.3	3	10.32	1	5.77E+05		(K)TKDGQII	(K)T\K\D G Q I\L/P\V|P/N V V V R(D)		148.3	545.6573	1634.959	-0.0015	-0.9	8.41	56825.2	9.49	HUMAN	Q9P258	Protein RCC2
9693	dirMS_041712_NAR_50mM_plus2.16214.16214.3	3	10.32	1	3.41E+05		(K)YAVLYQ	(K)Y/A|V\L/Y Q P L F D K R(F)		152.38	504.9436	1512.821	-0.0047	-3.1	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
9694	dirMS_041712_NAR_120mM_minus.9409.9409.3	3	10.31	0	1.67E+06		(K)EFHLNE!	(K)E F H L N E|S/G D/P S S K(S)		106.17	482.8881	1446.65	0.0002	0.1	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
9695	dirMS_041712_NAR_20mM_minus.12278.12278.3	3	10.31	0	5.35E+05	M73m	(R)AVLVDLI	(R)A V\L\V\D L E/P G T|m D S V R(S)	m:Oxidized methionine	172.08	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
9696	dirMS_041712_NAR_30mM_minus2.8604.8604.2	2	10.31	0	2.24E+05		(R)NVLLNN	(R)N V|L/L|N N S E K(M)		101.18	515.7847	1030.553	0.0094	9.1	6	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b

9697	dirMS_041712_NAR_50mM_minus2.10495.10495.3	3	10.31	0	2.90E+05	M35m	(K)AASDIAr	(K)A A/S D I|A/m T E L/P/P T H P I R(L)	m:Oxidized methionine	127.85	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
9698	dirMS_041712_NAR_50mM_minus2.16308.16308.3	3	10.31	0	1.38E+05		(R)DLKPSNI	(R)D L|K P S N\L\L|I/N T/T C D L/K(I)	C:Carbamidomethylation	160.43	615.6611	1844.979	-0.0099	-5.4	5.96	30925	5.63	HUMAN	B3KR49	Mitogen-activated protein kinase 3
9699	dirMS_041712_NAR_50mM_minus2.17898.17898.3	3	10.31	0	4.73E+03		(K)YPLVFSP	(K)Y P/L V F S P Q M/V G F/Y I K(Q)		170.72	596.9846	1788.939	-0.0001	0	8.5	321004.1	7.11	HUMAN	O75691	Small subunit processome component 20 homolog
9700	dirMS_041712_NAR_50mM_minus2.7188.7188.3	3	10.31	0	1.66E+05		(R)ETPHSP(	(R)E T P H\S P G\V/E/D/A/P I A K(V)		107.98	516.5936	1547.77	-0.0038	-2.4	4.65	67446.5	5.63	HUMAN	F8VQE1	LIM domain and actin-binding protein 1
9701	dirMS_041712_NAR_50mM_minus2.7877.7877.3	3	10.31	1	1.50E+05		(K)TAVCDIF	(K)T A\V/C D/I P P R G L K(M)	C:Carbamidomethylation	111.93	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
9702	dirMS_041712_NAR_60mM_minus.13815.13815.3	3	10.31	0	1.42E+05		(K)ADFCIIH	(K)A D|F C I/I/H Y A G K(V)	C:Carbamidomethylation	137.43	432.2132	1294.625	0.0002	0.1	6.79	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
9703	dirMS_041712_NAR_120mM_plus.11464.11464.2	2	10.31	0	7.40E+05		(R)FAQHGT	(R)F A/Q/H/G/T/F E Y/E/Y S Q R(W)		113.27	881.8929	1762.782	-0.0035	-2	5.4	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
9704	dirMS_041712_NAR_120mM_plus.9213.9213.3	3	10.31	1	1.62E+05		(K)LNRYNY	(K)L/N/R Y|N|Y|I/E G T K(M)		102.02	457.5737	1370.706	0.0003	0.2	8.5	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
9705	dirMS_041712_NAR_20mM_plus.10126.10126.2	2	10.31	0	4.14E+04		(K)LVSESSD	(K)L/V|S/E S/S D V L|P K(-)		142.18	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
9706	dirMS_041712_NAR_20mM_plus.10556.10556.2	2	10.31	0	5.11E+04		(R)ELAEDG'	(R)E/L A/E D/G/Y/S/G V E V R(V)		145.7	712.3373	1423.67	-0.0026	-1.9	4	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
9707	dirMS_041712_NAR_20mM_plus.12471.12471.2	2	10.31	0	1.93E+05		(R)GVEICIA	(R)G V/E\I/C I/A/T/P G R(L)	C:Carbamidomethylation	158.7	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
9708	dirMS_041712_NAR_20mM_plus.16463.16463.3	3	10.31	0	1.35E+05		(R)QAQEYE	(R)Q A Q E\Y/E/A\L L/N I/K(V)		184.45	473.9191	1419.748	-0.0051	-3.6	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9709	dirMS_041712_NAR_20mM_plus.8003.8003.2	2	10.31	0	4.21E+05	M239m	(K)EVDEQm	(K)E V/D/E|Q m L/N V Q/N K(N)	m:Oxidized methionine	125.1	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
9710	dirMS_041712_NAR_30mM_plus2.11007.11007.2	2	10.31	0	6.53E+05		(K)NFVDPV	(K)N F|V/D P V T K(K)		110.97	460.2505	919.488	0.0054	5.8	5.84	334221.3	6.44	HUMAN	P15924	Desmoplakin
9711	dirMS_041712_NAR_30mM_plus2.12758.12758.2	2	10.31	0	5.53E+05		(R)CNNVLY	(R)C N N|V/L/Y I/R(G)	C:Carbamidomethylation	120.78	526.2726	1051.535	0.0026	2.5	8.75	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F
9712	dirMS_041712_NAR_30mM_plus2.5499.5499.2	2	10.31	0	1.45E+05		(R)QLAAEE	(R)Q L|A/A/E E E/R(R)		83.65	473.2296	945.464	-0.0117	-12.4	4.25	533778	5.74	HUMAN	Q15149	Plectin
9713	dirMS_041712_NAR_50mM_plus2.10830.10830.3	3	10.31	1	4.68E+05		(R)ALRETLF	(R)A L R E T L|P/A/E Q D/L T T K(N)		125.08	562.6377	1685.907	-0.0083	-4.9	4.68	26790	6.25	HUMAN	F5GX11	Proteasome subunit alpha type-1
9714	dirMS_041712_NAR_50mM_plus2.5850.5850.3	3	10.31	1	1.71E+05		(R)ATEGM\	(R)A T|E/G M V V A D K N/C S K(I)	C:Carbamidomethylation	94.28	503.9061	1509.704	0.0002	0.1	6.11	15607.8	9.99	HUMAN	B4E0P1	Proteasome (Prosome, macropain) subunit, beta type, 7, isoform CRA_b
9715	dirMS_041712_NAR_60mM_plus.12731.12731.3	3	10.31	1	9.60E+05	M230m	(R)mSMKE\	(R)m S M K E V D\E/Q/M|L N V/Q/N K(N)	m:Oxidized methionine	123.5	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
9716	dirMS_041712_NAR_50mM_minus2.14616.14759.3	3	10.3	1	1.82E+05		(K)ELKIDIIP	(K)E L K I D I\I|P/N/P Q E/R(T)		151.52	522.2945	1564.869	-0.0004	-0.2	4.68	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
9717	dirMS_041712_NAR_50mM_minus2.6842.6842.3	3	10.3	1	7.27E+03	M628m	(K)AQALRD	(K)A Q|A L R D N S T/M/G/Y/m A A/K(K)	m:Oxidized methionine	105.55	581.9436	1727.82	15.9959	0.6	8.63	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
9718	dirMS_041712_NAR_60mM_minus.13879.13879.3	3	10.3	1	1.90E+05		(R)VEVTEFE	(R)V E|V/T E F E/D I K S G Y R(I)		137.38	557.9508	1671.822	0.0154	9.2	4.41	30992.3	4.14	HUMAN	B2REB8	Protein SET
9719	dirMS_041712_NAR_60mM_minus.6810.7055.3	3	10.3	0	1.27E+06	M437m	(R)LESGMC	(R)L/E|S G M Q N m S I/H/T K(T)	m:Oxidized methionine	97.23	497.9023	1475.698	15.9942	-0.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
9720	dirMS_041712_NAR_30mM_plus2.6856.6856.2	2	10.3	0	6.17E+04		(R)VYSTSV1	(R)V/Y|S/T/S V T/G S R(E)		90.47	528.7673	1056.532	-0.0047	-4.4	8.72	9437.4	9.69	HUMAN	Q5T123	SH3 domain binding glutamic acid-rich protein like 3
9721	dirMS_041712_NAR_50mM_plus2.8685.8685.3	3	10.3	0	1.55E+05		(K)VVQVSA	(K)V V|Q/V/S A G D S H T A A L T D D G R(V)		113.17	633.6509	1898.92	0.0179	9.4	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
9722	dirMS_041712_NAR_60mM_plus.11646.11646.3	3	10.3	0	4.51E+05		(R)NRPPFG	(R)N R/P P F\G/Q/G Y/T Q|P G P G Y R(-)		118.27	631.3105	1891.92	-0.0029	-1.5	9.99	43076.8	5.01	HUMAN	G5E9V1	Protein TFG
9723	dirMS_041712_NAR_60mM_plus.8496.8496.3	3	10.3	0	5.94E+05		(K)GQVCVN	(K)G Q|V/C V/M/I/H S G S R(G)	C:Carbamidomethylation	103.07	444.2219	1330.636	0.0157	11.8	9.75	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
9724	dirMS_041712_NAR_120mM_minus.12798.12798.3	3	10.29	0	2.13E+04		(K)TFTAWC	(K)T F|T/A W C/N S/H/L R(K)	C:Carbamidomethylation	124.13	464.8871	1392.648	-0.001	-0.7	9.44	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
9725	dirMS_041712_NAR_20mM_minus.12204.12204.3	3	10.29	0	5.07E+05	M256m	(R)SLDmDS	(R)S\L D m D S/I/I A/E/V/K(A)	m:Oxidized methionine	171.02	446.227	1320.671	15.9949	0	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
9726	dirMS_041712_NAR_20mM_minus.9780.9780.2	2	10.29	0	3.36E+05		(K)IGGIGTV	(K)I/G|G/I/G\T V/P V G R(V)		147.47	513.3075	1025.61	-0.0025	-2.4	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
9727	dirMS_041712_NAR_30mM_minus2.17072.17072.2	2	10.29	0	8.98E+04		(R)IMNTFS'	(R)I M|N\T/F/S V/V/P S\P K(V)		146	660.3534	1319.703	-0.0033	-2.5	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
9728	dirMS_041712_NAR_30mM_minus2.20468.20468.2	2	10.29	0	4.58E+05		(R)FLTWILN	(R)F/L|T/W I/L N R(Y)		175.92	531.8089	1062.61	0.001	1	9.75	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
9729	dirMS_041712_NAR_50mM_minus2.7192.7192.3	3	10.29	0	1.52E+04		(K)EQEPMF	(K)E Q E/P/M/P T V D/S H E P/R(L)		107.72	551.2498	1651.738	-0.0032	-1.9	4.4	18962.9	9.6	HUMAN	A6NGP5	Hematological and neurological-expressed 1-like protein
9730	dirMS_041712_NAR_50mM_minus2.8656.8692.3	3	10.29	1	2.14E+05		(R)VAIEPG/	(R)V/A/I/E|P G A P R E N D E F/C K(M)	C:Carbamidomethylation	117.37	611.2923	1831.864	-0.002	-1.1	4.41	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
9731	dirMS_041712_NAR_50mM_minus2.9669.9669.3	3	10.29	1	7.87E+04		(R)SVLGEAI	(R)S V/L/G E/A D/Q/K G\S L V A P D R(L)		123.27	581.2998	1741.908	-0.0231	-13.2	4.56	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
9732	dirMS_041712_NAR_60mM_minus.14974.15058.3	3	10.29	1	2.72E+05		(K)NLKVTA'	(K)N L K/V T A\V|P/T L L K(Y)		143.95	432.9457	1296.825	-0.0024	-1.9	10	11462.8	5.18	HUMAN	I3L2R6	Thioredoxin domain-containing protein 17
9733	dirMS_041712_NAR_60mM_minus.16235.16235.3	3	10.29	1	5.67E+05		(K)LKLSILYF	(K)L K L S I L\Y|P/A/T T G R(N)		150.53	478.2883	1432.852	-0.0019	-1.3	9.99	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
9734	dirMS_041712_NAR_60mM_minus.6087.6087.3	3	10.29	1	2.64E+05		(K)LEEAEK/	(K)L E|E A/E K A/A D E S E/R(G)		92.57	492.8981	1476.681	-0.0015	-1	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
9735	dirMS_041712_NAR_120mM_plus.21084.21084.3	3	10.29	2	1.18E+06		(R)TLAEIAK	(R)T L|A/E I A K V E L D/N M/P L R G K(Q)		163.05	666.7047	1998.105	-0.0057	-2.8	5.85	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
9736	dirMS_041712_NAR_20mM_plus.18647.18647.2	2	10.29	0	2.84E+05		(K)LAVEALS	(K)L A V|E/A/L|S/S L D G D L A G R(Y)		200.47	793.9214	1586.838	-0.0029	-1.8	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
9737	dirMS_041712_NAR_20mM_plus.9317.9317.2	2	10.29	0	1.02E+05		(R)ANIQAV	(R)A/N|I|Q/A/V|S L K(I)		135.67	472.2851	943.557	0.0058	6.2	8.8	25103.6	5.88	HUMAN	O43633	Charged multivesicular body protein 2a
9738	dirMS_041712_NAR_20mM_plus.9531.9531.2	2	10.29	0	1.43E+05		(R)GTGIVS/	(R)G T/G I|V|S A/P V/P\K(K)		136.92	513.3057	1025.599	0.0052	5	8.75	21898	11.33	HUMAN	E9PM36	40S ribosomal protein S2
9739	dirMS_041712_NAR_30mM_plus2.10215.10215.2	2	10.29	0	4.86E+05		(R)LGAPAL'	(R)L/G\A/P A|L/T S R(Q)		106.93	443.2607	885.515	-0.0011	-1.3	9.75	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
9740	dirMS_041712_NAR_30mM_plus2.14105.14105.2	2	10.29	0	3.30E+05		(R)YVDIAIP	(R)Y V|D/I/A|I\P C N/N K(G)	C:Carbamidomethylation	126.98	653.8256	1306.646	-0.0021	-1.6	5.83	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
9741	dirMS_041712_NAR_30mM_plus2.17079.17079.2	2	10.29	0	2.27E+05		(K)ACGNFG	(K)A C|G N F/G I\P C\E/L R(V)	C:Carbamidomethylation	142.65	697.3237	1393.635	0.005	3.6	6.05	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
9742	dirMS_041712_NAR_30mM_plus2.22585.22585.2	2	10.29	0	1.01E+06		(R)FLTWILN	(R)F/L/T|W I\L N R(Y)		175.88	531.8078	1062.61	-0.0012	-1.1	9.75	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
9743	dirMS_041712_NAR_30mM_plus2.7204.7204.2	2	10.29	0	1.83E+04		(R)SGGGGC	(R)S G/G\G G/G G/G L/G S G/G\S/I/R(S)		92.03	616.8023	1232.598	-0.0005	-0.4	9.47	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
9744	dirMS_041712_NAR_30mM_plus2.9324.9912.2	2	10.29	0	9.85E+06		(R)LASYLDF	(R)L/A|S/Y L D/R(V)		104.55	419.2286	837.447	0.0034	4.1	5.83	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9745	dirMS_041712_NAR_40mM_plus2.14391.14391.3	3	10.29	1	3.72E+05		(R)IINEPTA	(R)I I|N E/P T A/A A/I A Y G L D K K(V)		150.73	596.6671	1787.99	-0.0034	-1.9	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
9746	dirMS_041712_NAR_40mM_plus2.15148.15148.3	3	10.29	0	2.29E+05		(R)EVIDLLK	(R)E V|I/D L L/K/P D Q V/E G I Q K(S)		155.13	608.6749	1824.011	-0.0012	-0.6	4.32	156557.7	5.52	HUMAN	Q86UP2	Kinectin
9747	dirMS_041712_NAR_40mM_plus2.8899.8899.2	2	10.29	0	1.19E+05		(R)GYSFTT1	(R)G Y/S|F/T/T/T/A E R(E)		114.9	566.7672	1132.527	0.0002	0.2	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
9748	dirMS_041712_NAR_50mM_plus2.15400.15400.3	3	10.29	0	1.63E+05		(K)VALLLLD	(K)V A\L|L L/L/D Q G A/S/P H A A A K(N)		148.48	558.9877	1674.954	-0.0052	-3.1	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
9749	dirMS_041712_NAR_50mM_plus2.8893.8893.3	3	10.29	0	1.99E+05		(K)VVQVSA	(K)V V/Q|V S/A G D S H T/A A L T D D G R(V)		113.48	633.6509	1898.92	0.0179	9.4	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
9750	dirMS_041712_NAR_60mM_plus.13781.13781.3	3	10.29	0	2.15E+05		(R)LFFQPH(	(R)L/F/F Q/P H Q/A G L/S K(V)		128.93	458.2494	1372.737	-0.0035	-2.6	8.76	8684.1	9.22	HUMAN	C9J0F6	Ubiquitin-like modifier-activating enzyme 5 (Fragment)
9751	dirMS_041712_NAR_60mM_plus.16424.16424.3	3	10.29	0	4.22E+05		(R)FVFDRPI	(R)F/V/F/D|R P L P V S R(L)		142.53	444.917	1332.742	-0.0058	-4.4	9.6	18685.5	9.45	HUMAN	B4DEV8	Proteasome subunit alpha type
9752	dirMS_041712_NAR_120mM_minus.17635.17635.4	4	10.28	1	3.14E+05		(K)KTTIENI(	(K)K\T T I E N/I/Q L/P H/T/L L S/R(F)		151.25	466.7676	1864.065	-0.0165	-8.9	8.76	95792.4	6.36	HUMAN	J3KPV4	DNA replication licensing factor MCM4
9753	dirMS_041712_NAR_120mM_minus.20826.20826.4	4	10.28	1	5.83E+05		(R)SLHDAL(	(R)S L H D A\L/C/V|L A Q/T V K D/S R(T)	C:Carbamidomethylation	173.1	479.0049	1912.991	0.0068	3.6	6.47	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
9754	dirMS_041712_NAR_30mM_minus2.12419.12928.2	2	10.28	0	7.93E+05		(R)GVVGPE	(R)G V|V|G/P E L Y G/R(L)		122.53	523.7834	1046.563	-0.0034	-3.2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
9755	dirMS_041712_NAR_30mM_minus2.15828.15965.2	2	10.28	0	1.63E+05		(K)ELPELLQ	(K)E L|P|E/L L Q/R(N)		140.1	499.2869	997.568	-0.0011	-1.2	4.53	96649	6.13	HUMAN	Q8WUM4	Programmed cell death 6-interacting protein
9756	dirMS_041712_NAR_50mM_minus2.5281.5287.3	3	10.28	0	8.24E+05		(K)TATPQQ	(K)T A|T/P Q Q/A Q E V/H E K(L)		88.02	489.5768	1466.723	-0.0075	-5.1	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
9757	dirMS_041712_NAR_50mM_minus2.9535.9535.2	2	10.28	1	7.15E+05		(R)DGKLVS	(R)D/G/K\L\V\S|E S S D\V/L|P K(-)		121.97	737.3927	1473.78	-0.0014	-0.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
9758	dirMS_041712_NAR_60mM_minus.20123.20123.3	3	10.28	0	4.05E+05		(K)GHYTEG	(K)G H Y/T E G A E/L|V/D S V/L D V V/R(K)		184.27	653.6647	1958.982	-0.0022	-1.1	4.31	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
9759	dirMS_041712_NAR_30mM_plus2.9691.9691.2	2	10.28	0	7.42E+05		(K)EAESSPF	(K)E/A/E/S S/P F V/E\R(L)		105.1	575.7726	1150.537	0.0004	0.4	4.25	92752.5	4.76	HUMAN	P14625	Endoplasmin
9760	dirMS_041712_NAR_40mM_plus2.13051.13051.3	3	10.28	0	5.11E+04		(R)IVATKPL	(R)I/V/A T K/P/L Y\V/A L A Q/R(K)		143.25	514.9835	1542.937	-0.0007	-0.4	9.99	65918.2	9.74	HUMAN	E7EQV3	Polyadenylate-binding protein 1
9761	dirMS_041712_NAR_40mM_plus2.19299.19299.3	3	10.28	0	1.75E+05		(R)LQQAQL	(R)L Q/Q/A\Q L\Y/P\I A I/F I K/P K(S)		180.67	624.3737	1871.115	-0.0088	-4.7	9.7	94175.4	6.59	HUMAN	Q5JUW8	Discs, large homolog 3 (Neuroendocrine-dlg, Drosophila)
9762	dirMS_041712_NAR_50mM_plus2.12513.12513.3	3	10.28	1	8.84E+05		(R)ELISNSSI	(R)E L|I/S/N/S S D A L D/K I R(Y)		134.15	520.9473	1560.823	0.0046	2.9	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
9763	dirMS_041712_NAR_50mM_plus2.19971.19971.3	3	10.28	0	4.53E+05		(K)HSQFIG\	(K)H S Q F I\G\Y|P|I/T L Y L E K(E)		173.75	603.6541	1808.958	-0.0104	-5.7	6.75	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
9764	dirMS_041712_NAR_50mM_plus2.8616.8616.3	3	10.28	1	1.17E+05		(K)TENSGE/	(K)T E|N/S G E A L/A\K V/E D S N P Q/K(T)		112.38	639.6441	1916.92	-0.0018	-1	4.41	13579.2	9.99	HUMAN	E9PPQ6	Thymocyte nuclear protein 1 (Fragment)
9765	dirMS_041712_NAR_60mM_plus.14365.14439.3	3	10.28	1	6.81E+05		(R)KMMAD	(R)K\M M A D E\A|L|G|S/G/L/V S R(V)		131.82	522.2648	1564.782	-0.0023	-1.5	6.07	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
9766	dirMS_041712_NAR_60mM_plus.8291.8291.2	2	10.28	1	4.67E+05	M174m	(R)VKYETEL	(R)V/K|Y E|T E L/A m R(Q)	m:Oxidized methionine	101.53	628.3208	1239.64	15.9941	-0.6	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9767	dirMS_041712_NAR_60mM_plus.8615.8615.3	3	10.28	1	3.99E+04		(R)LLEEEDS	(R)L L E/E/E D/S K L/K(G)		103.8	401.8861	1203.647	-0.003	-2.5	4.41	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
9768	dirMS_041712_NAR_120mM_minus.12443.12443.4	4	10.27	1	4.42E+05		(R)IPFIRPAI	(R)I/P/F I R P A/D Q Y K D/P Q S K(K)		121.2	476.5062	1903.007	-0.0043	-2.2	8.5	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
9769	dirMS_041712_NAR_120mM_minus.8369.8369.3	3	10.27	1	1.00E+06		(K)KGTVEG	(K)K G T V E\G\F\E|P A D/N K(C)		100.1	464.5648	1391.68	-0.0003	-0.2	4.68	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
9770	dirMS_041712_NAR_120mM_minus.8857.8914.2	2	10.27	0	5.68E+05		(K)HFVALS1	(K)H/F|V|A|L\S T N/T T K(V)		103.28	609.8267	1218.648	-0.0016	-1.3	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
9771	dirMS_041712_NAR_20mM_minus.12072.12072.2	2	10.27	0	7.89E+05	M313m	(R)TVQSLEI	(R)T V/Q/S/L/E/I\D L/D S m R(N)	m:Oxidized methionine	170.33	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9772	dirMS_041712_NAR_30mM_minus2.11332.11332.2	2	10.27	0	1.24E+06		(K)FSASGEI	(K)F/S|A|S G E/L/G N G N I K(L)		114.93	647.3253	1293.643	0	0	6	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
9773	dirMS_041712_NAR_30mM_minus2.16980.16980.2	2	10.27	0	9.39E+04		(R)IMNTFS'	(R)I/M|N T F/S/V/V/P S P K(V)		145.97	660.3534	1319.703	-0.0033	-2.5	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
9774	dirMS_041712_NAR_30mM_minus2.17845.17880.2	2	10.27	0	1.89E+05		(R)YVANIFF	(R)Y/V|A/N I F/P Y/K(G)		151.32	557.7997	1114.593	-0.001	-0.9	8.5	23312.3	5.53	HUMAN	B4DFH3	Inorganic pyrophosphatase 2, mitochondrial
9775	dirMS_041712_NAR_40mM_minus2.10296.10296.2	2	10.27	0	1.15E+06		(R)VAPDEH	(R)V/A|P D E H P I L L/T E|A P L/N/P K(I)		143.48	977.5343	1954.064	-0.0031	-1.6	4.65	42344.8	5.39	HUMAN	Q562R1	Beta-actin-like protein 2
9776	dirMS_041712_NAR_40mM_minus2.5897.5897.2	2	10.27	0	1.24E+06		(K)AGFAGD	(K)A G/F/A|G/D/D A/P R(A)		98.1	488.7279	976.448	0.0002	0.2	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
9777	dirMS_041712_NAR_60mM_minus.9643.9643.3	3	10.27	0	7.10E+04		(R)IHGTEE(	(R)I H/G T E/E/G Q Q/I L/K(Q)		113.55	451.583	1352.717	0.0176	13	5.4	6847.8	5.79	HUMAN	F5GWA2	Nuclear mitotic apparatus protein 1 (Fragment)
9778	dirMS_041712_NAR_120mM_plus.5574.5574.3	3	10.27	1	7.62E+04		(R)YGEDNR	(R)Y/G/E D/N/R G Y/G G S Q/G G G/R(G)		82.97	543.9055	1629.7	0.0019	1.2	6.07	26157.9	4.57	HUMAN	K7EL85	TATA-binding protein-associated factor 2N (Fragment)
9779	dirMS_041712_NAR_20mM_plus.10658.10658.2	2	10.27	0	4.28E+04	M414m	(K)mDATAN	(K)m D A/T|A|N D/V/P S/P Y E V R(G)	m:Oxidized methionine	146.12	840.8792	1664.758	15.9927	-1.3	4.03	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
9780	dirMS_041712_NAR_20mM_plus.18502.18502.3	3	10.27	0	1.88E+04		(R)APVPAS	(R)A P V P A S E L\L/A/S/G V L\S R(A)		199.92	522.9655	1566.885	-0.003	-1.9	6.05	533778	5.74	HUMAN	Q15149	Plectin
9781	dirMS_041712_NAR_30mM_plus2.10027.10027.2	2	10.27	0	3.07E+05		(K)LAEQFPI	(K)L/A|E/Q F/P/R(Q)		105.68	430.7352	860.462	0.0006	0.7	6	15778.8	9.12	HUMAN	E9PL10	Transcription factor BTF3 homolog 4
9782	dirMS_041712_NAR_30mM_plus2.13211.13211.2	2	10.27	0	2.83E+05		(R)TNEGVII	(R)T N|E/G V/I/E/F R(S)		122.2	532.7727	1064.537	0.001	1	4.53	39700.2	11.49	HUMAN	Q13247	Serine/arginine-rich splicing factor 6
9783	dirMS_041712_NAR_30mM_plus2.14436.14436.2	2	10.27	0	2.63E+05		(R)ELLELAS	(R)E L/L/E/L/A S/R(M)		128.55	465.7671	930.525	0.0015	1.6	4.53	109301.2	7.85	HUMAN	H0Y394	Vigilin (Fragment)
9784	dirMS_041712_NAR_30mM_plus2.6202.6202.2	2	10.27	0	1.67E+05		(K)VSDYEM	(K)V/S|D Y E/M/K(L)		86.68	436.1974	871.387	0.0009	1.1	4.37	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
9785	dirMS_041712_NAR_40mM_plus2.13218.13350.2	2	10.27	0	8.98E+04		(K)FFVGGN	(K)F/F|V|G G N W K(M)		144.42	477.7448	954.483	-0.0009	-0.9	8.75	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
9786	dirMS_041712_NAR_40mM_plus2.16418.16418.3	3	10.27	1	1.23E+05		(R)DFSMAD	(R)D F/S M A D K V\L/P T I/P K(E)		163.32	521.2832	1561.829	0.0056	3.6	5.96	99900.1	5.04	HUMAN	B4DZI8	Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b
9787	dirMS_041712_NAR_50mM_plus2.22211.22211.3	3	10.27	1	5.40E+05		(R)ELAILLG	(R)E L A I/L/L G/M L D/P A E K D/E K(G)		190.32	629.004	1884.999	-0.0012	-0.7	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
9788	dirMS_041712_NAR_60mM_plus.16639.16639.3	3	10.27	1	2.17E+04	M557m	(K)mFGIDR	(K)m/F/G I D R D/A/I/A Q|A V R(G)	m:Oxidized methionine	143.9	526.9346	1562.811	15.9785	-10.4	5.71	63448.4	7.29	HUMAN	B4E022	Transketolase
9789	dirMS_041712_NAR_60mM_plus.17224.17224.3	3	10.27	1	4.50E+05		(R)GPIKFN\	(R)G P\I K F N V|W/D|T/A/G Q E K(F)		146.72	563.9572	1689.86	-0.0024	-1.4	6.07	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
9790	dirMS_041712_NAR_60mM_plus.18523.18523.3	3	10.27	1	2.64E+05		(R)RGDINLI	(R)R G D I N L\L\M|L/G D/P G/T A K(S)		154.48	557.6331	1670.889	-0.0047	-2.8	5.96	78390.7	9.27	HUMAN	B1AHB1	DNA replication licensing factor MCM5
9791	dirMS_041712_NAR_60mM_plus.7960.7960.3	3	10.27	1	3.30E+05	M254m	(R)LmEEIM	(R)L/m/E/E I/M S E K\E\N K(T)	m:Oxidized methionine	99.77	499.5719	1480.702	15.999	2.7	4.49	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
9792	dirMS_041712_NAR_120mM_minus.21436.21436.3	3	10.26	0	8.12E+05		(R)LHFFMP	(R)L H F F\M\P G\F\A|P\L T S R(G)		182.17	540.9497	1620.835	-0.001	-0.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
9793	dirMS_041712_NAR_120mM_minus.7416.7416.3	3	10.26	0	1.69E+05		(K)AVTEQG	(K)A V|T|E Q G H E/L/S N E E R(N)		94.8	533.5856	1598.741	0.0017	1.1	4.48	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
9794	dirMS_041712_NAR_40mM_minus2.5912.5912.2	2	10.26	0	1.31E+06		(K)AGFAGD	(K)A G/F|A|G/D/D A P R(A)		98.15	488.7279	976.448	0.0002	0.2	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
9795	dirMS_041712_NAR_40mM_minus2.8296.8296.3	3	10.26	1	4.45E+04		(R)VGLQAC	(R)V G L/Q\A Q|P V|P D E I V K/K(I)		129.47	540.9825	1620.932	0.001	0.6	6.04	112066.5	5.59	HUMAN	B1AQT2	Ankyrin 3, node of Ranvier (Ankyrin G)
9796	dirMS_041712_NAR_50mM_minus2.12815.12815.3	3	10.26	1	2.33E+05		(R)QATKDA	(R)Q A T K D A G T\I|A/G L N V L/R(I)		140.57	543.3085	1627.913	-0.0016	-1	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
9797	dirMS_041712_NAR_60mM_minus.9707.9707.3	3	10.26	1	2.91E+04		(K)VDVGKD	(K)V|D/V/G K|D Q E F T V/K(S)		113.57	455.5752	1364.706	0.0054	4	4.56	283472.4	5.71	HUMAN	P21333	Filamin-A
9798	dirMS_041712_NAR_20mM_plus.12775.12974.2	2	10.26	0	1.58E+05		(R)LVVPAS(	(R)L V|V|P A/S Q C G S L I G K(G)	C:Carbamidomethylation	161.72	714.8991	1428.788	0.003	2.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
9799	dirMS_041712_NAR_20mM_plus.16508.16508.3	3	10.26	0	5.15E+04	M178m	(R)LmTDTII	(R)L m T D T/I/N E/P/I/L/L/C R(F)	C:Carbamidomethylation m:Oxid	184.57	568.9602	1688.871	15.9951	0.1	4.37	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
9800	dirMS_041712_NAR_20mM_plus.7820.7820.2	2	10.26	0	2.10E+05		(R)ALANSL/	(R)A L|A N S|L A/C/Q G K(Y)	C:Carbamidomethylation	123.85	566.7967	1132.578	0.0082	7.2	8.8	13951.6	9.48	HUMAN	H3BR68	Fructose-bisphosphate aldolase A (Fragment)
9801	dirMS_041712_NAR_30mM_plus2.16134.16134.2	2	10.26	0	2.91E+04	M148m	(R)DLTDYLr	(R)D L|T/D/Y/L/m K(I)	m:Oxidized methionine	137.32	507.7505	998.486	16.0074	12.3	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
9802	dirMS_041712_NAR_30mM_plus2.22053.22053.2	2	10.26	0	1.56E+05		(R)QSSFALI	(R)Q S|S/F/A/L/L G D L T K(A)		170.63	640.3472	1279.689	-0.0021	-1.7	5.84	46579.3	4.96	HUMAN	E5RI07	Transportin-1
9803	dirMS_041712_NAR_40mM_plus2.19968.19968.3	3	10.26	1	1.48E+06		(R)ELAILLG	(R)E L/A|I/L|L G M L D/P A E K D E K(G)		189.07	629.003	1884.999	-0.0042	-2.3	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
9804	dirMS_041712_NAR_40mM_plus2.5443.5443.2	2	10.26	0	3.24E+04		(R)YYNQVC	(R)Y/Y|N/Q V G R(K)		88.93	450.2218	899.437	-0.0007	-0.7	8.59	37238.2	9.57	HUMAN	K7ELX4	Ferrochelatase, mitochondrial (Fragment)
9805	dirMS_041712_NAR_50mM_plus2.19872.19872.3	3	10.26	0	4.03E+05		(K)HSQFIG\	(K)H S Q F I G|Y/P I/T L Y L/E/K(E)		173.63	603.6541	1808.958	-0.0104	-5.7	6.75	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta

9806	dirMS_041712_NAR_50mM_plus2.5961.5961.3	3	10.26	0	8.73E+04		(K)AVTEQG	(K)A/V|T/E Q/G H/E/L S N E E\R(N)		95.48	533.5846	1598.741	-0.0013	-0.8	4.48	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
9807	dirMS_041712_NAR_50mM_plus2.7292.7292.3	3	10.26	0	1.68E+05		(R)SGSSQEI	(R)S G/S S Q/E|L/D/V K/P S A S P Q E R(S)		103.85	634.6443	1901.92	-0.0016	-0.8	4.68	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
9808	dirMS_041712_NAR_60mM_plus.11928.11928.3	3	10.26	0	9.79E+05		(K)FYEEVHI	(K)F/Y/E E V/H/D L E/R(K)		119.13	446.2162	1336.617	0.0172	12.9	4.4	18209.2	5.03	HUMAN	A8MXH2	Nucleosome assembly protein 1-like 4 (Fragment)
9809	dirMS_041712_NAR_60mM_plus.12521.12521.3	3	10.26	1	3.54E+06		(K)VKLEAEI	(K)V K L E A E|I/A/T/Y R(R)		122.98	431.5782	1292.721	-0.0008	-0.6	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9810	dirMS_041712_NAR_60mM_plus.16504.16504.3	3	10.26	1	3.69E+05		(-)MKLNISF	(-)M K/L N I S/F/P/A/T G C Q K(L)	C:Carbamidomethylation	142.85	532.2733	1594.808	-0.0026	-1.7	10	10471.9	5.4	HUMAN	A2A3R7	40S ribosomal protein S6
9811	dirMS_041712_NAR_120mM_minus.13843.13843.3	3	10.25	1	1.94E+05		(R)IAWDDE	(R)I/A|W D D/E E/T R D G F/R(L)		129.68	537.2494	1609.724	0.0095	5.9	4.11	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
9812	dirMS_041712_NAR_120mM_minus.4541.4541.2	2	10.25	0	2.84E+06	M46m M4	(R)HQGVm	(R)H/Q|G V m V G m/G/Q/K(D)	m:Oxidized methionine	73.83	602.2834	1171.571	31.9885	-1.1	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
9813	dirMS_041712_NAR_20mM_minus.9713.9713.2	2	10.25	0	1.57E+05		(K)LSELEPG	(K)L S E L/E/P G T G D\L R(F)		147.78	643.8318	1286.659	-0.0023	-1.8	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
9814	dirMS_041712_NAR_30mM_minus2.11379.11379.2	2	10.25	0	2.19E+05		(K)ATAVMI	(K)A T A|V|M|P D G Q F K(D)		115.47	582.7922	1164.572	0.0054	4.6	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
9815	dirMS_041712_NAR_30mM_minus2.5721.5721.2	2	10.25	0	4.13E+04		(R)AAEDDE	(R)A/A/E/D\D E/D D D\V/D/T K(K)		85.35	719.2778	1437.55	-0.0016	-1.1	3.5	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
9816	dirMS_041712_NAR_50mM_minus2.10058.10058.3	3	10.25	1	8.36E+05		(R)MQKEIT	(R)M Q K E I T/A/L/A/P S T M K(I)		124.62	516.9426	1548.812	0.0008	0.5	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
9817	dirMS_041712_NAR_50mM_minus2.11328.11328.3	3	10.25	1	1.14E+05		(K)AVAFSP	(K)A V\A/F/S P V/T E L K K(D)		132.35	430.585	1289.746	-0.0059	-4.6	8.64	85815.7	7.35	HUMAN	P17858	6-phosphofructokinase, liver type
9818	dirMS_041712_NAR_60mM_minus.11865.11984.3	3	10.25	0	1.71E+06		(K)SQIHDIV	(K)S Q I H D I\V|L|V/G/G S T R(I)		126.72	494.6084	1481.807	0.0036	2.4	6.46	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
9819	dirMS_041712_NAR_60mM_minus.14441.14441.3	3	10.25	1	2.71E+05		(R)TEMENE	(R)T/E|M/E N E F/V L/I/K K(D)		140.07	494.2594	1480.772	-0.0079	-5.4	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
9820	dirMS_041712_NAR_120mM_plus.11667.11689.4	4	10.25	2	3.86E+04		(K)KVTQLD	(K)K\V\T Q\L|D/L/D|G P K E L S/R(R)		112.93	425.4899	1698.939	-0.0007	-0.4	6.12	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
9821	dirMS_041712_NAR_120mM_plus.9945.9945.4	4	10.25	0	2.44E+05		(R)GHAAFT	(R)G H\A\A\F T S D|P K P T\I E/V S G/K(K)		105.2	461.2368	1841.939	-0.0138	-7.5	6.75	15844.7	6.65	HUMAN	E5RI06	Glutathione reductase, mitochondrial (Fragment)
9822	dirMS_041712_NAR_20mM_plus.12733.12733.2	2	10.25	0	2.51E+05	M316m	(R)ISEQFTA	(R)I/S\E/Q/F/T/A m F R(R)	m:Oxidized methionine	161.18	623.3012	1229.598	15.9968	1.5	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
9823	dirMS_041712_NAR_20mM_plus.14441.14441.3	3	10.25	0	1.18E+05	M174m	(K)AmGAA	(K)A m G A A Q\V|V\V T/D L S A/T/R(L)	m:Oxidized methionine	171.28	535.9457	1589.832	15.991	-2.5	5.88	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
9824	dirMS_041712_NAR_20mM_plus.7418.7418.3	3	10.25	0	2.14E+05		(K)TGQAPG	(K)T G Q A P G\Y|S/Y/T/A A N K(N)		119.53	476.8963	1428.675	-0.001	-0.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
9825	dirMS_041712_NAR_20mM_plus.9140.9140.2	2	10.25	0	2.17E+05		(R)VLTVINC	(R)V L/T|V/I/N Q T Q K(E)		133.3	572.3399	1143.673	-0.0007	-0.6	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
9826	dirMS_041712_NAR_30mM_plus2.10388.10531.2	2	10.25	0	2.22E+05		(R)SLSYSPV	(R)S L|S|Y/S P/V E/R(R)		108.27	519.2668	1037.526	0.0001	0.1	5.72	9057.8	12.09	HUMAN	I3L4U6	Serine/arginine repetitive matrix protein 2 (Fragment)
9827	dirMS_041712_NAR_30mM_plus2.11387.11387.2	2	10.25	0	6.40E+05		(R)MGESDI	(R)M/G|E/S/D D\S I L R(L)		113.7	561.7585	1122.51	0.0002	0.1	4.03	9225.3	9.16	HUMAN	P63220	40S ribosomal protein S21
9828	dirMS_041712_NAR_30mM_plus2.18209.18209.2	2	10.25	0	3.13E+05		(R)SQVEEEI	(R)S Q|V|E/E E L/F S V R(V)		149.2	661.8302	1322.659	-0.0055	-4.2	4.25	533778	5.74	HUMAN	Q15149	Plectin
9829	dirMS_041712_NAR_30mM_plus2.7881.8258.2	2	10.25	0	1.13E+06		(R)DYDDM	(R)D Y|D|D\M/S/P R(R)		96.22	499.6972	998.388	-0.0013	-1.3	3.93	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
9830	dirMS_041712_NAR_40mM_plus2.12929.12929.3	3	10.25	1	1.22E+04		(K)SGEISLP	(K)S G\E/I/S L P I K E E/P S P I/S K(M)		142.55	604.3276	1810.98	-0.0114	-6.3	4.78	119334.1	5.73	HUMAN	B4DGT8	MKL/myocardin-like 2, isoform CRA_a
9831	dirMS_041712_NAR_50mM_plus2.6644.6644.3	3	10.25	0	5.18E+05	M434m	(R)LESGmC	(R)L/E/S G/m Q N/M/S/I/H T K(T)	m:Oxidized methionine	99.12	497.9026	1475.698	15.9951	0.1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
9832	dirMS_041712_NAR_50mM_plus2.8286.8310.3	3	10.25	0	5.15E+05		(R)LEPKPQI	(R)L E|P K/P Q/P/P V/A E A T P R(S)		110.33	543.9631	1629.896	-0.0211	-13	6.14	14468.1	6.76	HUMAN	K7EJ51	Septin-9 (Fragment)
9833	dirMS_041712_NAR_60mM_plus.12188.12188.3	3	10.25	0	9.36E+05		(K)LDEAVA	(K)L/D E A V A/E/A H/L/G/K(L)		121.18	418.2255	1252.653	0.0088	7	4.65	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
9834	dirMS_041712_NAR_20mM_minus.12035.12035.2	2	10.24	0	2.13E+05	M185m	(K)LAVNm	(K)L/A/V/N/m V/P F P R(L)	m:Oxidized methionine	170.08	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
9835	dirMS_041712_NAR_40mM_minus2.6669.6669.2	2	10.24	0	4.17E+05		(R)LASYLDI	(R)L A/S/Y L D/R(V)		108.32	419.2267	837.447	-0.0004	-0.4	5.83	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9836	dirMS_041712_NAR_50mM_minus2.8552.8552.3	3	10.24	1	2.43E+05		(R)AGTGVD	(R)A G T G/V/D/N V/D L E/A A T R K(G)		116.55	539.6119	1616.824	-0.0027	-1.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
9837	dirMS_041712_NAR_50mM_minus2.9425.9425.2	2	10.24	1	7.15E+05		(R)DGKLVS	(R)D G K|L|V|S/E/S S D V L\P K(-)		121.97	737.3927	1473.78	-0.0014	-0.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
9838	dirMS_041712_NAR_120mM_plus.24504.24524.4	4	10.24	1	1.18E+06		(R)GHYTIGI	(R)G H\Y T\I\G K/E I I D\L/V/L D/R(I)		184.3	461.2589	1842.012	0.0018	1	5.38	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
9839	dirMS_041712_NAR_20mM_plus.13924.13924.2	2	10.24	0	1.84E+04		(R)GLCAIA	(R)G L C/A/I/A|Q A/E S L R(Y)	C:Carbamidomethylation	167.55	644.8389	1288.668	0.0027	2.1	6	18529.2	9.98	HUMAN	E9PL45	40S ribosomal protein S3
9840	dirMS_041712_NAR_20mM_plus.15674.15674.3	3	10.24	0	2.11E+05		(R)GVVDSE	(R)G V V D S/E/D I/P/L N L S R(E)		179.38	505.2667	1513.786	-0.0001	-0.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
9841	dirMS_041712_NAR_20mM_plus.16443.16443.2	2	10.24	0	8.33E+04		(R)LGSTVF	(R)L G S/T/V/F|V/A N L D/Y K(V)		184.9	713.8819	1426.758	-0.0011	-0.8	5.83	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
9842	dirMS_041712_NAR_20mM_plus.18199.18199.2	2	10.24	0	1.02E+05		(R)AILVDLE	(R)A I|L V/D/L|E|P G T M D S V R(S)		196.63	808.419	1615.836	-0.0053	-3.3	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
9843	dirMS_041712_NAR_20mM_plus.18209.18209.2	2	10.24	0	9.83E+04		(R)APGSGL	(R)A/P|G/S G L A/L L/P L K(I)		196.67	568.8548	1136.704	-0.0014	-1.3	8.8	266161	5.68	HUMAN	E9PPU0	Epiplakin
9844	dirMS_041712_NAR_20mM_plus.19236.19236.3	3	10.24	0	2.77E+05		(R)LAGTQP	(R)L A\G T Q P\L E\V|L/E/A V/Q R(S)		204.3	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
9845	dirMS_041712_NAR_20mM_plus.19366.19366.2	2	10.24	0	1.41E+05		(R)TGAIVD	(R)T G\A\I|V|D/V/P V\G E E L/L G R(V)		204.68	812.9497	1624.891	0.0017	1	4.14	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
9846	dirMS_041712_NAR_40mM_plus2.11317.11317.3	3	10.24	0	3.11E+04		(K)LQALAN	(K)L Q/A\L A\N E Q|A|A/A A H/E L E K(M)		132.83	602.981	1806.935	-0.006	-3.3	4.75	156557.7	5.52	HUMAN	Q86UP2	Kinectin
9847	dirMS_041712_NAR_40mM_plus2.12989.12989.3	3	10.24	0	5.72E+04		(R)LQAYHT	(R)L Q/A Y H T Q T\T/P L/I/E Y Y R(K)		143.12	666.3423	1997.013	-0.0004	-0.2	6.75	21283.1	6.45	HUMAN	F8VY04	Adenylate kinase 2, mitochondrial
9848	dirMS_041712_NAR_40mM_plus2.14717.14717.2	2	10.24	0	6.02E+04		(R)GLFIIDG	(R)G L/F|I I D/G K(G)		153.32	431.7546	862.503	-0.0014	-1.6	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
9849	dirMS_041712_NAR_40mM_plus2.15165.15165.3	3	10.24	0	4.25E+05		(K)FTISDHP	(K)F/T/I/S D H\P Q P I D P L L/K(N)		156.52	574.3118	1720.927	-0.006	-3.5	5.21	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
9850	dirMS_041712_NAR_50mM_plus2.10280.10301.3	3	10.24	1	1.76E+05		(R)QELILSN	(R)Q E/L/I/L/S N S E D K/S/I R(V)		121.43	544.624	1631.86	-0.0024	-1.5	4.68	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
9851	dirMS_041712_NAR_50mM_plus2.14489.14694.3	3	10.24	1	3.42E+06		(R)VTPTRTI	(R)V/T|P T R T E I\I/I/L/A T R(T)		144.88	528.6537	1583.948	-0.0014	-0.9	9.57	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
9852	dirMS_041712_NAR_50mM_plus2.17131.17131.3	3	10.24	1	9.92E+05		(K)DNNGVI	(K)D N N/G/V/I/G L/L E/P M K K(S)		158.5	509.9448	1527.82	-0.0001	-0.1	6.07	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
9853	dirMS_041712_NAR_60mM_plus.9383.9383.3	3	10.24	1	4.91E+05		(R)GSNKLV	(R)G S N K L V\I|E/E/A/E/R(S)		107.13	448.9043	1344.712	-0.0134	-10	4.79	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
9854	dirMS_041712_NAR_120mM_minus.16724.16724.3	3	10.23	0	5.06E+05		(R)EHALLA	(R)E H A\L\L A|Y/T|L G V/K(Q)		145.65	438.9186	1314.742	-0.0004	-0.3	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
9855	dirMS_041712_NAR_120mM_minus.19361.19361.3	3	10.23	1	1.46E+05		(K)YNQLLRI	(K)Y/N|Q/L/L R I E E E/L G S K(A)		160.73	564.6367	1691.896	-0.0007	-0.4	4.79	47510.4	7.04	HUMAN	P06733	Alpha-enolase
9856	dirMS_041712_NAR_30mM_minus2.11637.11637.2	2	10.23	0	2.59E+04		(K)LLPLNDC	(K)L/L|P/L/N D/C R(Y)	C:Carbamidomethylation	116.88	500.7644	1000.524	-0.0029	-2.9	5.84	17030.4	8.91	HUMAN	G3V5P4	Cofilin 2 (Muscle), isoform CRA_d
9857	dirMS_041712_NAR_30mM_minus2.12465.12466.2	2	10.23	0	2.51E+05		(K)STLTDSL	(K)S T|L|T/D S\L V/C/K(A)	C:Carbamidomethylation	121.8	562.2838	1123.566	-0.006	-5.4	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
9858	dirMS_041712_NAR_30mM_minus2.16217.16217.2	2	10.23	0	3.06E+05		(R)GEVTAA	(R)G E V|T|A/A/D L F N S/R(V)		141.75	640.3185	1279.628	0.002	1.6	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
9859	dirMS_041712_NAR_30mM_minus2.16852.16852.2	2	10.23	0	2.03E+05		(R)ASLEAAI	(R)A S L E\A/A/I/A D/A/E Q R(G)		144.77	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
9860	dirMS_041712_NAR_40mM_minus2.10925.10925.3	3	10.23	0	1.05E+05	M56m	(K)VAIVKPC	(K)V/A\I/V K P G V|P m E/I V L N K(E)	m:Oxidized methionine	147.12	575.0112	1707.024	15.9953	0.2	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
9861	dirMS_041712_NAR_50mM_minus2.11097.11097.3	3	10.23	0	1.40E+05		(R)DLEAEH	(R)D L/E/A E H V/E\V E/D T/T L N R(C)		131.17	623.9684	1869.882	0.0082	4.4	4.07	10027.3	8.44	HUMAN	H3BTW0	Uncharacterized protein (Fragment)
9862	dirMS_041712_NAR_50mM_minus2.17279.17279.3	3	10.23	1	1.35E+05		(K)VIAATNI	(K)V I/A A|T N R V\D I L/D/P A L L R(S)		166.88	617.366	1850.086	-0.0024	-1.3	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
9863	dirMS_041712_NAR_50mM_minus2.6122.6122.3	3	10.23	1	5.69E+04	M322m	(K)AAGSGE	(K)A/A/G/S G E L G V T m K G P K(G)	m:Oxidized methionine	97.78	473.5826	1402.736	15.9974	1.7	8.64	258215.9	5.48	HUMAN	E7EN95	Filamin-B
9864	dirMS_041712_NAR_60mM_minus.4673.4673.3	3	10.23	1	9.42E+04		(K)AGADEE	(K)A/G|A/D/E E R/A E T A R(L)		77.88	425.8679	1275.592	-0.0032	-2.5	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
9865	dirMS_041712_NAR_60mM_minus.6973.6973.3	3	10.23	1	3.61E+05		(K)LDEREA	(K)L/D|E R E A\G I/T E/K(V)		98.2	420.8852	1260.643	-0.002	-1.6	4.41	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
9866	dirMS_041712_NAR_20mM_plus.13892.13892.2	2	10.23	0	1.26E+05	M62m	(R)DASLmV	(R)D A S L/m|V/T\N D G A\T I L K(N)	m:Oxidized methionine	167.72	782.8922	1548.794	15.9833	-7.4	4.21	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
9867	dirMS_041712_NAR_40mM_plus2.17575.17575.3	3	10.23	0	1.64E+05		(R)VYAILTH	(R)V Y|A\I/L T/H G I F S G P A I S R(I)		169.48	601.3376	1801.996	0.0023	1.3	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
9868	dirMS_041712_NAR_120mM_minus.13546.13546.3	3	10.22	0	7.83E+04		(K)LSLGTYA	(K)L/S|L/G T/Y A/S L H G R(I)		128.13	425.5623	1274.685	-0.0128	-10.1	8.75	67446.5	5.63	HUMAN	F8VQE1	LIM domain and actin-binding protein 1
9869	dirMS_041712_NAR_120mM_minus.9060.9060.2	2	10.22	0	5.98E+05		(K)HFVALST	(K)H\F|V/A L S T N\T T/K(V)		103.33	609.8267	1218.648	-0.0016	-1.3	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
9870	dirMS_041712_NAR_20mM_minus.12311.12311.2	2	10.22	0	8.42E+05	M313m	(R)TVQSLEI	(R)T V|Q/S L/E/I D L D S m R(N)	m:Oxidized methionine	171.25	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9871	dirMS_041712_NAR_50mM_minus2.11155.11155.3	3	10.22	1	3.83E+05		(R)VVDLMA	(R)V V|D/L\M A H M A/S K E(-)		131.37	444.2213	1330.649	0	0	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
9872	dirMS_041712_NAR_50mM_minus2.14638.14638.3	3	10.22	0	6.01E+03		(R)LVLEVAC	(R)L V/L/E V A/Q H L G E S T V/R(T)		150.93	550.9791	1650.917	0.0054	3.3	5.4	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
9873	dirMS_041712_NAR_60mM_minus.14916.14916.3	3	10.22	1	7.20E+04		(K)LTEDKAI	(K)L T|E D K A D V/Q/S/I/I/G\L Q R(F)		143.08	595.9938	1785.97	-0.0037	-2	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
9874	dirMS_041712_NAR_60mM_minus.4658.4662.3	3	10.22	0	6.11E+05	M46m M4	(R)HQGVm	(R)H Q\G\V\m|V/G m G Q K(D)	m:Oxidized methionine	77.87	401.8579	1171.571	31.9881	-1.4	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
9875	dirMS_041712_NAR_60mM_minus.5096.5096.3	3	10.22	1	4.16E+04		(K)VSQGVE	(K)V/S|Q G V E/D/G P D/T K R(A)		83.18	463.2294	1387.681	-0.0076	-5.4	4.56	33726	7.84	HUMAN	B3KNJ4	SUMO-1 activating enzyme subunit 1, isoform CRA_a
9876	dirMS_041712_NAR_120mM_plus.5720.5720.3	3	10.22	1	7.30E+05		(R)TAQEVE	(R)T/A|Q/E/V/E T Y R R(S)		83.77	418.2137	1252.628	-0.0015	-1.2	5.81	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
9877	dirMS_041712_NAR_120mM_plus.8506.8506.2	2	10.22	1	1.84E+06	M174m	(R)VKYETEL	(R)V/K|Y|E T E L A m R(Q)	m:Oxidized methionine	97.78	628.314	1239.64	15.9805	-11.4	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9878	dirMS_041712_NAR_20mM_plus.14508.14508.2	2	10.22	0	1.39E+05		(K)LVILANN	(K)L V\I L|A/N N C P A L/R(K)	C:Carbamidomethylation	171.7	677.3851	1353.767	-0.0042	-3.1	9.75	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
9879	dirMS_041712_NAR_20mM_plus.16565.16565.2	2	10.22	0	1.38E+05		(K)TVDNFV	(K)T V|D/N|F/V A/L A T G E K(G)		185.88	682.8565	1364.706	0.0001	0.1	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
9880	dirMS_041712_NAR_20mM_plus.18933.18933.3	3	10.22	0	1.01E+05		(R)AAVPSG	(R)A A V|P S G A S T G I|Y E A L/E L R(D)		201.5	602.3183	1804.944	-0.0036	-2	4.53	43048.9	4.99	HUMAN	B7Z2X9	Enolase
9881	dirMS_041712_NAR_30mM_plus2.7404.7438.2	2	10.22	0	1.11E+06		(R)GGTPSA	(R)G G/T|P/S/A F D/R(I)		94	454.2173	907.427	0.0005	0.6	5.84	26413	9.18	HUMAN	B1APP6	6-phosphofructokinase type C (Fragment)
9882	dirMS_041712_NAR_50mM_plus2.11262.11376.3	3	10.22	1	4.23E+05		(R)LYPPSAE	(R)L Y|P/P/S/A E Y/P D/L R K(H)		127.25	516.9418	1548.806	0.0052	3.3	6.07	16450.4	6.98	HUMAN	C9J8F6	Creatine kinase U-type, mitochondrial (Fragment)
9883	dirMS_041712_NAR_50mM_plus2.9203.9203.3	3	10.22	1	7.16E+05		(K)TAVCDI	(K)T A|V/C/D I/P P R G L K(M)	C:Carbamidomethylation	115.77	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
9884	dirMS_041712_NAR_20mM_minus.7382.7382.2	2	10.21	0	9.15E+04		(K)VEIIAND	(K)V E|I|I/A/N D Q/G N R(T)		122.15	614.8166	1228.628	-0.0021	-1.7	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
9885	dirMS_041712_NAR_50mM_minus2.5264.5264.3	3	10.21	0	7.53E+05	M434m M	(R)LESGmC	(R)L/E/S/G m Q N m S I/H T K(T)	m:Oxidized methionine	87.88	503.2361	1475.698	31.9956	3.9	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
9886	dirMS_041712_NAR_50mM_minus2.7790.7790.3	3	10.21	0	3.55E+04		(R)VILGSEA	(R)V/I|L/G S/E A/A Q Q H P E E V R(G)		111.43	588.3055	1762.908	-0.0063	-3.6	4.75	19458.5	4.89	HUMAN	E9PKK8	Dipeptidyl peptidase 3 (Fragment)
9887	dirMS_041712_NAR_60mM_minus.17874.17874.3	3	10.21	0	1.80E+04		(K)VSHLLGI	(K)V S H L L G I N V|T/D/F T R(G)		160.52	524.623	1571.854	0.0004	0.3	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
9888	dirMS_041712_NAR_20mM_plus.16970.16970.2	2	10.21	0	2.55E+05		(K)VQIAVA	(K)V Q\I\A|V/A/N A/Q E L|L Q\R(M)		188.03	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
9889	dirMS_041712_NAR_20mM_plus.6655.6655.2	2	10.21	0	7.09E+04	M266m	(R)TQPmT	(R)T Q/P m T/A/Q A A S Y R(A)	m:Oxidized methionine	110.62	670.8169	1324.631	15.9951	0.1	8.41	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
9890	dirMS_041712_NAR_30mM_plus2.15526.15526.2	2	10.21	0	4.01E+05		(R)MAGAI	(R)M/A/G\A/I/A/Q G L I/R(A)		133.67	550.816	1100.624	0.0002	0.2	9.5	4449.1	11.42	HUMAN	F8WEI0	Pyrroline-5-carboxylate reductase 3
9891	dirMS_041712_NAR_40mM_plus2.11289.11289.3	3	10.21	0	1.21E+05		(K)EAGELKI	(K)E A G\E/L/K P E E E|I|T/V/G\P V Q K(L)		132.8	651.6782	1953.017	0.0025	1.3	4.32	108281.4	5.72	HUMAN	P53618	Coatomer subunit beta
9892	dirMS_041712_NAR_50mM_plus2.15043.15043.3	3	10.21	0	4.96E+05		(K)TTISVAH	(K)T T|I/S V/A/H/L L A A/R(Q)		146.45	418.2499	1252.737	-0.002	-1.6	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
9893	dirMS_041712_NAR_50mM_plus2.18879.18879.3	3	10.21	1	4.83E+05	M1m	(-)mDELQLI	(-)m D/E/L/Q L F R/G D T V L/L/K(G)	m:Oxidized methionine	166.87	598.6527	1777.952	15.9919	-1.7	4.56	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
9894	dirMS_041712_NAR_50mM_plus2.20387.20387.3	3	10.21	2	2.12E+05	T121t	(K)EPVIAQI	(K)E P V/I/A Q K Q K/H/t G A V R(A)	t:N-acetylglucosamine (T)	176.32	622.3526	1661.945	203.0987	10.4	10	39291.8	6.3	HUMAN	B4DGE3	Protein transport protein Sec31B
9895	dirMS_041712_NAR_50mM_plus2.6168.6168.3	3	10.21	0	4.66E+04		(R)LQVEQA	(R)L/Q|V E Q A/P H/S S/P G A K(L)		96.6	483.5916	1448.749	0.011	7.6	6.75	16834.6	6.3	HUMAN	H0YKT9	Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase MESH1 (Fragment)
9896	dirMS_041712_NAR_60mM_plus.9019.9019.3	3	10.21	1	2.35E+05	M316m	(K)mADEAI	(K)m/A/D/E/A I L Q E R E R(G)	m:Oxidized methionine	105.45	492.9088	1460.716	15.9956	0.5	4.41	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
9897	dirMS_041712_NAR_60mM_plus.9485.9485.3	3	10.21	1	3.92E+05		(K)VGIRETI	(K)V/G/I R E T/P E N/L A/K(L)		107.65	442.9125	1326.738	-0.0146	-11	6.11	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
9898	dirMS_041712_NAR_50mM_minus2.8214.8214.3	3	10.2	2	2.34E+05	M299m	(K)KDVDAA	(K)K D/V/D A A F m/N K V E L Q A K(V)	m:Oxidized methionine	115.43	608.3087	1806.942	15.9697	-13.8	6.12	66410.1	8.82	HUMAN	Q01546	Keratin, type II cytoskeletal 2 oral
9899	dirMS_041712_NAR_60mM_minus.11631.11631.3	3	10.2	0	7.51E+05		(K)TKPYIQV	(K)T K|P Y I Q/V/D\I/G G/G Q T/K(T)		124.67	535.6216	1604.864	-0.014	-8.7	8.17	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
9900	dirMS_041712_NAR_60mM_minus.19995.19995.3	3	10.2	1	7.87E+05		(R)LIALLEVI	(R)L I/A/L/L/E V L/S Q K R(M)		182.07	461.6287	1382.873	-0.0014	-1	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
9901	dirMS_041712_NAR_60mM_minus.7987.7987.3	3	10.2	1	4.61E+05		(R)YLAEVA	(R)Y/L/A E/V/A/T G E K R(A)		104.33	412.8902	1236.658	-0.0022	-1.8	6.14	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
9902	dirMS_041712_NAR_120mM_plus.9499.9499.3	3	10.2	0	1.07E+05		(K)STAGDT	(K)S T|A/G D T/H/L/G G\E D\F/D N R(M)		103.08	564.579	1691.726	-0.0031	-1.9	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
9903	dirMS_041712_NAR_20mM_plus.11426.11426.2	2	10.2	0	2.15E+05		(R)YALYDA	(R)Y A|L|Y/D/A T Y E/T\K(E)		151.13	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
9904	dirMS_041712_NAR_20mM_plus.15878.15878.2	2	10.2	0	1.02E+04		(K)ALTLIAG	(K)A L/T|L/I/A|G S/P L/K(I)		180.78	542.3395	1083.677	-0.0055	-5.1	8.8	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
9905	dirMS_041712_NAR_30mM_plus2.12664.12664.2	2	10.2	0	1.62E+05		(K)NAGVEG	(K)N A|G|V|E G/S L I V E/K(I)		120.17	608.3313	1215.658	-0.0026	-2.2	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
9906	dirMS_041712_NAR_30mM_plus2.18388.18388.2	2	10.2	0	2.29E+05		(K)TTFEDLI	(K)T T|F E/D/L I Q/R(C)		149.35	561.7934	1122.579	0.0006	0.5	4.37	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
9907	dirMS_041712_NAR_30mM_plus2.20200.20200.2	2	10.2	0	2.11E+05		(K)AWDIAI	(K)A W|D|I/A I A T\M\K(V)		159.67	560.3022	1119.587	0.0104	9.3	5.88	9623.9	6.07	HUMAN	F5H1U3	Peptidyl-prolyl cis-trans isomerase (Fragment)
9908	dirMS_041712_NAR_40mM_plus2.5721.5721.2	2	10.2	0	1.12E+05		(R)FSSSSGY	(R)F S|S S/S/G/Y/G G G S S R(V)		90.98	618.2686	1235.529	0.0012	1	8.75	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
9909	dirMS_041712_NAR_50mM_plus2.12382.12382.3	3	10.2	1	7.86E+05		(K)IEVEKPF	(K)I/E|V E K/P F A I A K E(-)		133.12	458.5944	1373.767	0.0012	0.8	5.01	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
9910	dirMS_041712_NAR_60mM_plus.16305.16329.3	3	10.2	0	3.26E+05		(R)FVFDRPI	(R)F/V|F D/R/P L P V S/R(L)		142.5	444.917	1332.742	-0.0058	-4.4	9.6	18685.5	9.45	HUMAN	B4DEV8	Proteasome subunit alpha type
9911	dirMS_041712_NAR_60mM_plus.17575.17575.3	3	10.2	1	4.62E+05		(R)AKELLGC	(R)A K\E L L G Q/G\L|L/L|R(S)		148.82	437.6093	1310.815	-0.0021	-1.6	8.79	106155.7	5.45	HUMAN	B5ME19	Eukaryotic translation initiation factor 3 subunit C
9912	dirMS_041712_NAR_60mM_plus.19433.19433.3	3	10.2	0	1.22E+05		(R)NSVSNF	(R)N/S\V/S N F L/H S L E R(G)		161.22	468.2401	1402.707	-0.0016	-1.1	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
9913	dirMS_041712_NAR_120mM_minus.8484.8484.3	3	10.19	1	2.08E+05		(R)LREDEN	(R)L R E D E N\A\E|P V/G T T Y/Q K(T)		100.38	617.3002	1849.893	-0.0066	-3.6	4.41	76925.9	4.46	HUMAN	A8MV58	Drebrin
9914	dirMS_041712_NAR_120mM_minus.9714.9714.3	3	10.19	1	3.90E+05		(K)YAGKDG	(K)Y/A/G K D G Y N Y T L S/K(T)		107.5	493.9089	1479.711	0.0007	0.5	8.38	11854.4	6.57	HUMAN	P31949	Protein S100-A11

9915	dirMS_041712_NAR_30mM_minus2.14737.14737.2	2	10.19	0	1.82E+05		(K)NLQEAE	(K)N L|Q/E/A/E/E/W Y\K(S)		133.95	655.3063	1309.606	-0.0006	-0.4	4.25	49709.6	5.19	HUMAN	B0YJC4	Vimentin
9916	dirMS_041712_NAR_30mM_minus2.16579.16579.2	2	10.19	0	2.83E+05		(R)ASLEAAI	(R)A S L E A/A/I/A/D A E Q R(G)		143.77	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
9917	dirMS_041712_NAR_30mM_minus2.17121.17121.2	2	10.19	0	1.88E+05		(R)SIQEELC	(R)S I Q/E/E L/Q Q|L/R(Q)		146.55	622.3359	1243.664	0.0004	0.3	4.53	533778	5.74	HUMAN	Q15149	Plectin
9918	dirMS_041712_NAR_30mM_minus2.17232.17232.2	2	10.19	0	1.84E+05		(R)IYNVIGT	(R)I Y/N|V/I/G T L R(G)		146.95	524.8092	1048.615	-0.0038	-3.7	8.75	84557.3	6.5	HUMAN	Q04609	Glutamate carboxypeptidase 2
9919	dirMS_041712_NAR_50mM_minus2.11332.11332.3	3	10.19	1	2.04E+05		(K)MLVSGA	(K)M L|V/S G A/G D I/K L T/K(D)		132.4	444.9227	1332.756	-0.002	-1.5	8.35	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
9920	dirMS_041712_NAR_50mM_minus2.16727.16727.3	3	10.19	1	9.23E+04		(R)DSEQVA	(R)D S|E/Q/V\A E L K/Q E L A T L K(S)		163.05	601.3217	1801.954	-0.0036	-2	4.41	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
9921	dirMS_041712_NAR_50mM_minus2.6655.6655.3	3	10.19	1	6.22E+04		(R)EGVLTG	(R)E G V/L/T/G S/P/E Q K E E A A K(A)		104.1	558.2834	1672.839	-0.0032	-1.9	4.49	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
9922	dirMS_041712_NAR_120mM_plus.19414.19431.3	3	10.19	1	6.90E+05		(K)YNQLLRI	(K)Y/N/Q/L/L/R I E E E L G S K(A)		155.23	564.6353	1691.896	-0.0049	-2.9	4.79	47510.4	7.04	HUMAN	P06733	Alpha-enolase
9923	dirMS_041712_NAR_20mM_plus.6654.6654.2	2	10.19	0	7.77E+04	M357m	(K)AELDDTI	(K)A E|L/D|D/T P m/R(G)	m:Oxidized methionine	110.62	532.24	1047.478	15.9952	0.3	4.03	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
9924	dirMS_041712_NAR_20mM_plus.9660.9660.2	2	10.19	0	1.19E+05		(K)VAGQDC	(K)V A|G Q|D/G S/V\V/Q/F K(I)		138.08	617.8225	1234.643	-0.0049	-4	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
9925	dirMS_041712_NAR_30mM_plus2.15235.15235.2	2	10.19	0	1.49E+05		(K)AFQNVF	(K)A F/Q N/V|F/A/P R(N)		132.4	525.2819	1049.553	0.0038	3.7	9.79	60786.2	8.94	HUMAN	B4DYH8	N-acetylglucosamine-6-sulfatase
9926	dirMS_041712_NAR_30mM_plus2.19427.19427.2	2	10.19	0	2.25E+05		(K)NFSGAE	(K)N F|S/G A/E\L E G L V R(A)		155.5	646.3361	1291.664	0.0008	0.6	4.53	71924.9	6.25	HUMAN	B4DFA2	Vesicle-fusing ATPase
9927	dirMS_041712_NAR_30mM_plus2.19951.19951.2	2	10.19	0	5.91E+05		(R)NAVWA	(R)N A|V|W/A/L S N L C R(G)	C:Carbamidomethylation	157.43	652.3414	1303.658	0.018	13.8	9.75	37228.9	5.22	HUMAN	C9JYI4	Importin subunit alpha-1 (Fragment)
9928	dirMS_041712_NAR_30mM_plus2.21122.21122.2	2	10.19	0	3.78E+05		(K)AIDLFTD	(K)A/I|D\L/F T D A I K(L)		164.97	553.8012	1106.609	-0.0141	-12.7	4.21	18141.9	4.7	HUMAN	F6VDH7	Hsc70-interacting protein (Fragment)
9929	dirMS_041712_NAR_30mM_plus2.4870.4870.2	2	10.19	1	2.29E+05		(R)NTKGGD	(R)N T\K G G D|A P A|A\G\E\D A(-)		77.03	637.286	1273.565	-0.0008	-0.6	4.03	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
9930	dirMS_041712_NAR_30mM_plus2.8095.8095.2	2	10.19	0	1.31E+06		(K)QGGGG	(K)Q G G/G G G/G|G S V/P G I E R(M)		97.13	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
9931	dirMS_041712_NAR_30mM_plus2.8557.8557.2	2	10.19	0	8.96E+05		(R)LGLGEG	(R)L/G L/G|E|G A E E K(S)		99.07	501.7639	1002.51	0.0103	10.3	4.25	40096.8	9.24	HUMAN	C9JW69	Regulator of chromosome condensation (Fragment)
9932	dirMS_041712_NAR_30mM_plus2.9272.9272.2	2	10.19	0	3.15E+05		(K)LAAAEG	(K)L/A/A\A/E G/E L K(I)		101.32	451.2545	901.499	0.0028	3.1	4.53	464687.9	5.7	HUMAN	Q8WXX0	Dynein heavy chain 7, axonemal
9933	dirMS_041712_NAR_40mM_plus2.10722.10722.3	3	10.19	1	4.29E+05		(R)DGKLVS	(R)D G K\L V\S\E|S/S/D V/L/P/K(-)		128.63	491.9315	1473.78	0.0004	0.3	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
9934	dirMS_041712_NAR_50mM_plus2.17436.17436.3	3	10.19	1	5.87E+05		(R)LNRLPA	(R)L N R L P\A A\G\V|G D/M V M A/T V K(K)		160.33	614.9984	1842.993	-0.0122	-6.6	8.75	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
9935	dirMS_041712_NAR_50mM_plus2.8954.8954.3	3	10.19	1	1.66E+05		(K)TTSPPEV	(K)T T/S|P/P E V/S G Y S Y E K T E/R(S)		113.7	644.3093	1930.903	0.0105	5.4	4.78	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
9936	dirMS_041712_NAR_60mM_plus.20184.20184.3	3	10.19	0	2.36E+05		(K)ALSAIAD	(K)A L|S\A/I A D L/L T/N E H E R(V)		165.23	551.6246	1652.86	-0.001	-0.6	4.65	105417.2	6.41	HUMAN	C9JZR2	Catenin delta-1
9937	dirMS_041712_NAR_30mM_minus2.11134.11252.2	2	10.18	0	5.48E+04		(K)MLVIEQ	(K)M/L|V|I/E/Q/C K(N)	C:Carbamidomethylation	114.78	510.7635	1020.522	-0.0019	-1.9	5.75	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
9938	dirMS_041712_NAR_30mM_minus2.11604.11604.2	2	10.18	0	1.08E+06		(K)LEAEIAT	(K)L/E|A|E/I A T Y R(R)		116.33	533.2797	1065.557	-0.0054	-5	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
9939	dirMS_041712_NAR_30mM_minus2.16648.16648.2	2	10.18	0	3.60E+04		(R)IGNLQTI	(R)I|G/N L/Q/T|D L S D G L R(L)		144.9	701.3701	1401.733	-0.0003	-0.2	4.21	280326.9	5.48	HUMAN	O75369	Filamin-B
9940	dirMS_041712_NAR_30mM_minus2.7604.7604.2	2	10.18	0	7.71E+04		(K)NCTYTQ	(K)N/C|T/Y/T Q V/Q T/R(S)	C:Carbamidomethylation	95.8	635.7938	1270.584	-0.0041	-3.3	8.75	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
9941	dirMS_041712_NAR_40mM_minus2.13597.13597.3	3	10.18	0	2.83E+04	M211m	(K)LAKPLSS	(K)L A K P L S S\L/T/P L/I/m A A K(E)	m:Oxidized methionine	163.85	557.3348	1653.997	15.9927	-1.3	10	24711.4	5.19	HUMAN	H7C1X3	PAK-2p34 (Fragment)
9942	dirMS_041712_NAR_50mM_minus2.11167.11167.3	3	10.18	0	1.66E+04		(R)VVVLMC	(R)V V|V/L M G S T/S D L/G H C E K(I)	C:Carbamidomethylation	132.28	577.9535	1731.84	0.0055	3.2	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
9943	dirMS_041712_NAR_60mM_minus.14461.14461.3	3	10.18	1	2.79E+05		(K)KSDIDEI	(K)K\S D I D\E\I\V\L|V/G G S T R(I)		139.93	530.2846	1588.854	-0.0148	-9.3	4.56	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
9944	dirMS_041712_NAR_60mM_minus.7855.7855.3	3	10.18	1	3.67E+04		(R)LREDEN	(R)L R E D E N A E|P/V G/T T Y Q K(T)		103.67	617.3015	1849.893	-0.0027	-1.5	4.41	76925.9	4.46	HUMAN	A8MV58	Drebrin
9945	dirMS_041712_NAR_20mM_plus.18696.18696.2	2	10.18	0	1.46E+05	M332m	(R)IVSQLLT	(R)I V|S Q/L|L/T L m D G L K(Q)	m:Oxidized methionine	199.58	723.9145	1430.829	15.993	-1.3	5.84	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
9946	dirMS_041712_NAR_30mM_plus2.20842.20842.2	2	10.18	0	3.47E+05		(K)LTQILSYI	(K)L T|Q/I|L S Y/L R(Q)		163.88	553.831	1106.657	-0.0021	-1.9	8.75	65715.2	6.26	HUMAN	Q13123	Protein Red
9947	dirMS_041712_NAR_30mM_plus2.21909.21909.2	2	10.18	0	2.34E+05		(R)EGDVLT	(R)E G D\V/L|T/L/L E|S E R(E)		170.72	680.8538	1360.696	0.0049	3.6	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
9948	dirMS_041712_NAR_30mM_plus2.7747.7771.2	2	10.18	0	3.38E+06		(R)AVDFAE	(R)A/V|D/F A E/R(H)		95.48	404.2048	807.399	0.0028	3.4	4.37	24115.6	11.59	HUMAN	E9PIZ3	60S ribosomal protein L8
9949	dirMS_041712_NAR_30mM_plus2.8905.8905.2	2	10.18	0	7.37E+05		(R)GMGPG	(R)G M/G/P G T|P A G Y G R(G)		100.28	560.7657	1120.52	0.0037	3.3	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
9950	dirMS_041712_NAR_40mM_plus2.14358.14358.3	3	10.18	1	1.77E+05		(K)IMASSPI	(K)I/M|A S/S/P D M D L A T/V S A L R K(M)		151.22	635.9975	1905.977	0.0007	0.4	5.96	36208.1	7.21	HUMAN	B4DMU0	Pyrroline-5-carboxylate reductase
9951	dirMS_041712_NAR_50mM_plus2.14685.14685.3	3	10.18	1	8.16E+05	M85m	(K)TVTAmD	(K)T/V|T A\m D V/V Y/A L K R(Q)	m:Oxidized methionine	145.5	494.9387	1466.804	15.998	2.1	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
9952	dirMS_041712_NAR_50mM_plus2.19411.19411.3	3	10.18	1	2.25E+05		(K)DGKTLN	(K)D G K/T L N D E/L/E/I|I E G M/K(F)		169.82	602.3071	1804.9	0.007	3.9	4.18	23782.2	9.5	HUMAN	E7EXB4	60 kDa heat shock protein, mitochondrial (Fragment)
9953	dirMS_041712_NAR_50mM_plus2.8840.8840.3	3	10.18	0	7.69E+05		(R)AALAHS	(R)A A/L/A H S/E E V\T/A S/Q V\A\A T K(T)		113.47	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
9954	dirMS_041712_NAR_120mM_minus.19093.19093.4	4	10.17	1	1.69E+05		(R)SLRDLTF	(R)S L R D\L T/P E/H/L/P/L/L R(N)		158.92	415.7434	1659.954	-0.0023	-1.4	6.47	38779.2	5.93	HUMAN	Q96C86	m7GpppX diphosphatase
9955	dirMS_041712_NAR_50mM_minus2.15122.15122.3	3	10.17	0	3.71E+05		(R)LQQELD	(R)L/Q/Q/E/L D D L T V/D L D H Q R(Q)		153.18	646.6559	1937.956	-0.0032	-1.6	4.03	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
9956	dirMS_041712_NAR_50mM_minus2.17635.17635.3	3	10.17	1	2.09E+04		(K)TGISDVF	(K)T G I S/D\V F A K N D/L|A V/V D\V R(I)		168.85	640.346	1919.023	0.0002	0.1	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
9957	dirMS_041712_NAR_50mM_minus2.18360.18360.3	3	10.17	0	4.62E+05		(K)ALIEVLQ	(K)A L\I/E/V/L Q/P L I/A E H Q A R(R)		175.42	601.0139	1801.033	-0.0059	-3.3	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
9958	dirMS_041712_NAR_50mM_minus2.9032.9032.3	3	10.17	1	1.70E+05		(K)ITIKNDP	(K)I/T\I K N D\P S/L P E/P K(C)		119.82	484.6056	1451.81	-0.0082	-5.6	6.07	20203.8	9.79	HUMAN	B4DG16	Asparagine--tRNA ligase, cytoplasmic
9959	dirMS_041712_NAR_50mM_minus2.9555.9555.2	2	10.17	1	7.15E+05		(R)DGKLVS	(R)D/G K/L\V|S E S S D/V/L|P K(-)		121.97	737.3927	1473.78	-0.0014	-0.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
9960	dirMS_041712_NAR_60mM_minus.13611.13611.3	3	10.17	1	1.05E+05		(K)LVKELEG	(K)L/V/K E L E/G V I/T/K(A)		135.83	410.2539	1228.751	-0.004	-3.2	6.14	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
9961	dirMS_041712_NAR_60mM_minus.15566.15566.3	3	10.17	1	1.55E+06		(R)KDDPVT	(R)K D D\P V\T N L/N|N/A/F/E V/A E K(Y)		147.42	635.317	1903.94	-0.0032	-1.7	4.32	21601.4	6.27	HUMAN	K7EJH8	Alpha-actinin-4 (Fragment)
9962	dirMS_041712_NAR_30mM_plus2.19262.19262.2	2	10.17	0	2.73E+05		(K)TVDNFV	(K)T V|D\N F/V/A L/A/T G E K(G)		154.77	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
9963	dirMS_041712_NAR_30mM_plus2.19887.19887.3	3	10.17	0	2.45E+05		(R)IIPGFMC	(R)I I/P G F M/C Q/G G D/F T/R(H)	C:Carbamidomethylation	157.77	533.5865	1598.745	-0.0004	-0.3	5.84	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
9964	dirMS_041712_NAR_30mM_plus2.20719.20792.2	2	10.17	0	4.58E+05		(R)SLVPAAI	(R)S L|V|P A/A/E L L E S R(V)		162.2	642.8602	1284.716	-0.0027	-2.1	4.53	533778	5.74	HUMAN	Q15149	Plectin
9965	dirMS_041712_NAR_40mM_plus2.6626.6626.2	2	10.17	0	5.65E+04		(K)AGFAGD	(K)A G/F/A/G D/D A P R(A)		98.63	488.728	976.448	0.0004	0.4	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
9966	dirMS_041712_NAR_50mM_plus2.10742.10742.3	3	10.17	1	2.46E+06		(R)MQKEIT	(R)M/Q K E I T/A\L|A/P S/T\M K(I)		124.03	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
9967	dirMS_041712_NAR_50mM_plus2.14244.14244.3	3	10.17	1	5.13E+05		(R)YSVDIPL	(R)Y/S/V/D I/P L D K T V V N/K(D)		143.52	530.9567	1590.874	-0.0182	-11.4	5.96	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
9968	dirMS_041712_NAR_50mM_plus2.21361.21361.3	3	10.17	1	4.92E+05	M145m	(R)GVmLA	(R)G V|m\L/A/V/D A V I/A E L K K(Q)	m:Oxidized methionine	182.35	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
9969	dirMS_041712_NAR_60mM_plus.13949.14374.3	3	10.17	0	1.99E+06		(K)GIHPTIIS	(K)G I\H\P T I|I/S/E/S F Q K(A)		130.72	486.2646	1456.78	-0.0002	-0.1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
9970	dirMS_041712_NAR_60mM_plus.16049.16049.3	3	10.17	0	8.90E+05		(K)SLTNDW	(K)S L/T N D W/E D H L/A/V K(H)		141.57	509.919	1527.744	-0.0014	-0.9	4.53	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
9971	dirMS_041712_NAR_60mM_plus.8169.8217.3	3	10.17	1	8.51E+05		(R)FEPYANI	(R)F E|P/Y/A/N P T K R(Y)		101.18	408.2176	1222.622	0.0167	13.7	8.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
9972	dirMS_041712_NAR_60mM_plus.8430.8431.3	3	10.17	1	2.13E+05		(R)SSSASSP	(R)S S|S/A/S/S/P E M K D/G L P\R(T)		102.22	516.921	1548.732	0.0162	10.5	5.79	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
9973	dirMS_041712_NAR_120mM_minus.12227.12227.3	3	10.16	0	7.30E+05		(K)TFTAWC	(K)T F|T\A W/C/N S H/L/R(K)	C:Carbamidomethylation	121.4	464.8871	1392.648	-0.001	-0.7	9.44	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
9974	dirMS_041712_NAR_30mM_minus2.18543.18837.2	2	10.16	0	5.53E+05		(R)SSIAGLL	(R)S S|I/A/G L/L L K(A)		157.1	451.2891	901.572	-0.0008	-0.9	8.47	533778	5.74	HUMAN	Q15149	Plectin
9975	dirMS_041712_NAR_50mM_minus2.11181.11181.3	3	10.16	1	1.86E+05		(R)DNKQA	(R)D N K Q A\G|V/F/E/P T/I V K(V)		132.05	515.9485	1545.827	0.0038	2.5	6.07	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
9976	dirMS_041712_NAR_50mM_minus2.12755.12755.3	3	10.16	1	1.29E+05		(R)TEMENE	(R)T|E|M E N E F V L/I/K K(D)		140.62	494.2621	1480.772	0.0002	0.1	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
9977	dirMS_041712_NAR_50mM_minus2.9410.9410.3	3	10.16	0	6.17E+04		(R)DLSKPIG	(R)D L/S K/P I/G A/L N/P K(R)		121.75	418.2465	1252.726	-0.001	-0.8	8.59	84798.4	5.92	HUMAN	B7Z2H9	Neurobeachin
9978	dirMS_041712_NAR_60mM_minus.15731.15952.3	3	10.16	0	5.31E+05	M260m	(K)GISDLAC	(K)G I|S/D/L A/Q/H/Y L m R(A)	m:Oxidized methionine	148.23	473.9047	1403.71	15.9896	-3.8	6.74	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
9979	dirMS_041712_NAR_60mM_minus.18308.18308.3	3	10.16	1	1.37E+05		(R)SELELTL	(R)S E\L/E/L/T/L G K L/E Q V R(S)		163.05	538.9724	1614.906	-0.0035	-2.1	4.78	533778	5.74	HUMAN	Q15149	Plectin
9980	dirMS_041712_NAR_60mM_minus.8604.8604.3	3	10.16	0	3.02E+05		(K)EFHLNES	(K)E F/H L\N\E|S/G D/P/S S K(S)		108.08	482.8882	1446.65	0.0005	0.3	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
9981	dirMS_041712_NAR_20mM_plus.16660.16660.3	3	10.16	0	2.21E+05		(K)VQIAVA	(K)V Q\I|A V\A\N A Q E/L/L Q R(M)		186.37	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
9982	dirMS_041712_NAR_20mM_plus.18584.18584.2	2	10.16	0	1.98E+05		(R)VFIGNLN	(R)V/F|I|G/N/L N T L V|V K(K)		200.12	658.8999	1316.794	-0.0011	-0.9	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
9983	dirMS_041712_NAR_30mM_plus2.18825.18845.2	2	10.16	0	3.71E+05		(R)IYISLLK(	(R)I/Y|I S L/L/K(E)		152.37	425.2732	849.544	-0.0053	-6.2	8.59	105417.2	6.41	HUMAN	C9JZR2	Catenin delta-1
9984	dirMS_041712_NAR_30mM_plus2.22227.22227.2	2	10.16	0	2.13E+05		(K)NSSYFVE	(K)N S\S Y/F/V E/W\I|P N N V\K(V)		171.88	848.9189	1696.833	-0.0024	-1.4	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
9985	dirMS_041712_NAR_40mM_plus2.11585.11585.2	2	10.16	0	5.28E+04		(R)TFEDFVI	(R)T/F/E/D/F V R(I)		134.22	457.2245	913.441	0.0003	0.3	4.37	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
9986	dirMS_041712_NAR_50mM_plus2.14474.14559.3	3	10.16	1	1.32E+05		(K)NLKVTA	(K)N L K V T A\V/P/T L/L K(Y)		144.67	432.9459	1296.825	-0.0018	-1.4	10	11462.8	5.18	HUMAN	I3L2R6	Thioredoxin domain-containing protein 17
9987	dirMS_041712_NAR_50mM_plus2.6940.6940.3	3	10.16	1	8.61E+05		(K)IVADKD	(K)I/V/A D K D Y/S/V/T A N/S K(I)		101.48	504.2628	1510.775	-0.0009	-0.6	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
9988	dirMS_041712_NAR_20mM_minus.9218.9218.2	2	10.15	0	9.72E+04	M267m	(R)LITLEEEr	(R)L I|T L/E/E E m T K(Y)	m:Oxidized methionine	142.02	611.8143	1206.629	15.9927	-1.8	4.25	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
9989	dirMS_041712_NAR_30mM_minus2.18113.18113.2	2	10.15	0	2.46E+05		(K)EGMNIV	(K)E G/M/N I/V E/A M E R(F)		152.32	639.7955	1278.582	0.002	1.6	4.25	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
9990	dirMS_041712_NAR_30mM_minus2.7349.7349.2	2	10.15	0	1.61E+05		(R)AQAAGS	(R)A Q|A|A/G\S\S V L/R(E)		94.8	480.2603	959.527	-0.0135	-14.1	9.79	38843.2	6.48	HUMAN	Q96EK9	Protein KTI12 homolog
9991	dirMS_041712_NAR_50mM_minus2.12439.12439.3	3	10.15	0	2.81E+05		(K)AASDIAI	(K)A A|S D/I/A M T\E L/P/P T H P I R(L)		139.2	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
9992	dirMS_041712_NAR_60mM_minus.18888.18888.3	3	10.15	0	1.36E+06		(R)IHFPLAT	(R)I H F|P L A T|Y/A|P V I S A E K(A)		166.23	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
9993	dirMS_041712_NAR_60mM_minus.7578.7578.3	3	10.15	1	1.06E+05	M195m	(R)GSNmDI	(R)G S/N/m/D/F R E/P T E/E/E R(A)	m:Oxidized methionine	102.05	571.578	1696.723	15.9963	0.8	4.25	27441.6	6.68	HUMAN	Q15056	Eukaryotic translation initiation factor 4H
9994	dirMS_041712_NAR_120mM_plus.4667.4667.3	3	10.15	0	8.70E+05		(R)YINTEHC	(R)Y/I/N T E/H/G/G S Q A R(F)		74.22	444.8857	1332.629	0.0134	10.1	6.75	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
9995	dirMS_041712_NAR_20mM_plus.8587.8587.2	2	10.15	0	6.29E+04		(R)LDAEPRI	(R)L D A E|P R|P P/P/T\Q\E A\A(-)		129.63	746.3743	1491.744	-0.0025	-1.7	4.14	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
9996	dirMS_041712_NAR_30mM_plus2.15216.15216.2	2	10.15	0	1.49E+05		(K)AFQNVF	(K)A F/Q N/V|F/A/P R(N)		132.4	525.2819	1049.553	0.0038	3.7	9.79	60786.2	8.94	HUMAN	B4DYH8	N-acetylglucosamine-6-sulfatase
9997	dirMS_041712_NAR_30mM_plus2.16193.16612.2	2	10.15	0	1.12E+06		(R)IFIGTFK(	(R)I/F|I/G T/F K(A)		138.45	413.2445	825.487	-0.0052	-6.3	8.75	25246.3	11.45	HUMAN	B3KVR1	Small nuclear ribonucleoprotein-associated protein
9998	dirMS_041712_NAR_30mM_plus2.18329.18329.2	2	10.15	0	3.72E+05		(R)SQVEEEI	(R)S Q|V/E|E/E L F|S V R(V)		149.42	661.8302	1322.659	-0.0055	-4.2	4.25	533778	5.74	HUMAN	Q15149	Plectin
9999	dirMS_041712_NAR_30mM_plus2.21986.21986.2	2	10.15	0	1.55E+05		(K)ANFLQN	(K)A N|F\L/Q|N M/I/E D R(T)		170.25	675.8282	1350.647	0.0021	1.5	4.37	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
10000	dirMS_041712_NAR_30mM_plus2.22432.22432.2	2	10.15	0	3.56E+05		(R)VGNLGL	(R)V G N\L\G L|A/T S F/F\N E R(N)		172.88	762.8926	1524.781	-0.0026	-1.7	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
10001	dirMS_041712_NAR_40mM_plus2.6239.6386.2	2	10.15	0	4.41E+05		(K)NAGFTP	(K)N A|G|F|T/P Q E R(Q)		96.23	510.2487	1019.491	-0.0004	-0.4	6	29474.8	6.94	HUMAN	G3V3M6	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
10002	dirMS_041712_NAR_40mM_plus2.7672.7672.2	2	10.15	0	7.03E+04		(K)YIDQEEL	(K)Y I/D Q E/E L N\K(T)		105.2	576.2811	1151.558	-0.003	-2.6	4.14	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
10003	dirMS_041712_NAR_50mM_plus2.13280.13280.3	3	10.15	1	1.66E+05		(K)GQILMP	(K)G Q|I/L|M/P N I G Y G S N K K(T)		137.87	540.6161	1619.857	-0.0236	-14.6	9.7	15730.4	11.67	HUMAN	D3YTB1	60S ribosomal protein L32 (Fragment)
10004	dirMS_041712_NAR_50mM_plus2.19035.19035.3	3	10.15	1	4.78E+04		(K)LIQLMEI	(K)L I/Q/L M\E E I/M A E K E N/K(T)		168.75	606.9845	1818.934	0.005	2.7	4.49	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
10005	dirMS_041712_NAR_50mM_plus2.20844.20844.3	3	10.15	0	2.17E+05		(K)GLEHVT	(K)G L E H V T V D D\L|V/A E I T/P K(G)		178.28	612.6632	1835.975	0.0001	0.1	4.31	11429.2	9.63	HUMAN	E5RHX8	Enhancer of yellow 2 transcription factor homolog
10006	dirMS_041712_NAR_50mM_plus2.7482.7482.3	3	10.15	0	3.69E+05		(R)VGQAVD	(R)V/G|Q A V D V V/G Q A/G K/P K(T)		105.72	484.9438	1452.817	-0.0001	0	8.56	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
10007	dirMS_041712_NAR_60mM_plus.10754.10754.3	3	10.15	1	1.26E+06		(R)YLAEFAT	(R)Y L|A E/F/A/T/G N D R K(E)		113.08	462.2281	1384.686	-0.0158	-11.4	6.07	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
10008	dirMS_041712_NAR_60mM_plus.6888.6888.3	3	10.15	1	7.28E+05		(R)SGAPAA	(R)S G\A/P A/A E/S K E I/V R(G)		94.78	438.904	1314.701	-0.0038	-2.9	5.87	14003.4	5.66	HUMAN	Q9NRX4	14 kDa phosphohistidine phosphatase
10009	dirMS_041712_NAR_20mM_minus.7860.7860.2	2	10.14	0	1.69E+05		(K)SVEAAA	(K)S V|E/A/A A/E/L S A K(D)		128.45	538.2838	1075.563	-0.0027	-2.5	4.53	12131.5	11.14	HUMAN	F5GXR3	Parathymosin
10010	dirMS_041712_NAR_20mM_minus.7878.7878.2	2	10.14	0	1.69E+05		(K)SVEAAA	(K)S V|E/A/A A/E\L S A K(D)		128.45	538.2838	1075.563	-0.0027	-2.5	4.53	12131.5	11.14	HUMAN	F5GXR3	Parathymosin
10011	dirMS_041712_NAR_50mM_minus2.10797.10797.3	3	10.14	1	5.75E+05		(R)IAEFTTN	(R)I/A|E F/T/T N L/T E E E E K S K(S)		130.37	623.6418	1868.912	-0.0015	-0.8	4.32	227783.5	5.5	HUMAN	P35579	Myosin-9
10012	dirMS_041712_NAR_60mM_minus.10286.10286.3	3	10.14	1	2.36E+04	M88m	(K)DVDEAY	(K)D V/D/E\A/Y/m N K/V E L E|S R(L)	m:Oxidized methionine	116.03	605.2791	1797.832	15.9904	-2.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
10013	dirMS_041712_NAR_60mM_minus.14851.14851.3	3	10.14	1	2.10E+05		(K)IDSRLEQ	(K)I D|S R L E\Q\Y/T/S A/I E G T K(S)		142.88	604.3095	1810.918	-0.0042	-2.3	4.68	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
10014	dirMS_041712_NAR_60mM_minus.15485.15485.3	3	10.14	1	4.47E+05		(R)LLDAQL	(R)L/L|D A Q/L/A/T G G L V C P A R R(L)	C:Carbamidomethylation	146.07	604.3344	1810.996	-0.007	-3.8	9.6	266161	5.68	HUMAN	E9PPU0	Epiplakin
10015	dirMS_041712_NAR_60mM_minus.6983.6983.3	3	10.14	1	2.78E+05		(R)VKVEPA	(R)V K V E|P A|V|D T S/R(I)		97.4	400.8938	1200.658	0.0086	7.1	6.04	258215.9	5.48	HUMAN	E7EN95	Filamin-B
10016	dirMS_041712_NAR_60mM_minus.8735.8735.3	3	10.14	0	3.02E+05		(K)EFHLNES	(K)E\F H L\N\E S/G D/P/S S K(S)		108.08	482.8882	1446.65	0.0005	0.3	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
10017	dirMS_041712_NAR_20mM_plus.14687.14687.2	2	10.14	0	8.06E+04		(K)NLYIISV	(K)N L|Y|I/I S/V K(G)		173.1	475.2896	949.572	0.0002	0.2	8.59	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
10018	dirMS_041712_NAR_20mM_plus.18981.18981.2	2	10.14	0	1.75E+05		(R)VCTLAII	(R)V C/T\L|A|I|I|D P G D S D I I R(S)	C:Carbamidomethylation	202.62	879.4578	1757.91	-0.0019	-1.1	3.93	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
10019	dirMS_041712_NAR_30mM_plus2.6661.6661.2	2	10.14	0	5.75E+04		(K)TVGVEP	(K)T V|G V E/P A A/D G K(G)		89.45	522.2782	1043.537	0.0124	11.8	4.37	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
10020	dirMS_041712_NAR_50mM_plus2.10083.10135.3	3	10.14	0	2.23E+05		(R)TITVALA	(R)T I|T/V/A/L A D/G G/R P D N T G R(G)		120.23	571.9661	1713.888	-0.0041	-2.4	5.63	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
10021	dirMS_041712_NAR_50mM_plus2.9104.9104.3	3	10.14	1	2.65E+05		(K)EVPAVP	(K)E V/P/A V/P E/T L K K(K)		115.48	404.2395	1210.704	-0.0002	-0.2	6.24	29282.3	10.71	HUMAN	P18124	60S ribosomal protein L7
10022	dirMS_041712_NAR_60mM_plus.12002.12002.3	3	10.14	1	3.89E+05		(R)NLKASLE	(R)N L/K A S L/E|N S L/R(E)		120.05	415.5712	1244.696	0.0033	2.7	8.75	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10023	dirMS_041712_NAR_60mM_plus.5226.5226.3	3	10.14	1	4.08E+05		(K)VSSAEG	(K)V/S/S A E G A\A K E E P K(R)		85.05	434.8867	1302.654	-0.008	-6.2	4.79	4801.6	11.17	HUMAN	F2Z2W6	Non-histone chromosomal protein HMG-14

10024	dirMS_041712_NAR_60mM_plus.5630.5630.3	3	10.14	0	1.11E+06		(K)TATPQQ	(K)T A|T/P/Q Q A Q/E V H E K(L)		87.6	489.5727	1466.723	-0.0198	-13.5	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
10025	dirMS_041712_NAR_120mM_minus.18211.18211.4	4	10.13	1	3.15E+05		(K)ILGSGIS	(K)I L G S G I/S S/S/S/V L/H G M V F K K(E)		154.12	487.5223	1947.073	-0.0058	-3	10	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
10026	dirMS_041712_NAR_20mM_minus.10274.10274.2	2	10.13	0	2.40E+04		(R)AQAALA	(R)A Q|A\A L|A/V/N I S A A R(G)		152.12	628.3558	1255.712	-0.0074	-5.9	9.79	58479.6	6.23	HUMAN	P40227	T-complex protein 1 subunit zeta
10027	dirMS_041712_NAR_20mM_minus.13350.13350.2	2	10.13	1	2.53E+05		(R)LVLDSV	(R)L V|L/D S V K L E/A(-)		184.13	543.825	1086.641	0.0022	2	4.37	10137.3	4.59	HUMAN	E5RIW3	Tubulin-specific chaperone A
10028	dirMS_041712_NAR_40mM_minus2.9197.9197.3	3	10.13	1	7.60E+04		(K)LIADVA	(K)L I/A/D V/A P S A I R E N D/I K(S)		136.5	575.6561	1724.954	-0.0004	-0.2	4.56	18388.8	6.85	HUMAN	F5H1Y3	Flap endonuclease 1 (Fragment)
10029	dirMS_041712_NAR_50mM_minus2.12797.12797.3	3	10.13	0	2.97E+05		(K)EGKPTIV	(K)E G K P T\I\V|E/E/D D/P E/L F K(Q)		140.95	615.9772	1845.912	0.0054	2.9	4.08	29841.1	9.04	HUMAN	O75937	DnaJ homolog subfamily C member 8
10030	dirMS_041712_NAR_50mM_minus2.13788.13788.3	3	10.13	0	3.00E+04		(K)TGEEIFG	(K)T|G\E|E/I/F/G T I G M R P N A K(N)		146.93	574.2947	1720.869	0.0009	0.5	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
10031	dirMS_041712_NAR_50mM_minus2.14564.14564.3	3	10.13	1	2.41E+05		(R)GFPTIYF	(R)G F/P/T/I Y F S/P A N K K(L)		150.63	490.5972	1469.779	-0.0017	-1.1	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
10032	dirMS_041712_NAR_60mM_minus.10955.10955.3	3	10.13	1	2.32E+05		(K)VTVAGL	(K)V T/V/A/G/L A/G K D/P V Q C S R(D)	C:Carbamidomethylation	121.08	553.2923	1657.869	-0.0067	-4	8.72	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
10033	dirMS_041712_NAR_120mM_plus.8636.8636.2	2	10.13	0	7.61E+05		(K)HFVALS	(K)H\F|V/A L S/T/N\T T K(V)		99	609.8311	1218.648	0.0072	5.9	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
10034	dirMS_041712_NAR_20mM_plus.15575.15575.3	3	10.13	0	7.61E+04		(-)SDVLELT	(-)S D V\L/E L T D D N/F/E/S R(I)		179.2	547.2518	1639.745	-0.0037	-2.3	3.77	13747.3	6.8	HUMAN	H7BZJ3	Thioredoxin (Fragment)
10035	dirMS_041712_NAR_30mM_plus2.12163.12336.2	2	10.13	0	7.36E+05		(K)VNLLYSF	(K)V/N|L|L Y/S/R(D)		117.3	432.7483	864.494	-0.0045	-5.2	8.72	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
10036	dirMS_041712_NAR_30mM_plus2.5823.5823.2	2	10.13	0	3.59E+04	M119m	(K)VTmQNI	(K)V/T|m/Q N L/N D/R(L)	m:Oxidized methionine	84.63	553.7615	1090.531	15.9848	-9.2	5.81	51902.9	5.09	HUMAN	P02533	Keratin, type I cytoskeletal 14
10037	dirMS_041712_NAR_30mM_plus2.9581.9581.2	2	10.13	0	4.57E+05		(K)QTTCWI	(K)Q T T|C/W/D|G V/R(N)	C:Carbamidomethylation	104.4	561.7585	1122.5	0.0101	9	5.84	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1
10038	dirMS_041712_NAR_40mM_plus2.17121.17121.3	3	10.13	1	7.56E+04		(K)VIAATNI	(K)V I/A A/T/N R V D/I L/D/P A L L R(S)		166.93	617.3636	1850.086	-0.0096	-5.2	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
10039	dirMS_041712_NAR_50mM_plus2.17607.17644.3	3	10.13	1	2.09E+05		(R)EVQLEEI	(R)E V Q/L/E/E/L/E A A R D L V S K(E)		160.73	610.3302	1828.965	0.011	6	4.25	45984.6	6.24	HUMAN	B4E1G6	Galactokinase
10040	dirMS_041712_NAR_50mM_plus2.6610.6610.3	3	10.13	1	5.14E+04		(R)AGGEEL	(R)A/G G/E/E L/D/E|G V A K D N A K(I)		99	534.9257	1602.761	0.002	1.2	4.18	89879.1	4.58	HUMAN	Q32MZ4	Leucine-rich repeat flightless-interacting protein 1
10041	dirMS_041712_NAR_60mM_plus.11319.11319.3	3	10.13	1	9.12E+04		(K)LTSDDVI	(K)L/T/S D D/V K/E Q I/Y/K(L)		116.7	480.2511	1438.742	-0.0037	-2.5	4.56	12573.5	10.39	HUMAN	E9PS50	40S ribosomal protein S13 (Fragment)
10042	dirMS_041712_NAR_60mM_plus.13046.13047.3	3	10.13	0	6.26E+05		(K)VFEGNR	(K)V/F|E/G N R\P T N S I\V F T/K(L)		124.57	570.3039	1708.902	-0.0045	-2.7	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
10043	dirMS_041712_NAR_60mM_plus.6472.6472.2	2	10.13	1	1.46E+05		(K)GSGTAE	(K)G/S\G T/A E V/E\L K\K(G)		92.38	559.806	1118.605	-0.0005	-0.4	6.14	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
10044	dirMS_041712_NAR_120mM_minus.19677.19677.3	3	10.12	0	7.14E+05		(R)NSVSNF	(R)N S/V|S N/F/L/H S L E/R(G)		162.22	468.2346	1402.707	-0.0181	-12.9	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
10045	dirMS_041712_NAR_120mM_minus.4729.4729.3	3	10.12	1	3.56E+05		(K)AGADEE	(K)A/G|A/D/E E R A E T A R(L)		76.68	425.8687	1275.592	-0.0008	-0.7	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
10046	dirMS_041712_NAR_120mM_minus.5081.5081.3	3	10.12	1	4.65E+05		(R)AAEEED	(R)A A/E/E/E D E A D/P K R(Q)		79.6	453.8716	1359.602	-0.002	-1.5	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
10047	dirMS_041712_NAR_120mM_minus.8619.8769.3	3	10.12	0	7.90E+05		(R)QYDISDI	(R)Q Y/D/I/S D/P Q/R P/R(L)		101.62	458.8971	1374.676	0.0007	0.5	5.96	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
10048	dirMS_041712_NAR_20mM_minus.11698.11698.2	2	10.12	0	9.34E+04	M148m	(R)DLTDYL	(R)D L|T/D/Y L m K(I)	m:Oxidized methionine	164.67	507.7443	998.486	15.995	0.1	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
10049	dirMS_041712_NAR_20mM_minus.12176.12176.2	2	10.12	0	1.07E+06	M313m	(R)TVQSLEI	(R)T V/Q|S/L/E\I D\L/D S m R(N)	m:Oxidized methionine	170.67	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10050	dirMS_041712_NAR_20mM_minus.9233.9233.2	2	10.12	0	1.90E+05	M239m	(K)EITALAP	(K)E I|T|A|L/A/P S T m K(I)	m:Oxidized methionine	141.92	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
10051	dirMS_041712_NAR_30mM_minus2.12846.12846.2	2	10.12	0	3.00E+04		(R)GQVVSL	(R)G Q/V|V/S L I/R(M)		123.58	436.2706	871.536	-0.0021	-2.4	9.75	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
10052	dirMS_041712_NAR_30mM_minus2.15782.15802.2	2	10.12	0	4.68E+04		(R)INEILSN	(R)I/N|E|I/L/S/N A L K(R)		139.15	557.8242	1114.647	-0.0055	-5	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
10053	dirMS_041712_NAR_30mM_minus2.20274.20274.2	2	10.12	0	5.68E+05		(K)IGFPWSI	(K)I G/F|P W S/E I R(N)		172.05	552.7932	1104.584	-0.0045	-4.1	6	71218.8	6.3	HUMAN	A7YIJ8	Radixin
10054	dirMS_041712_NAR_40mM_minus2.13849.13849.3	3	10.12	1	3.93E+05		(R)VTFSGLI	(R)V/T/F S/G L R D\T\V/T/P G E L L K(A)		164.75	611.6742	1833.012	-0.0036	-2	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
10055	dirMS_041712_NAR_50mM_minus2.10973.10973.3	3	10.12	1	4.01E+05		(R)INVYYNI	(R)I/N|V/Y Y/N E A T G G K Y/V/P R(A)		131.28	615.3184	1843.934	0.0069	3.8	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
10056	dirMS_041712_NAR_60mM_minus.13961.13961.3	3	10.12	0	3.42E+05		(K)LHLGTT	(K)L H L\G T T Q N S\L/T/E/A D/F R(E)		137.48	601.6438	1802.903	0.0137	7.6	5.32	49472.3	6.75	HUMAN	O75351	Vacuolar protein sorting-associated protein 4B
10057	dirMS_041712_NAR_60mM_minus.6437.6437.3	3	10.12	2	7.61E+04		(R)EQREKE	(R)E/Q/R E K E E/I/E/K(Y)		94.62	439.8929	1317.665	-0.0003	-0.3	4.65	107721.8	8.85	HUMAN	O94906	Pre-mRNA-processing factor 6
10058	dirMS_041712_NAR_60mM_minus.6841.7267.3	3	10.12	0	1.27E+06	M434m	(R)LESGmC	(R)L/E|S G m Q N\M/S I/H T/K(T)	m:Oxidized methionine	97.23	497.9023	1475.698	15.9942	-0.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
10059	dirMS_041712_NAR_120mM_plus.16058.16058.4	4	10.12	1	8.06E+05		(K)THLPGF	(K)T\H\L P G F|V E Q A/E A L K A K(G)		137.05	435.4926	1738.949	-0.0001	0	6.42	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
10060	dirMS_041712_NAR_20mM_plus.12491.12491.3	3	10.12	0	3.48E+05		(K)IISNASC	(K)I I S N\A|S C T T/N|C L|A/P L/A/K(V)	C:Carbamidomethylation	159.53	611.9768	1833.92	-0.0039	-2.1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
10061	dirMS_041712_NAR_20mM_plus.18194.18194.2	2	10.12	0	1.70E+05		(R)LTGQLFI	(R)L T|G Q/L\F/L|G G S I V/K(G)		197.02	666.8962	1332.789	-0.0034	-2.6	8.75	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
10062	dirMS_041712_NAR_20mM_plus.7935.7935.2	2	10.12	0	1.89E+05		(R)FGQGG	(R)F G Q|G G/A/G|P V/G/G Q/G P R(G)		125.1	671.3361	1341.666	-0.0009	-0.7	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
10063	dirMS_041712_NAR_30mM_plus2.13851.13893.2	2	10.12	0	3.42E+05		(R)SISLYYT	(R)S I|S|L/Y/Y/T G E K(G)		125.95	580.796	1160.583	0.0013	1.2	5.72	32503.1	5.29	HUMAN	H7BY16	Nucleolin (Fragment)
10064	dirMS_041712_NAR_30mM_plus2.15941.15941.2	2	10.12	0	3.76E+05		(K)EIIDPVLI	(K)E I/I|D/P V/L D R(I)		136.5	535.2996	1069.589	0.0031	2.9	4.03	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
10065	dirMS_041712_NAR_30mM_plus2.17247.17247.2	2	10.12	0	2.66E+05		(K)SQLLSYII	(K)S Q|L/L/S/Y\I D/R(L)		142.83	547.7952	1094.584	-0.0009	-0.8	5.55	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
10066	dirMS_041712_NAR_30mM_plus2.18694.18694.3	3	10.12	0	4.97E+05		(R)SSFYVN	(R)S S\F Y V N\G L/T/L/G G Q/K(C)		150.95	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
10067	dirMS_041712_NAR_30mM_plus2.19852.19852.2	2	10.12	0	2.31E+05		(K)LLQDFFI	(K)L L/Q D/F F/N G R(D)		156.9	555.2902	1109.574	-0.0007	-0.6	5.84	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
10068	dirMS_041712_NAR_30mM_plus2.21100.21100.2	2	10.12	0	6.57E+05		(K)IPDWFLI	(K)I/P/D\W F/L N R(Q)		165.75	530.785	1060.557	0.0053	5	5.84	9767.1	11.41	HUMAN	J3JS69	40S ribosomal protein S18
10069	dirMS_041712_NAR_40mM_plus2.13728.13728.3	3	10.12	0	1.25E+05		(K)NLPPSG	(K)N L/P P S G A V/P V T G I/P P H V V\K(V)		146.85	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
10070	dirMS_041712_NAR_50mM_plus2.14997.14997.3	3	10.12	0	6.71E+05		(R)QIFHPE	(R)Q I/F/H/P E|Q L I/T G K(E)		147.27	470.9293	1410.774	-0.0006	-0.4	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
10071	dirMS_041712_NAR_60mM_plus.13023.13107.3	3	10.12	1	5.76E+05		(R)VVNGKV	(R)V/V|N G K V E Y F/L/K(W)		124.92	432.5826	1295.736	-0.0026	-2	8.47	11857.8	9.63	HUMAN	B8ZZ43	Chromobox homolog 3 (HP1 gamma homolog, Drosophila), isoform CRA_b
10072	dirMS_041712_NAR_60mM_plus.15604.15604.2	2	10.12	1	4.11E+05		(R)TEMENE	(R)T E|M/E N/E F V L I/K/K(D)		138.27	740.8875	1480.772	-0.0039	-2.6	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
10073	dirMS_041712_NAR_60mM_plus.17761.17761.3	3	10.12	1	3.50E+05		(R)LMDLLG	(R)L/M|D\L|L G E|G L K R(S)		149.5	415.5712	1244.703	-0.0041	-3.3	6.07	52817.9	6.2	HUMAN	F5H3T8	Arginine--tRNA ligase, cytoplasmic
10074	dirMS_041712_NAR_20mM_minus.14667.14667.3	3	10.11	0	3.68E+05		(K)LAVEALS	(K)L A V E A L/S/S L/D/G D/L/A G R(Y)		201.3	529.6163	1586.838	-0.0041	-2.6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
10075	dirMS_041712_NAR_20mM_minus.8847.8847.2	2	10.11	0	1.75E+05		(K)IVVVTA	(K)I V|V/V|T A G V R(Q)		137.98	457.2947	913.583	-0.0008	-0.9	9.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
10076	dirMS_041712_NAR_30mM_minus2.17284.17754.2	2	10.11	0	2.11E+05		(R)ILELDQF	(R)I/L|E/L/D Q F/K(G)		147.17	503.2871	1005.562	0.0054	5.4	4.37	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
10077	dirMS_041712_NAR_30mM_minus2.19599.19599.2	2	10.11	0	2.41E+05		(R)ILVATNL	(R)I L/V/A/T\N L F/G/R(G)		162.35	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
10078	dirMS_041712_NAR_50mM_minus2.17016.17016.3	3	10.11	1	5.94E+04		(R)EFTRLEI	(R)E F\T R L E I/C/N/L/T/P D A L K(S)	C:Carbamidomethylation	164.93	640.6675	1919.989	-0.0016	-0.8	4.68	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
10079	dirMS_041712_NAR_50mM_minus2.6706.6706.3	3	10.11	1	1.91E+05	M23m	(R)LAEQAE	(R)L/A|E/Q/A E R Y D D m A S/A M K(A)	m:Oxidized methionine	104.88	615.6099	1828.82	15.9947	-0.1	4.32	7741.6	5.25	HUMAN	A2IDB1	14-3-3 protein eta
10080	dirMS_041712_NAR_60mM_minus.15802.16054.3	3	10.11	1	3.10E+05		(K)ELKIDIIP	(K)E L K I\D\I\I|P N/P Q E R(T)		148.9	522.2935	1564.869	-0.0034	-2.2	4.68	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
10081	dirMS_041712_NAR_60mM_minus.8318.8437.3	3	10.11	0	4.60E+05	M148m	(R)AHSSmV	(R)A H\S S\m\V|G|V/N L/P Q K(A)	m:Oxidized methionine	106.77	461.9064	1367.71	15.9947	-0.2	8.8	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
10082	dirMS_041712_NAR_20mM_plus.14323.14323.3	3	10.11	0	7.24E+03		(R)VPTANV	(R)V\P T A N V\S V/V/D L/T C R(L)	C:Carbamidomethylation	169.75	510.9348	1530.795	-0.0046	-3	5.81	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
10083	dirMS_041712_NAR_20mM_plus.17995.17995.3	3	10.11	0	1.85E+05		(R)TVQSLEI	(R)T V\Q S/L\E|I/D\L/D S M R(N)		195.08	502.9236	1506.747	0.0094	6.2	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10084	dirMS_041712_NAR_20mM_plus.9405.9405.3	3	10.11	0	1.27E+05		(K)SVTNED	(K)S V\T N E\D\V/T Q/E E/L/G/G A/K(T)		136	559.6039	1676.797	-0.0002	-0.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
10085	dirMS_041712_NAR_30mM_plus2.10236.10236.2	2	10.11	0	5.41E+05		(K)FVIATST	(K)F V/I A/T/S T K(I)		107.35	433.7497	866.498	-0.0061	-7	8.75	25891.4	10.67	HUMAN	F8W181	60S ribosomal protein L6 (Fragment)
10086	dirMS_041712_NAR_30mM_plus2.19470.19470.2	2	10.11	0	2.67E+05		(K)TVDNFV	(K)T V|D N F/V/A/L/A T G E K(G)		155.35	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
10087	dirMS_041712_NAR_30mM_plus2.19744.19744.2	2	10.11	0	2.35E+05		(K)APDFVF	(K)A/P/D|F/V/F/Y/A P R(L)		156.72	591.8008	1182.594	0.0001	0.1	5.88	71218.8	6.3	HUMAN	A7YIJ8	Radixin
10088	dirMS_041712_NAR_50mM_plus2.18951.18951.3	3	10.11	0	4.14E+05		(R)AGLGSG	(R)A G L/G/S/G/L/S L/S/G L V/H P/E\L S R(S)		167.17	617.3412	1850.013	-0.004	-2.2	6.79	73325.2	9.19	HUMAN	F5H2A9	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial
10089	dirMS_041712_NAR_50mM_plus2.20753.20753.3	3	10.11	1	1.70E+05		(R)VNSKFD	(R)V N/S K F/D T I/Y Q I L L K(K)		177.62	561.3209	1681.952	-0.0042	-2.5	8.47	72626.7	9.13	HUMAN	Q14258	E3 ubiquitin/ISG15 ligase TRIM25
10090	dirMS_041712_NAR_50mM_plus2.8937.8937.3	3	10.11	1	3.10E+05		(K)TAVCDII	(K)T A|V C D/I/P/P R G L K(M)	C:Carbamidomethylation	114.82	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
10091	dirMS_041712_NAR_60mM_plus.11220.11220.3	3	10.11	1	2.81E+05	M61m	(K)NQVAm	(K)N Q|V|A/m N\P T N T V/F D A K R(L)	m:Oxidized methionine	116.13	607.9666	1805.896	15.989	-3.3	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
10092	dirMS_041712_NAR_60mM_plus.13681.13681.3	3	10.11	1	4.71E+05		(R)KYEMFA	(R)K\Y E M F|A Q/T|L/Q Q S/R(G)		128.72	543.9389	1629.805	-0.0032	-2	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
10093	dirMS_041712_NAR_30mM_minus2.10071.10071.2	2	10.1	0	1.87E+05		(K)SPSESFI	(K)S/P/S E/S F/I G/R(E)		109.8	490.2513	979.484	0.011	11.2	5.72	103815.5	6.12	HUMAN	F8WBA3	Serine/threonine-protein kinase D
10094	dirMS_041712_NAR_30mM_minus2.9923.10005.2	2	10.1	0	5.32E+05		(R)GNIPTLN	(R)G N|I|P/T/L N R(M)		108.3	442.7519	884.495	0.0017	1.9	9.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
10095	dirMS_041712_NAR_40mM_minus2.14090.14090.3	3	10.1	0	1.84E+05		(K)LQAVEV	(K)L/Q|A V\E V V/I T H L A P G T K(H)		167.1	559.3273	1675.974	-0.0068	-4	6.75	16120	9.05	HUMAN	Q9Y2V2	Calcium-regulated heat stable protein 1
10096	dirMS_041712_NAR_50mM_minus2.10715.10715.3	3	10.1	1	3.93E+05		(R)IAEFTTN	(R)I/A/E|F T T\N L T/E E E E K S K(S)		130.12	623.6418	1868.912	-0.0015	-0.8	4.32	227783.5	5.5	HUMAN	P35579	Myosin-9
10097	dirMS_041712_NAR_50mM_minus2.12878.12879.3	3	10.1	0	4.17E+06	M84m	(K)YPIEHGI	(K)Y/P I E H G I I|T/N|W/D D\m E K(I)	m:Oxidized methionine	141.65	659.6398	1960.911	15.9939	-0.5	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
10098	dirMS_041712_NAR_20mM_plus.18578.18578.3	3	10.1	0	1.88E+04		(R)APVPAS	(R)A P V\P A S E\L L|A|S/G V/L/S R(A)		199.92	522.9655	1566.885	-0.003	-1.9	6.05	533778	5.74	HUMAN	Q15149	Plectin
10099	dirMS_041712_NAR_30mM_plus2.19762.19803.2	2	10.1	0	2.98E+05		(K)LFLVQLC	(K)L/F|L/V/Q L Q E/K(A)		157.4	559.3295	1117.662	-0.0098	-8.8	6	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
10100	dirMS_041712_NAR_30mM_plus2.8537.8537.2	2	10.1	0	8.93E+05		(R)LGLGEG	(R)L/G/L|G/E G A E E K(S)		98.92	501.7639	1002.51	0.0103	10.3	4.25	40096.8	9.24	HUMAN	C9JW69	Regulator of chromosome condensation (Fragment)
10101	dirMS_041712_NAR_40mM_plus2.17442.17442.3	3	10.1	1	3.14E+05		(K)TGISDVF	(K)T G I/S/D/V/F A K N D L A\V/V D/V R(I)		169.33	640.3451	1919.023	-0.0025	-1.3	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
10102	dirMS_041712_NAR_50mM_plus2.15650.15650.3	3	10.1	1	1.23E+06		(K)VQGGAI	(K)V Q/G/G A L E D S Q L/V A/G V A F K K(T)		150.83	639.6848	1917.044	-0.0042	-2.2	6.04	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
10103	dirMS_041712_NAR_60mM_plus.10022.10503.3	3	10.1	1	8.18E+05		(K)TAVCDII	(K)T/A|V/C/D I/P P R G L K(M)	C:Carbamidomethylation	111.95	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
10104	dirMS_041712_NAR_60mM_plus.17067.17067.3	3	10.1	1	7.69E+06		(K)LKVPEW	(K)L K/V P E/W|V/D T V K(L)		145.67	438.5872	1313.746	0.0007	0.5	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
10105	dirMS_041712_NAR_20mM_minus.11115.11115.2	2	10.09	0	8.27E+04		(K)VIDPATA	(K)V I/D/P A/T/A T/S V D/L R(D)		158.45	679.3706	1357.732	0.0018	1.3	4.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
10106	dirMS_041712_NAR_30mM_minus2.19090.19090.2	2	10.09	1	2.15E+05		(K)SKLEFSI	(K)S K L E F S\I\Y|P A|P(-)		158.93	626.334	1251.662	-0.0012	-1	5.72	21962.5	5.85	HUMAN	C9JJQ8	Tubulin alpha-4A chain (Fragment)
10107	dirMS_041712_NAR_30mM_minus2.5776.5776.2	2	10.09	0	6.55E+04		(K)TSETLSC	(K)T S\E/T/L/S Q A G Q\K(A)		85.58	575.2877	1149.575	-0.0065	-5.6	5.66	25978.5	4.91	HUMAN	C9J502	Prostate leucine zipper variant 2
10108	dirMS_041712_NAR_30mM_minus2.7012.7012.2	2	10.09	0	2.65E+05		(R)CGCLDE	(R)C/G|C|L|D/E D/T Q R(Q)	C:Carbamidomethylation	93.03	627.2485	1253.488	0.0012	1	4.03	266161	5.68	HUMAN	E9PPU0	Epiplakin
10109	dirMS_041712_NAR_50mM_minus2.13687.13687.3	3	10.09	1	1.15E+05		(K)LTEDKAI	(K)L T/E D\K A D V/Q\S I/I/G L Q R(F)		146.42	595.9939	1785.97	-0.0034	-1.9	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
10110	dirMS_041712_NAR_50mM_minus2.17673.17673.3	3	10.09	1	2.72E+04		(K)IILDLISE	(K)I I/L D/L/I S E/S/P I K G R(A)		170.7	518.6444	1553.926	-0.0075	-4.8	6.07	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
10111	dirMS_041712_NAR_60mM_minus.11178.11178.3	3	10.09	1	6.58E+04		(K)IDKTDYN	(K)I D K T D Y M|V/G/S Y/G P R(A)		122.35	534.591	1601.763	-0.0044	-2.7	5.96	21671	5.37	HUMAN	J3KTF8	Rho GDP-dissociation inhibitor 1 (Fragment)
10112	dirMS_041712_NAR_60mM_minus.7844.7863.3	3	10.09	1	4.87E+05		(K)IQDKEGI	(K)I/Q D K E G I|P/P/D/Q Q R(L)		103.45	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
10113	dirMS_041712_NAR_60mM_minus.8443.8443.3	3	10.09	0	1.10E+05		(K)VDNDEN	(K)V/D/N/D\E N E/H Q L S L/R(T)		107.02	523.5817	1568.73	0.0006	0.4	4.31	6862.5	4.32	HUMAN	E5RGW4	Nucleophosmin (Fragment)
10114	dirMS_041712_NAR_20mM_plus.10767.10767.2	2	10.09	0	3.14E+04		(K)IGGIGTV	(K)I/G/G/I/G T/V/P V G R(V)		146.8	513.3057	1025.61	-0.0061	-5.9	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
10115	dirMS_041712_NAR_20mM_plus.15039.15039.2	2	10.09	0	1.04E+05		(R)ILNVPQI	(R)I L|N|V/P Q/E L Y/E K(G)		174.7	673.3693	1345.736	-0.0049	-3.6	4.53	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
10116	dirMS_041712_NAR_20mM_plus.16847.16847.2	2	10.09	0	3.45E+05		(K)VQIAVA	(K)V Q\I/A V/A/N A/Q E L L Q R(M)		187.37	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
10117	dirMS_041712_NAR_20mM_plus.18588.18588.2	2	10.09	0	2.58E+05		(K)LAVEALS	(K)L A V E/A/L/S/S/L|D G D L A G R(Y)		200.4	793.9214	1586.838	-0.0029	-1.8	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
10118	dirMS_041712_NAR_30mM_plus2.19769.19769.2	2	10.09	0	1.32E+05		(R)NTWLYC	(R)N/T/W|L/Y Q A L R(E)		157.08	582.8112	1164.616	-0.0009	-0.8	8.75	49457.5	6.47	HUMAN	P56545	C-terminal-binding protein 2
10119	dirMS_041712_NAR_30mM_plus2.22761.22761.2	2	10.09	0	2.69E+05		(R)ELSDFIS	(R)E L|S D F/I\S Y/L/Q R(E)		177.22	685.8507	1370.695	-0.0009	-0.7	4.37	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
10120	dirMS_041712_NAR_40mM_plus2.10700.10700.3	3	10.09	1	4.10E+05		(R)DGKLVS	(R)D G K\L V\S/E|S/S D\V|L/P K(-)		128.58	491.9315	1473.78	0.0004	0.3	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
10121	dirMS_041712_NAR_50mM_plus2.11690.11690.3	3	10.09	1	1.92E+05		(K)TGQPMI	(K)T G Q|P/M/I N L/Y T D R/E\T G K(L)		129.08	608.6361	1823.896	-0.0019	-1	5.73	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
10122	dirMS_041712_NAR_50mM_plus2.12035.12035.3	3	10.09	0	4.17E+05		(K)QADLYIS	(K)Q A D L/Y/I/S/E/G/L/H P R(I)		131.4	500.2606	1498.765	0.0024	1.6	5.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
10123	dirMS_041712_NAR_50mM_plus2.9811.9811.3	3	10.09	1	2.54E+05		(K)TTDMAI	(K)T T|D/M/A/P S\K E T E M A L A K(D)		119.22	575.2802	1723.824	0.0019	1.1	4.68	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
10124	dirMS_041712_NAR_60mM_plus.16607.16607.2	2	10.09	0	7.96E+05		(R)EHALLA	(R)E/H|A|L|L/A Y/T L G V K(Q)		143.78	657.8735	1314.742	-0.0019	-1.4	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
10125	dirMS_041712_NAR_60mM_plus.17945.17945.3	3	10.09	1	3.36E+05		(K)YAVLYQ	(K)Y/A|V/L Y Q/P\L F/D/K R(F)		151.35	504.9379	1512.821	-0.0218	-14.4	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
10126	dirMS_041712_NAR_60mM_plus.8462.8462.2	2	10.09	1	4.35E+05		(K)EAIEGTY	(K)E A|I/E/G T Y I D\K/K(C)		102.33	633.8318	1266.658	-0.0013	-1	4.68	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
10127	dirMS_041712_NAR_50mM_minus2.11704.11704.3	3	10.08	0	2.57E+05	M291m	(K)TGEEIFG	(K)T\G/E/E I/F G/T/I G m R P N A K(N)	m:Oxidized methionine	134.28	579.6239	1720.869	15.9885	-3.7	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
10128	dirMS_041712_NAR_50mM_minus2.16150.16150.3	3	10.08	1	2.15E+05		(R)NILGGT	(R)N I/L/G G/T/V F R E P I I C K(N)	C:Carbamidomethylation	160.25	572.9848	1716.947	-0.0067	-3.9	8.75	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
10129	dirMS_041712_NAR_50mM_minus2.17162.17162.3	3	10.08	0	7.69E+03		(K)ALSAIAD	(K)A L|S A/I|A/D L L/T N E H E R(V)		165.92	551.6261	1652.86	0.0035	2.1	4.65	105417.2	6.41	HUMAN	C9JZR2	Catenin delta-1
10130	dirMS_041712_NAR_60mM_minus.15078.15078.3	3	10.08	1	3.39E+05		(K)AKLEQLI	(K)A K L E Q\L|F/Q/D E V A/K(A)		144.37	506.9421	1518.816	-0.0045	-3	4.68	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
10131	dirMS_041712_NAR_60mM_minus.7672.7672.3	3	10.08	1	5.65E+05		(R)YLAEVA	(R)Y/L/A E/V A/A G D D/K K(G)		102.07	427.222	1279.653	-0.0014	-1.1	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
10132	dirMS_041712_NAR_120mM_plus.4222.4222.2	2	10.08	1	1.34E+06	M310m	(R)TKTEISE	(R)T/K|T/E I/S E m N R(N)	m:Oxidized methionine	69.9	612.7976	1208.594	15.994	-0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8

10133	dirMS_041712_NAR_120mM_plus.8906.8906.2	2	10.08	0	5.81E+05		(R)NGVMP	(R)N G\V|M|P S H F S R(G)		99.88	566.274	1131.536	0.0043	3.8	9.75	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
10134	dirMS_041712_NAR_20mM_plus.16409.16409.2	2	10.08	0	2.38E+04		(R)VVSEDFI	(R)V V/S/E D\F\L/Q/D/V S/A S T K(S)		184.55	812.9055	1624.806	-0.0027	-1.7	4.03	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
10135	dirMS_041712_NAR_20mM_plus.18304.18304.2	2	10.08	0	1.62E+04		(R)LGYILTC	(R)L G Y I L/T/C|P S N L G T G L R(A)	C:Carbamidomethylation	197.53	867.9606	1734.921	-0.0068	-3.9	8.75	47435.3	9.08	HUMAN	P12532	Creatine kinase U-type, mitochondrial
10136	dirMS_041712_NAR_30mM_plus2.14951.14951.2	2	10.08	0	1.26E+06		(R)LCFEGLF	(R)L/C|F/E G L R(S)	C:Carbamidomethylation	130.87	447.7285	894.45	-0.0005	-0.5	6	533778	5.74	HUMAN	Q15149	Plectin
10137	dirMS_041712_NAR_30mM_plus2.22233.22405.2	2	10.08	0	3.01E+05		(K)CMPTFC	(K)C M|P/T F/Q F F/K(K)	C:Carbamidomethylation	172.77	603.2777	1205.548	-0.0001	-0.1	8.75	9680	5.77	HUMAN	B1ALW1	Thioredoxin
10138	dirMS_041712_NAR_30mM_plus2.9794.9824.2	2	10.08	0	7.30E+05		(K)MINTDL	(K)M/I|N/T D/L S R(I)		105.27	475.2445	949.477	0.0046	4.8	5.59	37884.5	11.27	HUMAN	H3BM89	60S ribosomal protein L4
10139	dirMS_041712_NAR_40mM_plus2.7230.7708.2	2	10.08	0	2.20E+05		(R)SGYFDEI	(R)S/G|Y|F D/E R(Y)		104.03	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
10140	dirMS_041712_NAR_50mM_plus2.11539.11539.3	3	10.08	1	2.80E+06	M72m	(R)TEmENE	(R)T E/m E N E|F V L/I K/K(D)	m:Oxidized methionine	127.98	499.5943	1480.772	15.9968	1.2	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
10141	dirMS_041712_NAR_50mM_plus2.17273.17273.3	3	10.08	1	1.24E+05		(K)LLVYEAL	(K)L L/V/Y E\A|L/E Y A K R(A)		159.85	489.9441	1467.821	-0.0028	-1.9	6.14	32535.6	9.19	HUMAN	B4DZW6	Regulator of microtubule dynamics protein 1
10142	dirMS_041712_NAR_50mM_plus2.22320.22320.3	3	10.08	0	5.24E+05		(R)GGHPPA	(R)G G H P P A I Q S L/I|N L|L|A/D N R(Y)		191.88	629.3448	1886.024	-0.0044	-2.3	6.74	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
10143	dirMS_041712_NAR_50mM_plus2.5200.5200.3	3	10.08	0	1.37E+06		(K)TATPQQ	(K)T A|T/P Q Q/A/Q/E V H E K(L)		86.38	489.5774	1466.723	-0.0057	-3.9	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
10144	dirMS_041712_NAR_60mM_plus.11660.11660.3	3	10.08	0	3.34E+05		(R)SVIHSLA	(R)S V/I H/S L A|S/V/E A Q K(S)		118.18	456.9206	1368.748	-0.0009	-0.7	6.47	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
10145	dirMS_041712_NAR_60mM_plus.17995.17995.3	3	10.08	1	1.04E+06		(R)ARFEELN	(R)A R F E E\L|N|A|D/L F\R(G)		150.85	494.2554	1480.754	-0.0027	-1.8	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
10146	dirMS_041712_NAR_60mM_plus.20507.20507.3	3	10.08	1	4.16E+05		(K)NAAGAL	(K)N/A/A/G A L/D L L K E L K(N)		166.93	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
10147	dirMS_041712_NAR_60mM_plus.20587.20587.3	3	10.08	1	7.00E+05		(K)IKYPENF	(K)I K/Y P E N/F|F/L L/R(G)		167.98	480.6056	1439.805	-0.0023	-1.6	8.59	33222.3	5.74	HUMAN	A6NNR3	Serine/threonine-protein phosphatase
10148	dirMS_041712_NAR_120mM_minus.10844.10844.2	2	10.07	1	1.13E+06		(K)IKIIAPPE	(K)I/K|I/I/A\P P E R(K)		113.33	518.8303	1036.651	0.002	1.9	8.75	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
10149	dirMS_041712_NAR_20mM_minus.8255.8255.2	2	10.07	0	5.74E+03		(K)DQVANS	(K)D Q\V|A/N/S A F V E\R(L)		131.7	618.3098	1235.602	0.0108	8.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
10150	dirMS_041712_NAR_30mM_minus2.17463.17568.2	2	10.07	0	4.37E+05		(R)EQLAIAE	(R)E\Q|L|A/I/A E F A R(S)		150.25	574.3084	1147.611	-0.0011	-0.9	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
10151	dirMS_041712_NAR_30mM_minus2.7828.7828.2	2	10.07	0	4.24E+05		(K)IYSSEAI	(K)I/Y|S S/E A I K(S)		97.78	455.7458	910.488	-0.0037	-4.1	6	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
10152	dirMS_041712_NAR_50mM_minus2.10972.10972.3	3	10.07	1	4.01E+05		(R)INVYYNI	(R)I/N/V/Y/Y N/E/A/T/G G K/Y V P R(A)		131.28	615.3184	1843.934	0.0069	3.8	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
10153	dirMS_041712_NAR_50mM_minus2.13403.13403.3	3	10.07	1	1.91E+05		(K)TITLEVEI	(K)T I|T|L/E/V E P S D T I/E N V/K A K(I)		144.63	663.0226	1987.059	-0.0061	-3.1	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
10154	dirMS_041712_NAR_50mM_minus2.9203.9203.3	3	10.07	1	4.00E+04		(R)QELILSN	(R)Q E|L/I/L/S/N S/E D K S I R(V)		120.57	544.6228	1631.86	-0.006	-3.7	4.68	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
10155	dirMS_041712_NAR_60mM_minus.10102.10102.3	3	10.07	0	1.99E+04		(R)LSNRPAI	(R)L/S N R/P A/F\M|P S E G R(M)		115.98	487.9154	1461.727	0.0049	3.4	9.6	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
10156	dirMS_041712_NAR_60mM_minus.15808.15931.3	3	10.07	0	5.31E+05	M260m	(K)GISDLAC	(K)G I/S/D/L A/Q/H Y/L m R(A)	m:Oxidized methionine	148.23	473.9047	1403.71	15.9896	-3.8	6.74	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
10157	dirMS_041712_NAR_60mM_minus.9949.9949.3	3	10.07	1	4.21E+04	M61m	(K)NQVAm	(K)N Q|V/A/m/N P T N T V/F D/A K R(L)	m:Oxidized methionine	115.03	607.9739	1805.896	16.0109	8.7	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
10158	dirMS_041712_NAR_120mM_plus.19094.19251.4	4	10.07	1	1.05E+06		(K)FQIPPN	(K)F Q\I|P P N A E L K/Y E L H/L K(S)		153.18	485.7703	1940.064	-0.0046	-2.4	6.75	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
10159	dirMS_041712_NAR_120mM_plus.6110.6110.2	2	10.07	1	2.26E+06		(K)IREEYPD	(K)I R/E E/Y\P D|R(I)		84.95	539.2694	1077.532	-0.0008	-0.8	4.68	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
10160	dirMS_041712_NAR_20mM_plus.7885.7885.3	3	10.07	0	1.18E+05		(K)VEIIAND	(K)V E\I\I\A N/D Q/G N R(T)		124.5	410.2139	1228.628	-0.0009	-0.7	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
10161	dirMS_041712_NAR_30mM_plus2.18446.18446.2	2	10.07	0	2.09E+05		(K)GVEGLI	(K)G V|E G L|I/D I\E\N/P/N/R(V)		149.52	713.3669	1425.733	-0.0067	-4.7	4.14	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
10162	dirMS_041712_NAR_40mM_plus2.17655.17655.3	3	10.07	0	3.79E+04		(R)AGLGSG	(R)A G L G S|G L/S L|S G L V H P E/L S R(S)		170.98	617.3431	1850.013	0.0017	0.9	6.79	73325.2	9.19	HUMAN	F5H2A9	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial
10163	dirMS_041712_NAR_40mM_plus2.18048.18048.3	3	10.07	1	1.63E+04		(R)EQIPAG	(R)E Q/I/P/A G T L L L/A V E D P E/K R(V)		172.2	660.3654	1979.081	0.0009	0.4	4.41	19773.1	4.48	HUMAN	B4DEU5	L-fucose kinase
10164	dirMS_041712_NAR_60mM_plus.18739.18739.3	3	10.07	1	3.96E+06		(R)VSFELFA	(R)V/S|F E L/F\A D/K V P/K(T)		155.83	460.5914	1379.757	0.0027	2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
10165	dirMS_041712_NAR_20mM_minus.12451.12451.2	2	10.06	0	8.61E+04		(K)LVSIGAE	(K)L V/S/I/G A E/E I V D G N A K(M)		172.12	757.9044	1514.806	-0.0045	-3	4.14	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
10166	dirMS_041712_NAR_20mM_minus.13208.13208.2	2	10.06	0	2.38E+04	M329m	(K)ALELNm	(K)A L/E|L|N/m/L S/L K(G)	m:Oxidized methionine	183.02	574.3232	1131.644	15.9949	0	6.05	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
10167	dirMS_041712_NAR_20mM_minus.13737.13737.2	2	10.06	0	3.87E+05		(K)LGGSAV	(K)L/G\G S A/V/I S L E\G K/P L(-)		188.65	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
10168	dirMS_041712_NAR_30mM_minus2.6879.6879.2	2	10.06	0	2.07E+05		(K)VTEGGE	(K)V T|E/G/G E|P Y/R(L)		91.93	504.238	1007.479	-0.0105	-10.4	4.53	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
10169	dirMS_041712_NAR_30mM_minus2.6944.6944.2	2	10.06	0	2.29E+05		(K)ELGNDA	(K)E L/G N/D/A/Y/K(K)		91.3	455.2195	909.431	0.0005	0.5	4.37	60404.6	6.4	HUMAN	F5H0T1	Stress-induced-phosphoprotein 1
10170	dirMS_041712_NAR_30mM_minus2.7203.7203.2	2	10.06	0	1.61E+05	M88m	(K)DVDEAY	(K)D/V/D/E/A/Y m N K(V)	m:Oxidized methionine	92.92	550.7326	1084.462	15.9964	1.3	4.03	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
10171	dirMS_041712_NAR_50mM_minus2.10367.10367.3	3	10.06	0	1.66E+05		(K)LQAEAP	(K)L Q|A/E A P/H\I/V V/G T P G R(V)		127.08	515.6179	1544.854	-0.0152	-9.8	6.75	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
10172	dirMS_041712_NAR_50mM_minus2.11309.11309.3	3	10.06	0	1.66E+04		(R)VVVLM	(R)V V|V/L/M/G S T S D L G H C E K(I)	C:Carbamidomethylation	132.28	577.9535	1731.84	0.0055	3.2	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
10173	dirMS_041712_NAR_50mM_minus2.14415.14416.3	3	10.06	1	1.04E+06		(K)EAFSLF	(K)E A/F/S/L/F/D K D/G D G T I T T K(E)		150	615.6336	1844.891	-0.005	-2.7	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
10174	dirMS_041712_NAR_50mM_minus2.15263.15263.3	3	10.06	1	3.99E+05		(R)VCENIPI	(R)V/C|E N I P I V L/C G N K V D|I K(D)	C:Carbamidomethylation	155.53	657.6803	1971.04	-0.0138	-7	6.04	14844.8	5.89	HUMAN	B4DV51	GTP-binding nuclear protein Ran
10175	dirMS_041712_NAR_50mM_minus2.17755.17755.3	3	10.06	0	4.30E+04		(R)IHFPLAT	(R)I H F P L A\T Y/A/P/V I S A E K(A)		169.93	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
10176	dirMS_041712_NAR_50mM_minus2.7047.7047.3	3	10.06	0	2.09E+05		(K)VSYGIG	(K)V S/Y/G I/G/D/E E/H D Q E G R(V)		106.65	564.249	1690.73	0.0021	1.3	4.17	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
10177	dirMS_041712_NAR_60mM_minus.16706.16706.3	3	10.06	0	1.78E+05		(R)LLIHQSL	(R)L/L/I H Q S L|A\G G/I I G V K(G)		153.38	506.9823	1518.937	-0.0043	-2.8	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
10178	dirMS_041712_NAR_60mM_minus.19989.19989.3	3	10.06	1	7.97E+05		(R)LIALLEVI	(R)L/I/A L|L E V/L S Q K R(M)		182.05	461.6287	1382.873	-0.0014	-1	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
10179	dirMS_041712_NAR_60mM_minus.9398.9398.3	3	10.06	0	1.14E+06		(R)QSVEND	(R)Q S V/E N D I/H/G L/R(K)		112.07	423.218	1267.639	0.0005	0.4	5.32	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10180	dirMS_041712_NAR_120mM_plus.10623.10645.3	3	10.06	1	1.09E+07		(R)VKYETEL	(R)V K Y E T\E|L/A/M/R(Q)		107.95	413.8849	1239.64	0	0	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10181	dirMS_041712_NAR_20mM_plus.17902.17993.2	2	10.06	0	2.04E+05		(R)SLVPAAI	(R)S L/V|P A/A/E/L L E S R(V)		194.93	642.8613	1284.716	-0.0005	-0.4	4.53	533778	5.74	HUMAN	Q15149	Plectin
10182	dirMS_041712_NAR_20mM_plus.18347.18347.2	2	10.06	0	1.62E+04		(R)LGYILTC	(R)L G Y I\L/T C/P S/N L G T/G/L R(A)	C:Carbamidomethylation	197.53	867.9606	1734.921	-0.0068	-3.9	8.75	47435.3	9.08	HUMAN	P12532	Creatine kinase U-type, mitochondrial
10183	dirMS_041712_NAR_30mM_plus2.10193.10193.2	2	10.06	0	3.98E+04		(R)NAMGSI	(R)N/A|M/G S L A S/Q A T K(D)		106.68	589.7934	1178.583	-0.0039	-3.3	8.75	21119.9	4.34	HUMAN	H0Y3Y9	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
10184	dirMS_041712_NAR_40mM_plus2.15510.15510.3	3	10.06	1	7.33E+04		(K)VLDSGA	(K)V L/D S|G A P I K I/P V G P E T L G R(I)		158.12	640.3668	1919.096	-0.0102	-5.3	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
10185	dirMS_041712_NAR_40mM_plus2.9676.9676.2	2	10.06	0	1.27E+05		(K)FYEAFSK	(K)F/Y|E A F/S/K(N)		120.15	446.2159	891.425	-0.0002	-0.2	6	20127.1	9.4	HUMAN	H0Y598	Heat shock protein HSP 90-beta (Fragment)
10186	dirMS_041712_NAR_50mM_plus2.16893.16893.3	3	10.06	1	4.67E+05		(K)VLDSGA	(K)V/L|D|S G A/P I K I P/V G/P/E T L G R(I)		156.78	640.3623	1919.096	-0.0237	-12.3	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
10187	dirMS_041712_NAR_50mM_plus2.20434.20434.3	3	10.06	1	2.43E+05		(R)GGPNIIT	(R)G G/P N/I/I T L A D I V K D P V S R(T)		176.55	622.3526	1865.049	-0.0058	-3.1	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
10188	dirMS_041712_NAR_50mM_plus2.8926.8926.3	3	10.06	0	1.80E+05		(K)TPVEPE	(K)T|P\V E/P/E|V/A I/H R(I)		113.98	416.5627	1247.674	-0.0007	-0.6	5.37	5429.1	9.6	HUMAN	E5RIP1	40S ribosomal protein S20
10189	dirMS_041712_NAR_60mM_plus.12102.12102.3	3	10.06	1	6.89E+05		(R)MGIVGF	(R)M/G\I V/G/P/E F/K D K(L)		120.63	407.5532	1220.634	0.0107	8.7	5.82	533778	5.74	HUMAN	Q15149	Plectin
10190	dirMS_041712_NAR_60mM_plus.9368.9368.3	3	10.06	1	3.60E+05		(R)QAVTNF	(R)Q A V/T/N/P N N T/F Y/A/T K R(L)		107.17	575.6283	1724.872	-0.0011	-0.6	9.99	6809.6	9.69	HUMAN	D6RA73	Stress-70 protein, mitochondrial (Fragment)
10191	dirMS_041712_NAR_30mM_minus2.16145.16145.2	2	10.05	0	6.11E+04		(R)NELESY	(R)N/E|L/E/S Y A Y/S L/K(N)		141.13	658.8239	1316.637	0.0037	2.8	4.53	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
10192	dirMS_041712_NAR_30mM_minus2.5180.5180.2	2	10.05	0	5.83E+05		(R)TDTGEP	(R)T D|T/G/E\P/M G R(G)		81.85	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
10193	dirMS_041712_NAR_40mM_minus2.9028.9028.3	3	10.05	1	9.47E+04		(K)LAEIGAF	(K)L/A/E|I/G/A P I Q G N R E E L V E R(L)		136.07	665.3586	1994.066	-0.0053	-2.6	4.49	38572.2	6.31	HUMAN	E9PJ04	Splicing factor 3B subunit 2 (Fragment)
10194	dirMS_041712_NAR_50mM_minus2.8528.8569.3	3	10.05	1	2.43E+05		(R)AGTGVD	(R)A G|T|G V/D/N V/D/L/E/A A T R K(G)		116.55	539.6119	1616.824	-0.0027	-1.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
10195	dirMS_041712_NAR_60mM_minus.13705.13705.3	3	10.05	1	7.02E+04		(R)ALEEALE	(R)A/L|E/E A/L E A K E E F E R(Q)		136.33	555.2761	1663.817	-0.0036	-2.2	4.2	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
10196	dirMS_041712_NAR_120mM_plus.14604.14604.4	4	10.05	2	9.63E+05		(R)YLYTLVI	(R)Y L\Y T|L V/I T D K E K/A E K(L)		130.57	454.2533	1813.995	-0.0032	-1.8	6.18	7621.9	10.1	HUMAN	J3KT73	60S ribosomal protein L38
10197	dirMS_041712_NAR_120mM_plus.14929.14929.2	2	10.05	0	3.37E+06		(R)DWSHYI	(R)D W|S/H/Y/F/K(I)		132	491.725	982.442	0.001	1	6.74	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10198	dirMS_041712_NAR_120mM_plus.21191.21191.4	4	10.05	1	1.06E+06		(R)DYLHLPI	(R)D Y L H L P/P|E I/V/P A T L R/R(S)		164.38	473.2689	1890.06	-0.0058	-3.1	6.75	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
10199	dirMS_041712_NAR_20mM_plus.8323.8323.2	2	10.05	0	2.60E+04		(K)SPVESTT	(K)S P\V/E/S|T/T E/P P A V R(A)		127.48	685.3502	1369.696	-0.0027	-1.9	4.53	38808	7.85	HUMAN	B4DZT4	Protein transport protein Sec24C
10200	dirMS_041712_NAR_20mM_plus.8511.8511.2	2	10.05	0	5.30E+03		(K)VVTDTD	(K)V/V/T/D/T D E/T E L A R(Q)		128.77	674.8318	1348.659	-0.0027	-2	3.91	36396.8	5.02	HUMAN	P05198	Eukaryotic translation initiation factor 2 subunit 1
10201	dirMS_041712_NAR_30mM_plus2.17348.17348.3	3	10.05	0	1.07E+06		(R)ASLEAAI	(R)A S L E\A/A I/A/D/A E Q/R(G)		144.27	448.8963	1344.675	-0.001	-0.8	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
10202	dirMS_041712_NAR_30mM_plus2.4852.4852.2	2	10.05	1	2.39E+05		(R)NTKGGI	(R)N T K G G D/A\P\A|A|G E|D A(-)		76.97	637.286	1273.565	-0.0008	-0.6	4.03	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
10203	dirMS_041712_NAR_40mM_plus2.12816.12816.3	3	10.05	0	1.96E+05		(K)NLPPSG	(K)N L|P/P S\G A V P V/T G I/P P H V V K(V)		142	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
10204	dirMS_041712_NAR_50mM_plus2.12436.12436.3	3	10.05	1	4.78E+05		(K)ILDSVGI	(K)I/L/D S/V/G I E|A D D D R L N K(V)		132.88	591.6385	1772.902	-0.0015	-0.9	4.04	11664.7	4.42	HUMAN	P05387	60S acidic ribosomal protein P2
10205	dirMS_041712_NAR_50mM_plus2.9202.9202.3	3	10.05	1	7.16E+05		(K)TAVCDIF	(K)T A|V/C D/I/P/P R G L/K(M)	C:Carbamidomethylation	115.77	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
10206	dirMS_041712_NAR_60mM_plus.17496.17516.3	3	10.05	1	2.28E+04		(R)AITGASL	(R)A I|T G A/S/L/A/D I/M A K R(N)		148.45	473.2654	1417.783	-0.0015	-1.1	8.79	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
10207	dirMS_041712_NAR_120mM_minus.11632.11632.3	3	10.04	1	3.47E+06		(R)FPGQLN	(R)F/P/G Q/L N/A/D L R K(L)		118.25	420.2348	1258.69	-0.0004	-0.3	8.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
10208	dirMS_041712_NAR_120mM_minus.12568.12696.3	3	10.04	1	2.67E+05		(K)ARLENEI	(K)A R\L E N E/I/A/T/Y/R(N)		122.42	445.9006	1335.701	-0.0143	-10.7	6.19	51115.6	4.9	HUMAN	O76014	Keratin, type I cuticular Ha7
10209	dirMS_041712_NAR_120mM_minus.16850.16850.3	3	10.04	0	4.31E+05		(K)HLEINPI	(K)H|L|E I N P/D H/S|I I E T L R(Q)		146.63	596.3176	1786.945	-0.0064	-3.6	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
10210	dirMS_041712_NAR_30mM_minus2.12431.12431.2	2	10.04	0	2.53E+05		(R)TLSGME	(R)T L|S/G M/E\S/Y\C V R(A)	C:Carbamidomethylation	121.98	651.795	1302.582	0.001	0.8	5.66	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
10211	dirMS_041712_NAR_30mM_minus2.16084.16084.2	2	10.04	0	9.26E+04		(R)LVQAFQ	(R)L V/Q/A/F Q F T D K(H)		140.68	598.8155	1196.631	-0.0073	-6.1	5.84	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
10212	dirMS_041712_NAR_30mM_minus2.16909.16954.2	2	10.04	0	3.39E+05		(K)FANPFP	(K)F A|N|P F/P A A V R(G)		146.38	545.2937	1089.584	-0.0039	-3.5	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
10213	dirMS_041712_NAR_30mM_minus2.5917.5917.2	2	10.04	0	5.74E+04		(R)LAEAEE	(R)L/A|E/A/E E T A R(T)		86.62	495.2478	989.49	-0.0015	-1.5	4.25	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
10214	dirMS_041712_NAR_30mM_minus2.8335.8335.2	2	10.04	0	4.59E+05		(K)SFQQSSI	(K)S F|Q/Q/S/S L S/R(D)		100.27	520.2591	1039.517	-0.0058	-5.6	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
10215	dirMS_041712_NAR_40mM_minus2.14730.14730.3	3	10.04	0	8.77E+04		(K)LVLIGSN	(K)L V/L I/G/S N/H/S L P F L K(F)		171.58	513.3088	1537.91	0.0018	1.2	8.76	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
10216	dirMS_041712_NAR_60mM_minus.6551.6551.3	3	10.04	1	4.07E+04		(K)SPPREG	(K)S P P R E G S Q G E\L|T|P A N S Q S R(M)		95.02	666.6591	1997.964	-0.0008	-0.4	5.87	53941.6	6.3	HUMAN	C9JFE4	COP9 signalosome complex subunit 1
10217	dirMS_041712_NAR_60mM_minus.6562.6562.3	3	10.04	0	9.81E+04		(K)CIGKPG	(K)C\I|G K/P G G S L D/N/S E Q K(C)	C:Carbamidomethylation	95.25	530.5892	1589.759	-0.0057	-3.6	6.07	9122.2	9.22	HUMAN	K7EIT2	Mitochondrial import inner membrane translocase subunit Tim13
10218	dirMS_041712_NAR_20mM_plus.13431.13431.2	2	10.04	0	1.18E+05	M98m	(R)TLTIVDT	(R)T L/T I|V/D T G I G m/T K(A)	m:Oxidized methionine	165.38	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
10219	dirMS_041712_NAR_20mM_plus.17453.17514.2	2	10.04	0	1.59E+05		(K)DVDLEFI	(K)D V|D|L/E F L/A/K(M)		192.67	525.2795	1049.551	0.0004	0.4	4.03	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
10220	dirMS_041712_NAR_20mM_plus.19155.19155.2	2	10.04	0	9.47E+04		(R)DLLFQAI	(R)D L|L/F/Q/A L G R(T)		203.37	516.7952	1032.584	-0.0005	-0.5	5.84	66742	6.4	HUMAN	Q9NSD9	Phenylalanine--tRNA ligase beta subunit
10221	dirMS_041712_NAR_20mM_plus.19210.19210.2	2	10.04	0	1.33E+05		(R)EGDVLT	(R)E G D\V|L/T L|L/E S E R(E)		203.58	680.8536	1360.696	0.0045	3.3	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
10222	dirMS_041712_NAR_20mM_plus.8764.8764.2	2	10.04	0	1.90E+04		(R)AVLIAG	(R)A V|L|I/A G Q/P G T\G K(T)		130.77	556.3256	1111.647	-0.0031	-2.8	8.8	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
10223	dirMS_041712_NAR_30mM_plus2.8214.8214.2	2	10.04	0	1.36E+06		(K)QGGGG	(K)Q G G G/G/G/G G S V|P G I/E R(M)		97.17	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
10224	dirMS_041712_NAR_40mM_plus2.11139.11139.3	3	10.04	1	7.39E+04		(K)AVEEED	(K)A V/E/E E D K/M T\P E Q L A/I/K(N)		131.87	610.9764	1830.915	-0.0007	-0.4	4.25	34747.6	6.06	HUMAN	O00487	26S proteasome non-ATPase regulatory subunit 14
10225	dirMS_041712_NAR_40mM_plus2.13196.13196.3	3	10.04	0	8.76E+05		(R)VVIIGAG	(R)V V|I I/G A G K/P\A/A V/V\L Q T K(G)		143.25	555.3527	1664.047	-0.0034	-2	10	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
10226	dirMS_041712_NAR_40mM_plus2.17319.17319.3	3	10.04	1	1.97E+05		(R)GDSVIV	(R)G D S V|I/V V L R N P L I A|G K(-)		168.73	551.0007	1650.99	-0.0026	-1.6	8.75	6144.3	10.23	HUMAN	K7EJB5	Small nuclear ribonucleoprotein Sm D2
10227	dirMS_041712_NAR_50mM_plus2.12656.12656.3	3	10.04	1	8.84E+05		(R)ELISNSSI	(R)E L/I/S/N S/S/D A\L D K I R(Y)		134.15	520.9473	1560.823	0.0046	2.9	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
10228	dirMS_041712_NAR_50mM_plus2.9283.9283.3	3	10.04	1	2.65E+05		(K)EVPAVP	(K)E V/P/A V/P E T L K K(K)		115.48	404.2395	1210.704	-0.0002	-0.2	6.24	29282.3	10.71	HUMAN	P18124	60S ribosomal protein L7
10229	dirMS_041712_NAR_60mM_plus.19484.19484.3	3	10.04	0	1.33E+05		(R)NSVSNF	(R)N S|V/S N F/L/H/S L E/R(G)		161.23	468.2401	1402.707	-0.0016	-1.1	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
10230	dirMS_041712_NAR_60mM_plus.19771.19771.3	3	10.04	0	7.84E+03		(K)SFLIWV	(K)S F|L I|W V N E E D/H T R(V)		162.93	549.2699	1645.797	-0.0017	-1.1	4.65	29478.9	6.26	HUMAN	E9PCP8	Creatine kinase U-type, mitochondrial
10231	dirMS_041712_NAR_60mM_plus.20203.20203.3	3	10.04	0	1.49E+05		(R)IDILDSA	(R)I/D|I/L D/S A/L\L R P G/R(I)		165.77	480.2825	1438.838	-0.0047	-3.3	5.96	44954.5	8.44	HUMAN	A8K3Z3	26S protease regulatory subunit 8
10232	dirMS_041712_NAR_20mM_minus.8935.8935.2	2	10.03	0	2.78E+05		(R)ALGQNF	(R)A L|G Q|N/P T N A E/V\L K(V)		138.8	677.871	1354.733	0.0022	1.6	6.05	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
10233	dirMS_041712_NAR_30mM_minus2.18826.18884.2	2	10.03	0	1.06E+05		(K)NLIDAG	(K)N L|I|D/A/G V D A L R(V)		157.17	578.811	1156.632	-0.0173	-15	4.21	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
10234	dirMS_041712_NAR_40mM_minus2.10881.10881.3	3	10.03	0	1.15E+05	M56m	(K)VAIVKP	(K)V/A/I/V/K/P G V/P m E I V L N K(E)	m:Oxidized methionine	147	575.0112	1707.024	15.9953	0.2	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
10235	dirMS_041712_NAR_50mM_minus2.11899.11899.3	3	10.03	0	1.72E+04	M425m M	(R)VFITDDI	(R)V F|I/T/D D\F H/D m m P K(Y)	m:Oxidized methionine	135.92	543.2416	1595.723	31.987	-1.7	4.41	92752.5	4.76	HUMAN	P14625	Endoplasmin
10236	dirMS_041712_NAR_50mM_minus2.7040.7040.3	3	10.03	0	2.09E+05		(K)VSYGIG	(K)V/S|Y/G I/G D E E/H D Q E G R(V)		106.65	564.249	1690.73	0.0021	1.3	4.17	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
10237	dirMS_041712_NAR_60mM_minus.19011.19011.3	3	10.03	0	5.21E+05		(R)LGFHLPI	(R)L G F H L|P L E|V/A/Y Q R(G)		168.48	514.9512	1542.843	-0.0037	-2.4	6.75	533778	5.74	HUMAN	Q15149	Plectin
10238	dirMS_041712_NAR_60mM_minus.8188.8201.3	3	10.03	1	1.36E+05		(R)LSQIGVE	(R)L/S|Q/I/G/V/E N T E E N R R(L)		106.02	548.9481	1644.83	-0.0002	-0.1	4.79	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
10239	dirMS_041712_NAR_20mM_plus.18141.18141.2	2	10.03	0	7.51E+04		(R)LSVLGAI	(R)L S V/L/G A|I/T\S V Q Q R(L)		196.28	686.3953	1371.795	-0.0121	-8.8	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
10240	dirMS_041712_NAR_30mM_plus2.17243.17244.2	2	10.03	0	2.83E+05		(R)LIVNVNI	(R)L I|V/N/V|N D L/R(R)		143.7	528.3113	1055.621	-0.0054	-5.2	5.84	91606.8	5.53	HUMAN	P25205	DNA replication licensing factor MCM3
10241	dirMS_041712_NAR_30mM_plus2.20941.20941.2	2	10.03	0	1.27E+05	M153m	(K)VVTYGm	(K)V V T/Y/G/m/A N L L T\G/P K(R)	m:Oxidized methionine	163.65	740.3971	1463.793	15.9943	-0.4	8.56	28454.5	6.24	HUMAN	B0AZP7	Synaptic vesicle membrane protein VAT-1 homolog

10242	dirMS_041712_NAR_30mM_plus2.22726.22731.3	3	10.03	0	4.63E+05		(R)ELSDFIS'	(R)E L S D F I/S/Y/L/Q R(E)		177.23	457.5693	1370.695	-0.0017	-1.2	4.37	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
10243	dirMS_041712_NAR_30mM_plus2.7926.7926.2	2	10.03	0	2.20E+05		(K)IAVAAQ	(K)I/A|V|A/A/Q/N C Y K(V)	C:Carbamidomethylation	96.05	569.2905	1137.572	0.0016	1.4	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
10244	dirMS_041712_NAR_40mM_plus2.5836.5836.2	2	10.03	1	1.68E+05		(R)SKQAEE	(R)S K Q A\E\E\E|F(-)		92.1	484.2219	967.437	-0.0002	-0.2	4.25	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
10245	dirMS_041712_NAR_50mM_plus2.12566.12566.3	3	10.03	1	3.50E+05		(R)IVAPGK(	(R)I V|A/P G K G I L/A A D\E S T/G S I A K(R)		133.95	633.3555	1898.059	-0.0074	-3.9	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
10246	dirMS_041712_NAR_50mM_plus2.13039.13039.3	3	10.03	1	1.36E+06		(R)VVDALG	(R)V/V|D/A/L/G N A I/D G K G P I G S K(T)		137.37	570.9829	1710.939	-0.0043	-2.5	5.93	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
10247	dirMS_041712_NAR_50mM_plus2.14974.14975.3	3	10.03	1	7.65E+05		(K)VTLPGLk	(K)V/T/L/P G L K E/D S Q I L/K(I)		146.35	514.2992	1540.895	-0.0114	-7.4	6.04	228081	6.98	HUMAN	A6NHR9	Structural maintenance of chromosomes flexible hinge domain-containing protein 1
10248	dirMS_041712_NAR_60mM_plus.10101.10101.2	2	10.03	0	2.03E+06		(K)GIVEFSG	(K)G I|V|E\F/S G K/P A A R(K)		111.3	616.3425	1231.679	-0.0016	-1.3	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
10249	dirMS_041712_NAR_60mM_plus.14838.14838.3	3	10.03	1	3.66E+05		(R)FFGDSA.	(R)F/F/G D/S A A S/M A I K N/P K(A)		134.58	528.5983	1583.789	-0.0083	-5.2	8.59	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
10250	dirMS_041712_NAR_60mM_plus.16515.16523.3	3	10.03	0	5.40E+05		(R)VHIGQV	(R)V H I\G Q|V|I|M/S I/R(T)		144.23	418.2478	1252.719	0.0094	7.5	9.73	18819.6	10.31	HUMAN	F8W7C6	60S ribosomal protein L10
10251	dirMS_041712_NAR_60mM_plus.16982.16982.3	3	10.03	1	6.61E+06		(K)LKVPEW	(K)L K\V/P/E/W V/D/T/V K(L)		145.77	438.5872	1313.746	0.0007	0.5	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
10252	dirMS_041712_NAR_60mM_plus.18865.18865.3	3	10.03	1	3.96E+06		(R)VSFELFA	(R)V/S|F/E L F A D K V/P K(T)		155.83	460.5914	1379.757	0.0027	2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
10253	dirMS_041712_NAR_60mM_plus.20910.20910.3	3	10.03	1	1.36E+05		(K)TFVNITP	(K)T F/V/N/I T P A/E V\G V\L V G K D R(S)		170.58	639.0248	1915.065	-0.0049	-2.6	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
10254	dirMS_041712_NAR_60mM_plus.5742.5742.3	3	10.03	1	8.61E+04	M117m	(R)ARQENC	(R)A R Q\E\N G\m|P E/E/P A T T A R(G)	m:Oxidized methionine	88.33	591.9441	1757.824	15.9942	-0.4	4.79	64356.2	9.96	HUMAN	O96013	Serine/threonine-protein kinase PAK 4
10255	dirMS_041712_NAR_120mM_minus.18843.18843.4	4	10.02	1	1.79E+05		(K)LHDNLII:	(K)L H D N L\I/I/S/D/L E N T V K K(L)		158.4	463.7605	1852.017	0.0027	1.5	5.38	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
10256	dirMS_041712_NAR_20mM_minus.8506.8506.2	2	10.02	0	7.57E+04		(R)IIYGGSV	(R)I I|Y/G G S/V/T G A T C/K(E)	C:Carbamidomethylation	134.28	663.8403	1326.672	0.0011	0.8	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
10257	dirMS_041712_NAR_30mM_minus2.19481.19481.2	2	10.02	0	3.18E+05		(R)ASLSLW	(R)A S L/S|L/W\Q A M/E K(G)		162.37	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
10258	dirMS_041712_NAR_30mM_minus2.6797.6877.2	2	10.02	0	2.56E+05		(R)IGDEDV(	(R)I/G|D|E/D/V/G R(V)		91.67	430.7116	860.411	0.0051	5.9	4.03	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
10259	dirMS_041712_NAR_30mM_minus2.9500.9688.2	2	10.02	0	2.86E+06		(K)VGVNGF	(K)V/G|V/N|G F/G R(I)		106.32	403.2183	805.432	-0.0022	-2.7	9.72	36223.7	8.79	HUMAN	P04406	Glyceraldehyde-3-phosphate dehydrogenase
10260	dirMS_041712_NAR_40mM_minus2.15658.15658.3	3	10.02	1	4.96E+05		(K)ALFEEVF	(K)A L|F E/E V/P E L L T E/A E K K(E)		181.8	615.9988	1845.984	-0.0026	-1.4	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
10261	dirMS_041712_NAR_60mM_minus.15374.15374.3	3	10.02	0	2.13E+05		(K)EGHVEV	(K)E G H V E V\V/S|E/L/L Q/R(E)		145.9	498.9349	1494.791	-0.0009	-0.6	4.75	48586.6	9.32	HUMAN	D6RCB2	Ankyrin-3
10262	dirMS_041712_NAR_60mM_minus.18561.18561.3	3	10.02	1	1.72E+05		(K)VVLDDK	(K)V V|L/D/D K/D Y F L F R(D)		165.12	510.6099	1529.8	0.0153	10	4.43	5189.9	4.56	HUMAN	B8ZZ54	10 kDa heat shock protein, mitochondrial
10263	dirMS_041712_NAR_120mM_plus.18403.18546.4	4	10.02	1	1.64E+06		(K)FQIPPN/	(K)F Q\I\P/P N/A E L K/Y E L H L K(S)		150.1	485.7703	1940.064	-0.0046	-2.4	6.75	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
10264	dirMS_041712_NAR_20mM_plus.12209.12546.2	2	10.02	0	4.54E+05		(K)VLLGVG	(K)V L/L G|V|G\D P/K(I)		158.47	449.2728	897.54	-0.0021	-2.3	5.81	66448.1	9.42	HUMAN	O00567	Nucleolar protein 56
10265	dirMS_041712_NAR_20mM_plus.9364.9364.2	2	10.02	0	8.16E+04		(R)ALEESN\	(R)A L|E/E/S N Y E/L E/G K(I)		136.32	691.3246	1381.648	-0.0062	-4.5	4.09	59054.3	5.14	HUMAN	P13645	Keratin, type I cytoskeletal 10
10266	dirMS_041712_NAR_30mM_plus2.13526.13526.2	2	10.02	0	1.00E+06		(K)ELSDIAL	(K)E L/S/D/I/A L R(I)		123.78	458.7641	916.51	0.0111	12.1	4.37	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
10267	dirMS_041712_NAR_30mM_plus2.18037.18037.2	2	10.02	0	3.59E+05		(R)NGGQIL	(R)N G|G Q|I/L I A D/L R(G)		147.35	585.3347	1169.664	-0.0016	-1.3	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
10268	dirMS_041712_NAR_30mM_plus2.21683.21683.2	2	10.02	0	1.29E+05		(R)IITLAGP'	(R)I I\T\L/A/G P T N A I F K(A)		168.37	679.9016	1358.804	-0.0083	-6.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
10269	dirMS_041712_NAR_50mM_plus2.17332.17332.3	3	10.02	0	3.44E+05		(K)DIPVVH(	(K)D I|P V V/H/Q/L L T R(Y)		159.57	430.9226	1290.753	0.0004	0.3	6.74	57147.5	7.81	HUMAN	P30419	Glycylpeptide N-tetradecanoyltransferase 1
10270	dirMS_041712_NAR_60mM_plus.14184.14184.3	3	10.02	0	1.15E+05		(K)LAQANG	(K)L A/Q A N/G W/G/V M\V S H R(S)		131.63	509.2606	1525.769	-0.002	-1.3	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
10271	dirMS_041712_NAR_120mM_minus.16954.16954.3	3	10.01	0	4.24E+05		(K)HLEINPD	(K)H/L E I N\P D|H/S\I I E T L/R(Q)		146.92	596.3176	1786.945	-0.0064	-3.6	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
10272	dirMS_041712_NAR_30mM_minus2.12618.12618.2	2	10.01	0	2.70E+05		(R)TLSGME	(R)T L|S|G/M/E/S Y C V R(A)	C:Carbamidomethylation	122.03	651.795	1302.582	0.001	0.8	5.66	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
10273	dirMS_041712_NAR_30mM_minus2.16434.16434.2	2	10.01	0	2.13E+05		(K)NAAGAL	(K)N A|A/G\A/L D L/L K(E)		143.42	493.2881	985.568	0.0013	1.3	5.84	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
10274	dirMS_041712_NAR_50mM_minus2.16556.16557.3	3	10.01	1	1.60E+05		(K)VVSSVL(	(K)V/V|S S V L/Q F G N I/S F K K(E)		162	551.6488	1652.937	-0.0052	-3.1	10	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
10275	dirMS_041712_NAR_120mM_plus.10787.10826.3	3	10.01	1	2.01E+05		(K)VSRDTL\	(K)V/S R D T\L|Y/E/A V/R(E)		109.42	436.8969	1308.691	-0.0145	-11.1	6.04	25002	10.06	HUMAN	P62906	60S ribosomal protein L10a
10276	dirMS_041712_NAR_120mM_plus.19998.19998.4	4	10.01	1	6.21E+05		(K)AAIDWF	(K)A/A/I/D/W/F D/G K E F/H G N I I K(V)		158.17	491.0027	1960.992	-0.0026	-1.3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
10277	dirMS_041712_NAR_120mM_plus.21001.21001.3	3	10.01	2	1.39E+06		(R)TLAEIAK	(R)T L|A E I A/K/V E L D N\M/P L R G K(Q)		162.92	666.7047	1998.105	-0.0057	-2.8	5.85	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
10278	dirMS_041712_NAR_30mM_plus2.16205.16205.2	2	10.01	0	2.91E+04	M148m	(R)DLTDYLr	(R)D/L|T/D/Y L/m\K(I)	m:Oxidized methionine	137.32	507.7505	998.486	16.0074	12.3	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
10279	dirMS_041712_NAR_30mM_plus2.16663.16663.2	2	10.01	0	4.44E+05		(K)GCSFLPI	(K)G C S/F|L|P D/P Y Q/K(Q)	C:Carbamidomethylation	140.57	656.306	1311.604	0.0009	0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
10280	dirMS_041712_NAR_30mM_plus2.19052.19052.2	2	10.01	0	4.46E+05		(R)LIDFLES(	(R)L/I|D|F L E/S G K(T)		152.1	511.2819	1021.556	0.0001	0.1	4.37	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
10281	dirMS_041712_NAR_30mM_plus2.7089.7089.2	2	10.01	0	1.37E+05		(R)TTTGSYI	(R)T/T|T/G/S Y I A/N/R(V)		91.82	542.274	1083.543	-0.0022	-2	8.41	10799.8	5.07	HUMAN	I3L3X7	Proteasome subunit beta type-6 (Fragment)
10282	dirMS_041712_NAR_40mM_plus2.17758.17758.3	3	10.01	0	2.88E+05		(K)LLYDLAI	(K)L L/Y D/L/A D Q L H A/A V G A S/R(A)		171.33	604.9967	1812.96	0.0153	8.4	5.21	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
10283	dirMS_041712_NAR_40mM_plus2.7505.7505.2	2	10.01	0	3.99E+05		(K)ASLENSI	(K)A S|L/E/N\S L R(E)		105.08	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10284	dirMS_041712_NAR_50mM_plus2.10126.10126.3	3	10.01	1	5.94E+04		(K)ITIKNDP	(K)I/T I K N D/P/S/L P E/P K(C)		120.53	484.6079	1451.81	-0.0013	-0.9	6.07	20203.8	9.79	HUMAN	B4DG16	Asparagine--tRNA ligase, cytoplasmic
10285	dirMS_041712_NAR_60mM_plus.17206.17206.3	3	10.01	0	1.75E+04		(R)IYSHSLLI	(R)I/Y S H|S L/L/P/V L R(S)		147.6	433.2569	1297.763	-0.0065	-5	8.75	60871.9	6.3	HUMAN	B4DJ93	Phosphoribosylformylglycinamidine cyclo-ligase
10286	dirMS_041712_NAR_60mM_plus.17536.17536.3	3	10.01	1	1.76E+05		(R)RTVQSLI	(R)R T V\Q S L E|I/D\L|D S M R(N)		148.8	554.954	1662.848	-0.0005	-0.3	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10287	dirMS_041712_NAR_60mM_plus.20399.20399.3	3	10.01	1	4.21E+05		(K)NAAGAL	(K)N A|A/G/A/L/D L/L K E/L K(N)		166.93	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
10288	dirMS_041712_NAR_120mM_minus.5146.5146.3	3	10	1	1.60E+05		(R)LKQSAEI	(R)L K Q S A E\E|Q/A/Q/A/R(A)		80.68	453.5713	1358.702	-0.0029	-2.1	6.14	533778	5.74	HUMAN	Q15149	Plectin
10289	dirMS_041712_NAR_120mM_minus.7407.7407.3	3	10	0	1.20E+05		(R)NIDEHA	(R)N/I/D E/H A/N E/D/V E R(M)		94.67	480.884	1440.635	0.0025	1.7	4.17	22768.7	8.94	HUMAN	P61026	Ras-related protein Rab-10
10290	dirMS_041712_NAR_30mM_minus2.7411.7427.2	2	10	0	1.37E+05		(R)VQESAD	(R)V/Q|E|S/A/D/E L Q K(M)		94.82	573.7846	1146.564	-0.0018	-1.6	4.14	17163.6	6.74	HUMAN	C9J1Z8	ADP-ribosylation factor 5 (Fragment)
10291	dirMS_041712_NAR_30mM_minus2.9523.9544.2	2	10	0	8.89E+05		(R)GGGQIII	(R)G G\G|Q|I|I|P T A R(R)		106.4	485.2762	969.548	-0.0025	-2.6	9.75	15036.9	7.16	HUMAN	K7EJ74	116 kDa U5 small nuclear ribonucleoprotein component (Fragment)
10292	dirMS_041712_NAR_40mM_minus2.15541.15581.3	3	10	1	7.01E+05		(K)LLPLVSD	(K)L L|P/L/V S D E V F I R D/V A K(V)		180.3	605.3511	1814.042	-0.0035	-1.9	4.56	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
10293	dirMS_041712_NAR_60mM_minus.11330.11330.3	3	10	1	1.02E+04		(R)ALEEAM	(R)A L/E|E\A/M E Q K A E L E/R(L)		123.13	549.6071	1646.805	0.0013	0.8	4.33	227783.5	5.5	HUMAN	P35579	Myosin-9
10294	dirMS_041712_NAR_120mM_plus.16791.16823.4	4	10	1	7.23E+05		(R)GHYTIGI	(R)G/H\Y\T I G K\E I\V D L/V/L/D/R(I)		141.4	457.7478	1827.996	-0.027	-14.7	5.38	50643.3	4.98	HUMAN	Q13748	Tubulin alpha-3C/D chain
10295	dirMS_041712_NAR_20mM_plus.14220.14220.2	2	10	0	8.76E+04		(K)GVVDSD	(K)G V/V/D|S D D L|P L N/V/S R(E)		170.28	743.3789	1485.754	-0.0038	-2.6	3.93	92752.5	4.76	HUMAN	P14625	Endoplasmin
10296	dirMS_041712_NAR_30mM_plus2.18536.18536.2	2	10	0	4.58E+05		(R)GYISPYF	(R)G Y\I|S|P Y F I N T/S K(G)		149.9	695.3554	1389.705	-0.0014	-1	8.5	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
10297	dirMS_041712_NAR_30mM_plus2.18703.18703.2	2	10	0	9.94E+04		(R)GLPWSC	(R)G/L|P W/S\C S A D/E V M R(F)	C:Carbamidomethylation	151.4	754.3298	1507.667	-0.0145	-9.6	4.37	49548	5.89	HUMAN	P55795	Heterogeneous nuclear ribonucleoprotein H2
10298	dirMS_041712_NAR_30mM_plus2.6897.6897.3	3	10	0	3.70E+04		(R)VIGSGCI	(R)V I G S G C/N|L/D/S A/R(F)	C:Carbamidomethylation	90.48	416.8708	1248.6	-0.0023	-1.8	5.81	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
10299	dirMS_041712_NAR_50mM_plus2.8662.8662.3	3	10	0	9.82E+04		(K)TPHPVL'	(K)T P H/P V L T|P\V/A A/N Q A K(Q)		112.42	515.284	1543.859	-0.0217	-14	8.44	94320	8.88	HUMAN	H0Y837	Nuclear pore complex protein Nup214 (Fragment)
10300	dirMS_041712_NAR_50mM_plus2.9534.9534.3	3	10	1	3.51E+05	M61m	(K)NQVAm	(K)N\Q|V/A/m N/P T N T V F D A K R(L)	m:Oxidized methionine	117.07	607.9678	1805.896	15.9926	-1.3	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
10301	dirMS_041712_NAR_50mM_plus2.9868.9925.3	3	10	0	4.35E+05		(K)AQVARP	(K)A Q|V/A R P G G D T I/F/G/K(I)		119.4	472.9249	1416.759	0.0008	0.5	8.79	7323.5	9.4	HUMAN	D6RC06	Histidine triad nucleotide-binding protein 1
10302	dirMS_041712_NAR_120mM_minus.8199.8199.2	2	9.99	0	4.37E+05		(R)HQGVM	(R)H/Q|G/V\M\V|G M/G Q K(D)		99.03	586.2907	1171.571	0.0031	2.6	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
10303	dirMS_041712_NAR_30mM_minus2.11594.11614.2	2	9.99	0	1.26E+05		(R)QVLFSAI	(R)Q V|L/F/S A/D/D/R(V)		116.8	525.7639	1050.521	-0.0009	-0.9	4.21	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
10304	dirMS_041712_NAR_30mM_minus2.18033.18033.2	2	9.99	0	1.88E+05		(K)FFFDPS/	(K)F/F|F/D/P S A/R(D)		151.68	493.7405	986.473	0.0007	0.7	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin
10305	dirMS_041712_NAR_120mM_plus.13245.13245.2	2	9.99	0	8.76E+04		(R)DYLHYIR	(R)D/Y|L/H|Y I/R(K)		122.77	490.2536	979.5	0.0003	0.3	6.74	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
10306	dirMS_041712_NAR_120mM_plus.17116.17116.4	4	9.99	1	1.12E+06		(K)FLSDVYF	(K)F L\S D V Y/P/D G F K/G H M L T K(S)		143.28	489.4962	1954.973	-0.0102	-5.2	6.74	15838.9	7.03	HUMAN	H0Y5U0	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
10307	dirMS_041712_NAR_120mM_plus.5416.5416.2	2	9.99	0	3.43E+05	M49m	(R)HQGVM	(R)H/Q|G V/M|V/G m G Q K(D)	m:Oxidized methionine	81.55	594.2868	1171.571	15.9953	0.3	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
10308	dirMS_041712_NAR_120mM_plus.7905.7905.4	4	9.99	0	6.18E+04		(K)AVVTHS	(K)A/V/V/T/H/S S G N H G Q A L T Y/A A K(L)		95.07	478.7463	1911.967	-0.0038	-2	8.65	11029.5	9.89	HUMAN	I3L3N0	Serine racemase (Fragment)
10309	dirMS_041712_NAR_120mM_plus.8922.8922.3	3	9.99	0	2.20E+06		(K)HTGPNS	(K)H T G P N\S P D T|A/N/D/G/F V R(L)		99.5	562.26	1684.767	-0.0019	-1.2	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
10310	dirMS_041712_NAR_20mM_plus.14245.14245.3	3	9.99	0	7.97E+05	M73m	(R)AVLVDLI	(R)A V\L V D L E/P G T/m/D S V/R(S)	m:Oxidized methionine	170.97	539.9421	1601.82	15.9914	-2.2	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
10311	dirMS_041712_NAR_30mM_plus2.18445.18445.2	2	9.99	0	1.65E+05		(K)QFLSQFI	(K)Q F/L|S Q/F/E/M Q/S R(K)		150.25	700.8358	1400.663	0.0016	1.2	6	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
10312	dirMS_041712_NAR_40mM_plus2.9829.9829.2	2	9.99	0	9.33E+04		(R)GYFSEEI	(R)G Y/F/S/E E M N R(V)		121.55	566.7355	1132.473	-0.0091	-8	4.53	533778	5.74	HUMAN	Q15149	Plectin
10313	dirMS_041712_NAR_50mM_plus2.16334.16334.3	3	9.99	0	2.89E+05		(K)ACQSIYF	(K)A C\Q/S/I/Y/P L H D V F V R(K)	C:Carbamidomethylation	154.4	568.9562	1704.853	0.0014	0.8	6.79	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
10314	dirMS_041712_NAR_60mM_plus.15483.15483.3	3	9.99	0	2.24E+05		(R)ILHCLGL	(R)I L H C\L G\L/A|E E I/Q/K(Y)	C:Carbamidomethylation	137.7	508.6121	1523.825	-0.0033	-2.2	5.4	33713.1	6.06	HUMAN	P53004	Biliverdin reductase A
10315	dirMS_041712_NAR_60mM_plus.16741.16779.3	3	9.99	1	8.72E+05		(R)STNKGT.	(R)S T N K G T\A\Y\T/F|F/T\P G N L K(Q)		144.73	616.3117	1846.933	-0.0128	-7	9.7	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
10316	dirMS_041712_NAR_20mM_minus.12294.12294.2	2	9.98	0	9.01E+05	M313m	(R)TVQSLEI	(R)T/V|Q/S\L/E|I D L D S m R(N)	m:Oxidized methionine	171.18	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10317	dirMS_041712_NAR_20mM_minus.12474.12474.2	2	9.98	0	5.50E+05	M185m	(K)LAVNm\	(K)L A/V/N/m V/P F P R(L)	m:Oxidized methionine	172.62	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
10318	dirMS_041712_NAR_20mM_minus.13288.13288.2	2	9.98	0	1.10E+06	M73m	(R)AILVDLE	(R)A I|L\V/D\L/E|P G/T m D S V R(S)	m:Oxidized methionine	182.8	816.4184	1615.836	15.9935	-0.8	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
10319	dirMS_041712_NAR_30mM_minus2.14711.14711.2	2	9.98	0	3.86E+05		(K)DLAGSII(	(K)D L|A/G S I/I G K(G)		133.22	437.2551	873.504	-0.0011	-1.2	5.84	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
10320	dirMS_041712_NAR_30mM_minus2.18015.18015.2	2	9.98	0	6.98E+04		(R)SSFYVN(	(R)S S F Y|V/N/G L/T\L G G Q K(C)		152.25	735.8825	1470.759	-0.001	-0.7	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
10321	dirMS_041712_NAR_50mM_minus2.13032.13032.3	3	9.98	1	3.31E+05		(R)ALPAVQ	(R)A L/P A V Q Q N N L D E/D L I R K(L)		142.8	646.3522	1937.045	-0.003	-1.6	4.56	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
10322	dirMS_041712_NAR_50mM_minus2.14713.14713.3	3	9.98	1	2.98E+05		(R)EAVTEIL	(R)E A/V/T/E/I/L G I E/P D R E K(G)		152.25	566.9683	1698.891	-0.0005	-0.3	4.25	25685.9	6.4	HUMAN	E9PGT1	Translin
10323	dirMS_041712_NAR_60mM_minus.11152.11216.3	3	9.98	1	2.22E+05	M183m	(R)VEVERD	(R)V/E|V/E R D N\L\A/E/D I m R(L)	m:Oxidized methionine	122.3	568.9449	1688.827	15.9929	-1.2	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
10324	dirMS_041712_NAR_60mM_minus.11866.11943.3	3	9.98	0	1.71E+06		(K)SQIHDIV	(K)S Q I H D I\V|L|V/G/G S T R(I)		126.72	494.6084	1481.807	0.0036	2.4	6.46	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
10325	dirMS_041712_NAR_60mM_minus.7247.7247.3	3	9.98	1	3.04E+05		(R)ELFESST	(R)E L/F/E/S S T N N\N K D/T K(Q)		98.72	542.9247	1626.761	-0.001	-0.6	4.68	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
10326	dirMS_041712_NAR_60mM_minus.8144.8144.3	3	9.98	1	1.61E+05		(K)DISTNYY	(K)D/I|S T/N Y/Y/A S Q K K(T)		105.07	473.231	1417.696	-0.0173	-12.2	8.43	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
10327	dirMS_041712_NAR_30mM_plus2.11495.11495.2	2	9.98	0	3.82E+05		(K)VAGQD(	(K)V/A|G Q/D/G S V V/Q F K(I)		113.82	617.8214	1234.643	-0.0071	-5.8	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
10328	dirMS_041712_NAR_30mM_plus2.17127.17127.2	2	9.98	0	1.93E+05		(R)AVAQAL	(R)A V|A\Q/A L E V I/P/R(T)		142.8	583.8476	1166.689	-0.0013	-1.1	6.05	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
10329	dirMS_041712_NAR_30mM_plus2.20272.20272.2	2	9.98	0	1.59E+05		(K)GSFSEQ(	(K)G S F/S\E Q/G/I N\E/F L\R(E)		160.9	742.362	1483.718	-0.0009	-0.6	4.53	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
10330	dirMS_041712_NAR_30mM_plus2.22068.22068.2	2	9.98	0	3.21E+05		(R)SFITWLF	(R)S F|I|T/W L/R(D)		170.53	461.7608	922.515	-0.0002	-0.2	9.47	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
10331	dirMS_041712_NAR_30mM_plus2.7036.7036.2	2	9.98	0	2.58E+05		(K)MAQFD/	(K)M/A|Q F D/A/K(K)		91.35	405.6961	810.381	0.0035	4.3	5.59	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
10332	dirMS_041712_NAR_30mM_plus2.9682.9682.2	2	9.98	0	1.36E+06		(R)QLSSGV:	(R)Q L|S S G V/S E I R(H)		104.9	538.2855	1075.574	-0.0105	-9.8	6	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
10333	dirMS_041712_NAR_40mM_plus2.10372.10372.2	2	9.98	0	2.39E+04		(R)CNNVLY	(R)C N|N|V/L\Y/I/R(G)	C:Carbamidomethylation	125.85	526.2705	1051.535	-0.0016	-1.5	8.75	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F
10334	dirMS_041712_NAR_40mM_plus2.11801.11801.2	2	9.98	0	2.55E+05		(R)NLLSVA\	(R)N/L/L/S V/A Y\K(N)		135.27	454.2649	907.525	-0.0022	-2.4	8.59	18789.1	6.77	HUMAN	A2IDB2	14-3-3 protein eta (Fragment)
10335	dirMS_041712_NAR_40mM_plus2.19114.19114.3	3	9.98	1	3.19E+05		(R)GGPNIIT	(R)G G P/N/I/I/T L A D I V K D/P V S R(T)		178.95	622.3522	1865.049	-0.007	-3.8	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
10336	dirMS_041712_NAR_50mM_plus2.9348.9348.3	3	9.98	1	1.90E+05		(R)EVLEKQI	(R)E V L E K/Q P V/L/S Q T E A R(D)		116.27	576.3137	1726.933	-0.0068	-4	4.79	29260.8	5.72	HUMAN	P28070	Proteasome subunit beta type-4
10337	dirMS_041712_NAR_60mM_plus.7819.7819.3	3	9.98	1	5.75E+05		(K)EASKQA	(K)E A/S K Q\A D\V/N/L/V/N A K(L)		98.83	496.2656	1486.786	-0.0038	-2.5	6.17	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
10338	dirMS_041712_NAR_60mM_plus.8586.8586.3	3	9.98	1	1.35E+06		(K)MQASIE	(K)M/Q|A S I/E K/G G S L/P K(V)		103.18	449.2449	1345.714	0.0057	4.3	8.35	32745.6	4.64	HUMAN	P06748	Nucleophosmin
10339	dirMS_041712_NAR_20mM_minus.11534.11534.2	2	9.97	0	1.40E+05	M98m	(R)TLTIVDT	(R)T L|T/I|V D T G\I G m T K(A)	m:Oxidized methionine	163.17	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
10340	dirMS_041712_NAR_30mM_minus2.10797.10797.2	2	9.97	0	3.05E+05		(R)FVTLSAT	(R)F V/T/L/S A T N A K(T)		112.58	526.2919	1051.578	-0.0017	-1.6	8.75	72873.4	5.73	HUMAN	Q96S55	ATPase WRNIP1
10341	dirMS_041712_NAR_30mM_minus2.19165.19165.2	2	9.97	1	2.15E+05		(K)SKLEFSI\	(K)S K L E\F/S I|Y|P\A|P(-)		158.93	626.334	1251.662	-0.0012	-1	5.72	21962.5	5.85	HUMAN	C9JJQ8	Tubulin alpha-4A chain (Fragment)
10342	dirMS_041712_NAR_30mM_minus2.20020.20020.2	2	9.97	0	2.44E+04		(K)SLNILTA	(K)S L/N|I/L/T A\F Q K(K)		168.82	567.8283	1134.652	-0.0024	-2.1	8.47	18172.6	7.77	HUMAN	F8VY02	Endoplasmic reticulum resident protein 29
10343	dirMS_041712_NAR_40mM_minus2.8989.8989.3	3	9.97	0	2.56E+04		(K)AASAGV	(K)A A/S/A G V/P Y/H G/E/V P V S L A R(A)		135.53	594.3141	1780.934	-0.0063	-3.5	6.79	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
10344	dirMS_041712_NAR_50mM_minus2.5749.5749.3	3	9.97	1	9.21E+04		(K)LEEAEK/	(K)L/E/E A E/K/A/A D E/S E R(G)		94.08	492.8982	1476.681	-0.0012	-0.8	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
10345	dirMS_041712_NAR_60mM_minus.15059.15059.3	3	9.97	0	5.83E+04		(R)DLSYCLS	(R)D L|S/Y C/L S/G M Y D H/R(Y)	C:Carbamidomethylation	143.88	539.566	1616.683	0.0003	0.2	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
10346	dirMS_041712_NAR_120mM_plus.18042.18042.3	3	9.97	0	4.73E+05		(R)HLLQAP'	(R)H L|L\Q A P V D D\A/Q E/I L H/S R(F)		148.32	648.0088	1942.014	-0.0023	-1.2	5.21	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
10347	dirMS_041712_NAR_20mM_plus.13922.13922.2	2	9.97	0	6.12E+04		(K)IVPNVLL	(K)I V/P N V/L L/E/Q G K(A)		167.72	605.3616	1209.72	-0.0042	-3.5	6	50659.2	7.87	HUMAN	B4DJV2	Citrate synthase
10348	dirMS_041712_NAR_20mM_plus.17108.17173.2	2	9.97	0	9.83E+04		(R)AVLVDLI	(R)A V\L|V|D L/E|P G T M D/S V R(S)		189.48	801.414	1601.82	0.0004	0.2	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
10349	dirMS_041712_NAR_20mM_plus.8091.8091.2	2	9.97	0	1.06E+05		(K)VTEDTS:	(K)V/T|E/D\T/S S V L\R(S)		126.02	553.7889	1106.569	0.0017	1.6	4.37	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
10350	dirMS_041712_NAR_30mM_plus2.10889.10889.2	2	9.97	0	4.67E+05		(K)LTAQFV/	(K)L/T|A/Q/F V/A R(N)		110.68	453.2619	905.52	-0.0038	-4.2	9.75	88941.6	5.15	HUMAN	Q15459	Splicing factor 3A subunit 1

10351	dirMS_041712_NAR_30mM_plus2.16023.16023.2	2	9.97	0	4.95E+05		(R)MGPNIY	(R)M/G|P|N/I/Y E/L R(T)		136.88	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
10352	dirMS_041712_NAR_30mM_plus2.20016.20016.2	2	9.97	0	8.31E+04		(R)FEELTNL	(R)F E/E|L|T N L I R(T)		158.62	567.8152	1134.615	0.0078	6.9	4.53	106155.7	5.45	HUMAN	B5ME19	Eukaryotic translation initiation factor 3 subunit C
10353	dirMS_041712_NAR_30mM_plus2.7351.7440.2	2	9.97	0	4.59E+05		(K)FENLCK(	(K)F/E|N/L/C/K(I)	C:Carbamidomethylation	93.2	405.6961	810.381	0.0035	4.3	6	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
10354	dirMS_041712_NAR_30mM_plus2.9799.9839.2	2	9.97	0	2.05E+05		(K)LNCSPD:	(K)L/N|C/S/P D/S F R(C)	C:Carbamidomethylation	104.85	548.2495	1095.489	0.003	2.7	5.84	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
10355	dirMS_041712_NAR_40mM_plus2.12317.12317.3	3	9.97	0	3.63E+04		(R)VLTEDEI	(R)V L/T E/D E M G H/P E I G D A I A R(L)		138.75	651.6493	1952.938	-0.0049	-2.5	4.17	40874	5.06	HUMAN	E9PCI9	Farnesyl pyrophosphate synthase
10356	dirMS_041712_NAR_40mM_plus2.16139.16139.3	3	9.97	0	4.91E+05		(R)FGVPVI/	(R)F G\V|P V/I/A D G G I Q N V G H I A K(A)		162.27	631.3436	1892.039	-0.0226	-12	6.74	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
10357	dirMS_041712_NAR_50mM_plus2.17620.17680.3	3	9.97	1	8.31E+05		(R)DSEQVA	(R)D S|E/Q|V/A E/L K/Q E L A T L K(S)		161.07	601.322	1801.954	-0.0027	-1.5	4.41	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
10358	dirMS_041712_NAR_50mM_plus2.18489.18489.3	3	9.97	0	4.12E+05		(R)VYAILTH	(R)V/Y|A/I L T H G I F S G P A I S\R(I)		165.83	601.3347	1801.996	-0.0064	-3.5	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
10359	dirMS_041712_NAR_50mM_plus2.18502.18502.3	3	9.97	0	4.06E+05		(R)AVSILPL	(R)A V|S I/L/P L L G/H G\V/P R(L)		165.87	476.9615	1428.869	0.0014	1	9.8	66841.7	7.74	HUMAN	F5H721	WW domain-binding protein 11
10360	dirMS_041712_NAR_50mM_plus2.20096.20096.3	3	9.97	0	3.62E+05		(R)NEVSFVI	(R)N/E/V|S F V I/H/N/L P V L A K(M)		174.27	560.6531	1679.948	-0.0032	-1.9	6.75	35663.7	5.91	HUMAN	B4DWK0	Selenide, water dikinase 1
10361	dirMS_041712_NAR_50mM_plus2.7940.7940.3	3	9.97	1	3.43E+04	M250m	(K)TTDmAF	(K)T/T/D m A/P S K E T/E M A L A K(D)	m:Oxidized methionine	108.27	580.6104	1723.824	15.9925	-1.4	4.68	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
10362	dirMS_041712_NAR_60mM_plus.7290.7290.3	3	9.97	0	3.00E+05		(K)ITPAHD(	(K)I T|P/A H D Q N D/Y E V/G Q R(H)		96.68	581.6074	1742.809	-0.0016	-0.9	4.54	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
10363	dirMS_041712_NAR_120mM_minus.18894.18894.4	4	9.96	1	4.11E+05		(R)HATALEI	(R)H A T A L\E|E|L/S E Q L E Q A K/R(F)		158.27	489.0065	1953.004	0.0006	0.3	4.91	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
10364	dirMS_041712_NAR_120mM_minus.8854.8854.3	3	9.96	0	8.92E+05		(K)HTGPNS	(K)H T G\P N\S P\D\T A/N/D/G F V/R(L)		103.08	562.2599	1684.767	-0.0022	-1.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
10365	dirMS_041712_NAR_30mM_minus2.14456.14540.2	2	9.96	0	3.58E+05		(R)VDFNVP	(R)V/D|F/N V|P/M K(N)		132.32	475.2457	949.481	0.003	3.1	5.81	30303.6	9.08	HUMAN	E7ERH5	Phosphoglycerate kinase
10366	dirMS_041712_NAR_40mM_minus2.10965.10965.3	3	9.96	0	7.67E+05		(R)QVSASE	(R)Q V/S A/S E L H T\S G I L/G/P E T L R(D)		148.73	665.6822	1995.051	-0.0185	-9.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
10367	dirMS_041712_NAR_50mM_minus2.14824.14824.3	3	9.96	1	4.43E+04		(R)SLSELES	(R)S L|S E|L/E S L K/L P A E S N/E K(I)		152.55	625.3311	1873.975	0.0034	1.8	4.49	90274.8	6.92	HUMAN	P22059	Oxysterol-binding protein 1
10368	dirMS_041712_NAR_60mM_minus.17911.17911.3	3	9.96	1	4.58E+05		(R)KVESLQI	(R)K V E S L|Q\E/E/I/A F/L/K(K)		160.27	511.9529	1533.852	-0.0081	-5.3	4.79	49709.6	5.19	HUMAN	B0YJC4	Vimentin
10369	dirMS_041712_NAR_120mM_plus.17677.17677.4	4	9.96	1	1.48E+05		(R)GFGHIG	(R)G F G H I G I/A\V|P/D V Y S/A C K R(F)	C:Carbamidomethylation	146.95	487.5024	1946.991	-0.0028	-1.4	8.6	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
10370	dirMS_041712_NAR_120mM_plus.18072.18072.4	4	9.96	0	9.38E+04		(R)HLLQAP'	(R)H L L Q A|P V/D D A Q/E/I/L/H S R(F)		148.65	486.2589	1942.014	-0.0003	-0.2	5.21	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
10371	dirMS_041712_NAR_20mM_plus.15424.15424.2	2	9.96	0	3.88E+04	M73m	(R)AILVDLE	(R)A I\L|V/D\L E|P/G T m D S V R(S)	m:Oxidized methionine	178.07	816.4181	1615.836	15.9929	-1.2	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
10372	dirMS_041712_NAR_20mM_plus.15892.15892.2	2	9.96	0	1.34E+05		(K)SILFVPT:	(K)S I|L/F|V/P T S A P R(G)		181.07	594.3403	1187.678	-0.005	-4.2	9.47	92752.5	4.76	HUMAN	P14625	Endoplasmin
10373	dirMS_041712_NAR_20mM_plus.18920.18920.2	2	9.96	0	5.15E+04		(R)NLTALGI	(R)N L/T/A\L/G L\N L V A/S G G\T A K(A)		201.48	800.4534	1599.906	-0.0069	-4.3	8.75	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
10374	dirMS_041712_NAR_30mM_plus2.14371.14371.2	2	9.96	0	2.23E+05		(R)ELFEMA	(R)E L/F/E/M/A R(T)		128.55	448.2205	895.434	-0.0005	-0.5	4.53	33615.3	9.15	HUMAN	B7Z5E2	26S protease regulatory subunit 7
10375	dirMS_041712_NAR_30mM_plus2.16497.16497.2	2	9.96	0	8.98E+04		(R)LIFSTITS	(R)L I|F S T I/T/S K(M)		139.15	505.3008	1009.593	0.0015	1.5	8.75	47479.5	5.09	HUMAN	P43686	26S protease regulatory subunit 6B
10376	dirMS_041712_NAR_30mM_plus2.18225.18274.2	2	9.96	0	3.78E+04		(K)AILFVPR	(K)A I|L|F/V/P/R(R)		149.07	408.2604	815.514	-0.0003	-0.3	9.79	57660.2	6.38	HUMAN	Q9NQH7	Probable Xaa-Pro aminopeptidase 3
10377	dirMS_041712_NAR_30mM_plus2.21993.22010.2	2	9.96	0	1.95E+04		(R)VIFGLFG	(R)V/I|F/G L/F/G K(T)		170.62	440.7682	880.529	0	0	8.72	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
10378	dirMS_041712_NAR_50mM_plus2.10937.10937.3	3	9.96	1	7.02E+05		(R)DISTNK\	(R)D I|S\T N K V E Q\I/P Y G E R(I)		124.22	583.6304	1748.881	-0.0047	-2.7	4.68	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
10379	dirMS_041712_NAR_50mM_plus2.12154.12154.3	3	9.96	1	1.30E+06		(K)MLVSGA	(K)M/L/V/S/G A G D I K L T K(D)		131.4	444.9236	1332.756	0.0007	0.5	8.35	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
10380	dirMS_041712_NAR_50mM_plus2.12600.12600.3	3	9.96	0	5.15E+05		(R)IMDPNI'	(R)I M/D/P N I/V/G S E H Y D/V\A R(G)		134.6	605.9694	1815.869	0.0242	13.3	4.54	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
10381	dirMS_041712_NAR_50mM_plus2.15129.15129.3	3	9.96	1	3.83E+05		(K)TKDGQII	(K)T K D G Q I\L|P V/P/N V V V R(D)		147.9	545.6573	1634.959	-0.0015	-0.9	8.41	56825.2	9.49	HUMAN	Q9P258	Protein RCC2
10382	dirMS_041712_NAR_50mM_plus2.15647.15647.3	3	9.96	0	1.49E+06		(R)LASTLVH	(R)L A|S/T L V H L\G E Y Q A|A V/D/G A R(K)		149.7	657.6802	1971.029	-0.0034	-1.7	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
10383	dirMS_041712_NAR_120mM_minus.10302.10422.3	3	9.95	1	6.18E+04		(R)KEEELQ/	(R)K E E E\L|Q|A/A/L/A/R(A)		111.02	419.8975	1257.68	-0.0018	-1.4	4.79	232239.1	5.52	HUMAN	F2Z2U8	Myosin-14
10384	dirMS_041712_NAR_120mM_minus.6304.6304.3	3	9.95	1	9.55E+05		(R)TEERAEI	(R)T/E/E R A\E L|A/E/S R(C)		88.9	430.8806	1290.628	-0.0012	-0.9	4.49	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
10385	dirMS_041712_NAR_120mM_minus.8672.8672.3	3	9.95	0	5.76E+05		(R)THYSNIE	(R)T H\Y\S N I|E/A|N/E/S E E V/R(Q)		102.13	593.2723	1777.799	0.0036	2	4.48	21983.3	4.68	HUMAN	K7EIV0	Calpain small subunit 1
10386	dirMS_041712_NAR_30mM_minus2.10770.10770.2	2	9.95	0	3.96E+05		(K)AVLENA	(K)A V|L/E/N A L R(N)		111.92	443.2601	885.515	-0.0023	-2.6	6.05	33605.6	6.56	HUMAN	A6NJ11	Ubiquitin fusion degradation protein 1 homolog
10387	dirMS_041712_NAR_30mM_minus2.15829.15829.2	2	9.95	0	1.25E+05		(R)TINEVEN	(R)T I|N\E|V/E N Q I L/T R(D)		139.6	715.3834	1429.765	-0.005	-3.5	4.53	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
10388	dirMS_041712_NAR_30mM_minus2.7332.7332.2	2	9.95	0	1.55E+05		(R)AQAAG:	(R)A Q|A|A/G\S\S V L R(E)		94.77	480.2603	959.527	-0.0135	-14.1	9.79	38843.2	6.48	HUMAN	Q96EK9	Protein KTI12 homolog
10389	dirMS_041712_NAR_30mM_minus2.8103.8103.2	2	9.95	0	8.16E+04		(K)SLAAEEE	(K)S L/A|A/E/E E A/A R(Q)		98.37	523.7597	1046.511	0.0008	0.8	4.25	533778	5.74	HUMAN	Q15149	Plectin
10390	dirMS_041712_NAR_50mM_minus2.17465.17465.3	3	9.95	0	3.93E+05		(K)VAHALA	(K)V A H A L A E G\L G\V|I/A C I/G E/K(L)	C:Carbamidomethylation	168.68	603.3247	1807.974	-0.0139	-7.7	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
10391	dirMS_041712_NAR_60mM_minus.13436.13436.3	3	9.95	1	1.40E+06		(R)QLREYQ	(R)Q L R E Y Q/E|L/M N V K(L)		135.27	517.6033	1550.8	-0.0042	-2.7	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
10392	dirMS_041712_NAR_60mM_minus.13674.13674.3	3	9.95	0	4.50E+05		(R)ANPQV(	(R)A N|P Q/V G/V A F/P/H I/K(H)		135.95	459.9265	1377.764	0.0012	0.9	8.8	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
10393	dirMS_041712_NAR_60mM_minus.6917.6917.3	3	9.95	1	2.74E+05		(R)IVDGKV'	(R)I V/D/G/K V V S E T N D T/K(V)		97.95	502.2642	1504.785	-0.0073	-4.8	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
10394	dirMS_041712_NAR_120mM_plus.11714.11714.3	3	9.95	1	1.18E+06		(K)MKEIAE/	(K)M K/E I A E/A/Y/L/G K(T)		114.3	418.2253	1252.661	0.0008	0.6	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
10395	dirMS_041712_NAR_120mM_plus.6785.6785.3	3	9.95	1	6.52E+05		(R)NKQTYS	(R)N K\Q T\Y S T E/P N/N/L K(A)		88.83	512.9261	1536.765	-0.0015	-1	8.5	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
10396	dirMS_041712_NAR_30mM_plus2.15047.15270.2	2	9.95	0	6.95E+05		(K)SADTLW	(K)S A|D|T/L|W/G I Q/K(E)		132.23	559.7963	1118.584	0.0013	1.1	5.55	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
10397	dirMS_041712_NAR_30mM_plus2.21745.21745.2	2	9.95	0	3.49E+05		(R)FSWNV\	(R)F S/W/N/V W|P/S/S R(L)		169.25	633.3085	1265.606	0.0035	2.8	9.75	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
10398	dirMS_041712_NAR_30mM_plus2.5313.5313.2	2	9.95	0	5.33E+05		(K)VSSFEEK	(K)V/S/S F E/E K(M)		81.62	413.203	825.399	-0.0002	-0.2	4.53	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
10399	dirMS_041712_NAR_30mM_plus2.6838.6879.2	2	9.95	0	6.17E+04		(R)VYSTSVT	(R)V/Y|S T/S V/T/G S R(E)		90.47	528.7673	1056.532	-0.0047	-4.4	8.72	9437.4	9.69	HUMAN	Q5T123	SH3 domain binding glutamic acid-rich protein like 3
10400	dirMS_041712_NAR_50mM_plus2.13140.13188.3	3	9.95	1	1.61E+06		(K)LIADVAF	(K)L I|A/D V A/P S A I R E N D/I K(S)		136.73	575.6533	1724.954	-0.0088	-5.1	4.56	18388.8	6.85	HUMAN	F5H1Y3	Flap endonuclease 1 (Fragment)
10401	dirMS_041712_NAR_50mM_plus2.16246.16246.3	3	9.95	1	2.46E+06		(K)LLQDFFI	(K)L/L/Q D/F F N/G K E L N K(S)		154.7	522.6137	1565.832	-0.0057	-3.6	6.07	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
10402	dirMS_041712_NAR_50mM_plus2.22206.22206.3	3	9.95	1	5.40E+05		(R)ELAILLG	(R)E L/A I/L/L G M L D/P A E K D/E K(G)		190.32	629.004	1884.999	-0.0012	-0.7	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
10403	dirMS_041712_NAR_60mM_plus.15914.15914.3	3	9.95	1	1.41E+06		(R)MSMKE'	(R)M S M K E V D E Q|M\L/N V/Q/N K(N)		140.88	641.9696	1923.897	-0.003	-1.6	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
10404	dirMS_041712_NAR_120mM_minus.13764.13764.4	4	9.94	1	1.60E+06		(K)ASIHEA\	(K)A/S/I H/E A/W/T D\G/K E A M L K(H)		129.97	447.476	1786.879	0.0029	1.6	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
10405	dirMS_041712_NAR_120mM_minus.18565.18565.3	3	9.94	1	3.30E+05		(R)ARFEEL(	(R)A R\F E E\L/C/S D/L/F/R(S)	C:Carbamidomethylation	156.88	514.9175	1542.737	0.001	0.7	4.68	25598.3	6.45	HUMAN	E7EP11	Heat shock 70 kDa protein 1A/1B
10406	dirMS_041712_NAR_30mM_minus2.9360.9360.2	2	9.94	0	5.80E+05		(K)VTEDTS:	(K)V/T|E/D/T S/S\V L R(S)		105.12	553.7841	1106.569	-0.0079	-7.1	4.37	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
10407	dirMS_041712_NAR_40mM_minus2.12370.12370.3	3	9.94	1	1.79E+04		(K)VVEEAP:	(K)V V|E E/A|P S I F L D A E T R R(A)		155.72	611.3244	1831.955	0.0038	2.1	4.41	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
10408	dirMS_041712_NAR_50mM_minus2.7896.7896.3	3	9.94	0	4.58E+04		(R)QLSQAG	(R)Q L/S Q A/G/S/F S D/G T H/G G L R(Y)		111.92	573.2875	1717.825	0.0227	13.2	6.74	266161	5.68	HUMAN	E9PPU0	Epiplakin
10409	dirMS_041712_NAR_60mM_minus.8265.8307.3	3	9.94	1	8.21E+05	M174m	(R)VKYETEL	(R)V K Y E T E/L/A/m/R(Q)	m:Oxidized methionine	106.05	419.2169	1239.64	15.996	0.8	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10410	dirMS_041712_NAR_20mM_plus.12722.12722.2	2	9.94	0	4.99E+04	M17m M2(	(K)GAEEmE	(K)G A E E m E T/V\I|P V/D V m R(R)	m:Oxidized methionine	160.18	854.3998	1675.803	31.9894	-0.3	4	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
10411	dirMS_041712_NAR_20mM_plus.14951.14951.2	2	9.94	0	1.26E+05		(R)LLDAQL:	(R)L L/D\A/Q|L|S T G G I/V D/P S K(S)		174.67	807.4389	1613.874	-0.004	-2.5	4.21	533778	5.74	HUMAN	Q15149	Plectin
10412	dirMS_041712_NAR_20mM_plus.15884.15884.2	2	9.94	0	1.13E+05		(K)VGINYQ	(K)V G I N/Y Q/P/P T V V/P G/G D L A K(V)		179.87	912.9952	1824.985	-0.0023	-1.3	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
10413	dirMS_041712_NAR_20mM_plus.16101.16101.2	2	9.94	0	4.27E+05		(K)DAGTIA(	(K)D A/G T I/A/G/L N V/L|R(I)		183.53	600.3422	1199.674	0.0029	2.4	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
10414	dirMS_041712_NAR_20mM_plus.16955.16955.2	2	9.94	0	1.21E+05		(K)LGGSAV	(K)L G/G S A\V/I/S L/E G K|P L(-)		187.37	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
10415	dirMS_041712_NAR_20mM_plus.7075.7075.2	2	9.94	0	4.35E+05		(R)IQEAGTI	(R)I Q|E|A/G T E V/V K(A)		115.37	537.2946	1073.584	-0.0018	-1.7	4.53	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
10416	dirMS_041712_NAR_20mM_plus.7427.7427.3	3	9.94	0	2.14E+05		(K)TGQAPG	(K)T G Q A P G\Y S/Y/T/A A N K(N)		119.53	476.8963	1428.675	-0.001	-0.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
10417	dirMS_041712_NAR_40mM_plus2.11553.11714.2	2	9.94	0	2.64E+05		(R)NLLSVA'	(R)N L|L/S/V/A/Y|K(N)		135.17	454.2649	907.525	-0.0022	-2.4	8.59	18789.1	6.77	HUMAN	A2IDB2	14-3-3 protein eta (Fragment)
10418	dirMS_041712_NAR_40mM_plus2.17839.17839.3	3	9.94	0	1.64E+05		(K)LAKPLSS	(K)L A K\P L S S\L\T|P L I/M A A K(E)		171.68	552.0052	1653.997	0.0039	2.3	10	24711.4	5.19	HUMAN	H7C1X3	PAK-2p34 (Fragment)
10419	dirMS_041712_NAR_40mM_plus2.8963.8963.2	2	9.94	0	1.19E+05		(R)GYSFTTI	(R)G Y|S/F/T/T/T A E R(E)		114.9	566.7672	1132.527	0.0002	0.2	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
10420	dirMS_041712_NAR_50mM_plus2.10076.10076.3	3	9.94	1	3.09E+05		(R)LGLPGD	(R)L/G L|P G/D E V/D/N K V K(G)		120.28	461.9229	1383.748	0.0063	4.6	4.56	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
10421	dirMS_041712_NAR_50mM_plus2.12178.12178.3	3	9.94	0	4.76E+05		(R)GAIQFV'	(R)G A I/Q/F/V/T Q Y Q H S S G/Q R(R)		131.62	602.9721	1806.888	0.0136	7.5	8.75	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
10422	dirMS_041712_NAR_50mM_plus2.18861.18861.3	3	9.94	1	4.32E+05		(K)ITQDIFQ	(K)I/T/Q D/I F/Q Q L L K/R(G)		167.02	501.627	1502.869	-0.0025	-1.7	8.75	72796.9	6.75	HUMAN	A6NC17	Methionine--tRNA ligase, cytoplasmic
10423	dirMS_041712_NAR_60mM_plus.17258.17258.3	3	9.94	0	1.03E+06		(R)QIFHPE(	(R)Q I F/H/P E Q L/I/T G/K(E)		147.05	470.9225	1410.774	-0.021	-14.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
10424	dirMS_041712_NAR_30mM_minus2.16726.16726.2	2	9.93	0	2.51E+05		(R)ASLEAAI	(R)A S/L E/A/A I/A|D/A/E Q R(G)		144.4	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
10425	dirMS_041712_NAR_30mM_minus2.6906.6906.2	2	9.93	0	2.56E+05		(R)IGDEDV(	(R)I/G/D/E/D/V/G/R(V)		91.67	430.7116	860.411	0.0051	5.9	4.03	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
10426	dirMS_041712_NAR_50mM_minus2.14062.14062.3	3	9.93	1	1.28E+05		(R)IIEFVPTI	(R)I I|E F V/P T K T P Y/D/P R(W)		148.32	559.3044	1675.905	-0.0067	-4	6.07	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
10427	dirMS_041712_NAR_60mM_minus.19248.19318.3	3	9.93	0	1.04E+06		(R)SLHDAL(	(R)S L H\D A\L\C|V|L A/Q T V K(D)	C:Carbamidomethylation	171.22	518.9484	1554.831	-0.0002	-0.1	6.46	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
10428	dirMS_041712_NAR_60mM_minus.9807.9807.3	3	9.93	1	2.83E+05		(R)TNAENE	(R)T/N|A/E N E F V/T I K K(D)		114.3	465.2487	1393.732	-0.0006	-0.4	5.81	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
10429	dirMS_041712_NAR_30mM_plus2.13066.13107.2	2	9.93	0	9.98E+05		(R)MVVPA/	(R)M/V|V|P A A L/K(V)		122.72	414.7506	828.501	-0.0072	-8.7	8.5	23633.9	11.02	HUMAN	P40429	60S ribosomal protein L13a
10430	dirMS_041712_NAR_30mM_plus2.16309.16309.2	2	9.93	0	2.45E+05		(K)TLGDFA/	(K)T/L|G D F A A E/Y A K(S)		138.32	593.2933	1185.579	0.0007	0.6	4.37	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
10431	dirMS_041712_NAR_30mM_plus2.4840.4840.2	2	9.93	0	8.10E+05		(R)MGQTN	(R)M/G Q|T M/E/R(I)		76.92	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
10432	dirMS_041712_NAR_30mM_plus2.8536.8536.2	2	9.93	0	8.93E+05		(R)LGLGEG.	(R)L/G/L|G E/G A E E\K(S)		98.92	501.7639	1002.51	0.0103	10.3	4.25	40096.8	9.24	HUMAN	C9JW69	Regulator of chromosome condensation (Fragment)
10433	dirMS_041712_NAR_50mM_plus2.13364.13364.3	3	9.93	0	1.99E+05		(K)LVRPPV(	(K)L V R P P V|Q|V/Y/G/I E/G R(Y)		138.6	528.3069	1582.906	-0.0002	-0.2	8.75	8249.6	10.2	HUMAN	H7C086	ATP synthase subunit O, mitochondrial (Fragment)
10434	dirMS_041712_NAR_50mM_plus2.18722.18854.3	3	9.93	1	4.36E+05		(K)AAIDWF	(K)A A|I/D|W/F\D G K E F S G N P I K(V)		167.18	632.3186	1894.933	0.0079	4.1	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
10435	dirMS_041712_NAR_50mM_plus2.7730.7730.3	3	9.93	1	2.65E+05		(K)GGIMLP	(K)G/G I|M L/P/E K S Q G/K(V)		106.62	415.5609	1244.667	0.0014	1.1	8.59	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
10436	dirMS_041712_NAR_60mM_plus.11403.11403.3	3	9.93	0	4.84E+05		(K)NFYVEH	(K)N/F/Y/V/E/H/P E V A R(L)		117.65	454.2286	1360.664	0.0068	5	5.4	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
10437	dirMS_041712_NAR_60mM_plus.15296.15296.3	3	9.93	1	1.76E+05		(R)VEVTEFE	(R)V/E|V/T E F E/D I K S G Y R(I)		136.78	557.9447	1671.822	-0.0029	-1.7	4.41	30992.3	4.14	HUMAN	B2REB8	Protein SET
10438	dirMS_041712_NAR_60mM_plus.18499.18499.3	3	9.93	1	1.57E+05		(R)CRVDLP	(R)C R V D\L|P L|A\V/L/S K(M)	C:Carbamidomethylation	154.17	457.599	1370.782	0	0	8.75	7765.6	8.23	HUMAN	H3BSA6	dCTP pyrophosphatase 1
10439	dirMS_041712_NAR_60mM_plus.7419.7419.3	3	9.93	0	5.01E+05		(R)SSGHSS:	(R)S S G H S S S E/L/S/P D A V/E K(A)		96.95	539.584	1616.74	-0.0024	-1.5	4.65	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
10440	dirMS_041712_NAR_60mM_plus.8587.8587.3	3	9.93	1	1.58E+06		(K)GGIMLP	(K)G G I/M/L/P E K S Q G/K(V)		103.33	415.5607	1244.667	0.0008	0.7	8.59	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
10441	dirMS_041712_NAR_20mM_minus.10110.10110.2	2	9.92	0	1.24E+05		(R)YALYDA'	(R)Y A|L\Y/D A T Y E T K(E)		150.82	669.3156	1337.626	-0.0021	-1.5	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
10442	dirMS_041712_NAR_30mM_minus2.16292.16292.2	2	9.92	0	1.24E+05		(R)EGVAAF	(R)E\G|V A A F Y|K(G)		142.03	442.7308	884.451	0.0031	3.5	6.1	17934.5	10.31	HUMAN	H7C4Z4	Calcium-binding mitochondrial carrier protein SCaMC-2 (Fragment)
10443	dirMS_041712_NAR_30mM_minus2.16621.16621.2	2	9.92	0	2.62E+05	M2243m	(K)mSIYQA	(K)m S|I|Y/Q/A/M/W K(G)	m:Oxidized methionine	144.13	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
10444	dirMS_041712_NAR_40mM_minus2.12356.12377.3	3	9.92	0	1.88E+05		(R)GAPPSSI	(R)G A/P/P S S N I E/D/F/H G L L P/K(G)		155.82	593.6401	1778.907	-0.0014	-0.8	5.32	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
10445	dirMS_041712_NAR_40mM_minus2.6978.6978.2	2	9.92	0	5.85E+05		(R)GYSFTTI	(R)G Y S/F/T/T T A E/R(E)		111.95	566.7661	1132.527	-0.002	-1.8	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
10446	dirMS_041712_NAR_50mM_minus2.10738.10738.3	3	9.92	0	1.80E+05		(R)LLELGPK	(R)L/L\E/L G/P K P E/V A Q Q\T R(K)		128.97	560.3182	1678.949	-0.0086	-5.1	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
10447	dirMS_041712_NAR_50mM_minus2.11724.11724.3	3	9.92	1	5.53E+05		(R)ELISNSSI	(R)E L I/S N/S|S D/A|L D K I R(Y)		135.78	520.9445	1560.823	-0.0038	-2.5	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
10448	dirMS_041712_NAR_50mM_minus2.14269.14269.3	3	9.92	1	2.08E+05		(R)DLAALG	(R)D L\A|A/L/G D K V N S\L/G E T A E/R(L)		149.15	620.3204	1858.95	-0.0038	-2.1	4.32	285798.6	5.23	HUMAN	A6NG51	Spectrin alpha chain, non-erythrocytic 1
10449	dirMS_041712_NAR_50mM_minus2.16959.16959.3	3	9.92	0	1.53E+05		(R)LLEVLSG	(R)L/L\E/V/L/S G E I/L P K P T K(G)		165.33	546.3329	1636.988	-0.0042	-2.6	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
10450	dirMS_041712_NAR_50mM_minus2.5876.5876.3	3	9.92	0	8.40E+04		(K)ANESSPI	(K)A N/E S S P K/P V/G/P/P\P E R(D)		95.83	521.2695	1561.797	-0.0029	-1.9	6.19	10501.2	5.81	HUMAN	A6PVM9	Allograft inflammatory factor 1-like
10451	dirMS_041712_NAR_60mM_minus.14372.14372.3	3	9.92	1	1.30E+06		(R)MSMKE'	(R)M S/M K E V D\E\Q|M/L/N V/Q N K(N)		140.47	641.9701	1923.897	-0.0015	-0.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
10452	dirMS_041712_NAR_20mM_plus.13722.13722.2	2	9.92	0	2.41E+05	M98m	(R)TLTIVDT	(R)T L|T/I|V/D T G I/G m T K(A)	m:Oxidized methionine	166.97	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
10453	dirMS_041712_NAR_20mM_plus.13726.13726.3	3	9.92	0	1.01E+05		(K)IFVGNV:	(K)I F V G N V S A A/C/T S/Q E L R(S)	C:Carbamidomethylation	166.68	584.6279	1751.874	-0.0053	-3.1	6	37433.2	9.17	HUMAN	B0LM41	Protein RBM14-RBM4
10454	dirMS_041712_NAR_30mM_plus2.10344.10344.2	2	9.92	0	5.36E+04		(K)TAVCDII	(K)T A|V|C D I|P|P R(G)	C:Carbamidomethylation	108.98	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
10455	dirMS_041712_NAR_30mM_plus2.15045.15239.2	2	9.92	0	4.92E+05		(K)LYLADPI	(K)L/Y|L/A/D/P M K(A)		131.93	475.7563	950.502	0.0038	4	5.83	7781.8	6.82	HUMAN	E9PE20	Signal recognition particle 9 kDa protein
10456	dirMS_041712_NAR_40mM_plus2.12558.12558.3	3	9.92	0	3.85E+05		(K)AASDIAI	(K)A A/S D I/A M T E/L/P P T H P I R(L)		140.05	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
10457	dirMS_041712_NAR_50mM_plus2.10127.10127.3	3	9.92	1	5.94E+04		(K)ITIKNDP	(K)I T/I K/N D|P S L P E/P K(C)		120.53	484.6079	1451.81	-0.0013	-0.9	6.07	20203.8	9.79	HUMAN	B4DG16	Asparagine--tRNA ligase, cytoplasmic
10458	dirMS_041712_NAR_50mM_plus2.12945.12945.3	3	9.92	0	1.82E+05		(K)SLLVPDI	(K)S L|L/V/P D/H V/I T R(L)		136.25	417.2467	1249.726	-0.0008	-0.6	6.46	19837.4	6.59	HUMAN	D3DQ64	Adenylate kinase isoenzyme 4, mitochondrial
10459	dirMS_041712_NAR_50mM_plus2.15204.15204.3	3	9.92	1	2.90E+05		(R)VEKIPG(	(R)V E K I P G G I|I/E/D S/C V|L R(G)	C:Carbamidomethylation	146.65	595.6548	1784.958	-0.0076	-4.3	4.68	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma

10460	dirMS_041712_NAR_50mM_plus2.7774.7774.3	3	9.92	0	2.10E+05		(R)DGQVIN	(R)D G\Q|V/I|N E/T/S Q H/H D D L E(-)		106.82	612.9457	1836.8	0.0231	12.6	4.28	53707.8	5.06	HUMAN	P08670	Vimentin
10461	dirMS_041712_NAR_50mM_plus2.8170.8170.3	3	9.92	1	9.41E+04		(R)QAVTNF	(R)Q A|V/T N/P/N/N T F Y A T K R(L)		109.92	575.628	1724.872	-0.002	-1.2	9.99	6809.6	9.69	HUMAN	D6RA73	Stress-70 protein, mitochondrial (Fragment)
10462	dirMS_041712_NAR_50mM_plus2.9500.9500.3	3	9.92	1	3.39E+05		(R)AGTGVD	(R)A G T/G V/D/N V D L/E/A/A T R K(G)		117.4	539.6108	1616.824	-0.006	-3.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
10463	dirMS_041712_NAR_60mM_plus.12074.12074.3	3	9.92	1	7.57E+05		(R)ARQEEL	(R)A R Q E E L|Y|S/E/L Q A/R(E)		120.1	531.6013	1592.803	-0.0134	-8.4	4.79	533778	5.74	HUMAN	Q15149	Plectin
10464	dirMS_041712_NAR_120mM_minus.10027.10027.4	4	9.91	0	3.14E+05		(K)LITQTFS	(K)L I/T Q/T/F S H/H/N Q L/A Q/K(T)		108.88	442.2355	1765.934	-0.0142	-8.1	8.76	38299.3	5.27	HUMAN	Q9Y266	Nuclear migration protein nudC
10465	dirMS_041712_NAR_120mM_minus.19116.19116.4	4	9.91	1	1.62E+05		(R)SLRDLTF	(R)S L R D\L T/P E/H/L/P L L R(N)		158.97	415.7434	1659.954	-0.0023	-1.4	6.47	38779.2	5.93	HUMAN	Q96C86	m7GpppX diphosphatase
10466	dirMS_041712_NAR_120mM_minus.21393.21393.3	3	9.91	0	8.12E+05		(R)LHFFMP	(R)L H\F F M/P G\F\A/P\L T S/R(G)		182.17	540.9497	1620.835	-0.001	-0.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
10467	dirMS_041712_NAR_120mM_minus.4736.4806.3	3	9.91	1	5.33E+05		(K)AGADEE	(K)A/G|A/D\E/E R A E T A/R(L)		77.15	425.8687	1275.592	-0.0008	-0.7	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
10468	dirMS_041712_NAR_20mM_minus.12157.12157.2	2	9.91	0	1.51E+05		(R)AAVIGPI	(R)A A/V|I/G/P D V F A K(L)		170.9	544.3103	1087.615	-0.0013	-1.2	5.88	266161	5.68	HUMAN	E9PPU0	Epiplakin
10469	dirMS_041712_NAR_20mM_minus.12336.12336.2	2	9.91	0	7.12E+05	M185m	(K)LAVNm	(K)L A\V/N/m V/P F P R(L)	m:Oxidized methionine	171.97	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
10470	dirMS_041712_NAR_30mM_minus2.18241.18241.3	3	9.91	0	4.14E+05		(R)QAQEYE	(R)Q A Q E\Y/E/A|L L N/I K(V)		154.48	473.9196	1419.748	-0.0036	-2.5	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10471	dirMS_041712_NAR_30mM_minus2.19054.19054.2	2	9.91	0	1.74E+05		(K)IISNLFL	(K)I I|S\N\L F/L G R(A)		157.72	516.8122	1032.62	-0.0029	-2.8	9.75	234333.2	6.01	HUMAN	J3KNX9	Unconventional myosin-XVIIIa
10472	dirMS_041712_NAR_30mM_minus2.7755.7827.2	2	9.91	0	5.46E+05		(K)TQLAVC	(K)T Q|L|A|V|C/Q Q R(I)	C:Carbamidomethylation	96.65	552.2842	1103.563	-0.0015	-1.3	9.41	9740.1	10.08	HUMAN	H0YFG2	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed (Fragment)
10473	dirMS_041712_NAR_40mM_minus2.6932.6940.2	2	9.91	0	5.85E+05		(R)GYSFTT	(R)G Y|S/F/T/T/T/A E R(E)		111.95	566.7661	1132.527	-0.002	-1.8	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
10474	dirMS_041712_NAR_40mM_minus2.9797.9797.2	2	9.91	0	2.04E+06		(R)VAPEEH	(R)V A/P E E H|P V L L T E/A/P L N|P K(A)		140.28	977.5343	1954.064	-0.0031	-1.6	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
10475	dirMS_041712_NAR_50mM_minus2.14949.14950.3	3	9.91	1	2.05E+05		(K)VVEEAP	(K)V/V\E/E/A/P S I\F L D A E T R R(A)		153.7	611.3243	1831.955	0.0035	1.9	4.41	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
10476	dirMS_041712_NAR_60mM_minus.12613.12613.3	3	9.91	1	1.60E+05		(K)LSAEKVE	(K)L S\A E K V/E I/A/T/L/T R(E)		130.73	477.6112	1430.821	-0.0023	-1.6	6.14	26661.1	7.81	HUMAN	H0YL69	Proteasome subunit alpha type (Fragment)
10477	dirMS_041712_NAR_60mM_minus.14631.14631.3	3	9.91	1	2.82E+04		(R)MSMKE	(R)M S M K E V D E Q/M|L N V Q\N K(N)		141.58	641.9701	1923.897	-0.0015	-0.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
10478	dirMS_041712_NAR_60mM_minus.18424.18424.3	3	9.91	1	6.80E+03	M834m	(K)MmALD	(K)M/m/A/L D R E V Q Y|L L N K(A)	m:Oxidized methionine	164.07	580.6293	1723.887	15.9864	-4.9	5.82	105005	5.57	HUMAN	E9PL22	Hypoxia up-regulated protein 1
10479	dirMS_041712_NAR_60mM_minus.8420.8420.3	3	9.91	1	6.45E+04		(K)QGIETPE	(K)Q G I/E/T/P E D Q/N D/L R/K(M)		106.97	548.2737	1642.803	0.0034	2.1	4.32	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
10480	dirMS_041712_NAR_120mM_plus.8485.8505.2	2	9.91	1	1.84E+06	M174m	(R)VKYETEL	(R)V/K|Y|E/T/E L A m R(Q)	m:Oxidized methionine	97.78	628.314	1239.64	15.9805	-11.4	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10481	dirMS_041712_NAR_120mM_plus.9904.9904.3	3	9.91	0	1.95E+05		(R)LESGMC	(R)L/E/S G M Q N/M/S I H/T|K(T)		104.98	492.5707	1475.698	-0.0006	-0.4	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
10482	dirMS_041712_NAR_20mM_plus.10783.10783.2	2	9.91	0	8.63E+04		(R)FLEQQN	(R)F L|E/Q Q/N Q\V L Q\T/K(W)		146.73	738.3942	1475.785	-0.0041	-2.8	6	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
10483	dirMS_041712_NAR_20mM_plus.10786.10786.2	2	9.91	0	2.19E+05	M33m	(K)VAGmD	(K)V A G m/D|V|E/L T V/E/E R(N)	m:Oxidized methionine	147.28	732.3555	1447.71	15.994	-0.6	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
10484	dirMS_041712_NAR_20mM_plus.15638.15638.2	2	9.91	0	8.60E+04		(-)SDVLELT	(-)S D V\L/E\L/T/D D N/F E S R(I)		179.3	820.3754	1639.745	-0.0011	-0.6	3.77	13747.3	6.8	HUMAN	H7BZJ3	Thioredoxin (Fragment)
10485	dirMS_041712_NAR_40mM_plus2.18052.18052.3	3	9.91	0	9.77E+04	M159m	(R)SVAAIH	(R)S V|A/A/I/H P S L E I/P m L I/P K(E)	m:Oxidized methionine	172.8	611.3472	1816.04	15.9869	-4.4	6.47	31606.3	6.72	HUMAN	B4E329	Phosphoribosyl pyrophosphate synthase-associated protein 2
10486	dirMS_041712_NAR_50mM_plus2.20252.20252.3	3	9.91	0	3.15E+05		(R)NEVSFV	(R)N E/V/S F/V I/H N/L P V L/A K(M)		174.45	560.6531	1679.948	-0.0032	-1.9	6.75	35663.7	5.91	HUMAN	B4DWK0	Selenide, water dikinase 1
10487	dirMS_041712_NAR_50mM_plus2.7465.7465.3	3	9.91	1	4.80E+04		(K)LYQEKG	(K)L/Y Q/E K G W G D T E F S K(Q)		105.13	563.2693	1687.796	-0.0029	-1.7	4.68	12143.3	5.16	HUMAN	H0Y5R3	1-acyl-sn-glycerol-3-phosphate acyltransferase delta (Fragment)
10488	dirMS_041712_NAR_60mM_plus.16563.16563.3	3	9.91	0	1.92E+05		(R)LSQYQE	(R)L S/Q/Y Q/E/P L/H L P G V R(V)		143.7	546.297	1636.881	-0.0041	-2.5	6.75	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
10489	dirMS_041712_NAR_60mM_plus.6409.6409.3	3	9.91	1	4.32E+05		(R)ARSDEG	(R)A R S D\E G\Q|L/S/P A/T R(G)		92.5	463.233	1387.692	-0.008	-5.8	6.12	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
10490	dirMS_041712_NAR_60mM_plus.8693.8693.3	3	9.91	0	6.69E+05		(K)GQVCV	(K)G Q|V/C/V/M I H/S G S R(G)	C:Carbamidomethylation	103.05	444.2219	1330.636	0.0157	11.8	9.75	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
10491	dirMS_041712_NAR_120mM_minus.17527.17527.3	3	9.9	1	3.04E+05		(R)RAPFDLI	(R)R A P F\D|L/F/E/N K(K)		150.7	412.8849	1236.637	0.003	2.4	6.07	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
10492	dirMS_041712_NAR_120mM_minus.7187.7187.3	3	9.9	1	2.57E+05		(K)DSYVGD	(K)D S/Y/V/G D E A/Q S K R(G)		92.62	452.2134	1354.623	0.0023	1.7	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
10493	dirMS_041712_NAR_120mM_minus.7821.7821.3	3	9.9	1	2.74E+06	M281m	(R)SRAEAE	(R)S R\A\E A\E|S/m/Y Q/I\K(Y)	m:Oxidized methionine	96.75	476.8951	1412.684	15.9869	-5.6	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
10494	dirMS_041712_NAR_120mM_minus.9883.9883.2	2	9.9	0	1.28E+05		(R)IGAEVY	(R)I/G|A|E|V/Y H\N L/K(N)		108.12	572.3123	1143.616	0.0016	1.4	6.75	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
10495	dirMS_041712_NAR_30mM_minus2.14059.14059.2	2	9.9	0	2.61E+05		(K)CDFPIM	(K)C/D|F/P I/M/K(F)	C:Carbamidomethylation	129.72	455.7144	910.416	0.0054	5.9	5.84	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
10496	dirMS_041712_NAR_30mM_minus2.9130.9130.2	2	9.9	0	2.14E+05		(R)LGEYED	(R)L/G\E/Y/E D V S/R(V)		102.85	534.2599	1067.5	0.0121	11.4	4.14	23811.2	6.78	HUMAN	A8MVD5	Tubulin-folding cofactor B
10497	dirMS_041712_NAR_50mM_minus2.12760.12760.3	3	9.9	0	2.90E+05		(K)EGKPTIV	(K)E G K P T I V E E/D D/P E L/F/K(Q)		140.92	615.9772	1845.912	0.0054	2.9	4.08	29841.1	9.04	HUMAN	O75937	DnaJ homolog subfamily C member 8
10498	dirMS_041712_NAR_60mM_minus.15482.15482.3	3	9.9	1	2.23E+05		(R)GPIKFN	(R)G P\I K\F N\V|W/D\T/A G Q E K(F)		146.48	563.9575	1689.86	-0.0015	-0.9	6.07	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
10499	dirMS_041712_NAR_120mM_plus.12518.12518.2	2	9.9	0	7.45E+05		(K)HLSVND	(K)H/L|S V/N D|L P V G R(S)		119.2	603.8321	1206.659	-0.002	-1.7	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
10500	dirMS_041712_NAR_20mM_plus.9253.9253.2	2	9.9	0	4.54E+04		(R)IIYGGSV	(R)I I|Y/G/G S V T G A T C K(E)	C:Carbamidomethylation	135.4	663.8412	1326.672	0.0029	2.2	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
10501	dirMS_041712_NAR_30mM_plus2.21199.21199.2	2	9.9	0	3.48E+03		(R)GAFQNL	(R)G A/F/Q/N/L/F Q S V/R(E)		164.47	633.8315	1266.659	-0.0032	-2.5	9.75	68629.9	5.59	HUMAN	E7EVX6	Androgen receptor
10502	dirMS_041712_NAR_30mM_plus2.6323.6323.2	2	9.9	0	1.25E+05		(K)ACGSEI	(K)A/C|G S E/I/M Q/K(K)	C:Carbamidomethylation	87.17	512.2281	1023.46	-0.0109	-10.6	6.05	334221.3	6.44	HUMAN	P15924	Desmoplakin
10503	dirMS_041712_NAR_30mM_plus2.8346.8346.2	2	9.9	0	2.20E+05		(R)VAIEPG	(R)V A\I|E/P G A P R(E)		97.7	455.2602	909.515	-0.0021	-2.3	5.97	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
10504	dirMS_041712_NAR_40mM_plus2.9439.9439.2	2	9.9	0	8.85E+04		(R)INVYYN	(R)I/N|V\Y/Y\N E/A T G G K(Y)		118.58	664.8248	1328.648	-0.0058	-4.4	6	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
10505	dirMS_041712_NAR_50mM_plus2.11505.11505.3	3	9.9	1	6.68E+04		(R)IAEFTTN	(R)I/A|E F T T N L/T E E E E/K S K(S)		128.28	623.6413	1868.912	-0.003	-1.6	4.32	227783.5	5.5	HUMAN	P35579	Myosin-9
10506	dirMS_041712_NAR_50mM_plus2.12157.12157.3	3	9.9	0	4.76E+05		(R)GAIQFV	(R)G A\I|Q/F V/T Q Y Q/H\S S G Q R(R)		131.62	602.9721	1806.888	0.0136	7.5	8.75	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
10507	dirMS_041712_NAR_60mM_plus.11511.11511.3	3	9.9	0	3.70E+05		(R)SLGTAD	(R)S L/G\T A|D V/H F E R(K)		116.88	411.2075	1231.607	0.0014	1.1	5.3	27557.2	11.05	HUMAN	E9PB61	THO complex subunit 4
10508	dirMS_041712_NAR_60mM_plus.12450.12759.3	3	9.9	0	3.37E+06		(R)TFIAIKP	(R)T F|I/A/I/K/P D/G V\Q R(G)		122.53	448.9229	1344.763	-0.0093	-6.9	8.41	6640.6	8.25	HUMAN	C9K028	Nucleoside diphosphate kinase A (Fragment)
10509	dirMS_041712_NAR_120mM_minus.16621.16621.3	3	9.89	0	6.39E+05		(R)EHALLA	(R)E H\A L\L/A|Y/T/L G V K(Q)		145.22	438.9186	1314.742	-0.0004	-0.3	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
10510	dirMS_041712_NAR_120mM_minus.18970.18970.4	4	9.89	1	2.04E+05		(K)LHDNLII	(K)L H D N L\I/I/S/D/L E N T V K/K(L)		158.65	463.7605	1852.017	0.0027	1.5	5.38	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
10511	dirMS_041712_NAR_120mM_minus.5578.5578.3	3	9.89	1	1.46E+05		(R)KLGQSE	(R)K L G Q S\E/S\Q/G|P/P/R(A)		83.77	428.5624	1283.67	0.0024	1.9	8.75	20025.3	6.6	HUMAN	F5GX23	26S proteasome non-ATPase regulatory subunit 9
10512	dirMS_041712_NAR_30mM_minus2.8113.8113.2	2	9.89	0	3.65E+04		(K)QLQEED	(K)Q L|Q E/E/D|L K(A)		98.77	501.7573	1002.51	-0.0029	-2.9	4.14	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
10513	dirMS_041712_NAR_50mM_minus2.10394.10394.3	3	9.89	0	1.30E+05		(K)NAQLNI	(K)N A|Q/L N/I E/L E A A/H H(-)		127.23	487.2478	1459.729	0	0	5.23	13452	8.89	HUMAN	F5H246	Protein NAMPTL
10514	dirMS_041712_NAR_50mM_minus2.11915.11915.3	3	9.89	1	1.64E+05		(K)TVNVVC	(K)T V/N V/V/Q/F/E P S K G A I G K(A)		136.02	558.6442	1673.922	-0.004	-2.4	8.26	83905.8	6.62	HUMAN	P41250	Glycine--tRNA ligase
10515	dirMS_041712_NAR_60mM_minus.13183.13183.3	3	9.89	0	5.10E+05		(K)GIHPTIIS	(K)G I H\P T I|I/S/E S F/Q/K(A)		133.38	486.2642	1456.78	-0.0014	-1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
10516	dirMS_041712_NAR_60mM_minus.17895.17895.3	3	9.89	1	3.70E+05		(K)NLRDID	(K)N L R\D I D\E|V|S/S L/L/R(T)		160.93	510.6099	1529.828	-0.013	-8.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
10517	dirMS_041712_NAR_60mM_minus.6416.6416.3	3	9.89	0	7.28E+04		(R)IVNTQE	(R)I/V|N T/Q/E Q/L N H R(W)		94.57	451.2405	1351.708	-0.0007	-0.5	6.75	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
10518	dirMS_041712_NAR_120mM_plus.10701.10701.3	3	9.89	0	8.92E+05		(R)YYDSRP	(R)Y/Y/D/S R/P G G Y G Y G Y G R(S)		108.68	577.5892	1730.756	-0.0027	-1.6	8.38	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
10519	dirMS_041712_NAR_30mM_plus2.6260.6260.2	2	9.89	0	3.31E+05	M369m	(R)FGSGM	(R)F/G|S/G M/N m/G/R(I)	m:Oxidized methionine	87.53	486.7048	956.408	15.9946	-0.3	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
10520	dirMS_041712_NAR_40mM_plus2.15122.15122.3	3	9.89	0	2.97E+05		(K)GVTIIGP	(K)G V/T\I/I/G/P A T V G G I K/P G C F K(I)	C:Carbamidomethylation	156.1	624.683	1872.041	-0.0067	-3.6	10	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
10521	dirMS_041712_NAR_40mM_plus2.9768.9768.3	3	9.89	0	2.45E+05		(R)AAEDPV	(R)A A|E/D/P/V A A A P R P L P A G G R(L)		121.1	572.6438	1715.919	-0.0019	-1.1	6.12	73966.7	10.21	HUMAN	B3KWK6	Alpha-L-iduronidase
10522	dirMS_041712_NAR_50mM_plus2.19570.19570.3	3	9.89	1	5.69E+05		(R)VLEALLP	(R)V L|E/A/L L/P L K G L E/E R(V)		172	527.318	1579.942	-0.0023	-1.5	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
10523	dirMS_041712_NAR_50mM_plus2.20474.20474.3	3	9.89	1	2.66E+05		(R)GGPNIIT	(R)G G/P N I|I/T L/A D I V K D/P V S R(T)		176.7	622.3526	1865.049	-0.0058	-3.1	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
10524	dirMS_041712_NAR_50mM_plus2.21806.21806.3	3	9.89	1	2.08E+05		(R)KVPELM	(R)K\V P E L\M/E\M|F L/P A/T K(N)		185.52	545.2925	1633.869	-0.0063	-3.8	6.14	95051	6.63	HUMAN	B3KXW5	AP-1 complex subunit gamma-1
10525	dirMS_041712_NAR_60mM_plus.10674.10674.3	3	9.89	1	8.35E+05		(R)LKAEAEI	(R)L K A E A E\L|L/Q\Q Q/K(E)		112.82	466.9362	1398.795	-0.0011	-0.8	6.14	533778	5.74	HUMAN	Q15149	Plectin
10526	dirMS_041712_NAR_60mM_plus.15758.15758.3	3	9.89	1	2.94E+04		(R)VEVERD	(R)V/E|V E R D N\L A/E/D I M R(L)		139.05	563.613	1688.827	-0.0028	-1.6	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
10527	dirMS_041712_NAR_30mM_minus2.17069.17069.2	2	9.88	0	1.94E+05		(R)IYNVIGT	(R)I/Y|N/V\I/G/T L R(G)		146.9	524.8092	1048.615	-0.0038	-3.7	8.75	84557.3	6.5	HUMAN	Q04609	Glutamate carboxypeptidase 2
10528	dirMS_041712_NAR_50mM_minus2.14735.14735.3	3	9.88	0	4.12E+05		(K)QLEAID	(K)Q L/E/A/I D Q L H L E Y A K(R)		152.43	557.6327	1670.875	0.0087	5.2	4.65	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
10529	dirMS_041712_NAR_120mM_plus.16310.16310.4	4	9.88	2	2.49E+06		(K)KQGGLG	(K)K\Q G G L\G|P M N I/P/L/V S D/P K R(T)		139.62	477.5186	1907.053	-0.0006	-0.3	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
10530	dirMS_041712_NAR_120mM_plus.7960.7960.2	2	9.88	0	4.64E+05		(K)STTTGHI	(K)S T/T T G H L\I Y|K(C)		95.25	560.8014	1120.6	-0.0042	-3.7	8.34	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
10531	dirMS_041712_NAR_20mM_plus.16982.16982.2	2	9.88	0	2.55E+05		(K)VQIAVA	(K)V Q/I A\V|A/N/A Q E L/L\Q R(M)		188.03	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
10532	dirMS_041712_NAR_20mM_plus.18593.18593.3	3	9.88	0	1.88E+04		(R)APVPAS	(R)A P V\P A S E\L\L|A/S/G V/L S R(A)		199.92	522.9655	1566.885	-0.003	-1.9	6.05	533778	5.74	HUMAN	Q15149	Plectin
10533	dirMS_041712_NAR_20mM_plus.8466.8466.2	2	9.88	0	9.13E+04		(K)VVTDTD	(K)V V|T/D|T/D E T E L A R(Q)		128.17	674.8318	1348.659	-0.0027	-2	3.91	36396.8	5.02	HUMAN	P05198	Eukaryotic translation initiation factor 2 subunit 1
10534	dirMS_041712_NAR_30mM_plus2.12506.12797.2	2	9.88	0	3.99E+05		(K)LVPVLS	(K)L V|P/V/L/S\A K(A)		119.25	413.7745	826.54	0.0021	2.5	8.75	37710.6	6.36	HUMAN	P37837	Transaldolase
10535	dirMS_041712_NAR_30mM_plus2.18249.18249.2	2	9.88	0	2.50E+05		(K)TTFEDLI	(K)T T/F|E/D L/I Q R(C)		148.95	561.7934	1122.579	0.0006	0.5	4.37	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
10536	dirMS_041712_NAR_30mM_plus2.18421.18421.2	2	9.88	0	2.36E+05		(K)GNFNYII	(K)G N F|N/Y/I/E F T R(I)		150.27	630.8035	1260.601	-0.001	-0.8	6	20513.6	4.62	HUMAN	J3QRS3	Myosin regulatory light chain 12A
10537	dirMS_041712_NAR_30mM_plus2.18655.18655.2	2	9.88	0	3.19E+05		(R)FVNVVP	(R)F V|N|V|V P/T F G K(K)		151.33	554.3087	1107.62	-0.0096	-8.7	8.75	10904.6	11.56	HUMAN	E9PR30	40S ribosomal protein S30
10538	dirMS_041712_NAR_30mM_plus2.7127.7127.2	2	9.88	1	2.66E+05		(R)AAEAAA	(R)A A E|A A A S S\R T/P/G R(E)		91.63	622.8143	1244.634	-0.0129	-10.3	9.64	24482	9.78	HUMAN	C9J8C4	Cordon-bleu protein-like 1 (Fragment)
10539	dirMS_041712_NAR_30mM_plus2.8552.8552.2	2	9.88	0	7.57E+05		(R)FSELTAE	(R)F/S/E/L/T A/E/K(L)		99.25	462.7408	924.467	0.007	7.6	4.53	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
10540	dirMS_041712_NAR_30mM_plus2.9081.9081.2	2	9.88	0	4.87E+05		(R)LATNTS	(R)L A/T N/T/S A P D/L/K(N)		100.75	565.801	1130.605	-0.0105	-9.2	5.84	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
10541	dirMS_041712_NAR_40mM_plus2.15454.15454.3	3	9.88	1	3.14E+04	S54s	(R)LLIYGAS	(R)L L|I/Y\G A S s R A/T G I P D R(F)	s:N-acetylglucosamine (S)	157.58	631.6874	1689.928	203.1194	21.1	8.75	11889	9.11	HUMAN	P01620	Ig kappa chain V-III region SIE
10542	dirMS_041712_NAR_50mM_plus2.6228.6228.3	3	9.88	1	1.09E+05		(R)VVSSIEC	(R)V/V|S S/I E Q K T E G/A E/K(K)		96.73	502.2651	1504.785	-0.0046	-3	4.79	8491.4	6.28	HUMAN	E5RIR4	14-3-3 protein zeta/delta (Fragment)
10543	dirMS_041712_NAR_60mM_plus.12231.12231.3	3	9.88	1	8.16E+05		(K)NQLTSN	(K)N Q|L|T/S N/P E N T V F D A K/R(L)		121.12	611.9737	1833.909	-0.0024	-1.3	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
10544	dirMS_041712_NAR_60mM_plus.5777.5777.3	3	9.88	1	8.96E+04		(R)NTAELQ	(R)N/T\A E L Q/P/E S G K R(K)		88.4	443.8995	1329.676	0.0082	6.2	6.14	59955.3	4.28	HUMAN	O15355	Protein phosphatase 1G
10545	dirMS_041712_NAR_60mM_plus.9224.9352.3	3	9.88	0	4.66E+05	M89m	(K)VYNYNH	(K)V/Y|N/Y N H/L/m/P T R(Y)	m:Oxidized methionine	106.8	475.2309	1407.684	15.9944	-0.4	8.57	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
10546	dirMS_041712_NAR_120mM_minus.16731.16731.3	3	9.87	0	3.68E+05		(K)HLEINPD	(K)H L|E/I/N/P\D\H/S\I/I E T L R(Q)		146.42	596.3176	1786.945	-0.0064	-3.6	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
10547	dirMS_041712_NAR_120mM_minus.7737.7863.2	2	9.87	1	1.08E+06		(R)AQYDEL	(R)A/Q|Y/D|E/L A R K(N)		96.87	547.2876	1093.564	0.0043	3.9	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10548	dirMS_041712_NAR_30mM_minus2.17458.17458.2	2	9.87	0	2.37E+05		(R)NGGQIL	(R)N G\G/Q I|L I/A D/L R(G)		149.13	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
10549	dirMS_041712_NAR_50mM_minus2.7146.7146.3	3	9.87	1	3.00E+04		(R)GIEPTG	(R)G I|E/P/T G N M V K Q P A/K(F)		107.48	490.5972	1469.778	-0.001	-0.7	8.59	258215.9	5.48	HUMAN	E7EN95	Filamin-B
10550	dirMS_041712_NAR_60mM_minus.8065.8065.3	3	9.87	1	2.69E+05		(K)LNVTEQ	(K)L/N|V/T/E Q/E/K I D K(L)		105.47	439.57	1316.706	-0.0102	-7.7	4.68	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
10551	dirMS_041712_NAR_60mM_minus.9297.9297.3	3	9.87	1	2.37E+05		(R)QDSAA	(R)Q/D|S A/A/V/G|F D Y K E K(L)		111.87	486.5639	1457.691	-0.0136	-9.3	4.56	61756.2	5.24	HUMAN	Q14247	Src substrate cortactin
10552	dirMS_041712_NAR_120mM_plus.14240.14240.4	4	9.87	1	7.06E+05		(R)ETNLDSI	(R)E T N L D S L/P L/V/D T H S K/R(T)		127.78	456.9906	1824.945	-0.0044	-2.4	5.38	53707.8	5.06	HUMAN	P08670	Vimentin
10553	dirMS_041712_NAR_20mM_plus.18878.18878.2	2	9.87	0	2.38E+05		(K)IYVDDGI	(K)I Y|V/D D G\L I/S L Q V K(Q)		200.77	731.9068	1462.815	-0.0088	-6	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
10554	dirMS_041712_NAR_20mM_plus.7352.7352.3	3	9.87	0	2.14E+05		(K)TGQAPG	(K)T G Q A\P G Y/S/Y/T/A/A N K(N)		119.53	476.8963	1428.675	-0.001	-0.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
10555	dirMS_041712_NAR_30mM_plus2.16741.16741.2	2	9.87	0	1.25E+05		(R)MGPAM	(R)M G/P A|M|G/P A\L/G\A G/I E R(M)		140.25	714.3615	1427.713	0.0024	1.7	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
10556	dirMS_041712_NAR_30mM_plus2.17045.17137.2	2	9.87	0	3.29E+05		(K)SQLLSYII	(K)S Q|L|L/S/Y I D/R(L)		142.57	547.7952	1094.584	-0.0009	-0.8	5.55	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
10557	dirMS_041712_NAR_40mM_plus2.19414.19414.3	3	9.87	1	1.46E+05		(R)TEGLSVL	(R)T/E|G L/S V L/S Q/A M A V I/K E K(I)		181.77	602.0005	1803.988	-0.0015	-0.8	5.81	31604.9	6.88	HUMAN	G3V4T5	Eukaryotic translation initiation factor 2 subunit 1 (Fragment)
10558	dirMS_041712_NAR_50mM_plus2.16030.16030.3	3	9.87	0	3.20E+05		(R)VSPHAS	(R)V S P H A S L Q E\L|A/P/I I C S K(C)	C:Carbamidomethylation	152.33	617.3317	1849.984	-0.0035	-1.9	6.72	24482	9.78	HUMAN	C9J8C4	Cordon-bleu protein-like 1 (Fragment)
10559	dirMS_041712_NAR_120mM_minus.20204.20277.3	3	9.86	0	3.92E+05		(K)VHLVGII	(K)V H\L\V G\I|D|I/F T/G K(K)		166.45	433.5866	1298.747	-0.0015	-1.1	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
10560	dirMS_041712_NAR_20mM_minus.13102.13102.2	2	9.86	0	8.53E+03		(K)TITLEVEI	(K)T I T/L E|V/E|P S D T I E N V K(A)		182.07	894.4654	1787.927	-0.0038	-2.1	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
10561	dirMS_041712_NAR_40mM_minus2.8130.8130.3	3	9.86	1	3.18E+05		(R)DGKLVS	(R)D G K\L V\S/E|S/S D V L/P K(-)		128.2	491.9311	1473.78	-0.0008	-0.5	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
10562	dirMS_041712_NAR_50mM_minus2.11574.11703.3	3	9.86	0	2.84E+05	M291m	(K)TGEEIFG	(K)T|G|E/E|I/F G/T I G m R P N A K(N)	m:Oxidized methionine	134.17	579.6239	1720.869	15.9885	-3.7	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
10563	dirMS_041712_NAR_50mM_minus2.13396.13396.3	3	9.86	0	1.85E+04		(R)LQAYHT	(R)L Q/A Y H\T Q T T/P/L/I E/Y Y R(K)		144.52	666.3408	1997.013	-0.0049	-2.4	6.75	21283.1	6.45	HUMAN	F8VY04	Adenylate kinase 2, mitochondrial
10564	dirMS_041712_NAR_60mM_minus.11344.11344.3	3	9.86	1	3.12E+04		(R)NVDSN	(R)N V/D S N N K E/L/S/I/A I/R(G)		123.32	524.9451	1572.834	-0.0133	-8.4	6.07	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
10565	dirMS_041712_NAR_60mM_minus.18224.18224.3	3	9.86	1	1.08E+05		(K)TVTAMD	(K)T V|T A M/D V/V/Y A L K R(Q)		162.23	489.6057	1466.804	-0.001	-0.7	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
10566	dirMS_041712_NAR_120mM_plus.8115.8115.3	3	9.86	0	2.72E+05		(K)HEQNID	(K)H E\Q N\I/D|C/G G G Y V/K(L)	C:Carbamidomethylation	96.22	492.8886	1476.654	-0.0024	-1.6	5.32	48311.8	4.29	HUMAN	P27797	Calreticulin
10567	dirMS_041712_NAR_20mM_plus.11597.11597.2	2	9.86	0	2.12E+04		(R)TIAQDY	(R)T/I|A Q/D/Y G V L K(A)		152.38	554.3056	1107.604	-0.0005	-0.5	5.5	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
10568	dirMS_041712_NAR_20mM_plus.17945.17945.2	2	9.86	0	9.12E+04		(K)SLESLDT	(K)S L|E/S L/D/T/S L/F A K(N)		195.25	655.8428	1310.684	-0.0055	-4.2	4.37	52796.2	5.19	HUMAN	E7EUT8	Splicing factor 3A subunit 3

10569	dirMS_041712_NAR_30mM_plus2.10385.10385.2	2	9.86	0	2.67E+05		(K)LVIEEAE	(K)L V|I/E/E/A E/R(S)		107.93	479.7648	958.52	0.0019	2	4.25	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
10570	dirMS_041712_NAR_30mM_plus2.10433.10538.2	2	9.86	0	1.84E+06		(K)TEWLDG	(K)T/E|W/L/D/G K(H)		108.43	424.7147	848.415	0.0073	8.6	4.37	18393.6	9.55	HUMAN	A2BFH1	Peptidyl-prolyl cis-trans isomerase A-like 4G
10571	dirMS_041712_NAR_30mM_plus2.11395.11395.2	2	9.86	0	9.73E+04		(R)VEFMD	(R)V E|F/M|D/D/T S R(S)		112.67	550.2401	1099.473	0.0005	0.4	4.03	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
10572	dirMS_041712_NAR_30mM_plus2.11823.11823.2	2	9.86	0	7.46E+05		(R)SSTDSLP	(R)S S/T/D S L/P G P I S\R(Q)		115.2	608.8101	1216.617	-0.0039	-3.2	5.55	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
10573	dirMS_041712_NAR_30mM_plus2.17228.17228.2	2	9.86	0	2.54E+05		(R)ISWYLR	(R)I/S/W/Y/L/R(D)		143.02	419.2286	837.462	-0.0118	-14.1	8.75	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
10574	dirMS_041712_NAR_30mM_plus2.18401.18401.2	2	9.86	0	3.72E+05		(R)SQVEEEI	(R)S Q|V|E/E/E L/F S V R(V)		149.55	661.8302	1322.659	-0.0055	-4.2	4.25	533778	5.74	HUMAN	Q15149	Plectin
10575	dirMS_041712_NAR_50mM_plus2.10617.10617.3	3	9.86	1	2.36E+06		(R)MQKEIT	(R)M Q|K E I\T A|L/A/P/S T M K(I)		123.98	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
10576	dirMS_041712_NAR_50mM_plus2.20693.20693.3	3	9.86	0	1.04E+05		(R)LQQELD	(R)L Q/Q/E/L/D D L L/V/D L D H Q R(Q)		177.52	650.6675	1949.993	-0.0047	-2.4	4.03	227783.5	5.5	HUMAN	P35579	Myosin-9
10577	dirMS_041712_NAR_50mM_plus2.6227.6227.3	3	9.86	1	1.09E+05		(R)VVSSIEC	(R)V/V|S S I E/Q K T E/G A E K(K)		96.73	502.2651	1504.785	-0.0046	-3	4.79	8491.4	6.28	HUMAN	E5RIR4	14-3-3 protein zeta/delta (Fragment)
10578	dirMS_041712_NAR_50mM_plus2.9054.9054.3	3	9.86	1	4.14E+05		(K)TAVCDIF	(K)T/A\V/C D I/P/P R G L K(M)	C:Carbamidomethylation	115.08	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
10579	dirMS_041712_NAR_60mM_plus.10455.10455.2	2	9.86	1	4.41E+06		(R)LQAEIEC	(R)L Q|A\E\I E/G\L K/G Q R(A)		112.33	671.3774	1341.748	-0.001	-0.7	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
10580	dirMS_041712_NAR_60mM_plus.7426.7426.3	3	9.86	1	5.48E+04		(K)QLELRQ	(K)Q/L/E/L/R Q E/E/E/R(R)		96.97	443.8995	1329.676	0.0082	6.2	4.49	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
10581	dirMS_041712_NAR_120mM_minus.5728.5728.3	3	9.85	1	7.04E+04		(R)REGGDC	(R)R E G G\D\G\E\E\Q D/V/G/D A G R(L)		84.48	549.5713	1646.7	-0.0007	-0.5	4.02	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
10582	dirMS_041712_NAR_120mM_minus.8583.8603.3	3	9.85	1	1.64E+05		(R)LAEDEAI	(R)L/A/E/D/E/A F Q R R(R)		101.83	412.21	1234.618	-0.002	-1.6	4.68	533778	5.74	HUMAN	Q15149	Plectin
10583	dirMS_041712_NAR_30mM_minus2.16252.16252.2	2	9.85	0	8.38E+03		(R)SNFGYN	(R)S N|F/G\Y/N I P L K(H)		141.98	576.8043	1152.605	-0.0035	-3	8.31	20458.8	4.99	HUMAN	G3V4X5	Proteasome subunit alpha type-3
10584	dirMS_041712_NAR_30mM_minus2.5960.5960.2	2	9.85	0	2.08E+05		(K)TSEVNC	(K)T S/E/V/N C Y R(C)	C:Carbamidomethylation	86.8	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
10585	dirMS_041712_NAR_40mM_minus2.11973.11973.3	3	9.85	1	4.82E+04		(R)SLGEIPI	(R)S L|G E/I/P/I V E S E I K K(E)		153.6	514.6302	1541.879	-0.0025	-1.6	4.78	108281.4	5.72	HUMAN	P53618	Coatomer subunit beta
10586	dirMS_041712_NAR_50mM_minus2.7232.7232.3	3	9.85	0	1.66E+05		(R)ETPHSP	(R)E T P H/S P G V/E/D/A/P I/A K(V)		107.98	516.5936	1547.77	-0.0038	-2.4	4.65	67446.5	5.63	HUMAN	F8VQE1	LIM domain and actin-binding protein 1
10587	dirMS_041712_NAR_50mM_minus2.7874.7874.3	3	9.85	0	4.58E+04		(R)QLSQAG	(R)Q L/S Q/A/G/S F S D G T/H/G G L R(Y)		111.92	573.2875	1717.825	0.0227	13.2	6.74	266161	5.68	HUMAN	E9PPU0	Epiplakin
10588	dirMS_041712_NAR_60mM_minus.15707.15707.3	3	9.85	1	5.22E+05	M81m	(K)EVNKFQ	(K)E V/N/K F Q m/A/Y/S N L L R(A)	m:Oxidized methionine	146.85	576.9619	1712.879	15.9923	-1.5	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
10589	dirMS_041712_NAR_60mM_minus.8227.8227.3	3	9.85	1	3.12E+05		(K)TVDDVII	(K)T V/D D/V I K/E Q/N R(E)		105.67	439.5636	1316.68	-0.0042	-3.2	4.55	20828.6	6.05	HUMAN	C9J0A7	Charged multivesicular body protein 2b
10590	dirMS_041712_NAR_120mM_plus.10590.10590.3	3	9.85	1	3.83E+05		(K)KGENYV	(K)K G E N Y\V|Y|I/N E A T/R(H)		108.4	519.5943	1556.77	-0.002	-1.3	6.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
10591	dirMS_041712_NAR_120mM_plus.4380.4380.3	3	9.85	1	2.54E+05		(R)AAEEED	(R)A A|E|E/E D E A D P K R(Q)		72.18	453.8721	1359.602	-0.0005	-0.4	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
10592	dirMS_041712_NAR_30mM_plus2.19659.19727.2	2	9.85	0	2.84E+05		(R)IYGISFPI	(R)I/Y|G\I|S F/P D|P K(M)		156.92	568.8061	1136.599	0.0063	5.5	5.83	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
10593	dirMS_041712_NAR_50mM_plus2.11359.11359.3	3	9.85	1	2.98E+05		(R)ETGVDL	(R)E T|G V/D/L/T K D N M/A L Q R(V)		127.18	564.2856	1690.843	-0.0006	-0.4	4.56	73964.5	5.87	HUMAN	P38646	Stress-70 protein, mitochondrial
10594	dirMS_041712_NAR_50mM_plus2.13565.13565.3	3	9.85	0	2.25E+06		(K)AGVVGF	(K)A G V|V/G/P E L/H E Q L L S A E K(A)		138.68	592.986	1776.949	-0.0056	-3.1	4.75	533778	5.74	HUMAN	Q15149	Plectin
10595	dirMS_041712_NAR_60mM_plus.10658.10658.3	3	9.85	1	3.21E+04		(R)LRQLAEI	(R)L R Q L A/E\E D|L/A/Q Q R(A)		112.7	523.9486	1569.834	-0.0031	-2	4.68	533778	5.74	HUMAN	Q15149	Plectin
10596	dirMS_041712_NAR_60mM_plus.20464.20464.3	3	9.85	1	7.78E+04		(R)LFVGNLI	(R)L F|V|G N/L/P A D I T E D E F K R(L)		167.3	655.3407	1964.012	-0.0048	-2.5	4.32	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
10597	dirMS_041712_NAR_60mM_plus.9453.9453.2	2	9.85	0	1.98E+06		(R)IGAEVYI	(R)I/G\A|E/V/Y H N\L K(N)		107.55	572.3143	1143.616	0.0056	4.9	6.75	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
10598	dirMS_041712_NAR_120mM_minus.5402.5402.3	3	9.84	1	2.17E+05		(R)KQQTLE	(R)K\Q Q T\L/E/A E/E A K(R)		82.88	425.5623	1274.659	0.0137	10.7	4.79	76925.9	4.46	HUMAN	A8MV58	Drebrin
10599	dirMS_041712_NAR_120mM_minus.8352.8352.3	3	9.84	1	4.70E+05		(R)ASRDEIF	(R)A S R D\E|I|F/A Q/S K(E)		99.97	417.8786	1251.633	-0.0115	-9.2	6.12	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
10600	dirMS_041712_NAR_20mM_minus.11509.11509.2	2	9.84	0	1.84E+05		(R)GDLGIEI	(R)G D/L/G\I E I/P A E K(V)		163.73	571.3078	1141.61	-0.0016	-1.4	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
10601	dirMS_041712_NAR_30mM_minus2.10204.10341.2	2	9.84	0	1.14E+06		(R)ANIQAV	(R)A N|I|Q/A/V|S L K(I)		110	472.2815	943.557	-0.0014	-1.5	8.8	25103.6	5.88	HUMAN	O43633	Charged multivesicular body protein 2a
10602	dirMS_041712_NAR_30mM_minus2.16882.16882.2	2	9.84	0	1.43E+05		(R)IMNTFS	(R)I M/N T/F/S/V/V/P S P K(V)		145.78	660.3534	1319.703	-0.0033	-2.5	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
10603	dirMS_041712_NAR_50mM_minus2.16749.16749.3	3	9.84	0	1.11E+04		(K)NVEQSS	(K)N V/E/Q|S S D L Q D/Q L N H L L K(-)		163.27	661.0005	1980.998	-0.0116	-5.8	4.54	11621	6.27	HUMAN	Q96B45	UPF0693 protein C10orf32
10604	dirMS_041712_NAR_50mM_minus2.8923.8923.3	3	9.84	1	1.31E+05	M227m	(R)mQKEIT	(R)m Q K E I\T/A\L/A/P S T M K(I)	m:Oxidized methionine	119.48	522.2727	1548.812	15.9911	-2.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
10605	dirMS_041712_NAR_60mM_minus.11696.11696.3	3	9.84	0	2.25E+05		(K)ADDGRF	(K)A/D/D G R P F|P/Q V I K(S)		124.53	448.2371	1342.711	-0.0146	-10.9	6	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
10606	dirMS_041712_NAR_60mM_minus.17805.17805.3	3	9.84	1	2.37E+05	M148m	(R)LDLAGR	(R)L/D|L A/G R D L T D/Y L m K(I)	m:Oxidized methionine	159.5	547.2829	1623.841	15.9931	-1.1	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
10607	dirMS_041712_NAR_20mM_plus.17559.17559.3	3	9.84	0	1.38E+04	M199m	(K)SmVPVC	(K)S m V/P V Q|V|Q/L D V/P V V K(V)	m:Oxidized methionine	192.58	551.9759	1637.93	15.9837	-6.8	5.55	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
10608	dirMS_041712_NAR_20mM_plus.18163.18163.2	2	9.84	0	7.51E+04		(R)LSVLGAI	(R)L S V/L|G\A\I/T\S\V/Q Q R(L)		196.38	686.3953	1371.795	-0.0121	-8.8	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
10609	dirMS_041712_NAR_20mM_plus.9376.9376.3	3	9.84	0	1.27E+05		(K)SVTNED	(K)S V T N E D V|T/Q/E/E L/G G A K(T)		136	559.6039	1676.797	-0.0002	-0.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
10610	dirMS_041712_NAR_30mM_plus2.18356.18356.2	2	9.84	0	3.77E+05		(R)SQVEEEI	(R)S Q|V/E/E/E L F/S V/R(V)		149.47	661.8302	1322.659	-0.0055	-4.2	4.25	533778	5.74	HUMAN	Q15149	Plectin
10611	dirMS_041712_NAR_30mM_plus2.20807.20807.2	2	9.84	0	6.44E+04		(R)YLTVAA	(R)Y L|T|V/A/A V/F R(G)		162.78	520.2996	1039.593	-0.0016	-1.5	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
10612	dirMS_041712_NAR_30mM_plus2.22145.22145.2	2	9.84	0	2.34E+05		(R)VGNLGL	(R)V G/N L/G L/A T/S/F F/N E/R(N)		172.53	762.8926	1524.781	-0.0026	-1.7	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
10613	dirMS_041712_NAR_50mM_plus2.15135.15135.3	3	9.84	0	7.04E+05		(R)QIFHPEC	(R)Q I|F\H/P E Q L I/T/G K(E)		147.5	470.9293	1410.774	-0.0006	-0.4	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
10614	dirMS_041712_NAR_50mM_plus2.17171.17171.3	3	9.84	1	3.30E+05		(R)VSFELFA	(R)V/S/F E\L F A/D K V/P K(T)		158.78	460.5906	1379.757	0.0003	0.2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
10615	dirMS_041712_NAR_60mM_plus.7250.7250.2	2	9.84	1	1.84E+05		(K)EMDEEC	(K)E M/D/E/E D/K A/F/K(Q)		96	621.2724	1241.535	0.0021	1.7	4.18	7066.2	10	HUMAN	Q9Y2S6	Translation machinery-associated protein 7
10616	dirMS_041712_NAR_20mM_minus.11755.11755.2	2	9.83	0	2.96E+05		(R)GALQNI	(R)G A L Q|N/I|I P A S/T G A A K(A)		165.4	706.3976	1411.79	-0.0024	-1.7	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
10617	dirMS_041712_NAR_20mM_minus.14422.14422.2	2	9.83	0	2.29E+05		(K)DAGVIA	(K)D A G\V|I/A/G\L N V L R(I)		198.17	599.3503	1197.695	-0.0017	-1.4	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
10618	dirMS_041712_NAR_40mM_minus2.14293.14293.3	3	9.83	1	1.61E+05		(K)TGISDVF	(K)T G/I|S D V\F\A K N D\L/A|V/V D/V R(I)		168.48	640.3454	1919.023	-0.0016	-0.8	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
10619	dirMS_041712_NAR_60mM_minus.4652.4652.3	3	9.83	0	6.11E+05	M46m M4	(R)HQGVm	(R)H Q G V\m|V/G m G Q K(D)	m:Oxidized methionine	77.87	401.8579	1171.571	31.9881	-1.4	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
10620	dirMS_041712_NAR_20mM_plus.11618.11618.3	3	9.83	0	9.97E+04		(R)AQAALA	(R)A Q\A\A/L\A V N/I S A A/R(G)		153.2	419.2429	1255.712	0.0024	1.9	9.79	58479.6	6.23	HUMAN	P40227	T-complex protein 1 subunit zeta
10621	dirMS_041712_NAR_30mM_plus2.19684.19684.2	2	9.83	0	2.62E+05		(K)LFLVQLC	(K)L/F|L V/Q L Q/E K(A)		157.23	559.3295	1117.662	-0.0098	-8.8	6	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
10622	dirMS_041712_NAR_30mM_plus2.20226.20226.2	2	9.83	0	3.58E+04		(R)TLMNLG	(R)T L|M/N/L|G G L/A/V/A R(D)		159.42	608.3434	1215.688	-0.0083	-6.8	9.41	22562.2	8.8	HUMAN	P37802	Transgelin-2
10623	dirMS_041712_NAR_30mM_plus2.22396.22396.2	2	9.83	0	2.87E+05		(K)CMPTFC	(K)C M|P/T/F Q/F/F K(K)	C:Carbamidomethylation	172.83	603.2777	1205.548	-0.0001	-0.1	8.75	9680	5.77	HUMAN	B1ALW1	Thioredoxin
10624	dirMS_041712_NAR_30mM_plus2.6830.6830.2	2	9.83	0	1.29E+05		(K)AVELAAI	(K)A V|E/L|A A/N T K(G)		90.6	458.7641	916.51	0.0111	12.1	6.05	63448.4	7.29	HUMAN	B4E022	Transketolase
10625	dirMS_041712_NAR_30mM_plus2.7112.7242.2	2	9.83	0	1.72E+06		(R)AQVIYTI	(R)A Q|V/I/Y/T/R(N)		92.9	425.7397	850.478	-0.006	-7.1	8.79	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
10626	dirMS_041712_NAR_30mM_plus2.7944.7944.2	2	9.83	0	2.20E+05		(K)IAVAAQ	(K)I A|V/A/A|Q N/C Y K(V)	C:Carbamidomethylation	96.05	569.2905	1137.572	0.0016	1.4	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
10627	dirMS_041712_NAR_50mM_plus2.17408.17408.3	3	9.83	1	9.28E+05		(K)DNNGVI	(K)D N/N G V I/G/L/L E/P M K K(S)		159.22	509.9448	1527.82	-0.0001	-0.1	6.07	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
10628	dirMS_041712_NAR_50mM_plus2.21428.21428.3	3	9.83	1	4.21E+05	M145m	(R)GVmLA	(R)G V/m|L/A\V D A V/I A E L K K(Q)	m:Oxidized methionine	182.52	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
10629	dirMS_041712_NAR_50mM_plus2.22142.22142.3	3	9.83	1	8.18E+05		(R)ELAILLG	(R)E L/A I/L/L G/M L D/P A E/K D E K(G)		190.47	629.004	1884.999	-0.0012	-0.7	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
10630	dirMS_041712_NAR_50mM_plus2.6155.6155.3	3	9.83	0	6.16E+04		(K)VDCTAH	(K)V/D/C T/A H S D V/C S/A Q G\V R(G)	C:Carbamidomethylation	96.33	587.9271	1761.764	0.0025	1.4	5.21	41053.3	5.58	HUMAN	Q86UY0	TXNDC5 protein
10631	dirMS_041712_NAR_50mM_plus2.7545.7545.3	3	9.83	1	2.58E+05		(K)SEETLDE	(K)S E|E/T/L D E G/P P K Y/T K(S)		105.8	531.9261	1593.764	-0.0005	-0.3	4.41	25233.4	9.34	HUMAN	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3
10632	dirMS_041712_NAR_50mM_plus2.7758.7758.3	3	9.83	1	9.26E+04		(R)FNEVAA	(R)F N/E|V|A A/Q Y/S E\D K A R(Q)		106.63	543.2611	1627.771	-0.0023	-1.4	4.68	14236.2	10.25	HUMAN	F5H1P5	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4
10633	dirMS_041712_NAR_50mM_plus2.8408.8408.3	3	9.83	0	5.15E+05		(R)LEPKPQI	(R)L E\P K P/Q/P/P/V/A E A T P R(S)		110.33	543.9631	1629.896	-0.0211	-13	6.14	14468.1	6.76	HUMAN	K7EJ51	Septin-9 (Fragment)
10634	dirMS_041712_NAR_50mM_plus2.8592.8592.3	3	9.83	1	7.86E+04		(K)VLADTKI	(K)V/L/A/D T K/E L V\S S K(V)		112.17	430.5844	1289.731	0.0075	5.8	6.04	18189.2	5.2	HUMAN	K7EL96	Perilipin-3 (Fragment)
10635	dirMS_041712_NAR_30mM_minus2.11840.11840.2	2	9.82	0	1.01E+05		(R)SGYLLPD	(R)S G Y|L|L/P D/T K(A)		116.68	497.265	993.525	-0.0024	-2.4	5.55	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
10636	dirMS_041712_NAR_30mM_minus2.14087.14087.2	2	9.82	0	1.79E+05		(R)VPELFAI	(R)V/P/E/L/F A N/R(G)		129.88	473.2631	945.515	0.0037	3.9	5.97	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
10637	dirMS_041712_NAR_40mM_minus2.13166.13166.3	3	9.82	1	9.20E+04		(K)VLDSGA	(K)V L|D S G A/P I\K I/P\V G P E T L G R(I)		160.87	640.3618	1919.096	-0.0252	-13.1	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
10638	dirMS_041712_NAR_40mM_minus2.13531.13531.3	3	9.82	1	3.72E+04		(K)VTLVVG	(K)V T/L/V/V/G A S Q/D I I/P Q L K K(K)		163.58	603.696	1809.084	-0.011	-6.1	8.56	25180.2	5.34	HUMAN	E7EMS6	Catechol O-methyltransferase (Fragment)
10639	dirMS_041712_NAR_40mM_minus2.14516.14516.3	3	9.82	1	1.99E+05		(R)GLLPGLI	(R)G L/L|P G/L L/P A P A D K L/T P K(G)		169.47	567.6813	1701.031	-0.0016	-0.9	8.59	153084.9	5.55	HUMAN	Q6P2E9	Enhancer of mRNA-decapping protein 4
10640	dirMS_041712_NAR_40mM_minus2.9467.9467.3	3	9.82	0	2.15E+05	M114m M	(R)AGKPVI	(R)A G K\P V I\C A T\Q/m/L E/S m I/K(K)	C:Carbamidomethylation m:Oxid	138.18	636.9906	1876.969	31.9879	-1	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
10641	dirMS_041712_NAR_60mM_minus.13550.13607.3	3	9.82	1	1.64E+05		(R)QRYEILT	(R)Q R Y E\I\L|T|P N S I/P K(G)		135.68	520.2902	1558.859	-0.0027	-1.7	8.59	227783.5	5.5	HUMAN	P35579	Myosin-9
10642	dirMS_041712_NAR_60mM_minus.5104.5104.3	3	9.82	1	6.90E+04		(K)EEASGS	(K)E\E/A/S/G/S S V T A E E A/K K(F)		83.3	508.2453	1522.723	-0.0018	-1.2	4.49	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
10643	dirMS_041712_NAR_60mM_minus.8509.8509.3	3	9.82	1	2.71E+04		(R)ELAEQEI	(R)E/L/A/E/Q/E L E K Q/R(Q)		107.28	458.2407	1372.707	0.0009	0.6	4.49	533778	5.74	HUMAN	Q15149	Plectin
10644	dirMS_041712_NAR_60mM_minus.9587.9608.3	3	9.82	1	3.49E+05	M64m	(K)LmDQLE	(K)L/m D Q|L/E/A L K K(Q)	m:Oxidized methionine	113.47	402.2246	1188.666	15.9936	-1.1	6.07	34163.9	5.87	HUMAN	Q9NP79	Vacuolar protein sorting-associated protein VTA1 homolog
10645	dirMS_041712_NAR_120mM_plus.10444.10630.3	3	9.82	1	8.75E+05		(K)IKGEHP	(K)I/K/G E H|P G L S I G D|V A/K(K)		108.22	507.6167	1520.843	-0.0076	-5	6.75	24408.7	5.92	HUMAN	B2RPK0	Putative high mobility group protein B1-like 1
10646	dirMS_041712_NAR_120mM_plus.4322.4333.3	3	9.82	1	3.08E+05		(K)AGADEE	(K)A/G|A|D/E E R A E/T A R(L)		71.55	425.869	1275.592	0.0001	0.1	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
10647	dirMS_041712_NAR_20mM_plus.8788.8788.2	2	9.82	0	1.87E+05	M224m	(K)GGKPEP	(K)G G K|P E/P P A m|P Q/P V|P T A(-)	m:Oxidized methionine	130.62	795.402	1573.804	15.9924	-1.6	6	25541.5	9.92	HUMAN	E9PL09	40S ribosomal protein S3
10648	dirMS_041712_NAR_30mM_plus2.12691.12691.2	2	9.82	0	3.52E+05		(R)ELAEDG	(R)E/L/A E/D G Y/S/G V/E/V/R(V)		120.57	712.3382	1423.67	-0.0008	-0.6	4	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
10649	dirMS_041712_NAR_30mM_plus2.6497.6497.2	2	9.82	0	1.82E+05		(K)TLNAGA	(K)T L|N/A/G A Y\S K(V)		88.78	462.7408	924.479	-0.0042	-4.5	8.26	30197.4	7.91	HUMAN	E9PMG2	Palmitoyl-protein thioesterase 1 (Fragment)
10650	dirMS_041712_NAR_40mM_plus2.13604.13604.3	3	9.82	1	1.31E+04		(K)DMELPT	(K)D M/E|L/P/T E K E V A L V/K(D)		146.4	534.6192	1601.845	-0.0024	-1.5	4.41	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
10651	dirMS_041712_NAR_50mM_plus2.12018.12018.3	3	9.82	1	4.97E+05	M327m	(R)VAGGPC	(R)V/A/G G/P Q m I/Q/L/S L\D G K R(L)	m:Oxidized methionine	131.13	562.6377	1669.905	15.9931	-1	8.72	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
10652	dirMS_041712_NAR_50mM_plus2.12052.12052.3	3	9.82	0	4.44E+05		(K)QADLYIS	(K)Q A D L Y I/S/E/G L/H P R(I)		131.48	500.2606	1498.765	0.0024	1.6	5.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
10653	dirMS_041712_NAR_50mM_plus2.14748.14748.3	3	9.82	0	9.00E+05	N483n	(K)LYSILQA	(K)L Y|S/I/L Q A n S/P T K(W)	n:N-acetylglucosamine (N)	145.9	513.2859	1334.731	203.1117	21	8.59	118702.2	8.83	HUMAN	E7ET15	U2 snRNP-associated SURP motif-containing protein
10654	dirMS_041712_NAR_50mM_plus2.17532.17602.3	3	9.82	1	5.87E+05		(R)LNRLPA	(R)L N R L\P A A\G\V|G/D\M/V/M A T V K(K)		160.33	614.9984	1842.993	-0.0122	-6.6	8.75	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
10655	dirMS_041712_NAR_50mM_plus2.7248.7248.3	3	9.82	1	1.07E+05	M628m	(K)AQALRD	(K)A Q|A L R D N S|T/M G Y m A A K(K)	m:Oxidized methionine	103.58	581.944	1727.82	15.9971	1.3	8.63	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
10656	dirMS_041712_NAR_60mM_plus.16451.16451.3	3	9.82	1	3.80E+04		(R)LGVFRA	(R)L/G/V F R A E S E\E/G/P/D V\L R(W)		142.8	591.9752	1773.913	-0.0019	-1.1	4.41	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
10657	dirMS_041712_NAR_120mM_minus.6561.6561.2	2	9.81	1	2.24E+05		(R)KLLEGEE	(R)K|L|L/E G E E S R(I)		89.75	530.7845	1060.563	-0.0016	-1.5	4.79	49709.6	5.19	HUMAN	B0YJC4	Vimentin
10658	dirMS_041712_NAR_20mM_minus.12131.12131.3	3	9.81	0	4.28E+05	M256m	(R)SLDmDS	(R)S L D/m D S I/I A E V K(A)	m:Oxidized methionine	170.6	446.227	1320.671	15.9949	0	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
10659	dirMS_041712_NAR_30mM_minus2.10668.10725.2	2	9.81	1	3.18E+05	M57m S58	(R)AESPms	(R)A E S|P m s|R Q E K(D)	m:Oxidized methionine s:N-a	111.98	691.3271	1162.552	219.0948	14.9	6.19	57837.4	9.85	HUMAN	Q6ZUT6	Uncharacterized protein C15orf52
10660	dirMS_041712_NAR_30mM_minus2.9322.9344.2	2	9.81	0	1.46E+05		(K)NDPSLPI	(K)N D|P/S/L/P E/P K(C)		105.2	498.7592	996.5	0.0115	11.5	4.37	20203.8	9.79	HUMAN	B4DG16	Asparagine--tRNA ligase, cytoplasmic
10661	dirMS_041712_NAR_50mM_minus2.10705.10705.3	3	9.81	0	2.72E+05		(K)VFEGNR	(K)V F|E/G N R P T N S I V/F T K(L)		129.18	570.3032	1708.902	-0.0066	-3.9	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
10662	dirMS_041712_NAR_50mM_minus2.13263.13263.3	3	9.81	0	1.69E+05		(K)MLDAEC	(K)M/L/D/A/E D I V G T A R P D E K(A)		143.52	587.2894	1759.853	0.0006	0.3	4.1	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
10663	dirMS_041712_NAR_50mM_minus2.17909.18001.3	3	9.81	1	1.42E+04		(K)GVPTGF	(K)G V|P/T/G F/I/L P\I\R D/I\R(A)		171.02	518.6444	1553.916	0.0024	1.6	9.6	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
10664	dirMS_041712_NAR_60mM_minus.13095.13095.3	3	9.81	1	9.10E+05		(K)DVDEAY	(K)D V/D/E A Y/M N K V/E\L E S R(L)		133.75	599.9463	1797.832	-0.008	-4.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
10665	dirMS_041712_NAR_120mM_plus.16886.16930.4	4	9.81	2	2.31E+06		(R)ALAEIAK	(R)A L\A E/I/A|K/A E L D D/T P M R G R(Q)		141.97	490.0116	1957.017	0.0074	3.8	4.78	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
10666	dirMS_041712_NAR_120mM_plus.20407.20407.3	3	9.81	0	2.97E+05		(R)INLWHL	(R)I/N\L/W/H/L/E I/T D R(S)		159.57	470.5889	1409.754	-0.0014	-1	5.32	52204.6	5.82	HUMAN	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
10667	dirMS_041712_NAR_20mM_plus.13612.13612.2	2	9.81	0	5.50E+04		(K)IFVGGLS	(K)I F\V|G G L/S/P D/T|P E\E K(I)		165.28	744.8731	1488.758	-0.0191	-12.8	4.14	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
10668	dirMS_041712_NAR_20mM_plus.18317.18317.2	2	9.81	0	3.78E+04		(R)GSYGDL	(R)G S Y G\D L\G G/P I I|T T Q V T I/P K(D)		197.32	959.0189	1917.033	-0.0022	-1.2	5.83	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
10669	dirMS_041712_NAR_30mM_plus2.16658.16658.2	2	9.81	0	3.87E+05		(R)LWDLTT	(R)L W|D|L|T T/G/T/T T R(R)		140.25	632.8304	1264.653	0.0003	0.3	5.84	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
10670	dirMS_041712_NAR_30mM_plus2.18891.19113.2	2	9.81	0	2.77E+05		(R)SWSLAT	(R)S W|S/L/A/T F/R(T)		152.77	484.2579	967.5	0.0089	9.2	9.47	533778	5.74	HUMAN	Q15149	Plectin
10671	dirMS_041712_NAR_30mM_plus2.20936.20936.2	2	9.81	0	1.52E+06		(R)LFDQAF	(R)L F|D/Q A/F G L/P R(L)		163.32	582.3164	1163.621	0.0048	4.1	5.84	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
10672	dirMS_041712_NAR_60mM_plus.10744.10744.4	4	9.81	1	8.96E+05	M61m N63	(K)mLnHEN	(K)m L n H E/N/V V/K F Y G H R(R)	m:Oxidized methionine n:N-	114.63	491.4815	1743.875	219.0294	-22.9	8.39	19759.3	5.26	HUMAN	E9PJI4	Serine/threonine-protein kinase Chk1 (Fragment)
10673	dirMS_041712_NAR_60mM_plus.17321.17321.3	3	9.81	0	2.04E+05		(K)THLPGF	(K)T\H\L\P G F\V/E Q A/E/A L K(A)		147.35	513.9442	1539.817	0.0015	1	5.37	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
10674	dirMS_041712_NAR_60mM_plus.18048.18048.3	3	9.81	1	6.16E+05		(K)EVNKFQ	(K)E\V N K F Q M/A|Y/S N L L R(A)		152.37	571.6293	1712.879	-0.0055	-3.2	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
10675	dirMS_041712_NAR_20mM_minus.8513.8513.2	2	9.8	0	7.57E+04		(R)IIYGGSV	(R)I I|Y/G/G S V/T G A T C K(E)	C:Carbamidomethylation	134.28	663.8403	1326.672	0.0011	0.8	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
10676	dirMS_041712_NAR_30mM_minus2.19036.19036.2	2	9.8	0	2.46E+05		(K)SYELPDC	(K)S Y\E\L|P D\G Q/V I/T I G N E R(F)		158.82	895.9492	1790.892	-0.0008	-0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
10677	dirMS_041712_NAR_40mM_minus2.7887.7887.3	3	9.8	0	1.26E+05		(K)QAAASA	(K)Q A/A\A/S A/T/Q T/I/A A A Q H A A S T P K(A)		126.05	665.6822	1995.025	0.0067	3.3	8.76	260187.7	6.1	HUMAN	Q5TCU6	Talin 1

10678	dirMS_041712_NAR_40mM_minus2.8159.8159.3	3	9.8	1	3.18E+05		(R)DGKLVS	(R)D G\K L V\S E/S S/D V/L/P K(-)		128.2	491.9311	1473.78	-0.0008	-0.5	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
10679	dirMS_041712_NAR_50mM_minus2.13325.13325.3	3	9.8	0	1.55E+05		(R)IVATKPL	(R)I V/A T K/P L/Y|V/A/L A Q R(K)		144.08	514.9821	1542.937	-0.0049	-3.2	9.99	65918.2	9.74	HUMAN	E7EQV3	Polyadenylate-binding protein 1
10680	dirMS_041712_NAR_50mM_minus2.15262.15262.3	3	9.8	1	4.43E+05		(K)GADFLV	(K)G A/D/F/L/V/T E V E N/G G S L G S K K(G)		155.53	636.662	1907.971	0.0005	0.3	4.68	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
10681	dirMS_041712_NAR_50mM_minus2.16452.16452.3	3	9.8	0	1.75E+05	M1m	(-)mKPLVVI	(-)m K\P L\V V/F|V|L/G/G/P G A G K(G)	m:Oxidized methionine	161.27	529.3077	1569.919	15.99	-3.1	10	22450.2	5.44	HUMAN	P30085	UMP-CMP kinase
10682	dirMS_041712_NAR_60mM_minus.12253.12253.3	3	9.8	1	4.75E+05		(R)INVYYN	(R)I/N|V/Y Y N E A T/G G K Y V P R(A)		127.67	615.3145	1843.934	-0.0048	-2.6	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
10683	dirMS_041712_NAR_60mM_minus.17766.17766.3	3	9.8	1	2.29E+05		(R)LGLSTLG	(R)L/G/L/S T/L/G E/L K Q N L S R(S)		159.48	543.6476	1628.933	-0.0047	-2.9	8.75	22294.4	5.26	HUMAN	O43399	Tumor protein D54
10684	dirMS_041712_NAR_60mM_minus.8319.8319.3	3	9.8	0	7.55E+04		(K)HTGPNS	(K)H T G P N\S\P/D/T/A|N/D/G F V R(L)		106.42	562.2608	1684.767	0.0005	0.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
10685	dirMS_041712_NAR_60mM_minus.9780.9780.3	3	9.8	1	2.83E+05		(R)TNAENE	(R)T N|A\E N E/F/V T I/K K(D)		114.3	465.2487	1393.732	-0.0006	-0.4	5.81	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
10686	dirMS_041712_NAR_120mM_plus.11543.11543.3	3	9.8	2	3.74E+05		(K)KGEKDIF	(K)K\G E\K D I|P G\L|T D T|T V P R(R)		113.53	576.3192	1726.933	0.0097	5.6	6.12	25082	11.29	HUMAN	A2A3R5	40S ribosomal protein S6
10687	dirMS_041712_NAR_120mM_plus.13849.13849.4	4	9.8	1	9.40E+05		(K)AGKFPSI	(K)A G K/F\P S/L/L/T/H N E N M V A K(V)		126.23	464.9972	1856.969	-0.0018	-0.9	8.64	25002	10.06	HUMAN	P62906	60S ribosomal protein L10a
10688	dirMS_041712_NAR_120mM_plus.14317.14317.3	3	9.8	1	2.66E+04	M313m	(R)RTVQSLI	(R)R T/V Q S\L|E|I/D/L/D/S m R(N)	m:Oxidized methionine	127.45	560.2841	1662.848	15.9898	-3	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10689	dirMS_041712_NAR_20mM_plus.14431.14431.2	2	9.8	0	5.25E+04		(K)ATLEVSS	(K)A T|L/E V/S/S I\I K(K)		170.97	530.8166	1060.625	0.0011	1	6.05	16689.5	9	HUMAN	B0QYV8	ADP-ribosylation factor GTPase activating protein 3 (Fragment)
10690	dirMS_041712_NAR_20mM_plus.17830.17830.2	2	9.8	0	8.88E+04		(K)VDFPQD	(K)V D/F/P Q\D Q\L T/A/L T/G R(I)		194.77	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
10691	dirMS_041712_NAR_20mM_plus.7887.7887.2	2	9.8	0	8.93E+04	M21m	(K)ATAVm	(K)A T A/V/m|P D/G/Q F K(D)	m:Oxidized methionine	124.48	590.7861	1164.572	15.9932	-1.5	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
10692	dirMS_041712_NAR_30mM_plus2.21358.21358.2	2	9.8	0	3.21E+05		(K)FDGILG	(K)F D\G I/L/G M/A/Y|P R(I)		167.32	620.3199	1239.619	0.0135	10.9	5.83	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
10693	dirMS_041712_NAR_40mM_plus2.17977.18000.3	3	9.8	0	1.24E+05		(R)GFGFITF	(R)G F/G\F/I/T|F T N P E H/A S/V/A M R(A)		172.02	661.3289	1981.959	0.0133	6.7	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
10694	dirMS_041712_NAR_50mM_plus2.11467.11467.3	3	9.8	0	1.38E+05		(R)ALQDLE	(R)A L/Q/D/L E N A A/S G D A A/V\H Q R(I)		127.67	622.6353	1865.91	-0.0187	-10	4.54	13862.5	4.75	HUMAN	K7EP82	Regulation of nuclear pre-mRNA domain-containing protein 1A (Fragment)
10695	dirMS_041712_NAR_50mM_plus2.5943.5943.3	3	9.8	0	1.85E+04		(R)VEAKPE	(R)V E/A K/P E V Q|S Q P P R(V)		95.3	488.9312	1464.781	-0.0015	-1	6.11	54177.2	5.41	HUMAN	Q9UN86	Ras GTPase-activating protein-binding protein 2
10696	dirMS_041712_NAR_60mM_plus.10127.10127.3	3	9.8	1	1.48E+06		(K)IFRDGEE	(K)I F/R D G E E\A G\A/Y\D G P R(T)		111.47	551.593	1652.766	-0.0019	-1.1	4.32	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
10697	dirMS_041712_NAR_60mM_plus.12199.12303.3	3	9.8	1	3.54E+06		(R)EIAQDF	(R)E I/A/Q/D/F K T D/L R(F)		121.45	445.9046	1335.69	0.0089	6.7	4.56	14166.5	11.62	HUMAN	B4DEB1	Histone H3
10698	dirMS_041712_NAR_60mM_plus.13903.13903.3	3	9.8	1	1.40E+06		(R)EMDRET	(R)E M D/R E T\L|I/D/V A R(T)		128.93	483.2457	1447.721	0.0016	1.1	4.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
10699	dirMS_041712_NAR_60mM_plus.16328.16404.3	3	9.8	0	4.61E+05		(R)FVFDRPI	(R)F/V/F/D R|P L/P V S R(L)		142.33	444.917	1332.742	-0.0058	-4.4	9.6	18685.5	9.45	HUMAN	B4DEV8	Proteasome subunit alpha type
10700	dirMS_041712_NAR_60mM_plus.17157.17157.3	3	9.8	0	2.04E+05		(K)THLPGF	(K)T\H L\P G F V/E/Q|A E A/L K(A)		147.35	513.9442	1539.817	0.0015	1	5.37	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
10701	dirMS_041712_NAR_20mM_minus.10404.10404.2	2	9.79	0	9.30E+04		(R)NTGIICT	(R)N T\G\I|I/C/T I G P A S R(S)	C:Carbamidomethylation	152.63	680.3561	1359.705	0	0	9.75	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
10702	dirMS_041712_NAR_20mM_minus.13135.13135.2	2	9.79	0	2.34E+05		(R)GVVDSE	(R)G V|V/D/S/E/D I P L N/L S R(E)		183.02	757.3944	1513.786	-0.0041	-2.7	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
10703	dirMS_041712_NAR_30mM_minus2.14783.14783.2	2	9.79	0	2.81E+05		(R)LDIDSPP	(R)L D I/D/S/P P/I T\A R(N)		134.17	599.3249	1197.647	-0.0049	-4.1	4.21	5755.5	5.75	HUMAN	H3BN34	Pyruvate kinase isozymes M1/M2 (Fragment)
10704	dirMS_041712_NAR_30mM_minus2.16552.16886.2	2	9.79	0	5.71E+05	M834m T8	(R)mTQLtV	(R)m T|Q|L/t V E K(V)	m:Oxidized methionine t:N-a	144.43	584.7961	949.502	219.0826	7.1	5.75	271875.5	5.65	HUMAN	A2RRP1	Neuroblastoma-amplified sequence
10705	dirMS_041712_NAR_40mM_minus2.6180.6184.2	2	9.79	0	9.42E+05		(R)STFSTN	(R)S T|F/S/T/N Y/R(S)		101.98	488.2302	975.453	0.0001	0.1	8.46	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10706	dirMS_041712_NAR_60mM_minus.11526.11526.3	3	9.79	1	1.64E+05		(K)NVDILK	(K)N/V/D/I/L K D/P/E/T V K(Q)		124.33	457.5867	1370.753	-0.007	-5.1	4.56	124524.8	5.71	HUMAN	O14980	Exportin-1
10707	dirMS_041712_NAR_60mM_minus.18196.18196.3	3	9.79	1	1.56E+06		(K)SLLGKD	(K)S L|L G K/D V L F L K(D)		163.42	411.5912	1232.761	-0.0022	-1.8	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
10708	dirMS_041712_NAR_60mM_minus.8714.8714.3	3	9.79	1	2.84E+05		(R)LGTPELS	(R)L/G\T/P/E L S/T A E R K(E)		108.45	434.572	1301.706	-0.0045	-3.5	6.14	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
10709	dirMS_041712_NAR_120mM_plus.21260.21260.4	4	9.79	0	1.48E+05		(K)ALEHAF	(K)A L E H A F/Q/L E H/I|M D L T R(L)		164.35	481.7493	1923.975	0.0008	0.4	5.27	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
10710	dirMS_041712_NAR_120mM_plus.23897.23897.3	3	9.79	1	3.41E+05	M145m	(R)GVmLA	(R)G V/m\L/A/V D A V I/A E L K K(Q)	m:Oxidized methionine	179.73	524.9713	1556.908	15.9913	-2.3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
10711	dirMS_041712_NAR_20mM_plus.12812.12812.2	2	9.79	0	1.33E+05		(K)IDIIPNP	(K)I D|I|I|P N P Q E R(T)		160.57	597.8227	1194.648	-0.0096	-8	4.37	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
10712	dirMS_041712_NAR_30mM_plus2.4186.4186.2	2	9.79	0	1.22E+06	M299m M	(K)NmmAA	(K)N m|m/A|A\C D|P R(H)	C:Carbamidomethylation m:Oxid	69.57	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
10713	dirMS_041712_NAR_40mM_plus2.12399.12399.3	3	9.79	1	1.76E+05		(K)IINADSE	(K)I I|N A/D S E D/P K Y I I N V K(Q)		139.05	611.3255	1831.98	-0.0181	-9.9	4.56	14693.3	4.69	HUMAN	C9JLS9	26S protease regulatory subunit 7 (Fragment)
10714	dirMS_041712_NAR_40mM_plus2.14091.14091.3	3	9.79	0	1.15E+05		(R)LVLEVA	(R)L V/L/E/V A Q/H L G E S T V R(T)		149.2	550.9762	1650.917	-0.0033	-2	5.4	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
10715	dirMS_041712_NAR_40mM_plus2.8230.8230.2	2	9.79	0	1.89E+05		(K)SFYMQR	(K)S F/Y/M/Q/R(C)		108.48	416.1954	831.382	0.0017	2.1	8.46	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
10716	dirMS_041712_NAR_50mM_plus2.12867.12867.3	3	9.79	0	5.97E+05		(R)FDAERP	(R)F/D/A/E R P V D C S V|I/V V N K(Q)	C:Carbamidomethylation	135.82	616.6476	1847.932	-0.0038	-2	4.56	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
10717	dirMS_041712_NAR_50mM_plus2.7685.7685.3	3	9.79	1	5.19E+04		(R)SQCLQV	(R)S\Q|C/L/Q/V P E R E A Q D A Q K(Q)	C:Carbamidomethylation	106.08	629.6395	1886.902	0.0014	0.8	4.68	23297.7	6.12	HUMAN	K7ESF4	Uncharacterized protein (Fragment)
10718	dirMS_041712_NAR_60mM_plus.10502.10525.2	2	9.79	1	1.58E+06		(R)VKYETEL	(R)V/K|Y/E|T E L/A M R(Q)		113.07	620.326	1239.64	0.0045	3.7	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10719	dirMS_041712_NAR_60mM_plus.13973.13973.3	3	9.79	0	1.21E+06		(K)GIHPTIIS	(K)G I H\P T I\I|S/E/S\F Q/K(A)		130.18	486.2646	1456.78	-0.0002	-0.1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
10720	dirMS_041712_NAR_60mM_plus.14873.14873.3	3	9.79	1	1.45E+05		(R)ARICCDL	(R)A R I C\C D|L/D/V L/A S K(K)	C:Carbamidomethylation	134.32	507.5883	1520.756	-0.0056	-3.7	6	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
10721	dirMS_041712_NAR_120mM_minus.9689.9689.3	3	9.78	0	3.90E+05		(K)NCPHIV	(K)N C|P/H\I\V/V/G T/P G/R(I)	C:Carbamidomethylation	107.48	436.2293	1306.669	0.0049	3.7	9.75	28185.1	10.76	HUMAN	B4DIJ6	Spliceosome RNA helicase DDX39B
10722	dirMS_041712_NAR_30mM_minus2.13626.13626.2	2	9.78	0	5.94E+05		(R)LILIESR(I	(R)L/I/L|I/E/S R(I)		128.2	422.2686	843.53	0.0001	0.1	6	17222	10.53	HUMAN	P62277	40S ribosomal protein S13
10723	dirMS_041712_NAR_30mM_minus2.15075.15075.2	2	9.78	0	6.28E+05		(R)AGLQFP	(R)A G L\Q|F|P V|G R(I)		135.13	472.7669	944.531	-0.0047	-5	9.79	6891.8	11.07	HUMAN	A8MQC5	Histone H2A
10724	dirMS_041712_NAR_40mM_minus2.14195.14195.3	3	9.78	1	1.47E+05		(K)ITSDEPL	(K)I/T/S/D\E/P L T K D D/I|P V F L R(H)		168.18	653.6833	1959.043	-0.008	-4.1	4.23	22313.1	4.9	HUMAN	B1AHE4	Ataxin 10 (Fragment)
10725	dirMS_041712_NAR_50mM_minus2.17945.17970.3	3	9.78	1	9.88E+04		(K)ILDVASL	(K)I/L|D|V/A|S L/E V L N E V N R R(S)		171.25	614.0139	1840.029	-0.0015	-0.8	4.68	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
10726	dirMS_041712_NAR_60mM_minus.18213.18213.3	3	9.78	1	5.46E+05		(K)IKTLFPLI	(K)I K T L F/P/L/I/E/A K(K)		162.7	424.9345	1272.793	-0.0036	-2.9	8.59	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
10727	dirMS_041712_NAR_60mM_minus.7890.7890.3	3	9.78	1	3.82E+05	M230m M	(R)mSmKE	(R)m S m K E V D E\Q\m|L/N|V/Q\N K(N)	m:Oxidized methionine	103.83	657.9647	1923.897	47.9823	-1.3	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
10728	dirMS_041712_NAR_120mM_plus.13614.13614.4	4	9.78	2	1.02E+06	M100m	(K)KQGGLG	(K)K Q\G G L G\P m N I/P L/V/S D P K/R(T)	m:Oxidized methionine	123.85	481.5167	1907.053	15.9918	-1.6	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
10729	dirMS_041712_NAR_20mM_plus.16768.16768.3	3	9.78	0	3.01E+05		(K)VQIAVA	(K)V Q\I\A\V A N A/Q/E L/L Q R(M)		186.93	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
10730	dirMS_041712_NAR_20mM_plus.19151.19151.3	3	9.78	0	1.90E+05		(K)TLETQS	(K)T L\E T Q S\A\L/G/P/A L/Q A A F K(L)		202.63	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
10731	dirMS_041712_NAR_30mM_plus2.16443.16510.2	2	9.78	0	3.15E+06		(R)INEILSN	(R)I/N|E|I/L/S N A L/K(R)		138.22	557.8307	1114.647	0.0075	6.7	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
10732	dirMS_041712_NAR_30mM_plus2.6639.6726.2	2	9.78	0	2.16E+05		(K)TLNAGA	(K)T L|N/A/G A/Y/S K(V)		89.35	462.7408	924.479	-0.0042	-4.5	8.26	30197.4	7.91	HUMAN	E9PMG2	Palmitoyl-protein thioesterase 1 (Fragment)
10733	dirMS_041712_NAR_40mM_plus2.9084.9084.2	2	9.78	0	5.44E+05		(K)SSFFSD	(K)S S|F/F|S/D\R(G)		116.2	423.1935	845.379	0.0009	1.1	5.55	15031.5	6.72	HUMAN	B4DLA0	ATP-dependent RNA helicase DDX3X
10734	dirMS_041712_NAR_50mM_plus2.6600.6600.3	3	9.78	1	1.11E+05		(R)ITGDPY	(R)I/T/G/D/P Y K V/Q Q A K(E)		99.47	449.9102	1347.727	-0.0106	-7.9	8.5	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
10735	dirMS_041712_NAR_60mM_plus.13851.13851.3	3	9.78	0	9.24E+05		(K)GIHPTIIS	(K)G I H P T I\I|S E/S/F Q K(A)		129.48	486.2646	1456.78	-0.0002	-0.1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
10736	dirMS_041712_NAR_60mM_plus.16316.16316.3	3	9.78	0	6.18E+05		(K)MTHLPE	(K)M T H L P E L/D|T|L|S/S E/R(A)		142.28	543.6023	1628.795	-0.0025	-1.5	4.65	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
10737	dirMS_041712_NAR_60mM_plus.16324.16324.3	3	9.78	1	1.84E+05		(K)KAPDFV	(K)K A P D F\V|F/Y/A P R(L)		141.8	437.5685	1310.689	0.0018	1.3	8.59	71218.8	6.3	HUMAN	A7YIJ8	Radixin
10738	dirMS_041712_NAR_60mM_plus.5466.5466.3	3	9.78	1	1.34E+05		(K)CDSSPD	(K)C D|S S/P D S A E/D/V R K(V)	C:Carbamidomethylation	86.15	489.2128	1465.622	0.0015	1	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
10739	dirMS_041712_NAR_120mM_minus.11949.11949.3	3	9.77	1	3.07E+05		(R)LKGYLIS	(R)L K G Y L\I|S/G S/S Y A R(S)		119.55	472.2599	1414.769	-0.0037	-2.6	9.7	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
10740	dirMS_041712_NAR_120mM_minus.17470.17470.4	4	9.77	2	3.00E+05		(R)NLKASLE	(R)N L K A/S L/E/N S/L R E V E A R(Y)		150.28	458.0011	1828.988	-0.005	-2.7	6.23	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10741	dirMS_041712_NAR_120mM_minus.5617.5617.3	3	9.77	1	1.23E+05		(K)CDSSPD	(K)C D|S/S|P/D S A E D/V R K(V)	C:Carbamidomethylation	83.98	489.2132	1465.622	0.0027	1.8	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
10742	dirMS_041712_NAR_120mM_minus.8011.8011.2	2	9.77	0	4.26E+05		(K)FHSQLM	(K)F/H|S Q/L M R(L)		97.85	459.7343	918.461	-0.0001	-0.1	9.75	10225.7	7.97	HUMAN	P49458	Signal recognition particle 9 kDa protein
10743	dirMS_041712_NAR_120mM_minus.8103.8103.3	3	9.77	0	5.42E+04		(K)KPMVLG	(K)K|P M V L G H E/A S/G T\V\E\K(V)		98.37	528.2771	1582.826	-0.009	-5.7	6.76	10868.5	9.4	HUMAN	B7Z3A6	Sorbitol dehydrogenase
10744	dirMS_041712_NAR_30mM_minus2.6043.6043.2	2	9.77	0	2.56E+05		(K)TSEVNC	(K)T/S|E|V N C Y R(C)	C:Carbamidomethylation	87.2	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
10745	dirMS_041712_NAR_30mM_minus2.7285.7285.2	2	9.77	0	2.36E+05		(R)AVEDISS	(R)A V|E/D I/S/S/S R(T)		93.98	482.244	963.474	0.0066	6.8	4.37	68767.9	5.93	HUMAN	E9PMH5	Baculoviral IAP repeat-containing protein 2
10746	dirMS_041712_NAR_50mM_minus2.11705.11705.3	3	9.77	1	5.05E+05		(R)ELISNSSI	(R)E L/I/S N/S S D A L D/K I R(Y)		135.73	520.9445	1560.823	-0.0038	-2.5	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
10747	dirMS_041712_NAR_50mM_minus2.16640.16640.3	3	9.77	0	1.37E+05		(K)VSHLLGI	(K)V S H L\L G I\N|V/T/D F T\R(G)		162.22	524.6237	1571.854	0.0025	1.6	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
10748	dirMS_041712_NAR_50mM_minus2.9259.9260.3	3	9.77	1	2.01E+05		(K)GITEQQI	(K)G I|T/E Q Q K E/G L E I V K(M)		120.58	524.6237	1571.864	-0.0074	-4.7	4.79	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
10749	dirMS_041712_NAR_60mM_minus.15612.15612.3	3	9.77	1	5.26E+04		(R)LTFLVAC	(R)L T|F/L/V/A Q K D F R(K)		147.03	446.5885	1337.758	-0.0067	-5	8.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
10750	dirMS_041712_NAR_60mM_minus.16040.16040.3	3	9.77	1	3.74E+05		(K)LKLSILYF	(K)L K\L S I L|Y/P A/T T G R(N)		150	478.2883	1432.852	-0.0019	-1.3	9.99	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
10751	dirMS_041712_NAR_60mM_minus.18861.18861.3	3	9.77	0	4.58E+04	M195m	(R)LHFFmP	(R)L H F F m|P/G|F/A/P L T S/R(G)	m:Oxidized methionine	167.23	546.2843	1620.835	16.0028	4.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
10752	dirMS_041712_NAR_120mM_plus.8376.8376.4	4	9.77	1	1.72E+05		(R)LLSDAT	(R)L L/S D A T V E K D E S H A G/K(V)		97.25	425.7164	1699.85	-0.0059	-3.5	4.75	40240.9	6.39	HUMAN	Q14320	Protein FAM50A
10753	dirMS_041712_NAR_20mM_plus.16517.16517.2	2	9.77	0	2.36E+05		(R)ADLIAYL	(R)A/D/L/I/A/Y/L K(K)		184.45	453.7678	906.529	-0.0012	-1.3	5.88	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
10754	dirMS_041712_NAR_20mM_plus.17546.17546.3	3	9.77	0	6.52E+04		(K)ITNLTQ	(K)I T N L T Q Q|L/E Q A/S I V/K(K)		192.92	562.6523	1685.943	-0.0009	-0.5	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
10755	dirMS_041712_NAR_30mM_plus2.7988.8015.2	2	9.77	0	1.64E+05		(K)SDPVVS	(K)S D/P/V/V/S Y/R(E)		96.37	461.7327	922.463	-0.0047	-5.1	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
10756	dirMS_041712_NAR_50mM_plus2.10084.10084.3	3	9.77	0	6.15E+05		(K)VGQEIE	(K)V/G/Q E/I E/V R P G/I V S/K(D)		121.05	504.2907	1510.859	-0.0012	-0.8	6.11	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
10757	dirMS_041712_NAR_50mM_plus2.12409.12409.3	3	9.77	1	3.54E+04		(K)ILIANTG	(K)I/L|I/A/N/T G M D T D K I K(I)		133.33	511.6172	1532.835	0.0018	1.2	5.96	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
10758	dirMS_041712_NAR_50mM_plus2.12562.12562.3	3	9.77	0	2.30E+05		(K)TVTSATI	(K)T/V|T S/A T/I/V Y/H L A R(Q)		133.57	477.9357	1431.795	-0.0029	-2	8.44	125655.3	6.18	HUMAN	Q92900	Regulator of nonsense transcripts 1
10759	dirMS_041712_NAR_50mM_plus2.12877.12877.3	3	9.77	1	6.20E+04		(K)LIADVAF	(K)L I/A/D/V/A/P S A I R E N D/I K(S)		135.47	575.6533	1724.954	-0.0088	-5.1	4.56	18388.8	6.85	HUMAN	F5H1Y3	Flap endonuclease 1 (Fragment)
10760	dirMS_041712_NAR_50mM_plus2.14159.14159.3	3	9.77	1	6.91E+04		(K)VVSSSIV	(K)V V|S S S I/V D K/Y I/G E S A R(L)		142.2	570.6392	1709.907	-0.0038	-2.2	6.04	29938.9	6.07	HUMAN	H0YJC0	26S protease regulatory subunit 10B (Fragment)
10761	dirMS_041712_NAR_60mM_plus.21675.21675.3	3	9.77	1	6.76E+05		(K)EIIDLVL	(K)E I/I/D/L/V L D R I R(K)		180.82	452.2733	1354.805	0.0001	0.1	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
10762	dirMS_041712_NAR_60mM_plus.6214.6214.3	3	9.77	1	3.16E+05		(R)GSCSTE	(R)G S\C/S T E/V/E K E/T Q E|K(M)	C:Carbamidomethylation	91.05	537.9088	1611.717	-0.0048	-3	4.49	13871.4	9.22	HUMAN	O75348	V-type proton ATPase subunit G 1
10763	dirMS_041712_NAR_20mM_minus.14551.14551.3	3	9.76	0	3.53E+03		(R)APVPAS	(R)A P V P A S E L\L|A/S/G V/L/S R(A)		200.08	522.9653	1566.885	-0.0036	-2.3	6.05	533778	5.74	HUMAN	Q15149	Plectin
10764	dirMS_041712_NAR_30mM_minus2.16117.16117.2	2	9.76	0	1.41E+05		(K)GCSFLP	(K)G C/S/F/L|P D/P Y\Q/K(Q)	C:Carbamidomethylation	141.02	656.3051	1311.604	-0.0009	-0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
10765	dirMS_041712_NAR_30mM_minus2.17950.17950.2	2	9.76	0	1.74E+05		(R)YVANIFF	(R)Y V|A N I F P Y K(G)		151.42	557.7997	1114.593	-0.001	-0.9	8.5	23312.3	5.53	HUMAN	B4DFH3	Inorganic pyrophosphatase 2, mitochondrial
10766	dirMS_041712_NAR_30mM_minus2.9420.9420.2	2	9.76	0	4.41E+05		(K)NSNPAL	(K)N S|N|P A/L|N D N L E K(G)		105.48	664.8273	1328.644	0.0032	2.4	4.37	27264.5	5.09	HUMAN	O00299	Chloride intracellular channel protein 1
10767	dirMS_041712_NAR_40mM_minus2.12613.12613.3	3	9.76	1	5.98E+05		(R)VCENIPI	(R)V C/E/N I|P I V/L C G N K V/D|I K(D)	C:Carbamidomethylation	157.7	657.6842	1971.04	-0.0021	-1.1	6.04	14844.8	5.89	HUMAN	B4DV51	GTP-binding nuclear protein Ran
10768	dirMS_041712_NAR_40mM_minus2.14344.14344.3	3	9.76	0	6.01E+05		(R)IHFPLAT	(R)I H F\P L A T\Y/A|P/V I S A E K(A)		167.95	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
10769	dirMS_041712_NAR_50mM_minus2.15997.15997.3	3	9.76	1	5.72E+04		(K)FLSPQD	(K)F/L|S/P Q D T F E A L K R(N)		158.78	517.9421	1551.817	-0.0048	-3.1	6.07	97622	8.94	HUMAN	Q9NTZ6	RNA-binding protein 12
10770	dirMS_041712_NAR_60mM_minus.14289.14308.3	3	9.76	1	2.53E+05		(R)VEVERD	(R)V/E\V E R D N\L|A/E D/I M/R(L)		139.93	563.6139	1688.827	-0.0001	0	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
10771	dirMS_041712_NAR_60mM_minus.14362.14362.3	3	9.76	1	1.30E+06		(R)MSMKE	(R)M S M K E V\D E Q|M/L/N\V/Q N/K(N)		140.47	641.9701	1923.897	-0.0015	-0.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
10772	dirMS_041712_NAR_60mM_minus.19212.19212.3	3	9.76	0	6.06E+03		(-)MKPLVV	(-)M K P L V/V\F\V\L|G/G P G A G K(G)		170.37	523.9758	1569.919	-0.0057	-3.6	10	22450.2	5.44	HUMAN	P30085	UMP-CMP kinase
10773	dirMS_041712_NAR_120mM_plus.9799.9887.4	4	9.76	1	3.56E+06		(K)DTGKTP	(K)D T\G K T\P V E P/E/V A/I/H R(I)		104.8	412.9719	1648.865	0.0005	0.3	5.45	5429.1	9.6	HUMAN	E5RIP1	40S ribosomal protein S20
10774	dirMS_041712_NAR_20mM_plus.14879.14879.2	2	9.76	0	1.45E+05		(K)VLEQLT	(K)V L/E Q\L/T|G Q T\P V/F S/K(A)		174.65	773.9244	1546.848	-0.006	-3.9	5.97	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
10775	dirMS_041712_NAR_20mM_plus.17171.17171.2	2	9.76	0	8.06E+04		(K)VNIIPIIA	(K)V N\I|I/P I/I/A/K(A)		189.38	490.8283	980.65	-0.001	-1	8.72	51212	5.84	HUMAN	A6NFQ9	Septin-8
10776	dirMS_041712_NAR_30mM_plus2.15815.15857.2	2	9.76	0	3.25E+05		(R)FDVSGY	(R)F D|V|S/G/Y/P T I K(I)		136.32	563.7923	1126.578	-0.0006	-0.5	5.83	73273.4	4.96	HUMAN	P13667	Protein disulfide-isomerase A4
10777	dirMS_041712_NAR_30mM_plus2.20875.20875.2	2	9.76	0	1.06E+05		(K)VAELLSE	(K)V A E|L/L/S E/E E R(E)		163.27	587.8038	1174.595	0.0053	4.5	4.09	98698.5	5.53	HUMAN	Q5VZ66	Janus kinase and microtubule-interacting protein 3
10778	dirMS_041712_NAR_30mM_plus2.8725.8854.3	3	9.76	0	7.01E+05		(K)VEIIAND	(K)V E\I\I\A/N D/Q/G N/R(T)		99.73	410.2146	1228.628	0.0012	1	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
10779	dirMS_041712_NAR_50mM_plus2.6052.6052.3	3	9.76	0	3.54E+04		(K)QPPTAA	(K)Q P/P/T/A A/G R P V D/A|S P R(V)		95.98	507.2698	1519.798	-0.0027	-1.8	9.6	43421.2	6.21	HUMAN	E9PHI6	Cytoplasmic dynein 1 light intermediate chain 1
10780	dirMS_041712_NAR_60mM_plus.10856.10858.3	3	9.76	1	2.86E+05		(R)QQEGFK	(R)Q Q/E G F K/G T F/P/D/A R(E)		114.17	494.2424	1480.718	-0.0053	-3.6	6.07	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
10781	dirMS_041712_NAR_60mM_plus.4891.4891.3	3	9.76	1	2.77E+04		(R)AAEEED	(R)A A/E E E/D/E A D/P K/R(Q)		80.98	453.872	1359.602	-0.0008	-0.6	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
10782	dirMS_041712_NAR_120mM_minus.10868.10868.3	3	9.75	0	3.40E+06		(K)YPTPPS	(K)Y P T P\P S Q H S Y A S/S/N A A E R(T)		113.67	654.9729	1962.894	0.0101	5.1	6.75	279264.6	4.96	HUMAN	Q04721	Neurogenic locus notch homolog protein 2
10783	dirMS_041712_NAR_20mM_minus.14556.14556.2	2	9.75	0	6.88E+03		(K)LAVEALS	(K)L A/V E A/L/S|S L D G D/L/A/G R(Y)		200	793.922	1586.838	-0.0017	-1.1	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
10784	dirMS_041712_NAR_30mM_minus2.14110.14111.2	2	9.75	0	1.93E+05		(R)IYGFYDE	(R)I/Y|G/F/Y D/E C K(R)	C:Carbamidomethylation	130.57	597.7605	1194.514	0.0001	0.1	4.37	33222.3	5.74	HUMAN	A6NNR3	Serine/threonine-protein phosphatase
10785	dirMS_041712_NAR_40mM_minus2.5856.5856.2	2	9.75	0	7.61E+05		(K)AGFAGD	(K)A G|F/A/G D/D A P R(A)		97.77	488.7279	976.448	0.0002	0.2	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
10786	dirMS_041712_NAR_50mM_minus2.12647.12647.3	3	9.75	1	4.52E+05	M100m	(K)QGGLGF	(K)Q G G\L|G/P m N I/P L/V S D/P K R(T)	m:Oxidized methionine	140.3	598.988	1778.958	15.9913	-2	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1

10787	dirMS_041712_NAR_50mM_minus2.13236.13236.3	3	9.75	0	4.03E+05		(K)VTHAVV	(K)V T\H A V V\T\V|P/A/Y/F N D A Q R(Q)		143.43	629.9954	1887.971	0.0005	0.3	6.71	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
10788	dirMS_041712_NAR_50mM_minus2.15772.15772.3	3	9.75	1	8.21E+04		(K)DANAKL	(K)D A N A|K L S E|L|E/A/A L Q\R(A)		158.97	543.6248	1628.86	-0.0004	-0.2	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
10789	dirMS_041712_NAR_60mM_minus.16477.16477.3	3	9.75	1	1.35E+05		(K)KLSTIAL	(K)K\L S T I A/L A|L/G V E R(T)		151.77	457.6153	1370.837	-0.0052	-3.8	8.75	52669.1	4.73	HUMAN	A8MY67	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform
10790	dirMS_041712_NAR_60mM_minus.9465.9465.3	3	9.75	1	2.04E+05	M118m	(R)LSFDKD	(R)L/S/F D K D/A/m V A/R(A)	m:Oxidized methionine	112.4	423.5497	1252.635	15.9991	3.3	5.96	35556.4	9.3	HUMAN	F2Z393	Transaldolase
10791	dirMS_041712_NAR_120mM_plus.10518.10518.3	3	9.75	1	1.41E+07		(R)VKYETEL	(R)V/K Y E T E|L A/M/R(Q)		107.73	413.8849	1239.64	0	0	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10792	dirMS_041712_NAR_20mM_plus.11995.11995.2	2	9.75	0	1.00E+05		(K)VSTAVLS	(K)V S\T/A V/L/S/I T A\K(A)		156.42	545.3252	1089.651	-0.0083	-7.6	8.72	106861.4	5.24	HUMAN	Q99460	26S proteasome non-ATPase regulatory subunit 1
10793	dirMS_041712_NAR_20mM_plus.12294.12294.3	3	9.75	0	2.90E+05		(K)VNQIGS	(K)V N Q I G S V|T/E/S/I Q/A C K(L)	C:Carbamidomethylation	157.67	545.2781	1633.821	-0.0016	-1	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
10794	dirMS_041712_NAR_40mM_plus2.13471.13471.3	3	9.75	0	4.66E+05		(R)VAPEEH	(R)V/A|P E E H P V L L T/E A/P L N/P K(A)		145.25	652.0252	1954.064	-0.0034	-1.7	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
10795	dirMS_041712_NAR_40mM_plus2.18651.18651.3	3	9.75	0	4.72E+04		(R)NEVSFV	(R)N/E|V/S/F V/I H N L P\V L A K(M)		175.93	560.6533	1679.948	-0.0026	-1.5	6.75	35663.7	5.91	HUMAN	B4DWK0	Selenide, water dikinase 1
10796	dirMS_041712_NAR_40mM_plus2.6212.6212.2	2	9.75	1	2.84E+05		(R)YSGGNY	(R)Y S|G G N Y/R D N Y|D|N(-)		95.58	719.2857	1437.567	-0.0024	-1.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
10797	dirMS_041712_NAR_50mM_plus2.14309.14309.3	3	9.75	0	7.47E+05		(R)LQAYHT	(R)L Q|A|Y H T Q T T/P L/I/E Y Y R(K)		143.55	666.341	1997.013	-0.0043	-2.1	6.75	21283.1	6.45	HUMAN	F8VY04	Adenylate kinase 2, mitochondrial
10798	dirMS_041712_NAR_50mM_plus2.15231.15231.3	3	9.75	0	6.29E+05		(K)LHIIEVG	(K)L H\I\I E V G\T|P/P T G N Q P F P K(K)		147.33	649.0216	1945.054	-0.0039	-2	6.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
10799	dirMS_041712_NAR_50mM_plus2.18110.18110.3	3	9.75	0	3.28E+05		(R)YPSLSLH	(R)Y/P/S L S L/H G I E G A F/S G S G A K(T)		163.3	626.6508	1877.939	-0.0014	-0.7	6.75	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
10800	dirMS_041712_NAR_50mM_plus2.6695.6695.3	3	9.75	0	4.53E+04		(K)ITPAHD	(K)I/T|P A/H D Q N D Y E/V/G Q R(H)		100.07	581.6074	1742.809	-0.0016	-0.9	4.54	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
10801	dirMS_041712_NAR_60mM_plus.16346.16346.3	3	9.75	0	4.27E+05		(R)EAYPGD	(R)E A|Y/P/G D V F Y L/H S R(L)		142.45	518.5855	1553.738	0.0036	2.3	5.32	48851.3	9.2	HUMAN	K7EK63	ATP synthase subunit alpha, mitochondrial
10802	dirMS_041712_NAR_60mM_plus.16725.16725.3	3	9.75	1	2.29E+04		(R)YRSDGA	(R)Y/R S D G A L L|L/G/A/S/S L/S G R(C)		143.73	574.9718	1722.913	-0.0125	-7.2	8.75	30278.5	5.29	HUMAN	B4DP38	Methylosome protein 50
10803	dirMS_041712_NAR_120mM_minus.6725.6725.2	2	9.74	1	7.21E+04		(K)GSGTAE	(K)G/S|G T/A/E V/E L\K/K(G)		91.03	559.8072	1118.605	0.0019	1.7	6.14	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
10804	dirMS_041712_NAR_30mM_minus2.13058.13058.2	2	9.74	0	2.81E+05		(K)LSELEPG	(K)L S E/L/E|P G T G D/L R(F)		124.52	643.8325	1286.659	-0.0009	-0.7	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
10805	dirMS_041712_NAR_30mM_minus2.17208.17347.2	2	9.74	0	1.15E+04		(K)VIVPNM	(K)V I|V|P N M E/F R(A)		147.4	552.7932	1104.587	-0.0079	-7.2	5.97	86098.8	5.31	HUMAN	B4DUC5	Exportin-2
10806	dirMS_041712_NAR_30mM_minus2.7159.7159.2	2	9.74	0	4.82E+05		(K)DAQGQI	(K)D A/Q/G Q|P G/L E R(A)		92.98	535.762	1070.523	-0.0058	-5.4	4.37	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
10807	dirMS_041712_NAR_40mM_minus2.7391.7391.3	3	9.74	0	1.00E+05		(K)ASQEPSI	(K)A S Q\E|P S P K|P G T E V I/P A A P R(K)		119.13	644.6737	1932.018	-0.012	-6.2	6.19	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
10808	dirMS_041712_NAR_60mM_minus.13967.13967.3	3	9.74	0	4.53E+05		(K)DCGATV	(K)D C/G A T W/V/V/L/G H S E R(R)	C:Carbamidomethylation	138.03	529.5838	1586.738	-0.0012	-0.7	5.32	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
10809	dirMS_041712_NAR_60mM_minus.14008.14008.3	3	9.74	0	2.23E+05		(R)VQIEHIS	(R)V Q|I E/H/I S S L I K(L)		137.73	422.9181	1266.742	-0.0019	-1.5	6.72	47748.2	6.08	HUMAN	O00231	26S proteasome non-ATPase regulatory subunit 11
10810	dirMS_041712_NAR_60mM_minus.16782.16782.3	3	9.74	1	2.50E+05		(R)YRVPDV	(R)Y R V P D\V\L|V A D/P/P I A R(L)		154.48	560.9843	1680.943	-0.0048	-2.9	5.96	96499.9	5.43	HUMAN	F5H6X6	Neutral alpha-glucosidase AB
10811	dirMS_041712_NAR_60mM_minus.8526.8526.3	3	9.74	1	2.71E+04		(R)ELAEQEI	(R)E L/A/E/Q E L E/K\Q/R(Q)		107.28	458.2407	1372.707	0.0009	0.6	4.49	533778	5.74	HUMAN	Q15149	Plectin
10812	dirMS_041712_NAR_120mM_plus.6690.6690.2	2	9.74	0	3.02E+05	M88m	(R)NGVmP	(R)N G|V|m/P/S H F S R(G)	m:Oxidized methionine	88.17	574.2686	1131.536	15.9935	-1.2	9.75	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
10813	dirMS_041712_NAR_20mM_plus.11127.11127.2	2	9.74	0	2.58E+03		(R)TAAALA	(R)T A A/A|L/A|P/A S L T S A R(M)		148.3	650.862	1300.722	-0.0052	-4	9.41	300351.7	12.1	HUMAN	Q9UQ35	Serine/arginine repetitive matrix protein 2
10814	dirMS_041712_NAR_20mM_plus.14306.14306.2	2	9.74	0	8.76E+04		(K)GVVDSD	(K)G V V/D/S\D D/L|P L N/V/S\R(E)		170.28	743.3789	1485.754	-0.0038	-2.6	3.93	92752.5	4.76	HUMAN	P14625	Endoplasmin
10815	dirMS_041712_NAR_20mM_plus.17727.17727.3	3	9.74	0	1.12E+04		(R)IINEPTA	(R)I I N/E P T A\A A|I/A/Y G L/D R(T)		193.42	563.3055	1687.901	0.0006	0.3	4.37	25598.3	6.45	HUMAN	E7EP11	Heat shock 70 kDa protein 1A/1B
10816	dirMS_041712_NAR_20mM_plus.19357.19357.3	3	9.74	0	2.32E+05		(R)LAGTQP	(R)L A G T Q\P\L/E|V|L/E A V Q R(S)		204.48	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
10817	dirMS_041712_NAR_30mM_plus2.18576.18614.3	3	9.74	0	1.66E+05		(-)SDVLELT	(-)S D V\L E L T D/D N F/E S R(I)		150.85	547.2595	1639.745	0.0194	11.8	3.77	13747.3	6.8	HUMAN	H7BZJ3	Thioredoxin (Fragment)
10818	dirMS_041712_NAR_30mM_plus2.18931.18931.2	2	9.74	0	3.63E+05		(R)NLVCTD	(R)N L|V|C/T D L F T/R(G)	C:Carbamidomethylation	152.18	619.8128	1238.62	-0.0015	-1.2	5.84	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
10819	dirMS_041712_NAR_30mM_plus2.19973.19973.2	2	9.74	0	5.38E+05		(R)NAVWA	(R)N A V|W/A/L\S/N L/C R(G)	C:Carbamidomethylation	157.48	652.3414	1303.658	0.018	13.8	9.75	37228.9	5.22	HUMAN	C9JYI4	Importin subunit alpha-1 (Fragment)
10820	dirMS_041712_NAR_30mM_plus2.9300.9300.2	2	9.74	0	4.83E+05		(K)ATFDAIS	(K)A T|F/D A I/S K(T)		102.47	426.7266	852.446	-0.0002	-0.3	5.88	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
10821	dirMS_041712_NAR_40mM_plus2.9875.9875.2	2	9.74	0	2.32E+05		(K)EQFAWI	(K)E Q|F/A/W/R(H)		122.82	418.706	836.405	-0.0002	-0.3	6.1	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
10822	dirMS_041712_NAR_50mM_plus2.12605.12763.3	3	9.74	1	6.75E+05		(K)SAPSIPK	(K)S A|P/S/I/P/K E N F/S C L T R(L)	C:Carbamidomethylation	135.18	569.6265	1706.853	0.0119	7	8.46	23209	6.92	HUMAN	B9A041	Malate dehydrogenase, cytoplasmic
10823	dirMS_041712_NAR_50mM_plus2.19805.19805.3	3	9.74	1	2.87E+05		(K)DRDVTF	(K)D R D V T F\S|P/A|T\I/E/N E L I/K(F)		172.58	650.0048	1948.002	-0.0024	-1.2	4.32	8027.1	8.38	HUMAN	H7C2D6	Mesencephalic astrocyte-derived neurotrophic factor (Fragment)
10824	dirMS_041712_NAR_50mM_plus2.20556.20556.3	3	9.74	1	1.67E+04		(K)SSVLENF	(K)S S/V/L|E/N F/V G R D F L P\R(G)		177.28	579.3128	1735.913	0.0113	6.5	5.79	73288.1	8.96	HUMAN	E5RHK8	Dynamin-3
10825	dirMS_041712_NAR_60mM_plus.5664.5664.3	3	9.74	0	7.68E+04		(R)TAEHEA	(R)T A\E H E A A\Q|Q/D\L/Q S K(F)		87.8	519.2487	1555.735	-0.0031	-2	4.65	156557.7	5.52	HUMAN	Q86UP2	Kinectin
10826	dirMS_041712_NAR_30mM_minus2.6970.7008.2	2	9.73	0	1.47E+05		(K)ISTVVSS	(K)I/S|T/V/V/S S K(E)		92.48	410.7405	820.477	-0.0037	-4.6	8.75	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
10827	dirMS_041712_NAR_30mM_minus2.7178.7178.2	2	9.73	0	1.28E+05		(R)LYAGST	(R)L/Y/A/G S T/V K(C)		93.52	419.7351	838.467	-0.004	-4.7	8.59	55287.2	6.08	HUMAN	B2R5P6	Thioredoxin reductase 1, cytoplasmic
10828	dirMS_041712_NAR_50mM_minus2.14393.14393.3	3	9.73	1	1.07E+06		(K)EAFSLFD	(K)E A/F/S/L/F D K D G D G T I T T K(E)		149.97	615.6336	1844.891	-0.005	-2.7	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
10829	dirMS_041712_NAR_50mM_minus2.15520.15520.3	3	9.73	1	4.15E+05		(K)QGGLGF	(K)Q G G L/G/P\M N I|P/L/V S D P K R(T)		157.37	593.6566	1778.958	-0.0029	-1.6	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
10830	dirMS_041712_NAR_50mM_minus2.6633.6633.3	3	9.73	1	6.22E+04		(R)EGVLTG	(R)E G\V\L/T/G S/P E Q K E E A A K(A)		104.1	558.2834	1672.839	-0.0032	-1.9	4.49	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
10831	dirMS_041712_NAR_50mM_minus2.8928.8928.3	3	9.73	0	2.36E+05		(R)VMLGET	(R)V/M|L/G E T N/P A D S K P G/T I R(G)		118.3	595.9744	1785.916	-0.0077	-4.3	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
10832	dirMS_041712_NAR_50mM_minus2.9080.9080.3	3	9.73	0	5.92E+04		(R)ASSLNE	(R)A S|S/L/N/E N V/D H S A L L K(L)		119.95	533.2774	1597.818	-0.0004	-0.2	5.32	89361.6	4.91	HUMAN	Q96SB3	Neurabin-2
10833	dirMS_041712_NAR_60mM_minus.16349.16372.3	3	9.73	0	1.48E+05		(R)FQSGDF	(R)F Q/S G/D F/H/V/I N G V L R(T)		150.9	530.2846	1588.823	0.0162	10.2	6.74	104619	5.75	HUMAN	F8W904	Exportin-2
10834	dirMS_041712_NAR_60mM_minus.16978.16978.3	3	9.73	1	2.47E+05		(K)YAVLYQ	(K)Y A|V/L/Y Q/P L F D K/R(F)		154.63	504.9409	1512.821	-0.0128	-8.4	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
10835	dirMS_041712_NAR_60mM_minus.9093.9093.3	3	9.73	1	1.62E+05	M232m M:	(R)MSmKE	(R)M/S m K E V\D\E Q|m/L/N V|Q N K(N)	m:Oxidized methionine	110.57	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
10836	dirMS_041712_NAR_120mM_plus.15924.15943.4	4	9.73	1	3.61E+05	M108m	(K)FLSDVYI	(K)F L\S D V|Y/P/D\G F K G H m L T K(S)	m:Oxidized methionine	137.13	493.498	1954.973	15.997	1.1	6.74	15838.9	7.03	HUMAN	H0Y5U0	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
10837	dirMS_041712_NAR_120mM_plus.7143.7143.3	3	9.73	1	1.11E+06		(R)SDYDGI	(R)S D|Y/D/G I G S R G D R(S)		91.03	433.1967	1297.577	-0.0012	-0.9	4.43	15031.5	6.72	HUMAN	B4DLA0	ATP-dependent RNA helicase DDX3X
10838	dirMS_041712_NAR_20mM_plus.10872.10872.2	2	9.73	1	1.70E+04	M336m	(K)LSmKDV	(K)L/S m K\D V/T/V E\K(A)	m:Oxidized methionine	147.23	583.3065	1149.618	15.9873	-6.5	6.07	51195.3	5.26	HUMAN	Q8WUX9	Charged multivesicular body protein 7
10839	dirMS_041712_NAR_20mM_plus.11406.11406.2	2	9.73	0	3.45E+05		(K)LITPAVV	(K)L I|T|P A V V S E R(L)		151	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
10840	dirMS_041712_NAR_20mM_plus.18976.18976.3	3	9.73	0	1.01E+05		(R)AAVPSG	(R)A A V|P S G A S T/G I/Y E A L E/L R(D)		201.5	602.3183	1804.944	-0.0036	-2	4.53	43048.9	4.99	HUMAN	B7Z2X9	Enolase
10841	dirMS_041712_NAR_20mM_plus.7300.7300.2	2	9.73	0	3.28E+05	M281m	(R)AEAESm	(R)A E|A/E|S m Y\Q I/K(Y)	m:Oxidized methionine	118.58	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
10842	dirMS_041712_NAR_30mM_plus2.12628.12628.2	2	9.73	0	9.15E+05		(R)YSGSYN	(R)Y S|G S/Y/N D/Y L R(A)		119.53	619.2776	1237.548	-0.0005	-0.4	5.83	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
10843	dirMS_041712_NAR_30mM_plus2.14334.14523.2	2	9.73	0	3.97E+05		(R)ELFEMA	(R)E/L/F/E/M/A R(T)		129.48	448.2205	895.434	-0.0005	-0.5	4.53	33615.3	9.15	HUMAN	B7Z5E2	26S protease regulatory subunit 7
10844	dirMS_041712_NAR_30mM_plus2.4989.4989.2	2	9.73	0	5.46E+05	S333s	(R)MQGAsI	(R)M/Q G/A s/R(L)	s:N-acetylglucosamine (S)	77.6	426.6906	649.309	203.0653	-16.5	9.5	206020.3	6.34	HUMAN	Q8TEM1	Nuclear pore membrane glycoprotein 210
10845	dirMS_041712_NAR_30mM_plus2.9473.9473.2	2	9.73	0	5.99E+05		(R)GGGQII	(R)G G G Q/I|I/P T A R(R)		104.05	485.2772	969.548	-0.0005	-0.5	9.75	15036.9	7.16	HUMAN	K7EJ74	116 kDa U5 small nuclear ribonucleoprotein component (Fragment)
10846	dirMS_041712_NAR_40mM_plus2.12736.12736.3	3	9.73	0	1.65E+05		(K)NLPPSG	(K)N L/P\P S/G A V/P V T G/I/P P H V V K(V)		141.78	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
10847	dirMS_041712_NAR_40mM_plus2.13779.13779.3	3	9.73	1	3.43E+05		(R)QVFGEA	(R)Q V/F G E/A T K Q/P G I/T F I A A/K(F)		147.45	636.0176	1906.043	-0.005	-2.6	8.59	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
10848	dirMS_041712_NAR_40mM_plus2.9176.9176.3	3	9.73	0	7.25E+03	M115m	(R)VmLGET	(R)V m|L/G E T/N/P/A/D S K P G T I R(G)	m:Oxidized methionine	117.13	601.3077	1785.916	15.9922	-1.5	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
10849	dirMS_041712_NAR_50mM_plus2.21636.21636.3	3	9.73	1	1.96E+05		(K)LKVNFLI	(K)L K V N F L|P E/I/I T L S K(E)		184.32	539.0011	1614.983	0.0058	3.6	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
10850	dirMS_041712_NAR_50mM_plus2.7401.7401.3	3	9.73	1	2.78E+05		(R)IVEQDTI	(R)I/V/E/Q\D T M/P P K G V R(H)		105.25	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
10851	dirMS_041712_NAR_60mM_plus.11121.11133.3	3	9.73	0	8.16E+05		(K)NFYQEH	(K)N/F/Y/Q/E/H/P D/L A R(R)		116	463.8897	1389.655	0	0	5.32	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
10852	dirMS_041712_NAR_60mM_plus.16453.16453.3	3	9.73	1	3.80E+04		(R)LGVFRA	(R)L/G/V|F R A E\S E\E/G P/D V|L R(W)		142.8	591.9752	1773.913	-0.0019	-1.1	4.41	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
10853	dirMS_041712_NAR_60mM_plus.21439.21439.3	3	9.73	1	3.68E+05		(R)ARDDLI	(R)A R\D D L\I|T/D/L/L N E A K(Q)		177.42	529.6165	1586.838	-0.0035	-2.2	4.23	23653.1	9.28	HUMAN	C9J8H1	V-type proton ATPase subunit E 1 (Fragment)
10854	dirMS_041712_NAR_60mM_plus.5778.5778.3	3	9.73	0	1.46E+05	M116m	(R)ATAPQT	(R)A/T/A/P Q T Q/H/V S P m R(Q)	m:Oxidized methionine	88.28	480.5724	1423.711	15.9916	-2.3	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
10855	dirMS_041712_NAR_60mM_plus.7341.7467.3	3	9.73	0	1.34E+05		(K)ALLQTHI	(K)A/L|L/Q/T H/P E A Q R(A)		95.23	421.8971	1263.68	-0.0037	-2.9	6.79	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
10856	dirMS_041712_NAR_120mM_minus.7037.7037.3	3	9.72	1	5.77E+05		(K)DSYVGD	(K)D S|Y/V/G D/E A/Q S K R(G)		92.07	452.2134	1354.623	0.0023	1.7	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
10857	dirMS_041712_NAR_20mM_minus.10156.10156.3	3	9.72	0	3.04E+04		(K)IEDLSQC	(K)I/E\D L\S Q Q A/Q L/A A A E K(F)		151.12	538.9478	1614.833	-0.0045	-2.8	4.14	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
10858	dirMS_041712_NAR_50mM_minus2.10498.10498.3	3	9.72	0	2.90E+05	M35m	(K)AASDIA	(K)A A\S D|I/A/m T E/L/P P T H P I R(L)	m:Oxidized methionine	127.85	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
10859	dirMS_041712_NAR_50mM_minus2.11016.11016.3	3	9.72	1	1.16E+05		(K)QIDLSTV	(K)Q/I/D|L S T/V D L/K/K(L)		131.17	420.5783	1259.72	-0.0002	-0.2	5.96	21156.2	9.41	HUMAN	P55145	Mesencephalic astrocyte-derived neurotrophic factor
10860	dirMS_041712_NAR_60mM_minus.11171.11196.3	3	9.72	1	2.22E+05	M183m	(R)VEVERD	(R)V/E|V/E R D N\L\A/E/D I m R(L)	m:Oxidized methionine	122.3	568.9449	1688.827	15.9929	-1.2	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
10861	dirMS_041712_NAR_60mM_minus.16699.16699.3	3	9.72	0	8.86E+04		(R)NSSHAG	(R)N S S H A/G A F\V I|V/T E/E A/I A K(G)		152.82	615.3243	1843.955	0.0035	1.9	5.4	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
10862	dirMS_041712_NAR_20mM_plus.14384.14384.2	2	9.72	0	1.59E+04		(K)TVFGVEI	(K)T V|F/G\V\E P/D L T R(E)		171.18	617.3237	1233.647	-0.0073	-5.9	4.37	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
10863	dirMS_041712_NAR_20mM_plus.17578.17578.3	3	9.72	0	3.61E+04	M74m	(R)mIAGQ	(R)m I A G Q V|L\D\I/N/L|A|A E/P K(V)	m:Oxidized methionine	193.18	566.9751	1682.915	15.9962	0.7	4.37	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
10864	dirMS_041712_NAR_20mM_plus.17886.17903.2	2	9.72	0	1.98E+05		(R)SLVPAAI	(R)S/L|V|P A A E L L E\S R(V)		194.83	642.8613	1284.716	-0.0005	-0.4	4.53	533778	5.74	HUMAN	Q15149	Plectin
10865	dirMS_041712_NAR_20mM_plus.18501.18501.3	3	9.72	0	2.24E+05		(R)LSVEEA	(R)L S V\E E A V A A G\V\V/G/G E/I Q E K(L)		198.52	629.0001	1884.991	-0.0056	-2.9	4.09	266161	5.68	HUMAN	E9PPU0	Epiplakin
10866	dirMS_041712_NAR_20mM_plus.18918.18918.2	2	9.72	0	1.05E+05		(K)DTSYLFI	(K)D T\S Y\L\F/I/T/G P D V/V/K(S)		201.92	777.9049	1554.805	-0.0025	-1.6	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
10867	dirMS_041712_NAR_30mM_plus2.12838.12838.2	2	9.72	0	2.21E+05		(K)NAGVEC	(K)N A|G\V/E/G S L/I V E K(I)		120.17	608.3313	1215.658	-0.0026	-2.2	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
10868	dirMS_041712_NAR_30mM_plus2.13367.13391.3	3	9.72	0	1.29E+05		(K)ALIAAQ	(K)A L|I A\A\Q/Y|S/G A Q V R(V)		123.35	449.9171	1347.738	-0.0012	-0.9	8.79	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
10869	dirMS_041712_NAR_40mM_plus2.11316.11316.3	3	9.72	0	3.11E+04		(K)LQALAN	(K)L Q|A/L/A\N E/Q A A A A H E L E K(M)		132.83	602.981	1806.935	-0.006	-3.3	4.75	156557.7	5.52	HUMAN	Q86UP2	Kinectin
10870	dirMS_041712_NAR_40mM_plus2.7639.7639.2	2	9.72	0	6.28E+04		(R)AQYDEL	(R)A Q/Y/D E/L A R(K)		105.2	483.2372	965.469	-0.0016	-1.6	4.37	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10871	dirMS_041712_NAR_40mM_plus2.9891.9891.2	2	9.72	0	2.34E+05		(K)EQFAWI	(K)E/Q/F/A W/R(H)		122.82	418.706	836.405	-0.0002	-0.3	6.1	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
10872	dirMS_041712_NAR_50mM_plus2.10919.10919.3	3	9.72	0	2.31E+05		(K)TKPYIQ	(K)T K/P Y\I Q V D|I/G/G G Q T K(T)		125.32	535.6231	1604.864	-0.0095	-5.9	8.17	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
10873	dirMS_041712_NAR_50mM_plus2.14157.14157.3	3	9.72	0	5.08E+05		(K)VTHAVV	(K)V T H A\V V\T V/P A Y/F/N/D A Q R(Q)		142.7	629.9955	1887.971	0.0008	0.4	6.71	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
10874	dirMS_041712_NAR_50mM_plus2.14433.14433.3	3	9.72	1	5.76E+05		(R)SEGVVA	(R)S E|G V|V/A V L/L T K K(S)		144.37	415.2585	1243.762	-0.0011	-0.9	8.31	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
10875	dirMS_041712_NAR_50mM_plus2.20790.20790.3	3	9.72	0	2.17E+05		(K)GLEHVT	(K)G L E H V\T V D D\L|V/A|E\I/T P K(G)		178.28	612.6632	1835.975	0.0001	0.1	4.31	11429.2	9.63	HUMAN	E5RHX8	Enhancer of yellow 2 transcription factor homolog
10876	dirMS_041712_NAR_50mM_plus2.6128.6128.3	3	9.72	0	1.25E+05		(R)SGSMDI	(R)S G S/M/D/P S/G A H P/S V R(Q)		96.5	462.214	1384.627	0.0001	0	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
10877	dirMS_041712_NAR_50mM_plus2.6325.6325.3	3	9.72	0	2.09E+05	M70m	(K)EAPPmE	(K)E A/P/P m/E K/P\E V V K(T)	m:Oxidized methionine	97.97	457.2387	1353.708	15.9933	-1.2	4.79	14798.1	10.35	HUMAN	K7EJ78	40S ribosomal protein S15 (Fragment)
10878	dirMS_041712_NAR_50mM_plus2.9220.9220.3	3	9.72	1	2.75E+05		(R)TNAENE	(R)T N/A\E N|E F/V T I/K K(D)		115.83	465.2518	1393.732	0.0087	6.2	5.81	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
10879	dirMS_041712_NAR_120mM_minus.15270.15270.4	4	9.71	1	2.25E+05		(K)THLPGF	(K)T H\L\P G F\V/E Q/A/E A L K A/K(G)		137.72	435.4914	1738.949	-0.0049	-2.8	6.42	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
10880	dirMS_041712_NAR_20mM_minus.10326.10326.2	2	9.71	0	8.40E+04		(K)ALDFIAS	(K)A L|D\F\I/A/S K(G)		152	432.7455	864.482	0.0012	1.4	5.88	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
10881	dirMS_041712_NAR_30mM_minus2.17801.17992.2	2	9.71	0	1.60E+05		(R)VPFSLLR	(R)V/P|F/S/L L R(G)		151.43	416.2578	831.509	-0.0004	-0.5	9.72	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
10882	dirMS_041712_NAR_30mM_minus2.18793.18793.2	2	9.71	0	2.45E+05		(K)LLQDFFI	(K)L/L|Q/D/F F/N G/R(D)		157.37	555.2906	1109.574	0.0001	0.1	5.84	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
10883	dirMS_041712_NAR_30mM_minus2.7261.7261.2	2	9.71	0	2.75E+05		(K)SAVLQE	(K)S A/V/L|Q\E A R(I)		94.43	437.2408	873.479	-0.0045	-5.2	5.72	28218.2	9.35	HUMAN	F6X838	Coatomer subunit gamma-2
10884	dirMS_041712_NAR_30mM_minus2.9348.9348.2	2	9.71	0	1.01E+06		(K)QADVNI	(K)Q A/D/V/N/L|V/N A/K(L)		105.43	536.2917	1071.579	-0.0032	-3	5.84	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
10885	dirMS_041712_NAR_40mM_minus2.14507.14507.3	3	9.71	0	2.27E+05		(R)DIKPQN	(R)D I K P Q N|L\L|L D/P/D/T A V L K(L)		169.67	631.6945	1893.069	-0.0002	-0.1	4.43	47257	9.38	HUMAN	P49841	Glycogen synthase kinase-3 beta
10886	dirMS_041712_NAR_50mM_minus2.16774.16774.3	3	9.71	0	4.35E+05		(K)NILFVIT	(K)N I|L/F V/I T K/P D V Y/K(S)		164.05	517.2991	1549.899	-0.0161	-10.4	8.5	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
10887	dirMS_041712_NAR_60mM_minus.13987.13987.3	3	9.71	0	9.95E+05		(K)LGDVYV	(K)L/G D\V/Y V/N D A F G T A H R(A)		136.97	545.603	1634.792	0.0023	1.4	5.21	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
10888	dirMS_041712_NAR_60mM_minus.9004.9004.3	3	9.71	1	3.60E+05	M232m M:	(R)MSmKE	(R)M/S m K E V\D E|Q\m/L/N\V\Q N K(N)	m:Oxidized methionine	110.3	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
10889	dirMS_041712_NAR_20mM_plus.10158.10158.2	2	9.71	0	1.58E+05		(K)GEATVS	(K)G E A\T|V\S/F D D/P/P S A K(A)		142.07	710.8324	1420.659	-0.0015	-1.1	4.03	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
10890	dirMS_041712_NAR_20mM_plus.16853.16853.2	2	9.71	0	3.34E+05		(K)VQIAVA	(K)V Q|I A/V|A|N A Q E/L L Q R(M)		187.42	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
10891	dirMS_041712_NAR_20mM_plus.17940.17940.3	3	9.71	0	1.99E+05		(R)TVQSLEI	(R)T V Q S\L/E|I|D L/D S M R(N)		195	502.9236	1506.747	0.0094	6.2	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10892	dirMS_041712_NAR_20mM_plus.19225.19225.2	2	9.71	0	1.30E+05		(R)EGDVLT	(R)E G D\V/L|T/L\L/E/S E R(E)		203.6	680.8536	1360.696	0.0045	3.3	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
10893	dirMS_041712_NAR_20mM_plus.8253.8261.2	2	9.71	0	3.33E+05	M176m	(K)VLEGmE	(K)V/L|E|G m E V V/R(K)	m:Oxidized methionine	126.95	524.278	1031.555	15.9933	-1.5	4.53	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
10894	dirMS_041712_NAR_20mM_plus.8988.8988.2	2	9.71	0	2.27E+05		(R)VLTVINC	(R)V L/T\V/I|N\Q T Q/K(E)		132.87	572.3399	1143.673	-0.0007	-0.6	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
10895	dirMS_041712_NAR_20mM_plus.9395.9395.2	2	9.71	0	7.19E+04		(R)QTVAVG	(R)Q T/V/A V/G V/I K(A)		135.88	457.7856	914.567	-0.003	-3.3	8.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1

10896	dirMS_041712_NAR_30mM_plus2.10613.10734.2	2	9.71	0	8.18E+05		(R)INVELST	(R)I/N|V|E L/S T K(G)		109.37	452.2602	903.515	-0.0014	-1.6	6	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
10897	dirMS_041712_NAR_30mM_plus2.14537.14537.2	2	9.71	0	5.85E+05		(K)IGLDFCK	(K)I/G/L/D F C K(Y)	C:Carbamidomethylation	129.58	426.7164	852.428	-0.0029	-3.4	5.84	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
10898	dirMS_041712_NAR_30mM_plus2.6217.6217.2	2	9.71	0	1.67E+05		(K)VQEQEL	(K)V/Q|E/Q E/L T R(L)		86.78	501.7639	1002.521	-0.0009	-0.9	4.53	334221.3	6.44	HUMAN	P15924	Desmoplakin
10899	dirMS_041712_NAR_40mM_plus2.12500.12500.3	3	9.71	1	3.43E+04	M357m	(R)ALAEIAK	(R)A L/A/E|I A K/A E L D D T/P m R(G)	m:Oxidized methionine	139.65	587.3006	1743.895	15.9927	-1.3	4.32	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
10900	dirMS_041712_NAR_50mM_plus2.18890.18890.3	3	9.71	0	2.33E+05		(R)LPVPPLC	(R)L P\V/P P L Q/Q/S L D H Y L/K(A)		167.4	583.336	1747.974	0.0193	11	6.74	18575.3	9.69	HUMAN	A6PVN3	Carnitine O-acetyltransferase
10901	dirMS_041712_NAR_50mM_plus2.21419.21419.3	3	9.71	1	1.71E+05		(K)TGLSSEC	(K)T G/L/S/S/E/Q T/V\N V L A Q I L K R(L)		183	653.0385	1957.108	-0.0067	-3.4	8.41	48481.7	6.95	HUMAN	E7EUG6	General transcription factor IIF subunit 1
10902	dirMS_041712_NAR_60mM_plus.18617.18617.3	3	9.71	1	6.61E+05		(R)IRIDSLS	(R)I R I D S\L|S|A\Q|L/S Q L Q\K(Q)		154.47	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
10903	dirMS_041712_NAR_120mM_minus.12910.12910.3	3	9.7	1	1.79E+05		(R)NKQEVN	(R)N K Q\E|V\M I/S/D/L/E E/R(L)		124.15	530.9318	1590.779	0.0016	1	4.41	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
10904	dirMS_041712_NAR_120mM_minus.17718.17718.3	3	9.7	1	1.82E+05		(R)AGKLDP	(R)A G K L D/P/H/L\V L/D Q L R(C)		151.47	525.6385	1574.901	-0.0004	-0.2	6.79	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
10905	dirMS_041712_NAR_20mM_minus.7897.7897.2	2	9.7	0	1.26E+05		(R)LAPEYE	(R)L/A|P E/Y/E A A A T R(L)		128.68	596.302	1191.6	-0.0037	-3.1	4.53	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
10906	dirMS_041712_NAR_20mM_minus.9316.9316.2	2	9.7	0	5.66E+05		(K)YEELQSL	(K)Y/E|E/L Q S L/A G K(H)		143.23	569.2917	1137.579	-0.0025	-2.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
10907	dirMS_041712_NAR_40mM_minus2.13859.13891.3	3	9.7	0	5.98E+04		(R)LLAEIGA	(R)L/L\A/E|I G A/V/T L V S A P R P D/S R(H)		165.87	655.7064	1965.113	-0.0081	-4.1	6.07	27279.2	9.51	HUMAN	A9C4B9	tRNA splicing endonuclease 34 homolog (S. cerevisiae) (Fragment)
10908	dirMS_041712_NAR_50mM_minus2.18398.18398.3	3	9.7	0	1.54E+04		(K)ALESPEF	(K)A L|E/S/P E R/P/F L A I/L G G A K(V)		176.02	590.3356	1768.996	-0.0033	-1.9	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
10909	dirMS_041712_NAR_50mM_minus2.9354.9354.3	3	9.7	0	2.43E+05		(K)TGVAVN	(K)T G/V/A V/N/K/P A E F T V D/A K(H)		121.9	549.6316	1646.875	0.0054	3.3	5.73	283472.4	5.71	HUMAN	P21333	Filamin-A
10910	dirMS_041712_NAR_60mM_minus.15192.15192.3	3	9.7	1	4.91E+04		(K)YMACCL	(K)Y/M/A C/C\L L Y R G D V/V/P K(E)	C:Carbamidomethylation	145.53	615.6321	1844.886	-0.0038	-2.1	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
10911	dirMS_041712_NAR_20mM_plus.17477.17477.2	2	9.7	0	2.22E+05		(K)LLYAFAE	(K)L L/Y/A F A E A T V/P K(V)		192.97	661.8712	1322.736	-0.0003	-0.3	6	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
10912	dirMS_041712_NAR_20mM_plus.8584.8584.2	2	9.7	0	7.92E+04		(K)ILGPQGI	(K)I L|G\P/Q|G N T I K(R)		129.25	520.8068	1040.61	-0.0035	-3.4	8.75	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
10913	dirMS_041712_NAR_20mM_plus.8617.8617.2	2	9.7	0	1.46E+05		(K)TAVCDIF	(K)T A|V/C/D/I/P\P R(G)	C:Carbamidomethylation	129.67	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
10914	dirMS_041712_NAR_30mM_plus2.21690.21690.2	2	9.7	0	1.20E+05		(R)NSILAQ	(R)N S/I\L|A|Q|V/L/D Q S A R(A)		169.72	707.8889	1414.765	0.0057	4	5.84	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
10915	dirMS_041712_NAR_30mM_plus2.4454.4732.2	2	9.7	0	1.24E+06	M571m	(R)mGANSI	(R)m/G/A/N/S/L/E/R(M)	m:Oxidized methionine	74.87	447.2119	877.42	15.9969	2.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
10916	dirMS_041712_NAR_30mM_plus2.4489.4489.2	2	9.7	0	3.76E+05		(R)SYTSGPC	(R)S Y/T/S/G P G S\R(I)		73.17	456.2155	911.422	0.002	2.2	8.46	19288.4	10.19	HUMAN	F8VQY3	Keratin, type II cytoskeletal 8 (Fragment)
10917	dirMS_041712_NAR_40mM_plus2.10339.10339.2	2	9.7	0	9.40E+04		(K)IGGIGTV	(K)I/G/G\I/G/T V|P V G R(V)		125.75	513.3081	1025.61	-0.0013	-1.2	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
10918	dirMS_041712_NAR_40mM_plus2.14749.14849.3	3	9.7	0	3.03E+05		(R)IEGDMI	(R)I E\G D|M/I|V C/A A Y\A H E L/P K(Y)	C:Carbamidomethylation	153.93	639.6498	1916.925	0.0104	5.4	4.65	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
10919	dirMS_041712_NAR_50mM_plus2.15543.15543.3	3	9.7	1	8.44E+05		(K)VQGGAL	(K)V Q|G\G A L/E D S\Q L V/A G V A F K K(T)		150.45	639.6848	1917.044	-0.0042	-2.2	6.04	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
10920	dirMS_041712_NAR_50mM_plus2.19008.19008.3	3	9.7	1	5.18E+06		(R)LFVGNLI	(R)L F/V/G/N L/P A/D I/T E D E F K/R(L)		166.85	655.3417	1964.012	-0.0018	-0.9	4.32	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
10921	dirMS_041712_NAR_60mM_plus.16028.16028.3	3	9.7	0	4.93E+05		(R)VWYVSN	(R)V W|Y/V S N I D/G T H I A/K(T)		140.15	534.9464	1602.828	-0.0028	-1.8	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
10922	dirMS_041712_NAR_20mM_minus.13676.13676.2	2	9.69	0	1.54E+05		(K)ALQQGL	(K)A/L/Q/Q/G/L V/G/L E L K(E)		187.58	634.8811	1268.757	-0.0023	-1.8	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
10923	dirMS_041712_NAR_20mM_minus.8626.8688.2	2	9.69	0	1.86E+05		(K)LVLVGD	(K)L V|L|V/G/D G G T/G K(T)		136.13	508.2919	1015.578	-0.0017	-1.7	5.84	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
10924	dirMS_041712_NAR_30mM_minus2.16060.16060.2	2	9.69	0	1.18E+05		(K)SSEELLS	(K)S S/E/E L|L|S A L Q/K(K)		141.45	602.816	1204.642	-0.0172	-14.3	4.53	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
10925	dirMS_041712_NAR_30mM_minus2.16337.16337.2	2	9.69	0	1.59E+05		(R)ASLEAAI	(R)A S L E/A A|I/A\D/A E Q R(G)		143.13	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
10926	dirMS_041712_NAR_40mM_minus2.11149.11149.3	3	9.69	0	3.97E+05		(R)DAGEGL	(R)D A|G E\G L/L A V/Q I T D/Q E G\K P K(R)		148.28	657.0157	1969.024	0.0089	4.5	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
10927	dirMS_041712_NAR_40mM_minus2.15635.15635.3	3	9.69	1	3.98E+05	M145m	(R)GVmLA	(R)G V/m/L|A V D A V/I/A/E L K K(Q)	m:Oxidized methionine	181.67	524.9715	1556.908	15.9919	-1.9	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
10928	dirMS_041712_NAR_40mM_minus2.9114.9180.3	3	9.69	1	7.60E+04		(K)LIADVAF	(K)L/I|A/D V A/P S A I R E N D/I K(S)		136.5	575.6561	1724.954	-0.0004	-0.2	4.56	18388.8	6.85	HUMAN	F5H1Y3	Flap endonuclease 1 (Fragment)
10929	dirMS_041712_NAR_50mM_minus2.12729.12729.3	3	9.69	0	3.18E+06	M84m	(K)YPIEHGI	(K)Y/P I E H G I I/T N W/D D m E K(I)	m:Oxidized methionine	141.42	659.6398	1960.911	15.9939	-0.5	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
10930	dirMS_041712_NAR_50mM_minus2.9114.9114.3	3	9.69	1	1.70E+05		(K)ITIKNDP	(K)I/T\I K N D|P S/L/P E\P K(C)		119.82	484.6056	1451.81	-0.0082	-5.6	6.07	20203.8	9.79	HUMAN	B4DG16	Asparagine--tRNA ligase, cytoplasmic
10931	dirMS_041712_NAR_60mM_minus.11231.11231.3	3	9.69	1	2.22E+05	M183m	(R)VEVERD	(R)V/E|V E R D N L/A/E/D I m R(L)	m:Oxidized methionine	122.3	568.9449	1688.827	15.9929	-1.2	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
10932	dirMS_041712_NAR_60mM_minus.14550.14550.3	3	9.69	1	4.46E+05		(K)VLAGDK	(K)V/L/A G D K N F|I/T A E/E L R(R)		140.4	559.3035	1675.901	-0.0054	-3.2	4.68	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
10933	dirMS_041712_NAR_60mM_minus.14821.14821.3	3	9.69	1	5.91E+05		(K)TDKTLVL	(K)T/D K T L\V L|L/M/G K(E)		142.57	406.9088	1218.713	-0.0008	-0.6	8.26	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
10934	dirMS_041712_NAR_60mM_minus.15483.15483.3	3	9.69	1	2.23E+05		(R)GPIKFN	(R)G P\I/K F N\V|W/D\T A G Q E K(F)		146.48	563.9575	1689.86	-0.0015	-0.9	6.07	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
10935	dirMS_041712_NAR_120mM_plus.11540.11540.3	3	9.69	2	7.51E+05		(R)DLDRIAC	(R)D L D R I A/G Q|V|A/A A N K K(H)		112.65	523.9602	1569.871	-0.0047	-3	8.59	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
10936	dirMS_041712_NAR_120mM_plus.12805.12805.3	3	9.69	0	3.45E+05		(K)HVTSECI	(K)H V\T S E C/L/G W/M R(Q)	C:Carbamidomethylation	120.88	459.2138	1375.625	0.0023	1.7	6.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
10937	dirMS_041712_NAR_20mM_plus.17113.17113.2	2	9.69	0	2.44E+05		(K)LFLVQLC	(K)L F|L|V Q L Q E K(A)		189.62	559.3342	1117.662	-0.0004	-0.4	6	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
10938	dirMS_041712_NAR_20mM_plus.19148.19185.2	2	9.69	0	2.21E+05		(K)ILTFDQL	(K)I L|T|F/D Q/L/A L D/S\P K(G)		203.25	730.9063	1460.8	0.0058	4	4.21	14643	11.93	HUMAN	F8VUA6	60S ribosomal protein L18 (Fragment)
10939	dirMS_041712_NAR_50mM_plus2.10520.10520.3	3	9.69	1	5.68E+05		(K)GCGVVK	(K)G C/G V V/K F E/S/P E/V A E R(A)	C:Carbamidomethylation	123.78	555.2753	1663.811	0.0005	0.3	4.79	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
10940	dirMS_041712_NAR_50mM_plus2.18161.18161.3	3	9.69	1	1.63E+06		(R)ELIKVLEI	(R)E L I K V L E E\A|N/Q/A I N/P K(L)		163.57	603.6741	1809.012	-0.0039	-2.2	4.79	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
10941	dirMS_041712_NAR_60mM_plus.14849.14849.3	3	9.69	1	1.45E+05		(R)ARICCDI	(R)A R I\C\C D|L/D V/L A S K(K)	C:Carbamidomethylation	134.32	507.5883	1520.756	-0.0056	-3.7	6	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
10942	dirMS_041712_NAR_60mM_plus.9270.9270.3	3	9.69	0	3.00E+05		(K)QEYDES	(K)Q E/Y/D E/S/G P S/I V H/R(K)		106.35	506.2392	1516.703	0.0004	0.3	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
10943	dirMS_041712_NAR_50mM_minus2.12296.12296.3	3	9.68	1	4.17E+04		(K)QLGGSV	(K)Q L/G G S V E/L/V D/I/G K Q K(L)		138.1	524.2969	1570.88	-0.0038	-2.4	6.07	9475.6	4.64	HUMAN	J3KRD5	Cytosolic non-specific dipeptidase (Fragment)
10944	dirMS_041712_NAR_50mM_minus2.13116.13116.3	3	9.68	1	2.73E+04		(K)VVSSSIV	(K)V/V|S S S I V D K Y I/G E S A R(L)		142.6	570.6413	1709.907	0.0025	1.5	6.04	29938.9	6.07	HUMAN	H0YJC0	26S protease regulatory subunit 10B (Fragment)
10945	dirMS_041712_NAR_50mM_minus2.14419.14419.3	3	9.68	1	1.40E+05		(R)GDVVPK	(R)G D V/V/P K D V N A A/I/A T I K(T)		150.42	537.6375	1610.911	-0.0133	-8.2	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
10946	dirMS_041712_NAR_50mM_minus2.14795.14795.3	3	9.68	0	2.98E+05		(R)ELSPDIA	(R)E L S/P/D/I/A H/L A S L K(T)		152.82	465.2561	1393.769	-0.0148	-10.6	5.32	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
10947	dirMS_041712_NAR_50mM_minus2.9495.9495.3	3	9.68	0	1.82E+05		(R)AIGSASE	(R)A I|G\S/A S/E G A/Q/S S L/Q E V Y H K(S)		122.55	654.6559	1961.956	-0.0032	-1.6	5.4	20148.5	4.65	HUMAN	B4E2V4	Proteasome (Prosome, macropain) subunit, alpha type, 5, isoform CRA_c
10948	dirMS_041712_NAR_120mM_plus.11637.11637.2	2	9.68	0	3.00E+05		(K)HMLPTV	(K)H/M|L/P T V L/R(M)		113.93	483.7811	966.555	-0.0004	-0.4	9.75	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
10949	dirMS_041712_NAR_20mM_plus.9963.9963.2	2	9.68	0	2.48E+05		(K)VASGCLI	(K)V/A|S|G/C\L/D\I\N S S V K(G)	C:Carbamidomethylation	139.83	675.3376	1349.673	-0.005	-3.7	5.81	56837	7.19	HUMAN	E7ETT1	Propionyl-CoA carboxylase beta chain, mitochondrial
10950	dirMS_041712_NAR_30mM_plus2.10608.10609.2	2	9.68	0	1.14E+06		(K)LNLSQVI	(K)L/N|L/S/Q/V/R(F)		108.68	415.2469	829.489	-0.0025	-3	9.75	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
10951	dirMS_041712_NAR_40mM_plus2.8903.9002.2	2	9.68	0	1.05E+05		(K)FYEQFSK	(K)F/Y/E/Q F|S K(N)		115.03	474.7301	948.446	0.0068	7.1	6	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
10952	dirMS_041712_NAR_50mM_plus2.10299.10299.3	3	9.68	1	5.90E+05		(K)YGEPGE	(K)Y/G\E|P G E/V F/I N K G K(G)		121.75	479.9177	1437.737	0.0013	0.9	6.14	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
10953	dirMS_041712_NAR_50mM_plus2.11410.11410.3	3	9.68	0	3.52E+05		(R)MLTGPV	(R)M L/T|G P V\Y S Q/S T A/L T H/K(Q)		127.67	578.6334	1733.889	-0.0034	-2	8.37	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
10954	dirMS_041712_NAR_50mM_plus2.14907.14907.3	3	9.68	0	5.02E+05		(K)TTISVAH	(K)T T/I/S V/A H/L/L/A A/R(Q)		146.45	418.2499	1252.737	-0.002	-1.6	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
10955	dirMS_041712_NAR_50mM_plus2.17432.17458.3	3	9.68	0	9.60E+05		(R)VLDPFTI	(R)V/L\D/P F T/I K P L D/R(K)		160.52	471.9408	1413.81	-0.0022	-1.5	5.93	63448.4	7.29	HUMAN	B4E022	Transketolase
10956	dirMS_041712_NAR_50mM_plus2.5189.5189.3	3	9.68	0	5.44E+04		(K)AAGPSLS	(K)A A|G|P S L S H T S/G G T Q/S K(V)		86.15	495.9137	1485.729	-0.0027	-1.8	8.8	68764.6	6.96	HUMAN	P27694	Replication protein A 70 kDa DNA-binding subunit
10957	dirMS_041712_NAR_50mM_plus2.8494.8494.3	3	9.68	0	5.53E+05		(R)ASGNYA	(R)A/S/G N|Y/A T V I/S H N P E/T K(K)		111.85	563.6145	1688.824	0.0051	3	6.79	24115.6	11.59	HUMAN	E9PIZ3	60S ribosomal protein L8
10958	dirMS_041712_NAR_60mM_plus.10561.10690.2	2	9.68	1	1.68E+06		(R)VKYETEL	(R)V/K|Y/E/T E L/A/M R(Q)		113.15	620.326	1239.64	0.0045	3.7	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10959	dirMS_041712_NAR_60mM_plus.17019.17019.3	3	9.68	1	2.18E+05		(R)ASLISAV	(R)A S/L/I/S/A/V/S D K L R(W)		145.88	420.5832	1259.732	0.0033	2.6	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
10960	dirMS_041712_NAR_60mM_plus.7739.7872.3	3	9.68	0	1.06E+06		(R)SAHATA	(R)S A H A T A\P\V/N|I/A G S R(T)		99.03	451.2397	1351.708	-0.0031	-2.3	9.49	300351.7	12.1	HUMAN	Q9UQ35	Serine/arginine repetitive matrix protein 2
10961	dirMS_041712_NAR_120mM_minus.10625.10625.3	3	9.67	1	2.46E+05		(R)YLAEFAT	(R)Y L/A E/F A/T/G/N D R K(E)		111.73	462.2338	1384.686	0.0013	0.9	6.07	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
10962	dirMS_041712_NAR_120mM_minus.12838.12838.2	2	9.67	1	1.76E+05		(K)VKLEAEI	(K)V/K/L|E/A\E I/A T Y\R(R)		123.82	646.8634	1292.721	-0.0014	-1	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10963	dirMS_041712_NAR_120mM_minus.13037.13037.3	3	9.67	1	1.49E+05		(R)KQITME	(R)K Q I T\M/E/E/L V/R(S)		125.65	416.2324	1246.682	0.0003	0.2	6.14	533778	5.74	HUMAN	Q15149	Plectin
10964	dirMS_041712_NAR_20mM_minus.14705.14705.2	2	9.67	0	1.40E+05		(R)IITLAGP	(R)I I/T|L/A/G/P T N A I F K(A)		202.17	679.9047	1358.804	-0.0021	-1.5	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
10965	dirMS_041712_NAR_30mM_minus2.19388.19388.2	2	9.67	0	1.93E+05		(R)ILVATNL	(R)I L|V/A/T N/L F G R(G)		161.85	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
10966	dirMS_041712_NAR_50mM_minus2.10508.10881.3	3	9.67	0	2.96E+05		(K)VFEGNR	(K)V F|E/G N R P T N S I V\F/T K(L)		129.28	570.3032	1708.902	-0.0066	-3.9	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
10967	dirMS_041712_NAR_50mM_minus2.18069.18069.3	3	9.67	0	8.78E+04		(R)EAVELPL	(R)E A/V E/L/P/L T H F E L Y K(Q)		171.98	563.634	1688.889	-0.002	-1.2	4.75	47479.5	5.09	HUMAN	P43686	26S protease regulatory subunit 6B
10968	dirMS_041712_NAR_50mM_minus2.7127.7127.3	3	9.67	0	1.74E+05		(R)SAEEEA	(R)S A|E E/E/A/A/D/L P T K P T K(I)		106.92	529.6012	1586.791	-0.0018	-1.1	4.41	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
10969	dirMS_041712_NAR_50mM_minus2.8307.8307.3	3	9.67	1	8.11E+04		(K)VAQPTIT	(K)V A|Q/P/T I T D/N K D G T V T V R(Y)		115.13	605.6545	1814.961	-0.0117	-6.5	5.93	83264.1	6.04	HUMAN	E9PHF0	Filamin-A
10970	dirMS_041712_NAR_60mM_minus.15870.15870.3	3	9.67	1	3.86E+05		(K)KANLQII	(K)K A N L Q I D\Q\I/N/T/D|L/N L E R(S)		148.07	666.6911	1998.061	-0.0027	-1.3	4.56	227783.5	5.5	HUMAN	P35579	Myosin-9
10971	dirMS_041712_NAR_60mM_minus.17044.17044.3	3	9.67	0	1.00E+05		(R)LLANQQ	(R)L L|A/N Q Q/V/F H I/S C F/R(C)	C:Carbamidomethylation	154.67	578.3012	1732.895	-0.0061	-3.5	9.75	67446.5	5.63	HUMAN	F8VQE1	LIM domain and actin-binding protein 1
10972	dirMS_041712_NAR_120mM_plus.11673.11673.2	2	9.67	1	8.55E+05		(R)NLKASLE	(R)N/L/K/A|S/L E N S L R(E)		114.02	622.8511	1244.696	-0.0008	-0.6	8.75	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10973	dirMS_041712_NAR_20mM_plus.19238.19238.2	2	9.67	0	1.28E+05		(R)EGDVLT	(R)E G D V|L|T/L/L E/S E R(E)		203.63	680.8536	1360.696	0.0045	3.3	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
10974	dirMS_041712_NAR_20mM_plus.7635.7635.2	2	9.67	0	2.01E+05	M328m	(K)ALmDEV	(K)A/L|m/D E V V|K(A)	m:Oxidized methionine	122.5	460.741	904.481	15.9939	-1.1	4.37	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
10975	dirMS_041712_NAR_30mM_plus2.5804.5804.2	2	9.67	0	6.56E+04		(K)NTCTSV	(K)N T/C T/S/V/Y/T K(D)	C:Carbamidomethylation	84.92	537.2502	1073.493	-0.0001	-0.1	8.59	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
10976	dirMS_041712_NAR_50mM_plus2.13720.13720.3	3	9.67	0	4.46E+05		(K)FLSDPQ	(K)F/L/S D/P Q V/H T V L V E/R(S)		140.13	547.2984	1639.88	0.0004	0.3	5.32	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
10977	dirMS_041712_NAR_50mM_plus2.17939.17939.3	3	9.67	0	7.62E+04		(K)LNLSCIH	(K)L/N\L|S/C I H S/P V/V N E L M R(G)	C:Carbamidomethylation	162.23	627.9943	1881.967	0.001	0.5	6.75	60090.6	9.25	HUMAN	Q9Y2X3	Nucleolar protein 58
10978	dirMS_041712_NAR_50mM_plus2.21895.21895.3	3	9.67	1	1.23E+04	S645s	(R)LDsQLEI	(R)L\D/s Q L/E I/L\S/P S R S A R(V)	s:N-acetylglucosamine (S)	186.87	625.6716	1671.902	203.0978	9.8	6.07	98435.9	8.21	HUMAN	Q53R41	FAST kinase domain-containing protein 1
10979	dirMS_041712_NAR_60mM_plus.10785.10952.3	3	9.67	0	7.88E+05		(R)ISNRPAF	(R)I/S/N R P A\F\M|P S E/G K(M)		114.92	478.578	1433.721	-0.0011	-0.8	8.75	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
10980	dirMS_041712_NAR_60mM_plus.16135.16135.3	3	9.67	0	5.46E+05		(R)ETHSALC	(R)E T H S A L|G/P\A/L Q A A F K(L)		141.77	514.2744	1540.812	-0.0032	-2.1	6.85	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
10981	dirMS_041712_NAR_60mM_plus.16836.16836.3	3	9.67	1	5.36E+06		(K)LKVPEW	(K)L K V P E W/V D/T V/K(L)		145.55	438.5872	1313.746	0.0007	0.5	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
10982	dirMS_041712_NAR_120mM_minus.13434.13434.4	4	9.66	1	9.52E+05		(K)SVHSSVI	(K)S V H S\S V/P L/L/N S K D/P I/D R(I)		127.53	466.7525	1863.992	-0.0041	-2.2	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
10983	dirMS_041712_NAR_50mM_minus2.11009.11009.3	3	9.66	0	2.62E+05		(K)VTVLFAC	(K)V T|V/L/F/A/G Q H/I S K(S)		130.92	433.9205	1299.742	0.005	3.8	8.73	258215.9	5.48	HUMAN	E7EN95	Filamin-B
10984	dirMS_041712_NAR_50mM_minus2.11619.11619.3	3	9.66	0	2.76E+05	M291m	(K)TGEEIFG	(K)T G\E/E|I/F/G/T I/G m R P N A K(N)	m:Oxidized methionine	134.2	579.6239	1720.869	15.9885	-3.7	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
10985	dirMS_041712_NAR_50mM_minus2.12735.12735.3	3	9.66	0	9.95E+05	M114m M	(R)AGKPVIC	(R)A G K\P V\I|C\A\T\Q/m/L E|S m I K(K)	C:Carbamidomethylation m:Oxid	139.97	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
10986	dirMS_041712_NAR_50mM_minus2.14447.14447.3	3	9.66	1	1.81E+04		(R)AACLLDC	(R)A A|C/L\L D/G\V/P V A L K K(V)	C:Carbamidomethylation	150.35	485.6161	1454.84	-0.0062	-4.3	8.64	9312.6	9.1	HUMAN	F8WAG2	Serine/threonine-protein kinase Nek7 (Fragment)
10987	dirMS_041712_NAR_50mM_minus2.9884.9884.3	3	9.66	0	3.71E+05	M147m	(K)LQmEAF	(K)L Q|m E/A/P/H I|I/V G T P G R(V)	m:Oxidized methionine	124.88	545.6267	1618.873	15.9922	-1.7	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
10988	dirMS_041712_NAR_120mM_plus.12437.12437.4	4	9.66	1	1.78E+06		(K)TLTTVQC	(K)T L T T/V Q/G|I/A D/D/Y D K K K(L)		117.78	449.7412	1795.944	-0.0006	-0.4	5.71	13778.5	7.96	HUMAN	K7EM18	Eukaryotic translation initiation factor 1
10989	dirMS_041712_NAR_20mM_plus.13994.13994.3	3	9.66	0	3.16E+05	M313m	(R)TVQSLEI	(R)T\V Q S L E\I/D|L/D/S m R(N)	m:Oxidized methionine	168.57	508.2519	1506.747	15.9943	-0.4	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
10990	dirMS_041712_NAR_20mM_plus.16912.16912.3	3	9.66	0	1.96E+05		(R)AIVAIEN	(R)A I|V A I E N/P A D V/S V/I S S R(N)		188.73	580.9864	1740.949	-0.0044	-2.5	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
10991	dirMS_041712_NAR_20mM_plus.18608.18608.2	2	9.66	0	2.01E+05		(K)IYVDDGI	(K)I Y|V/D/D G L/I S L Q V/K(Q)		200.52	731.9068	1462.815	-0.0088	-6	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
10992	dirMS_041712_NAR_30mM_plus2.11771.11771.2	2	9.66	0	4.85E+05		(R)AMGEQ	(R)A M|G/E/Q/A/V/A L A/R(A)		114.22	558.7944	1116.583	-0.0015	-1.3	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
10993	dirMS_041712_NAR_30mM_plus2.12815.12919.2	2	9.66	0	3.54E+05		(R)NLGLYVI	(R)N L|G/L Y/V/K(T)		120.72	403.7418	806.477	-0.0007	-0.9	8.59	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
10994	dirMS_041712_NAR_30mM_plus2.7817.7817.2	2	9.66	0	4.12E+05		(K)CNLLAEI	(K)C/N|L/L/A/E/K(Q)	C:Carbamidomethylation	94.87	424.2213	847.434	0.0011	1.3	6	40209.9	5.43	HUMAN	C9JV77	Alpha-2-HS-glycoprotein
10995	dirMS_041712_NAR_40mM_plus2.10614.10614.3	3	9.66	0	1.02E+05	M147m	(K)LQmEAF	(K)L Q/m E/A/P H/I/I V G T P G R(V)	m:Oxidized methionine	127.23	545.6274	1618.873	15.9943	-0.4	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
10996	dirMS_041712_NAR_50mM_plus2.12123.12123.3	3	9.66	1	5.72E+05		(R)DNKQAC	(R)D N/K Q A\G\V|F/E/P T I V K(V)		131.55	515.9483	1545.827	0.0032	2.1	6.07	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
10997	dirMS_041712_NAR_50mM_plus2.7723.7723.3	3	9.66	1	1.94E+05		(R)IVEQDTI	(R)I V/E Q D/T M/P P K G V R(H)		106.05	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
10998	dirMS_041712_NAR_60mM_plus.20419.20419.3	3	9.66	0	1.25E+06		(R)IHFPLAT	(R)I H F P L A T/Y/A/P/V I S A E/K(A)		166.1	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
10999	dirMS_041712_NAR_120mM_minus.15059.15059.3	3	9.65	1	2.52E+05		(R)IQLVEEE	(R)I Q|L/V/E E E L D R A Q E/R(L)		136.88	576.6344	1727.892	-0.0036	-2.1	4.25	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
11000	dirMS_041712_NAR_120mM_minus.15309.15309.4	4	9.65	2	1.28E+04		(R)EDLRLPE	(R)E/D L R L/P/E G/D L G K E I E Q K(Y)		137.83	493.0108	1969.024	-0.0023	-1.2	4.36	16346.3	4.85	HUMAN	I3L397	Eukaryotic translation initiation factor 5A-1 (Fragment)
11001	dirMS_041712_NAR_20mM_minus.9331.9331.2	2	9.65	0	1.05E+04		(R)AQIFAN	(R)A Q|I/F A/N/T/V/D N A R(I)		143	660.3388	1319.67	0.0001	0.1	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11002	dirMS_041712_NAR_40mM_minus2.10535.10956.3	3	9.65	1	3.00E+06		(K)TITLEVEI	(K)T I\T|L/E/V E/P S D T I E N V K A K(I)		146.03	663.0226	1987.059	-0.0061	-3.1	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
11003	dirMS_041712_NAR_40mM_minus2.14411.14411.3	3	9.65	0	2.72E+05		(R)DVCTELI	(R)D V/C/T/E L L/P L/I K P Q G R(V)	C:Carbamidomethylation	168.95	580.3211	1738.952	-0.0033	-1.9	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
11004	dirMS_041712_NAR_40mM_minus2.15223.15223.3	3	9.65	0	2.58E+06		(K)ALESPEF	(K)A L|E/S/P E R P F L A I L G G A K(V)		174.8	590.3353	1768.996	-0.0042	-2.4	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase

11005	dirMS_041712_NAR_50mM_minus2.8551.8551.3	3	9.65	1	2.43E+05		(R)AGTGVD	(R)A G/T/G/V/D N V D L/E/A/A T R K(G)		116.55	539.6119	1616.824	-0.0027	-1.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
11006	dirMS_041712_NAR_50mM_minus2.9397.9412.3	3	9.65	1	9.84E+04		(K)TATPEIV	(K)T A|T/P E/I V/D N K/D/G T V T\V R(Y)		121.37	605.9853	1815.945	-0.0033	-1.8	4.55	258215.9	5.48	HUMAN	E7EN95	Filamin-B
11007	dirMS_041712_NAR_60mM_minus.14676.14676.3	3	9.65	0	1.65E+06		(K)SLTNDW	(K)S L|T/N D W E D/H/L A V K(H)		142.13	509.9191	1527.744	-0.0011	-0.7	4.53	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
11008	dirMS_041712_NAR_120mM_plus.14830.14831.3	3	9.65	1	8.47E+05		(K)LDKSQIH	(K)L D K S Q I/H D|I|V|L\V|G G S T R(I)		131	613.3369	1838.013	-0.0169	-9.2	6.75	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
11009	dirMS_041712_NAR_20mM_plus.11573.11573.2	2	9.65	0	1.63E+05		(K)VGLQVV	(K)V/G/L|Q|V V/A/V K(A)		151.8	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
11010	dirMS_041712_NAR_20mM_plus.12549.12549.2	2	9.65	0	1.42E+05		(K)DLAGSII	(K)D L|A/G S I/I/G K(G)		158.77	437.2558	873.504	0.0003	0.4	5.84	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
11011	dirMS_041712_NAR_20mM_plus.12679.12679.2	2	9.65	0	5.51E+04		(K)YGQISE\	(K)Y G\Q/I/S E\V/V V V/K(D)		160.02	610.8456	1220.689	-0.0046	-3.8	6	28815.3	9.52	HUMAN	B4E2X2	Cold-inducible RNA-binding protein
11012	dirMS_041712_NAR_30mM_plus2.15081.15266.2	2	9.65	0	8.11E+05		(K)LYANMF	(K)L/Y|A|N/M/F E/R(L)		132.37	522.2535	1043.498	0.0018	1.8	6	9740.1	10.08	HUMAN	H0YFG2	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed (Fragment)
11013	dirMS_041712_NAR_30mM_plus2.6638.6638.2	2	9.65	0	2.00E+05		(K)TLNAGA	(K)T L/N/A/G A Y|S K(V)		89.22	462.7408	924.479	-0.0042	-4.5	8.26	30197.4	7.91	HUMAN	E9PMG2	Palmitoyl-protein thioesterase 1 (Fragment)
11014	dirMS_041712_NAR_30mM_plus2.6871.6871.2	2	9.65	0	2.73E+05		(K)AEYLCR(	(K)A E|Y/L/C R(I)	C:Carbamidomethylation	90.82	406.1945	811.377	0.005	6.2	6.04	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
11015	dirMS_041712_NAR_30mM_plus2.8408.8408.2	2	9.65	0	2.24E+05		(R)VAIEPG/	(R)V A/I/E/P G A/P/R(E)		97.73	455.2602	909.515	-0.0021	-2.3	5.97	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
11016	dirMS_041712_NAR_40mM_plus2.16107.16107.3	3	9.65	1	1.95E+05		(R)VYAEDP	(R)V/Y|A/E/D P Y K S F G L/P S/I G R(L)		161.6	633.6593	1898.965	-0.0013	-0.7	6.04	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
11017	dirMS_041712_NAR_50mM_plus2.17220.17220.3	3	9.65	1	8.65E+05		(R)VYAEDP	(R)V/Y|A E/D/P Y K S F G L/P S I G/R(L)		159.17	633.6509	1898.965	-0.0265	-14	6.04	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
11018	dirMS_041712_NAR_50mM_plus2.18500.18500.3	3	9.65	1	5.52E+05		(K)NAAGAL	(K)N A/A|G A L/D L L K E L K(N)		165.92	452.601	1355.789	-0.0008	-0.6	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
11019	dirMS_041712_NAR_50mM_plus2.7185.7185.3	3	9.65	1	1.94E+05		(R)DSFDGR	(R)D S/F/D/G R/G P\P G P E/S Q/S R(A)		103.85	563.592	1688.762	-0.0009	-0.5	4.56	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
11020	dirMS_041712_NAR_50mM_plus2.7677.7677.3	3	9.65	1	5.17E+04		(K)AAAAAS	(K)A A\A|A/A|S|A A G P G G L V A G K E E K(K)		106.4	575.9777	1725.913	0.0056	3.2	6.18	28364.3	5.45	HUMAN	A6NIH7	Protein unc-119 homolog B
11021	dirMS_041712_NAR_60mM_plus.18702.18702.3	3	9.65	0	1.99E+05		(K)GSDHSA	(K)G S D H S A S L\E|P G E/L|A E L V R(S)		155.43	622.9778	1866.919	-0.0003	-0.2	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
11022	dirMS_041712_NAR_60mM_plus.8939.9085.3	3	9.65	1	7.38E+05		(R)VVDSMI	(R)V/V|D/S M/E/D/E V Q R R(L)		105.27	488.2367	1462.696	0.0001	0.1	4.32	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
11023	dirMS_041712_NAR_120mM_minus.6034.6034.3	3	9.64	1	2.07E+04		(K)NVICDK(	(K)N V|I/C D/K C E G R(G)	C:Carbamidomethylation	86.4	417.525	1250.562	-0.0012	-0.9	6.07	45609.1	6.66	HUMAN	P31689	DnaJ homolog subfamily A member 1
11024	dirMS_041712_NAR_20mM_minus.12338.12338.3	3	9.64	0	7.28E+05	M73m	(R)AVLVDLI	(R)A V|L\V D\L E/P/G/T|m D S V R(S)	m:Oxidized methionine	172.38	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
11025	dirMS_041712_NAR_20mM_minus.7248.7248.2	2	9.64	0	1.47E+04	M33m	(R)IDEmPE/	(R)I/D\E/m|P E A A/V K(S)	m:Oxidized methionine	120.43	559.7733	1102.545	15.9944	-0.4	4.14	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
11026	dirMS_041712_NAR_30mM_minus2.11585.11587.2	2	9.64	0	3.24E+05		(K)EIAEAYL	(K)E I/A/E/A Y/L/G K(T)		115.95	497.265	993.525	-0.0024	-2.4	4.53	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
11027	dirMS_041712_NAR_30mM_minus2.12053.12053.2	2	9.64	0	3.05E+05		(K)GLVQAL	(K)G L/V/Q/A/L/Q/T K(V)		118.83	479.288	957.573	-0.004	-4.2	8.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
11028	dirMS_041712_NAR_30mM_minus2.7247.7247.2	2	9.64	0	2.75E+05		(K)SAVLQE/	(K)S A|V|L/Q|E A R(I)		94.43	437.2408	873.479	-0.0045	-5.2	5.72	28218.2	9.35	HUMAN	F6X838	Coatomer subunit gamma-2
11029	dirMS_041712_NAR_30mM_minus2.7578.7578.2	2	9.64	0	3.77E+05		(R)MGANSI	(R)M/G/A/N S L/E R(M)		95.93	439.2149	877.42	0.0029	3.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
11030	dirMS_041712_NAR_50mM_minus2.7404.7404.3	3	9.64	0	3.24E+04		(K)ATAGDT	(K)A T/A|G D T H/L G G E D/F D/N R(L)		109.13	559.2493	1675.731	0.0027	1.6	4.22	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
11031	dirMS_041712_NAR_120mM_plus.20605.20605.4	4	9.64	1	2.15E+05		(K)AAIDWF	(K)A/A|I/D W/F/D G K E F H G N/I I K(V)		161.23	491.0027	1960.992	-0.0026	-1.3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
11032	dirMS_041712_NAR_20mM_plus.14535.14535.2	2	9.64	0	6.56E+05	M73m	(R)AVLVDLI	(R)A V L\V|D/L|E|P G T m D S V R(S)	m:Oxidized methionine	171.07	809.4082	1601.82	15.9888	-3.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
11033	dirMS_041712_NAR_20mM_plus.16501.16501.3	3	9.64	0	2.12E+05		(K)TVTNAV	(K)T V T N A V\V T V/P A Y/F N D S Q R(Q)		184.58	661.3368	1981.998	-0.0019	-1	5.5	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
11034	dirMS_041712_NAR_30mM_plus2.13335.13335.2	2	9.64	0	5.70E+05		(K)CPFTGN	(K)C P/F|T/G N V S I/R(G)	C:Carbamidomethylation	122.88	575.7876	1150.567	0.0006	0.5	9.75	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
11035	dirMS_041712_NAR_30mM_plus2.18869.18869.2	2	9.64	0	5.13E+04		(R)MGPGIG	(R)M/G/P/G\I|G A I L E/R(S)		152.52	557.3091	1113.609	0.0024	2.2	5.75	14175.1	9.89	HUMAN	H0YKS1	Myelin expression factor 2 (Fragment)
11036	dirMS_041712_NAR_40mM_plus2.17823.17823.3	3	9.64	1	7.73E+04	M116m	(R)ELAILLG	(R)E L/A I/L L/G/m/L D P A E K D E K(G)	m:Oxidized methionine	171.67	634.3333	1884.999	15.9867	-4.3	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
11037	dirMS_041712_NAR_50mM_plus2.12038.12038.3	3	9.64	1	2.40E+05		(R)FNVPVS	(R)F N V/P/V/S L/E S K K(A)		131.27	416.5714	1247.699	0.0002	0.2	8.59	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
11038	dirMS_041712_NAR_50mM_plus2.6167.6167.3	3	9.64	0	1.85E+05		(R)ATAPQT	(R)A/T/A/P Q T Q/H V/S P M\R(Q)		96.3	475.2418	1423.711	-0.0002	-0.1	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
11039	dirMS_041712_NAR_60mM_plus.13312.13312.3	3	9.64	1	9.50E+05		(R)ISVYYNE	(R)I S|V/Y/Y N E A T G G K Y V P R(A)		126.05	606.3113	1816.923	-0.0035	-1.9	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
11040	dirMS_041712_NAR_60mM_plus.16925.16925.3	3	9.64	0	8.46E+05		(K)TTISVAH	(K)T T|I/S/V A/H L L A A/R(Q)		144.68	418.2478	1252.737	-0.0083	-6.7	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
11041	dirMS_041712_NAR_60mM_plus.21126.21211.3	3	9.64	1	4.03E+05		(R)KAIIIFVP	(R)K A I I\I\F\V|P V P Q L K(S)		174.23	489.3205	1465.95	-0.0035	-2.4	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
11042	dirMS_041712_NAR_60mM_plus.6423.6423.3	3	9.64	1	7.26E+06		(K)DSYVGD	(K)D S|Y/V/G D/E A Q S K R(G)		91.98	452.213	1354.623	0.0011	0.8	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
11043	dirMS_041712_NAR_30mM_minus2.12223.12223.2	2	9.63	0	1.29E+05		(R)TLSGME	(R)T L|S/G M/E/S Y C/V R(A)	C:Carbamidomethylation	119.48	651.795	1302.582	0.001	0.8	5.66	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
11044	dirMS_041712_NAR_30mM_minus2.17100.17100.2	2	9.63	0	8.32E+05		(R)LVNWPE	(R)L V|N/W P E/H L R(S)		146.1	582.315	1163.632	-0.0093	-8	6.75	25352.6	11.4	HUMAN	K7ENP0	Matrix metalloproteinase-28
11045	dirMS_041712_NAR_40mM_minus2.13847.13847.3	3	9.63	1	4.48E+04		(K)FGEVVD	(K)F/G|E/V/V\D C T L/K L D P I T G R(S)	C:Carbamidomethylation	165.3	640.6656	1919.989	-0.0073	-3.8	4.56	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
11046	dirMS_041712_NAR_50mM_minus2.10723.10841.3	3	9.63	0	2.85E+05		(K)VFEGNR	(K)V/F/E|G N\R P T N S I V F T/K(L)		129.3	570.3032	1708.902	-0.0066	-3.9	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
11047	dirMS_041712_NAR_50mM_minus2.17559.17559.3	3	9.63	0	4.20E+05		(K)VAHALA	(K)V A H A L A E G\L/G\V|I/A C I G E/K(L)	C:Carbamidomethylation	168.75	603.3247	1807.974	-0.0139	-7.7	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
11048	dirMS_041712_NAR_60mM_minus.18071.18084.3	3	9.63	1	2.77E+05		(R)TRIEGLL	(R)T R I\E G\L|L|A A F/P K(L)		161.67	439.2618	1315.773	-0.0024	-1.8	8.41	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
11049	dirMS_041712_NAR_60mM_minus.6089.6089.3	3	9.63	1	2.64E+05		(K)LEEAEK/	(K)L E|E/A E/K/A A D/E S E R(G)		92.57	492.8981	1476.681	-0.0015	-1	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
11050	dirMS_041712_NAR_60mM_minus.7510.7510.3	3	9.63	0	8.37E+04		(K)ALLQTHI	(K)A L/L Q T H/P E A Q R(A)		101.33	421.8989	1263.68	0.0017	1.4	6.79	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
11051	dirMS_041712_NAR_60mM_minus.9005.9005.3	3	9.63	1	3.60E+05	M232m M	(R)MSmKE\	(R)M S/m K E V D E Q|m|L N/V/Q N K(N)	m:Oxidized methionine	110.3	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
11052	dirMS_041712_NAR_20mM_plus.13062.13062.2	2	9.63	0	6.61E+04		(R)LAPDYD.	(R)L A/P/D Y D/A L D V A N K(I)		162.6	702.8524	1404.7	-0.003	-2.1	3.93	22029.9	10.62	HUMAN	A8MUS3	60S ribosomal protein L23a
11053	dirMS_041712_NAR_20mM_plus.13992.13992.3	3	9.63	0	1.26E+04		(K)AIANEC(	(K)A I/A N E\C Q/A/N F I/S/I K(G)	C:Carbamidomethylation	168.03	526.9365	1578.795	0.0005	0.3	6.05	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
11054	dirMS_041712_NAR_20mM_plus.14246.14246.2	2	9.63	0	8.76E+04		(K)GVVDSD	(K)G V/V D/S/D/D L/P L N V/S\R(E)		170.28	743.3789	1485.754	-0.0038	-2.6	3.93	92752.5	4.76	HUMAN	P14625	Endoplasmin
11055	dirMS_041712_NAR_20mM_plus.14966.14966.2	2	9.63	0	8.31E+04		(K)VVNIVP\	(K)V V|N|I/V P V/I A/K(A)		174.67	526.3453	1051.687	-0.0041	-3.9	8.72	22387.6	9.64	HUMAN	K7EK18	Septin-9 (Fragment)
11056	dirMS_041712_NAR_20mM_plus.7673.7673.2	2	9.63	0	1.34E+05		(K)YICENQI	(K)Y/I|C|E N Q D S I/S/S K(L)	C:Carbamidomethylation	122.43	722.3246	1443.642	-0.0001	-0.1	4.37	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
11057	dirMS_041712_NAR_30mM_plus2.11451.11511.2	2	9.63	0	4.42E+05		(R)LAELSDY	(R)L/A|E/L/S D/Y/R(R)		113.73	483.7442	966.489	-0.008	-8.2	4.37	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
11058	dirMS_041712_NAR_30mM_plus2.14891.14891.2	2	9.63	0	6.56E+04		(R)EYSLQVI	(R)E Y/S/L Q/V/L/K(N)		129.9	490.2728	979.546	-0.0076	-7.7	6.1	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
11059	dirMS_041712_NAR_30mM_plus2.18483.18483.2	2	9.63	0	2.36E+05		(K)GNFNYII	(K)G N\F/N|Y/I/E/F T R(I)		150.27	630.8035	1260.601	-0.001	-0.8	6	20513.6	4.62	HUMAN	J3QRS3	Myosin regulatory light chain 12A
11060	dirMS_041712_NAR_30mM_plus2.6900.7034.2	2	9.63	0	5.05E+05		(K)ISDSEGF	(K)I/S|D/S E/G F/K(A)		91.13	441.7168	882.42	0.006	6.8	4.37	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
11061	dirMS_041712_NAR_40mM_plus2.19280.19280.3	3	9.63	1	1.93E+05		(K)TSAQVV	(K)T S|A/Q V/V L/D G L V D K I G D V K(C)		180.37	619.6811	1857.033	-0.004	-2.2	4.43	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
11062	dirMS_041712_NAR_50mM_plus2.13523.13523.3	3	9.63	0	1.54E+06		(R)VLVVHD	(R)V L|V V/H/D G/F E G L/A K(G)		139.83	461.9229	1383.763	-0.0089	-6.5	5.32	18719.9	6.91	HUMAN	F8VP00	6-phosphofructokinase, muscle type (Fragment)
11063	dirMS_041712_NAR_60mM_plus.11579.11579.3	3	9.63	1	1.25E+06		(K)FGQYNK	(K)F/G Q/Y N K/E D|P T S F/R(L)		117.23	530.2507	1588.739	-0.0015	-0.9	6.07	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
11064	dirMS_041712_NAR_60mM_plus.17430.17430.3	3	9.63	1	3.74E+05		(R)KVPGVT	(R)K V|P G V T A\I\E|L/D E/D T/G T/F R(I)		148.18	650.0017	1948.002	-0.0117	-6	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
11065	dirMS_041712_NAR_120mM_minus.11508.11508.3	3	9.62	1	1.32E+06	M406m	(R)QLREYQ	(R)Q L R E Y Q E|L m/N\V/K(L)	m:Oxidized methionine	116.77	522.9361	1550.8	15.9942	-0.5	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
11066	dirMS_041712_NAR_120mM_minus.20087.20087.3	3	9.62	0	4.52E+05	M195m	(R)LHFFmP	(R)L H F F m P G F|A/P L T S R(G)	m:Oxidized methionine	166.07	546.2809	1620.835	15.9926	-1.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
11067	dirMS_041712_NAR_120mM_minus.4263.4263.3	3	9.62	1	3.43E+05		(R)MEQER(	(R)M/E|Q E R Q E Q E/E R(E)		70.83	497.8941	1491.649	0.0185	12.4	4.32	76925.9	4.46	HUMAN	A8MV58	Drebrin
11068	dirMS_041712_NAR_20mM_minus.12168.12306.2	2	9.62	0	1.19E+06	M313m	(R)TVQSLEI	(R)T V/Q/S\L|E/I D L/D S m R(N)	m:Oxidized methionine	170.82	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11069	dirMS_041712_NAR_20mM_minus.8306.8306.2	2	9.62	0	1.25E+05		(K)VTADVII	(K)V T/A/D\V/I/N/A A E K(L)		132.47	565.8065	1130.605	0.0005	0.5	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
11070	dirMS_041712_NAR_30mM_minus2.13765.13765.2	2	9.62	0	4.09E+05		(R)AIENELL	(R)A/I|E/N E L|L/A R(N)		127.68	514.79	1028.574	-0.0008	-0.7	4.53	40519.5	5.04	HUMAN	B6F210	Glutathione synthetase
11071	dirMS_041712_NAR_30mM_minus2.16055.16055.2	2	9.62	0	9.84E+04		(R)LVQAFQ	(R)L V|Q/A/F Q F T D K(H)		140.62	598.8155	1196.631	-0.0073	-6.1	5.84	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
11072	dirMS_041712_NAR_30mM_minus2.17278.17278.2	2	9.62	0	2.21E+05		(R)NGGQIL	(R)N\G\G|Q/I|L I/A D/L R(G)		148.1	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
11073	dirMS_041712_NAR_30mM_minus2.20039.20039.2	2	9.62	0	8.03E+04		(K)SLNILTA	(K)S L|N/I|L/T/A F Q K(K)		169.83	567.8283	1134.652	-0.0024	-2.1	8.47	18172.6	7.77	HUMAN	F8VY02	Endoplasmic reticulum resident protein 29
11074	dirMS_041712_NAR_60mM_minus.10736.10736.3	3	9.62	0	5.06E+04		(R)AYADSY	(R)A Y/A/D S Y Y Y/E/D/G G M K P R(V)		119.78	629.2712	1885.806	-0.0071	-3.8	4.56	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
11075	dirMS_041712_NAR_60mM_minus.14010.14010.3	3	9.62	1	8.34E+04		(K)SKLTFSC	(K)S K L T F S C|L/G/G/S D N F K(H)	C:Carbamidomethylation	138.07	554.2737	1660.8	0.0066	4	8.31	15014.9	3.9	HUMAN	B4DHP2	Prostaglandin E synthase 3
11076	dirMS_041712_NAR_60mM_minus.6605.6605.3	3	9.62	0	5.20E+04		(R)ATAPQT	(R)A T/A/P/Q\T Q H\V/S P M/R(Q)		95.48	475.2404	1423.711	-0.0044	-3.1	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
11077	dirMS_041712_NAR_60mM_minus.8694.8694.3	3	9.62	1	2.84E+05		(R)LGTPELS	(R)L/G\T/P E L/S T A E R K(E)		108.45	434.572	1301.706	-0.0045	-3.5	6.14	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
11078	dirMS_041712_NAR_20mM_plus.16559.16559.2	2	9.62	0	1.72E+05		(R)LLEAQIA	(R)L L\E\A/Q/I/A\T G G I\I|D|P K(E)		185.52	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
11079	dirMS_041712_NAR_20mM_plus.19223.19223.3	3	9.62	0	2.77E+05		(R)LAGTQP	(R)L A G T Q\P\L E V/L\E A/V Q R(S)		204.3	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
11080	dirMS_041712_NAR_20mM_plus.7340.7340.2	2	9.62	0	2.86E+05		(K)TGQAPC	(K)T G/Q|A|P/G Y S Y/T A A N K(N)		119.52	714.8394	1428.675	-0.0039	-2.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
11081	dirMS_041712_NAR_40mM_plus2.19228.19228.3	3	9.62	1	1.93E+05		(K)TSAQVV	(K)T/S\A/Q V/V L D/G L V D/K I G D V K(C)		180.37	619.6811	1857.033	-0.004	-2.2	4.43	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
11082	dirMS_041712_NAR_50mM_plus2.10612.10648.3	3	9.62	1	2.32E+05		(R)LVGGPN	(R)L/V|G/G/P M D A S/V E E E/G V R R(A)		123.63	600.9675	1800.891	-0.0029	-1.6	4.41	16027.2	9.57	HUMAN	P01034	Cystatin-C
11083	dirMS_041712_NAR_120mM_minus.4490.4490.3	3	9.61	1	1.50E+07	M310m	(R)TKTEISEI	(R)T K\T E\I|S/E/m/N R(N)	m:Oxidized methionine	72.87	408.8693	1208.594	15.9994	3.7	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
11084	dirMS_041712_NAR_120mM_minus.7449.7470.3	3	9.61	1	2.03E+05		(K)SESPKEP	(K)S E|S/P/K/E/P E Q L R(K)		94.95	433.8886	1299.654	-0.0027	-2.1	4.78	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
11085	dirMS_041712_NAR_20mM_minus.8693.8693.2	2	9.61	0	1.03E+05	M23m	(K)LYLADPr	(K)L Y/L/A/D/P m K(A)	m:Oxidized methionine	135.8	483.7514	950.502	15.994	-1	5.83	7781.8	6.82	HUMAN	E9PE20	Signal recognition particle 9 kDa protein
11086	dirMS_041712_NAR_30mM_minus2.15002.15154.2	2	9.61	0	5.86E+05		(K)VYFDLR(	(K)V/Y|F D/L/R(I)		135.32	406.7193	812.43	0.0012	1.5	5.8	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
11087	dirMS_041712_NAR_50mM_minus2.11290.11290.3	3	9.61	0	1.66E+04		(R)VVVLMC	(R)V V|V|L/M G S T S D L G H C E K(I)	C:Carbamidomethylation	132.28	577.9535	1731.84	0.0055	3.2	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
11088	dirMS_041712_NAR_50mM_minus2.7980.7980.3	3	9.61	0	8.88E+04		(K)TAVEHA	(K)T A/V E H|A T/D E D I L/A K(G)		112.23	504.9229	1512.754	0.0001	0.1	4.31	288852.1	5.33	HUMAN	E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein
11089	dirMS_041712_NAR_120mM_plus.9643.9643.3	3	9.61	1	7.40E+04		(R)TFKEICA	(R)T/F|K E I C/A\V/S/R(I)	C:Carbamidomethylation	102.52	404.2141	1210.625	0.0029	2.4	8.41	25558.6	9.3	HUMAN	B1APE1	General transcription factor IIB (Fragment)
11090	dirMS_041712_NAR_120mM_plus.9649.9649.3	3	9.61	1	1.21E+05		(R)QQEGES	(R)Q Q/E/G E/S R L/N L V Q R(N)		104	519.6066	1556.814	-0.0087	-5.6	6.14	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
11091	dirMS_041712_NAR_20mM_plus.10226.10226.2	2	9.61	0	9.56E+04		(K)LEAEIAT	(K)L/E|A E/I A T Y/R(R)		143.43	533.2797	1065.557	-0.0054	-5	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11092	dirMS_041712_NAR_20mM_plus.17910.17910.2	2	9.61	0	9.08E+04		(K)SLESLDT	(K)S L/E S/L/D T S L|F A K(N)		195.17	655.8428	1310.684	-0.0055	-4.2	4.37	52796.2	5.19	HUMAN	E7EUT8	Splicing factor 3A subunit 3
11093	dirMS_041712_NAR_20mM_plus.18099.18099.2	2	9.61	0	1.58E+05		(K)VANVSL	(K)V A\N\V/S L L A L Y K(G)		195.55	595.8558	1190.714	-0.01	-8.4	8.56	15978.4	10.84	HUMAN	P62266	40S ribosomal protein S23
11094	dirMS_041712_NAR_30mM_plus2.18885.18885.2	2	9.61	0	5.39E+05		(R)NFWVS(	(R)N F|W|V|S/G L S S T T R(A)		151.82	677.8411	1354.675	-0.0001	0	9.75	103309.5	5.34	HUMAN	A0AV56	SAFB protein
11095	dirMS_041712_NAR_30mM_plus2.22259.22259.3	3	9.61	0	3.06E+05		(K)NSSYFVI	(K)N S\S Y F V E/W|I/P N N V K(V)		171.93	566.2872	1696.833	0.0141	8.3	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
11096	dirMS_041712_NAR_30mM_plus2.7247.7247.2	2	9.61	0	3.05E+05		(K)GSAITGI	(K)G S A|I|T G/P V/A K(E)		92.77	450.7605	900.515	-0.0012	-1.3	8.75	8956.4	10.28	HUMAN	J3KTJ3	60S ribosomal protein L23
11097	dirMS_041712_NAR_30mM_plus2.8954.8954.2	2	9.61	0	5.36E+05		(K)QADVNI	(K)Q/A|D/V/N L/V/N A K(L)		100.82	536.2922	1071.579	-0.0022	-2	5.84	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
11098	dirMS_041712_NAR_40mM_plus2.13927.13927.3	3	9.61	1	3.86E+05		(R)QVFGEA	(R)Q V/F/G E/A T\K Q/P G I T F I A/A K(F)		147.62	636.0176	1906.043	-0.005	-2.6	8.59	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
11099	dirMS_041712_NAR_40mM_plus2.17383.17383.3	3	9.61	0	2.47E+04		(R)GTEDITS	(R)G T/E|D/I/T S/P H G I P L D\L\L D/R(V)		169.42	650.3372	1948.997	-0.0004	-0.2	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
11100	dirMS_041712_NAR_40mM_plus2.7952.7952.3	3	9.61	1	1.36E+05		(K)GAVAED	(K)G A\V/A/E/D G D E L\R T E/P E A/K(K)		107.38	596.2867	1786.845	0.0002	0.1	4.08	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
11101	dirMS_041712_NAR_50mM_plus2.11146.11146.3	3	9.61	1	3.14E+05		(R)DLDRIA(	(R)D L/D R I A/G\Q\V/A/A A N K(K)		126.77	481.2661	1441.776	0.008	5.5	5.96	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
11102	dirMS_041712_NAR_50mM_plus2.15286.15286.3	3	9.61	0	2.34E+05		(R)LASTLVH	(R)L A|S|T L V H L G E Y/Q/A/A V D/G A R(K)		148.03	657.6802	1971.029	-0.0034	-1.7	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
11103	dirMS_041712_NAR_50mM_plus2.15586.15586.3	3	9.61	1	1.01E+06		(R)KVPGVT	(R)K V/P G V T A I E\L/D|E/D T/G T F R(I)		149.87	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
11104	dirMS_041712_NAR_50mM_plus2.15860.15860.3	3	9.61	0	9.09E+05		(R)GHVFEE	(R)G H V F E E S\Q\V/A/G T/P M F V V K(A)		151.5	654.657	1961.979	-0.0225	-11.5	5.4	96306.4	6.41	HUMAN	P13639	Elongation factor 2
11105	dirMS_041712_NAR_50mM_plus2.17660.17686.3	3	9.61	0	3.57E+05		(R)LLLDIPL(	(R)L L|L D I|P L/Q T P H K(L)		160.8	463.2819	1387.831	0.0004	0.3	6.74	198852.6	5.95	HUMAN	A6NKT7	RanBP2-like and GRIP domain-containing protein 3
11106	dirMS_041712_NAR_50mM_plus2.21429.21429.3	3	9.61	1	1.97E+05		(R)LIALLEVI	(R)L I/A L/L/E V L/S Q K R(M)		183.25	461.6293	1382.873	0.0004	0.3	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
11107	dirMS_041712_NAR_50mM_plus2.21625.21625.3	3	9.61	1	1.96E+05		(K)LKVNFLF	(K)L K V N F\L|P/E I/I T L S K(E)		184.32	539.0011	1614.983	0.0058	3.6	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
11108	dirMS_041712_NAR_60mM_plus.17470.17470.3	3	9.61	1	3.74E+05		(R)KVPGVT	(R)K\V\P G V T A\I E|L/D E|D/T G\T F R(I)		148.18	650.0017	1948.002	-0.0117	-6	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
11109	dirMS_041712_NAR_60mM_plus.18494.18494.3	3	9.61	1	7.19E+05		(R)IRIDSLS/	(R)I R I D\S L\S\A/Q|L/S Q L Q K(Q)		154.07	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
11110	dirMS_041712_NAR_60mM_plus.20746.20746.3	3	9.61	0	6.69E+05		(R)LGFHLPI	(R)L G F H L P/L|E|V A/Y Q R(G)		168.7	514.9568	1542.843	0.0131	8.5	6.75	533778	5.74	HUMAN	Q15149	Plectin
11111	dirMS_041712_NAR_30mM_minus2.7236.7236.2	2	9.6	0	3.86E+05		(K)QQTLEA	(K)Q Q|T L/E/A E E A/K(R)		93.4	573.7846	1146.564	-0.0018	-1.6	4.25	76925.9	4.46	HUMAN	A8MV58	Drebrin
11112	dirMS_041712_NAR_30mM_minus2.9997.10009.2	2	9.6	0	2.19E+05		(R)GVTIKPT	(R)G V|T/I K/P T V/D|D D(-)		108.62	580.294	1159.584	-0.0034	-2.9	4.17	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
11113	dirMS_041712_NAR_50mM_minus2.12980.12980.3	3	9.6	0	4.04E+06	M84m	(K)YPIEHGI	(K)Y/P/I E H G I I|T/N/W D D m E K(I)	m:Oxidized methionine	141.68	659.6398	1960.911	15.9939	-0.5	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle

11114	dirMS_041712_NAR_50mM_minus2.13575.13575.3	3	9.6	0	2.72E+05		(K)VIQYLAY	(K)V I|Q Y L/A Y/V/A S S H K(S)		144.7	493.6043	1478.8	-0.0018	-1.2	8.48	227783.5	5.5	HUMAN	P35579	Myosin-9
11115	dirMS_041712_NAR_60mM_minus.12222.12222.3	3	9.6	1	1.44E+05		(R)FNVPVS	(R)F N/V|P V S/L E S K K(A)		127.98	416.571	1247.699	-0.001	-0.8	8.59	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
11116	dirMS_041712_NAR_60mM_minus.18954.18961.3	3	9.6	1	2.48E+05		(R)DSIVAEL	(R)D S/I/V/A/E L/D R E M S R(S)		168.02	507.5858	1520.737	0.0055	3.6	4.32	34709.6	4.98	HUMAN	O14579	Coatomer subunit epsilon
11117	dirMS_041712_NAR_20mM_plus.18297.18297.2	2	9.6	0	1.95E+05		(R)AAVEEG	(R)A A V E E/G/I|V|L|G G/G C A\L\L R(C)	C:Carbamidomethylation	197.9	842.9549	1684.905	-0.0025	-1.5	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
11118	dirMS_041712_NAR_30mM_plus2.6286.6286.2	2	9.6	0	2.52E+05		(K)GEGQLG	(K)G E|G Q/L|G/P A E R(A)		87.53	507.2537	1013.501	-0.0009	-0.9	4.53	96306.4	6.41	HUMAN	P13639	Elongation factor 2
11119	dirMS_041712_NAR_40mM_plus2.17614.17614.3	3	9.6	1	1.96E+05		(R)LKLPSIPI	(R)L K L P S I\P\L\V|P V\S A Q K(R)		170.73	530.671	1589.999	-0.0004	-0.3	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
11120	dirMS_041712_NAR_40mM_plus2.17922.17922.3	3	9.6	0	1.24E+05		(R)GFGFITF	(R)G F/G F/I/T F T N P E H A S V A M R(A)		172.02	661.3289	1981.959	0.0133	6.7	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
11121	dirMS_041712_NAR_50mM_plus2.11471.11471.3	3	9.6	1	3.38E+05		(R)ICCDLDV	(R)I/C/C D L D/V L/A S K K(V)	C:Carbamidomethylation	128.37	474.5801	1421.713	0.013	9.2	5.96	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
11122	dirMS_041712_NAR_50mM_plus2.17350.17350.3	3	9.6	0	3.46E+05		(K)DIPVVH	(K)D I/P/V V H/Q L L T R(Y)		159.6	430.9226	1290.753	0.0004	0.3	6.74	57147.5	7.81	HUMAN	P30419	Glycylpeptide N-tetradecanoyltransferase 1
11123	dirMS_041712_NAR_50mM_plus2.20271.20271.3	3	9.6	0	2.12E+05		(R)DYLHLPI	(R)D Y L H L\P\P E\I/V|P A/T L R(R)		174.1	578.658	1733.959	0.001	0.6	5.32	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
11124	dirMS_041712_NAR_50mM_plus2.7391.7391.3	3	9.6	0	1.54E+04		(R)ASLQETI	(R)A S/L/Q|E T H F D/S/T Q T K(Q)		104.73	531.5968	1592.755	0.0208	13	5.32	37597.1	4.91	HUMAN	C9JAT7	UBX domain-containing protein 7
11125	dirMS_041712_NAR_50mM_plus2.9583.9583.3	3	9.6	0	5.99E+05		(K)GAVDG	(K)G A|V/D G G L/S I/P H S T K(R)		117.25	446.9057	1338.701	0.0013	1	6.74	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
11126	dirMS_041712_NAR_60mM_plus.12585.12585.3	3	9.6	1	3.67E+05		(R)YIEVFKS	(R)Y I/E/V F/K S/S/Q E E V R(S)		122.33	538.6083	1613.817	-0.0066	-4.1	4.79	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
11127	dirMS_041712_NAR_30mM_minus2.17003.17003.2	2	9.59	0	1.94E+05		(R)IYNVIGT	(R)I/Y|N/V/I G T L R(G)		146.9	524.8092	1048.615	-0.0038	-3.7	8.75	84557.3	6.5	HUMAN	Q04609	Glutamate carboxypeptidase 2
11128	dirMS_041712_NAR_30mM_minus2.18996.19203.2	2	9.59	0	2.84E+05		(R)LTIAILR	(R)L T|I/A I/L/R(H)		159.23	400.2731	799.54	-0.0011	-1.3	9.75	87498	6.43	HUMAN	C9J266	E3 ubiquitin-protein ligase RNF123
11129	dirMS_041712_NAR_30mM_minus2.9019.9085.2	2	9.59	0	8.36E+05		(R)ALANSL	(R)A L|A|N/S/L A/C/Q/G K(Y)	C:Carbamidomethylation	103.73	566.7927	1132.578	0.0002	0.2	8.8	13951.6	9.48	HUMAN	H3BR68	Fructose-bisphosphate aldolase A (Fragment)
11130	dirMS_041712_NAR_50mM_minus2.10545.10545.3	3	9.59	0	7.23E+03		(R)ALQDLE	(R)A L/Q/D/L/E N A/A S G D A A V/H\Q R(I)		127.82	622.6372	1865.91	-0.013	-7	4.54	13862.5	4.75	HUMAN	K7EP82	Regulation of nuclear pre-mRNA domain-containing protein 1A (Fragment)
11131	dirMS_041712_NAR_60mM_minus.4801.4801.3	3	9.59	1	7.13E+05	M137m	(R)mQNDT	(R)m/Q/N/D T A E\N E T T E K E\E/K(S)	m:Oxidized methionine	79.37	638.2735	1896.813	15.9932	-0.9	4.14	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
11132	dirMS_041712_NAR_60mM_minus.9070.9070.3	3	9.59	0	2.42E+05		(K)SVIHSGF	(K)S/V/I H S G P/F/T/E/S Q/K(S)		110.93	472.9099	1416.712	0.0034	2.4	6.47	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
11133	dirMS_041712_NAR_120mM_plus.17356.17356.3	3	9.59	2	8.10E+05		(R)NLKASLE	(R)N L/K/A/S L/E N/S L R E V E/A R(Y)		143.8	610.332	1828.988	-0.0061	-3.3	6.23	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11134	dirMS_041712_NAR_20mM_plus.14450.14450.2	2	9.59	0	1.24E+05		(K)LVILANN	(K)L V|I/L/A/N N C P A L R(K)	C:Carbamidomethylation	171.38	677.3851	1353.767	-0.0042	-3.1	9.75	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
11135	dirMS_041712_NAR_20mM_plus.8251.8258.2	2	9.59	0	3.33E+05	M176m	(K)VLEGmE	(K)V/L|E/G m E V V R(K)	m:Oxidized methionine	126.95	524.278	1031.555	15.9933	-1.5	4.53	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
11136	dirMS_041712_NAR_30mM_plus2.13703.13808.2	2	9.59	0	2.91E+05		(R)TIAQDY	(R)T I|A/Q/D/Y G V L K(A)		125.23	554.3087	1107.604	0.0057	5.1	5.5	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
11137	dirMS_041712_NAR_30mM_plus2.19582.19582.2	2	9.59	0	2.61E+05		(K)APDFVF	(K)A P/D/F V/F Y/A/P/R(L)		156.63	591.8008	1182.594	0.0001	0.1	5.88	71218.8	6.3	HUMAN	A7YIJ8	Radixin
11138	dirMS_041712_NAR_30mM_plus2.8309.8309.2	2	9.59	0	1.96E+05		(R)TENCLSS	(R)T E/N C/L|S S/C V D\R(F)	C:Carbamidomethylation	97.15	670.7815	1340.557	-0.0012	-0.9	4.37	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
11139	dirMS_041712_NAR_40mM_plus2.11068.11068.3	3	9.59	0	1.00E+05	M35m	(K)AASDIA	(K)A A/S D I A m/T E L/P P T H P I R(L)	m:Oxidized methionine	131.03	612.652	1819.937	16.0044	5.1	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
11140	dirMS_041712_NAR_40mM_plus2.17368.17368.3	3	9.59	1	8.46E+04		(R)NAAALS	(R)N A|A|A/L/S Q/A L R L E A P E L P V K(V)		168.6	664.3784	1991.128	-0.0078	-3.9	6.14	10558	9.4	HUMAN	H0YE28	Protein C11orf31 (Fragment)
11141	dirMS_041712_NAR_50mM_plus2.10604.10604.3	3	9.59	1	2.19E+05		(K)SVEAAA	(K)S V\E/A/A A E L/S A K D L/K(E)		122.85	477.9286	1431.769	0.0023	1.6	4.68	12131.5	11.14	HUMAN	F5GXR3	Parathymosin
11142	dirMS_041712_NAR_50mM_plus2.12655.12655.3	3	9.59	1	8.84E+05		(R)ELISNSS	(R)E/L/I/S N S/S D A\L D K I R(Y)		134.15	520.9473	1560.823	0.0046	2.9	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
11143	dirMS_041712_NAR_60mM_plus.13793.13793.2	2	9.59	1	2.17E+06		(K)FASFIDK	(K)F/A|S|F/I/D K V/R(F)		129.18	541.8029	1082.599	-0.0008	-0.7	8.75	19569.8	9.88	HUMAN	F8VRG4	Keratin, type II cytoskeletal 8 (Fragment)
11144	dirMS_041712_NAR_60mM_plus.7124.7124.3	3	9.59	1	5.16E+05		(K)GLVPED	(K)G L/V/P E D D T K/E K(I)		95.55	410.8799	1230.621	0.0039	3.2	4.32	81733.5	5.24	HUMAN	E9PAW1	Splicing factor 3A subunit 1
11145	dirMS_041712_NAR_60mM_plus.7198.7198.2	2	9.59	0	1.72E+06		(K)STTTGHI	(K)S/T|T/T/G H\L I/Y/K(C)		95.58	560.8031	1120.6	-0.0008	-0.7	8.34	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
11146	dirMS_041712_NAR_120mM_minus.17462.17462.3	3	9.58	1	3.65E+05		(R)RTVQSLI	(R)R T V Q S\L/E|I/D L/D S M R(N)		149.57	554.9552	1662.848	0.0031	1.9	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11147	dirMS_041712_NAR_20mM_minus.13372.13372.2	2	9.58	1	2.45E+05		(R)LVLDSV	(R)L V|L/D/S V K L\E/A(-)		184.18	543.825	1086.641	0.0022	2	4.37	10137.3	4.59	HUMAN	E5RIW3	Tubulin-specific chaperone A
11148	dirMS_041712_NAR_30mM_minus2.10744.10744.2	2	9.58	0	6.30E+05		(K)GFSLESC	(K)G F/S/L/E/S C/R(S)	C:Carbamidomethylation	112.08	478.2237	955.43	0.0099	10.4	6	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
11149	dirMS_041712_NAR_30mM_minus2.12364.12364.2	2	9.58	0	2.35E+04		(K)GDYPLE	(K)G D Y|P/L/E A V\R(M)		119.97	510.2598	1019.516	-0.0033	-3.2	4.37	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
11150	dirMS_041712_NAR_30mM_minus2.16565.17076.2	2	9.58	0	7.70E+05		(K)MIFVGIK	(K)M/I|F/V/G I/K(K)		145.97	404.2383	807.48	-0.0104	-12.9	8.5	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
11151	dirMS_041712_NAR_50mM_minus2.10417.10417.3	3	9.58	0	1.27E+05		(K)NAQLNI	(K)N\A Q L/N I/E/L/E/A A H/H(-)		127.27	487.2478	1459.729	0	0	5.23	13452	8.89	HUMAN	F5H246	Protein NAMPTL
11152	dirMS_041712_NAR_50mM_minus2.15100.15100.3	3	9.58	0	2.48E+05	M118m	(R)AGKPVI	(R)A G K P V\I\C\A T/Q/M/L E S m I K(K)	C:Carbamidomethylation m:Oxid	154.47	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
11153	dirMS_041712_NAR_60mM_minus.11655.11676.3	3	9.58	1	1.63E+05		(K)ARLENEI	(K)A R L E\N E/I/A/T/Y/R(N)		124.97	445.91	1335.701	0.0139	10.4	6.19	51115.6	4.9	HUMAN	O76014	Keratin, type I cuticular Ha7
11154	dirMS_041712_NAR_60mM_minus.8596.8596.3	3	9.58	0	9.13E+04		(R)ISVYYNE	(R)I/S|V/Y Y/N E A/S S H K(Y)		107.72	466.5604	1397.67	-0.0029	-2.1	6.75	18402.2	5.06	HUMAN	G3V2N6	HCG1983504, isoform CRA_d
11155	dirMS_041712_NAR_120mM_plus.12073.12073.4	4	9.58	1	2.00E+06		(K)TLTTVQ	(K)T L T T V Q/G I/A/D D/Y D K K/K(L)		116.93	449.7412	1795.944	-0.0006	-0.4	5.71	13778.5	7.96	HUMAN	K7EM18	Eukaryotic translation initiation factor 1
11156	dirMS_041712_NAR_120mM_plus.5500.5524.3	3	9.58	1	2.28E+06		(R)QREMEE	(R)Q R E M|E|E/Q/M/R(R)		82	412.8549	1236.546	0.0042	3.4	4.79	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
11157	dirMS_041712_NAR_20mM_plus.13857.13857.2	2	9.58	0	1.26E+05	M62m	(R)DASLmV	(R)D A S/L/m|V|T N D G A/T I L K(N)	m:Oxidized methionine	167.72	782.8922	1548.794	15.9833	-7.4	4.21	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
11158	dirMS_041712_NAR_20mM_plus.18054.18054.2	2	9.58	0	1.02E+05		(K)VDFPQD	(K)V D/F/P Q D Q L|T A|L T G R(I)		195.67	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
11159	dirMS_041712_NAR_20mM_plus.8418.8418.2	2	9.58	0	2.56E+04		(R)NDAPTP	(R)N D\A|P T|P G T S T T\P G L R(S)		127.98	742.8666	1484.734	-0.008	-5.4	5.84	83912.5	6.73	HUMAN	E9PD64	Transducin-like enhancer protein 3
11160	dirMS_041712_NAR_30mM_plus2.10969.10969.2	2	9.58	0	4.85E+06		(R)QTVAVG	(R)Q T/V/A/V G V/I/K(A)		110.2	457.7881	914.567	0.002	2.2	8.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
11161	dirMS_041712_NAR_30mM_plus2.17042.17042.2	2	9.58	0	2.05E+05		(R)VFSGLVS	(R)V/F|S G L/V S T G L K(V)		141.95	554.322	1107.641	-0.0041	-3.7	8.72	96306.4	6.41	HUMAN	P13639	Elongation factor 2
11162	dirMS_041712_NAR_40mM_plus2.8307.8307.2	2	9.58	0	9.24E+04		(R)QLSSGV	(R)Q\L/S/S/G V/S E/I/R(H)		109.58	538.2862	1075.574	-0.0091	-8.5	6	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
11163	dirMS_041712_NAR_40mM_plus2.9172.9172.2	2	9.58	0	9.50E+04		(R)LSIYEAR	(R)L/S|I/Y E/A/R(C)		116.22	426.2316	851.462	-0.0062	-7.3	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
11164	dirMS_041712_NAR_60mM_plus.16276.16276.3	3	9.58	1	3.69E+05		(-)MKLNISF	(-)M K L N I S F|P/A/T G C Q K(L)	C:Carbamidomethylation	142.85	532.2733	1594.808	-0.0026	-1.7	10	10471.9	5.4	HUMAN	A2A3R7	40S ribosomal protein S6
11165	dirMS_041712_NAR_60mM_plus.20504.20504.3	3	9.58	1	3.02E+05		(R)AQFEGI	(R)A Q/F/E/G I V/T D/L I R R(T)		167.4	506.6178	1517.843	-0.0046	-3	6.12	18505.2	10.14	HUMAN	H0YBG6	Stress-70 protein, mitochondrial (Fragment)
11166	dirMS_041712_NAR_60mM_plus.5825.5825.3	3	9.58	1	8.67E+04		(R)CLSSATD	(R)C L/S S A/T/D/P Q/T K R(K)	C:Carbamidomethylation	88.38	455.226	1363.663	0	0	8.75	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
11167	dirMS_041712_NAR_20mM_minus.13300.13355.2	2	9.57	1	2.53E+05		(R)LVLDSV	(R)L/V|L|D S/V K L E A(-)		184.13	543.825	1086.641	0.0022	2	4.37	10137.3	4.59	HUMAN	E5RIW3	Tubulin-specific chaperone A
11168	dirMS_041712_NAR_30mM_minus2.14335.14335.2	2	9.57	0	7.55E+04		(R)TPYGASI	(R)T/P|Y|G\A/S I/F|Q\S K(E)		131.18	599.8093	1198.61	0.0011	0.9	8.26	44815.8	6.62	HUMAN	B3KQ29	Transducin-like enhancer protein 4
11169	dirMS_041712_NAR_50mM_minus2.15552.15552.3	3	9.57	0	2.09E+05		(R)QVVQGI	(R)Q V V Q/G L L/S E/T Y L E A/H/R(I)		156.7	614.9953	1842.971	0.0005	0.3	5.4	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
11170	dirMS_041712_NAR_120mM_plus.13425.13425.4	4	9.57	1	1.43E+06		(K)SVHSSVI	(K)S V H S S\V/P L/L N/S K/D P I D/R(I)		123.27	466.7533	1863.992	-0.0009	-0.5	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
11171	dirMS_041712_NAR_120mM_plus.21028.21028.4	4	9.57	0	3.21E+05		(K)ALEHAF	(K)A/L E H/A F Q L E H/I M/D/L T R(L)		163.55	481.7493	1923.975	0.0008	0.4	5.27	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
11172	dirMS_041712_NAR_120mM_plus.25704.25704.3	3	9.57	1	4.62E+05		(R)GVMLA	(R)G V\M|L/A/V D/A V/I A E L K/K(Q)		193.3	519.6402	1556.908	-0.002	-1.3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
11173	dirMS_041712_NAR_20mM_plus.13908.13908.2	2	9.57	0	3.21E+04	M178m	(K)GGIVGm	(K)G G I V/G/m|T L/P I/A/R(D)	m:Oxidized methionine	167.35	600.8402	1184.682	15.9911	-3.1	9.75	27150.8	7.95	HUMAN	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2
11174	dirMS_041712_NAR_20mM_plus.18280.18280.2	2	9.57	0	5.62E+04		(K)LFIGGLN	(K)L/F/I G/G L/N V Q/T S E S G L R(G)		197.5	845.9573	1690.912	-0.0049	-2.9	6	31011.2	9.5	HUMAN	Q13151	Heterogeneous nuclear ribonucleoprotein A0
11175	dirMS_041712_NAR_20mM_plus.7438.7438.3	3	9.57	0	2.14E+05		(K)TGQAPG	(K)T G Q A\P G|Y/S/Y/T A A/N K(N)		119.53	476.8963	1428.675	-0.001	-0.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
11176	dirMS_041712_NAR_20mM_plus.8744.8744.2	2	9.57	0	5.31E+03		(R)AVLIAG	(R)A V/L/I|A|G\Q/P G T G K(T)		130.05	556.3256	1111.647	-0.0031	-2.8	8.8	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
11177	dirMS_041712_NAR_30mM_plus2.20201.20201.2	2	9.57	0	3.58E+04		(R)TLMNLG	(R)T L|M|N|L|G G/L/A V A R(D)		159.42	608.3434	1215.688	-0.0083	-6.8	9.41	22562.2	8.8	HUMAN	P37802	Transgelin-2
11178	dirMS_041712_NAR_30mM_plus2.20657.20657.2	2	9.57	0	2.60E+05		(R)ASLSLW	(R)A S\L/S|L/W/Q A M E/K(G)		162.9	632.3231	1263.64	-0.0013	-1	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
11179	dirMS_041712_NAR_30mM_plus2.5568.5568.2	2	9.57	0	5.21E+04		(R)GGAGV	(R)G G|A/G/V/G S M T K(I)		84.05	432.7161	864.424	0.0005	0.6	8.75	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
11180	dirMS_041712_NAR_50mM_plus2.10401.10401.3	3	9.57	1	1.59E+05		(K)VELDNM	(K)V/E|L|D N M P L R G K(Q)		122.23	424.5659	1271.678	0.0055	4.3	6.04	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
11181	dirMS_041712_NAR_50mM_plus2.19180.19180.3	3	9.57	1	4.32E+05		(R)LKVPPAI	(R)L K|V|P/P A\I/N/Q F/T Q/A/L D R(Q)		169.82	604.3351	1811.017	-0.0266	-14.7	8.75	30166.2	10.79	HUMAN	P62424	60S ribosomal protein L7a
11182	dirMS_041712_NAR_50mM_plus2.21648.21648.3	3	9.57	1	1.95E+05		(K)LKVNFLF	(K)L K V N F L|P/E I/I/T L S K(E)		184.33	539.0011	1614.983	0.0058	3.6	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
11183	dirMS_041712_NAR_60mM_plus.5715.5715.3	3	9.57	1	1.53E+05	M131m	(R)QmGQP	(R)Q\m G Q/P C D/A/Y Q K/R(L)	C:Carbamidomethylation m:Oxid	87.98	499.8898	1481.662	15.9925	-1.6	8.59	334221.3	6.44	HUMAN	P15924	Desmoplakin
11184	dirMS_041712_NAR_60mM_plus.6352.6362.3	3	9.57	0	1.67E+05		(R)SQTSSIP	(R)S Q|T/S/S I/P Q K/P Q T N K(S)		91.88	515.2771	1543.807	0.0093	6	10	40335.7	7.39	HUMAN	H0Y5H6	Ubiquitin-associated protein 2-like (Fragment)
11185	dirMS_041712_NAR_120mM_minus.18172.18172.4	4	9.56	1	3.15E+05		(K)ILGSGIS	(K)I L G S G I/S/S S S V/L/H G M V F K K(E)		154.12	487.5223	1947.073	-0.0058	-3	10	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
11186	dirMS_041712_NAR_30mM_minus2.14633.14633.2	2	9.56	0	1.01E+05		(R)LDIDSPP	(R)L D\I/D/S/P P I T A R(N)		133.55	599.3249	1197.647	-0.0049	-4.1	4.21	5755.5	5.75	HUMAN	H3BN34	Pyruvate kinase isozymes M1/M2 (Fragment)
11187	dirMS_041712_NAR_40mM_minus2.12446.12446.3	3	9.56	1	2.37E+05	S80s	(R)LVEKPSF	(R)L/V E K/P/S R G s E E/H/L K(S)	s:N-acetylglucosamine (S)	155.97	604.6573	1608.87	203.087	4.2	6.76	52348.8	7.1	HUMAN	D5MNW9	Ankyrin repeat and SOCS box protein 10
11188	dirMS_041712_NAR_40mM_minus2.15456.15456.3	3	9.56	0	1.77E+05		(R)ETSSDV	(R)E T|S S/D V A|L/A S/H I L T A L R(E)		178.45	595.3178	1783.955	-0.016	-9	5.32	36920.6	4.68	HUMAN	O00273	DNA fragmentation factor subunit alpha
11189	dirMS_041712_NAR_40mM_minus2.6984.6984.2	2	9.56	0	5.85E+05		(R)GYSFTTT	(R)G/Y/S|F/T T/T A E/R(E)		111.95	566.7661	1132.527	-0.002	-1.8	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
11190	dirMS_041712_NAR_50mM_minus2.13425.13425.3	3	9.56	1	5.31E+05		(K)LTEDKAI	(K)L/T/E D K A D V Q/S\I\/G L Q/R(F)		144.8	595.9939	1785.97	-0.0034	-1.9	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
11191	dirMS_041712_NAR_50mM_minus2.7434.7434.3	3	9.56	0	1.45E+05		(K)IVIGYQS	(K)I V|I/G Y Q S H A D T A T/K(S)		109.47	501.9321	1503.78	0.0016	1	6.74	28739.8	8.54	HUMAN	D6RBW1	Eukaryotic translation initiation factor 4E
11192	dirMS_041712_NAR_50mM_minus2.9662.9662.3	3	9.56	0	1.24E+05		(K)MIVDPV	(K)M I\V/D/P/V/E P H G E M K(F)		122.52	494.5757	1481.713	-0.0002	-0.1	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
11193	dirMS_041712_NAR_60mM_minus.10623.10623.3	3	9.56	0	2.57E+05		(R)SVIHSLA	(R)S V/I/H S L A/S\V/E/A Q K(S)		119.02	456.9195	1368.748	-0.0042	-3.1	6.47	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
11194	dirMS_041712_NAR_60mM_minus.14037.14037.3	3	9.56	1	2.40E+05		(R)VVISLQL	(R)V/V|I/S L/Q L/T A E/K R(V)		138.07	452.9408	1356.821	-0.0131	-9.6	8.72	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
11195	dirMS_041712_NAR_60mM_minus.17970.17970.3	3	9.56	0	3.59E+03		(R)GGYVLH	(R)G G Y/V\L/H/I/G T I/Y G D/L K(V)		161.65	535.9574	1605.863	-0.0059	-3.7	6.74	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
11196	dirMS_041712_NAR_60mM_minus.7745.7745.3	3	9.56	1	5.37E+05		(R)YLAEVA	(R)Y L/A E V A/A/G D D K K(G)		102.12	427.222	1279.653	-0.0014	-1.1	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
11197	dirMS_041712_NAR_60mM_minus.9047.9047.3	3	9.56	0	2.35E+05		(K)SVIHSGF	(K)S V/I H\S G\P|F/T/E S Q K(S)		110.9	472.9099	1416.712	0.0034	2.4	6.47	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
11198	dirMS_041712_NAR_120mM_plus.15174.15174.4	4	9.56	2	6.75E+05		(K)TVGVEP	(K)T V|G V/E/P A A D G K G V V V V I K/R(R)		132.43	474.2836	1894.112	0.0005	0.3	8.26	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
11199	dirMS_041712_NAR_120mM_plus.18063.18063.3	3	9.56	0	4.73E+05		(R)HLLQAP	(R)H L|L|Q A|P V D D A Q E I/L H/S R(F)		148.32	648.0088	1942.014	-0.0023	-1.2	5.21	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
11200	dirMS_041712_NAR_120mM_plus.18087.18087.4	4	9.56	0	9.38E+04		(R)HLLQAP	(R)H L\L Q A|P|V D D A Q/E I L/H S R(F)		148.65	486.2589	1942.014	-0.0003	-0.2	5.21	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
11201	dirMS_041712_NAR_20mM_plus.18255.18255.2	2	9.56	0	1.70E+05		(K)DAGVIA	(K)D A G\V|I/A|G/L N V L R(I)		196.73	599.3505	1197.695	-0.0013	-1.1	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
11202	dirMS_041712_NAR_30mM_plus2.16727.16727.2	2	9.56	0	1.25E+05		(R)MGPAM	(R)M G/P A/M|G/P A L G\A G I E R(M)		140.25	714.3615	1427.713	0.0024	1.7	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
11203	dirMS_041712_NAR_30mM_plus2.19162.19162.2	2	9.56	0	2.24E+05		(K)TVDNFV	(K)T/V/D N F/V/A/L A/T G E K(G)		154.3	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
11204	dirMS_041712_NAR_30mM_plus2.4255.4255.2	2	9.56	0	4.81E+05	M558m	(R)mGANN	(R)m/G/A|N N/L/E/R(M)	m:Oxidized methionine	70.2	460.7158	904.431	15.9938	-1.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
11205	dirMS_041712_NAR_40mM_plus2.11992.11992.3	3	9.56	0	5.37E+04		(R)TVVSGS	(R)T V|V/S G S C A A/H S L L I T T E/G K(L)	C:Carbamidomethylation	136.67	644.3327	1930.99	-0.0067	-3.5	6.41	56825.2	9.49	HUMAN	Q9P258	Protein RCC2
11206	dirMS_041712_NAR_40mM_plus2.14995.14995.3	3	9.56	0	2.29E+05		(R)EVIDLLK	(R)E V|I/D L\L K/P D Q V/E G I Q K(S)		155.13	608.6749	1824.011	-0.0012	-0.6	4.32	156557.7	5.52	HUMAN	Q86UP2	Kinectin
11207	dirMS_041712_NAR_50mM_plus2.11697.11697.3	3	9.56	1	1.31E+05		(K)IGRIEDV	(K)I G R I E D\V T P\I/P/S/D/S T R(R)		128.73	585.9784	1755.924	-0.0029	-1.7	4.56	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
11208	dirMS_041712_NAR_50mM_plus2.14267.14282.3	3	9.56	1	8.83E+05		(K)ATLPSPD	(K)A T|L/P S P/D K L/P G F K(M)		143.57	457.5906	1370.768	-0.0106	-7.7	8.64	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
11209	dirMS_041712_NAR_50mM_plus2.19126.19126.3	3	9.56	0	5.12E+05		(R)GFGFITF	(R)G F|G/F/I/T/F T/N/P E H A S V A M R(A)		168.95	661.3258	1981.959	0.004	2	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
11210	dirMS_041712_NAR_50mM_plus2.19149.19169.3	3	9.56	0	7.58E+05		(R)LGFHLPI	(R)L G\F H L\P L/E|V/A/Y Q R(G)		168.23	514.9522	1542.843	-0.0007	-0.4	6.75	533778	5.74	HUMAN	Q15149	Plectin
11211	dirMS_041712_NAR_60mM_plus.12830.12830.3	3	9.56	0	1.38E+05		(R)LFGGNF	(R)L/F|G G/N F A H Q A S V A/R(V)		124.15	492.2556	1474.755	-0.0027	-1.8	9.75	61760.3	6.01	HUMAN	O14773	Tripeptidyl-peptidase 1
11212	dirMS_041712_NAR_120mM_minus.19474.19474.3	3	9.55	1	1.00E+05		(K)LEALKDI	(K)L E A L K D|L/A S\L S/R(D)		161.92	439.2616	1315.758	0.0123	9.3	6.07	18679.9	4.7	HUMAN	C9IZR8	Engulfment and cell motility protein 1 (Fragment)
11213	dirMS_041712_NAR_120mM_minus.8629.8682.2	2	9.55	1	1.51E+06	M174m	(R)VKYETEI	(R)V/K|Y|E|T/E L A m R(Q)	m:Oxidized methionine	101.97	628.3209	1239.64	15.9943	-0.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11214	dirMS_041712_NAR_120mM_minus.9412.9707.3	3	9.55	0	8.55E+05		(K)SPQYCQ	(K)S/P|Q|Y C Q/V I/H/R(L)	C:Carbamidomethylation	106.37	429.8855	1287.626	0.0157	12.2	8.49	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
11215	dirMS_041712_NAR_30mM_minus2.18992.19035.2	2	9.55	0	2.33E+05		(K)MAILQIN	(K)M/A|I/L/Q I\M/K(E)		158.23	474.2745	947.542	0.0001	0.1	8.5	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
11216	dirMS_041712_NAR_30mM_minus2.5856.5856.2	2	9.55	0	2.27E+05		(R)VVSSIEQ	(R)V V|S/S I/E Q K(T)		86.03	445.2523	889.499	-0.0016	-1.8	5.97	8491.4	6.28	HUMAN	E5RIR4	14-3-3 protein zeta/delta (Fragment)
11217	dirMS_041712_NAR_30mM_minus2.9617.9617.2	2	9.55	0	5.10E+04		(R)VTVVDV	(R)V T|V/V/D|V N E S R(I)		106.58	559.2986	1117.585	0.0051	4.6	4.37	6026	6.52	HUMAN	D6RHF4	UDP-glucose 6-dehydrogenase (Fragment)
11218	dirMS_041712_NAR_40mM_minus2.16061.16061.3	3	9.55	1	7.03E+05		(R)ELAILLG	(R)E L A/I/L/L G M L D/P A E K D E K(G)		189.45	629.0034	1884.999	-0.003	-1.6	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
11219	dirMS_041712_NAR_50mM_minus2.12910.12910.3	3	9.55	0	2.95E+05		(R)ETNLDSI	(R)E T N L/D S L/P L/V/D T H S K(R)		142.23	556.9529	1668.844	0.0002	0.1	4.53	53707.8	5.06	HUMAN	P08670	Vimentin
11220	dirMS_041712_NAR_50mM_minus2.5780.5780.3	3	9.55	1	1.15E+05		(K)EAVSTPS	(K)E A|V S T P S R M/A H|R(D)		94.6	447.8956	1341.669	0.0031	2.3	9.7	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
11221	dirMS_041712_NAR_50mM_minus2.9636.9636.3	3	9.55	1	2.92E+05		(R)ALEEAM	(R)A L/E\E\A M E Q/K/A E/L E R(L)		122.23	549.6072	1646.805	0.0016	1	4.33	227783.5	5.5	HUMAN	P35579	Myosin-9
11222	dirMS_041712_NAR_60mM_minus.13297.13297.3	3	9.55	1	5.45E+05	M313m	(R)RTVQSLI	(R)R T V\Q\S\L E|I/D/L D/S/m R(N)	m:Oxidized methionine	134.57	560.2852	1662.848	15.9931	-1.1	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18

11223	dirMS_041712_NAR_60mM_minus.18143.18143.3	3	9.55	1	1.76E+04		(R)VTFSGLF	(R)V/T|F/S/G L R D T V T|P G E L L K(A)		162.32	611.6719	1833.012	-0.0105	-5.7	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
11224	dirMS_041712_NAR_30mM_plus2.10803.10803.2	2	9.55	0	1.07E+05		(R)GYSFTTT	(R)G Y|S\F/T T T A E R(E)		110	566.7674	1132.527	0.0006	0.5	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
11225	dirMS_041712_NAR_30mM_plus2.11312.11312.2	2	9.55	0	5.16E+04		(R)MGESDI	(R)M/G|E|S D D S I/L R(L)		112.17	561.7585	1122.51	0.0002	0.1	4.03	9225.3	9.16	HUMAN	P63220	40S ribosomal protein S21
11226	dirMS_041712_NAR_30mM_plus2.16700.16700.2	2	9.55	0	3.82E+05		(R)LWDLTT	(R)L W/D|L/T/T/G T T T R(R)		140.33	632.8304	1264.653	0.0003	0.3	5.84	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
11227	dirMS_041712_NAR_30mM_plus2.5463.5463.2	2	9.55	0	8.55E+04		(R)GGAGV(	(R)G G|A|G|V/G S/M T K(I)		82.32	432.7161	864.424	0.0005	0.6	8.75	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
11228	dirMS_041712_NAR_30mM_plus2.7697.7697.2	2	9.55	0	1.18E+05		(R)NVLLNN	(R)N V|L/L/N/N S/E K(M)		94.35	515.7855	1030.553	0.011	10.6	6	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b
11229	dirMS_041712_NAR_40mM_plus2.11140.11140.3	3	9.55	1	7.39E+04		(K)AVEEED	(K)A V/E E E D K M/T/P E/Q L A I K(N)		131.87	610.9764	1830.915	-0.0007	-0.4	4.25	34747.6	6.06	HUMAN	O00487	26S proteasome non-ATPase regulatory subunit 14
11230	dirMS_041712_NAR_40mM_plus2.13744.13744.3	3	9.55	1	2.58E+05		(R)GDVVPK	(R)G D V|V/P K/D V N|A A I A T I K(T)		147.32	537.6381	1610.911	-0.0115	-7.1	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
11231	dirMS_041712_NAR_40mM_plus2.20066.20066.3	3	9.55	1	1.41E+06		(R)ELAILLG	(R)E L\A I/L/L G M L/D/P A E K D E/K(G)		189.22	629.003	1884.999	-0.0042	-2.3	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
11232	dirMS_041712_NAR_50mM_plus2.10491.10491.3	3	9.55	0	5.29E+04		(R)LQAQQI	(R)L Q/A/Q Q D/A V/N I/V C H S K(T)	C:Carbamidomethylation	123.17	570.9571	1710.859	-0.0024	-1.4	6.74	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
11233	dirMS_041712_NAR_50mM_plus2.11256.11289.3	3	9.55	1	3.31E+05		(K)DLFPYEE	(K)D L|F|P/Y|E E S K E K(F)		127.05	462.2257	1384.663	-0.0005	-0.4	4.41	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
11234	dirMS_041712_NAR_50mM_plus2.12289.12289.3	3	9.55	1	2.80E+05		(R)ESDVPLI	(R)E/S D V/P L/K\T E E F E V T K(T)		132.68	584.2981	1750.874	0.0052	3	4.25	18909	6.21	HUMAN	Q969H8	UPF0556 protein C19orf10
11235	dirMS_041712_NAR_50mM_plus2.17126.17126.3	3	9.55	0	4.47E+05		(R)DLKPSNI	(R)D L/K P S N L\L|I/N T T C D L K(I)	C:Carbamidomethylation	158.28	615.664	1844.979	-0.0012	-0.6	5.96	30925	5.63	HUMAN	B3KR49	Mitogen-activated protein kinase 3
11236	dirMS_041712_NAR_60mM_plus.16744.16744.2	2	9.55	0	7.84E+05		(R)EHALLA\	(R)E/H|A|L/L\A/Y T L/G V/K(Q)		144.03	657.8735	1314.742	-0.0019	-1.4	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
11237	dirMS_041712_NAR_120mM_minus.11792.11792.3	3	9.54	1	3.96E+05		(R)QSVEAD	(R)Q S/V/E/A/D/I N G\L R/R(V)		118.45	453.244	1357.718	-0.0008	-0.6	6.07	19213.2	4.66	HUMAN	K7EMD9	Keratin, type I cytoskeletal 13 (Fragment)
11238	dirMS_041712_NAR_20mM_minus.12870.12870.2	2	9.54	0	3.41E+05		(R)FAIQDIS	(R)F A|I/Q D/I S V E/E/T S A K(E)		178.75	769.3885	1537.774	-0.0047	-3.1	4.14	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
11239	dirMS_041712_NAR_20mM_minus.13616.13616.2	2	9.54	0	1.33E+05		(K)ALQQGL	(K)A L\Q/Q|G/L V/G L E L K(E)		187.42	634.8811	1268.757	-0.0023	-1.8	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
11240	dirMS_041712_NAR_20mM_minus.7195.7195.2	2	9.54	0	1.49E+04	M33m	(R)IDEmPE/	(R)I D|E m|P E A A V/K(S)	m:Oxidized methionine	120.27	559.7733	1102.545	15.9944	-0.4	4.14	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
11241	dirMS_041712_NAR_30mM_minus2.18244.18244.2	2	9.54	0	7.87E+04		(R)NLVCTD	(R)N L|V/C/T D L F/T R(G)	C:Carbamidomethylation	153.68	619.8134	1238.62	-0.0003	-0.2	5.84	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
11242	dirMS_041712_NAR_50mM_minus2.11641.11641.3	3	9.54	1	1.90E+05		(K)IEVEKPF	(K)I/E|V/E/K/P F A I A K E(-)		134.4	458.5927	1373.767	-0.0039	-2.9	5.01	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
11243	dirMS_041712_NAR_50mM_minus2.18079.18079.3	3	9.54	0	2.87E+05		(R)SLHDAL(	(R)S L H/D A L\C|V/L/A/Q T V K(D)	C:Carbamidomethylation	171.73	518.9488	1554.831	0.001	0.6	6.46	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
11244	dirMS_041712_NAR_50mM_minus2.6801.6801.3	3	9.54	0	5.92E+05		(R)EATNPP'	(R)E A/T/N/P/P V I Q E E K/P K(K)		105.52	527.2846	1579.833	0.0066	4.2	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
11245	dirMS_041712_NAR_60mM_minus.11543.11543.3	3	9.54	1	2.94E+05		(R)VFDKEG	(R)V/F/D K E G\N G T V/M/G A E I/R(H)		124.35	574.9539	1722.848	-0.0008	-0.5	4.68	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
11246	dirMS_041712_NAR_60mM_minus.14263.14264.3	3	9.54	1	2.99E+05	M108m	(R)DSIVAEL	(R)D S|I|V/A E/L D R E m S R(S)	m:Oxidized methionine	138.78	512.9153	1520.737	15.994	-0.6	4.32	34709.6	4.98	HUMAN	O14579	Coatomer subunit epsilon
11247	dirMS_041712_NAR_60mM_minus.5593.5593.3	3	9.54	1	1.14E+05	M1m	(-)mDSETD	(-)m/D/S/E T/D M V R Q I R(A)	m:Oxidized methionine	87.43	499.5724	1480.688	16.0144	13	4.56	28693	5.27	HUMAN	E9PJ36	Vacuolar protein sorting-associated protein 51 homolog (Fragment)
11248	dirMS_041712_NAR_60mM_minus.6988.6988.3	3	9.54	1	3.61E+05		(K)LDEREA(	(K)L/D/E R E\A/G I/T E K(V)		98.2	420.8852	1260.643	-0.002	-1.6	4.41	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
11249	dirMS_041712_NAR_60mM_minus.8498.8498.3	3	9.54	1	1.00E+05		(R)VVASDK	(R)V V|A/S D K/E T Y E L R(Y)		107.3	470.5828	1409.727	0.0068	4.8	4.68	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
11250	dirMS_041712_NAR_20mM_plus.17465.17465.2	2	9.54	0	1.61E+05	M74m	(R)mIAGQ\	(R)m I/A\G Q/V|L D/I N L A A E/P K(V)	m:Oxidized methionine	192.85	849.9568	1682.915	15.9918	-1.9	4.37	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
11251	dirMS_041712_NAR_30mM_plus2.18641.18693.2	2	9.54	0	3.23E+05		(R)FVNVVP	(R)F V|N|V|V\P T F G K(K)		151.3	554.3087	1107.62	-0.0096	-8.7	8.75	10904.6	11.56	HUMAN	E9PR30	40S ribosomal protein S30
11252	dirMS_041712_NAR_40mM_plus2.17245.17245.3	3	9.54	1	1.60E+04		(R)LFVGNLI	(R)L F|V/G N/L P T/D/I/T E E D F K R(L)		167.72	665.3502	1994.023	0.0131	6.6	4.32	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
11253	dirMS_041712_NAR_40mM_plus2.18505.18523.3	3	9.54	1	6.91E+04		(R)KAIIIFVP	(R)K A I I\I F|V|P V/P Q L K(S)		175.18	489.3186	1465.95	-0.0092	-6.3	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
11254	dirMS_041712_NAR_50mM_plus2.12846.12846.3	3	9.54	0	5.97E+05		(R)FDAERP'	(R)F/D|A E R P V D C\S\V I V V/N K(Q)	C:Carbamidomethylation	135.82	616.6476	1847.932	-0.0038	-2	4.56	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
11255	dirMS_041712_NAR_50mM_plus2.17423.17423.3	3	9.54	1	7.82E+05	T375t	(K)tLPEISRI	(K)t/L/P E I S R I S Q S/M A E/K(W)	t:N-acetylglucosamine (T)	159.35	631.6637	1689.884	203.0926	7	5.81	116607.6	8.76	HUMAN	Q8IVU3	Probable E3 ubiquitin-protein ligase HERC6
11256	dirMS_041712_NAR_50mM_plus2.5319.5319.3	3	9.54	0	3.81E+05	M116m	(R)ATAPQT	(R)A T\A/P Q/T Q/H/V/S P m R(Q)	m:Oxidized methionine	87.6	480.5727	1423.711	15.9925	-1.7	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
11257	dirMS_041712_NAR_50mM_plus2.6662.6662.3	3	9.54	0	2.83E+05		(K)TIEAEAA	(K)T I|E A E/A A/H/G T V T\R(H)		99.78	452.5685	1355.691	-0.0004	-0.3	5.37	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
11258	dirMS_041712_NAR_50mM_plus2.7820.7820.3	3	9.54	0	6.35E+04		(K)QEYDES	(K)Q E/Y D E S/G/P S/I/V H R(K)		106.95	506.2382	1516.703	-0.0026	-1.7	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
11259	dirMS_041712_NAR_50mM_plus2.8184.8204.3	3	9.54	1	3.71E+05		(R)VLVNDA	(R)V L|V|N D/A Q K V/T E/G Q Q E R(L)		109.88	605.3151	1813.94	-0.0095	-5.2	4.68	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
11260	dirMS_041712_NAR_60mM_plus.10796.10796.2	2	9.54	1	1.07E+06		(R)VKYETEI	(R)V/K|Y/E/T E L A M R(Q)		113.57	620.326	1239.64	0.0045	3.7	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11261	dirMS_041712_NAR_60mM_plus.5567.5567.3	3	9.54	0	3.12E+05	M111m	(R)MEELHN	(R)M/E/E/L H/N\Q E m Q K(R)	m:Oxidized methionine	87.4	478.2118	1416.625	15.9962	0.9	4.75	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
11262	dirMS_041712_NAR_120mM_minus.8061.8061.3	3	9.53	1	7.83E+05		(K)IQDKEGI	(K)I Q\D K E G I/P|P D/Q Q R(L)		97.97	508.5981	1523.781	-0.0015	-1	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
11263	dirMS_041712_NAR_20mM_minus.12044.12044.3	3	9.53	0	2.54E+05	M256m	(R)SLDmDS	(R)S L D\m D\S/I/I A E/V/K(A)	m:Oxidized methionine	170.07	446.227	1320.671	15.9949	0	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
11264	dirMS_041712_NAR_30mM_minus2.16727.16727.2	2	9.53	0	2.51E+05		(R)ASLEAAI	(R)A S/L|E\A A I/A/D A/E Q R(G)		144.4	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
11265	dirMS_041712_NAR_50mM_minus2.14329.14329.3	3	9.53	0	4.31E+05		(R)QIFHPE(	(R)Q\I F H/P E Q L I/T/G K(E)		149.72	470.9286	1410.774	-0.0027	-1.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
11266	dirMS_041712_NAR_50mM_minus2.17079.17079.3	3	9.53	1	8.56E+04		(K)YVLINW'	(K)Y V|L\I/N W V G E D V P\D A R/K(C)		165.32	625.3311	1873.981	-0.0019	-1	4.56	76925.9	4.46	HUMAN	A8MV58	Drebrin
11267	dirMS_041712_NAR_50mM_minus2.8304.8304.3	3	9.53	0	1.80E+05	M389m	(K)MIVDPV	(K)M\I/V/D/P V E/P H G E m K(F)	m:Oxidized methionine	114.72	499.9082	1481.713	15.9973	1.6	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
11268	dirMS_041712_NAR_50mM_minus2.9144.9144.3	3	9.53	1	2.01E+05		(K)GITEQQI	(K)G I/T E/Q Q/K/E/G L E I V K(M)		120.58	524.6237	1571.864	-0.0074	-4.7	4.79	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
11269	dirMS_041712_NAR_50mM_minus2.9970.9970.3	3	9.53	0	5.80E+05	M147m	(K)LQmEAF	(K)L Q|m E A\P H I/I/V/G T/P G R(V)	m:Oxidized methionine	125.35	545.6267	1618.873	15.9922	-1.7	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
11270	dirMS_041712_NAR_60mM_minus.14847.14847.3	3	9.53	0	3.64E+05		(K)AVGHPF	(K)A V/G H|P F\V I/Q/L/G R(I)		142.13	431.9182	1293.743	-0.0026	-2	9.8	124524.8	5.71	HUMAN	O14980	Exportin-1
11271	dirMS_041712_NAR_60mM_minus.17218.17218.3	3	9.53	1	3.11E+05		(K)DANAKL	(K)D A\N A K\L S E L|E/A/A/L/Q R(A)		156.03	543.6239	1628.86	-0.0031	-1.9	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
11272	dirMS_041712_NAR_20mM_plus.14679.14679.2	2	9.53	0	1.95E+05	M179m M:	(K)mFVLDE	(K)m F|V|L|D/E/A/D E m L S/R(G)	m:Oxidized methionine	173.58	794.3555	1555.713	31.9906	0.5	3.91	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
11273	dirMS_041712_NAR_20mM_plus.8756.8756.2	2	9.53	0	1.90E+04		(R)AVLIAG(	(R)A V L\I/A/G/Q/P G T G K(T)		130.77	556.3256	1111.647	-0.0031	-2.8	8.8	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
11274	dirMS_041712_NAR_30mM_plus2.18310.18310.2	2	9.53	0	1.64E+04		(K)VVNSILA	(K)V V|N/S|I L A F R(E)		149.52	509.8031	1018.604	-0.0055	-5.4	9.72	56564.1	6.56	HUMAN	B4DNW0	Aminoacylase-1
11275	dirMS_041712_NAR_50mM_plus2.18317.18335.3	3	9.53	0	1.31E+06		(K)ALSAIAD	(K)A L|S A I/A/D L/L/T N E H E\R(V)		163.87	551.6254	1652.86	0.0014	0.9	4.65	105417.2	6.41	HUMAN	C9JZR2	Catenin delta-1
11276	dirMS_041712_NAR_60mM_plus.16164.16164.3	3	9.53	1	1.12E+06		(K)TDKTLVI	(K)T/D\K T L V/L/L/M/G/K(E)		141.08	406.908	1218.713	-0.0032	-2.6	8.26	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
11277	dirMS_041712_NAR_60mM_plus.21672.21672.3	3	9.53	1	6.81E+05		(K)EIIDLVLI	(K)E I/I/D/L/V L D/R I R(K)		180.8	452.2733	1354.805	0.0001	0.1	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
11278	dirMS_041712_NAR_20mM_minus.7402.7402.2	2	9.52	0	1.52E+05	M21m	(K)ATAVmF	(K)A T A V/m|P D/G Q/F K(D)	m:Oxidized methionine	122.22	590.7864	1164.572	15.9938	-1	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
11279	dirMS_041712_NAR_20mM_minus.9234.9234.2	2	9.52	0	9.72E+04	M267m	(R)LITLEEEr	(R)L I|T/L E/E E/m T K(Y)	m:Oxidized methionine	142.02	611.8143	1206.629	15.9927	-1.8	4.25	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
11280	dirMS_041712_NAR_30mM_minus2.16964.16964.2	2	9.52	0	9.39E+04		(R)IMNTFS'	(R)I M/N/T\F/S V V/P/S P K(V)		145.97	660.3534	1319.703	-0.0033	-2.5	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
11281	dirMS_041712_NAR_50mM_minus2.13590.13590.3	3	9.52	1	5.31E+05		(K)LTEDKAI	(K)L T/E D K A D V Q S/I/I/G L Q R(F)		144.8	595.9939	1785.97	-0.0034	-1.9	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
11282	dirMS_041712_NAR_60mM_minus.11384.11384.3	3	9.52	1	1.19E+04		(K)KVEEAEI	(K)K V E E A E|P/E/E F V/V E K(V)		123.62	554.6136	1661.827	-0.0006	-0.4	4.2	11857.8	9.63	HUMAN	B8ZZ43	Chromobox homolog 3 (HP1 gamma homolog, Drosophila), isoform CRA_b
11283	dirMS_041712_NAR_60mM_minus.17250.17250.3	3	9.52	1	1.10E+05		(R)CRVDLP	(R)C R V D\L|P|L A V L/S K(M)	C:Carbamidomethylation	156	457.5982	1370.782	-0.0024	-1.7	8.75	7765.6	8.23	HUMAN	H3BSA6	dCTP pyrophosphatase 1
11284	dirMS_041712_NAR_60mM_minus.4993.4993.3	3	9.52	1	1.11E+05		(K)DSYVGD	(K)D S Y/V/G D E A/Q S K/R(G)		82.27	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
11285	dirMS_041712_NAR_60mM_minus.6447.6455.3	3	9.52	1	1.71E+05		(R)AQLGGF	(R)A Q|L/G G P E A A K S D E/T/A A K(-)		94.9	548.6116	1643.824	-0.0033	-2	4.68	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
11286	dirMS_041712_NAR_60mM_minus.9776.9776.2	2	9.52	1	4.41E+05		(R)LQAEIEG	(R)L Q|A\E I E/G/L/K/G/Q R(A)		114.13	671.3768	1341.748	-0.0022	-1.6	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
11287	dirMS_041712_NAR_120mM_plus.5567.5567.3	3	9.52	1	3.76E+05		(K)TCEESSF	(K)T/C/E/E S/S F C K/R(Q)	C:Carbamidomethylation	82.18	435.1877	1303.541	0.008	6.1	5.81	10576.1	11.44	HUMAN	E9PRF8	Neutral alpha-glucosidase AB
11288	dirMS_041712_NAR_20mM_plus.19146.19146.3	3	9.52	0	2.04E+05		(R)LAGTQP	(R)L A G T Q|P L/E V\L/E/A V Q R(S)		204.02	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
11289	dirMS_041712_NAR_30mM_plus2.10060.10418.2	2	9.52	0	4.04E+05		(R)NIVEAA/	(R)N I|V|E/A/A/A V R(D)		107.17	471.772	942.537	0	0	6	13229.4	11.62	HUMAN	F8VZW7	Protein LOC100996747
11290	dirMS_041712_NAR_30mM_plus2.17627.17627.3	3	9.52	0	5.51E+05		(R)SIQEELC	(R)S I\Q\E E/L/Q Q/L R(Q)		146.05	415.225	1243.664	-0.0036	-2.9	4.53	533778	5.74	HUMAN	Q15149	Plectin
11291	dirMS_041712_NAR_30mM_plus2.6685.6685.2	2	9.52	0	5.75E+04		(K)TVGVEP.	(K)T/V/G\V/E/P A A D G K(G)		89.45	522.2782	1043.537	0.0124	11.8	4.37	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
11292	dirMS_041712_NAR_30mM_plus2.7847.8140.2	2	9.52	0	4.96E+05		(K)SDPVVS'	(K)S D|P/V|V/S Y R(E)		94.37	461.7327	922.463	-0.0047	-5.1	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
11293	dirMS_041712_NAR_40mM_plus2.17021.17021.3	3	9.52	0	3.68E+05		(R)IHFPLAT	(R)I H\F\P L A\T/Y\A|P V/I S/A E K(A)		167.4	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
11294	dirMS_041712_NAR_40mM_plus2.17624.17624.3	3	9.52	1	2.71E+05		(K)TGISDVF	(K)T G/I/S D V F A K N D L/A|V V D|V R(I)		169.5	640.3451	1919.023	-0.0025	-1.3	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
11295	dirMS_041712_NAR_50mM_plus2.10870.10870.3	3	9.52	1	2.43E+06		(R)MQKEIT	(R)M Q K E I\T A/L A|P/S T M K(I)		124.03	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
11296	dirMS_041712_NAR_50mM_plus2.14616.14616.3	3	9.52	1	5.76E+05		(R)SEGVVA	(R)S|E|G/V V/A V/L L T K K(S)		144.37	415.2585	1243.762	-0.0011	-0.9	8.31	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
11297	dirMS_041712_NAR_50mM_plus2.15064.15064.3	3	9.52	1	3.25E+05		(R)LDDLVST	(R)L/D/D\L\V|S T/G K L/N L S Q V R(F)		146.93	586.6631	1757.976	-0.0008	-0.5	5.96	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
11298	dirMS_041712_NAR_50mM_plus2.6643.6643.3	3	9.52	0	5.18E+05	M434m	(R)LESGmC	(R)L E|S/G m Q N/M S I H/T K(T)	m:Oxidized methionine	99.12	497.9026	1475.698	15.9951	0.1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
11299	dirMS_041712_NAR_60mM_plus.15608.15608.3	3	9.52	0	2.27E+05		(R)NFDLTA	(R)N F/D L T A|I/P C A N H K(M)	C:Carbamidomethylation	138.13	500.9145	1500.726	0.0026	1.7	6.74	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
11300	dirMS_041712_NAR_60mM_plus.16090.16090.3	3	9.52	1	5.53E+05		(R)IKIGDPL	(R)I K I G D/P\L L/E/D/T R(M)		141.48	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
11301	dirMS_041712_NAR_20mM_minus.12597.12597.2	2	9.51	0	1.62E+05		(R)LVNWPE	(R)L V|N W P E/H L R(S)		173.37	582.3186	1163.632	-0.0021	-1.8	6.75	25352.6	11.4	HUMAN	K7ENP0	Matrix metalloproteinase-28
11302	dirMS_041712_NAR_20mM_minus.13201.13201.2	2	9.51	0	1.40E+05		(K)VGINYQ	(K)V G I N/Y Q|P P T V\V/P G G D/L A K(V)		183.15	912.9938	1824.985	-0.0051	-2.8	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
11303	dirMS_041712_NAR_20mM_minus.7286.7286.2	2	9.51	0	1.32E+05	M374m	(R)mAPTPII	(R)m A|P T/P I P T R(S)	m:Oxidized methionine	121.02	500.2679	983.534	15.9943	-0.7	9.5	76925.9	4.46	HUMAN	A8MV58	Drebrin
11304	dirMS_041712_NAR_30mM_minus2.12809.12809.2	2	9.51	0	4.06E+04		(R)GGEPQ(	(R)G G E/P\Q/G P P F\I K(Y)		122.6	563.7964	1126.589	-0.0036	-3.2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
11305	dirMS_041712_NAR_30mM_minus2.16921.16921.2	2	9.51	0	1.50E+05		(R)TLINELV	(R)T/L|I/N/E L/V K(G)		146.02	465.2877	929.567	0.0015	1.6	5.66	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
11306	dirMS_041712_NAR_60mM_minus.11416.11416.3	3	9.51	1	8.45E+05	M232m	(R)MSmKE\	(R)M S m K E V D E/Q|M|L/N V Q N K(N)	m:Oxidized methionine	122.85	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
11307	dirMS_041712_NAR_60mM_minus.12201.12201.3	3	9.51	1	2.58E+05		(R)TVSKVD	(R)T V/S K V D D|F/L/A/N E A/K(G)		128.07	512.9419	1536.79	0.0207	13.5	4.55	52385	7.18	HUMAN	B4DQJ8	6-phosphogluconate dehydrogenase, decarboxylating
11308	dirMS_041712_NAR_60mM_minus.13678.13678.3	3	9.51	0	2.56E+05		(K)VSHVST(	(K)V/S H V\S T\G G G\A/S/L/E L/L/E\G K(V)		136.42	580.9746	1740.913	-0.0034	-2	5.4	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
11309	dirMS_041712_NAR_60mM_minus.17743.17743.3	3	9.51	1	3.77E+05		(K)YGKLEV/	(K)Y G K L E V|A/N L|L L Q K(S)		159.53	496.9631	1488.878	-0.0037	-2.5	8.5	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
11310	dirMS_041712_NAR_120mM_plus.9639.9639.3	3	9.51	0	1.73E+05		(K)QEYDES	(K)Q E/Y|D E/S/G/P S I V/H R(K)		103.82	506.2393	1516.703	0.0007	0.5	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
11311	dirMS_041712_NAR_120mM_plus.9961.9961.2	2	9.51	0	5.50E+05		(K)HLTDAYI	(K)H/L|T/D A Y|F/K(K)		105.57	497.7567	994.499	0.0069	6.9	6.74	25891.4	10.67	HUMAN	F8W181	60S ribosomal protein L6 (Fragment)
11312	dirMS_041712_NAR_20mM_plus.15616.15616.2	2	9.51	0	5.93E+03		(R)SSFYVN(	(R)S S F\Y|V|N/G\L\T\L/G G Q K(C)		178.63	735.8818	1470.759	-0.0024	-1.6	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
11313	dirMS_041712_NAR_20mM_plus.16564.16564.3	3	9.51	0	6.48E+04	M137m M:	(R)IIGATDS	(R)I I/G A/T D S S G\E L/m/F L/m K(W)	m:Oxidized methionine	185.8	582.2872	1712.86	31.9873	-1.5	4.37	19439.5	4.97	HUMAN	B5MD17	Chromobox protein homolog 1 (Fragment)
11314	dirMS_041712_NAR_30mM_plus2.16956.16956.2	2	9.51	1	2.62E+05		(R)FVLSQAI	(R)F V|L/S/Q A K D E L(-)		141.53	575.3104	1149.615	-0.0015	-1.3	4.37	41053.3	5.58	HUMAN	Q86UY0	TXNDC5 protein
11315	dirMS_041712_NAR_30mM_plus2.22027.22067.2	2	9.51	0	1.40E+05		(K)ETLLAM	(K)E T/L/L/A/M/F K(Y)		170.98	476.7621	952.517	-0.0003	-0.3	6.1	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
11316	dirMS_041712_NAR_40mM_plus2.11122.11122.3	3	9.51	1	7.28E+04		(K)AVEEED	(K)A V/E/E E D K M|T/P/E Q L A I K(N)		131.85	610.9764	1830.915	-0.0007	-0.4	4.25	34747.6	6.06	HUMAN	O00487	26S proteasome non-ATPase regulatory subunit 14
11317	dirMS_041712_NAR_40mM_plus2.13301.13301.3	3	9.51	1	1.17E+05		(R)ETFEKTF	(R)E\T/F E K T/P V\E/V/P V G G F K(G)		144.53	588.6444	1763.921	-0.0028	-1.6	4.79	533778	5.74	HUMAN	Q15149	Plectin
11318	dirMS_041712_NAR_50mM_plus2.6006.6021.3	3	9.51	1	6.47E+04		(R)GPPPPP'	(R)G P|P/P/P P T/A S E\P T R R(S)		95.75	487.2606	1459.765	0.002	1.4	9.6	124127.1	8.81	HUMAN	O14776	Transcription elongation regulator 1
11319	dirMS_041712_NAR_60mM_plus.17600.17600.3	3	9.51	1	2.04E+05	S110s	(R)LSTKDPL	(R)L S|T/K/D P\L P T I A s R(E)	s:N-acetylglucosamine (S)	149.18	534.6306	1398.795	203.0821	1.7	8.75	32994.3	10.02	HUMAN	A6NHR2	39S ribosomal protein L37, mitochondrial
11320	dirMS_041712_NAR_60mM_plus.6509.6509.3	3	9.51	1	2.36E+05		(R)IVENEKI	(R)I/V/E N E K I/N/A E K(S)		92.6	429.5691	1286.695	-0.0023	-1.8	4.79	13922.5	6.92	HUMAN	B4DIS3	Dpy-30-like protein, isoform CRA_b
11321	dirMS_041712_NAR_20mM_minus.12145.12145.2	2	9.5	0	1.92E+05	M73m	(R)AVLVDLI	(R)A V/L\V/D L/E|P G/T m D S V R(S)	m:Oxidized methionine	171.15	809.4088	1601.82	15.99	-3	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
11322	dirMS_041712_NAR_20mM_minus.13200.13200.3	3	9.5	0	1.06E+05		(R)GVVDSE	(R)G V V D/S E D I/P/L N/L/S R(E)		183	505.266	1513.786	-0.0022	-1.5	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
11323	dirMS_041712_NAR_20mM_minus.7531.7531.2	2	9.5	0	6.74E+05	M239m	(K)EVDEQn	(K)E V D/E/Q|m\L/N V/Q N K(N)	m:Oxidized methionine	123.7	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
11324	dirMS_041712_NAR_40mM_minus2.11715.11715.3	3	9.5	1	4.75E+04		(R)QVFGEA	(R)Q V F/G E A T K Q/P G I/T F I A A K(F)		152.53	636.0167	1906.043	-0.0077	-4.1	8.59	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
11325	dirMS_041712_NAR_50mM_minus2.15153.15153.3	3	9.5	0	1.70E+05		(R)NSSHAG	(R)N/S S H A G A F V\I/V/T E E A I A K(G)		154.27	615.3184	1843.955	-0.0142	-7.7	5.4	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
11326	dirMS_041712_NAR_50mM_minus2.18068.18068.3	3	9.5	1	1.52E+05		(R)GDLGIEI	(R)G D L|G I/E\I/P A E K V F L A Q K(M)		172.1	610.0112	1828.022	-0.0024	-1.3	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
11327	dirMS_041712_NAR_50mM_minus2.8721.8721.3	3	9.5	1	1.13E+05		(K)TAVCDIF	(K)T A/V/C D/I/P P R G L/K(M)	C:Carbamidomethylation	117.28	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
11328	dirMS_041712_NAR_60mM_minus.14072.14072.3	3	9.5	1	3.44E+05		(R)FVNVVP	(R)F V/N\V/V/P/T F G/K/K(K)		138.5	412.5738	1235.715	-0.0078	-6.3	10	10904.6	11.56	HUMAN	E9PR30	40S ribosomal protein S30
11329	dirMS_041712_NAR_60mM_minus.5077.5077.3	3	9.5	1	5.32E+04		(K)CDSSPD:	(K)C/D|S S/P D S A E D/V R K(V)	C:Carbamidomethylation	83.13	489.2127	1465.622	0.0012	0.8	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
11330	dirMS_041712_NAR_60mM_minus.9566.9566.3	3	9.5	1	3.49E+05	M64m	(K)LmDQLE	(K)L m D\Q\L|E/A L/K/K(Q)	m:Oxidized methionine	113.47	402.2246	1188.666	15.9936	-1.1	6.07	34163.9	5.87	HUMAN	Q9NP79	Vacuolar protein sorting-associated protein VTA1 homolog
11331	dirMS_041712_NAR_120mM_plus.15449.15449.4	4	9.5	1	2.83E+05		(R)IQKEALC	(R)I Q|K E A L G G Q A L Y/P H V L V K(N)		134.22	491.7882	1964.133	-0.0018	-0.9	8.51	86691.2	9.19	HUMAN	B7Z4B8	Heterogeneous nuclear ribonucleoprotein U-like protein 1

11332	dirMS_041712_NAR_120mM_plus.8223.8243.2	2	9.5	0	2.55E+05		(R)IGKPAPD	(R)I/G K|P A/P D|F K(A)		96.73	486.7785	972.551	-0.0016	-1.6	8.59	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
11333	dirMS_041712_NAR_20mM_plus.10731.10731.2	2	9.5	0	1.18E+05		(R)AGTGVD	(R)A G T G V/D\N/V/D|L/E A/A T R(K)		146.88	744.8731	1488.729	0.01	6.7	4.03	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
11334	dirMS_041712_NAR_20mM_plus.13172.13172.2	2	9.5	0	6.48E+04		(R)ILGADTS	(R)I L\G\A\D\T S V|D\L/E E T G R(V)		163.12	788.3928	1575.786	-0.0077	-4.9	3.91	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
11335	dirMS_041712_NAR_20mM_plus.7165.7220.2	2	9.5	0	3.68E+05	M532m M5	(R)mVPAGm	(R)m\V|P A/G m G A/G L E R(M)	m:Oxidized methionine	117.55	610.7907	1188.586	31.9877	-1.7	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
11336	dirMS_041712_NAR_20mM_plus.7970.7970.2	2	9.5	0	5.71E+04		(K)SVTEQG	(K)S V T E\Q/G A/E|L/S/N E E R(N)		124.88	774.8589	1548.714	-0.0031	-2	4.09	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
11337	dirMS_041712_NAR_30mM_plus2.21829.21829.3	3	9.5	0	1.83E+05		(K)GLVQAL	(K)G L V/Q A L/G L/S N/F N S R(Q)		169.45	492.6036	1475.796	-0.0003	-0.2	9.75	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
11338	dirMS_041712_NAR_40mM_plus2.11234.11234.3	3	9.5	1	7.92E+04		(K)AVEEED	(K)A V|E/E E D\K M\T/P E Q L A I K(N)		132.05	610.9764	1830.915	-0.0007	-0.4	4.25	34747.6	6.06	HUMAN	O00487	26S proteasome non-ATPase regulatory subunit 14
11339	dirMS_041712_NAR_40mM_plus2.11308.11308.3	3	9.5	0	1.21E+05		(K)EAGELKP	(K)E A/G E L/K P E E\E/I T/V/G/P V Q K(L)		132.8	651.6782	1953.017	0.0025	1.3	4.32	108281.4	5.72	HUMAN	P53618	Coatomer subunit beta
11340	dirMS_041712_NAR_40mM_plus2.17052.17052.3	3	9.5	0	1.19E+05		(K)LQAVEV	(K)L Q|A V/E V/V I T H L A P G T/K(H)		166.82	559.3259	1675.974	-0.011	-6.6	6.75	16120	9.05	HUMAN	Q9Y2V2	Calcium-regulated heat stable protein 1
11341	dirMS_041712_NAR_50mM_plus2.10699.10699.3	3	9.5	1	2.46E+06		(R)MQKEIT	(R)M/Q\K E I T\A\L/A|P\S/T M K(I)		124.03	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
11342	dirMS_041712_NAR_50mM_plus2.18984.18984.3	3	9.5	0	5.31E+05		(R)GFGFITF	(R)G F G F/I/T/F T/N P E H A S V A M R(A)		168.58	661.3258	1981.959	0.004	2	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
11343	dirMS_041712_NAR_50mM_plus2.9755.9755.3	3	9.5	1	1.04E+06		(K)LKGEATV	(K)L K G E A|T\V S/F/D/D|P P S\A K(A)		119.12	554.6155	1661.838	-0.0061	-3.7	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
11344	dirMS_041712_NAR_120mM_minus.18196.18196.3	3	9.49	1	2.92E+05		(R)KQSLGE	(R)K Q S L G E\L\I|G/T L/N A A K(V)		154.38	514.9655	1542.885	-0.003	-2	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
11345	dirMS_041712_NAR_120mM_minus.9713.9713.3	3	9.49	1	6.41E+05		(R)AREQAE	(R)A R E Q A\E A/E|V/A/S L N R(R)		107.8	515.2649	1543.782	-0.0022	-1.4	4.79	11017	4.8	HUMAN	D6R904	Tropomyosin alpha-3 chain
11346	dirMS_041712_NAR_20mM_minus.13328.13328.2	2	9.49	0	5.44E+05		(K)DAGTIAG	(K)D A G T|I|A/G L N V L/R(I)		184.68	600.3403	1199.674	-0.0009	-0.8	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
11347	dirMS_041712_NAR_20mM_minus.14641.14641.2	2	9.49	0	8.83E+04		(R)IITLTGPT	(R)I I|T|L/T G/P T N A I F K(A)		201.33	694.9107	1388.815	-0.0007	-0.5	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
11348	dirMS_041712_NAR_20mM_minus.7085.7085.2	2	9.49	0	4.77E+05	M281m	(R)AEAESm	(R)A E|A/E/S/m Y Q I K(Y)	m:Oxidized methionine	117.9	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
11349	dirMS_041712_NAR_30mM_minus2.14108.14108.2	2	9.49	0	2.19E+05		(R)GANDFM	(R)G A/N D/F/M/C D E/M E/R(S)	C:Carbamidomethylation	130.03	737.7725	1474.54	-0.0018	-1.2	3.91	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
11350	dirMS_041712_NAR_50mM_minus2.13630.13630.3	3	9.49	0	2.19E+04		(R)DLSHIGD	(R)D L S H I G D A\V\V/I|S C A K(D)	C:Carbamidomethylation	145.88	528.9397	1584.805	-0.0005	-0.3	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
11351	dirMS_041712_NAR_60mM_minus.8141.8156.3	3	9.49	0	1.91E+05		(R)QYDISDP	(R)Q/Y/D/I/S D/P Q R P R(L)		105.63	458.8971	1374.676	0.0007	0.5	5.96	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
11352	dirMS_041712_NAR_120mM_plus.14542.14560.3	3	9.49	1	5.07E+05		(K)LDKSQIH	(K)L D/K S/Q I H D/I|V|L V|G G S T R(I)		130.1	613.3369	1838.013	-0.0169	-9.2	6.75	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
11353	dirMS_041712_NAR_20mM_plus.15233.15233.2	2	9.49	0	5.88E+04		(R)EQLAIAE	(R)E Q|L/A/I/A E/F A R(S)		176.1	574.312	1147.611	0.0061	5.3	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
11354	dirMS_041712_NAR_20mM_plus.16047.16047.2	2	9.49	0	4.77E+04		(K)DAGTIAG	(K)D A\G\T I/A/G L N/V/L R(I)		182.22	600.3422	1199.674	0.0029	2.4	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
11355	dirMS_041712_NAR_20mM_plus.19129.19129.3	3	9.49	0	1.99E+05		(K)TLETQSA	(K)T L E T Q S/A/L/G/P A/L Q A A F K(L)		202.6	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
11356	dirMS_041712_NAR_30mM_plus2.10338.10587.2	2	9.49	0	7.88E+05		(K)VLVDMS	(K)V/L|V|D M\S/R(V)		108.9	410.2229	819.439	-0.0008	-0.9	5.81	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
11357	dirMS_041712_NAR_30mM_plus2.11283.11644.2	2	9.49	0	1.14E+06		(R)LVDMM	(R)L/V|D|M/M E/R(G)		113.78	447.2119	893.422	-0.0054	-6.1	4.37	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
11358	dirMS_041712_NAR_30mM_plus2.12548.12548.2	2	9.49	0	4.37E+05		(R)QGVDAD	(R)Q G\V|D/A/D/I N G L R(Q)		118.17	579.2997	1157.591	0.0012	1	4.21	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
11359	dirMS_041712_NAR_30mM_plus2.16203.16285.2	2	9.49	0	1.72E+05		(K)YIQELWR	(K)Y I|Q|E/L W/R(K)		138.08	504.2687	1007.531	-0.0008	-0.8	6	20608.6	11.48	HUMAN	E7ENU7	Ribosomal protein L15 (Fragment)
11360	dirMS_041712_NAR_30mM_plus2.16260.16260.2	2	9.49	0	1.38E+06		(R)GGIVDEG	(R)G G I|V|D E\G A L L R(A)		138.9	550.3082	1099.611	-0.0015	-1.3	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
11361	dirMS_041712_NAR_30mM_plus2.18680.18798.2	2	9.49	0	3.32E+05		(R)ESLEALL	(R)E S\L/E/A L/L/Q/R(A)		152.07	529.8026	1058.584	0.0139	13.1	4.53	107721.8	8.85	HUMAN	O94906	Pre-mRNA-processing factor 6
11362	dirMS_041712_NAR_40mM_plus2.6195.6195.2	2	9.49	1	2.84E+05		(R)YSGGNY	(R)Y/S\G G N/Y R D N\Y\D|N(-)		95.58	719.2857	1437.567	-0.0024	-1.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
11363	dirMS_041712_NAR_40mM_plus2.7271.7271.2	2	9.49	0	9.67E+04		(R)STFSTNY	(R)S T|F/S/T N Y R(S)		102.65	488.2297	975.453	-0.0009	-0.9	8.46	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11364	dirMS_041712_NAR_50mM_plus2.10993.11077.3	3	9.49	1	4.55E+05		(R)AIPNNQ	(R)A I/P N N Q V/L/G\K I E/R(A)		125.48	484.6151	1451.833	-0.0021	-1.5	8.79	16368.4	9.95	HUMAN	O60869	Endothelial differentiation-related factor 1
11365	dirMS_041712_NAR_50mM_plus2.21426.21426.3	3	9.49	0	4.50E+06		(R)LHFFMP	(R)L H\F F M\P G\F/A|P\L/T S R(G)		182.1	540.9498	1620.835	-0.0007	-0.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
11366	dirMS_041712_NAR_50mM_plus2.9280.9280.3	3	9.49	1	1.70E+06		(R)LQAEIEG	(R)L/Q|A E/I/E/G/L K G Q R(A)		115.58	447.921	1341.748	0	0	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
11367	dirMS_041712_NAR_60mM_plus.9354.9362.3	3	9.49	1	4.91E+05		(R)GSNKLV	(R)G S N K L\V|I|E/E/A E R(S)		107.13	448.9043	1344.712	-0.0134	-10	4.79	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
11368	dirMS_041712_NAR_30mM_minus2.11817.11817.2	2	9.48	0	3.78E+05		(K)MTISQQ	(K)M T|I|S Q/Q E/F/G/R(T)		117.88	598.7911	1196.573	0.0021	1.7	5.75	21119.9	4.34	HUMAN	H0Y3Y9	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
11369	dirMS_041712_NAR_30mM_minus2.16324.16324.2	2	9.48	0	1.91E+05		(K)ACGNFG	(K)A C|G N/F/G I\P C E L R(V)	C:Carbamidomethylation	142.52	697.3207	1393.635	-0.001	-0.7	6.05	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
11370	dirMS_041712_NAR_40mM_minus2.14402.14402.3	3	9.48	1	3.43E+04		(R)LKLPSIPL	(R)L K L\P S I/P\L\V/P V/S A Q K(R)		169.28	530.6703	1589.999	-0.0025	-1.6	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
11371	dirMS_041712_NAR_50mM_minus2.10503.10503.3	3	9.48	0	1.46E+05		(R)LLELGPK	(R)L L/E/L/G P K/P E V A Q Q T R(K)		128.35	560.3182	1678.949	-0.0086	-5.1	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
11372	dirMS_041712_NAR_50mM_minus2.15611.15611.3	3	9.48	1	4.72E+05		(K)QGGLGP	(K)Q G G L/G/P M/N\I|P L V/S D P K R(T)		157.45	593.6566	1778.958	-0.0029	-1.6	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
11373	dirMS_041712_NAR_50mM_minus2.17903.17903.3	3	9.48	0	4.27E+05	M203m	(R)DTGIFLD	(R)D T/G I/F L/D L m H L/K(K)	m:Oxidized methionine	170.33	473.5826	1402.74	15.9933	-1.1	5.21	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
11374	dirMS_041712_NAR_50mM_minus2.7751.7751.3	3	9.48	0	4.07E+04	M409m	(K)VLAmSG	(K)V L/A m/S G D/P N Y L H R(M)	m:Oxidized methionine	111.03	496.9173	1472.732	16.0059	7.4	6.71	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
11375	dirMS_041712_NAR_60mM_minus.10281.10281.3	3	9.48	0	5.66E+05		(K)AQVARP	(K)A Q|V|A R P G G D T I/F/G K(I)		117.83	472.9235	1416.759	-0.0034	-2.4	8.79	7323.5	9.4	HUMAN	D6RC06	Histidine triad nucleotide-binding protein 1
11376	dirMS_041712_NAR_60mM_minus.19329.19329.3	3	9.48	0	4.54E+05		(R)THNGES	(R)T H N G E S V\S|Y|L|F S H V|P L(-)		171.93	596.2923	1786.876	-0.0135	-7.6	5.92	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
11377	dirMS_041712_NAR_60mM_minus.7632.7632.3	3	9.48	1	7.96E+05		(K)IQDKEGI	(K)I/Q D K E G I/P/P D Q Q/R(L)		101.62	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
11378	dirMS_041712_NAR_60mM_minus.9147.9147.2	2	9.48	0	9.67E+05		(K)QEYDESG	(K)Q/E/Y D|E S G P S I V/H/R(K)		110.35	758.8539	1516.703	-0.0021	-1.4	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
11379	dirMS_041712_NAR_120mM_plus.7172.7172.2	2	9.48	1	4.77E+05		(K)SLDEME	(K)S/L/D/E/M/E K/Q Q R(E)		91.18	632.3059	1263.6	0.0047	3.8	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
11380	dirMS_041712_NAR_120mM_plus.9575.9575.3	3	9.48	1	5.95E+05		(R)NYRDNY	(R)N Y R D N|Y Q/A/F C/K(W)	C:Carbamidomethylation	103.37	493.5549	1478.648	0.002	1.4	8.49	334221.3	6.44	HUMAN	P15924	Desmoplakin
11381	dirMS_041712_NAR_20mM_plus.10457.10457.2	2	9.48	0	1.31E+03		(K)SYEPLED	(K)S Y|E/P/L E D/P G V K(S)		144.22	617.3053	1233.6	0.0036	2.9	4.14	35556.4	9.3	HUMAN	F2Z393	Transaldolase
11382	dirMS_041712_NAR_20mM_plus.17842.17842.2	2	9.48	0	1.79E+05		(K)GADFLV	(K)G A D F L|V/T E/V E/N G G/S L/G S K(K)		195.05	890.4414	1779.876	-0.0004	-0.2	4.14	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
11383	dirMS_041712_NAR_30mM_plus2.10020.10020.2	2	9.48	0	1.51E+06		(R)GVNVSA	(R)G V|N/V|S A L S R(D)		105.73	451.7509	902.505	-0.0109	-12.1	9.75	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
11384	dirMS_041712_NAR_30mM_plus2.21546.21645.2	2	9.48	0	2.77E+05		(R)NIPMLFV	(R)N I|P M/L/F V R(G)		167.75	495.2847	989.56	0.002	2.1	9.75	11845.2	4.58	HUMAN	P62310	U6 snRNA-associated Sm-like protein LSm3
11385	dirMS_041712_NAR_30mM_plus2.9076.9564.2	2	9.48	0	1.43E+06		(K)EVGSIIG	(K)E V/G S/I/I/G/K(K)		102.52	401.7331	802.467	-0.008	-9.9	6.1	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
11386	dirMS_041712_NAR_40mM_plus2.13321.13321.3	3	9.48	1	1.17E+05		(R)ETFEKTP	(R)E T F E/K T P V/E/V/P\V/G G F K(G)		144.53	588.6444	1763.921	-0.0028	-1.6	4.79	533778	5.74	HUMAN	Q15149	Plectin
11387	dirMS_041712_NAR_50mM_plus2.11062.11062.3	3	9.48	0	3.42E+05		(K)LQAEAP	(K)L Q|A E A P H I V/V G/T/P G R(V)		126.45	515.6223	1544.854	-0.002	-1.3	6.75	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
11388	dirMS_041712_NAR_50mM_plus2.12595.12595.3	3	9.48	1	3.83E+05		(K)LPGGELN	(K)L/P G G E L\N\P G E|D E V/E G L K R(L)		134.28	636.9936	1908.966	0.0001	0.1	4.25	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
11389	dirMS_041712_NAR_50mM_plus2.15508.15508.3	3	9.48	0	2.60E+05		(K)ANLLNN	(K)A N|L|L/N/N\E A H A I T M Q V/T K(S)		149.67	623.3237	1867.969	-0.0129	-6.9	6.79	74483	8.6	HUMAN	P46063	ATP-dependent DNA helicase Q1
11390	dirMS_041712_NAR_50mM_plus2.22311.22311.3	3	9.48	0	5.77E+05		(R)GGHPPA	(R)G G H P P A I Q/S L\I\N/L/L/A D/N R(Y)		191.82	629.3448	1886.024	-0.0044	-2.3	6.74	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
11391	dirMS_041712_NAR_60mM_plus.16315.16315.3	3	9.48	0	6.18E+05		(K)MTHLPE	(K)M T H\L P E L/D\T|L/S/S E R(A)		142.28	543.6023	1628.795	-0.0025	-1.5	4.65	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
11392	dirMS_041712_NAR_60mM_plus.7064.7064.3	3	9.48	0	1.22E+06	M434m	(R)LESGmQ	(R)L/E|S G/m Q N/M S I/H/T K(T)	m:Oxidized methionine	95.27	497.903	1475.698	15.9963	1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
11393	dirMS_041712_NAR_60mM_plus.9079.9092.3	3	9.48	0	2.11E+06		(K)NCPHIVV	(K)N/C\P H\I V/V/G/T/P G/R(I)	C:Carbamidomethylation	106.15	436.2272	1306.669	-0.0014	-1.1	9.75	28185.1	10.76	HUMAN	B4DIJ6	Spliceosome RNA helicase DDX39B
11394	dirMS_041712_NAR_120mM_minus.11363.11363.3	3	9.47	0	4.42E+05		(K)SAKPTKP	(K)S A K P T K P A A/S D\L|P V|P A E G V R(N)		116.37	664.3662	1991.092	-0.008	-4	8.31	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
11395	dirMS_041712_NAR_120mM_minus.6224.6224.3	3	9.47	1	7.84E+05		(R)TEERAEL	(R)T/E|E R A E L A/E/S R(C)		88.75	430.8806	1290.628	-0.0012	-0.9	4.49	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
11396	dirMS_041712_NAR_30mM_minus2.6802.6802.2	2	9.47	0	1.71E+05		(R)GCLDEET	(R)G/C|L/D/E E/T S R(A)	C:Carbamidomethylation	91.75	533.7297	1066.447	0.0052	4.8	4.14	533778	5.74	HUMAN	Q15149	Plectin
11397	dirMS_041712_NAR_50mM_minus2.11422.11422.3	3	9.47	0	9.15E+04		(R)DLQSNV	(R)D L/Q S/N/V/E/H/L T E/K(M)		133.58	471.5727	1412.702	0.0019	1.4	4.65	23167	8.94	HUMAN	B1APP8	6-phosphofructokinase type C
11398	dirMS_041712_NAR_50mM_minus2.12761.12761.3	3	9.47	1	4.30E+05	M100m	(K)QGGLGP	(K)Q G\G\L/G/P m N I|P/L V S D P K R(T)	m:Oxidized methionine	140.4	598.988	1778.958	15.9913	-2	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
11399	dirMS_041712_NAR_50mM_minus2.15695.15695.3	3	9.47	1	2.26E+05		(K)DVLFLKD	(K)D V/L/F L K D C V/G/P E V E/K(A)	C:Carbamidomethylation	156.53	583.3014	1747.893	-0.0039	-2.2	4.32	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
11400	dirMS_041712_NAR_50mM_minus2.17890.17890.3	3	9.47	0	3.01E+05		(R)IHFPLAT	(R)I H F/P L A T\Y|A/P V/I S A E K(A)		169.63	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
11401	dirMS_041712_NAR_60mM_minus.13905.13905.3	3	9.47	0	2.71E+05		(K)YGGELV	(K)Y/G G E/L V/P/H F P A R(V)		138.02	448.2371	1342.69	0.0065	4.8	6.75	258215.9	5.48	HUMAN	E7EN95	Filamin-B
11402	dirMS_041712_NAR_60mM_minus.14032.14032.3	3	9.47	0	2.23E+05		(R)VQIEHIS	(R)V Q/I E/H\I/S S L I/K(L)		137.73	422.9181	1266.742	-0.0019	-1.5	6.72	47748.2	6.08	HUMAN	O00231	26S proteasome non-ATPase regulatory subunit 11
11403	dirMS_041712_NAR_60mM_minus.18296.18296.3	3	9.47	1	1.37E+05		(R)SELELTLG	(R)S E|L\E L/T L/G K L/E Q V R(S)		163.05	538.9724	1614.906	-0.0035	-2.1	4.78	533778	5.74	HUMAN	Q15149	Plectin
11404	dirMS_041712_NAR_60mM_minus.18839.18839.3	3	9.47	0	1.43E+05		(K)VAHALA	(K)V A H A L A E G\L G\V|I/A C/I G E K(L)	C:Carbamidomethylation	166.95	603.3262	1807.974	-0.0094	-5.2	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
11405	dirMS_041712_NAR_60mM_minus.19259.19259.3	3	9.47	0	3.35E+05		(K)HGATVL	(K)H G A T\V\L T|A/L/G G I L K(K)		170.82	450.939	1350.81	-0.0079	-5.9	8.76	8125.3	9.3	HUMAN	B0QYF7	Myoglobin (Fragment)
11406	dirMS_041712_NAR_30mM_plus2.16781.16781.2	2	9.47	0	3.53E+05		(K)QLQEMI	(K)Q L/Q/E/M/L/G L S K(V)		140.73	573.8112	1146.619	-0.0036	-3.1	6	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
11407	dirMS_041712_NAR_30mM_plus2.21286.21286.2	2	9.47	0	8.98E+04		(R)QTLMW	(R)Q T/L M/W/S/A T W/P K(E)		166	674.8389	1348.672	-0.0013	-1	8.75	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
11408	dirMS_041712_NAR_30mM_plus2.8160.8160.2	2	9.47	0	2.73E+05		(K)EIAENAL	(K)E I/A/E N A/L/G\K(H)		96.92	472.755	944.505	-0.002	-2.1	4.53	36982.9	6.37	HUMAN	P31942	Heterogeneous nuclear ribonucleoprotein H3
11409	dirMS_041712_NAR_40mM_plus2.9017.9017.2	2	9.47	0	8.93E+04		(K)GSDFDC	(K)G S/D|F/D C/E L/R(L)	C:Carbamidomethylation	115.47	549.7296	1098.452	-0.0001	-0.1	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
11410	dirMS_041712_NAR_50mM_plus2.10962.10962.3	3	9.47	1	2.48E+05		(K)YGQISEV	(K)Y G|Q/I/S E/V/V\V V K D R(E)		125.47	497.9426	1491.817	-0.0033	-2.2	6.07	28815.3	9.52	HUMAN	B4E2X2	Cold-inducible RNA-binding protein
11411	dirMS_041712_NAR_20mM_minus.7113.7113.2	2	9.46	0	1.65E+05		(R)AAQVAQ	(R)A A Q V|A/Q/D/E E/I A/R(L)		118.82	650.8255	1300.649	-0.0054	-4.2	4.14	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
11412	dirMS_041712_NAR_30mM_minus2.15574.15574.2	2	9.46	0	3.35E+04	M1342m	(R)ASLSLW	(R)A/S/L|S/L|W Q/A m E K(G)	m:Oxidized methionine	138.07	640.3185	1263.64	15.9895	-4.2	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
11413	dirMS_041712_NAR_30mM_minus2.16511.16866.3	3	9.46	0	8.82E+05		(R)ASLEAAI	(R)A S\L E A A\I/A/D/A/E Q R(G)		144.05	448.8965	1344.675	-0.0004	-0.3	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
11414	dirMS_041712_NAR_30mM_minus2.19499.19499.2	2	9.46	0	3.70E+05		(R)ASLSLW	(R)A S/L/S/L/W Q A/M E K(G)		162.5	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
11415	dirMS_041712_NAR_40mM_minus2.15409.15409.3	3	9.46	1	3.49E+05		(R)GGPNIIT	(R)G G P\N I/I/T L A\D/I V K D P V S R(T)		178.23	622.3523	1865.049	-0.0067	-3.6	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
11416	dirMS_041712_NAR_40mM_minus2.9879.9879.2	2	9.46	0	1.95E+06		(R)VAPEEH	(R)V A/P E E/H|P V L/L\T E/A P L N/P K(A)		140.62	977.5343	1954.064	-0.0031	-1.6	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
11417	dirMS_041712_NAR_50mM_minus2.12079.12079.3	3	9.46	1	1.94E+05		(R)LATALQK	(R)L/A|T A/L Q K L/E E A E K(A)		137.03	481.9385	1443.805	-0.0044	-3	4.79	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
11418	dirMS_041712_NAR_50mM_minus2.12576.12576.3	3	9.46	1	1.30E+05		(R)SLIANLA	(R)S L|I A/N L/A/A A N C Y K K(E)	C:Carbamidomethylation	139.83	512.9454	1536.82	0.0014	0.9	9.7	36978.6	6.33	HUMAN	B7Z800	Adenosine kinase
11419	dirMS_041712_NAR_50mM_minus2.8991.8991.3	3	9.46	1	1.31E+05	M227m	(R)mQKEIT	(R)m Q K E I T|A|L|A/P/S T M K(I)	m:Oxidized methionine	119.48	522.2727	1548.812	15.9911	-2.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
11420	dirMS_041712_NAR_60mM_minus.10093.10094.3	3	9.46	0	3.39E+05		(K)LTPLSHE	(K)L T|P/L/S/H/E/V I S R(Q)		115.77	417.9007	1251.706	-0.018	-14.4	6.75	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
11421	dirMS_041712_NAR_60mM_minus.14090.14090.3	3	9.46	1	3.30E+05		(R)QATKDA	(R)Q A T K D A G/T/I|A|G L N V L R(I)		138.87	543.3073	1627.913	-0.0052	-3.2	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
11422	dirMS_041712_NAR_60mM_minus.16374.16374.3	3	9.46	1	1.44E+05		(K)KLSTIAL	(K)K\L S T I\A L/A|L/G/V E R(T)		151.45	457.6153	1370.837	-0.0052	-3.8	8.75	52669.1	4.73	HUMAN	A8MY67	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform
11423	dirMS_041712_NAR_120mM_plus.8064.8064.2	2	9.46	0	1.42E+06		(R)HQGVM	(R)H|Q|G\V M V/G M G Q/K(D)		96.13	586.2888	1171.571	-0.0007	-0.6	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
11424	dirMS_041712_NAR_20mM_plus.18196.18196.2	2	9.46	0	9.83E+04		(R)APGSGL	(R)A P/G S G L|A/L/L/P L/K(I)		196.67	568.8548	1136.704	-0.0014	-1.3	8.8	266161	5.68	HUMAN	E9PPU0	Epiplakin
11425	dirMS_041712_NAR_20mM_plus.19349.19349.2	2	9.46	0	8.40E+04		(R)ALIAGGG	(R)A L\I/A/G G G A|P E I E L A L R(L)		205.1	775.9467	1550.89	-0.0039	-2.5	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
11426	dirMS_041712_NAR_20mM_plus.8125.8125.2	2	9.46	0	3.83E+05	M239m	(K)EVDEQm	(K)E V D E|Q m L|N|V/Q/N/K(N)	m:Oxidized methionine	125.18	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
11427	dirMS_041712_NAR_30mM_plus2.20843.20843.2	2	9.46	0	1.02E+05		(R)DWVLNE	(R)D W|V/L N E F/K(H)		163.85	525.767	1050.526	0.0013	1.2	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
11428	dirMS_041712_NAR_30mM_plus2.6854.6854.2	2	9.46	0	7.31E+04		(R)ENPYYD	(R)E N/P/Y/Y/D/S R(V)		90.4	522.2255	1043.443	0.0009	0.8	4.37	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
11429	dirMS_041712_NAR_30mM_plus2.7834.7834.2	2	9.46	0	4.12E+05		(K)CNLLAEK	(K)C/N\L/L A\E/K(Q)	C:Carbamidomethylation	94.87	424.2213	847.434	0.0011	1.3	6	40209.9	5.43	HUMAN	C9JV77	Alpha-2-HS-glycoprotein
11430	dirMS_041712_NAR_30mM_plus2.9372.9372.2	2	9.46	0	3.54E+05		(R)LAAVDV	(R)L/A/A/V/D V S A R(A)		102.68	451.2545	901.51	-0.0084	-9.4	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin
11431	dirMS_041712_NAR_40mM_plus2.19541.19541.3	3	9.46	0	3.40E+04		(K)GAEILEV	(K)G A E/I L/E/V L/H/S L P A V R(Q)		183.02	535.3088	1603.917	-0.0048	-3	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
11432	dirMS_041712_NAR_40mM_plus2.7487.7487.2	2	9.46	0	3.20E+05		(K)ASLENSL	(K)A/S/L/E/N S\L/R(E)		104.95	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11433	dirMS_041712_NAR_50mM_plus2.9453.9453.3	3	9.46	1	3.51E+05	M61m	(K)NQVAm	(K)N Q/V|A m/N/P T/N T V/F D A K R(L)	m:Oxidized methionine	117.07	607.9678	1805.896	15.9926	-1.3	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
11434	dirMS_041712_NAR_60mM_plus.17282.17282.3	3	9.46	0	2.04E+05		(K)THLPGFV	(K)T\H L\P G F|V|E|Q/A/E A L K(A)		147.35	513.9442	1539.817	0.0015	1	5.37	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
11435	dirMS_041712_NAR_120mM_minus.4996.4996.3	3	9.45	1	2.60E+05		(K)AGADEE	(K)A/G|A D/E E R/A E T A R(L)		78.72	425.8687	1275.592	-0.0008	-0.7	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
11436	dirMS_041712_NAR_120mM_minus.5191.5191.3	3	9.45	1	3.17E+05		(R)LRAETEQ	(R)L/R A E T\E|Q/G E/Q Q R(Q)		81.13	482.2432	1444.714	0.0012	0.8	4.79	533778	5.74	HUMAN	Q15149	Plectin
11437	dirMS_041712_NAR_20mM_minus.13662.13662.3	3	9.45	0	7.17E+05	M221m	(R)ALTVPEL	(R)A L\T V/P E L/T/Q/Q m/F D/A K(N)	m:Oxidized methionine	186.6	569.9577	1691.867	15.9913	-2.1	4.37	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
11438	dirMS_041712_NAR_30mM_minus2.13943.13943.3	3	9.45	1	5.56E+04	S187s	(R)SVMsTM	(R)S V/M s T/M/W/K N E R(R)	s:N-acetylglucosamine (S)	129.12	524.5723	1368.64	203.0625	-10.7	8.46	23918.2	10.17	HUMAN	P10966-8	Isoform 7 of T-cell surface glycoprotein CD8 beta chain
11439	dirMS_041712_NAR_40mM_minus2.13224.13224.3	3	9.45	1	2.01E+05	M148m	(R)LDLAGR	(R)L D|L/A/G R D/L T D Y L m K(I)	m:Oxidized methionine	161.12	547.2822	1623.841	15.991	-2.4	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
11440	dirMS_041712_NAR_50mM_minus2.10499.10499.3	3	9.45	0	2.90E+05	M35m	(K)AASDIAm	(K)A A|S/D/I/A/m T E L/P/P T H/P I R(L)	m:Oxidized methionine	127.85	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)

11441	dirMS_041712_NAR_50mM_minus2.16889.16889.3	3	9.45	0	2.44E+05		(R)LGIEGLS	(R)L/G\I/E G\L/S L H/N V/L K(L)		164.18	464.9452	1392.821	0.0001	0.1	6.75	177928	5.42	HUMAN	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1
11442	dirMS_041712_NAR_50mM_minus2.7208.7208.3	3	9.45	0	1.66E+05		(R)ETPHSP(	(R)E T P H S P G V|E|D/A P/I/A K(V)		107.98	516.5936	1547.77	-0.0038	-2.4	4.65	67446.5	5.63	HUMAN	F8VQE1	LIM domain and actin-binding protein 1
11443	dirMS_041712_NAR_120mM_plus.5714.5714.4	4	9.45	2	4.78E+05		(R)KTGQAP	(R)K\T G Q\A|P/G/Y S Y T/A A N K N K(G)		83.5	450.4826	1798.908	0.0003	0.2	9.83	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
11444	dirMS_041712_NAR_120mM_plus.6762.6762.2	2	9.45	0	5.08E+05		(R)HLTGEFI	(R)H/L|T G E\F E/K(K)		88.68	480.743	960.479	0.0002	0.2	5.4	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
11445	dirMS_041712_NAR_20mM_plus.10713.10713.2	2	9.45	0	8.05E+03		(R)LAEVEA/	(R)L/A|E/V E A/A/L/E K(Q)		146.92	536.7941	1072.589	-0.0075	-7	4.25	533778	5.74	HUMAN	Q15149	Plectin
11446	dirMS_041712_NAR_20mM_plus.14444.14444.2	2	9.45	0	1.59E+04		(K)TVFGVEI	(K)T V/F/G/V/E P\D L T R(E)		171.18	617.3237	1233.647	-0.0073	-5.9	4.37	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
11447	dirMS_041712_NAR_20mM_plus.14518.14576.2	2	9.45	0	6.71E+05	M73m	(R)AVLVDLI	(R)A V L|V/D L\E|P G T m/D S V\R(S)	m:Oxidized methionine	171.05	809.4082	1601.82	15.9888	-3.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
11448	dirMS_041712_NAR_30mM_plus2.18194.18194.2	2	9.45	0	1.98E+05		(R)QITLNDI	(R)Q I/T/L/N|D/L/P V G R(S)		148	613.3465	1225.69	-0.0042	-3.4	5.84	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
11449	dirMS_041712_NAR_40mM_plus2.15124.15124.3	3	9.45	0	3.53E+05		(R)DVQIGD	(R)D V|Q|I/G\D I V/T V G E C R P L S K(T)	C:Carbamidomethylation	156.92	662.6815	1986.033	-0.0025	-1.3	4.56	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
11450	dirMS_041712_NAR_40mM_plus2.7021.7021.2	2	9.45	0	1.61E+05		(R)QLETLG(	(R)Q L/E\T/L/G Q E K(L)		101.52	523.282	1045.552	0.0043	4.1	4.53	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
11451	dirMS_041712_NAR_40mM_plus2.7731.7731.2	2	9.45	0	8.63E+04		(R)FGQGGA	(R)F G/Q\G\G A|G|P V/G G Q G/P R(G)		105.47	671.3368	1341.666	0.0005	0.4	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
11452	dirMS_041712_NAR_50mM_plus2.13621.13621.3	3	9.45	1	7.51E+05		(K)LIQEIVD	(K)L I|Q/E I/V D/K S G V\V/R(V)		140.07	485.9552	1455.853	-0.0019	-1.3	6.07	66105.7	7.3	HUMAN	A8MQB8	Fragile X mental retardation protein 1
11453	dirMS_041712_NAR_50mM_plus2.20021.20021.3	3	9.45	1	1.08E+05		(K)SVISGGL	(K)S V|I/S/G G L D/A L E F I G K K(T)		174.18	545.3029	1633.916	-0.0218	-13.3	5.79	22133.2	4.82	HUMAN	E5RGF9	Protein FAM114A2 (Fragment)
11454	dirMS_041712_NAR_50mM_plus2.7078.7078.3	3	9.45	1	9.80E+04		(R)MLQADI	(R)M L/Q A D/P N K V/S A R(A)		102.4	443.9033	1329.694	0.001	0.8	8.5	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
11455	dirMS_041712_NAR_60mM_plus.8306.8306.3	3	9.45	1	5.02E+05		(R)LSQIGVE	(R)L/S|Q/I/G/V E N T E E N R R(L)		101.63	548.9468	1644.83	-0.0041	-2.5	4.79	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
11456	dirMS_041712_NAR_60mM_plus.8890.8932.3	3	9.45	1	1.50E+06	S98s	(R)ESKRHsS	(R)E S K/R/H/s/S S/K(R)	s:N-acetylglucosamine (S)	103.83	416.8777	1045.539	203.0801	0.5	10	69591.5	5.68	HUMAN	A6NJ88	Putative SAGE1-like protein
11457	dirMS_041712_NAR_120mM_minus.9097.9097.2	2	9.44	0	5.62E+05		(K)HFVALST	(K)H/F|V/A L S T N T/T K(V)		103.4	609.8267	1218.648	-0.0016	-1.3	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
11458	dirMS_041712_NAR_40mM_minus2.13123.13123.3	3	9.44	1	9.20E+04		(K)VLDSGA	(K)V L|D S G/A/P I K I/P V G P E/T/L G R(I)		160.87	640.3618	1919.096	-0.0252	-13.1	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
11459	dirMS_041712_NAR_40mM_minus2.15779.15779.3	3	9.44	0	6.68E+05		(K)GLAPDLI	(K)G L\A|P D L P E/D L Y/H L I/K(K)		184.38	565.3111	1693.916	0.0028	1.7	4.54	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
11460	dirMS_041712_NAR_40mM_minus2.8147.8147.3	3	9.44	0	2.15E+05	M35m	(K)AASDIAr	(K)A A|S D I/A/m T E L/P/P/T H P I R(L)	m:Oxidized methionine	128.43	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
11461	dirMS_041712_NAR_40mM_minus2.9260.9260.3	3	9.44	0	1.31E+05		(K)VQASLA	(K)V Q|A|S/L/A A N T\F T/I/T G H A E T K(Q)		137.35	654.0087	1960.013	-0.0019	-1	6.72	11802.2	5.6	HUMAN	D6RDG3	Transcription factor BTF3 (Fragment)
11462	dirMS_041712_NAR_50mM_minus2.12078.12078.3	3	9.44	1	1.94E+05		(R)LATALQI	(R)L/A|T/A/L Q K L E E A E K(A)		137.03	481.9385	1443.805	-0.0044	-3	4.79	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
11463	dirMS_041712_NAR_50mM_minus2.12465.12465.3	3	9.44	0	2.90E+05		(K)AASDIAN	(K)A A\S D I|A M/T E L/P P T H P I R(L)		139.23	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
11464	dirMS_041712_NAR_50mM_minus2.4950.4950.3	3	9.44	1	4.33E+05		(R)AAEDDE	(R)A/A|E\D/D E/D\D D/V D T K K(Q)		82.37	522.5522	1565.645	-0.0029	-1.8	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
11465	dirMS_041712_NAR_50mM_minus2.8943.8943.3	3	9.44	1	1.16E+05	M88m	(K)DVDEAY	(K)D V|D\E A/Y m N K V E L E S R(L)	m:Oxidized methionine	118.62	605.2817	1797.832	15.9982	1.8	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
11466	dirMS_041712_NAR_60mM_minus.11821.11821.3	3	9.44	1	4.61E+05	M232m	(R)MSmKE\	(R)M S m K E V\D E\Q\M/L\N V Q/N K(N)	m:Oxidized methionine	125.58	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
11467	dirMS_041712_NAR_60mM_minus.13352.13352.3	3	9.44	1	4.89E+05		(K)TKEVYEL	(K)T K E V Y E/L/L/D/S P/G/K(V)		134.43	493.5966	1478.774	0.0015	1	4.68	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
11468	dirMS_041712_NAR_60mM_minus.4986.4986.3	3	9.44	1	1.11E+05		(K)DSYVGD	(K)D S/Y/V/G D E A Q S K R(G)		82.27	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
11469	dirMS_041712_NAR_120mM_plus.6604.6604.2	2	9.44	0	5.24E+05	M46m	(R)HQGVm	(R)H/Q|G V m/V/G/M/G Q K(D)	m:Oxidized methionine	87.48	594.2868	1171.571	15.9953	0.3	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
11470	dirMS_041712_NAR_120mM_plus.8705.8705.3	3	9.44	1	4.30E+04		(R)RQQEEL	(R)R\Q Q E E\L|L|A/E E N Q R(L)		99.1	548.2767	1642.814	0.0012	0.7	4.49	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
11471	dirMS_041712_NAR_20mM_plus.11989.11989.2	2	9.44	0	6.74E+04		(K)VLIANN(	(K)V L|I|A N/N/G I\A A V K(C)		155.83	591.8632	1182.72	-0.0014	-1.2	8.72	269989.9	5.92	HUMAN	F8W8T8	Acetyl-CoA carboxylase 2
11472	dirMS_041712_NAR_20mM_plus.12512.12512.2	2	9.44	0	1.19E+05		(K)IISNASC	(K)I I/S N\A|S C T/T/N C L|A/P/L A K(V)	C:Carbamidomethylation	159.55	917.4626	1833.92	-0.0018	-1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
11473	dirMS_041712_NAR_20mM_plus.12895.12895.2	2	9.44	0	3.26E+05	M316m	(R)ISEQFTA	(R)I/S\E Q/F T/A m/F R(R)	m:Oxidized methionine	161.43	623.3012	1229.598	15.9968	1.5	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
11474	dirMS_041712_NAR_20mM_plus.8124.8124.2	2	9.44	0	3.83E+05	M239m	(K)EVDEQn	(K)E V/D E Q m L|N|V Q/N/K(N)	m:Oxidized methionine	125.18	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
11475	dirMS_041712_NAR_20mM_plus.8843.8871.2	2	9.44	0	5.76E+04		(R)GLDVED	(R)G L|D V/E D/V/K(F)		131.6	437.7292	874.452	-0.0005	-0.6	4.03	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
11476	dirMS_041712_NAR_30mM_plus2.15251.15251.2	2	9.44	0	5.29E+05		(R)IAAYLFK	(R)I/A/A/Y L/F K(G)		132.15	413.2445	825.487	-0.0052	-6.3	8.59	15830.9	5.16	HUMAN	J3KRF5	Clathrin heavy chain 1 (Fragment)
11477	dirMS_041712_NAR_30mM_plus2.4474.4474.2	2	9.44	0	3.69E+05		(R)SYTSGP(	(R)S Y|T/S G/P G S R(I)		73.02	456.2155	911.422	0.002	2.2	8.46	19288.4	10.19	HUMAN	F8VQY3	Keratin, type II cytoskeletal 8 (Fragment)
11478	dirMS_041712_NAR_30mM_plus2.5901.5901.2	2	9.44	0	1.75E+05		(R)EAEEVYI	(R)E A/E/E/V/Y R(N)		85.63	448.2113	895.416	-0.0003	-0.3	4.25	54793.4	10.51	HUMAN	B7Z4Q3	Putative RNA-binding protein Luc7-like 2
11479	dirMS_041712_NAR_50mM_plus2.13527.13527.3	3	9.44	1	1.88E+06		(R)QATKDA	(R)Q A T K D A G/T I/A/G L|N V L R(I)		140	543.3085	1627.913	-0.0016	-1	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
11480	dirMS_041712_NAR_60mM_plus.18436.18436.3	3	9.44	1	7.90E+05		(K)EVNKFQ	(K)E V N/K F Q M/A/Y/S/N L L/R(A)		153	571.6293	1712.879	-0.0055	-3.2	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
11481	dirMS_041712_NAR_120mM_minus.11534.11591.4	4	9.43	2	1.59E+06		(K)QAGPAS	(K)Q A G P A/S\V/P/L R T E E E F K/K(F)		117.18	472.5042	1886.997	-0.0021	-1.1	6.23	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
11482	dirMS_041712_NAR_30mM_minus2.11917.11917.3	3	9.43	0	3.96E+06		(R)AQIFAN	(R)A Q\I F|A N/T/V/D/N A R(I)		117.57	440.5617	1319.67	0.0003	0.2	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11483	dirMS_041712_NAR_30mM_minus2.12880.12899.2	2	9.43	0	6.88E+05		(R)IGLAEEII	(R)I/G|L|A/E E I R(H)		123.3	450.7604	900.515	-0.0014	-1.5	4.53	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
11484	dirMS_041712_NAR_30mM_minus2.5257.5257.2	2	9.43	0	6.21E+05		(R)TDTGEP	(R)T D|T/G/E\P M G/R(G)		82.35	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
11485	dirMS_041712_NAR_50mM_minus2.17059.17059.3	3	9.43	0	6.44E+04		(R)ILVTLLH	(R)I L/V/T L/L/H/T/L E R(M)		165.27	436.6057	1307.805	-0.002	-1.5	6.75	45212.4	9.41	HUMAN	B7Z233	Acetyl-CoA acetyltransferase, cytosolic
11486	dirMS_041712_NAR_60mM_minus.10246.10246.3	3	9.43	1	2.36E+04	M88m	(K)DVDEAY	(K)D V/D E/A Y m N K V/E/L/E S R(L)	m:Oxidized methionine	116.03	605.2791	1797.832	15.9904	-2.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
11487	dirMS_041712_NAR_60mM_minus.10626.10626.3	3	9.43	0	1.44E+05	M271m	(R)DLNYCF!	(R)D L|N/Y C/F/S/G m S D/H/R(Y)	C:Carbamidomethylation m:Oxid	119.2	539.8863	1601.647	15.9972	1.4	5.21	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
11488	dirMS_041712_NAR_60mM_minus.11607.11607.3	3	9.43	0	2.25E+05		(K)ADDGRF	(K)A/D|D/G R P F/P Q V/I/K(S)		124.53	448.2371	1342.711	-0.0146	-10.9	6	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
11489	dirMS_041712_NAR_60mM_minus.7094.7094.3	3	9.43	1	2.36E+04		(R)AGGEEL	(R)A/G|G/E E/L D E G V A K D N A\K(I)		98.43	534.9257	1602.761	0.002	1.2	4.18	89879.1	4.58	HUMAN	Q32MZ4	Leucine-rich repeat flightless-interacting protein 1
11490	dirMS_041712_NAR_120mM_plus.18491.18491.3	3	9.43	1	6.09E+04	M293m	(K)HEILEAS	(K)H E I L E A S H\m/I/Q T K E R(S)	m:Oxidized methionine	149.78	613.3075	1821.928	15.9804	-7.9	6.02	90088.3	5.78	HUMAN	Q8WXW3	Progesterone-induced-blocking factor 1
11491	dirMS_041712_NAR_30mM_plus2.11950.11950.2	2	9.43	0	6.83E+05		(K)CGDLVF.	(K)C/G\D|L/V/F A/K(M)	C:Carbamidomethylation	116.12	455.2298	909.45	0.0025	2.7	5.84	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
11492	dirMS_041712_NAR_30mM_plus2.18532.18532.2	2	9.43	0	1.54E+05		(R)AMLDQI	(R)A M|L/D Q/L/M/G T S/R(D)		150.35	611.8	1222.592	0.0009	0.7	5.88	5509.4	10.84	HUMAN	F8WB41	Putative RNA-binding protein Luc7-like 2
11493	dirMS_041712_NAR_30mM_plus2.19430.19430.2	2	9.43	0	1.85E+04		(K)MNEFLE	(K)M N\E/F/L/E N/F E/K(N)		155.87	650.7974	1300.588	-0.0003	-0.2	4.25	28580.2	9.35	HUMAN	Q9UFN0	Protein NipSnap homolog 3A
11494	dirMS_041712_NAR_40mM_plus2.10630.10630.3	3	9.43	0	1.85E+05		(K)VGSLDN	(K)V/G/S L D N V/G H L P A G G A V K(I)		128.15	530.9567	1590.86	-0.0043	-2.7	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
11495	dirMS_041712_NAR_50mM_plus2.9249.9249.3	3	9.43	1	5.88E+04		(R)IEDVTPII	(R)I/E|D V T P I P S D/S T R R(K)		115.63	529.2768	1585.818	-0.0022	-1.4	4.56	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
11496	dirMS_041712_NAR_60mM_plus.7984.8219.3	3	9.43	1	6.10E+05		(K)ALSRQEI	(K)A L/S R Q E M\Q/E/V/Q/S/S R(S)		100.33	550.2735	1648.807	-0.0012	-0.7	6.19	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
11497	dirMS_041712_NAR_20mM_minus.12104.12104.2	2	9.42	0	3.90E+05	M185m	(K)LAVNm\	(K)L/A\V|N/m\V/P F/P R(L)	m:Oxidized methionine	170.83	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
11498	dirMS_041712_NAR_20mM_minus.13756.13756.2	2	9.42	0	2.16E+05		(R)IVLLDSS	(R)I V|L L/D/S S L\E Y K(K)		189.05	640.3594	1279.714	-0.0029	-2.2	4.37	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
11499	dirMS_041712_NAR_20mM_minus.9733.9733.2	2	9.42	0	2.50E+05	M33m	(K)VAGmD'	(K)V A G\m D/V/E L|T V/E E R(N)	m:Oxidized methionine	147.53	732.355	1447.71	15.993	-1.3	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
11500	dirMS_041712_NAR_30mM_minus2.15827.15827.2	2	9.42	0	4.68E+04		(R)INEILSN/	(R)I/N|E\I/L S|N A L K(R)		139.15	557.8242	1114.647	-0.0055	-5	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
11501	dirMS_041712_NAR_40mM_minus2.11261.11261.3	3	9.42	1	1.92E+04	M250m	(R)DSDIIED	(R)D S|D/I/I/E/D V m V K D L Q K(L)	m:Oxidized methionine	149.23	588.6311	1747.878	16.0005	3.2	4.04	55757.3	5.55	HUMAN	O94919	Endonuclease domain-containing 1 protein
11502	dirMS_041712_NAR_40mM_minus2.8960.8960.3	3	9.42	1	5.45E+04		(R)IVAPGK(	(R)I V|A/P G K G I L A/A/D/E S/T G S I A K(R)		135.25	633.355	1898.059	-0.0089	-4.7	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
11503	dirMS_041712_NAR_50mM_minus2.14030.14030.3	3	9.42	1	1.03E+05		(R)RLLEEEII	(R)R|L/L/E E E I I A F S K(K)		148.02	483.2761	1447.815	-0.0018	-1.2	4.79	63742.6	6.4	HUMAN	B5ME97	Septin 10, isoform CRA_c
11504	dirMS_041712_NAR_50mM_minus2.7061.7061.3	3	9.42	0	2.09E+05		(K)VSYGIGI	(K)V S/Y/G/I G/D E E H D Q E G R(V)		106.65	564.249	1690.73	0.0021	1.3	4.17	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
11505	dirMS_041712_NAR_60mM_minus.18034.18034.3	3	9.42	1	1.25E+04		(K)RSIQFVD	(K)R S I Q\F\V|D/W/C P T G F K(V)	C:Carbamidomethylation	161.33	580.9568	1740.853	0.0032	1.8	8.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
11506	dirMS_041712_NAR_20mM_plus.19106.19106.3	3	9.42	0	2.37E+05		(R)VCTLAIII	(R)V C T L A\I/I/D/P G D/S D/I I R(S)	C:Carbamidomethylation	202.77	586.641	1757.91	-0.0018	-1	3.93	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
11507	dirMS_041712_NAR_30mM_plus2.4290.4435.2	2	9.42	0	4.13E+05		(R)SMPEQT	(R)S M/P/E/Q T G/E/K(-)		72.3	503.7289	1006.451	-0.0005	-0.5	4.53	12955	9.87	HUMAN	P62888	60S ribosomal protein L30
11508	dirMS_041712_NAR_50mM_plus2.12061.12061.3	3	9.42	0	3.79E+05		(K)FSVCVL(	(K)F S/V/C V/L G D/Q Q H C D E A/K(A)	C:Carbamidomethylation	131.38	631.6129	1892.827	-0.0024	-1.3	4.54	25002	10.06	HUMAN	P62906	60S ribosomal protein L10a
11509	dirMS_041712_NAR_50mM_plus2.15012.15012.3	3	9.42	0	6.71E+05		(R)QIFHPE(	(R)Q/I F H/P/E Q L/I T G K(E)		147.27	470.9293	1410.774	-0.0006	-0.4	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
11510	dirMS_041712_NAR_60mM_plus.11826.11826.2	2	9.42	1	2.66E+05		(K)TLQEVTI	(K)T L\Q/E\V|T E/M D S V K R(Y)		118.98	768.3889	1535.773	-0.0029	-1.9	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
11511	dirMS_041712_NAR_20mM_minus.7206.7206.2	2	9.41	0	1.40E+05		(K)VTLTSEE	(K)V/T|L/T|S E/E E/A R(L)		119.73	567.785	1134.564	-0.001	-0.9	4.25	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
11512	dirMS_041712_NAR_20mM_minus.8351.8351.2	2	9.41	0	1.25E+05		(K)VTADVII	(K)V/T|A/D V|I N A A E K(L)		132.47	565.8065	1130.605	0.0005	0.5	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
11513	dirMS_041712_NAR_50mM_minus2.12351.12351.3	3	9.41	1	3.32E+05		(R)DGRGAL	(R)D G R G A L Q\N\I|I|P/A S T G A A K(A)		138.33	580.6487	1739.94	-0.0083	-4.8	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
11514	dirMS_041712_NAR_50mM_minus2.16780.16780.3	3	9.41	0	2.54E+05		(K)ALVSHN	(K)A L\V S H N G S\L\I|N/V/G S/L/L Q R(A)		163.75	626.6879	1878.056	-0.0064	-3.4	9.8	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
11515	dirMS_041712_NAR_60mM_minus.10113.10113.3	3	9.41	0	3.39E+05		(K)LTPLSHE	(K)L T/P/L/S H/E V I S R(Q)		115.77	417.9007	1251.706	-0.018	-14.4	6.75	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
11516	dirMS_041712_NAR_60mM_minus.11401.11401.3	3	9.41	1	2.74E+05		(K)VVSKEE!	(K)V V|S K E E S\I|V/S S L R(L)		123.52	478.27	1432.801	-0.0051	-3.6	6.11	49283	6.89	HUMAN	C9JZR4	ADP-ribosylation factor GTPase-activating protein 3
11517	dirMS_041712_NAR_60mM_minus.13700.13700.3	3	9.41	0	3.78E+05		(-)MVNHFI/	(-)M/V|N H/F I A E/F K(R)		136.52	412.5461	1235.624	-0.0004	-0.3	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
11518	dirMS_041712_NAR_60mM_minus.15222.15222.2	2	9.41	0	4.20E+05		(R)EHALLA\	(R)E H|A|L|L|A/Y T L G V K(Q)		144.65	657.873	1314.742	-0.0029	-2.2	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
11519	dirMS_041712_NAR_60mM_minus.18373.18373.3	3	9.41	1	4.80E+05		(K)TQLNLLI	(K)T Q/L/N L L/L D K L/R(S)		163.37	442.9403	1326.81	-0.004	-3	8.41	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
11520	dirMS_041712_NAR_60mM_minus.18427.18427.3	3	9.41	0	1.09E+06		(R)IHFPLAT	(R)I H\F P L A T Y A|P V I S A E K(A)		165.12	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
11521	dirMS_041712_NAR_120mM_plus.12666.12666.2	2	9.41	0	7.62E+05		(K)HLSVND	(K)H L|S V/N D|L P V G R(S)		119.22	603.8321	1206.659	-0.002	-1.7	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
11522	dirMS_041712_NAR_120mM_plus.8675.8675.3	3	9.41	0	5.88E+05		(K)QHTFVE	(K)Q H T F V|E/T|E/S\V/R(Y)		98.15	444.8857	1332.654	-0.0117	-8.8	5.4	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
11523	dirMS_041712_NAR_20mM_plus.9541.9541.2	2	9.41	0	8.32E+04		(K)AVDSQII	(K)A/V|D S/Q I L/P/K(I)		137.07	485.7824	970.557	0.0008	0.8	5.88	25891.4	10.67	HUMAN	F8W181	60S ribosomal protein L6 (Fragment)
11524	dirMS_041712_NAR_30mM_plus2.19347.19347.2	2	9.41	0	2.23E+05		(K)NFSGAE	(K)N F|S/G A\E L E G L/V R(A)		155.35	646.3361	1291.664	0.0008	0.6	4.53	71924.9	6.25	HUMAN	B4DFA2	Vesicle-fusing ATPase
11525	dirMS_041712_NAR_30mM_plus2.20202.20243.2	2	9.41	0	2.03E+05		(R)FLGTEVI	(R)F/L/G|T E/V L L/R(L)		160.83	524.3115	1047.62	-0.004	-3.8	6	103045.5	7.1	HUMAN	B9ZVT1	RNA-binding protein 12B
11526	dirMS_041712_NAR_30mM_plus2.20587.20587.2	2	9.41	0	1.91E+05		(R)ASLSLW	(R)A S L/S|L/W Q/A M/E K(G)		162.67	632.3231	1263.64	-0.0013	-1	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
11527	dirMS_041712_NAR_40mM_plus2.6412.6412.2	2	9.41	0	1.45E+05		(K)SLESINSI	(K)S/L|E/S/I/N S R(L)		96.8	453.2358	905.469	-0.0044	-4.8	5.72	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
11528	dirMS_041712_NAR_50mM_plus2.14560.14560.3	3	9.41	1	5.76E+05		(R)SEGVVA	(R)S E|G\V/V/A V/L/L T K/K(S)		144.37	415.2585	1243.762	-0.0011	-0.9	8.31	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
11529	dirMS_041712_NAR_50mM_plus2.19351.19351.3	3	9.41	0	1.75E+05		(R)LHPVILA	(R)L H P V I L A S|I|V/D/S Y E/R(R)		169.85	571.3163	1711.938	-0.0034	-2	5.32	39260.1	5.25	HUMAN	B3KSH1	Eukaryotic translation initiation factor 3 subunit F
11530	dirMS_041712_NAR_60mM_plus.10551.10551.3	3	9.41	1	6.84E+05		(R)LKAEAEI	(R)L K\A E A\E\L/L/Q Q\Q K(E)		112.97	466.9362	1398.795	-0.0011	-0.8	6.14	533778	5.74	HUMAN	Q15149	Plectin
11531	dirMS_041712_NAR_120mM_minus.13525.13525.3	3	9.4	1	2.25E+05		(R)VIDRELY	(R)V/I/D/R E\L Y Q Q L/Q/R(G)		128.15	520.955	1560.849	0.0012	0.8	6.04	533778	5.74	HUMAN	Q15149	Plectin
11532	dirMS_041712_NAR_120mM_minus.19374.19374.3	3	9.4	0	1.84E+04		(R)NSVSNF	(R)N S/V S/N F/L/H/S/L E R(G)		160.98	468.2346	1402.707	-0.0181	-12.9	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
11533	dirMS_041712_NAR_120mM_minus.21422.21422.3	3	9.4	0	8.12E+05		(R)LHFFMP	(R)L H F F M P/G\F A|P\L/T S R(G)		182.17	540.9497	1620.835	-0.001	-0.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
11534	dirMS_041712_NAR_20mM_minus.13670.13670.2	2	9.4	0	1.53E+05		(K)ALQQGL	(K)A L/Q/Q/G L V/G/L E L K(E)		187.57	634.8811	1268.757	-0.0023	-1.8	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
11535	dirMS_041712_NAR_30mM_minus2.10369.10369.2	2	9.4	0	6.05E+05		(K)EAAENS	(K)E A|A E/N/S L/V A/Y/K(A)		110.8	597.8033	1194.6	-0.0008	-0.6	4.53	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
11536	dirMS_041712_NAR_30mM_minus2.6066.6066.2	2	9.4	0	2.64E+05		(K)TSEVNC	(K)T|S|E/V/N C Y R(C)	C:Carbamidomethylation	87.3	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
11537	dirMS_041712_NAR_40mM_minus2.12797.12797.3	3	9.4	0	3.24E+05		(R)DVQIGD	(R)D V\Q|I/G/D I V T V G E C R P L/S K(T)	C:Carbamidomethylation	159.63	662.684	1986.033	0.005	2.5	4.56	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
11538	dirMS_041712_NAR_40mM_minus2.7504.7504.3	3	9.4	1	1.82E+05	M88m	(K)DVDEAY	(K)D V/D/E A/Y m N K V/E L E/S R(L)	m:Oxidized methionine	120.62	605.2801	1797.832	15.9934	-0.8	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
11539	dirMS_041712_NAR_50mM_minus2.10080.10080.3	3	9.4	0	1.78E+05	M392m	(K)EmNPAL	(K)E m N/P/A L|G I|D C L H K(G)	C:Carbamidomethylation m:Oxid	125.77	505.2416	1497.719	15.9914	-2.3	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
11540	dirMS_041712_NAR_50mM_minus2.12841.12841.3	3	9.4	0	1.53E+05		(K)ASLASLP	(K)A S L A S L/P/P L H V A/K(L)		141.37	435.2622	1303.773	-0.0012	-0.9	8.8	141626	5.5	HUMAN	A8MY36	Dynactin subunit 1
11541	dirMS_041712_NAR_50mM_minus2.8720.8720.3	3	9.4	1	3.40E+04		(R)VEVGKD	(R)V/E|V G K D Q E F/T V D/T R(G)		117.13	541.605	1622.802	-0.0016	-1	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
11542	dirMS_041712_NAR_50mM_minus2.9475.9475.3	3	9.4	1	3.98E+04		(K)IQVLQQ	(K)I Q|V|L/Q\Q Q A D D A E E R A E\R(L)		122.12	666.9985	1998.984	-0.003	-1.5	4.18	26611.3	4.47	HUMAN	A6NL28	Putative tropomyosin alpha-3 chain-like protein
11543	dirMS_041712_NAR_60mM_minus.14945.14945.3	3	9.4	0	9.99E+04		(K)SLTNDW	(K)S/L/T/N D W E D|H L A V K(H)		144.35	509.9191	1527.744	-0.0011	-0.7	4.53	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
11544	dirMS_041712_NAR_60mM_minus.17723.17723.3	3	9.4	0	1.40E+05		(R)GGHVVE	(R)G G H V\V E G L\A/G E/L E/Q/L/R(A)		158.98	555.2959	1663.876	-0.0031	-1.8	4.75	106088.3	5.78	HUMAN	P10275	Androgen receptor
11545	dirMS_041712_NAR_60mM_minus.9454.9454.3	3	9.4	1	1.78E+05		(K)IFRDGEE	(K)I F R D G E E\A G\A|Y D/G P R(T)		112.25	551.5934	1652.766	-0.0007	-0.4	4.32	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
11546	dirMS_041712_NAR_120mM_plus.5593.5593.3	3	9.4	1	4.53E+05		(K)AQQELE	(K)A Q|Q/E L/E/E Q T R/R(A)		81.9	463.2395	1387.692	0.0115	8.3	4.79	67933	6.08	HUMAN	P26038	Moesin
11547	dirMS_041712_NAR_20mM_plus.18313.18313.2	2	9.4	0	5.62E+04		(K)LFIGGLN	(K)L F/I|G G L/N/V/Q/T S E S G L R(G)		197.5	845.9573	1690.912	-0.0049	-2.9	6	31011.2	9.5	HUMAN	Q13151	Heterogeneous nuclear ribonucleoprotein A0
11548	dirMS_041712_NAR_20mM_plus.18539.18539.2	2	9.4	0	7.65E+04		(K)STLINTLI	(K)S/T/L/I/N T L F K(S)		199.02	518.8058	1036.604	0.0006	0.6	8.47	18010.4	9.42	HUMAN	K7EIE4	Septin-9 (Fragment)
11549	dirMS_041712_NAR_30mM_plus2.10108.10108.2	2	9.4	0	3.60E+05		(K)GMPGF!	(K)G M/P G F/S T/S K(K)		106.38	456.2155	911.429	-0.0054	-5.9	8.75	16060.3	9.43	HUMAN	H0YKV0	Isovaleryl-CoA dehydrogenase, mitochondrial (Fragment)

11550	dirMS_041712_NAR_30mM_plus2.18387.18387.2	2	9.4	0	2.29E+05		(K)TTFEDLI	(K)T/T/F/E|D L\I Q R(C)		149.35	561.7934	1122.579	0.0006	0.5	4.37	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
11551	dirMS_041712_NAR_40mM_plus2.11531.11531.2	2	9.4	0	5.28E+04		(R)TFEDFV	(R)T/T/F|E/D/F V/R(I)		134.22	457.2245	913.441	0.0003	0.3	4.37	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
11552	dirMS_041712_NAR_40mM_plus2.11925.11968.2	2	9.4	0	2.48E+05		(K)LSELEAA	(K)L/S|E|L/E A/A|L/Q R(A)		136.62	565.3103	1129.621	-0.0078	-6.9	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
11553	dirMS_041712_NAR_40mM_plus2.12970.12970.3	3	9.4	0	2.00E+05		(R)VVLSVSS	(R)V V|L S/V/S S G G Q H T V L L/V/K(D)		143.48	575.0089	1723.011	0.0009	0.5	8.73	45424.7	7.24	HUMAN	P18754	Regulator of chromosome condensation
11554	dirMS_041712_NAR_40mM_plus2.9182.9182.2	2	9.4	0	1.45E+05		(R)QTVAVG	(R)Q T/V/A/V/G V I/K(A)		116.57	457.7854	914.567	-0.0034	-3.7	8.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
11555	dirMS_041712_NAR_50mM_plus2.12682.12682.3	3	9.4	1	3.83E+05		(K)LPGGEL	(K)L/P|G G E L N|P G/E D\E/V/E G L K R(L)		134.28	636.9936	1908.966	0.0001	0.1	4.25	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
11556	dirMS_041712_NAR_50mM_plus2.19905.19905.3	3	9.4	0	3.74E+05		(K)NGGLGH	(K)N G\G/L G H M N\I/A/L/L/S D L T K(Q)		173.03	585.311	1753.927	-0.0081	-4.6	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
11557	dirMS_041712_NAR_50mM_plus2.5559.5559.3	3	9.4	1	1.11E+05		(K)DSYVGD	(K)D S\Y/V/G D/E A Q S K R(G)		90.6	452.2114	1354.623	-0.0037	-2.7	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
11558	dirMS_041712_NAR_60mM_plus.18709.18709.3	3	9.4	1	1.58E+04	T225t	(R)TELMDH	(R)T/E L/M/D H S R/T t L Q R(E)	t:N-acetylglucosamine (T)	154.07	597.6338	1587.791	203.0961	9.3	6.42	37131.1	9.47	HUMAN	P29275	Adenosine receptor A2b
11559	dirMS_041712_NAR_60mM_plus.19885.19885.3	3	9.4	1	1.53E+05		(R)GMLRED	(R)G M/L R E D A\V/L/E Y L K(I)		163.87	512.9411	1536.809	-0.0003	-0.2	4.68	67933	6.08	HUMAN	P26038	Moesin
11560	dirMS_041712_NAR_60mM_plus.5695.5695.3	3	9.4	1	1.53E+05	M131m	(R)QmGQP	(R)Q m|G Q/P C/D/A Y Q K/R(L)	C:Carbamidomethylation m:Oxid	87.98	499.8898	1481.662	15.9925	-1.6	8.59	334221.3	6.44	HUMAN	P15924	Desmoplakin
11561	dirMS_041712_NAR_120mM_minus.11386.11407.3	3	9.39	1	4.08E+05		(K)VIADNV	(K)V/I/A/D N V/K/D W S K(V)		116.48	425.5623	1274.674	-0.0016	-1.2	5.93	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
11562	dirMS_041712_NAR_30mM_minus2.14020.14020.2	2	9.39	0	3.05E+05		(R)LAGLFN	(R)L A|G\L/F/N E Q\R(K)		129.57	524.2789	1047.558	-0.0076	-7.3	6	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
11563	dirMS_041712_NAR_50mM_minus2.10272.10272.3	3	9.39	0	1.66E+05		(K)LQAEAP	(K)L Q|A E A P H\I/V V/G T P G R(V)		127.08	515.6179	1544.854	-0.0152	-9.8	6.75	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
11564	dirMS_041712_NAR_60mM_minus.12137.12137.3	3	9.39	0	7.93E+05	M1m	(-)mVNHF	(-)m V/N\H F I/A E/F K(R)	m:Oxidized methionine	127.92	417.8768	1235.624	15.9917	-2.6	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
11565	dirMS_041712_NAR_60mM_minus.16941.16941.3	3	9.39	1	2.55E+05	M182m	(R)GmLRED	(R)G m L R E D A/V/L|E Y/L K(I)	m:Oxidized methionine	154.75	518.2737	1536.809	15.9975	1.7	4.68	67933	6.08	HUMAN	P26038	Moesin
11566	dirMS_041712_NAR_60mM_minus.5336.5336.3	3	9.39	0	1.65E+06		(K)TATPQQ	(K)T A/T|P Q Q A Q E/V H E K(L)		84.62	489.5763	1466.723	-0.009	-6.2	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
11567	dirMS_041712_NAR_120mM_plus.14000.14000.3	3	9.39	1	4.03E+05		(K)WKDSD	(K)W/K D\S D E A/D/L/V/L/A/K(E)		126.42	497.2584	1489.753	0.0073	4.9	4.23	20982.2	5.23	HUMAN	Q13185	Chromobox protein homolog 3
11568	dirMS_041712_NAR_20mM_plus.12999.12999.2	2	9.39	0	1.45E+05		(R)LVVPAS	(R)L V|V|P A S Q C G S/L I G K(G)	C:Carbamidomethylation	161.9	714.8991	1428.788	0.003	2.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
11569	dirMS_041712_NAR_30mM_plus2.15444.15444.2	2	9.39	0	3.31E+05		(R)GLPWS	(R)G L/P/W/S C S A D E V/Q R(F)	C:Carbamidomethylation	133.27	752.8375	1504.685	-0.0172	-11.4	4.37	4406.9	4.36	HUMAN	D6R9D3	Heterogeneous nuclear ribonucleoprotein H
11570	dirMS_041712_NAR_30mM_plus2.17409.17409.3	3	9.39	0	1.05E+06		(R)ASLEAAI	(R)A S L E A A\I|A/D/A/E Q/R(G)		144.43	448.8963	1344.675	-0.001	-0.8	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
11571	dirMS_041712_NAR_30mM_plus2.8973.9040.2	2	9.39	0	3.51E+05		(R)LFEQNV	(R)L/F|E/Q N V/Q/R(S)		100.77	517.2734	1033.543	-0.003	-2.9	6	21184.9	7.82	HUMAN	P61081	NEDD8-conjugating enzyme Ubc12
11572	dirMS_041712_NAR_40mM_plus2.13068.13069.3	3	9.39	0	2.26E+05		(R)VVLSVSS	(R)V/V|L/S/V S S G G Q H T V L L V K(D)		143.62	575.0089	1723.011	0.0009	0.5	8.73	45424.7	7.24	HUMAN	P18754	Regulator of chromosome condensation
11573	dirMS_041712_NAR_50mM_plus2.11561.11561.3	3	9.39	1	5.26E+05		(K)LIPDSIG	(K)L I/P/D S I G K D I E/K(A)		128.77	443.2514	1327.747	-0.0071	-5.4	4.56	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
11574	dirMS_041712_NAR_50mM_plus2.11884.11884.3	3	9.39	0	2.20E+05		(R)IELGDV	(R)I E L/G D V T/P/H N I K(Q)		130.6	445.9079	1335.727	-0.0175	-13.1	5.32	14942.8	8.71	HUMAN	C9J5D1	N-alpha-acetyltransferase 50
11575	dirMS_041712_NAR_50mM_plus2.16601.16601.3	3	9.39	0	4.08E+05		(K)SAIPHPL	(K)S A\I/P/H|P L/I M G\V I R(E)		155.43	468.6115	1403.819	0.0008	0.6	9.49	44513	5.59	HUMAN	B4DIH5	COP9 signalosome complex subunit 2
11576	dirMS_041712_NAR_50mM_plus2.18523.18523.3	3	9.39	0	4.45E+05	M195m	(R)LHFFmP	(R)L H/F F m\P/G|F A/P L/T S R(G)	m:Oxidized methionine	164.27	546.2803	1620.835	15.9908	-2.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
11577	dirMS_041712_NAR_50mM_plus2.22139.22139.3	3	9.39	1	8.06E+05		(R)ELAILLG	(R)E L/A/I/L/L G M L D P/A E K D E K(G)		190.45	629.004	1884.999	-0.0012	-0.7	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
11578	dirMS_041712_NAR_60mM_plus.16301.16301.3	3	9.39	1	1.84E+05		(K)KAPDFV	(K)K A P D F\V|F/Y A P/R(L)		141.8	437.5685	1310.689	0.0018	1.3	8.59	71218.8	6.3	HUMAN	A7YIJ8	Radixin
11579	dirMS_041712_NAR_60mM_plus.19363.19363.3	3	9.39	1	4.46E+04		(R)SLADIA	(R)S L|A/D I/A R E E A S N F/R(S)		159.53	526.9346	1578.787	0.0022	1.4	4.68	20458.8	4.99	HUMAN	G3V4X5	Proteasome subunit alpha type-3
11580	dirMS_041712_NAR_60mM_plus.4788.4788.3	3	9.39	1	1.78E+06		(R)AAEEED	(R)A A|E\E E/D E A D/P K R(Q)		80	453.872	1359.602	-0.0008	-0.6	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
11581	dirMS_041712_NAR_60mM_plus.9787.9787.3	3	9.39	1	1.29E+06		(K)EAALST	(K)E A/A/L/S/T/A/L S E K/R(T)		109.78	425.898	1275.69	-0.0109	-8.5	6.24	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
11582	dirMS_041712_NAR_120mM_minus.10450.10450.3	3	9.38	1	2.31E+05		(R)RQQEQ	(R)R/Q\Q E\Q\Q\V/P I/L E/K(F)		111.02	499.2772	1495.823	-0.0057	-3.8	6.14	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
11583	dirMS_041712_NAR_120mM_minus.10978.10978.3	3	9.38	1	2.36E+05		(R)TNEKVE	(R)T N/E K/V E\L|Q/E L/N D\R(F)		114.1	529.9368	1587.797	-0.0014	-0.9	4.41	49709.6	5.19	HUMAN	B0YJC4	Vimentin
11584	dirMS_041712_NAR_120mM_minus.8209.8209.3	3	9.38	1	2.76E+04		(K)SSGGRE	(K)S S|G G R E D\L\E/S/S/G L Q\R(R)		98.9	526.5882	1577.751	-0.0014	-0.9	4.68	11625.5	8.01	HUMAN	B8ZZT7	Hematological and neurological-expressed 1 protein
11585	dirMS_041712_NAR_20mM_minus.13334.13334.2	2	9.38	0	5.56E+05		(K)DAGTIA	(K)D A G T|I/A/G L N V L/R(I)		184.7	600.3403	1199.674	-0.0009	-0.8	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
11586	dirMS_041712_NAR_20mM_minus.7322.7322.2	2	9.38	0	1.32E+05	M374m	(R)mAPTPI	(R)m A|P T/P I/P T R(S)	m:Oxidized methionine	121.02	500.2679	983.534	15.9943	-0.7	9.5	76925.9	4.46	HUMAN	A8MV58	Drebrin
11587	dirMS_041712_NAR_30mM_minus2.10037.10055.2	2	9.38	0	1.87E+05		(K)SPSESFI	(K)S/P|S/E/S F/I G R(E)		109.8	490.2513	979.484	0.011	11.2	5.72	103815.5	6.12	HUMAN	F8WBA3	Serine/threonine-protein kinase D
11588	dirMS_041712_NAR_30mM_minus2.12508.12508.2	2	9.38	0	2.62E+05		(K)STLTDSL	(K)S T/L/T D/S L V/C K(A)	C:Carbamidomethylation	121.85	562.2838	1123.566	-0.006	-5.4	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
11589	dirMS_041712_NAR_30mM_minus2.15991.15991.2	2	9.38	0	3.18E+04		(K)NLILVVR	(K)N\L/I|L/V V/R(G)		139.73	413.7746	826.551	-0.009	-10.9	9.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
11590	dirMS_041712_NAR_30mM_minus2.5185.5185.2	2	9.38	0	5.79E+05		(R)TDTGEP	(R)T D|T|G E\P M G R(G)		81.87	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
11591	dirMS_041712_NAR_50mM_minus2.12677.12691.3	3	9.38	1	2.33E+05		(R)QATKDA	(R)Q A T K D A G T\I/A/G/L/N V/L R(I)		140.57	543.3085	1627.913	-0.0016	-1	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
11592	dirMS_041712_NAR_60mM_minus.12772.12772.3	3	9.38	1	1.96E+05		(K)LSAEKVE	(K)L/S/A E K V E\I|A/T/L T R(E)		130.97	477.6112	1430.821	-0.0023	-1.6	6.14	26661.1	7.81	HUMAN	H0YL69	Proteasome subunit alpha type (Fragment)
11593	dirMS_041712_NAR_60mM_minus.9722.9722.3	3	9.38	0	5.63E+05		(K)VFEHDS	(K)V F/E/H D S V/E/L\N C K(M)	C:Carbamidomethylation	112.98	492.8981	1476.679	0.001	0.7	4.65	31975.7	6.55	HUMAN	P10768	S-formylglutathione hydrolase
11594	dirMS_041712_NAR_120mM_plus.17100.17100.4	4	9.38	2	1.83E+06		(R)NLKASL	(R)N L/K A S\L/E/N S\L R E V/E/A R(Y)		143.23	458.0016	1828.988	-0.003	-1.6	6.23	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11595	dirMS_041712_NAR_120mM_plus.20626.20626.4	4	9.38	1	2.15E+05		(K)AAIDWF	(K)A A/I D/W F/D G K E/F H G N I I K(V)		161.23	491.0027	1960.992	-0.0026	-1.3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
11596	dirMS_041712_NAR_20mM_plus.15467.15467.2	2	9.38	0	2.97E+04		(R)VLELVS	(R)V L|E/L|V/S\I T A N K(N)		178.48	593.8535	1186.704	-0.0044	-3.7	5.97	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
11597	dirMS_041712_NAR_30mM_plus2.21964.21964.2	2	9.38	0	1.03E+05		(K)NFYFLE	(K)N F|Y|F/L E/M N T R(L)		170.5	667.8205	1334.62	0.0139	10.4	6	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
11598	dirMS_041712_NAR_40mM_plus2.13260.13260.3	3	9.38	0	1.97E+05		(R)DLSHIG	(R)D L/S H\I G D A\V/V|I S C A K(D)	C:Carbamidomethylation	144.35	528.9395	1584.805	-0.0011	-0.7	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
11599	dirMS_041712_NAR_40mM_plus2.6289.6289.2	2	9.38	1	2.84E+05		(R)YSGGNY	(R)Y S|G G N Y/R D/N Y/D\N(-)		95.58	719.2857	1437.567	-0.0024	-1.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
11600	dirMS_041712_NAR_50mM_plus2.18755.18755.3	3	9.38	0	4.45E+05		(R)DVCTEL	(R)D V|C/T/E L L/P L/I K/P Q/G R(V)	C:Carbamidomethylation	166.58	580.3229	1738.952	0.0021	1.2	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
11601	dirMS_041712_NAR_50mM_plus2.6112.6112.3	3	9.38	0	1.25E+05		(R)SGSMD	(R)S G S\M|D/P/S G A H P S V R(Q)		96.5	462.214	1384.627	0.0001	0	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
11602	dirMS_041712_NAR_50mM_plus2.7987.7987.3	3	9.38	0	9.70E+03		(K)STAGDT	(K)S/T/A G D T H L/G G E/D/F D N R(M)		108.98	564.5793	1691.726	-0.0022	-1.3	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
11603	dirMS_041712_NAR_60mM_plus.21668.21668.3	3	9.38	1	6.86E+05		(K)EIIDLVL	(K)E I/I/D/L V L D R I R(K)		180.8	452.2733	1354.805	0.0001	0.1	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
11604	dirMS_041712_NAR_30mM_minus2.12359.12359.2	2	9.37	0	2.96E+05		(K)STLTDSL	(K)S T/L/T/D S\L V C/K(A)	C:Carbamidomethylation	120.75	562.2838	1123.566	-0.006	-5.4	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
11605	dirMS_041712_NAR_30mM_minus2.14415.14623.2	2	9.37	0	4.74E+05		(K)QLFDQV	(K)Q L/F/D/Q V V/K(T)		132.43	488.7803	976.546	0.0071	7.3	5.84	71218.8	6.3	HUMAN	A7YIJ8	Radixin
11606	dirMS_041712_NAR_30mM_minus2.15213.15213.2	2	9.37	0	7.26E+05	M2249m	(K)MSIYQA	(K)M/S|I Y/Q/A m W K(G)	m:Oxidized methionine	135.75	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
11607	dirMS_041712_NAR_30mM_minus2.7217.7217.2	2	9.37	0	3.86E+05		(K)QQTLEA	(K)Q Q|T/L/E/A/E E/A K(R)		93.4	573.7846	1146.564	-0.0018	-1.6	4.25	76925.9	4.46	HUMAN	A8MV58	Drebrin
11608	dirMS_041712_NAR_30mM_minus2.7977.7977.2	2	9.37	0	2.08E+05		(K)SLAAEEE	(K)S L|A|A/E/E E A A R(Q)		96.68	523.7597	1046.511	0.0008	0.8	4.25	533778	5.74	HUMAN	Q15149	Plectin
11609	dirMS_041712_NAR_50mM_minus2.10989.10989.3	3	9.37	0	2.62E+05		(K)VTVLFA	(K)V T|V/L/F/A/G Q H I S K(S)		130.92	433.9205	1299.742	0.005	3.8	8.73	258215.9	5.48	HUMAN	E7EN95	Filamin-B
11610	dirMS_041712_NAR_50mM_minus2.11180.11180.3	3	9.37	1	1.86E+05		(R)DNKQA	(R)D N K Q A\G\V|F/E/P T I V K(V)		132.05	515.9485	1545.827	0.0038	2.5	6.07	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
11611	dirMS_041712_NAR_60mM_minus.10898.10898.3	3	9.37	1	2.20E+05		(K)VTVAGL	(K)V/T|V/A/G L A/G/K D/P V Q C S R(D)	C:Carbamidomethylation	121.02	553.2923	1657.869	-0.0067	-4	8.72	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
11612	dirMS_041712_NAR_60mM_minus.12795.12795.3	3	9.37	1	1.48E+05		(R)TPSDVK	(R)T P S D/V K E L|V/L/D N S/R(S)		131.33	524.9451	1572.823	-0.002	-1.3	4.55	20111	4.47	HUMAN	H0YN26	Acidic leucine-rich nuclear phosphoprotein 32 family member A
11613	dirMS_041712_NAR_60mM_minus.16421.16421.3	3	9.37	1	8.35E+04		(R)VRLGDV	(R)V R L G D\V\I\S\I Q|P C/P D/V K(Y)	C:Carbamidomethylation	151.82	599.3265	1795.974	-0.0085	-4.8	5.93	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
11614	dirMS_041712_NAR_60mM_minus.19196.19196.3	3	9.37	0	3.35E+05		(K)HGATVL	(K)H G A\T V L T/A/L/G/G I L/K(K)		170.82	450.939	1350.81	-0.0079	-5.9	8.76	8125.3	9.3	HUMAN	B0QYF7	Myoglobin (Fragment)
11615	dirMS_041712_NAR_120mM_plus.8172.8172.3	3	9.37	2	4.62E+05		(K)TPKGPS	(K)T/P K/G P S S|V|E/D I K A K(M)		96.4	486.2728	1456.801	0.0033	2.2	8.17	32745.6	4.64	HUMAN	P06748	Nucleophosmin
11616	dirMS_041712_NAR_20mM_plus.12470.12470.2	2	9.37	0	1.93E+05		(R)GVEICIA	(R)G V\E|I/C\I/A T|P G R(L)	C:Carbamidomethylation	158.7	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
11617	dirMS_041712_NAR_20mM_plus.15891.15891.3	3	9.37	0	2.06E+04	M73m	(R)AILVDLE	(R)A I|L\V\D L E/P G/T m D/S V R(S)	m:Oxidized methionine	181.03	544.6139	1615.836	15.9912	-2.3	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
11618	dirMS_041712_NAR_20mM_plus.16396.16396.3	3	9.37	0	1.35E+05		(R)QAQEYE	(R)Q A Q\E Y/E/A|L/L N I/K(V)		184.45	473.9191	1419.748	-0.0051	-3.6	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11619	dirMS_041712_NAR_20mM_plus.16692.16692.2	2	9.37	0	2.39E+05		(K)VQIAVA	(K)V Q\I A|V|A/N\A Q/E L L Q R(M)		186.53	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
11620	dirMS_041712_NAR_20mM_plus.17023.17023.3	3	9.37	0	2.28E+05		(K)VQIAVA	(K)V Q\I A\V A\N A/Q E/L/L/Q/R(M)		188.18	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
11621	dirMS_041712_NAR_20mM_plus.17050.17050.2	2	9.37	0	2.06E+05		(K)VQIAVA	(K)V Q|I|A\V|A/N A/Q E L/L Q R(M)		188.23	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
11622	dirMS_041712_NAR_20mM_plus.8072.8072.2	2	9.37	0	1.26E+05		(R)LLEAAS	(R)L/L|E/A A/S V/S S K(G)		125.97	502.7839	1004.562	-0.0017	-1.7	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
11623	dirMS_041712_NAR_20mM_plus.9358.9358.2	2	9.37	0	7.19E+04		(R)QTVAVG	(R)Q T|V/A V/G V/I/K(A)		135.88	457.7856	914.567	-0.003	-3.3	8.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
11624	dirMS_041712_NAR_30mM_plus2.13923.13949.2	2	9.37	0	5.99E+05		(R)LAGLFN	(R)L A|G\L/F/N E/Q/R(K)		126	524.279	1047.558	-0.0074	-7.1	6	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
11625	dirMS_041712_NAR_40mM_plus2.14695.14695.3	3	9.37	1	1.08E+05		(R)LPAAGV	(R)L/P\A A/G V G D\M/V/M/A T V/K K(G)		153.2	529.9585	1587.86	0.0013	0.8	8.59	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
11626	dirMS_041712_NAR_50mM_plus2.14686.14686.3	3	9.37	1	8.16E+05	M85m	(K)TVTAm	(K)T V|T/A/m D V V/Y A L K R(Q)	m:Oxidized methionine	145.5	494.9387	1466.804	15.998	2.1	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
11627	dirMS_041712_NAR_50mM_plus2.16112.16112.3	3	9.37	0	4.14E+04		(K)ACQSIY	(K)A C|Q/S I Y/P L/H D V F V R(K)	C:Carbamidomethylation	153.83	568.9562	1704.853	0.0014	0.8	6.79	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
11628	dirMS_041712_NAR_50mM_plus2.17580.17580.3	3	9.37	0	4.75E+05		(R)DLISHD	(R)D L|I/S H D E M F/S D I Y K(I)		160.08	571.5992	1712.784	-0.0006	-0.3	4.22	19709.1	4.83	HUMAN	P13693	Translationally-controlled tumor protein
11629	dirMS_041712_NAR_50mM_plus2.8863.8863.3	3	9.37	0	7.69E+05		(R)AALAHS	(R)A A/L A/H S E E V T/A|S Q\V\A A\T K(T)		113.47	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
11630	dirMS_041712_NAR_60mM_plus.17451.17451.3	3	9.37	1	3.74E+05		(R)KVPGVT	(R)K\V/P G V T A I E|L/D E/D|T/G T F R(I)		148.18	650.0017	1948.002	-0.0117	-6	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
11631	dirMS_041712_NAR_60mM_plus.20322.20322.3	3	9.37	0	2.10E+06		(K)VHLVGI	(K)V H\L\V\G I|D\I/F T G/K(K)		166.1	433.5839	1298.747	-0.0096	-7.4	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
11632	dirMS_041712_NAR_120mM_minus.12666.12666.3	3	9.36	0	6.72E+05		(K)TFTAWC	(K)T F|T/A/W/C N|S H L R(K)	C:Carbamidomethylation	122.37	464.8871	1392.648	-0.001	-0.7	9.44	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
11633	dirMS_041712_NAR_120mM_minus.4598.4598.2	2	9.36	0	2.75E+06	M46m M4	(R)HQGVm	(R)H/Q|G V\m\V G/m G Q K(D)	m:Oxidized methionine	73.87	602.2834	1171.571	31.9885	-1.1	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
11634	dirMS_041712_NAR_20mM_minus.14008.14008.2	2	9.36	0	8.06E+03		(R)DIIVIGN	(R)D I\I|V|I/G N D I\T Y R(I)		192.12	696.3778	1391.753	-0.0046	-3.3	4.21	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
11635	dirMS_041712_NAR_60mM_minus.17892.17912.3	3	9.36	1	4.78E+05		(R)KVESLQ	(R)K V E S L Q|E|E/I/A/F L K(K)		160.22	511.9529	1533.852	-0.0081	-5.3	4.79	49709.6	5.19	HUMAN	B0YJC4	Vimentin
11636	dirMS_041712_NAR_60mM_minus.18102.18102.3	3	9.36	1	1.71E+05		(R)IRVESLL	(R)I R V\E S L\L/V/T A/I S K(A)		162.43	476.9628	1428.878	-0.0046	-3.2	8.75	91730	7.16	HUMAN	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15
11637	dirMS_041712_NAR_120mM_plus.11578.11600.4	4	9.36	1	5.34E+05		(R)DFTVSA	(R)D F\T/V/S A/M/H/G D M D Q K E R(D)		113.75	467.4593	1866.811	0.0045	2.4	4.66	26945.8	8.07	HUMAN	J3KSZ0	Eukaryotic initiation factor 4A-I (Fragment)
11638	dirMS_041712_NAR_120mM_plus.5530.5530.3	3	9.36	0	4.50E+05		(K)GPKPAF	(K)G P|K|P A/F G Q Q/H Q Q Q P\K(S)		82.03	559.2878	1675.866	-0.0175	-10.4	10	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
11639	dirMS_041712_NAR_20mM_plus.13522.13522.2	2	9.36	0	1.03E+05		(K)IFVGGLS	(K)I/F V/G G/L|S P D T|P E E K(I)		165.33	744.8731	1488.758	-0.0191	-12.8	4.14	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
11640	dirMS_041712_NAR_20mM_plus.15872.15872.2	2	9.36	0	2.44E+05		(R)GVVDSE	(R)G V V D S/E/D\I|P/L/N\L S R(E)		179.95	757.3956	1513.786	-0.0017	-1.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
11641	dirMS_041712_NAR_30mM_plus2.17898.17898.2	2	9.36	0	1.29E+05		(K)FAEAFE	(K)F A|E/A/F/E/A I/P R(A)		146.62	575.798	1150.589	-0.0004	-0.4	4.53	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
11642	dirMS_041712_NAR_50mM_plus2.18822.18822.3	3	9.36	0	4.20E+05		(R)AGLGSG	(R)A G L/G S/G L/S L S\G L V/H P E\L S R(S)		167.15	617.3412	1850.013	-0.004	-2.2	6.79	73325.2	9.19	HUMAN	F5H2A9	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial
11643	dirMS_041712_NAR_50mM_plus2.9204.9204.3	3	9.36	1	2.75E+05		(R)TNAENE	(R)T/N|A E N E F/V/T I K K(D)		115.83	465.2518	1393.732	0.0087	6.2	5.81	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
11644	dirMS_041712_NAR_60mM_plus.15498.15498.2	2	9.36	1	4.90E+05		(K)VKEGM	(K)V/K|E\G M/N I V\E A/M E R(F)		137.75	753.3758	1505.745	-0.0007	-0.5	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
11645	dirMS_041712_NAR_60mM_plus.8269.8269.3	3	9.36	1	2.68E+06	M174m	(R)VKYETE	(R)V/K\Y E T/E|L/A/m R(Q)	m:Oxidized methionine	101.47	419.2169	1239.64	15.996	0.8	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11646	dirMS_041712_NAR_120mM_minus.7675.7675.3	3	9.35	1	2.74E+06	M281m	(R)SRAEAE	(R)S R A E\A\E|S/m/Y Q I/K(Y)	m:Oxidized methionine	96.75	476.8951	1412.684	15.9869	-5.6	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
11647	dirMS_041712_NAR_120mM_minus.9018.9018.3	3	9.35	0	9.66E+05		(K)HTGPNS	(K)H T G P N\S P D/T/A|N/D/G F/V R(L)		103.18	562.2599	1684.767	-0.0022	-1.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
11648	dirMS_041712_NAR_30mM_minus2.13229.13229.2	2	9.35	0	3.35E+04		(K)TGCNVL	(K)T G/C N/V/L/L/I Q K(S)	C:Carbamidomethylation	125.43	573.3186	1145.635	-0.0048	-4.2	8.41	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
11649	dirMS_041712_NAR_30mM_minus2.5815.5833.2	2	9.35	0	5.86E+05		(K)YAEAVT	(K)Y/A|E|A V/T/R(A)		86.43	405.2098	809.415	-0.0029	-3.5	6	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
11650	dirMS_041712_NAR_50mM_minus2.10848.10848.3	3	9.35	0	1.24E+05		(R)IMLFTN	(R)I M/L/F/T N E D N P H/G N D S A K(A)		129.73	634.9586	1902.865	-0.0038	-2	4.54	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
11651	dirMS_041712_NAR_60mM_minus.16731.16731.3	3	9.35	1	2.99E+05		(R)LKLPAV	(R)L K L P A\V|V/T/A D L R(L)		153.85	432.6056	1295.805	-0.0023	-1.8	8.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
11652	dirMS_041712_NAR_60mM_minus.18235.18235.3	3	9.35	1	1.37E+05		(R)SELELTL	(R)S E|L/E L/T/L G K L E Q V R(S)		163.05	538.9724	1614.906	-0.0035	-2.1	4.78	533778	5.74	HUMAN	Q15149	Plectin
11653	dirMS_041712_NAR_60mM_minus.18798.18798.3	3	9.35	1	2.67E+05		(K)NAAGAL	(K)N A|A/G A/L D L L K E/L K(N)		166.87	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
11654	dirMS_041712_NAR_120mM_plus.4344.4344.3	3	9.35	1	3.08E+05		(K)AGADEE	(K)A/G|A/D/E E/R A E T A R(L)		71.55	425.869	1275.592	0.0001	0.1	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
11655	dirMS_041712_NAR_120mM_plus.7707.7707.2	2	9.35	1	1.18E+06		(R)AQYDEL	(R)A/Q/Y/D/E L/A R\K(N)		93.33	547.2874	1093.564	0.0039	3.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11656	dirMS_041712_NAR_120mM_plus.8548.8570.3	3	9.35	0	1.29E+04		(K)MADHW	(K)M/A D H/W/E/T A/P/R(H)		97.3	405.188	1213.542	0.0076	6.2	5.3	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
11657	dirMS_041712_NAR_20mM_plus.10646.10646.3	3	9.35	0	8.07E+04		(K)TTTLSG	(K)T T\T L S G T A/P A|A/G V/V|P S R(V)		145.97	529.2872	1585.854	-0.0074	-4.6	9.41	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
11658	dirMS_041712_NAR_20mM_plus.14075.14075.2	2	9.35	0	2.09E+05	M256m	(R)SLDmDS	(R)S L|D m/D S I I A/E/V\K(A)	m:Oxidized methionine	168.68	668.8371	1320.671	15.9954	0.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8

11659	dirMS_041712_NAR_20mM_plus.18030.18030.2	2	9.35	0	1.34E+05		(R)LFDQAF	(R)L F/D/Q/A F\G L P/R(L)		195.53	582.3166	1163.621	0.0052	4.4	5.84	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
11660	dirMS_041712_NAR_30mM_plus2.22167.22167.2	2	9.35	0	2.79E+05		(R)VGNLGL	(R)V G N\L|G L/A|T/S F/F N E R(N)		172.62	762.8926	1524.781	-0.0026	-1.7	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
11661	dirMS_041712_NAR_30mM_plus2.22765.22765.2	2	9.35	0	2.69E+05		(R)ELSDFIS	(R)E L/S D F/I\S/Y L|Q R(E)		177.22	685.8507	1370.695	-0.0009	-0.7	4.37	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
11662	dirMS_041712_NAR_40mM_plus2.11290.11290.3	3	9.35	0	1.21E+05		(K)EAGELKI	(K)E A/G E\L/K P E E E I T/V/G/P V Q K(L)		132.8	651.6782	1953.017	0.0025	1.3	4.32	108281.4	5.72	HUMAN	P53618	Coatomer subunit beta
11663	dirMS_041712_NAR_40mM_plus2.17143.17143.3	3	9.35	0	6.64E+04		(R)IHFPLAT	(R)I H F P L A|T|Y A/P V I S A E K(A)		166.77	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
11664	dirMS_041712_NAR_50mM_plus2.13228.13228.3	3	9.35	1	9.46E+05		(K)ASLAET	(K)A/S|L/A/E T D K I T L E V/A/K(L)		137.47	530.2925	1588.879	-0.0163	-10.2	4.68	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
11665	dirMS_041712_NAR_50mM_plus2.21638.21638.3	3	9.35	1	1.45E+05		(K)AKNEIL	(K)A K N E\I L D E\V|I/S/L S Q V T P/K(H)		183.9	662.036	1984.096	-0.0027	-1.3	4.68	118312	7.77	HUMAN	E5KLJ5	Dynamin-like 120 kDa protein, mitochondrial
11666	dirMS_041712_NAR_50mM_plus2.5167.5167.3	3	9.35	0	1.37E+06		(K)TATPQQ	(K)T\A|T|P Q Q A/Q E/V H E/K(L)		86.38	489.5774	1466.723	-0.0057	-3.9	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
11667	dirMS_041712_NAR_60mM_plus.11018.11018.3	3	9.35	1	6.66E+05		(R)AVDERF	(R)A/V/D/E/R F/P G C M Q G R(T)	C:Carbamidomethylation	115.05	508.237	1522.689	0.0075	4.9	6.12	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
11668	dirMS_041712_NAR_60mM_plus.12688.12817.3	3	9.35	1	3.24E+05		(R)LLNTWT	(R)L/L/N/T W T N R Y/P D|A K(M)		123.17	531.2853	1591.823	0.0186	11.7	8.59	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
11669	dirMS_041712_NAR_60mM_plus.16452.16452.3	3	9.35	1	3.80E+04		(R)LGVFRA	(R)L/G/V F/R A E S E|E G/P D V\L R(W)		142.8	591.9752	1773.913	-0.0019	-1.1	4.41	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
11670	dirMS_041712_NAR_60mM_plus.7174.7174.3	3	9.35	0	4.32E+05		(K)HSGPNS	(K)H S\G P N S\A/D/S\A/N/D/G F V R(L)		95.72	544.2474	1630.72	0.0072	4.4	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
11671	dirMS_041712_NAR_60mM_plus.9662.9662.3	3	9.35	0	9.53E+05		(K)GHENVE	(K)G H E N V\E\A|A|Q/A E Y I E K(F)		107.98	563.2692	1687.792	0.0008	0.5	4.48	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
11672	dirMS_041712_NAR_120mM_minus.7029.7029.2	2	9.34	1	1.40E+05		(K)IIAPPERI	(K)I I|A|P P E R K(Y)		92.63	462.2871	923.567	-0.0004	-0.4	8.75	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
11673	dirMS_041712_NAR_30mM_minus2.11215.11215.2	2	9.34	0	1.32E+05		(R)AMGEQ	(R)A/M|G E Q/A V/A L A/R(A)		114.68	558.7916	1116.583	-0.0071	-6.3	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
11674	dirMS_041712_NAR_30mM_minus2.18760.18760.2	2	9.34	0	2.25E+05		(K)YPQLLP	(K)Y/P|Q|L L/P/G I/R(G)		156.45	528.816	1056.62	0.0047	4.4	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
11675	dirMS_041712_NAR_30mM_minus2.6232.6232.2	2	9.34	0	1.18E+05		(K)MAGAM	(K)M|A|G/A\M S T T A/K(T)		88.03	484.7299	968.454	-0.0014	-1.5	8.5	23963.2	8.9	HUMAN	Q9UQN3	Charged multivesicular body protein 2b
11676	dirMS_041712_NAR_50mM_minus2.12081.12081.3	3	9.34	1	1.78E+05		(K)SAPSIPK	(K)S A|P S I/P K E N F S/C L T/R(L)	C:Carbamidomethylation	137.22	569.6251	1706.853	0.0077	4.5	8.46	23209	6.92	HUMAN	B9A041	Malate dehydrogenase, cytoplasmic
11677	dirMS_041712_NAR_60mM_minus.8215.8215.3	3	9.34	2	1.02E+05		(K)NLKVPS	(K)N L K|V P S\G Q N A|D\V Q/K T D\N(-)		105.95	609.9772	1827.92	-0.0025	-1.4	5.96	11018.4	8.89	HUMAN	B0AZT5	N-alpha-acetyltransferase 50
11678	dirMS_041712_NAR_120mM_plus.8281.8281.4	4	9.34	2	1.05E+05		(R)TASFSES	(R)T A|S F/S E S R A D E V A/P A K K(A)		96.9	449.2325	1793.903	0.0054	3	5.85	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
11679	dirMS_041712_NAR_20mM_plus.17610.17610.2	2	9.34	0	9.20E+04	M148m	(K)TFAPEEI	(K)T F|A|P E E/I S/A m V L T K(M)	m:Oxidized methionine	193.48	776.8996	1536.798	15.9941	-0.5	4.53	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
11680	dirMS_041712_NAR_30mM_plus2.17462.17462.2	2	9.34	0	9.20E+04		(K)VFQFLN	(K)V/F/Q|F L N\A K(C)		144.02	483.7736	966.541	-0.0008	-0.8	8.72	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
11681	dirMS_041712_NAR_30mM_plus2.7065.7065.2	2	9.34	0	1.37E+05		(R)TTTGSYI	(R)T T|T/G/S Y/I A N/R(V)		91.82	542.274	1083.543	-0.0022	-2	8.41	10799.8	5.07	HUMAN	I3L3X7	Proteasome subunit beta type-6 (Fragment)
11682	dirMS_041712_NAR_30mM_plus2.7130.7130.2	2	9.34	0	1.35E+05		(K)ISDSEGF	(K)I/S/D/S/E G F K(A)		93.08	441.7168	882.42	0.006	6.8	4.37	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
11683	dirMS_041712_NAR_50mM_plus2.20862.20862.3	3	9.34	0	5.70E+05		(R)LHFFMP	(R)L H F F M\P G\F/A|P|L T S R(G)		179.53	540.9498	1620.835	-0.0007	-0.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
11684	dirMS_041712_NAR_60mM_plus.5174.5174.3	3	9.34	1	3.55E+05		(K)MSSPED	(K)M/S\S/P/E/D D/S D T K/R(L)		85.33	456.5289	1367.574	-0.0022	-1.6	4.23	103309.5	5.34	HUMAN	A0AV56	SAFB protein
11685	dirMS_041712_NAR_120mM_minus.7580.7580.3	3	9.33	1	1.52E+05		(R)YSERYD	(R)Y/S E R Y D/P/E/P/K(S)		95.63	428.5347	1283.59	-0.0007	-0.6	4.68	68315.4	6.01	HUMAN	Q14677	Clathrin interactor 1
11686	dirMS_041712_NAR_20mM_minus.10471.10471.2	2	9.33	0	1.44E+05		(R)IYVVDV	(R)I Y|V|V D/V G\S E P R(A)		152.93	617.3216	1233.647	-0.0115	-9.3	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
11687	dirMS_041712_NAR_30mM_minus2.13565.13565.2	2	9.33	0	2.62E+05		(K)LTVEEAF	(K)L/T/V E E/A/F K(A)		127.25	468.7559	936.504	0.0008	0.9	4.53	266161	5.68	HUMAN	E9PPU0	Epiplakin
11688	dirMS_041712_NAR_30mM_minus2.18979.18979.2	2	9.33	0	5.78E+05		(K)LALFQAI	(K)L/A|L F/Q A I/G/K(E)		158.65	480.7964	960.588	-0.0022	-2.2	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
11689	dirMS_041712_NAR_30mM_minus2.19386.19386.2	2	9.33	0	2.36E+05		(R)FEELNA	(R)F/E|E|L|N A|D/L F R(G)		160.92	627.3141	1253.616	0.0048	3.9	4.14	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
11690	dirMS_041712_NAR_50mM_minus2.14232.14232.3	3	9.33	0	1.56E+05	M13m	(R)DLISHDE	(R)D L/I/S/H D E m F S D I/Y K(I)	m:Oxidized methionine	149.13	576.9343	1712.784	16.0047	5.7	4.22	19709.1	4.83	HUMAN	P13693	Translationally-controlled tumor protein
11691	dirMS_041712_NAR_50mM_minus2.16218.16218.3	3	9.33	0	1.46E+05		(K)LDPHLVI	(K)L/D/P/H|L V L/D Q L R(C)		160.2	440.2533	1318.748	-0.0024	-1.8	5.21	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
11692	dirMS_041712_NAR_60mM_minus.5179.5179.3	3	9.33	0	1.89E+06		(K)TATPQQ	(K)T A|T/P Q Q\A Q E V H E K(L)		84.33	489.5763	1466.723	-0.009	-6.2	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
11693	dirMS_041712_NAR_30mM_plus2.10094.10277.2	2	9.33	0	8.37E+05		(K)FVIATST	(K)F/V|I|A T/S T K(I)		107.18	433.7497	866.498	-0.0061	-7	8.75	25891.4	10.67	HUMAN	F8W181	60S ribosomal protein L6 (Fragment)
11694	dirMS_041712_NAR_30mM_plus2.19936.19936.3	3	9.33	0	1.72E+05		(R)TTVPQLI	(R)T T\V P Q\L|L/A|S V Q R(W)		158.23	438.2563	1312.758	-0.004	-3	9.41	266161	5.68	HUMAN	E9PPU0	Epiplakin
11695	dirMS_041712_NAR_50mM_plus2.13518.13518.3	3	9.33	0	1.58E+07		(R)LIDLHSP	(R)L/I/D L H/S/P S E/I V K(Q)		138.68	450.9258	1350.763	0.0001	0.1	5.32	7304.3	9.39	HUMAN	G3XAN0	40S ribosomal protein S20
11696	dirMS_041712_NAR_50mM_plus2.14580.14580.3	3	9.33	1	5.76E+05		(R)SEGVVA	(R)S/E/G V V/A V L/L T K K(S)		144.37	415.2585	1243.762	-0.0011	-0.9	8.31	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
11697	dirMS_041712_NAR_50mM_plus2.15787.15808.3	3	9.33	1	5.93E+05		(R)ALASQL	(R)A L|A/S Q L Q D S L K/D/L K(A)		151.3	510.6214	1529.853	-0.0037	-2.4	6	124367.7	5.51	HUMAN	P18206	Vinculin
11698	dirMS_041712_NAR_50mM_plus2.16267.16267.3	3	9.33	1	2.64E+06		(K)LLQDFF	(K)L L/Q D/F/F N G K E L\N K(S)		154.72	522.6137	1565.832	-0.0057	-3.6	6.07	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
11699	dirMS_041712_NAR_50mM_plus2.18399.18399.2	2	9.33	0	6.08E+05		(R)IHFPLAT	(R)I H|F|P\L A\T Y A P V I S A E K(A)		164.85	878.9842	1756.963	-0.0021	-1.2	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
11700	dirMS_041712_NAR_50mM_plus2.18554.18554.3	3	9.33	1	5.28E+05		(K)TGISDV	(K)T G I/S D V F A\K N D\L/A V/V D/V R(I)		166.27	640.3449	1919.023	-0.0031	-1.6	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
11701	dirMS_041712_NAR_50mM_plus2.20724.20724.3	3	9.33	0	1.25E+04		(K)VIDLPG	(K)V I\D\L/P G G G A A/F/V M E H L K(M)		177.7	585.311	1753.931	-0.0121	-6.9	5.32	35398.8	7.15	HUMAN	Q9H479	Fructosamine-3-kinase
11702	dirMS_041712_NAR_50mM_plus2.20845.20845.3	3	9.33	1	2.60E+05		(R)NLQNLL	(R)N L|Q/N|L/L I L/T/A/I K A D R(T)		178.05	566.0067	1696.012	-0.006	-3.6	8.75	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
11703	dirMS_041712_NAR_120mM_minus.10866.11034.3	3	9.32	1	3.40E+06	S65s	(R)FIGDYEP	(R)F I G D Y E P|N T G/K L Y s/R(L)	s:N-acetylglucosamine (S)	113.67	654.9729	1759.865	203.0392	-20.5	6.07	27176.8	9.3	HUMAN	Q6T310	Ras-like protein family member 11A
11704	dirMS_041712_NAR_120mM_minus.20218.20218.3	3	9.32	0	3.92E+05		(K)VHLVGI	(K)V H L V G\I/D|I|F/T/G K(K)		166.45	433.5866	1298.747	-0.0015	-1.1	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
11705	dirMS_041712_NAR_20mM_minus.11270.11270.2	2	9.32	0	6.01E+04	M148m	(R)DLTDYL	(R)D L|T D/Y/L/m K(I)	m:Oxidized methionine	160.07	507.7443	998.486	15.995	0.1	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
11706	dirMS_041712_NAR_20mM_minus.13624.13624.2	2	9.32	0	2.17E+05		(K)LGGSAV	(K)L G/G S A/V/I/S L E G K|P L(-)		187.83	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
11707	dirMS_041712_NAR_30mM_minus2.13162.13162.2	2	9.32	0	6.98E+05		(R)VNFAMI	(R)V N\F|A/M/N V/G\K(A)		124.38	490.2513	979.503	-0.0076	-7.8	8.72	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
11708	dirMS_041712_NAR_30mM_minus2.7649.7669.2	2	9.32	0	7.42E+05	M4591m	(R)SmVEEG	(R)S m|V|E/E/G T G L R(L)	m:Oxidized methionine	96.38	547.7614	1078.52	15.9958	0.8	4.53	533778	5.74	HUMAN	Q15149	Plectin
11709	dirMS_041712_NAR_40mM_minus2.12802.12802.3	3	9.32	1	1.47E+04		(R)LDQEVA	(R)L/D/Q|E V/A E V D K N I E L L K(K)		158.83	619.3351	1856.001	-0.0104	-5.6	4.18	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
11710	dirMS_041712_NAR_50mM_minus2.15359.15359.3	3	9.32	1	3.43E+05		(R)VVVDAL	(R)V V/V/D/A L/S G L K G D L A G R(Y)		155.1	523.9677	1569.896	-0.0073	-4.7	5.93	26949.2	7.99	HUMAN	C9JSQ1	Creatine kinase U-type, mitochondrial (Fragment)
11711	dirMS_041712_NAR_50mM_minus2.17856.17856.3	3	9.32	0	2.19E+05		(R)LGFHLP	(R)L G\F H\L\P L|E|V/A Y Q R(G)		170.25	514.953	1542.843	0.0017	1.1	6.75	533778	5.74	HUMAN	Q15149	Plectin
11712	dirMS_041712_NAR_60mM_minus.14365.14365.3	3	9.32	1	2.64E+05		(R)VEVERD	(R)V/E/V E/R D N\L/A/E D/I M R(L)		139.98	563.6139	1688.827	-0.0001	0	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
11713	dirMS_041712_NAR_60mM_minus.7607.7607.3	3	9.32	1	5.65E+05		(R)YLAEVA	(R)Y/L/A E/V A/A/G D D K/K(G)		102.07	427.222	1279.653	-0.0014	-1.1	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
11714	dirMS_041712_NAR_60mM_minus.7803.7803.3	3	9.32	1	3.76E+05	M230m M	(R)mSmKE	(R)m S m K E V D\E Q\m/L/N/V/Q N K(N)	m:Oxidized methionine	103.82	657.9647	1923.897	47.9823	-1.3	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
11715	dirMS_041712_NAR_120mM_plus.9826.9826.4	4	9.32	1	3.56E+06		(K)DTGKTP	(K)D T\G K T/P V E P/E V A/I H/R(I)		104.8	412.9719	1648.865	0.0005	0.3	5.45	5429.1	9.6	HUMAN	E5RIP1	40S ribosomal protein S20
11716	dirMS_041712_NAR_20mM_plus.7493.7493.2	2	9.32	0	7.51E+04	M33m	(R)IDEmPE	(R)I/D|E m|P/E A A V/K(S)	m:Oxidized methionine	120.15	559.7742	1102.545	15.9962	1.2	4.14	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
11717	dirMS_041712_NAR_30mM_plus2.16022.16022.2	2	9.32	0	4.95E+05		(R)MGPNIY	(R)M/G|P/N/I/Y E L/R(T)		136.88	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
11718	dirMS_041712_NAR_30mM_plus2.19452.19452.2	2	9.32	0	4.01E+05		(-)MDELQL	(-)M|D/E\L|Q/L F R(G)		156.58	526.2726	1051.524	0.0138	13.2	4.37	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
11719	dirMS_041712_NAR_30mM_plus2.23397.23397.2	2	9.32	0	1.61E+06		(R)DLPLLLF	(R)D L|P L/L/L F R(T)		188.98	493.8049	986.603	-0.0008	-0.8	5.84	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
11720	dirMS_041712_NAR_30mM_plus2.7692.7772.2	2	9.32	0	8.85E+05		(K)FAEQTL	(K)F/A|E/Q/T L/R(Q)		94.45	432.7306	864.457	-0.0035	-4	6	533778	5.74	HUMAN	Q15149	Plectin
11721	dirMS_041712_NAR_30mM_plus2.7737.7760.2	2	9.32	0	1.20E+05		(R)VVFDSA	(R)V/V|F/D S A Q/R(S)		94.42	461.2413	921.479	-0.0035	-3.8	5.81	82756.6	5.34	HUMAN	C9JIF9	Acylamino-acid-releasing enzyme
11722	dirMS_041712_NAR_30mM_plus2.8072.8072.2	2	9.32	0	1.28E+06		(K)QGGGG	(K)Q/G/G G G\G/G G|S V|P/G I E R(M)		97.12	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
11723	dirMS_041712_NAR_50mM_plus2.7313.7313.3	3	9.32	0	1.68E+05		(R)SGSSQE	(R)S G S S Q/E/L D V K/P S A\S P Q E R(S)		103.85	634.6443	1901.92	-0.0016	-0.8	4.68	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
11724	dirMS_041712_NAR_60mM_plus.10646.10646.2	2	9.32	1	1.68E+06		(R)VKYETEL	(R)V/K|Y E|T E L/A M R(Q)		113.15	620.326	1239.64	0.0045	3.7	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11725	dirMS_041712_NAR_60mM_plus.18583.18583.3	3	9.32	0	1.67E+05		(K)DHGLEV	(K)D H\G L\E V\L/G/L V R(V)		153.92	403.2318	1207.679	0.0015	1.2	5.32	17732.8	5.85	HUMAN	F5GYJ1	U8 snoRNA-decapping enzyme
11726	dirMS_041712_NAR_20mM_minus.13550.13550.3	3	9.31	0	1.81E+05		(R)QAQEYE	(R)Q A Q E Y E|A|L/L N/I K(V)		186.67	473.9203	1419.748	-0.0015	-1	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11727	dirMS_041712_NAR_30mM_minus2.12428.12428.2	2	9.31	0	1.12E+05	M126m	(K)ImMEFE	(K)I/m|M/E/F E R(Q)	m:Oxidized methionine	121.77	486.2209	955.438	15.9969	2.1	4.53	25103.6	5.88	HUMAN	O43633	Charged multivesicular body protein 2a
11728	dirMS_041712_NAR_30mM_minus2.14369.14369.2	2	9.31	0	1.95E+05		(R)ELAFQIS	(R)E L/A F/Q/I/S K(E)		131.73	468.2614	935.52	-0.0041	-4.4	6.1	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
11729	dirMS_041712_NAR_30mM_minus2.17112.17112.2	2	9.31	0	7.89E+04		(R)IMNTFS	(R)I M|N|T F/S/V V/P/S P K(V)		146.1	660.3534	1319.703	-0.0033	-2.5	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
11730	dirMS_041712_NAR_30mM_minus2.6974.6974.2	2	9.31	0	1.28E+05		(R)ESAEAL	(R)E S/A/E/A/L/A/T K(L)		92.07	460.2363	919.473	-0.0078	-8.5	4.53	72152.1	5.27	HUMAN	A0MZ66	Shootin-1
11731	dirMS_041712_NAR_40mM_minus2.6708.6708.2	2	9.31	0	4.17E+05		(R)LASYLDF	(R)L/A/S/Y L D R(V)		108.32	419.2267	837.447	-0.0004	-0.4	5.83	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11732	dirMS_041712_NAR_50mM_minus2.10569.10589.3	3	9.31	0	2.14E+05		(K)VFEGNR	(K)V F|E G N R P T N S I\V/F/T K(L)		128.85	570.3032	1708.902	-0.0066	-3.9	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
11733	dirMS_041712_NAR_50mM_minus2.14210.14210.3	3	9.31	1	1.56E+05		(K)KGVNLP	(K)K\G V N\L\P G A\A\V/D L|P A V S E K(D)		148.73	588.9987	1764.985	-0.0039	-2.2	6.07	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
11734	dirMS_041712_NAR_50mM_minus2.8948.8948.3	3	9.31	1	1.31E+05	M227m	(R)mQKEIT	(R)m Q K E I\T|A|L|A/P S T M K(I)	m:Oxidized methionine	119.48	522.2727	1548.812	15.9911	-2.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
11735	dirMS_041712_NAR_60mM_minus.11993.11993.3	3	9.31	1	9.04E+04		(R)LKEVLEY	(R)L K E V\L E\Y/N A/I/G/G K(Y)		126.8	478.6037	1433.8	-0.0033	-2.3	6.14	40874	5.06	HUMAN	E9PCI9	Farnesyl pyrophosphate synthase
11736	dirMS_041712_NAR_120mM_plus.23670.23670.3	3	9.31	0	7.52E+05		(R)LHFFMP	(R)L H F F M P G\F|A|P|L/T S R(G)		179.08	540.9492	1620.835	-0.0025	-1.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
11737	dirMS_041712_NAR_120mM_plus.7649.7649.3	3	9.31	0	4.52E+05		(R)SGSMD	(R)S G|S M\D/P/S G A H P S V R(Q)		93.88	462.218	1384.627	0.0121	8.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
11738	dirMS_041712_NAR_20mM_plus.10396.10396.2	2	9.31	0	7.76E+04		(R)IEDVTPI	(R)I E D|V|T|P I/P/S D S T R(R)		144.5	715.3607	1429.717	-0.0028	-2	4.03	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
11739	dirMS_041712_NAR_20mM_plus.13797.13797.2	2	9.31	0	2.90E+04		(K)TGAAPII	(K)T G\A\A|P I/I D V V R(S)		167.35	556.3256	1111.647	-0.0031	-2.8	5.5	10240.9	10.46	HUMAN	E9PJD9	60S ribosomal protein L27a
11740	dirMS_041712_NAR_20mM_plus.15947.15947.2	2	9.31	0	1.50E+05		(K)DAGTIA	(K)D A\G/T|I/A/G L N V\L R(I)		181.92	600.3422	1199.674	0.0029	2.4	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
11741	dirMS_041712_NAR_20mM_plus.7133.7215.2	2	9.31	0	3.60E+05	M532m M	(R)mVPAG	(R)m V|P|A G m G A G L E R(M)	m:Oxidized methionine	117.53	610.7907	1188.586	31.9877	-1.7	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
11742	dirMS_041712_NAR_30mM_plus2.16938.16938.2	2	9.31	0	3.76E+04	M185m	(K)LAVNm	(K)L A|V/N m/V/P F/P/R(L)	m:Oxidized methionine	142.12	580.3176	1143.634	15.9936	-1.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
11743	dirMS_041712_NAR_30mM_plus2.19979.19979.2	2	9.31	0	5.04E+04		(K)TFESLVD	(K)T F|E/S/L V D F/S K(A)		158.22	586.793	1172.583	-0.0047	-4	4.37	35407.1	6.73	HUMAN	E9PF18	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial
11744	dirMS_041712_NAR_30mM_plus2.21508.21532.2	2	9.31	0	2.81E+05		(R)NIPMLF	(R)N I|P M/L/F/V R(G)		167.73	495.2847	989.56	0.002	2.1	9.75	11845.2	4.58	HUMAN	P62310	U6 snRNA-associated Sm-like protein LSm3
11745	dirMS_041712_NAR_30mM_plus2.4827.4827.2	2	9.31	0	7.47E+05	M571m	(R)mGANSI	(R)m G\A/N/S L/E R(M)	m:Oxidized methionine	76.53	447.2119	877.42	15.9969	2.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
11746	dirMS_041712_NAR_40mM_plus2.11939.12132.2	2	9.31	0	1.63E+05		(K)VYFDLR	(K)V/Y|F D/L R(I)		137.07	406.7184	812.43	-0.0006	-0.7	5.8	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
11747	dirMS_041712_NAR_40mM_plus2.17750.17750.3	3	9.31	1	1.96E+05		(R)LKLPSIPI	(R)L K L P\S I|P L V/P V S/A Q K(R)		170.73	530.671	1589.999	-0.0004	-0.3	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
11748	dirMS_041712_NAR_40mM_plus2.6706.6706.2	2	9.31	0	1.68E+04		(K)SLAAEEE	(K)S L|A|A/E/E E A A R(Q)		99.53	523.7589	1046.511	-0.0008	-0.7	4.25	533778	5.74	HUMAN	Q15149	Plectin
11749	dirMS_041712_NAR_40mM_plus2.9116.9116.2	2	9.31	0	5.34E+05		(R)GGNFGF	(R)G G N|F/G|F G D/S R(G)		116.42	507.2256	1013.444	0.0004	0.4	5.84	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
11750	dirMS_041712_NAR_50mM_plus2.11268.11296.3	3	9.31	0	9.26E+05		(R)TFIAIKP	(R)T F|I/A/I K/P D/G V Q R(G)		126.32	448.9241	1344.763	-0.0057	-4.2	8.41	6640.6	8.25	HUMAN	C9K028	Nucleoside diphosphate kinase A (Fragment)
11751	dirMS_041712_NAR_50mM_plus2.11796.11796.3	3	9.31	1	3.08E+05		(K)LIPDSIGI	(K)L I/P D S I/G K D/I E K(A)		130.23	443.2514	1327.747	-0.0071	-5.4	4.56	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
11752	dirMS_041712_NAR_50mM_plus2.14762.14762.3	3	9.31	1	9.20E+05		(K)MQSAAI	(K)M/Q|S\A A\F S I A/A D V/K D/V K(A)		145.55	560.9581	1680.863	-0.0028	-1.7	5.72	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
11753	dirMS_041712_NAR_50mM_plus2.17124.17162.3	3	9.31	1	3.27E+04		(R)AIYAYAL	(R)A I/Y A/Y A/L Q V F P S K K(S)		158.17	533.6359	1598.894	-0.0009	-0.6	9.53	107721.8	8.85	HUMAN	O94906	Pre-mRNA-processing factor 6
11754	dirMS_041712_NAR_60mM_plus.8477.8839.3	3	9.31	1	1.33E+06		(K)MQASIE	(K)M/Q|A/S I/E K G G S L/P K(V)		103.2	449.2449	1345.714	0.0057	4.3	8.35	32745.6	4.64	HUMAN	P06748	Nucleophosmin
11755	dirMS_041712_NAR_60mM_plus.9124.9124.3	3	9.31	1	8.62E+05		(K)AQAEVE	(K)A Q|A/E V E/G L G K G V A/R(L)		105.63	462.2549	1384.754	-0.0042	-3	6.19	533778	5.74	HUMAN	Q15149	Plectin
11756	dirMS_041712_NAR_120mM_minus.12331.12331.3	3	9.3	1	1.30E+06		(K)VKLEAEI	(K)V K L E\A E|I|A T|Y/R(R)		122.18	431.5783	1292.721	-0.0005	-0.4	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11757	dirMS_041712_NAR_120mM_minus.17529.17529.3	3	9.3	1	3.39E+05		(R)RTVQSLI	(R)R T V Q S\L\E|I/D L/D/S M R(N)		149.65	554.9552	1662.848	0.0031	1.9	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11758	dirMS_041712_NAR_120mM_minus.9019.9019.3	3	9.3	0	9.66E+05		(K)HTGPNS	(K)H T G P N|S P/D\T|A/N/D/G F V R(L)		103.18	562.2599	1684.767	-0.0022	-1.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
11759	dirMS_041712_NAR_30mM_minus2.15805.15805.2	2	9.3	0	2.16E+04		(R)NLQDPF	(R)N L|Q/D/P/F/Y/P R(G)		140.87	575.2877	1149.569	-0.0006	-0.5	5.83	24760.9	5.16	HUMAN	Q96EI5	Transcription elongation factor A protein-like 4
11760	dirMS_041712_NAR_30mM_minus2.16661.16959.2	2	9.3	0	1.34E+04		(K)AGIPVY	(K)A G I|P/V Y/A W K(G)		145.83	502.7828	1004.556	0.0019	1.9	8.63	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
11761	dirMS_041712_NAR_30mM_minus2.9340.9340.2	2	9.3	0	4.00E+05		(R)NQPQF	(R)N Q|P/Q F/Q Q M R(Q)		104.93	588.7841	1176.558	0.0031	2.6	9.75	35061.2	4.66	HUMAN	G5E9P0	RAD23 homolog B (S. cerevisiae), isoform CRA_a
11762	dirMS_041712_NAR_40mM_minus2.15664.15664.3	3	9.3	1	4.96E+05		(K)ALFEEV	(K)A L|F E E V/P E L L/T E/A E K K(E)		181.8	615.9988	1845.984	-0.0026	-1.4	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
11763	dirMS_041712_NAR_60mM_minus.10784.10784.3	3	9.3	0	5.06E+04		(R)AYADSY	(R)A Y|A\D S Y Y/Y/E D G G M K P R(V)		119.78	629.2712	1885.806	-0.0071	-3.8	4.56	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
11764	dirMS_041712_NAR_60mM_minus.13757.13757.3	3	9.3	1	2.57E+05		(K)KAEAAA	(K)K A/E A A A S A\L|A\D A D|A/D/L E E R(L)		136.4	639.6429	1916.92	-0.0054	-2.8	4.02	25103.6	5.88	HUMAN	O43633	Charged multivesicular body protein 2a
11765	dirMS_041712_NAR_60mM_minus.5187.5187.3	3	9.3	0	1.97E+06		(K)TATPQQ	(K)T A/T|P Q Q A Q E V/H\E K(L)		84.37	489.5763	1466.723	-0.009	-6.2	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
11766	dirMS_041712_NAR_120mM_plus.5464.5464.3	3	9.3	1	6.49E+04		(R)KLGQSE	(R)K\L G\Q S E|S|Q G/P P/R(A)		81.78	428.5626	1283.67	0.003	2.3	8.75	20025.3	6.6	HUMAN	F5GX23	26S proteasome non-ATPase regulatory subunit 9
11767	dirMS_041712_NAR_120mM_plus.8509.8509.3	3	9.3	0	1.29E+04		(K)MADHW	(K)M/A D/H W/E/T/A P R(H)		97.3	405.188	1213.542	0.0076	6.2	5.3	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1

11768	dirMS_041712_NAR_20mM_plus.18873.18873.2	2	9.3	0	1.05E+05		(K)DTSYLFI	(K)D T S Y L|F/I/T|G P D V V K(S)		201.92	777.9049	1554.805	-0.0025	-1.6	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
11769	dirMS_041712_NAR_30mM_plus2.10551.10551.2	2	9.3	0	2.50E+05		(R)MYAALG	(R)M/Y/A/A L/G D/P K(A)		109.03	483.2388	965.476	-0.0058	-6	5.59	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
11770	dirMS_041712_NAR_30mM_plus2.11317.11317.2	2	9.3	0	6.71E+05		(K)LTVDSAI	(K)L/T/V D S A/I A R(D)		113.02	473.2687	945.536	-0.0062	-6.6	5.84	334221.3	6.44	HUMAN	P15924	Desmoplakin
11771	dirMS_041712_NAR_40mM_plus2.12743.12743.3	3	9.3	1	5.65E+04		(K)VLCGGD	(K)V L|C G G D I Y|V/P E D P K/L K(D)	C:Carbamidomethylation	141.33	601.6538	1802.936	0.0111	6.2	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
11772	dirMS_041712_NAR_40mM_plus2.13018.13018.3	3	9.3	0	5.11E+04		(R)IVATKPL	(R)I V|A T K P/L Y/V/A|L/A Q R(K)		143.25	514.9835	1542.937	-0.0007	-0.4	9.99	65918.2	9.74	HUMAN	E7EQV3	Polyadenylate-binding protein 1
11773	dirMS_041712_NAR_40mM_plus2.20072.20072.3	3	9.3	1	5.88E+05		(K)EGGLGP	(K)E G G L/G/P L N/I/P L L A D V T R R(L)		189.8	631.0288	1891.076	-0.0041	-2.2	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
11774	dirMS_041712_NAR_40mM_plus2.6051.6051.2	2	9.3	0	2.48E+05		(R)MGANN	(R)M/G|A/N/N/L/E R(M)		94.25	452.7221	904.431	0.0064	7.1	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
11775	dirMS_041712_NAR_40mM_plus2.9000.9022.2	2	9.3	0	1.05E+05		(K)FYEQFSK	(K)F/Y|E Q F/S/K(N)		115.03	474.7301	948.446	0.0068	7.1	6	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
11776	dirMS_041712_NAR_50mM_plus2.10748.10748.3	3	9.3	0	4.20E+05		(K)TSEVDLA	(K)T/S|E/V/D L A K/P L V/K(F)		123.78	433.922	1299.752	-0.0004	-0.3	5.73	17178.3	5.63	HUMAN	C9IZF9	Programmed cell death 6-interacting protein (Fragment)
11777	dirMS_041712_NAR_50mM_plus2.13240.13240.3	3	9.3	1	5.25E+05		(R)VFDKDG	(R)V F/D K D G N G\Y\I/S A A E L R(H)		137.68	585.6264	1754.871	-0.0061	-3.5	4.56	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
11778	dirMS_041712_NAR_50mM_plus2.15520.15520.3	3	9.3	1	8.05E+05		(K)VQGGAL	(K)V Q|G G A/L/E D S Q L/V A G V A F K K(T)		150.4	639.6848	1917.044	-0.0042	-2.2	6.04	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
11779	dirMS_041712_NAR_50mM_plus2.17896.17920.3	3	9.3	0	7.62E+04		(K)LNLSCIH	(K)L N|L|S/C I H/S/P V V N E L M R(G)	C:Carbamidomethylation	162.23	627.9943	1881.967	0.001	0.5	6.75	60090.6	9.25	HUMAN	Q9Y2X3	Nucleolar protein 58
11780	dirMS_041712_NAR_60mM_plus.15087.15184.3	3	9.3	1	4.36E+05		(K)SLEELRL	(K)S L|E\E/L/R L E/D Y/Q A N R(K)		135.6	579.2911	1735.861	-0.0022	-1.3	4.41	178367.2	6.03	HUMAN	J3KP29	Nuclear pore complex protein Nup98-Nup96
11781	dirMS_041712_NAR_60mM_plus.17446.17446.3	3	9.3	1	7.56E+05		(R)VIKDFM	(R)V I K D F M\I Q/G/G D/F T R(G)		148.33	542.9482	1626.831	-0.0008	-0.5	5.93	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
11782	dirMS_041712_NAR_60mM_plus.21507.21507.3	3	9.3	0	7.55E+04		(R)LHFFMP	(R)L H F F M\P G\F|A/P\L/T/S R(G)		179.18	540.9492	1620.835	-0.0025	-1.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
11783	dirMS_041712_NAR_20mM_minus.13238.13238.2	2	9.29	1	8.37E+04		(K)EALVSQI	(K)E A|L|V S Q|L/S R G K(Q)		183.37	594.3411	1187.674	0.0007	0.6	8.85	224067.5	5.64	HUMAN	Q9UKX2	Myosin-2
11784	dirMS_041712_NAR_30mM_minus2.11798.11798.2	2	9.29	0	3.73E+05		(K)MTISQQ	(K)M/T|I/S Q/Q E F G R(T)		117.87	598.7911	1196.573	0.0021	1.7	5.75	21119.9	4.34	HUMAN	H0Y3Y9	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
11785	dirMS_041712_NAR_30mM_minus2.11884.11884.2	2	9.29	0	9.21E+05		(K)EVDEQM	(K)E V\D/E/Q|M L/N V/Q/N K(N)		117.53	723.8476	1446.689	-0.0014	-1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
11786	dirMS_041712_NAR_30mM_minus2.13605.13649.2	2	9.29	0	2.34E+05		(R)YLFVDR(	(R)Y/L|F V/D/R(A)		127.43	406.7193	812.43	0.0012	1.5	5.83	21781.4	5.48	HUMAN	E7ERA5	Myosin-10 (Fragment)
11787	dirMS_041712_NAR_30mM_minus2.14299.14299.2	2	9.29	0	7.55E+04		(R)TPYGASI	(R)T/P/Y/G A S I/F\Q S K(E)		131.18	599.8093	1198.61	0.0011	0.9	8.26	44815.8	6.62	HUMAN	B3KQ29	Transducin-like enhancer protein 4
11788	dirMS_041712_NAR_30mM_minus2.16826.16826.3	3	9.29	0	5.54E+05		(R)ASLEAAI	(R)A S L/E A A I/A\D/A/E/Q/R(G)		144.65	448.8965	1344.675	-0.0004	-0.3	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
11789	dirMS_041712_NAR_40mM_minus2.15105.15105.3	3	9.29	0	1.44E+05		(K)LFLFHTS	(K)L F/L F H T S L/P\I/A\E A P G K(L)		173.92	580.9924	1740.968	-0.0057	-3.3	6.75	108105.4	6.57	HUMAN	E7EP00	Protein transport protein Sec24C
11790	dirMS_041712_NAR_60mM_minus.15012.15205.3	3	9.29	1	1.06E+06	M3109m S	(K)GDmDV	(K)G D m D V s L|P|K V E G D m K(V)	m:Oxidized methionine s:N-a	144.13	619.2771	1620.761	235.056	-7.1	4.23	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
11791	dirMS_041712_NAR_120mM_plus.13488.13488.2	2	9.29	1	1.54E+06		(K)DKGFGF	(K)D/K/G F/G/F I/R(L)		123.33	470.2551	939.505	-0.0018	-1.9	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
11792	dirMS_041712_NAR_120mM_plus.7749.7895.2	2	9.29	0	8.49E+05		(K)HFEALAI	(K)H/F|E/A L/A N/R(A)		94.5	479.2487	957.49	0	0	6.75	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
11793	dirMS_041712_NAR_20mM_plus.16580.16765.2	2	9.29	0	1.82E+05		(K)IAFAITAI	(K)I/A|F/A/I T A I K(G)		185.42	474.2987	947.592	-0.0023	-2.4	8.75	17718.4	10.99	HUMAN	P62269	40S ribosomal protein S18
11794	dirMS_041712_NAR_20mM_plus.16959.16959.3	3	9.29	0	2.88E+05		(K)VQIAVA	(K)V Q I A V A N|A/Q/E/L/L Q R(M)		187.93	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
11795	dirMS_041712_NAR_20mM_plus.9394.9394.3	3	9.29	0	1.27E+05		(K)SVTNED	(K)S V\T N E D V|T Q E/E L/G G A K(T)		136	559.6039	1676.797	-0.0002	-0.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
11796	dirMS_041712_NAR_30mM_plus2.17768.17813.3	3	9.29	0	6.69E+05		(R)SIQEELC	(R)S I\Q/E\E\L/Q Q/L/R(Q)		146.3	415.225	1243.664	-0.0036	-2.9	4.53	533778	5.74	HUMAN	Q15149	Plectin
11797	dirMS_041712_NAR_40mM_plus2.18916.18916.3	3	9.29	1	3.28E+05		(R)TLAEIAK	(R)T L/A E|I A K V E L D/N M/P L R(G)		176.95	604.9967	1812.989	-0.0132	-7.3	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
11798	dirMS_041712_NAR_60mM_plus.13103.13604.3	3	9.29	0	2.02E+06		(K)NVDDILI	(K)N V/D|D I L/K/P|P\G R(E)		126.47	408.563	1223.674	0.0002	0.2	5.96	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
11799	dirMS_041712_NAR_60mM_plus.18019.18019.3	3	9.29	1	3.65E+04		(K)MFGIDR	(K)M/F/G/I/D/R D A I\A Q A V R(G)		152.48	521.6038	1562.811	-0.0139	-8.9	5.71	63448.4	7.29	HUMAN	B4E022	Transketolase
11800	dirMS_041712_NAR_60mM_plus.20626.20626.3	3	9.29	1	2.87E+05		(K)ITQDIFQ	(K)I/T Q/D I F/Q Q/L L K R(G)		168.08	501.626	1502.869	-0.0055	-3.7	8.75	72796.9	6.75	HUMAN	A6NC17	Methionine--tRNA ligase, cytoplasmic
11801	dirMS_041712_NAR_120mM_minus.21432.21432.3	3	9.28	0	8.12E+05		(R)LHFFMP	(R)L H\F F\M|P G|F|A/P\L/T S R(G)		182.17	540.9497	1620.835	-0.001	-0.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
11802	dirMS_041712_NAR_50mM_minus2.12362.12400.3	3	9.28	1	8.29E+04		(K)QLQALS	(K)Q L/Q/A/L S S E L/A/Q A R D E/T K(K)		138.55	629.9954	1887.977	-0.0054	-2.9	4.68	71218.8	6.3	HUMAN	A7YIJ8	Radixin
11803	dirMS_041712_NAR_50mM_minus2.13438.13438.3	3	9.28	0	1.50E+04		(R)VVIIGAG	(R)V V|I|I/G A G K P A A V V L Q T K(G)		144.4	555.3513	1664.047	-0.0076	-4.5	10	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
11804	dirMS_041712_NAR_50mM_minus2.15443.15443.3	3	9.28	1	1.02E+05		(K)YAVLYQ	(K)Y A|V/L Y Q/P L F D/K R(F)		155.68	504.9453	1512.821	0.0004	0.3	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
11805	dirMS_041712_NAR_50mM_minus2.17969.17969.3	3	9.28	1	1.70E+05		(K)AIDLFTD	(K)A I/D|L|F|T D A/I K L N P R(L)		171.33	529.6358	1586.89	0.0028	1.8	6	18141.9	4.7	HUMAN	F6VDH7	Hsc70-interacting protein (Fragment)
11806	dirMS_041712_NAR_30mM_plus2.10597.10597.2	2	9.28	0	1.78E+05		(R)VLTVING	(R)V L|T V/I/N Q T Q/K(E)		108.73	572.34	1143.673	-0.0005	-0.4	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
11807	dirMS_041712_NAR_40mM_plus2.15461.15461.3	3	9.28	0	2.58E+06		(R)VSLDVN	(R)V/S|L/D V N/H F A P D E L/T V/K(T)		156.68	595.3161	1783.922	0.0113	6.3	4.54	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
11808	dirMS_041712_NAR_40mM_plus2.15806.15806.3	3	9.28	0	1.62E+05		(K)VAIVKPG	(K)V A|I/V K/P G V/P M E I V L N K(E)		160.42	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
11809	dirMS_041712_NAR_50mM_plus2.11957.11957.3	3	9.28	1	6.76E+05		(R)ISVYYNE	(R)I/S/V/Y/Y N/E A T G G K Y V P R(A)		130.8	606.3123	1816.923	-0.0005	-0.3	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
11810	dirMS_041712_NAR_50mM_plus2.15250.15250.3	3	9.28	0	5.71E+05		(K)LHIIEVG	(K)L H\I I/E V G T|P/P T G N/Q P F P K(K)		147.4	649.0216	1945.054	-0.0039	-2	6.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
11811	dirMS_041712_NAR_50mM_plus2.16048.16342.3	3	9.28	1	1.22E+05		(R)EGIVTAT	(R)E G\I|V/T/A/T E Q E V K E D I A/K(L)		154.88	620.658	1859.96	-0.0002	-0.1	4.25	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
11812	dirMS_041712_NAR_50mM_plus2.17983.17983.3	3	9.28	0	2.43E+05		(K)AKPLLLC	(K)A K P L L\L Q|L/P I/G E/A K(T)		162.03	497.6447	1490.93	-0.0109	-7.3	8.64	32227.8	7.89	HUMAN	D6RAL1	Ribosome-releasing factor 2, mitochondrial (Fragment)
11813	dirMS_041712_NAR_50mM_plus2.20221.20221.3	3	9.28	0	2.34E+05		(K)GHVDILA	(K)G H V\D I L A|P T V/Q/E/L A/A L E K(E)		174.63	635.3536	1904.049	-0.0025	-1.3	4.65	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
11814	dirMS_041712_NAR_50mM_plus2.21430.21430.3	3	9.28	1	1.92E+05		(R)TEGLSVL	(R)T/E|G|L/S V/L S\Q A M A V I K E K(I)		182.82	602.0007	1803.988	-0.0009	-0.5	5.81	31604.9	6.88	HUMAN	G3V4T5	Eukaryotic translation initiation factor 2 subunit 1 (Fragment)
11815	dirMS_041712_NAR_50mM_plus2.8252.8252.3	3	9.28	1	3.49E+05		(R)VAVEAK	(R)V/A|V E A K/N P A D L/P/K(L)		110.53	451.2563	1351.758	-0.0036	-2.7	6.04	96306.4	6.41	HUMAN	P13639	Elongation factor 2
11816	dirMS_041712_NAR_50mM_plus2.8760.8760.3	3	9.28	1	7.58E+05	M112m S1	(R)SmLREA	(R)S m/L R E A\A|M G\I s V/T A K(D)	m:Oxidized methionine s:N-a	113.45	595.312	1564.819	219.1029	16	8.46	39257.7	9.69	HUMAN	Q8IYD2	Kelch domain-containing protein 8A
11817	dirMS_041712_NAR_60mM_plus.16349.16349.3	3	9.28	0	4.27E+05		(R)EAYPGD	(R)E A|Y/P G D V/F/Y L/H S R(L)		142.45	518.5855	1553.738	0.0036	2.3	5.32	48851.3	9.2	HUMAN	K7EK63	ATP synthase subunit alpha, mitochondrial
11818	dirMS_041712_NAR_60mM_plus.16742.16742.3	3	9.28	1	8.42E+05		(R)STNKGT	(R)S T N K G T A\Y T/F|F/T|P G N L K(Q)		144.7	616.3117	1846.933	-0.0128	-7	9.7	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
11819	dirMS_041712_NAR_60mM_plus.17053.17053.3	3	9.28	1	2.34E+05		(R)ASLISAV	(R)A S|L/I/S/A V S D K L R(W)		146.07	420.5832	1259.732	0.0033	2.6	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
11820	dirMS_041712_NAR_30mM_minus2.10162.10261.2	2	9.27	0	8.05E+05		(K)IGALEGY	(K)I/G|A|L/E/G Y/R(G)		109.53	439.737	878.473	-0.0063	-7.2	6	20203.8	9.79	HUMAN	B4DG16	Asparagine--tRNA ligase, cytoplasmic
11821	dirMS_041712_NAR_30mM_minus2.11910.11910.2	2	9.27	0	9.21E+05		(K)EVDEQM	(K)E V/D\E/Q|M\L\N V Q/N K(N)		117.53	723.8476	1446.689	-0.0014	-1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
11822	dirMS_041712_NAR_50mM_minus2.12521.12521.3	3	9.27	1	3.07E+05		(K)LYEQILA	(K)L Y|E Q/I L/A\E/N E K L K(A)		139.22	530.9592	1590.874	-0.0107	-6.7	4.79	22046.7	5.8	HUMAN	H0YIM2	Protein phosphatase 1 regulatory subunit 12A (Fragment)
11823	dirMS_041712_NAR_50mM_minus2.12743.12743.3	3	9.27	0	9.52E+04		(R)LLVGND	(R)L L/V/G N D D V/H I I A R(S)		140.98	478.9368	1434.806	-0.0105	-7.3	5.21	376926.5	4.99	HUMAN	H0Y5W0	E3 ubiquitin-protein ligase HUWE1 (Fragment)
11824	dirMS_041712_NAR_50mM_minus2.12777.12777.3	3	9.27	0	2.94E+05		(K)EGKPTIV	(K)E G K P T I V|E/E/D D/P E L/F K(Q)		140.93	615.9772	1845.912	0.0054	2.9	4.08	29841.1	9.04	HUMAN	O75937	DnaJ homolog subfamily C member 8
11825	dirMS_041712_NAR_50mM_minus2.15929.15929.3	3	9.27	1	8.21E+04		(K)DANAKL	(K)D A\N A K L S E\L/E|A/A/L Q R(A)		158.97	543.6248	1628.86	-0.0004	-0.2	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
11826	dirMS_041712_NAR_60mM_minus.17745.17759.3	3	9.27	1	4.16E+05	M148m	(R)LDLAGR	(R)L/D|L/A/G/R D L T D/Y L m K(I)	m:Oxidized methionine	159.32	547.2829	1623.841	15.9931	-1.1	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
11827	dirMS_041712_NAR_120mM_plus.14799.14799.3	3	9.27	1	9.20E+05		(K)LDKSQIH	(K)L D K/S/Q I H D\I|V\L V/G/G S T R(I)		130.88	613.3369	1838.013	-0.0169	-9.2	6.75	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
11828	dirMS_041712_NAR_20mM_plus.14557.14557.2	2	9.27	0	3.89E+04	M185m	(K)LAVNm\	(K)L A/V N|m/V|P F P R(L)	m:Oxidized methionine	172.75	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
11829	dirMS_041712_NAR_20mM_plus.18960.18960.3	3	9.27	0	1.74E+05		(K)TLETQSA	(K)T L E T Q S A\L|G/P A/L Q A A/F K(L)		202.38	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
11830	dirMS_041712_NAR_20mM_plus.7871.7871.2	2	9.27	0	8.65E+04	M21m	(K)ATAVmP	(K)A T A/V m/P D/G/Q/F/K(D)	m:Oxidized methionine	124.45	590.7861	1164.572	15.9932	-1.5	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
11831	dirMS_041712_NAR_30mM_plus2.20865.20865.2	2	9.27	0	2.00E+05		(K)VFSIGPV	(K)V F|S|I|G P V/F R(A)		164.37	511.2941	1021.583	-0.002	-2	9.72	57534.6	6.11	HUMAN	P14868	Aspartate--tRNA ligase, cytoplasmic
11832	dirMS_041712_NAR_30mM_plus2.22464.22464.2	2	9.27	0	1.02E+05		(R)SLDMDS	(R)S L|D M/D/S/I I A E V K(A)		173.67	660.8437	1320.671	0.0086	6.5	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
11833	dirMS_041712_NAR_30mM_plus2.8531.8655.2	2	9.27	0	1.02E+05		(R)YNYIEGT	(R)Y/N|Y|I/E/G T/K(M)		99.03	494.2448	987.478	0.0041	4.2	6	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
11834	dirMS_041712_NAR_40mM_plus2.17897.17897.3	3	9.27	0	1.66E+05		(K)LAKPLSS	(K)L A K P L S S\L/T/P L/I M A A K(E)		171.7	552.0052	1653.997	0.0039	2.3	10	24711.4	5.19	HUMAN	H7C1X3	PAK-2p34 (Fragment)
11835	dirMS_041712_NAR_50mM_plus2.9800.9800.3	3	9.27	1	4.42E+05		(K)TAVCDIP	(K)T A|V/C D I/P/P R G L K(M)	C:Carbamidomethylation	119.37	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
11836	dirMS_041712_NAR_60mM_plus.13135.13135.3	3	9.27	0	5.53E+05		(R)SGGMER	(R)S/G/G\M/E R/P F V\L/A R(A)		124.78	440.5673	1319.689	-0.0015	-1.2	9.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
11837	dirMS_041712_NAR_60mM_plus.8806.8806.3	3	9.27	1	8.20E+05		(R)SSGGSYI	(R)S S/G/G S/Y R\D S Y D/S Y A T H/N/E(-)		104.85	665.9403	1995.795	0.0112	5.6	4.81	18647.7	9.51	HUMAN	Q14011	Cold-inducible RNA-binding protein
11838	dirMS_041712_NAR_20mM_minus.14457.14457.2	2	9.26	0	1.01E+05		(K)AIDLFTD	(K)A I|D L/F T/D/A I K(L)		198.77	553.8085	1106.609	0.0005	0.5	4.21	18141.9	4.7	HUMAN	F6VDH7	Hsc70-interacting protein (Fragment)
11839	dirMS_041712_NAR_30mM_minus2.12125.12125.2	2	9.26	0	2.65E+05		(R)IFYDMK	(R)I/F|Y D/M/K(V)		119.18	408.702	816.396	0.0007	0.8	5.83	15739.2	9.3	HUMAN	F6RFD5	Destrin
11840	dirMS_041712_NAR_30mM_minus2.15211.15211.2	2	9.26	0	7.26E+05	M2249m	(K)MSIYQA	(K)M S\I/Y/Q/A/m W/K(G)	m:Oxidized methionine	135.75	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
11841	dirMS_041712_NAR_50mM_minus2.13584.13584.3	3	9.26	1	1.17E+05		(K)IDSRLEQ	(K)I/D/S R L E/Q\Y\T/S A I E G T K(S)		144.82	604.3145	1810.918	0.0108	6	4.68	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
11842	dirMS_041712_NAR_60mM_minus.10862.10862.3	3	9.26	0	7.56E+04		(R)TIVITSHI	(R)T I/V/I T S H/P G Q I V K(H)		120.03	464.9423	1392.821	-0.0086	-6.2	8.44	27999.4	5.61	HUMAN	B7Z5C0	DnaJ homolog subfamily A member 1
11843	dirMS_041712_NAR_60mM_minus.12593.12593.3	3	9.26	1	1.30E+04		(K)LSAEKVE	(K)L/S/A/E K/V E\I A/T L/T R(E)		130.48	477.6112	1430.821	-0.0023	-1.6	6.14	26661.1	7.81	HUMAN	H0YL69	Proteasome subunit alpha type (Fragment)
11844	dirMS_041712_NAR_60mM_minus.13722.13722.3	3	9.26	1	2.57E+05		(K)KAEAAA	(K)K A E A\A\A S A\L/A/D|A/D/A D/L E E R(L)		136.4	639.6429	1916.92	-0.0054	-2.8	4.02	25103.6	5.88	HUMAN	O43633	Charged multivesicular body protein 2a
11845	dirMS_041712_NAR_20mM_plus.17527.17527.2	2	9.26	0	1.44E+04	M199m	(K)SmVPVC	(K)S m|V|P V|Q V Q L D V|P V V K(V)	m:Oxidized methionine	192.52	827.4624	1637.93	15.988	-4.2	5.55	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
11846	dirMS_041712_NAR_20mM_plus.18840.18840.2	2	9.26	0	1.29E+05		(R)LFFLQVK	(R)L F|F/L Q/V K(E)		201.5	447.7765	894.545	0.001	1.1	8.75	71218.8	6.3	HUMAN	A7YIJ8	Radixin
11847	dirMS_041712_NAR_20mM_plus.19344.19344.3	3	9.26	0	9.30E+04		(R)ALIAGGG	(R)A L I A G G G A/P/E I/E L A L/R(L)		205.05	517.6345	1550.89	-0.0011	-0.7	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
11848	dirMS_041712_NAR_30mM_plus2.14342.14434.2	2	9.26	0	4.42E+05		(R)GIFTSEIG	(R)G I|F/T/S/E/I/G T K(Q)		129.17	526.7806	1052.562	-0.0083	-7.9	6	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
11849	dirMS_041712_NAR_30mM_plus2.20745.20745.2	2	9.26	0	1.27E+05		(K)SVVTSIF	(K)S V/V/T/S I F G/V/K(N)		162.85	518.799	1036.604	-0.013	-12.5	8.47	132902.3	5.82	HUMAN	J3KR24	Isoleucine--tRNA ligase, cytoplasmic
11850	dirMS_041712_NAR_30mM_plus2.21094.21094.2	2	9.26	0	1.02E+05		(K)VFSIGPV	(K)V/F|S\I/G/P V/F R(A)		164.3	511.2941	1021.583	-0.002	-2	9.72	57534.6	6.11	HUMAN	P14868	Aspartate--tRNA ligase, cytoplasmic
11851	dirMS_041712_NAR_40mM_plus2.11278.11278.3	3	9.26	0	1.21E+05		(K)EAGELKP	(K)E A G\E L K P E E E\I|T|V/G P V Q K(L)		132.8	651.6782	1953.017	0.0025	1.3	4.32	108281.4	5.72	HUMAN	P53618	Coatomer subunit beta
11852	dirMS_041712_NAR_40mM_plus2.19324.19324.3	3	9.26	0	1.75E+05		(R)LQQAQL	(R)L/Q|Q/A\Q L/Y/P I A I F I K P K(S)		180.67	624.3737	1871.115	-0.0088	-4.7	9.7	94175.4	6.59	HUMAN	Q5JUW8	Discs, large homolog 3 (Neuroendocrine-dlg, Drosophila)
11853	dirMS_041712_NAR_40mM_plus2.8753.8753.2	2	9.26	0	9.63E+04		(R)WVCSSL	(R)W|V/C S/S/L R(H)	C:Carbamidomethylation	113.6	454.2261	907.445	-0.0005	-0.6	9.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
11854	dirMS_041712_NAR_50mM_plus2.12543.12543.3	3	9.26	1	3.06E+05		(R)SGVGLS	(R)S G/V/G L/S/S Y L S T E K/D A S\P K(T)		133.63	609.3102	1825.918	-0.0018	-1	5.79	64248.4	9.08	HUMAN	Q9BW04	Specifically androgen-regulated gene protein
11855	dirMS_041712_NAR_50mM_plus2.6630.6630.3	3	9.26	1	3.80E+05		(R)IVDGKV	(R)I V|D G K/V V/S E T/N D T/K(V)		100.3	502.2651	1504.785	-0.0046	-3	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
11856	dirMS_041712_NAR_60mM_plus.19977.19977.3	3	9.26	1	3.34E+05		(K)GPVREG	(K)G P V R E|G\D V L/T L/L E/S E R(E)		165.02	590.6485	1769.939	-0.0083	-4.7	4.41	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
11857	dirMS_041712_NAR_60mM_plus.8195.8300.3	3	9.26	0	8.66E+05		(R)QYDISDP	(R)Q Y/D/I/S/D/P Q R P R(L)		100.88	458.8968	1374.676	-0.0002	-0.1	5.96	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
11858	dirMS_041712_NAR_120mM_minus.6080.6080.3	3	9.25	1	5.64E+05		(K)TCEESSF	(K)T/C/E/E S S F/C K/R(Q)	C:Carbamidomethylation	86.8	435.1849	1303.541	-0.0004	-0.3	5.81	10576.1	11.44	HUMAN	E9PRF8	Neutral alpha-glucosidase AB
11859	dirMS_041712_NAR_120mM_minus.8872.8872.3	3	9.25	0	8.92E+05		(K)HTGPNS	(K)H T G P N\S P/D T|A/N/D/G F V R(L)		103.08	562.2599	1684.767	-0.0022	-1.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
11860	dirMS_041712_NAR_20mM_minus.11555.11555.2	2	9.25	0	1.40E+05	M98m	(R)TLTIVDT	(R)T L|T I|V/D T/G I G m T K(A)	m:Oxidized methionine	163.17	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
11861	dirMS_041712_NAR_20mM_minus.14689.14689.2	2	9.25	0	9.62E+04		(K)IYVDDGI	(K)I/Y|V D|D G\L I/S/L Q\V K(Q)		201.6	731.9104	1462.815	-0.0016	-1.1	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
11862	dirMS_041712_NAR_30mM_minus2.13185.13185.2	2	9.25	0	2.72E+04	S105s	(R)TPVGsP	(R)T/P/V|G s P W/P R(V)	s:N-acetylglucosamine (S)	125.15	600.3148	996.526	203.0962	14	9.41	21117.9	12.16	HUMAN	P0DI83	Ras-related protein Rab-34, isoform NARR
11863	dirMS_041712_NAR_40mM_minus2.10800.10800.3	3	9.25	0	1.24E+05	M56m	(K)VAIVKPG	(K)V/A|I\V K P G V/P m E I V L N K(E)	m:Oxidized methionine	146.9	575.0112	1707.024	15.9953	0.2	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
11864	dirMS_041712_NAR_40mM_minus2.9472.9472.3	3	9.25	0	4.45E+04	M111m	(K)VADPTP	(K)V/A|D|P T P F H I Q/A E/V\T m K(T)	m:Oxidized methionine	138.23	600.6393	1783.905	15.9986	2.1	5.32	24897.7	9.84	HUMAN	A8MTM1	Carbonyl reductase [NADPH] 1
11865	dirMS_041712_NAR_50mM_minus2.10714.10714.3	3	9.25	1	3.93E+05		(R)IAEFTTN	(R)I/A|E F/T/T N L/T/E E E E K S K(S)		130.12	623.6418	1868.912	-0.0015	-0.8	4.32	227783.5	5.5	HUMAN	P35579	Myosin-9
11866	dirMS_041712_NAR_60mM_minus.6936.6936.3	3	9.25	1	2.74E+05		(R)IVDGKV	(R)I/V|D G K/V/V\S E T N D T K(V)		97.95	502.2642	1504.785	-0.0073	-4.8	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
11867	dirMS_041712_NAR_60mM_minus.8288.8288.3	3	9.25	1	1.02E+05		(R)AAERNP	(R)A A E R N\P\A|L|A|G S A I R(C)		106.15	466.2587	1396.766	-0.004	-2.9	9.64	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
11868	dirMS_041712_NAR_120mM_plus.4443.4443.3	3	9.25	1	2.93E+05		(R)AAEEED	(R)A/A\E\E E/D E/A D/P K R(Q)		72.37	453.8721	1359.602	-0.0005	-0.4	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
11869	dirMS_041712_NAR_120mM_plus.8339.8339.3	3	9.25	1	3.23E+06		(K)QLELRQ	(K)Q\L/E/L/R Q E/E/E/R(R)		97.02	443.8969	1329.676	0.0004	0.3	4.49	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
11870	dirMS_041712_NAR_20mM_plus.14693.14693.3	3	9.25	0	7.07E+04		(K)LVILANN	(K)L V\I L A N N|C/P A L R(K)	C:Carbamidomethylation	172.85	451.9268	1353.767	-0.0013	-0.9	9.75	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
11871	dirMS_041712_NAR_20mM_plus.17526.17526.2	2	9.25	0	1.44E+04	M199m	(K)SmVPVC	(K)S m/V|P V Q V\Q L|D\V/P V V K(V)	m:Oxidized methionine	192.52	827.4624	1637.93	15.988	-4.2	5.55	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
11872	dirMS_041712_NAR_20mM_plus.18121.18121.2	2	9.25	0	9.99E+04		(R)AILVDLE	(R)A I\L|V D L E/P G T M/D S V/R(S)		196.6	808.419	1615.836	-0.0053	-3.3	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
11873	dirMS_041712_NAR_30mM_plus2.11873.11873.2	2	9.25	0	1.53E+06		(R)NTDEMV	(R)N/T|D/E/M V/E/L R(I)		114.87	553.7615	1106.515	0.0011	1	4.14	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
11874	dirMS_041712_NAR_30mM_plus2.12737.12737.2	2	9.25	0	5.39E+05		(R)CNNVLY	(R)C N/N|V|L\Y/I/R(G)	C:Carbamidomethylation	120.77	526.2726	1051.535	0.0026	2.5	8.75	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F
11875	dirMS_041712_NAR_30mM_plus2.17646.17939.2	2	9.25	0	6.63E+05		(R)LMGLEA	(R)L/M|G L/E/A/L K(G)		146.52	437.7532	874.507	-0.0075	-8.6	6	4886.6	6.03	HUMAN	D6RIZ7	T-complex protein 1 subunit epsilon
11876	dirMS_041712_NAR_30mM_plus2.20961.20961.2	2	9.25	0	4.39E+04		(R)EMVLEII	(R)E\M/V/L/E/I I/R(E)		163.4	501.7877	1002.565	0.0029	2.9	4.53	61981.6	8.97	HUMAN	Q96I24	Far upstream element-binding protein 3

11877	dirMS_041712_NAR_30mM_plus2.5506.5529.2	2	9.25	0	1.51E+05	M67m	(R)AmNGE	(R)A m|N/G/E|S L D/G/R(Q)	m:Oxidized methionine	82.97	533.2363	1049.468	15.9973	2.2	4.37	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
11878	dirMS_041712_NAR_40mM_plus2.7501.7604.2	2	9.25	0	1.99E+05		(R)SGYFDE	(R)S/G/Y|F D/E/R(Y)		104.2	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
11879	dirMS_041712_NAR_50mM_plus2.16259.16259.3	3	9.25	1	2.76E+05		(K)YAVLYQ	(K)Y A|V L Y Q|P L F D/K R(F)		152.5	504.9436	1512.821	-0.0047	-3.1	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
11880	dirMS_041712_NAR_50mM_plus2.21120.21120.3	3	9.25	0	3.08E+05		(K)HSQFIG	(K)H S Q F\I G\Y|P/I T L F V E K(E)		180.18	593.6536	1778.948	-0.0013	-0.8	6.75	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
11881	dirMS_041712_NAR_60mM_plus.10151.10151.3	3	9.25	1	5.27E+05		(R)RQQEQ	(R)R Q\Q E Q Q|V/P/I L E K(F)		111.23	499.2786	1495.823	-0.0015	-1	6.14	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
11882	dirMS_041712_NAR_120mM_minus.17445.17445.4	4	9.24	1	5.36E+05		(R)GFGHIG	(R)G F/G H I G I A\V/P D V/Y S A C K R(F)	C:Carbamidomethylation	150.38	487.502	1946.991	-0.0044	-2.2	8.6	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
11883	dirMS_041712_NAR_30mM_minus2.18356.18356.2	2	9.24	0	5.54E+03		(R)LTAEDL	(R)L T|A E/D/L/F/E/A R(I)		153.52	582.7922	1164.59	-0.0124	-10.7	4.14	533778	5.74	HUMAN	Q15149	Plectin
11884	dirMS_041712_NAR_50mM_minus2.12722.12722.3	3	9.24	0	2.82E+05		(K)EGKPTI	(K)E G K P T I\V/E/E/D/D/P E L/F K(Q)		140.88	615.9772	1845.912	0.0054	2.9	4.08	29841.1	9.04	HUMAN	O75937	DnaJ homolog subfamily C member 8
11885	dirMS_041712_NAR_50mM_minus2.7966.7966.3	3	9.24	0	4.50E+04		(K)GSLTEG	(K)G S/L/T/E|G A L A/H S G N P V S K(G)		112.42	542.2789	1624.829	-0.0068	-4.2	6.75	110902.8	6.09	HUMAN	D6RD46	LIM and calponin homology domains-containing protein 1
11886	dirMS_041712_NAR_60mM_minus.10673.10673.3	3	9.24	1	5.44E+05	M239m	(R)MSMKE	(R)M/S M K E V D\E Q|m|L/N V Q/N K(N)	m:Oxidized methionine	119.9	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
11887	dirMS_041712_NAR_60mM_minus.15703.15703.3	3	9.24	1	3.03E+05		(R)GFPTIYF	(R)G F/P T I Y/F/S/P A N K/K(L)		147.2	490.5972	1469.779	-0.0017	-1.1	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
11888	dirMS_041712_NAR_60mM_minus.19006.19006.3	3	9.24	0	5.08E+05		(R)LGFHLP	(R)L G F H L\P\L E|V/A/Y Q R(G)		168.47	514.9512	1542.843	-0.0037	-2.4	6.75	533778	5.74	HUMAN	Q15149	Plectin
11889	dirMS_041712_NAR_120mM_plus.18717.18717.4	4	9.24	0	4.36E+04		(R)LGWDP	(R)L/G W D\P K/P G E G H L D/A L L R(G)		150.98	469.253	1873.992	-0.0017	-0.9	5.38	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
11890	dirMS_041712_NAR_120mM_plus.4177.4177.3	3	9.24	1	1.73E+07	M310m	(R)TKTEISE	(R)T K T\E I|S/E/m N R(N)	m:Oxidized methionine	69.83	408.8687	1208.594	15.9976	2.2	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
11891	dirMS_041712_NAR_120mM_plus.5230.5230.3	3	9.24	1	4.31E+05		(R)YEREQY	(R)Y/E/R E Q|Y/A D/R(A)		81.37	410.5196	1229.555	-0.0103	-8.4	4.68	37433.2	9.17	HUMAN	B0LM41	Protein RBM14-RBM4
11892	dirMS_041712_NAR_120mM_plus.7643.7643.3	3	9.24	1	2.02E+06	M281m	(R)SRAEAE	(R)S R A E A\E/S/m/Y Q I/K(Y)	m:Oxidized methionine	93.02	476.8977	1412.684	15.9947	-0.1	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
11893	dirMS_041712_NAR_20mM_plus.11273.11273.3	3	9.24	0	1.08E+05		(R)GCITIIG	(R)G C/I T I/I G G G D T/A/T C C\A/K(W)	C:Carbamidomethylation	150.18	585.5999	1754.787	-0.0019	-1.1	5.84	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
11894	dirMS_041712_NAR_20mM_plus.17745.17745.3	3	9.24	0	1.12E+04		(R)IINEPTA	(R)I I\N E P T A A\A|I/A/Y/G L D R(T)		193.42	563.3055	1687.901	0.0006	0.3	4.37	25598.3	6.45	HUMAN	E7EP11	Heat shock 70 kDa protein 1A/1B
11895	dirMS_041712_NAR_20mM_plus.7443.7443.2	2	9.24	0	7.99E+04		(R)GTSFDA	(R)G T S F D/A A|A|T S/G G S/A/S S E K(A)		119.65	815.8661	1630.719	0.0058	3.6	4.37	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
11896	dirMS_041712_NAR_20mM_plus.9247.9247.2	2	9.24	0	4.54E+04		(R)IIYGGSV	(R)I I|Y/G/G/S V T\G A T C K(E)	C:Carbamidomethylation	135.4	663.8412	1326.672	0.0029	2.2	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
11897	dirMS_041712_NAR_30mM_plus2.10730.10841.2	2	9.24	0	7.45E+05		(R)ANIQAV	(R)A N|I/Q|A/V/S L K(I)		109.55	472.2823	943.557	0.0002	0.2	8.8	25103.6	5.88	HUMAN	O43633	Charged multivesicular body protein 2a
11898	dirMS_041712_NAR_30mM_plus2.20144.20144.2	2	9.24	0	1.22E+04		(R)ALDTM	(R)A L/D/T\M|N F D/V I K(G)		159.3	633.8315	1266.64	0.0159	12.5	4.21	68197.9	9.58	HUMAN	B1ANR0	Poly(A) binding protein, cytoplasmic 4 (Inducible form)
11899	dirMS_041712_NAR_50mM_plus2.8297.8297.3	3	9.24	0	2.33E+05		(K)VQQAEL	(K)V Q|Q A E L H/T/G S\L P R(I)		110.33	479.2607	1435.765	0.0023	1.6	6.72	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
11900	dirMS_041712_NAR_50mM_plus2.8558.8558.3	3	9.24	1	2.16E+04		(R)AIDSSNL	(R)A/I/D/S/S/N L K D D Y S/T A/Q R(V)		111.82	595.2868	1783.846	0.0002	0.1	4.43	46656.7	9.19	HUMAN	Q5JVF3	PCI domain-containing protein 2
11901	dirMS_041712_NAR_60mM_plus.19234.19234.3	3	9.24	1	1.75E+05		(R)AGEAGK	(R)A/G|E/A G\K L E E V|M/Q E L R(A)		158.92	553.9525	1659.837	0.0059	3.6	4.49	54918.3	5.61	HUMAN	Q9BR76	Coronin-1B
11902	dirMS_041712_NAR_60mM_plus.6517.6517.2	2	9.24	0	1.48E+05		(K)TVEAEA	(K)T V|E|A|E/A A H/G T\V T R(H)		92.68	671.3399	1341.676	-0.0032	-2.4	5.37	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
11903	dirMS_041712_NAR_120mM_minus.20506.20506.3	3	9.23	1	1.51E+05		(R)GLFIIDD	(R)G L/F/I/I/D D/K G I L R(Q)		169.07	453.9371	1359.8	-0.0027	-2	5.96	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
11904	dirMS_041712_NAR_20mM_minus.8223.8223.2	2	9.23	0	5.74E+03		(K)DQVAN	(K)D Q|V/A/N/S A F V E R(L)		131.7	618.3098	1235.602	0.0108	8.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
11905	dirMS_041712_NAR_30mM_minus2.12417.12417.2	2	9.23	0	1.54E+05		(K)IGVTVLS	(K)I/G|V/T/V L S R(I)		120.92	422.7649	844.525	-0.0026	-3	9.75	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
11906	dirMS_041712_NAR_40mM_minus2.14656.14859.3	3	9.23	0	1.19E+06		(K)ISSIQSIV	(K)I/S|S I/Q/S I/V/P A L E I A/N A H R(K)		172.1	640.3618	1919.071	0	0	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
11907	dirMS_041712_NAR_40mM_minus2.8090.8090.3	3	9.23	0	1.24E+05	M147m	(K)LQmEA	(K)L Q/m E A/P H I/I/V\G\T P\G R(V)	m:Oxidized methionine	127.3	545.627	1618.873	15.9931	-1.1	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
11908	dirMS_041712_NAR_40mM_minus2.9506.9506.3	3	9.23	0	2.43E+03	M53m	(K)SGTGIA	(K)S G T/G I/A A/M S V M R P E Q I m K(S)	m:Oxidized methionine	137.67	641.6582	1906.955	16.0053	5.4	8.46	8797.3	9.3	HUMAN	H3BR50	V-type proton ATPase 16 kDa proteolipid subunit
11909	dirMS_041712_NAR_50mM_minus2.15280.15280.3	3	9.23	0	4.13E+05	M118m	(R)AGKPVI	(R)A G K\P V\I C A|T/Q\M/L/E\S m I/K(K)	C:Carbamidomethylation m:Oxid	155.22	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
11910	dirMS_041712_NAR_60mM_minus.10008.10008.3	3	9.23	1	3.17E+05		(K)LTSDDVI	(K)L/T/S D/D/V K E Q I Y K(L)		115.37	480.2484	1438.742	-0.0118	-8.2	4.56	12573.5	10.39	HUMAN	E9PS50	40S ribosomal protein S13 (Fragment)
11911	dirMS_041712_NAR_60mM_minus.10585.10585.3	3	9.23	0	2.08E+05		(R)LSNLAL	(R)L/S/N/L|A\L V/K P E K(T)		118.6	404.5829	1211.736	-0.0017	-1.4	8.59	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
11912	dirMS_041712_NAR_60mM_minus.17221.17221.3	3	9.23	0	9.52E+04	S93s	(R)ALWVH	(R)A L W V/H S S A|S|A s S A A S R(R)	s:N-acetylglucosamine (S)	156.02	597.6347	1587.787	203.1022	12.7	9.8	66338.4	9.55	HUMAN	Q9UJ88	Interferon-related IFRD2 (PC4-B) protein
11913	dirMS_041712_NAR_120mM_plus.18165.18165.3	3	9.23	1	3.37E+05		(R)ARFEEL	(R)A R F E E\L|N|A/D/L F/R(G)		147.97	494.2571	1480.754	0.0024	1.7	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
11914	dirMS_041712_NAR_20mM_plus.12142.12142.2	2	9.23	0	3.44E+04		(K)LQAFSA	(K)L Q|A|F S/A A I/E S C/N K(A)	C:Carbamidomethylation	156.63	719.8475	1438.699	-0.0118	-8.2	6	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
11915	dirMS_041712_NAR_20mM_plus.12590.12590.2	2	9.23	0	1.34E+05		(R)GVEICIA	(R)G V\E/I/C|I/A/T/P G R(L)	C:Carbamidomethylation	159.12	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
11916	dirMS_041712_NAR_20mM_plus.13985.13985.2	2	9.23	0	6.90E+04		(K)IEVLEEE	(K)I E|V/L/E E/E/L R(L)		168.03	565.3132	1129.61	0.0092	8.1	4.09	334221.3	6.44	HUMAN	P15924	Desmoplakin
11917	dirMS_041712_NAR_20mM_plus.15419.15419.2	2	9.23	0	3.88E+04	M73m	(R)AILVDLE	(R)A I|L/V/D\L E/P G T m/D S V R(S)	m:Oxidized methionine	178.07	816.4181	1615.836	15.9929	-1.2	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
11918	dirMS_041712_NAR_20mM_plus.15682.15682.3	3	9.23	0	2.07E+05		(K)TITLEVE	(K)T\I/T\L E V E/P/S D T I/E N V K(A)		179.07	596.6463	1787.927	-0.003	-1.7	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
11919	dirMS_041712_NAR_20mM_plus.18558.18558.2	2	9.23	0	7.52E+04		(K)STLINTL	(K)S T|L/I/N T L F K(S)		199.03	518.8058	1036.604	0.0006	0.6	8.47	18010.4	9.42	HUMAN	K7EIE4	Septin-9 (Fragment)
11920	dirMS_041712_NAR_20mM_plus.18956.18956.3	3	9.23	0	7.06E+04		(R)NLTALG	(R)N L\T A L\G L/N\L|V/A S G G T A K(A)		201.58	533.9719	1599.906	-0.0053	-3.3	8.75	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
11921	dirMS_041712_NAR_20mM_plus.7417.7449.2	2	9.23	0	2.44E+05		(R)TVGIVG	(R)T V|G\I|V|G N Q/P K(V)		119.85	506.7922	1012.579	-0.0014	-1.4	8.41	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
11922	dirMS_041712_NAR_20mM_plus.8110.8110.2	2	9.23	0	1.06E+05		(K)VTEDTS	(K)V/T/E/D|T S/S V L R(S)		126.02	553.7889	1106.569	0.0017	1.6	4.37	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
11923	dirMS_041712_NAR_20mM_plus.9365.9365.2	2	9.23	0	8.16E+04		(R)ALEESN	(R)A L|E/E/S N Y E L/E/G K(I)		136.32	691.3246	1381.648	-0.0062	-4.5	4.09	59054.3	5.14	HUMAN	P13645	Keratin, type I cytoskeletal 10
11924	dirMS_041712_NAR_30mM_plus2.14435.14435.2	2	9.23	0	5.64E+05		(R)IILLAEG	(R)I/I|L/L|A E G R(L)		129.25	442.7821	884.556	0.0005	0.6	6	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
11925	dirMS_041712_NAR_30mM_plus2.7372.7372.2	2	9.23	0	7.14E+04		(R)EVIINSR	(R)E V|I/I/N S R(F)		93.52	415.7394	830.473	-0.0015	-1.8	6.1	15838.9	7.03	HUMAN	H0Y5U0	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
11926	dirMS_041712_NAR_40mM_plus2.13239.13239.3	3	9.23	1	8.25E+05		(K)TITLEVE	(K)T I/T/L/E V E/P S D T I E N\V K A K(I)		143.68	663.0201	1987.059	-0.0136	-6.9	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
11927	dirMS_041712_NAR_50mM_plus2.12305.12305.3	3	9.23	1	3.20E+05		(K)LSAEKV	(K)L S/A E K V/E/I/A T/L\T R(E)		132.33	477.6113	1430.821	-0.002	-1.4	6.14	26661.1	7.81	HUMAN	H0YL69	Proteasome subunit alpha type (Fragment)
11928	dirMS_041712_NAR_50mM_plus2.18926.18926.3	3	9.23	1	2.97E+05		(R)DSIVAEL	(R)D S/I|V/A/E/L D R E M S/R(S)		167.37	507.5872	1520.737	0.0097	6.4	4.32	34709.6	4.98	HUMAN	O14579	Coatomer subunit epsilon
11929	dirMS_041712_NAR_50mM_plus2.21626.21626.3	3	9.23	0	1.01E+05		(K)THLPLA	(K)T H L P L A\L|L/P Q T L L D Q K(V)		183.97	601.0191	1801.058	-0.0154	-8.6	6.41	22243.5	7.91	HUMAN	E9PKR8	Sulfotransferase 1A2 (Fragment)
11930	dirMS_041712_NAR_60mM_plus.14227.14227.3	3	9.23	1	8.17E+05		(K)TTVKDL	(K)T\T/V K D L S/E|L|G S V/R(T)		131.13	468.9268	1404.769	-0.0034	-2.4	5.74	533778	5.74	HUMAN	Q15149	Plectin
11931	dirMS_041712_NAR_60mM_plus.14393.14393.2	2	9.23	1	3.44E+05		(K)DVDEAY	(K)D V\D/E/A\Y M/N K V/E/L E/S R(L)		131.83	899.42	1797.832	0.0004	0.2	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
11932	dirMS_041712_NAR_120mM_minus.20400.20400.4	4	9.22	0	2.45E+05		(K)ALEHAF	(K)A L|E H\A F/Q L E\H/I/M/D L T R(L)		167.78	481.7478	1923.975	-0.0052	-2.7	5.27	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
11933	dirMS_041712_NAR_120mM_minus.7188.7188.3	3	9.22	1	2.57E+05		(K)DSYVGD	(K)D S/Y/V/G|D/E A Q/S K/R(G)		92.62	452.2134	1354.623	0.0023	1.7	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
11934	dirMS_041712_NAR_20mM_minus.12403.12403.2	2	9.22	0	5.39E+05	M313m	(R)TVQSLE	(R)T V/Q/S L|E\I D L/D S m R(N)	m:Oxidized methionine	171.58	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
11935	dirMS_041712_NAR_30mM_minus2.20471.20474.2	2	9.22	0	4.58E+05		(R)FLTWIL	(R)F L|T|W I L/N R(Y)		175.92	531.8089	1062.61	0.001	1	9.75	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
11936	dirMS_041712_NAR_50mM_minus2.13269.13269.3	3	9.22	1	2.03E+05	M26m	(K)GAEEME	(K)G A/E|E/M/E T/V I/P V D V m R/R(A)	m:Oxidized methionine	143.72	616.6435	1831.904	16.0119	9.2	4.41	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
11937	dirMS_041712_NAR_50mM_minus2.13706.13706.3	3	9.22	1	3.91E+05		(K)ITDIIGKE	(K)I/T|D I|I/G K E E G I\G/P E N L R(G)		146.9	618.665	1853.997	-0.0163	-8.8	4.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
11938	dirMS_041712_NAR_50mM_minus2.14270.14270.3	3	9.22	0	1.56E+05	M13m	(R)DLISHDE	(R)D L|I/S H D E m/F S D I Y K(I)	m:Oxidized methionine	149.13	576.9343	1712.784	16.0047	5.7	4.22	19709.1	4.83	HUMAN	P13693	Translationally-controlled tumor protein
11939	dirMS_041712_NAR_50mM_minus2.7958.7958.3	3	9.22	0	8.88E+04		(K)TAVEHA	(K)T\A|V/E/H A T D E D I L A/K(G)		112.23	504.9229	1512.754	0.0001	0.1	4.31	288852.1	5.33	HUMAN	E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein
11940	dirMS_041712_NAR_60mM_minus.8038.8038.3	3	9.22	1	1.12E+05		(R)VIEETEE	(R)V I|E E T/E E/R L/S K(V)		105.03	444.903	1332.7	-0.0061	-4.6	4.49	558007.1	5.44	HUMAN	P58107	Epiplakin
11941	dirMS_041712_NAR_120mM_plus.5438.5438.2	2	9.22	0	3.43E+05	M49m	(R)HQGVM	(R)H/Q|G V\M V G m/G Q/K(D)	m:Oxidized methionine	81.55	594.2868	1171.571	15.9953	0.3	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
11942	dirMS_041712_NAR_120mM_plus.6495.6495.2	2	9.22	1	2.84E+05		(R)SIAKEGF	(R)S I|A/K/E G F E/K(I)		87.12	504.7715	1008.536	-0.0003	-0.3	5.86	17213.7	10.05	HUMAN	B7Z712	60 kDa heat shock protein, mitochondrial
11943	dirMS_041712_NAR_20mM_plus.12881.12881.2	2	9.22	0	1.46E+05		(R)LVVPAS	(R)L V|V/P A/S Q C G S L/I\G K(G)	C:Carbamidomethylation	161.6	714.8991	1428.788	0.003	2.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
11944	dirMS_041712_NAR_20mM_plus.16753.16753.2	2	9.22	0	1.25E+05		(R)LLEAQIA	(R)L L E/A/Q/I/A/T G G I I/D|P K(E)		185.92	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
11945	dirMS_041712_NAR_20mM_plus.17175.17175.2	2	9.22	0	8.87E+04		(K)VLDIIAT	(K)V/L|D\I/I A/T I/N K(G)		189.95	550.3381	1099.672	-0.0032	-2.9	5.81	19639	5.52	HUMAN	H0YA83	Beta-hexosaminidase subunit beta (Fragment)
11946	dirMS_041712_NAR_20mM_plus.8431.8431.2	2	9.22	0	1.06E+05		(K)TAVCDI	(K)T A/V/C/D/I/P\P R(G)	C:Carbamidomethylation	127.63	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
11947	dirMS_041712_NAR_40mM_plus2.6807.6807.2	2	9.22	0	2.58E+04		(K)YQAECS	(K)Y/Q|A E/C S Q F K(A)	C:Carbamidomethylation	100.03	580.7568	1160.504	0.0022	1.9	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
11948	dirMS_041712_NAR_50mM_plus2.11475.11475.3	3	9.22	1	2.80E+06	M72m	(R)TEmENE	(R)T|E|m E N E\F/V L I K K(D)	m:Oxidized methionine	127.98	499.5943	1480.772	15.9968	1.2	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
11949	dirMS_041712_NAR_50mM_plus2.15504.15504.3	3	9.22	1	7.67E+05		(K)VQGGAL	(K)V/Q|G G A/L/E D S Q L V A/G V A F K K(T)		150.35	639.6848	1917.044	-0.0042	-2.2	6.04	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
11950	dirMS_041712_NAR_50mM_plus2.17099.17099.3	3	9.22	0	5.71E+05		(R)QYYTLL	(R)Q Y Y|T/L/L N Q/A/P D\M L H R(K)		157.23	621.6447	1862.922	-0.0022	-1.2	6.74	4335.1	9.82	HUMAN	E5RH00	Ras GTPase-activating protein-binding protein 1
11951	dirMS_041712_NAR_50mM_plus2.20604.20604.3	3	9.22	1	2.42E+05		(R)GGPNIIT	(R)G G P/N I/I/T L A/D I/V K/D P V S R(T)		177	622.3526	1865.049	-0.0058	-3.1	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
11952	dirMS_041712_NAR_50mM_plus2.8946.8946.3	3	9.22	0	6.04E+05		(R)AALAHS	(R)A A L A H S E E\V|T|A/S Q V/A/A\T\K(T)		113.75	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
11953	dirMS_041712_NAR_60mM_plus.11530.11530.3	3	9.22	1	5.03E+05		(K)TAVCDI	(K)T A|V/C D I/P P R/G L K(M)	C:Carbamidomethylation	118.92	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
11954	dirMS_041712_NAR_60mM_plus.13104.13104.3	3	9.22	1	5.54E+05		(R)ICCDLD	(R)I C/C D\L D/V/L/A S K K(V)	C:Carbamidomethylation	125.25	474.5772	1421.713	0.0043	3.1	5.96	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
11955	dirMS_041712_NAR_60mM_plus.21446.21446.3	3	9.22	1	3.68E+05		(R)ARDDLI	(R)A R D D\L\I/T|D|L/L/N E A K(Q)		177.42	529.6165	1586.838	-0.0035	-2.2	4.23	23653.1	9.28	HUMAN	C9J8H1	V-type proton ATPase subunit E 1 (Fragment)
11956	dirMS_041712_NAR_60mM_plus.8318.8318.3	3	9.22	0	6.64E+05		(R)QYDISD	(R)Q Y/D/I/S D/P Q/R P/R(L)		101.42	458.8968	1374.676	-0.0002	-0.1	5.96	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
11957	dirMS_041712_NAR_30mM_minus2.15278.15278.2	2	9.21	0	7.59E+04		(R)QITVND	(R)Q\I/T V/N/D/L/P V G R(S)		136.35	606.3404	1211.674	-0.0007	-0.6	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
11958	dirMS_041712_NAR_30mM_minus2.9338.9421.2	2	9.21	0	3.76E+05		(R)AYEFAE	(R)A/Y|E/F/A E/R(C)		105.27	443.2099	885.41	0.0024	2.7	4.53	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
11959	dirMS_041712_NAR_40mM_minus2.12195.12195.3	3	9.21	0	4.30E+05		(K)IAILTCP	(K)I/A\I/L T C/P F\E/P P K P/K(T)	C:Carbamidomethylation	155.62	537.6382	1610.898	0.0026	1.6	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
11960	dirMS_041712_NAR_50mM_minus2.13616.13616.3	3	9.21	0	2.19E+04		(R)DLSHIG	(R)D L S H\I G D A V|V/I/S C A K(D)	C:Carbamidomethylation	145.88	528.9397	1584.805	-0.0005	-0.3	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
11961	dirMS_041712_NAR_50mM_minus2.17017.17017.3	3	9.21	0	1.02E+05		(K)LILPHVD	(K)L I L/P/H V D I Q/L K(Y)		164.9	430.2702	1288.799	-0.0027	-2.1	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
11962	dirMS_041712_NAR_50mM_minus2.9486.9486.3	3	9.21	0	1.37E+05		(K)MIVDPV	(K)M I V|D/P V/E/P\H G E M K(F)		122.28	494.5757	1481.713	-0.0002	-0.1	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
11963	dirMS_041712_NAR_60mM_minus.14938.14938.3	3	9.21	1	7.20E+04		(K)LTEDKA	(K)L/T|E D K A D V Q\S\I/I/G L Q R(F)		143.08	595.9938	1785.97	-0.0037	-2	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
11964	dirMS_041712_NAR_120mM_plus.7538.7538.3	3	9.21	1	2.02E+06	M281m	(R)SRAEAE	(R)S R A E A\E|S m/Y Q/I/K(Y)	m:Oxidized methionine	93.02	476.8977	1412.684	15.9947	-0.1	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
11965	dirMS_041712_NAR_20mM_plus.16094.16094.2	2	9.21	0	4.77E+04		(K)DAGTIA	(K)D A\G T|I|A/G L N V L R(I)		182.22	600.3422	1199.674	0.0029	2.4	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
11966	dirMS_041712_NAR_20mM_plus.16186.16186.3	3	9.21	0	1.63E+05	M223m	(K)VLNNmE	(K)V L N N\m E I G T/S/L/F D/E E/G A K(I)	m:Oxidized methionine	183.92	661.6522	1966.943	15.9994	2.3	4	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
11967	dirMS_041712_NAR_20mM_plus.16927.16927.3	3	9.21	0	9.87E+04		(R)AAFTAF	(R)A A F T A F/E E|A/Q/L/P R(L)		187.77	484.2492	1450.733	0.0005	0.4	4.53	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
11968	dirMS_041712_NAR_20mM_plus.19036.19036.2	2	9.21	0	1.05E+05		(K)DTSYLF	(K)D T S Y/L|F/I|T|G P D V V K(S)		201.92	777.9049	1554.805	-0.0025	-1.6	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
11969	dirMS_041712_NAR_20mM_plus.6648.6667.2	2	9.21	0	7.09E+04	M266m	(R)TQPmT	(R)T Q|P m/T A/Q A A/S Y R(A)	m:Oxidized methionine	110.62	670.8169	1324.631	15.9951	0.1	8.41	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
11970	dirMS_041712_NAR_40mM_plus2.10595.10595.3	3	9.21	0	1.85E+05		(K)VGSLDN	(K)V/G S L/D/N V G H/L P A G G/A V K(I)		128.15	530.9567	1590.86	-0.0043	-2.7	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
11971	dirMS_041712_NAR_40mM_plus2.17988.17988.3	3	9.21	1	4.73E+04		(K)TFVNITP	(K)T F|V\N I/T P/A E V/G V L V G K D R(S)		172.23	639.0251	1915.065	-0.004	-2.1	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
11972	dirMS_041712_NAR_50mM_plus2.17384.17559.3	3	9.21	1	4.78E+05		(R)ELELKV	(R)E/L E L K V/P/L/V/V/R(L)		159.83	432.2745	1294.809	-0.0004	-0.3	6.24	20422.4	5.35	HUMAN	H0Y852	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial (Fragment)
11973	dirMS_041712_NAR_50mM_plus2.9001.9001.3	3	9.21	0	8.58E+04		(R)SSTTSM	(R)S S/T/T/S/M T/S/V/P K P L/K(F)		114.5	488.597	1463.777	-0.001	-0.7	10	24799.7	5.16	HUMAN	C9JPC0	26S proteasome non-ATPase regulatory subunit 2 (Fragment)
11974	dirMS_041712_NAR_50mM_plus2.9044.9044.3	3	9.21	1	1.12E+05		(R)ALSTTA	(R)A L/S\T/T A/S T A A F D/K Q P Q S R(E)		114.4	627.3202	1879.951	-0.0048	-2.5	8.79	48446.2	8.53	HUMAN	C9J8T0	Selenocysteine-specific elongation factor
11975	dirMS_041712_NAR_120mM_minus.15045.15045.4	4	9.2	1	3.11E+05		(R)EALLSSA	(R)E A\L L/S/S A V/D/H G S D E V K F R(Q)		135.92	490.7539	1959.977	0.0167	8.5	4.75	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
11976	dirMS_041712_NAR_20mM_minus.11685.11685.2	2	9.2	0	4.32E+05		(R)GALQNI	(R)G A L Q/N/I|I\P A|S T G A A K(A)		165.02	706.3976	1411.79	-0.0024	-1.7	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
11977	dirMS_041712_NAR_20mM_minus.12518.12518.2	2	9.2	0	4.35E+05	M73m	(R)AVLVDL	(R)A V L/V/D L|E|P G T/m D S V R(S)	m:Oxidized methionine	172.9	809.4088	1601.82	15.99	-3	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
11978	dirMS_041712_NAR_30mM_minus2.15511.15511.2	2	9.2	0	3.29E+04		(K)FLMAN	(K)F L|M/A/N G Q L V K(M)		138.07	560.8108	1120.618	-0.004	-3.6	8.75	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
11979	dirMS_041712_NAR_30mM_minus2.17207.17207.2	2	9.2	0	1.94E+05		(R)IYNVIGT	(R)I Y/N|V|I\G T L R(G)		146.9	524.8092	1048.615	-0.0038	-3.7	8.75	84557.3	6.5	HUMAN	Q04609	Glutamate carboxypeptidase 2
11980	dirMS_041712_NAR_30mM_minus2.17437.17437.2	2	9.2	0	5.80E+04		(K)LLCGLLA	(K)L/L|C\G L|L A E R(L)	C:Carbamidomethylation	149.33	522.7963	1044.587	-0.0017	-1.6	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
11981	dirMS_041712_NAR_30mM_minus2.17459.17459.2	2	9.2	0	2.37E+05		(R)NGGQIL	(R)N G|G\Q|I/L I A D/L/R(G)		149.13	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
11982	dirMS_041712_NAR_40mM_minus2.10753.10753.3	3	9.2	0	1.27E+05	M56m	(K)VAIVKP	(K)V A|I/V K P G V|P m E I V L N K(E)	m:Oxidized methionine	146.87	575.0112	1707.024	15.9953	0.2	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
11983	dirMS_041712_NAR_50mM_minus2.14143.14143.3	3	9.2	0	3.40E+05		(K)SPAPPLL	(K)S/P|A/P/P L L H V A A L G Q K(Q)		148.45	500.2911	1498.874	-0.0153	-10.2	8.49	17549.1	10.39	HUMAN	E5RFJ3	DBIRD complex subunit KIAA1967 (Fragment)
11984	dirMS_041712_NAR_50mM_minus2.15046.15046.3	3	9.2	0	5.93E+05		(R)LLIHQSL	(R)L L/I H Q\S\L/A G G I I/G V K(G)		154.48	506.9833	1518.937	-0.0013	-0.8	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
11985	dirMS_041712_NAR_50mM_minus2.16377.16377.3	3	9.2	0	3.32E+04		(R)IMEIVD	(R)I M/E/I V/D/A I T T/T A Q S H Q R(T)		161.6	638.6598	1913.975	-0.0101	-5.3	5.32	94165.2	8.68	HUMAN	J3KNX3	6-phosphofructokinase

11986	dirMS_041712_NAR_50mM_minus2.17914.17914.3	3	9.2	1	1.70E+05		(K)IDPSKPE	(K)I D P S/K P/E S I L K M T/K(K)		171.33	529.6358	1586.882	0.0106	6.7	8.5	26247.3	7.75	HUMAN	Q14696	LDLR chaperone MESD
11987	dirMS_041712_NAR_50mM_minus2.6770.6770.3	3	9.2	1	2.55E+04		(K)LAQYEPI	(K)L A/Q/Y E/P/P Q E E K R A E(-)		104.98	563.2743	1687.829	-0.0202	-12	4.69	11966.5	5.71	HUMAN	Q99417	C-Myc-binding protein
11988	dirMS_041712_NAR_20mM_plus.12929.12929.2	2	9.2	0	1.13E+05	M137m	(K)IEVIEIm	(K)I E/V/I/E/I/m T D/R(G)	m:Oxidized methionine	161.12	617.8225	1218.64	15.9979	2.4	4.14	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
11989	dirMS_041712_NAR_20mM_plus.17505.17505.2	2	9.2	0	3.20E+04		(K)LFVTND	(K)L F|V/T/N D A/A/T I L R(E)		192.63	667.3752	1333.747	-0.0043	-3.2	5.84	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
11990	dirMS_041712_NAR_30mM_plus2.11435.11435.2	2	9.2	0	3.73E+05		(R)NGDFLP	(R)N G D|F L|P T|R(L)		113.47	460.2391	919.463	0.0077	8.4	5.84	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
11991	dirMS_041712_NAR_30mM_plus2.19392.19392.2	2	9.2	0	2.88E+04		(R)FLLADNI	(R)F L/L|A D|N L Y/C\K(A)	C:Carbamidomethylation	155.03	628.8226	1256.634	0.0036	2.8	5.83	22400.1	6.19	HUMAN	F5H2A7	Prefoldin subunit 3
11992	dirMS_041712_NAR_40mM_plus2.13376.13376.3	3	9.2	0	9.33E+04	M73m	(R)IEGDmI	(R)I/E\G\D m/I V/C A A Y A H E L|P K(Y)	C:Carbamidomethylation m:Oxid	144.87	644.9798	1916.925	16.0004	2.8	4.65	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
11993	dirMS_041712_NAR_40mM_plus2.16613.16613.3	3	9.2	1	2.47E+05		(R)VTFSGLF	(R)V/T|F/S/G L R D T V/T P G E L L K(A)		163.87	611.6744	1833.012	-0.003	-1.6	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
11994	dirMS_041712_NAR_40mM_plus2.19463.19463.3	3	9.2	1	4.58E+05		(K)ALFEEVF	(K)A L|F/E\E V/P E L L T E A E K K(E)		181.77	615.9991	1845.984	-0.0017	-0.9	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
11995	dirMS_041712_NAR_40mM_plus2.7321.7321.2	2	9.2	0	1.54E+05		(R)SGYFDEI	(R)S/G Y|F D E R(Y)		103.57	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
11996	dirMS_041712_NAR_50mM_plus2.11777.11777.3	3	9.2	1	1.65E+06		(K)TGQPMI	(K)T G Q/P M I N L Y/T D R E/T G K(L)		130.67	608.6361	1823.896	-0.0019	-1	5.73	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
11997	dirMS_041712_NAR_50mM_plus2.12937.12937.3	3	9.2	1	2.60E+05		(R)IHPEPVI	(R)I/H P E P/V I R/F H K(A)		136.17	458.2605	1372.785	-0.0179	-13	8.76	210550.5	6.46	HUMAN	G5E933	Myotubularin-related protein 5
11998	dirMS_041712_NAR_50mM_plus2.20583.20583.3	3	9.2	2	2.51E+05	T121t	(K)EPVIAQ	(K)E P V I/A Q/K/Q K/H t G A V R(A)	t:N-acetylglucosamine (T)	176.95	622.3526	1661.945	203.0987	10.4	10	39291.8	6.3	HUMAN	B4DGE3	Protein transport protein Sec31B
11999	dirMS_041712_NAR_50mM_plus2.9189.9189.3	3	9.2	0	1.75E+04		(R)GPPPTD	(R)G P|P|P T D/P Y G R P P P Y D R(G)		115.38	594.6247	1781.861	-0.001	-0.6	5.96	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
12000	dirMS_041712_NAR_60mM_plus.11198.11198.3	3	9.2	0	3.61E+05		(R)LVKPGN	(R)L V|K/P G N Q N/T/Q/V/T E A W N K(V)		116.13	643.0039	1927.003	-0.0061	-3.1	8.59	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
12001	dirMS_041712_NAR_60mM_plus.7202.7202.3	3	9.2	1	4.31E+05		(K)VVSETN	(K)V V|S/E/T N D T/K V\L R(H)		95.93	454.2511	1360.743	-0.0043	-3.2	6.04	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
12002	dirMS_041712_NAR_120mM_minus.14386.14386.3	3	9.19	1	1.43E+05	M313m	(R)RTVQSLI	(R)R T V\Q S\L\E|I|D/L/D S m R(N)	m:Oxidized methionine	133.25	560.2849	1662.848	15.9922	-1.6	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
12003	dirMS_041712_NAR_120mM_minus.17830.17830.3	3	9.19	1	2.41E+05		(R)RAPFDLI	(R)R\A P F/D\L|F/E/N K(K)		151.13	412.8849	1236.637	0.003	2.4	6.07	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
12004	dirMS_041712_NAR_120mM_minus.9312.9312.3	3	9.19	1	1.29E+05		(R)RADLNC	(R)R A D L N Q\G\I/G E|P Q/S P S R(R)		105.1	575.6264	1724.867	-0.0028	-1.6	6.07	26810.9	5.15	HUMAN	Q96C19	EF-hand domain-containing protein D2
12005	dirMS_041712_NAR_30mM_minus2.14355.14355.2	2	9.19	0	7.55E+04		(R)TPYGASI	(R)T/P|Y\G/A S I F/Q/S/K(E)		131.18	599.8093	1198.61	0.0011	0.9	8.26	44815.8	6.62	HUMAN	B3KQ29	Transducin-like enhancer protein 4
12006	dirMS_041712_NAR_30mM_minus2.8050.8050.2	2	9.19	0	2.56E+04		(R)CVSLEPK	(R)C/V/S L/E P/K(N)	C:Carbamidomethylation	96.93	416.7206	832.423	0.0106	12.7	6	104330.3	5.8	HUMAN	Q9H3U1	Protein unc-45 homolog A
12007	dirMS_041712_NAR_40mM_minus2.14250.14250.3	3	9.19	0	3.15E+04		(K)GVTIASC	(K)G V\T I/A/S/G/G V L/P N I H P E/L L A K(K)		168.03	662.715	1986.138	-0.0078	-3.9	6.75	17631.5	10.76	HUMAN	D6RCF2	Histone H2A
12008	dirMS_041712_NAR_40mM_minus2.9581.9581.3	3	9.19	0	2.91E+04	M5m	(R)EmQDVI	(R)E m/Q/D V D L/A/E V K P L/V E K(G)	m:Oxidized methionine	138.73	620.3199	1842.952	15.9934	-0.8	4.18	18328.6	4.58	HUMAN	E5RGM5	Protein NDRG1 (Fragment)
12009	dirMS_041712_NAR_60mM_minus.18183.18183.3	3	9.19	1	1.76E+04		(R)VTFSGLF	(R)V/T/F/S G L R D\T V T P G E L L K(A)		162.32	611.6719	1833.012	-0.0105	-5.7	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
12010	dirMS_041712_NAR_20mM_plus.10243.10256.2	2	9.19	0	2.01E+05		(K)LSDGVA	(K)L/S|D/G V A V/L/K(V)		143.02	451.2712	901.535	-0.0002	-0.2	5.84	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
12011	dirMS_041712_NAR_20mM_plus.15757.15757.2	2	9.19	0	3.01E+05		(K)VGINYQ	(K)V G I/N Y Q|P P T V V/P G G D/L A K(V)		179.15	912.9952	1824.985	-0.0023	-1.3	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
12012	dirMS_041712_NAR_20mM_plus.18903.18903.3	3	9.19	0	6.34E+04		(K)DTSYLFI	(K)D T S\Y L\F/I|T G P/D V V K(S)		201.93	518.9458	1554.805	0.0178	11.5	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
12013	dirMS_041712_NAR_30mM_plus2.20659.20855.2	2	9.19	0	2.32E+05		(K)EGLLLW	(K)E G\L|L|L|W/C/Q R(K)	C:Carbamidomethylation	162.88	587.8038	1174.604	-0.0034	-2.9	6.1	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
12014	dirMS_041712_NAR_40mM_plus2.15166.15166.3	3	9.19	1	2.11E+04		(R)TIAQDY	(R)T I|A Q/D/Y/G V L K A D E G I S F R(G)		155.8	661.6783	1983.018	0.0022	1.1	4.56	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
12015	dirMS_041712_NAR_50mM_plus2.18593.18593.3	3	9.19	0	1.81E+05		(K)ASVITQ	(K)A/S|V/I/T Q V F H V P L E/E/R(K)		166.42	575.6533	1724.933	0.0124	7.2	5.4	24511.6	6.62	HUMAN	C9J5E5	Vigilin (Fragment)
12016	dirMS_041712_NAR_50mM_plus2.21839.21839.3	3	9.19	1	2.08E+05		(R)KVPELM	(R)K\V P E L M\E|M/F L/P A T K(N)		185.52	545.2925	1633.869	-0.0063	-3.8	6.14	95051	6.63	HUMAN	B3KXW5	AP-1 complex subunit gamma-1
12017	dirMS_041712_NAR_60mM_plus.13662.13662.2	2	9.19	0	3.59E+05	S393s	(K)HLLHsV	(K)H/L|L H|s V/N Q\R(F)	s:N-acetylglucosamine (S)	128.45	653.8525	1103.607	203.0909	8.8	9.76	46725.5	6.13	HUMAN	Q9Y2U9	Kelch domain-containing protein 2
12018	dirMS_041712_NAR_60mM_plus.14544.14544.3	3	9.19	1	2.72E+05		(K)NKDQG	(K)N K D Q G T/Y E/D\Y|V/E G L/R(V)		133.2	596.2816	1786.824	0.006	3.4	4.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
12019	dirMS_041712_NAR_60mM_plus.17186.17186.3	3	9.19	0	1.75E+04		(R)IYSHSLLI	(R)I Y S/H/S L\L/P|V L R(S)		147.6	433.2569	1297.763	-0.0065	-5	8.75	60871.9	6.3	HUMAN	B4DJ93	Phosphoribosylformylglycinamidine cyclo-ligase
12020	dirMS_041712_NAR_120mM_minus.18402.18402.3	3	9.18	0	1.60E+05		(R)FHQLDI	(R)F H\Q\L\D\I|D\D|L/Q/S I R(A)		155.3	533.9425	1599.813	0.0004	0.3	4.41	24897.7	9.84	HUMAN	A8MTM1	Carbonyl reductase [NADPH] 1
12021	dirMS_041712_NAR_30mM_minus2.10142.10142.2	2	9.18	0	1.41E+05		(R)SPSTLLP	(R)S|P|S/T L/L/P/K(K)		109.23	421.7586	842.498	0.0117	13.9	8.47	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
12022	dirMS_041712_NAR_30mM_minus2.12097.12134.2	2	9.18	0	2.37E+05		(K)IGVTVLS	(K)I/G|V/T|V L S R(I)		119.13	422.7649	844.525	-0.0026	-3	9.75	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
12023	dirMS_041712_NAR_30mM_minus2.19110.19154.2	2	9.18	1	2.15E+05		(K)SKLEFSI	(K)S K L E\F S I|Y|P/A|P(-)		158.93	626.334	1251.662	-0.0012	-1	5.72	21962.5	5.85	HUMAN	C9JJQ8	Tubulin alpha-4A chain (Fragment)
12024	dirMS_041712_NAR_50mM_minus2.14727.14727.3	3	9.18	1	4.18E+05		(K)GCLELIK	(K)G C|L E L I/K E\T G V/P I/A G R(H)	C:Carbamidomethylation	151.82	571.6494	1712.936	-0.0027	-1.6	6.14	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
12025	dirMS_041712_NAR_60mM_minus.11449.11449.3	3	9.18	0	2.41E+04		(K)TKPYIQ	(K)T K|P Y I Q/V/D|I/G G/G Q T K(T)		123.8	535.6216	1604.864	-0.014	-8.7	8.17	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
12026	dirMS_041712_NAR_60mM_minus.5716.5716.3	3	9.18	1	2.78E+05		(K)EAEGAP	(K)E A E/G/A/P Q V/E A G K R(L)		87.38	447.8959	1341.676	-0.0026	-1.9	4.79	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
12027	dirMS_041712_NAR_20mM_plus.16630.16630.3	3	9.18	0	6.48E+04	M137m M	(R)IIGATDS	(R)I/I\G A T D S S/G E/L/m F L m/K(W)	m:Oxidized methionine	185.8	582.2872	1712.86	31.9873	-1.5	4.37	19439.5	4.97	HUMAN	B5MD17	Chromobox protein homolog 1 (Fragment)
12028	dirMS_041712_NAR_20mM_plus.6941.6941.2	2	9.18	0	9.56E+04		(K)AAAAAA	(K)A A/A|A|A\A/A L Q\A K(S)		114.28	478.7792	956.552	-0.0012	-1.3	8.8	37884.5	11.27	HUMAN	H3BM89	60S ribosomal protein L4
12029	dirMS_041712_NAR_30mM_plus2.18437.18437.2	2	9.18	0	2.36E+05		(K)GNFNYII	(K)G N\F/N/Y/I/E/F T/R(I)		150.27	630.8035	1260.601	-0.001	-0.8	6	20513.6	4.62	HUMAN	J3QRS3	Myosin regulatory light chain 12A
12030	dirMS_041712_NAR_30mM_plus2.21885.21885.3	3	9.18	0	3.56E+05		(R)NSILAQ	(R)N S I\L/A Q\V/L/D Q S A/R(A)		170.08	472.2638	1414.765	0.012	8.5	5.84	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
12031	dirMS_041712_NAR_30mM_plus2.22769.22769.2	2	9.18	0	2.69E+05		(R)ELSDFIS	(R)E L|S D/F/I/S Y|L/Q R(E)		177.22	685.8507	1370.695	-0.0009	-0.7	4.37	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
12032	dirMS_041712_NAR_40mM_plus2.11994.11994.3	3	9.18	0	2.25E+05		(K)VQASLA	(K)V Q/A\S L/A A N T/F T\I T G H A E/T K(Q)		137.38	654.0104	1960.013	0.0032	1.6	6.72	11802.2	5.6	HUMAN	D6RDG3	Transcription factor BTF3 (Fragment)
12033	dirMS_041712_NAR_40mM_plus2.16758.16758.3	3	9.18	0	3.49E+04	M64m	(R)GFGFITF	(R)G F G\F|I/T F/T\N/P E H A S V A m R(A)	m:Oxidized methionine	164.88	666.6524	1981.959	15.9838	-5.6	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
12034	dirMS_041712_NAR_50mM_plus2.14386.14386.3	3	9.18	0	2.60E+06		(R)LSQYQE	(R)L/S/Q/Y Q E/P L/H L P G V R(V)		144.53	546.2968	1636.881	-0.0047	-2.9	6.75	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
12035	dirMS_041712_NAR_60mM_plus.20538.20538.3	3	9.18	1	3.08E+05		(K)ITQDIFQ	(K)I/T/Q D I/F Q Q/L L K/R(G)		167.98	501.626	1502.869	-0.0055	-3.7	8.75	72796.9	6.75	HUMAN	A6NC17	Methionine--tRNA ligase, cytoplasmic
12036	dirMS_041712_NAR_120mM_minus.15889.15889.4	4	9.17	1	4.37E+05		(R)YAEIVHL	(R)Y A/E I V/H L/T L/P\D/G T K R(S)		140.9	428.9878	1712.933	-0.0036	-2.1	6.75	21230	6.36	HUMAN	H0YC04	V-type proton ATPase subunit B, brain isoform (Fragment)
12037	dirMS_041712_NAR_120mM_minus.8734.8734.3	3	9.17	0	5.76E+05		(R)THYSNIE	(R)T\H Y\S N I\E|A|N E/S E E V R(Q)		102.13	593.2723	1777.799	0.0036	2	4.48	21983.3	4.68	HUMAN	K7EIV0	Calpain small subunit 1
12038	dirMS_041712_NAR_20mM_minus.12578.12578.2	2	9.17	0	1.18E+04	M73m	(R)AVLVDLI	(R)A V L V/D/L/E|P/G T m D S V R(S)	m:Oxidized methionine	175.23	809.4088	1601.82	15.99	-3	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
12039	dirMS_041712_NAR_50mM_minus2.10496.10496.3	3	9.17	0	2.90E+05	M35m	(K)AASDIA	(K)A A|S D I/A m T E/L/P P T\H P I/R(L)	m:Oxidized methionine	127.85	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
12040	dirMS_041712_NAR_50mM_minus2.5829.5829.3	3	9.17	0	1.31E+05		(R)AGAAG	(R)A G\A|A/G/G P/E E E A E/K P V/K(T)		95.32	513.9233	1539.765	-0.0096	-6.2	4.49	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
12041	dirMS_041712_NAR_50mM_minus2.9404.9404.3	3	9.17	1	1.31E+05	M15m	(K)mLVSGA	(K)m/L|V/S G A G D I K L T K(D)	m:Oxidized methionine	121.65	450.2541	1332.756	15.9922	-2	8.35	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
12042	dirMS_041712_NAR_20mM_plus.10423.10441.2	2	9.17	0	1.10E+05	M267m	(R)LITLEEE	(R)L I|T\L/E E/E m T K(Y)	m:Oxidized methionine	145.17	611.8175	1206.629	15.9991	3.4	4.25	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
12043	dirMS_041712_NAR_20mM_plus.12112.12112.2	2	9.17	0	1.20E+05		(R)IYVVDV	(R)I Y|V|V D/V/G S E P R(A)		156.17	617.3237	1233.647	-0.0073	-5.9	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
12044	dirMS_041712_NAR_20mM_plus.12790.12790.2	2	9.17	0	1.23E+05	M137m	(K)IEVIEIm	(K)I E/V|I/E/I m T D R(G)	m:Oxidized methionine	160.93	617.8225	1218.64	15.9979	2.4	4.14	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
12045	dirMS_041712_NAR_20mM_plus.15191.15191.2	2	9.17	0	9.87E+04		(K)AILFVPR	(K)A/I|L/F/V P/R(R)		176.13	408.2606	815.514	0.0001	0.2	9.79	57660.2	6.38	HUMAN	Q9NQH7	Probable Xaa-Pro aminopeptidase 3
12046	dirMS_041712_NAR_20mM_plus.16206.16206.3	3	9.17	0	1.32E+05		(R)LLDAQL	(R)L L\D A Q\L A T G G I/V/D/P R(L)		183.53	513.6218	1538.854	-0.0028	-1.8	4.21	533778	5.74	HUMAN	Q15149	Plectin
12047	dirMS_041712_NAR_20mM_plus.6396.6396.2	2	9.17	0	1.60E+05		(K)DSYVGD	(K)D S/Y|V/G D E A\Q S K(R)		107.17	599.7645	1198.522	-0.0005	-0.4	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
12048	dirMS_041712_NAR_20mM_plus.8068.8068.3	3	9.17	0	4.57E+05	M239m	(K)EVDEQ	(K)E V D E Q\m/L/N V/Q/N/K(N)	m:Oxidized methionine	125.12	488.2328	1446.689	15.9945	-0.3	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
12049	dirMS_041712_NAR_20mM_plus.8896.8896.2	2	9.17	0	3.07E+05	M161m	(K)LLIEmEC	(K)L L|I/E/m E/Q R(L)	m:Oxidized methionine	132.45	524.278	1031.555	15.9933	-1.5	4.53	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
12050	dirMS_041712_NAR_30mM_plus2.8589.8589.2	2	9.17	0	6.11E+05		(K)VTMQN	(K)V/T|M/Q/N L N D R(L)		99.2	545.7703	1090.531	0.0024	2.2	5.81	51902.9	5.09	HUMAN	P02533	Keratin, type I cytoskeletal 14
12051	dirMS_041712_NAR_30mM_plus2.9117.9205.2	2	9.17	0	2.25E+05		(R)ALELEQ	(R)A L|E/L/E Q E/R(K)		101.35	494.2566	987.511	-0.0046	-4.7	4.25	67933	6.08	HUMAN	P26038	Moesin
12052	dirMS_041712_NAR_50mM_plus2.11337.11337.3	3	9.17	1	2.98E+05		(R)ETGVDL	(R)E T|G/V/D L/T K D N M A/L Q R(V)		127.18	564.2856	1690.843	-0.0006	-0.4	4.56	73964.5	5.87	HUMAN	P38646	Stress-70 protein, mitochondrial
12053	dirMS_041712_NAR_50mM_plus2.14361.14361.3	3	9.17	0	2.26E+06		(K)LQMEAF	(K)L/Q|M/E A P H I/I/V/G T P\G R(V)		143.97	540.2948	1618.873	-0.0035	-2.2	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
12054	dirMS_041712_NAR_50mM_plus2.19028.19028.3	3	9.17	0	8.17E+05		(R)CRPDQL	(R)C R P D Q|L|T\G L/S L/L|P L/S E K(A)	C:Carbamidomethylation	167.72	643.0148	1927.032	-0.0019	-1	6.07	533778	5.74	HUMAN	Q15149	Plectin
12055	dirMS_041712_NAR_50mM_plus2.20039.20039.3	3	9.17	1	1.59E+05		(K)EIEELKEI	(K)E I\E E L/K E L L/P E/I R(E)		173.57	537.6393	1610.9	0.0034	2.1	4.33	30121.3	4.2	HUMAN	E9PRH9	Nuclear autoantigenic sperm protein (Fragment)
12056	dirMS_041712_NAR_50mM_plus2.9180.9180.3	3	9.17	1	6.58E+05		(K)TAVCDIF	(K)T/A|V/C D/I/P P R G L K(M)	C:Carbamidomethylation	115.63	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
12057	dirMS_041712_NAR_50mM_plus2.9736.9756.3	3	9.17	0	9.82E+04		(K)YIQQTKI	(K)Y I|Q\Q/T/K/P L/T L E R(T)		118.75	497.2822	1489.837	-0.0053	-3.5	8.59	26283.8	8.96	HUMAN	O43809	Cleavage and polyadenylation specificity factor subunit 5
12058	dirMS_041712_NAR_60mM_plus.16355.16355.3	3	9.17	0	9.38E+05		(K)MTHLPE	(K)M T H\L\P E\L|D T|L/S/S E R(A)		141.98	543.6023	1628.795	-0.0025	-1.5	4.65	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
12059	dirMS_041712_NAR_60mM_plus.6154.6301.3	3	9.17	1	5.17E+05		(K)SVQATT	(K)S V|Q/A T T E N/K E/L K(T)		91.73	449.9085	1347.711	-0.0005	-0.4	5.86	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
12060	dirMS_041712_NAR_20mM_minus.7118.7118.2	2	9.16	0	1.65E+05		(R)AAQVAC	(R)A A Q|V/A Q D/E E I/A R(L)		118.82	650.8255	1300.649	-0.0054	-4.2	4.14	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
12061	dirMS_041712_NAR_30mM_minus2.5254.5254.2	2	9.16	0	6.21E+05		(R)TDTGEP	(R)T D|T/G E P M G R(G)		82.35	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
12062	dirMS_041712_NAR_40mM_minus2.14116.14116.3	3	9.16	0	3.46E+05		(R)LLEVLSG	(R)L L/E\V/L S/G E\I/L P K P T K(G)		166.62	546.333	1636.988	-0.0039	-2.4	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
12063	dirMS_041712_NAR_50mM_minus2.7186.7186.3	3	9.16	0	4.95E+04	M1369m	(K)QIATLH	(K)Q I/A/T/L/H/A Q V A D/m K(K)	m:Oxidized methionine	107.68	481.2527	1425.752	15.9917	-2.2	6.74	227783.5	5.5	HUMAN	P35579	Myosin-9
12064	dirMS_041712_NAR_60mM_minus.10497.10497.3	3	9.16	0	1.64E+05		(K)TTLAHII	(K)T/T L/A H I/I/A S N S/K(K)		118.65	419.2377	1255.7	-0.0019	-1.5	8.44	72873.4	5.73	HUMAN	Q96S55	ATPase WRNIP1
12065	dirMS_041712_NAR_60mM_minus.13451.13451.3	3	9.16	1	1.16E+05	M160m	(K)FRQDLm	(K)F R Q D L m N\I/A|G T/T L S S K(L)	m:Oxidized methionine	135.43	599.9744	1781.921	15.9872	-4.3	8.75	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
12066	dirMS_041712_NAR_20mM_plus.16603.16603.2	2	9.16	0	1.74E+05		(R)ELLIIGG	(R)E L\L/I/I/G/G V/A A/R(D)		185.93	556.3437	1111.683	-0.0032	-2.9	6.1	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
12067	dirMS_041712_NAR_20mM_plus.6720.6720.3	3	9.16	0	1.25E+05	M136m	(R)LVAGEm	(R)L V A G/E m G Q\N|E|P/D/Q G G Q R(G)	m:Oxidized methionine	111.45	601.2753	1785.818	15.9929	-1.1	4.14	17508.7	8.03	HUMAN	Q5H928	3-hydroxyacyl-CoA dehydrogenase type-2
12068	dirMS_041712_NAR_40mM_plus2.13827.13827.3	3	9.16	0	2.23E+05		(K)VALLLLD	(K)V A/L L|L\L/D Q G A S/P H|A A/A K(N)		148.13	558.9886	1674.954	-0.0025	-1.5	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
12069	dirMS_041712_NAR_40mM_plus2.7104.7104.2	2	9.16	0	3.74E+04		(K)GANPVE	(K)G A|N/P V/E/I\R(R)		101.82	428.2357	855.468	-0.0042	-4.9	6	17213.7	10.05	HUMAN	B7Z712	60 kDa heat shock protein, mitochondrial
12070	dirMS_041712_NAR_50mM_plus2.11712.11797.3	3	9.16	1	1.71E+06		(K)TGQPMI	(K)T/G Q|P M/I N L Y T D R E|T G K(L)		130.7	608.6361	1823.896	-0.0019	-1	5.73	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
12071	dirMS_041712_NAR_50mM_plus2.12435.12435.3	3	9.16	1	4.78E+05		(K)ILDSVGII	(K)I/L/D S V G I/E/A D D D/R L N K(V)		132.88	591.6385	1772.902	-0.0015	-0.9	4.04	11664.7	4.42	HUMAN	P05387	60S acidic ribosomal protein P2
12072	dirMS_041712_NAR_50mM_plus2.14933.14933.3	3	9.16	0	8.03E+05		(R)TIQVENS	(R)T I|Q V/E N S H L/I L|T G A G A L N K(V)		146.07	660.3668	1979.092	-0.0062	-3.1	6.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
12073	dirMS_041712_NAR_50mM_plus2.8254.8254.3	3	9.16	0	9.46E+04		(K)ATAGDT	(K)A T/A/G D/T H/L G G E D F D N R(L)		110.23	559.2487	1675.731	0.0009	0.5	4.22	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
12074	dirMS_041712_NAR_120mM_minus.4458.4746.2	2	9.15	0	2.84E+06	M46m M4	(R)HQGVm	(R)H/Q|G V m/V|G m G Q K(D)	m:Oxidized methionine	73.83	602.2834	1171.571	31.9885	-1.1	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
12075	dirMS_041712_NAR_20mM_minus.13869.13869.2	2	9.15	0	3.93E+05		(K)VLTPELY	(K)V L|T/P E L Y/A E L R(A)		190.82	652.3653	1303.726	-0.0023	-1.8	4.53	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
12076	dirMS_041712_NAR_30mM_minus2.16680.16680.2	2	9.15	0	2.95E+05		(K)MIFVGIK	(K)M/I/F/V/G I K(K)		144.85	404.2383	807.48	-0.0104	-12.9	8.5	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
12077	dirMS_041712_NAR_30mM_minus2.18354.18354.2	2	9.15	0	7.59E+04		(K)QIWQNI	(K)Q/I/W Q/N/L G L/D D/T K(I)		154.02	715.8676	1430.727	0.0005	0.4	4.21	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
12078	dirMS_041712_NAR_40mM_minus2.13777.13777.3	3	9.15	1	4.48E+04		(K)FGEVVD	(K)F/G|E/V V/D C T L K L/D/P I T G R(S)	C:Carbamidomethylation	165.3	640.6656	1919.989	-0.0073	-3.8	4.56	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
12079	dirMS_041712_NAR_40mM_minus2.6009.6009.2	2	9.15	0	1.03E+06		(K)AGFAGD	(K)A/G/F|A/G D D/A P R(A)		98.47	488.7279	976.448	0.0002	0.2	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
12080	dirMS_041712_NAR_50mM_minus2.14813.14813.3	3	9.15	0	4.12E+05		(K)YPIEHGI	(K)Y/P/I E H G I I|T N/W/D/D M E K(I)		152.48	654.3084	1960.911	-0.0003	-0.1	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
12081	dirMS_041712_NAR_60mM_minus.11699.11699.3	3	9.15	2	4.61E+05	M79m	(K)NMGAK	(K)N M G A K N V|C/L/m T D K N L S/K(L)	C:Carbamidomethylation m:Oxid	125.58	647.3196	1923.945	15.9993	2.3	9.7	14508.2	9.3	HUMAN	B4DFI7	Hydroxyacid-oxoacid transhydrogenase, mitochondrial
12082	dirMS_041712_NAR_60mM_minus.13401.13401.3	3	9.15	1	5.68E+05		(R)KLVIIEGI	(R)K\L V I\I\E G/D L/E/R(T)		135.13	428.9221	1284.752	-0.0004	-0.3	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
12083	dirMS_041712_NAR_60mM_minus.17790.17790.3	3	9.15	1	2.25E+05		(R)LGLSTLG	(R)L/G/L/S/T L/G E L K Q N L S R(S)		159.57	543.6476	1628.933	-0.0047	-2.9	8.75	22294.4	5.26	HUMAN	O43399	Tumor protein D54
12084	dirMS_041712_NAR_20mM_plus.10782.10782.2	2	9.15	0	8.63E+04		(R)FLEQQN	(R)F L|E/Q/Q/N Q/V L Q T K(W)		146.73	738.3942	1475.785	-0.0041	-2.8	6	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
12085	dirMS_041712_NAR_20mM_plus.14009.14009.2	2	9.15	0	8.18E+04		(K)LSILYPA	(K)L S I/L\Y/P A T T/G R(N)		168.48	596.3406	1191.673	0.0007	0.6	8.75	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
12086	dirMS_041712_NAR_20mM_plus.17947.17947.2	2	9.15	0	1.10E+05		(K)VDFPQD	(K)V D F/P Q D|Q L T/A/L T G R(I)		195.33	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
12087	dirMS_041712_NAR_30mM_plus2.21263.21263.2	2	9.15	0	8.98E+04		(R)QTLMW	(R)Q T|L|M/W/S A T W/P K(E)		166	674.8389	1348.672	-0.0013	-1	8.75	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
12088	dirMS_041712_NAR_30mM_plus2.8357.8357.2	2	9.15	0	1.34E+06		(K)QGGGG	(K)Q G G/G/G G/G G/S/V/P G I E R(M)		97.18	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
12089	dirMS_041712_NAR_30mM_plus2.9710.9710.2	2	9.15	0	7.62E+05		(K)EAESSPF	(K)E A/E/S/S/P F V E R(L)		105.13	575.7726	1150.537	0.0004	0.4	4.25	92752.5	4.76	HUMAN	P14625	Endoplasmin
12090	dirMS_041712_NAR_40mM_plus2.15275.15275.3	3	9.15	1	1.22E+05		(K)QGGLGF	(K)Q/G G L/G P M/N I/P/L/V/S D P K R(T)		156.57	593.6623	1778.958	0.0142	8	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
12091	dirMS_041712_NAR_50mM_plus2.18718.18718.3	3	9.15	0	1.19E+06		(R)LGFHLPI	(R)L G F H L\P L\E|V/A/Y Q R(G)		167.38	514.9522	1542.843	-0.0007	-0.4	6.75	533778	5.74	HUMAN	Q15149	Plectin
12092	dirMS_041712_NAR_50mM_plus2.21457.21457.3	3	9.15	1	1.49E+05		(K)ALFEEVF	(K)A L/F/E E V/P E L/L T E A E K K(E)		182.7	615.9987	1845.984	-0.0029	-1.6	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
12093	dirMS_041712_NAR_50mM_plus2.9314.9314.3	3	9.15	0	8.66E+04		(K)VEIMPPI	(K)V E\I M\P|P/P/P K P K(D)		115.37	411.5726	1232.707	-0.0039	-3.2	8.56	53885.5	9	HUMAN	P11182	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial
12094	dirMS_041712_NAR_60mM_plus.12652.12652.3	3	9.15	1	8.04E+05		(R)DLDRIA	(R)D L D R I A G Q|V/A/A A N\K(K)		123.35	481.263	1441.776	-0.0013	-0.9	5.96	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19

12095	dirMS_041712_NAR_60mM_plus.13689.13689.3	3	9.15	1	5.96E+05		(R)FKIPGSP	(R)F K I P G S|P P/E S/M/G R(G)		128.43	468.2401	1402.715	-0.009	-6.4	8.75	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
12096	dirMS_041712_NAR_60mM_plus.15583.15601.3	3	9.15	1	5.58E+05		(R)KGVEGL	(R)K G V E G\L\I|D\I|E/N/P N R(V)		138.17	518.6115	1553.828	-0.0082	-5.3	4.68	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
12097	dirMS_041712_NAR_120mM_minus.10130.10130.3	3	9.14	0	5.96E+05		(R)HGESAV	(R)H/G E S A\W/N/L/E/N R(F)		109.4	438.2098	1312.603	0.012	9.1	5.4	28917.5	6.68	HUMAN	P18669	Phosphoglycerate mutase 1
12098	dirMS_041712_NAR_120mM_minus.8833.8833.3	3	9.14	0	8.72E+05		(K)HTGPNS	(K)H T G\P N S P D T\A/N/D/G F V R(L)		103.07	562.2599	1684.767	-0.0022	-1.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
12099	dirMS_041712_NAR_20mM_minus.9700.9700.2	2	9.14	0	1.57E+05		(K)LSELEPG	(K)L S\E\L/E|P G T G\D/L R(F)		147.78	643.8318	1286.659	-0.0023	-1.8	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
12100	dirMS_041712_NAR_30mM_minus2.10091.10091.2	2	9.14	0	6.70E+05		(R)WVCSSL	(R)W/V/C/S/S/L/R(H)	C:Carbamidomethylation	109.05	454.2271	907.445	0.0015	1.6	9.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
12101	dirMS_041712_NAR_30mM_minus2.11797.11864.2	2	9.14	0	2.96E+05		(R)AFPGPL	(R)A F|P G/P L/A K(D)		117.87	400.7352	800.467	-0.0034	-4.2	8.8	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
12102	dirMS_041712_NAR_30mM_minus2.14993.14993.2	2	9.14	0	1.89E+05		(K)EFPGLA	(K)E F|P/G L\A G V/K(I)		134.88	459.2546	917.509	-0.0072	-7.8	6.1	41053.3	5.58	HUMAN	Q86UY0	TXNDC5 protein
12103	dirMS_041712_NAR_30mM_minus2.7082.7082.2	2	9.14	0	2.80E+05		(R)ASYISSA	(R)A/S|Y/I\S S A R(L)		93.03	427.7216	854.437	-0.0007	-0.9	8.79	59288.4	7.16	HUMAN	Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)
12104	dirMS_041712_NAR_50mM_minus2.16336.16336.3	3	9.14	0	1.75E+05	M1m	(-)mKPLVVI	(-)m K P L V\V\F|V|L/G G P G\A/G K(G)	m:Oxidized methionine	161.27	529.3077	1569.919	15.99	-3.1	10	22450.2	5.44	HUMAN	P30085	UMP-CMP kinase
12105	dirMS_041712_NAR_50mM_minus2.9205.9205.3	3	9.14	0	1.48E+05		(R)TITVALA	(R)T I/T V/A\L A D G G R P D N T G R(G)		120.08	571.9667	1713.888	-0.0023	-1.3	5.63	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
12106	dirMS_041712_NAR_60mM_minus.14705.14705.3	3	9.14	0	2.48E+05		(K)YYITIIDA	(K)Y Y|I T I I/D A|P G H R(D)		142.82	473.5815	1418.743	-0.0127	-9	6.74	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
12107	dirMS_041712_NAR_60mM_minus.14997.14997.3	3	9.14	1	5.05E+04		(K)KAPDFV	(K)K\A P D F\V/F/Y/A P R(L)		143.68	437.5685	1310.689	0.0018	1.3	8.59	71218.8	6.3	HUMAN	A7YIJ8	Radixin
12108	dirMS_041712_NAR_60mM_minus.17452.17452.3	3	9.14	1	2.25E+05		(K)GPREEIV	(K)G P R E E I V Y\L|P C I Y/R(N)	C:Carbamidomethylation	157.73	588.9733	1764.91	-0.0048	-2.7	6.14	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
12109	dirMS_041712_NAR_120mM_plus.7673.7673.2	2	9.14	0	8.35E+05		(K)HFEALAI	(K)H|F|E/A L A N/R(A)		94.48	479.2487	957.49	0	0	6.75	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
12110	dirMS_041712_NAR_20mM_plus.17080.17080.2	2	9.14	0	8.48E+04		(K)VNIIPIIA	(K)V/N|I/I/P I I A K(A)		189.25	490.8283	980.65	-0.001	-1	8.72	51212	5.84	HUMAN	A6NFQ9	Septin-8
12111	dirMS_041712_NAR_20mM_plus.17843.17843.2	2	9.14	0	9.16E+04		(K)VDFPQD	(K)V D/F/P Q D/Q L T A\L/T G R(I)		194.83	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
12112	dirMS_041712_NAR_20mM_plus.7204.7204.2	2	9.14	0	4.54E+03		(R)ITESEEV	(R)I T|E|S E|E V V/S R(E)		116.9	574.792	1148.579	-0.0026	-2.3	4.25	74423.5	6.57	HUMAN	P02545	Prelamin-A/C
12113	dirMS_041712_NAR_20mM_plus.7694.7694.2	2	9.14	0	1.57E+05		(K)IAVAAQ	(K)I A|V/A/A/Q N C Y K(V)	C:Carbamidomethylation	122.43	569.2902	1137.572	0.001	0.9	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
12114	dirMS_041712_NAR_20mM_plus.8713.8713.2	2	9.14	0	2.38E+05		(R)VPPPPPI	(R)V/P|P/P P P I A R(A)		130.58	472.2851	943.572	-0.0094	-10	9.72	32085.2	8.93	HUMAN	B4DY08	Heterogeneous nuclear ribonucleoproteins C1/C2
12115	dirMS_041712_NAR_30mM_plus2.18439.18439.2	2	9.14	0	3.53E+05		(R)SQVEEEI	(R)S Q|V/E/E/E\L F S V R(V)		149.63	661.8302	1322.659	-0.0055	-4.2	4.25	533778	5.74	HUMAN	Q15149	Plectin
12116	dirMS_041712_NAR_30mM_plus2.9817.9989.2	2	9.14	0	6.54E+05		(R)EEEMMI	(R)E\E/E/M/M/I/R(Q)		105.33	469.2135	937.412	0.008	8.5	4.25	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
12117	dirMS_041712_NAR_40mM_plus2.19409.19409.3	3	9.14	1	1.46E+05		(R)TEGLSVL	(R)T E/G L|S V L/S\Q A M A V I K E K(I)		181.77	602.0005	1803.988	-0.0015	-0.8	5.81	31604.9	6.88	HUMAN	G3V4T5	Eukaryotic translation initiation factor 2 subunit 1 (Fragment)
12118	dirMS_041712_NAR_50mM_plus2.10966.10966.3	3	9.14	0	6.36E+04		(K)MVMIQI	(K)M V/M|I/Q/D/G P Q N T G/A D K P L R(I)		125.3	657.663	1970.979	-0.0042	-2.1	5.71	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
12119	dirMS_041712_NAR_50mM_plus2.14770.14770.3	3	9.14	1	1.58E+04		(K)KGVNLP	(K)K G V N L P G A|A\V|D|L/P A V S\E K(D)		145.08	588.999	1764.985	-0.003	-1.7	6.07	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
12120	dirMS_041712_NAR_60mM_plus.10411.10411.3	3	9.14	1	1.61E+06		(R)TNAENE	(R)T N|A E N E/F/V T I K/K(D)		112.27	465.2512	1393.732	0.0069	4.9	5.81	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
12121	dirMS_041712_NAR_60mM_plus.15024.15024.3	3	9.14	1	4.21E+05		(K)SLEELRL	(K)S L/E/E/L R L E/D Y Q A N R(K)		135.57	579.2911	1735.861	-0.0022	-1.3	4.41	178367.2	6.03	HUMAN	J3KP29	Nuclear pore complex protein Nup98-Nup96
12122	dirMS_041712_NAR_60mM_plus.16169.16364.3	3	9.14	0	4.88E+05		(K)TTITMAI	(K)T/T|I/T M/A/H/L L A A/R(E)		141.72	433.5839	1298.725	0.0122	9.4	9.44	37589.6	5.96	HUMAN	Q52LJ0	Protein FAM98B
12123	dirMS_041712_NAR_60mM_plus.19475.19475.3	3	9.14	0	6.06E+05		(K)VSHLLGI	(K)V/S H L L G I N\V|T/D F T R(G)		159.95	524.6233	1571.854	0.0013	0.8	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
12124	dirMS_041712_NAR_60mM_plus.8288.8288.3	3	9.14	1	5.11E+05		(R)LSQIGVE	(R)L/S|Q/I/G\V/E N T E/E N R/R(L)		101.57	548.9468	1644.83	-0.0041	-2.5	4.79	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
12125	dirMS_041712_NAR_120mM_minus.14697.14697.4	4	9.13	2	3.07E+05		(K)AMGDA	(K)A M|G D/A/E I/K D G E R L P L A V/K(D)		134.3	479.0049	1913.016	-0.0183	-9.6	4.78	99900.1	5.04	HUMAN	B4DZI8	Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b
12126	dirMS_041712_NAR_20mM_minus.12076.12076.2	2	9.13	0	8.51E+05	M313m	(R)TVQSLEI	(R)T V|Q\S L|E|I D/L/D S m R(N)	m:Oxidized methionine	170.4	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
12127	dirMS_041712_NAR_20mM_minus.9195.9232.2	2	9.13	0	1.90E+05	M239m	(K)EITALAP	(K)E I|T\A/L|A/P S T m K(I)	m:Oxidized methionine	141.92	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
12128	dirMS_041712_NAR_30mM_minus2.14373.14373.2	2	9.13	0	2.19E+05		(R)YYFEGIK	(R)Y/Y/F/E/G I K(Q)		132.28	460.2363	919.456	0.0093	10.1	6	23092.1	6.93	HUMAN	G3V438	Activator of 90 kDa heat shock protein ATPase homolog 1 (Fragment)
12129	dirMS_041712_NAR_30mM_minus2.19084.19084.2	2	9.13	0	1.24E+04		(R)FEELTNL	(R)F/E|E L/T/N L I/R(T)		158.37	567.804	1134.615	-0.0146	-12.9	4.53	106155.7	5.45	HUMAN	B5ME19	Eukaryotic translation initiation factor 3 subunit C
12130	dirMS_041712_NAR_30mM_minus2.19498.19498.2	2	9.13	0	3.70E+05		(R)ASLSLW	(R)A S/L/S L\W Q/A|M E K(G)		162.5	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
12131	dirMS_041712_NAR_40mM_minus2.10963.10963.3	3	9.13	0	1.81E+05		(R)DLSHIGI	(R)D L S H I G D A\V/V|I S C A K(D)	C:Carbamidomethylation	147.4	528.9384	1584.805	-0.0044	-2.8	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
12132	dirMS_041712_NAR_40mM_minus2.14525.14525.3	3	9.13	1	1.99E+05		(R)GLLPGLI	(R)G L\L|P|G L L/P\A P A D K L T P K(G)		169.47	567.6813	1701.031	-0.0016	-0.9	8.59	153084.9	5.55	HUMAN	Q6P2E9	Enhancer of mRNA-decapping protein 4
12133	dirMS_041712_NAR_50mM_minus2.12575.12575.3	3	9.13	1	1.30E+05		(R)SLIANLA	(R)S L/I/A\N L/A A/A N C Y K\K(E)	C:Carbamidomethylation	139.83	512.9454	1536.82	0.0014	0.9	9.7	36978.6	6.33	HUMAN	B7Z800	Adenosine kinase
12134	dirMS_041712_NAR_50mM_minus2.12782.12782.3	3	9.13	1	3.77E+05		(K)NTVELL\	(K)N T/V|E/L/L/V E D K G N Q V Y R(C)		140.5	626.3309	1876.976	0.0018	1	4.68	258215.9	5.48	HUMAN	E7EN95	Filamin-B
12135	dirMS_041712_NAR_50mM_minus2.14359.14359.3	3	9.13	0	6.18E+04		(K)VALLLLD	(K)V A/L|L L L D Q/G/A S P H A A A K(N)		150.53	558.9883	1674.954	-0.0034	-2	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
12136	dirMS_041712_NAR_50mM_minus2.9530.9530.3	3	9.13	1	1.31E+05		(R)MQKEIT	(R)M Q/K\E I T A|L|A/P S T M K(I)		122.2	516.9426	1548.812	0.0008	0.5	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
12137	dirMS_041712_NAR_60mM_minus.14917.14917.3	3	9.13	1	7.20E+04		(K)LTEDKAI	(K)L/T|E D K A D V Q/S/I/I|G L Q R(F)		143.08	595.9938	1785.97	-0.0037	-2	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
12138	dirMS_041712_NAR_60mM_minus.8245.8266.3	3	9.13	1	8.21E+05	M174m	(R)VKYETEI	(R)V/K Y E T E|L/A/m R(Q)	m:Oxidized methionine	106.05	419.2169	1239.64	15.996	0.8	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
12139	dirMS_041712_NAR_20mM_plus.6398.6398.2	2	9.13	0	1.60E+05		(K)DSYVGD	(K)D S Y|V|G/D E A\Q S K(R)		107.17	599.7645	1198.522	-0.0005	-0.4	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
12140	dirMS_041712_NAR_30mM_plus2.19405.19405.2	2	9.13	0	2.27E+05		(K)NFSGAE	(K)N F|S/G/A/E/L E G L V/R(A)		155.47	646.3361	1291.664	0.0008	0.6	4.53	71924.9	6.25	HUMAN	B4DFA2	Vesicle-fusing ATPase
12141	dirMS_041712_NAR_30mM_plus2.20100.20100.3	3	9.13	0	4.52E+05		(K)SYELPDC	(K)S Y E L P D G Q/V/I/T I/G N E R(F)		159.72	597.6334	1790.892	-0.0063	-3.5	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
12142	dirMS_041712_NAR_40mM_plus2.13108.13413.3	3	9.13	0	3.96E+05		(K)NLPPSG	(K)N L/P P S\G A V/P V T G I/P P H V\V K(V)		144.37	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
12143	dirMS_041712_NAR_40mM_plus2.6727.6727.2	2	9.13	0	1.68E+04		(K)SLAAEEE	(K)S L|A|A E/E E/A A R(Q)		99.53	523.7589	1046.511	-0.0008	-0.7	4.25	533778	5.74	HUMAN	Q15149	Plectin
12144	dirMS_041712_NAR_50mM_plus2.12324.12324.3	3	9.13	1	4.91E+05		(K)ILDSVGII	(K)I/L|D/S/V/G I/E A D D D R L N K(V)		132.85	591.6385	1772.902	-0.0015	-0.9	4.04	11664.7	4.42	HUMAN	P05387	60S acidic ribosomal protein P2
12145	dirMS_041712_NAR_50mM_plus2.19980.19980.3	3	9.13	0	2.86E+05		(R)LQSLPFA	(R)L Q|S L/P F A L T H L/N\L K(A)		173.67	532.3178	1594.931	0.0073	4.6	8.76	175851.7	5.01	HUMAN	Q14160	Protein scribble homolog
12146	dirMS_041712_NAR_50mM_plus2.7293.7293.3	3	9.13	0	1.68E+05		(R)SGSSQEI	(R)S/G S/S/Q E|L D V\K/P S A S P Q E/R(S)		103.85	634.6443	1901.92	-0.0016	-0.8	4.68	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
12147	dirMS_041712_NAR_50mM_plus2.9493.9493.3	3	9.13	0	5.99E+05		(K)GAVDGC	(K)G A/V/D/G G L/S/I/P H S T\K(R)		117.25	446.9057	1338.701	0.0013	1	6.74	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
12148	dirMS_041712_NAR_60mM_plus.13760.13760.3	3	9.13	1	4.71E+05		(R)KYEMFA	(R)K\Y E M\F|A Q T|L/Q/Q S R(G)		128.72	543.9389	1629.805	-0.0032	-2	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
12149	dirMS_041712_NAR_60mM_plus.19769.19769.3	3	9.13	0	3.06E+05		(R)NSVSNF	(R)N/S\V/S|N F L/H/S L E R(G)		162.78	468.2401	1402.707	-0.0016	-1.1	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
12150	dirMS_041712_NAR_60mM_plus.20389.20389.3	3	9.13	1	4.21E+05		(K)NAAGAL	(K)N A/A|G/A/L D/L/L/K E L/K(N)		166.93	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
12151	dirMS_041712_NAR_60mM_plus.20614.20614.3	3	9.13	1	2.90E+05		(K)ITQDIFQ	(K)I/T|Q D/I/F/Q Q L L K R(G)		168.08	501.626	1502.869	-0.0055	-3.7	8.75	72796.9	6.75	HUMAN	A6NC17	Methionine--tRNA ligase, cytoplasmic
12152	dirMS_041712_NAR_60mM_plus.21681.21681.3	3	9.13	1	6.54E+05		(K)EIIDLVLI	(K)E I/I/D/L V/L/D R I R(K)		180.83	452.2733	1354.805	0.0001	0.1	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
12153	dirMS_041712_NAR_60mM_plus.7438.7438.3	3	9.13	0	5.01E+05		(R)SSGHSSS	(R)S S G H S S S E\L|S|P D A V E K(A)		96.95	539.584	1616.74	-0.0024	-1.5	4.65	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
12154	dirMS_041712_NAR_60mM_plus.8884.8884.3	3	9.13	1	7.11E+05		(R)QLQLAQ	(R)Q\L/Q/L/A Q/E/A A Q K/R(L)		104.87	461.9268	1383.77	-0.0044	-3.2	8.75	533778	5.74	HUMAN	Q15149	Plectin
12155	dirMS_041712_NAR_120mM_minus.13492.13492.3	3	9.12	2	9.83E+05		(R)AQKDEE	(R)A/Q|K/D E E K M\E/I\Q\E/I Q L K(E)		128.13	654.0058	1960.006	-0.0027	-1.4	4.58	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
12156	dirMS_041712_NAR_120mM_minus.19552.19552.4	4	9.12	1	1.11E+05		(K)MKPLMC	(K)M K P L M G V|I Y V/P|L/T D K E K(Q)		162.03	491.2741	1962.08	-0.0057	-2.9	8.19	20796.6	6.37	HUMAN	B7Z972	Protein-L-isoaspartate O-methyltransferase
12157	dirMS_041712_NAR_30mM_minus2.15614.15614.2	2	9.12	0	1.51E+05		(K)AMTGVI	(K)A M/T G V|E Q W/P Y R(A)		138.37	669.3172	1337.631	-0.0036	-2.7	6.04	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
12158	dirMS_041712_NAR_30mM_minus2.16167.16167.2	2	9.12	0	2.52E+04		(R)VFSGLVS	(R)V F|S/G L V/S T G L K(V)		141.38	554.3215	1107.641	-0.0051	-4.6	8.72	96306.4	6.41	HUMAN	P13639	Elongation factor 2
12159	dirMS_041712_NAR_30mM_minus2.19040.19040.2	2	9.12	0	1.24E+04		(R)FEELTNL	(R)F E|E/L T/N/L I\R(T)		158.37	567.804	1134.615	-0.0146	-12.9	4.53	106155.7	5.45	HUMAN	B5ME19	Eukaryotic translation initiation factor 3 subunit C
12160	dirMS_041712_NAR_50mM_minus2.12602.12602.3	3	9.12	0	1.09E+06	M114m M:	(R)AGKPVI(	(R)A G K\P V I\C\A|T Q m\L E/S m I K(K)	C:Carbamidomethylation m:Oxid	139.87	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
12161	dirMS_041712_NAR_50mM_minus2.13406.13406.3	3	9.12	0	2.46E+05		(K)VIQYLAY	(K)V I/Q/Y/L A\Y/V/A S S H K(S)		144.78	493.6043	1478.8	-0.0018	-1.2	8.48	227783.5	5.5	HUMAN	P35579	Myosin-9
12162	dirMS_041712_NAR_50mM_minus2.13830.13830.3	3	9.12	1	1.32E+05		(K)NLKVTA	(K)N L\K V\T A|V/P T L L/K(Y)		147.1	432.9468	1296.825	0.0009	0.7	10	11462.8	5.18	HUMAN	I3L2R6	Thioredoxin domain-containing protein 17
12163	dirMS_041712_NAR_50mM_minus2.15878.15878.3	3	9.12	0	9.69E+04		(K)INLEAAE	(K)I N/L E A/A E L G E/I S D/I H T K(L)		158.72	618.326	1852.965	-0.0016	-0.9	4.4	84268.2	6.32	HUMAN	Q9UHD2	Serine/threonine-protein kinase TBK1
12164	dirMS_041712_NAR_50mM_minus2.7748.7748.3	3	9.12	1	5.68E+04		(R)LGAAPE	(R)L/G\A|A|P E E E S A Y V/A/G E K R(Q)		111.32	592.9614	1776.876	-0.0066	-3.7	4.5	30276.7	5	HUMAN	F2Z2K0	NSFL1 cofactor p47
12165	dirMS_041712_NAR_60mM_minus.10565.10565.3	3	9.12	1	1.37E+05		(R)SATKVT/	(R)S A/T K V\T A/D V/I/N A A E/K(L)		118.73	506.6084	1517.817	-0.0063	-4.2	5.79	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
12166	dirMS_041712_NAR_60mM_minus.16751.16751.3	3	9.12	1	3.90E+05		(R)ARFEELI	(R)A R F E\E\L|N/A/D/L/F R(G)		153.97	494.2594	1480.754	0.0093	6.3	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
12167	dirMS_041712_NAR_60mM_minus.17829.17829.3	3	9.12	1	3.65E+05		(K)NLRDIDI	(K)N L R D I D E|V/S/S/L L R(T)		160.92	510.6099	1529.828	-0.013	-8.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
12168	dirMS_041712_NAR_60mM_minus.5051.5051.3	3	9.12	1	3.90E+04	M277m M:	(K)LGREEP/	(K)L G R E E/P A|m/S\m D A N|G K(I)	m:Oxidized methionine	82.83	546.5777	1605.736	31.9826	-4.4	4.68	99900.1	5.04	HUMAN	B4DZI8	Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b
12169	dirMS_041712_NAR_120mM_plus.10796.10798.3	3	9.12	1	7.48E+04		(K)KYEFGES	(K)K\Y E\F/G|E S\D/L/R(S)		109.63	415.205	1243.595	0.0051	4.1	4.68	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
12170	dirMS_041712_NAR_120mM_plus.4247.4395.3	3	9.12	0	2.42E+06	M46m M4	(R)HQGVm	(R)H Q\G V\m|V/G/m G Q K(D)	m:Oxidized methionine	70.95	401.8588	1171.571	31.9908	0.8	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
12171	dirMS_041712_NAR_20mM_plus.14241.14241.2	2	9.12	0	8.58E+04		(R)VFSGLVS	(R)V F|S/G L/V/S T G L K(V)		170.27	554.3224	1107.641	-0.0033	-3	8.72	96306.4	6.41	HUMAN	P13639	Elongation factor 2
12172	dirMS_041712_NAR_20mM_plus.17708.17708.3	3	9.12	0	1.12E+04		(R)IINEPTA	(R)I I N/E P T A A/A\I|A/Y/G L D R(T)		193.42	563.3055	1687.901	0.0006	0.3	4.37	25598.3	6.45	HUMAN	E7EP11	Heat shock 70 kDa protein 1A/1B
12173	dirMS_041712_NAR_40mM_plus2.15155.15155.3	3	9.12	0	1.16E+05		(R)QVVQGI	(R)Q V\V\Q|G L\L/S/E T Y/L E A H R(I)		155.72	614.9934	1842.971	-0.0052	-2.8	5.4	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
12174	dirMS_041712_NAR_50mM_plus2.16319.16319.3	3	9.12	1	2.53E+04		(K)GADFLV	(K)G A/D F|L/V T/E V E/N\G G S L G S K K(G)		153.82	636.6618	1907.971	-0.0001	0	4.68	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
12175	dirMS_041712_NAR_50mM_plus2.19894.19894.3	3	9.12	1	4.39E+05		(R)LFLDRDI	(R)L F L/D R/D L\M T|L/P I/Q N K(L)		173.45	606.3362	1816.999	-0.0049	-2.7	5.96	18188.9	10.98	HUMAN	K7EKP7	Ferrochelatase, mitochondrial (Fragment)
12176	dirMS_041712_NAR_60mM_plus.10366.10366.2	2	9.12	0	9.30E+05		(R)SSGPYG	(R)S S/G/P Y G/G G/G Q\Y/F A K/P\R(N)		112.17	814.8941	1628.782	-0.0007	-0.4	9.7	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
12177	dirMS_041712_NAR_60mM_plus.18645.18645.3	3	9.12	1	2.30E+05		(K)DANAKL	(K)D A N/A K L S E|L/E/A/A/L Q R(A)		154.87	543.6241	1628.86	-0.0025	-1.5	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
12178	dirMS_041712_NAR_60mM_plus.9182.9182.3	3	9.12	1	2.99E+05		(R)FVKQDC	(R)F V|K Q D/Q\V/C I|A R(L)	C:Carbamidomethylation	106	455.2428	1363.715	-0.0012	-0.9	8.75	53458.1	5.47	HUMAN	H3BR35	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A (Fragment)
12179	dirMS_041712_NAR_120mM_minus.10932.11024.3	3	9.11	0	1.08E+06		(R)AGHPVL	(R)A G H/P V L/Y C S/A R(T)	C:Carbamidomethylation	113.72	410.8753	1230.605	0.0065	5.3	8.8	52871.9	6.2	HUMAN	A8K327	NEU3 protein
12180	dirMS_041712_NAR_120mM_minus.13276.13276.3	3	9.11	2	2.61E+05		(R)AQKDEE	(R)A Q/K/D E/E/K M/E I|Q/E I/Q L K(E)		126.68	654.0058	1960.006	-0.0027	-1.4	4.58	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
12181	dirMS_041712_NAR_20mM_minus.10782.10782.3	3	9.11	0	1.40E+05		(K)VNQIGS	(K)V N Q\I G S V/T E/S/I Q/A/C K(L)	C:Carbamidomethylation	155.38	545.2807	1633.821	0.0062	3.8	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
12182	dirMS_041712_NAR_20mM_minus.13563.13563.2	2	9.11	0	8.44E+04		(R)ETTDTD	(R)E T T D/T/D|T A/D\Q V I/A/S F/K(V)		186.33	871.4073	1741.813	-0.0053	-3.1	3.84	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
12183	dirMS_041712_NAR_30mM_minus2.18598.18598.2	2	9.11	0	3.72E+05		(R)QAQEYE	(R)Q A/Q E/Y/E/A/L\L/N I K(V)		154.87	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
12184	dirMS_041712_NAR_30mM_minus2.19053.19053.2	2	9.11	0	2.56E+05		(R)LTIAILR(	(R)L T|I|A I/L R(H)		159.13	400.2731	799.54	-0.0011	-1.3	9.75	87498	6.43	HUMAN	C9J266	E3 ubiquitin-protein ligase RNF123
12185	dirMS_041712_NAR_50mM_minus2.11728.11728.3	3	9.11	1	1.79E+05		(K)IEVEKPF	(K)I E/V E K/P F/A I/A K E(-)		134.48	458.5927	1373.767	-0.0039	-2.9	5.01	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
12186	dirMS_041712_NAR_50mM_minus2.14672.14672.3	3	9.11	1	8.49E+05		(R)IINEPTA	(R)I I/N\E/P T A A A I A/Y G L D|K R(E)		152.52	606.0022	1815.996	-0.0043	-2.4	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
12187	dirMS_041712_NAR_50mM_minus2.14807.14807.3	3	9.11	0	3.91E+04		(K)IAILTCPF	(K)I A/I/L T C/P F E/P P K/P K(T)	C:Carbamidomethylation	152.75	537.6375	1610.898	0.0005	0.3	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
12188	dirMS_041712_NAR_50mM_minus2.8326.8326.3	3	9.11	0	4.10E+04		(R)DNIQGIT	(R)D N|I/Q G I/T/K P/A I R(R)		116.12	442.5888	1325.754	-0.0017	-1.3	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
12189	dirMS_041712_NAR_60mM_minus.11092.11092.3	3	9.11	0	2.62E+04		(K)LSHETVT	(K)L S H/E T\V|T/I E/L K(N)		121.97	423.9038	1269.705	-0.008	-6.3	5.4	5328.3	9.82	HUMAN	J3QLR7	Small nuclear ribonucleoprotein Sm D1
12190	dirMS_041712_NAR_20mM_plus.10131.10131.2	2	9.11	0	4.14E+04		(K)LVSESSD	(K)L V|S\E|S S D V/L/P K(-)		142.18	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
12191	dirMS_041712_NAR_20mM_plus.10425.10425.2	2	9.11	0	2.32E+05		(R)AQIFAN	(R)A/Q|I/F A/N T V D N A R(I)		145.25	660.3343	1319.67	-0.0089	-6.8	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
12192	dirMS_041712_NAR_20mM_plus.10477.10477.2	2	9.11	0	2.77E+03	M28m	(R)VFQVEY	(R)V F\Q/V E Y/A/m/K(A)	m:Oxidized methionine	144.78	565.7823	1114.56	15.9972	2	5.97	3930.3	4.78	HUMAN	G3V3W4	Proteasome subunit alpha type-3
12193	dirMS_041712_NAR_20mM_plus.10608.10608.2	2	9.11	0	2.04E+05		(K)NAGVEG	(K)N A|G\V|E/G S L/I/V E K(I)		146.07	608.3304	1215.658	-0.0044	-3.6	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
12194	dirMS_041712_NAR_20mM_plus.14622.14622.3	3	9.11	0	3.29E+05	M73m	(R)AVLVDLI	(R)A V/L\V D L E/P G/T m D S V R(S)	m:Oxidized methionine	172.4	539.9421	1601.82	15.9914	-2.2	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
12195	dirMS_041712_NAR_30mM_plus2.16790.16790.2	2	9.11	0	3.06E+05		(K)SNQQLV	(K)S N\Q\Q/L/V/D I/I/E/K(V)		141.15	643.8504	1286.695	-0.0015	-1.2	4.37	22568.6	6.35	HUMAN	B3KQ25	Proteasome activator complex subunit 3
12196	dirMS_041712_NAR_30mM_plus2.8724.8724.2	2	9.11	0	1.81E+05		(R)VGDYGS	(R)V/G/D|Y/G/S L/S G R(E)		99.42	505.7477	1010.49	-0.002	-2	5.8	34552	6.72	HUMAN	Q9UBR2	Cathepsin Z
12197	dirMS_041712_NAR_40mM_plus2.10220.10220.2	2	9.11	0	6.72E+04		(R)EYQELM	(R)E Y/Q/E L/M/N V K(L)		125	577.2823	1153.556	0.0015	1.3	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
12198	dirMS_041712_NAR_40mM_plus2.5911.5911.2	2	9.11	0	1.08E+05		(K)FNYSGS(	(K)F N|Y/S G/S G G R(S)		92.48	472.7171	944.422	0.0049	5.1	8.75	96205.6	9.06	HUMAN	G5E9M5	Interleukin enhancer binding factor 3, 90kDa, isoform CRA_b
12199	dirMS_041712_NAR_50mM_plus2.18127.18127.3	3	9.11	1	6.65E+05		(K)GYPPED	(K)G Y/P/P/E D I F/N L V G K K(V)		164.23	526.2834	1576.837	-0.0013	-0.8	6.07	40763.2	6.29	HUMAN	Q9NR45	Sialic acid synthase
12200	dirMS_041712_NAR_50mM_plus2.19717.19717.3	3	9.11	1	1.81E+05		(R)TSLLTLEI	(R)T S|L/L/T|L E D V K Q/E L I K(L)		172.12	577.3359	1729.995	-0.0014	-0.8	4.68	156316.8	8.61	HUMAN	Q7Z478	ATP-dependent RNA helicase DHX29
12201	dirMS_041712_NAR_60mM_plus.20484.20484.3	3	9.11	1	3.02E+05		(R)AQFEGI\	(R)A Q|F/E/G I V T D/L I R R(T)		167.4	506.6178	1517.843	-0.0046	-3	6.12	18505.2	10.14	HUMAN	H0YBG6	Stress-70 protein, mitochondrial (Fragment)
12202	dirMS_041712_NAR_60mM_plus.8670.8670.3	3	9.11	1	1.51E+06		(K)MQASIE	(K)M/Q|A/S/I E/K G G S L/P K(V)		103.35	449.2449	1345.714	0.0057	4.3	8.35	32745.6	4.64	HUMAN	P06748	Nucleophosmin
12203	dirMS_041712_NAR_120mM_minus.14755.14755.2	2	9.1	0	7.65E+05		(R)DWSHYI	(R)D/W/S/H/Y F/K(I)		135	491.725	982.442	0.001	1	6.74	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18

12204	dirMS_041712_NAR_120mM_minus.17356.17356.4	4	9.1	2	5.34E+05		(K)KDEKTD	(K)K D E K T D T L E D\L|F/P T T/K(I)		149.03	470.992	1880.949	-0.0026	-1.4	4.44	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
12205	dirMS_041712_NAR_30mM_minus2.13830.13830.2	2	9.1	0	3.56E+05		(R)LAGLFN	(R)L/A|G\L|F N E/Q R(K)		128.93	524.2789	1047.558	-0.0076	-7.3	6	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
12206	dirMS_041712_NAR_30mM_minus2.18805.18842.2	2	9.1	0	1.61E+05		(K)GWPLYL	(K)G W|P/L/Y L S T K(N)		157.23	532.7918	1064.578	-0.0012	-1.1	8.59	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
12207	dirMS_041712_NAR_30mM_minus2.18994.18994.2	2	9.1	0	2.28E+05		(K)SYELPD	(K)S Y E|L/P D G Q/V|I T I/G N E R(F)		158.73	895.9492	1790.892	-0.0008	-0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
12208	dirMS_041712_NAR_30mM_minus2.8105.8105.2	2	9.1	0	7.22E+04		(R)FLEETN	(R)F/L/E|E|T/N R(L)		98.53	454.7292	908.447	0.0039	4.3	4.53	28116.6	5.26	HUMAN	A6NE76	Cullin-4B (Fragment)
12209	dirMS_041712_NAR_40mM_minus2.10926.10926.3	3	9.1	1	1.14E+05	M362m	(R)EGSVmL	(R)E G\S V m/L Q|V D V/D/T V K G G L K(L)	m:Oxidized methionine	147.85	630.9989	1874.989	15.993	-1	4.56	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
12210	dirMS_041712_NAR_40mM_minus2.14416.14416.3	3	9.1	1	3.43E+04		(R)LKLPSIP	(R)L K L P S I|P\L\V/P V/S A Q K(R)		169.28	530.6703	1589.999	-0.0025	-1.6	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
12211	dirMS_041712_NAR_50mM_minus2.10779.10779.3	3	9.1	0	1.32E+05		(R)IMLFTN	(R)I M|L/F/T N E D N P H G N D S A/K(A)		129.5	634.9586	1902.865	-0.0038	-2	4.54	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
12212	dirMS_041712_NAR_50mM_minus2.11159.11159.3	3	9.1	1	1.86E+05		(R)DNKQA	(R)D N K Q A\G\V/F/E/P/T I V K(V)		132.05	515.9485	1545.827	0.0038	2.5	6.07	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
12213	dirMS_041712_NAR_50mM_minus2.16404.16404.3	3	9.1	0	5.96E+04	M114m	(R)AGKPVI	(R)A G K\P V I C A|T/Q/m/L E S M I/K(K)	C:Carbamidomethylation m:Oxid	160.87	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
12214	dirMS_041712_NAR_50mM_minus2.16441.16441.3	3	9.1	1	1.60E+05		(K)VVSSVL	(K)V/V|S S V L Q/F G N I S F K K(E)		162	551.6488	1652.937	-0.0052	-3.1	10	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
12215	dirMS_041712_NAR_50mM_minus2.7718.7718.3	3	9.1	0	2.44E+05		(R)LESGMC	(R)L/E|S G/M\Q/N M S I H T K(T)		111.27	492.5712	1475.698	0.0009	0.6	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
12216	dirMS_041712_NAR_50mM_minus2.8302.8302.3	3	9.1	1	8.27E+04	M61m	(K)NQVAm	(K)N Q|V|A/m N P T N/T V/F D A K R(L)	m:Oxidized methionine	114.92	607.968	1805.896	15.9932	-1	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
12217	dirMS_041712_NAR_60mM_minus.14871.14871.3	3	9.1	1	3.80E+05		(R)IKIGDPL	(R)I K I\G D P L|L|E D/T R(M)		142.73	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
12218	dirMS_041712_NAR_60mM_minus.4677.4677.3	3	9.1	1	9.42E+04		(K)AGADEE	(K)A/G/A/D/E E/R A E T A R(L)		77.88	425.8679	1275.592	-0.0032	-2.5	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
12219	dirMS_041712_NAR_120mM_plus.6282.6282.3	3	9.1	1	5.04E+05		(R)ARSDEG	(R)A R S D\E G Q|L|S|P A T R(G)		86.7	463.2395	1387.692	0.0115	8.3	6.12	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
12220	dirMS_041712_NAR_20mM_plus.11062.11062.2	2	9.1	0	6.40E+03	M94m	(R)FSmVV	(R)F S\m/V|V Q/D G I V/K(A)	m:Oxidized methionine	147.97	619.8249	1222.65	15.9925	-1.9	5.84	13010.7	9.97	HUMAN	A6NC19	Peroxiredoxin-5, mitochondrial
12221	dirMS_041712_NAR_20mM_plus.12589.12589.2	2	9.1	0	1.34E+05		(R)GVEICIA	(R)G V/E|I|C I/A T/P G R(L)	C:Carbamidomethylation	159.12	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
12222	dirMS_041712_NAR_30mM_plus2.12761.12960.2	2	9.1	0	3.54E+05		(R)NLGLYV	(R)N/L|G L/Y/V K(T)		120.72	403.7418	806.477	-0.0007	-0.9	8.59	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
12223	dirMS_041712_NAR_30mM_plus2.20222.20222.2	2	9.1	0	1.71E+05		(K)NIEDVIA	(K)N I|E/D/V/I\A Q G/I G K(L)		160.45	628.8445	1256.685	-0.0028	-2.2	4.37	9098.8	4.38	HUMAN	H0YDD8	60S acidic ribosomal protein P2 (Fragment)
12224	dirMS_041712_NAR_50mM_plus2.7612.7612.3	3	9.1	1	3.02E+05		(R)IVEQDT	(R)I/V|E/Q D/T M/P P K G V/R(H)		105.6	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
12225	dirMS_041712_NAR_60mM_plus.17130.17130.3	3	9.1	1	6.27E+06		(K)LKVPEW	(K)L K V/P E/W/V/D T V K(L)		145.87	438.5872	1313.746	0.0007	0.5	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
12226	dirMS_041712_NAR_60mM_plus.21265.21265.3	3	9.1	0	2.23E+05		(R)QARPTY	(R)Q A R P T Y A T/A M/L|Q S L/L K(-)		175.57	597.9953	1791.979	-0.0072	-4	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
12227	dirMS_041712_NAR_60mM_plus.6425.6425.3	3	9.1	1	1.35E+05		(R)SIPAGA	(R)S I/P/A/G A E/P G E K G S A\R(K)		92.35	476.2505	1426.728	0.0085	5.9	5.87	18962.9	9.6	HUMAN	A6NGP5	Hematological and neurological-expressed 1-like protein
12228	dirMS_041712_NAR_60mM_plus.8926.8926.3	3	9.1	1	8.20E+05		(R)SSGGSY	(R)S S|G G/S Y R/D S Y D S Y A T/H N/E(-)		104.85	665.9403	1995.795	0.0112	5.6	4.81	18647.7	9.51	HUMAN	Q14011	Cold-inducible RNA-binding protein
12229	dirMS_041712_NAR_120mM_minus.4865.4865.3	3	9.09	1	5.55E+05		(K)AGADEE	(K)A/G/A/D E E/R A E T A R(L)		77.53	425.8687	1275.592	-0.0008	-0.7	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
12230	dirMS_041712_NAR_30mM_minus2.19885.19994.2	2	9.09	0	1.54E+06		(R)LFFLQV	(R)L/F|F/L Q V K(E)		167.3	447.7757	894.545	-0.0006	-0.7	8.75	71218.8	6.3	HUMAN	A7YIJ8	Radixin
12231	dirMS_041712_NAR_30mM_minus2.7091.7112.2	2	9.09	0	2.75E+05		(R)ASYISSA	(R)A S|Y/I S/S/A/R(L)		93.9	427.7216	854.437	-0.0007	-0.9	8.79	59288.4	7.16	HUMAN	Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)
12232	dirMS_041712_NAR_50mM_minus2.14018.14035.3	3	9.09	1	4.43E+05		(R)LYSILGT	(R)L/Y\S I/L/G T/T L K D/E G K(L)		148.45	513.2863	1537.847	-0.0029	-1.9	6.07	66876.9	6.17	HUMAN	O75083	WD repeat-containing protein 1
12233	dirMS_041712_NAR_50mM_minus2.15041.15041.3	3	9.09	0	4.22E+05		(K)IAILTCP	(K)I/A\I/L T C/P F E/P/P K P K(T)	C:Carbamidomethylation	153.53	537.6375	1610.898	0.0005	0.3	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
12234	dirMS_041712_NAR_50mM_minus2.6130.6130.3	3	9.09	0	4.44E+05	M437m	(R)LESGMC	(R)L E|S G M Q N m S I/H/T K(T)	m:Oxidized methionine	97.77	497.9018	1475.698	15.9927	-1.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
12235	dirMS_041712_NAR_60mM_minus.15379.15379.3	3	9.09	1	2.23E+05		(R)GPIKFN	(R)G P I K F N V|W/D|T/A G Q E K(F)		146.48	563.9575	1689.86	-0.0015	-0.9	6.07	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
12236	dirMS_041712_NAR_60mM_minus.15732.15732.3	3	9.09	1	3.86E+05		(K)KANLQI	(K)K A N L\Q I D Q I|N/T/D L N L E R(S)		148.03	666.6911	1998.061	-0.0027	-1.3	4.56	227783.5	5.5	HUMAN	P35579	Myosin-9
12237	dirMS_041712_NAR_20mM_plus.15906.15907.3	3	9.09	0	2.06E+04	M73m	(R)AILVDLE	(R)A I\L\V D L E/P G T m/D/S V R(S)	m:Oxidized methionine	181.03	544.6139	1615.836	15.9912	-2.3	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
12238	dirMS_041712_NAR_30mM_plus2.21922.21922.3	3	9.09	0	3.43E+05		(R)NSILAQ	(R)N S I L A Q|V/L/D Q/S A/R(A)		170.13	472.2638	1414.765	0.012	8.5	5.84	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
12239	dirMS_041712_NAR_50mM_plus2.10915.10915.3	3	9.09	1	4.68E+05		(R)ALRETL	(R)A L R E T\L|P/A/E/Q D L T T/K(N)		125.08	562.6377	1685.907	-0.0083	-4.9	4.68	26790	6.25	HUMAN	F5GX11	Proteasome subunit alpha type-1
12240	dirMS_041712_NAR_50mM_plus2.13302.13302.3	3	9.09	1	2.89E+05		(K)TSLVAT	(K)T S/L/V/A T/P G I D K L T E K(S)		137.9	524.9717	1572.884	0.0162	10.3	5.73	89370.5	5.69	HUMAN	Q8IV36	Protein HID1
12241	dirMS_041712_NAR_50mM_plus2.13744.13744.3	3	9.09	1	7.51E+05		(K)LIQEIVD	(K)L/I|Q/E I V D K S G/V V R(V)		140.07	485.9552	1455.853	-0.0019	-1.3	6.07	66105.7	7.3	HUMAN	A8MQB8	Fragile X mental retardation protein 1
12242	dirMS_041712_NAR_50mM_plus2.16318.16318.3	3	9.09	1	2.53E+04		(K)GADFLV	(K)G A/D|F/L|V T E V E N G G S L G S K K(G)		153.82	636.6618	1907.971	-0.0001	0	4.68	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
12243	dirMS_041712_NAR_50mM_plus2.7823.7823.3	3	9.09	1	9.96E+04		(K)ELQAAG	(K)E L/Q|A A G K/S/P E D L E R(L)		106.57	514.9321	1542.776	0.0059	3.8	4.41	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
12244	dirMS_041712_NAR_60mM_plus.14488.14488.3	3	9.09	1	9.75E+05		(R)KFNALF	(R)K F N A L F|A|Q/G N Y/S E A A K(V)		132.12	586.9647	1758.881	-0.0014	-0.8	8.5	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
12245	dirMS_041712_NAR_60mM_plus.14832.14832.3	3	9.09	1	4.22E+05		(K)NKDQG	(K)N K\D Q\G T\Y E/D Y/V/E G/L R(V)		134.03	596.2816	1786.824	0.006	3.4	4.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
12246	dirMS_041712_NAR_60mM_plus.17726.17726.3	3	9.09	0	1.41E+05		(R)NHLLPD	(R)N H\L L P D I\V/T/C V/Q/S S R(K)	C:Carbamidomethylation	149.65	580.3035	1738.891	0.0055	3.1	6.74	20940.9	10.04	HUMAN	Q9BSD7	Cancer-related nucleoside-triphosphatase
12247	dirMS_041712_NAR_60mM_plus.20375.20375.3	3	9.09	1	4.21E+05		(K)NAAGAL	(K)N A/A/G/A/L D L L/K/E/L K(N)		166.93	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
12248	dirMS_041712_NAR_60mM_plus.20405.20564.3	3	9.09	1	3.02E+05		(R)AQFEGI	(R)A Q|F/E/G I/V T D L I R/R(T)		167.4	506.6178	1517.843	-0.0046	-3	6.12	18505.2	10.14	HUMAN	H0YBG6	Stress-70 protein, mitochondrial (Fragment)
12249	dirMS_041712_NAR_60mM_plus.6520.6520.3	3	9.09	1	2.57E+05		(R)ATEGM	(R)A/T/E/G M V/V/A D K N C S K(I)	C:Carbamidomethylation	92.68	503.9055	1509.704	-0.0016	-1.1	6.11	15607.8	9.99	HUMAN	B4E0P1	Proteasome (Prosome, macropain) subunit, beta type, 7, isoform CRA_b
12250	dirMS_041712_NAR_120mM_minus.12687.12687.3	3	9.08	0	6.33E+05		(K)TFTAWC	(K)T F|T A/W/C N S H L/R(K)	C:Carbamidomethylation	122.4	464.8871	1392.648	-0.001	-0.7	9.44	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
12251	dirMS_041712_NAR_120mM_minus.17742.17742.3	3	9.08	1	1.85E+05		(R)AGKLDP	(R)A G K\L D|P H/L V L D Q L R(C)		151.48	525.6385	1574.901	-0.0004	-0.2	6.79	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
12252	dirMS_041712_NAR_120mM_minus.7422.7422.3	3	9.08	1	3.19E+05		(K)IYEDGD	(K)I/Y/E/D G/D D D M K R(T)		94.63	452.8645	1356.574	0.0053	3.9	4.03	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
12253	dirMS_041712_NAR_30mM_minus2.10372.10372.2	2	9.08	0	2.81E+05		(R)ETAEAD	(R)E T/A|E/A/D/V|A S L N R(R)		110.08	638.3134	1275.618	0.002	1.6	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
12254	dirMS_041712_NAR_30mM_minus2.7198.7198.2	2	9.08	0	4.38E+05		(K)DAQGQ	(K)D A/Q/G Q/P G L E/R(A)		93.08	535.762	1070.523	-0.0058	-5.4	4.37	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
12255	dirMS_041712_NAR_40mM_minus2.9333.9333.3	3	9.08	1	6.96E+05	M356m	(K)VGEVIV	(K)V/G|E/V/I/V T K D D A m L L K(G)	m:Oxidized methionine	136.93	549.6354	1630.908	15.9832	-7.1	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
12256	dirMS_041712_NAR_50mM_minus2.12109.12109.3	3	9.08	0	9.09E+03		(K)AASAGV	(K)A/A|S A G V/P Y/H G E V/P V S L A R(A)		135.98	594.315	1780.934	-0.0036	-2	6.79	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
12257	dirMS_041712_NAR_50mM_minus2.14478.14478.3	3	9.08	0	4.07E+05		(R)QIFHPE	(R)Q I F H/P E\Q/L/I T/G K(E)		149.77	470.9286	1410.774	-0.0027	-1.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
12258	dirMS_041712_NAR_60mM_minus.15779.15779.3	3	9.08	1	3.93E+05		(R)IFDSEEI	(R)I/F/D S E E I/L/A G Y K R(E)		148.62	514.2713	1540.801	-0.0012	-0.8	4.68	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
12259	dirMS_041712_NAR_60mM_minus.17824.17836.3	3	9.08	1	5.88E+05		(R)KVESLQ	(R)K V E S\L\Q E|E|I/A F L/K(K)		159.98	511.9529	1533.852	-0.0081	-5.3	4.79	49709.6	5.19	HUMAN	B0YJC4	Vimentin
12260	dirMS_041712_NAR_60mM_minus.18637.18637.3	3	9.08	0	2.91E+05		(K)TFLVWV	(K)T F|L V/W V/N E E D/H L R(V)		165.78	553.2818	1657.833	-0.0024	-1.5	4.65	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
12261	dirMS_041712_NAR_60mM_minus.5307.5307.3	3	9.08	0	1.33E+05		(R)AEAEAG	(R)A E|A\E A/G S P R P D/P/R(E)		84.88	451.5562	1352.655	-0.0013	-0.9	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
12262	dirMS_041712_NAR_120mM_plus.10540.10540.2	2	9.08	1	1.86E+06		(R)VKYETE	(R)V/K|Y E/T E L/A M R(Q)		107.78	620.3237	1239.64	-0.0001	0	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
12263	dirMS_041712_NAR_120mM_plus.11518.11518.4	4	9.08	2	5.81E+05		(K)KGEKDI	(K)K\G E K D I P G L T D\T/T V/P R(R)		113.53	432.4918	1726.933	0.012	6.9	6.12	25082	11.29	HUMAN	A2A3R5	40S ribosomal protein S6
12264	dirMS_041712_NAR_120mM_plus.12771.12771.3	3	9.08	1	6.47E+05		(K)LFNLSKE	(K)L/F/N L/S K/E D D/V R(Q)		119.97	445.9007	1335.69	-0.0028	-2.1	4.56	25082	11.29	HUMAN	A2A3R5	40S ribosomal protein S6
12265	dirMS_041712_NAR_120mM_plus.7728.7728.2	2	9.08	1	1.15E+06		(R)AQYDEL	(R)A/Q|Y/D E/L A R\K(N)		93.35	547.2874	1093.564	0.0039	3.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
12266	dirMS_041712_NAR_120mM_plus.8329.8329.4	4	9.08	1	2.27E+05		(K)NKPGPY	(K)N K P G P\Y S S V/P/P/P S A/P/P P K K(S)		97.03	487.0187	1945.054	-0.0012	-0.6	10	73601.9	9.46	HUMAN	Q14978	Nucleolar and coiled-body phosphoprotein 1
12267	dirMS_041712_NAR_120mM_plus.9681.9681.4	4	9.08	2	3.92E+06		(R)VLTVIN	(R)V L T/V/I N/Q/T/Q K E/N L R K(F)		104.23	446.7653	1784.039	0.0005	0.3	9.99	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
12268	dirMS_041712_NAR_20mM_plus.14607.14607.3	3	9.08	0	1.37E+05		(R)LQEAGIL	(R)L Q E\A G I\L/S/A/E E/L Q R(L)		172.1	519.6131	1556.828	-0.0031	-2	4.25	533778	5.74	HUMAN	Q15149	Plectin
12269	dirMS_041712_NAR_20mM_plus.15118.15118.2	2	9.08	0	5.88E+04		(R)EQLAIA	(R)E Q/L|A|I/A E F A R(S)		176.1	574.312	1147.611	0.0061	5.3	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
12270	dirMS_041712_NAR_20mM_plus.15259.15259.2	2	9.08	0	9.43E+04		(K)GVEGLI	(K)G V\E G L/I D/I E N/P N R(V)		176.52	713.3667	1425.733	-0.0071	-5	4.14	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
12271	dirMS_041712_NAR_20mM_plus.18059.18059.2	2	9.08	0	1.29E+05		(R)LFDQAF	(R)L F/D Q/A/F G L/P R(L)		195.58	582.3166	1163.621	0.0052	4.4	5.84	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
12272	dirMS_041712_NAR_60mM_plus.10412.10412.3	3	9.08	1	6.69E+05	M86m	(K)mKEIAE	(K)m K E I|A/E A/Y/L/G/K(T)	m:Oxidized methionine	112.17	423.5533	1252.661	15.9848	-8	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
12273	dirMS_041712_NAR_60mM_plus.11898.11898.3	3	9.08	0	9.79E+05		(K)FYEEVH	(K)F/Y/E/E/V/H/D L E R(K)		119.13	446.2162	1336.617	0.0172	12.9	4.4	18209.2	5.03	HUMAN	A8MXH2	Nucleosome assembly protein 1-like 4 (Fragment)
12274	dirMS_041712_NAR_60mM_plus.14228.14250.3	3	9.08	1	9.08E+05		(K)TTVKDL	(K)T T|V K D L|S E|L/G S V/R(T)		131.28	468.9268	1404.769	-0.0034	-2.4	5.74	533778	5.74	HUMAN	Q15149	Plectin
12275	dirMS_041712_NAR_60mM_plus.15753.16125.3	3	9.08	1	1.62E+06		(R)KSEIEYY	(R)K\S E I\E|Y|Y/A/M L/A K(T)		140.15	482.5882	1445.735	0.0156	10.8	6.14	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
12276	dirMS_041712_NAR_120mM_minus.14187.14187.3	3	9.07	1	6.63E+04		(K)ASLENS	(K)A/S/L/E/N S L R\E V E A R(Y)		131.78	491.9266	1473.766	-0.0003	-0.2	4.79	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
12277	dirMS_041712_NAR_40mM_minus2.12200.12200.3	3	9.07	0	1.48E+05		(K)AAPEAS	(K)A A/P|E/A S S P P A S/P L/Q H L/L P G K(A)		154.52	656.6876	1968.055	-0.0067	-3.4	6.79	84649.8	5.82	HUMAN	Q96TA1	Niban-like protein 1
12278	dirMS_041712_NAR_40mM_minus2.8688.8688.3	3	9.07	2	5.46E+03		(K)VEVDLD	(K)V E/V/D/L D Q T Q R E R/K(M)		133.38	539.2818	1615.84	-0.009	-5.6	4.78	107120	9.75	HUMAN	Q7Z7M9	Polypeptide N-acetylgalactosaminyltransferase 5
12279	dirMS_041712_NAR_50mM_minus2.14286.14286.3	3	9.07	0	4.31E+05		(R)QIFHPE	(R)Q I/F/H/P E Q/L/I/T G K(E)		149.72	470.9286	1410.774	-0.0027	-1.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
12280	dirMS_041712_NAR_50mM_minus2.17313.17313.3	3	9.07	0	9.69E+04		(R)IDILDSA	(R)I/D/I/L/D S A L L R P G R(I)		166.83	480.2803	1438.838	-0.0113	-7.8	5.96	44954.5	8.44	HUMAN	A8K3Z3	26S protease regulatory subunit 8
12281	dirMS_041712_NAR_50mM_minus2.7036.7036.3	3	9.07	1	7.83E+05	M2747m	(K)TLQEVT	(K)T L/Q/E/V/T E m D S V K R(Y)	m:Oxidized methionine	106.27	517.9271	1535.773	15.9934	-1	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
12282	dirMS_041712_NAR_50mM_minus2.8571.8571.3	3	9.07	1	4.24E+05	M244m	(K)ILIANTG	(K)I L/I/A N T G/m D/T D K I K(I)	m:Oxidized methionine	117.38	516.9426	1532.835	15.978	-10.9	5.96	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
12283	dirMS_041712_NAR_60mM_minus.11736.11736.3	3	9.07	1	4.61E+05	M232m	(R)MSmKE	(R)M S m K E V D\E\Q|M\L/N/V|Q/N K(N)	m:Oxidized methionine	125.58	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
12284	dirMS_041712_NAR_60mM_minus.13969.14070.3	3	9.07	0	3.65E+05		(K)QLPLVK	(K)Q L/P L/V/K/P Y/L/R(S)		138.22	409.59	1226.762	-0.0065	-5.3	9.99	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
12285	dirMS_041712_NAR_60mM_minus.8095.8095.3	3	9.07	0	1.29E+05		(K)EAYPDH	(K)E A/Y/P/D/H T Q F E/K(N)		105.03	455.5427	1364.612	0.0018	1.3	4.65	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1
12286	dirMS_041712_NAR_120mM_plus.18722.18722.4	4	9.07	1	4.05E+05		(R)SKDVVE	(R)S K D V V E/P L/L R P Q W Y V R(C)		150.65	497.0291	1985.097	-0.0021	-1.1	8.31	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
12287	dirMS_041712_NAR_120mM_plus.18965.18965.4	4	9.07	1	1.35E+06		(K)FQIPPN	(K)F Q\I/P P N/A E/L K Y E L H L K(S)		152.7	485.7703	1940.064	-0.0046	-2.4	6.75	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
12288	dirMS_041712_NAR_20mM_plus.18243.18273.2	2	9.07	0	1.14E+04		(K)AIDLFTD	(K)A I|D|L/F T D A I K(L)		197.1	553.8073	1106.609	-0.0019	-1.7	4.21	18141.9	4.7	HUMAN	F6VDH7	Hsc70-interacting protein (Fragment)
12289	dirMS_041712_NAR_20mM_plus.6455.6455.2	2	9.07	0	2.02E+05	M216m	(R)DLmAC	(R)D L/m|A C A Q/T/G S/G K(T)	C:Carbamidomethylation m:Oxid	107.72	627.776	1238.55	15.9943	-0.5	5.84	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
12290	dirMS_041712_NAR_30mM_plus2.10493.10493.2	2	9.07	0	1.81E+05		(R)DGYDYD	(R)D G/Y|D/Y D/G Y R(L)		108.42	562.2211	1123.433	0.0022	2	3.93	28442.8	10.22	HUMAN	J3KTL2	Serine/arginine-rich-splicing factor 1
12291	dirMS_041712_NAR_30mM_plus2.15993.15993.2	2	9.07	0	2.62E+04		(K)FLMAN	(K)F/L|M A/N G Q L\V/K(M)		136.13	560.8126	1120.618	-0.0004	-0.4	8.75	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
12292	dirMS_041712_NAR_30mM_plus2.22037.22037.2	2	9.07	0	1.03E+05		(K)NFYFLE	(K)N F|Y|F/L\E M N T R(L)		170.5	667.8205	1334.62	0.0139	10.4	6	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
12293	dirMS_041712_NAR_30mM_plus2.23511.23511.2	2	9.07	0	1.80E+05		(R)IAIYELLF	(R)I/A|I/Y/E L\L F K(E)		190.25	555.3331	1109.661	-0.0016	-1.4	6	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
12294	dirMS_041712_NAR_30mM_plus2.6848.6869.2	2	9.07	0	2.27E+05		(R)NMGYV	(R)N/M|G|Y|V/Q\Q R(R)		90.27	498.2399	995.473	-0.0002	-0.2	8.75	28637.7	6.66	HUMAN	B4DDM6	Mitotic checkpoint protein BUB3
12295	dirMS_041712_NAR_40mM_plus2.17174.17174.3	3	9.07	0	7.36E+05		(R)IHFPLAT	(R)I H F\P L A T\Y/A/P/V I S A E K(A)		168.3	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
12296	dirMS_041712_NAR_40mM_plus2.17873.17873.3	3	9.07	0	1.66E+05		(K)LAKPLSS	(K)L A K\P L S S\L/T/P L/I/M A A K(E)		171.7	552.0052	1653.997	0.0039	2.3	10	24711.4	5.19	HUMAN	H7C1X3	PAK-2p34 (Fragment)
12297	dirMS_041712_NAR_50mM_plus2.18778.18778.3	3	9.07	0	3.83E+05		(R)IHFPLAT	(R)I H F P L A T Y\A/P V I S A E K(A)		166.62	586.3252	1756.963	-0.0022	-1.2	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
12298	dirMS_041712_NAR_50mM_plus2.19853.19853.3	3	9.07	0	5.26E+04		(K)GLCLLE	(K)G L/C|L/L/E Q I D S F K P P Q R(S)	C:Carbamidomethylation	172.9	634.3344	1900.995	-0.0063	-3.3	6.07	45536.8	9.03	HUMAN	B7Z1K2	HBS1-like protein
12299	dirMS_041712_NAR_60mM_plus.16554.16554.3	3	9.07	1	6.26E+05		(K)AAVEW	(K)A A|V|E/W F D/G K D F Q G S K(L)		143.05	562.2762	1684.797	0.0175	10.4	4.56	65213.5	9.57	HUMAN	B0QYK0	Ewing sarcoma breakpoint region 1
12300	dirMS_041712_NAR_120mM_minus.14275.14275.4	4	9.06	2	6.24E+05		(K)MEIATK	(K)M E|I\A T/K D/P L/N P I K/Q D/V K(K)		131.67	485.7686	1940.052	0.0004	0.2	5.88	33115.9	5.54	HUMAN	Q15181	Inorganic pyrophosphatase
12301	dirMS_041712_NAR_30mM_minus2.14791.14830.2	2	9.06	0	3.67E+04		(K)DVNAAL	(K)D V|N|A|A/I/A A I K(T)		132.78	493.2881	985.568	0.0013	1.3	5.84	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
12302	dirMS_041712_NAR_30mM_minus2.7890.8350.2	2	9.06	0	1.73E+06		(K)LLEAETC	(K)L/L|E|A|E/T Q/R(Q)		98.72	480.2603	959.516	-0.0023	-2.4	4.53	266161	5.68	HUMAN	E9PPU0	Epiplakin
12303	dirMS_041712_NAR_50mM_minus2.13145.13145.3	3	9.06	1	2.73E+04		(K)VVSSSIV	(K)V V|S/S S I/V D K Y I G E S A R(L)		142.6	570.6413	1709.907	0.0025	1.5	6.04	29938.9	6.07	HUMAN	H0YJC0	26S protease regulatory subunit 10B (Fragment)
12304	dirMS_041712_NAR_50mM_minus2.15496.15496.3	3	9.06	1	2.25E+04		(K)CEFQDA	(K)C E/F Q\D\A\Y V/L L/S E/K K(I)	C:Carbamidomethylation	156.05	577.2917	1729.847	0.014	8.1	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
12305	dirMS_041712_NAR_50mM_minus2.15511.15546.3	3	9.06	1	8.24E+04		(K)FLVYVA	(K)F/L|V Y V A N F D E K D|P R(T)		156.65	571.6268	1712.864	0.0016	0.9	4.56	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
12306	dirMS_041712_NAR_50mM_minus2.7028.7028.3	3	9.06	1	2.04E+05		(K)GAVAED	(K)G A V|A|E/D G D E L/R T E P E/A K(K)		106.92	596.2904	1786.845	0.0113	6.3	4.08	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
12307	dirMS_041712_NAR_50mM_minus2.8609.8609.3	3	9.06	1	2.14E+05		(R)VAIEPG	(R)V A\I\E/P G A P R E N D E/F C/K(M)	C:Carbamidomethylation	117.37	611.2923	1831.864	-0.002	-1.1	4.41	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
12308	dirMS_041712_NAR_60mM_minus.12156.12156.3	3	9.06	1	3.77E+05		(K)AAAGK	(K)A A|A G K A E L\E/L E/L/G R(I)		127.53	476.5974	1427.785	-0.0076	-5.3	4.79	533778	5.74	HUMAN	Q15149	Plectin
12309	dirMS_041712_NAR_60mM_minus.13898.13898.3	3	9.06	1	1.90E+05		(R)VEVTEF	(R)V/E|V/T/E/F E D I K S G Y R(I)		137.38	557.9508	1671.822	0.0154	9.2	4.41	30992.3	4.14	HUMAN	B2REB8	Protein SET
12310	dirMS_041712_NAR_60mM_minus.14896.14896.3	3	9.06	1	1.25E+05		(K)ESLKELS	(K)E S L K E L S L A G N\E/L/G D/E G A R(L)		143.02	663.341	1987.993	0.0154	7.7	4.25	31761.7	6.01	HUMAN	H0YCR7	Ribonuclease inhibitor (Fragment)
12311	dirMS_041712_NAR_60mM_minus.15291.15319.3	3	9.06	1	4.91E+04		(K)YMACCL	(K)Y/M|A/C/C L L Y R G D V\V/P K(E)	C:Carbamidomethylation	145.53	615.6321	1844.886	-0.0038	-2.1	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
12312	dirMS_041712_NAR_60mM_minus.18566.18566.3	3	9.06	1	1.31E+04		(R)VYEFLD	(R)V Y|E\F/L D K L D/V V R(S)		164.77	499.2763	1495.815	-0.0012	-0.8	4.56	41296.9	9.52	HUMAN	B4DT72	26S proteasome non-ATPase regulatory subunit 3

12313	dirMS_041712_NAR_20mM_plus.14707.14707.2	2	9.06	0	1.85E+05	M256m	(R)SLDmDS	(R)S L|D/m\D S I/I A E/V/K(A)	m:Oxidized methionine	172.47	668.8371	1320.671	15.9954	0.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
12314	dirMS_041712_NAR_20mM_plus.15149.15149.2	2	9.06	0	2.17E+05		(K)GLAITFV	(K)G L A\I/T|F\V|S D E N D A K(I)		175.3	740.3693	1479.733	-0.0012	-0.8	4.03	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
12315	dirMS_041712_NAR_20mM_plus.16207.16207.3	3	9.06	0	1.32E+05		(R)LLDAQL	(R)L/L D A Q L\A T/G/G\I/V D/P R(L)		183.53	513.6218	1538.854	-0.0028	-1.8	4.21	533778	5.74	HUMAN	Q15149	Plectin
12316	dirMS_041712_NAR_20mM_plus.18136.18136.3	3	9.06	0	1.36E+05		(R)AILVDLE	(R)A I\L\V D L E/P G/T M D S V R(S)		196.55	539.2833	1615.836	-0.0006	-0.4	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
12317	dirMS_041712_NAR_30mM_plus2.20645.20645.2	2	9.06	0	1.22E+05		(K)SVVTSIF	(K)S V|V/T/S I F/G V K(N)		162.82	518.799	1036.604	-0.013	-12.5	8.47	132902.3	5.82	HUMAN	J3KR24	Isoleucine--tRNA ligase, cytoplasmic
12318	dirMS_041712_NAR_30mM_plus2.20723.20723.2	2	9.06	0	1.27E+05		(K)SVVTSIF	(K)S V|V/T/S I/F/G V K(N)		162.85	518.799	1036.604	-0.013	-12.5	8.47	132902.3	5.82	HUMAN	J3KR24	Isoleucine--tRNA ligase, cytoplasmic
12319	dirMS_041712_NAR_30mM_plus2.6407.6407.2	2	9.06	0	2.46E+05		(R)SPDNPM	(R)S/P|D/N|P M N Q R(A)		88.32	529.7357	1058.468	-0.0042	-4	5.55	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
12320	dirMS_041712_NAR_40mM_plus2.7178.7178.2	2	9.06	0	2.67E+04		(K)IAVAAQ	(K)I A|V|A|A/Q N C/Y K(V)	C:Carbamidomethylation	102.12	569.2912	1137.572	0.003	2.7	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
12321	dirMS_041712_NAR_40mM_plus2.7734.7734.2	2	9.06	0	5.58E+04		(R)VIGSGC	(R)V/I|G/S/G C N L D S/A R(F)	C:Carbamidomethylation	105.37	624.8021	1248.6	-0.0032	-2.6	5.81	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
12322	dirMS_041712_NAR_50mM_plus2.11928.11928.3	3	9.06	1	4.35E+05		(K)QIDLSTV	(K)Q I/D/L/S\T V/D L K\K(L)		130.47	420.5781	1259.72	-0.0008	-0.6	5.96	21156.2	9.41	HUMAN	P55145	Mesencephalic astrocyte-derived neurotrophic factor
12323	dirMS_041712_NAR_50mM_plus2.7803.7803.3	3	9.06	0	8.07E+04		(R)ETPHSP	(R)E T/P H S\P G V/E/D/A P I/A K(V)		106.83	516.6001	1547.77	0.0157	10.2	4.65	67446.5	5.63	HUMAN	F8VQE1	LIM domain and actin-binding protein 1
12324	dirMS_041712_NAR_60mM_plus.18765.18765.3	3	9.06	1	1.60E+05		(R)IRLEETLI	(R)I R L E E\T/L/E Q L A/K(Q)		155.77	481.6118	1442.821	-0.0005	-0.3	4.79	90274.8	6.92	HUMAN	P22059	Oxysterol-binding protein 1
12325	dirMS_041712_NAR_120mM_minus.13536.13536.4	4	9.05	1	7.85E+05		(K)SVHSSVI	(K)S V H S\S V/P/L/L N S K D/P I D R(I)		127.8	466.7525	1863.992	-0.0041	-2.2	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
12326	dirMS_041712_NAR_30mM_minus2.10207.10223.2	2	9.05	0	6.17E+05		(R)AEGAIA	(R)A E|G\A|I/A G F/R(D)		109.75	446.2394	891.468	0.0032	3.6	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
12327	dirMS_041712_NAR_30mM_minus2.14332.14332.2	2	9.05	0	2.40E+05		(K)CCSGAII	(K)C/C|S/G A/I I\V L T/K(S)	C:Carbamidomethylation	131.97	611.3188	1221.633	-0.0027	-2.2	8.75	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
12328	dirMS_041712_NAR_40mM_minus2.15244.15244.3	3	9.05	0	7.36E+05		(K)ALIEVLQ	(K)A L|I/E/V\L/Q/P L I A E H Q A R(R)		175.33	601.0146	1801.033	-0.0038	-2.1	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
12329	dirMS_041712_NAR_50mM_minus2.14457.14457.3	3	9.05	0	3.46E+05		(K)LHIIEVG	(K)L H I\I E V\G T|P/P T G N Q P F/P K(K)		150.05	649.0215	1945.054	-0.0042	-2.2	6.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
12330	dirMS_041712_NAR_50mM_minus2.6704.6704.3	3	9.05	1	2.52E+05		(R)ASVDTK	(R)A/S/V/D T K E/A E G A|P Q V E A G K(R)		104.8	596.2904	1786.882	-0.0251	-14	4.41	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
12331	dirMS_041712_NAR_50mM_minus2.9289.9289.3	3	9.05	0	1.99E+05		(K)VGQEIE	(K)V/G/Q|E I E/V R P G I V S K(D)		120.43	504.2902	1510.859	-0.0027	-1.8	6.11	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
12332	dirMS_041712_NAR_60mM_minus.12571.12571.3	3	9.05	1	1.30E+04		(K)LSAEKVE	(K)L/S\A E\K V/E I|A T/L T R(E)		130.48	477.6112	1430.821	-0.0023	-1.6	6.14	26661.1	7.81	HUMAN	H0YL69	Proteasome subunit alpha type (Fragment)
12333	dirMS_041712_NAR_60mM_minus.15207.15207.3	3	9.05	1	3.39E+05		(K)AKLEQL	(K)A K L E Q|L\F/Q/D E|V A/K(A)		144.37	506.9421	1518.816	-0.0045	-3	4.68	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
12334	dirMS_041712_NAR_60mM_minus.17127.17127.3	3	9.05	1	4.89E+04		(R)STVRDID	(R)S T V R D I D|P Q|N\D L/T/F L R(I)		155.6	630.6628	1889.972	0.0023	1.2	4.43	16537.8	6.59	HUMAN	B1AKR6	Dynein light chain roadblock-type 1
12335	dirMS_041712_NAR_120mM_plus.10232.10232.3	3	9.05	0	1.24E+05		(R)IHDPQLI	(R)I H D\P Q|L|L T E/R(A)		106.38	407.8899	1221.659	-0.0035	-2.8	5.32	21721.5	5.37	HUMAN	H7BZ35	Aspartate--tRNA ligase, cytoplasmic (Fragment)
12336	dirMS_041712_NAR_120mM_plus.4807.4807.3	3	9.05	1	3.66E+05		(R)LRAETE	(R)L R A E T E|Q|G/E/Q/Q R(Q)		76.6	482.2449	1444.714	0.0063	4.3	4.79	533778	5.74	HUMAN	Q15149	Plectin
12337	dirMS_041712_NAR_120mM_plus.8498.8498.2	2	9.05	1	1.39E+05		(K)SGKYVL	(K)S/G/K/Y V/L|G Y/K(Q)		97.87	507.7834	1014.562	-0.0023	-2.3	9.52	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
12338	dirMS_041712_NAR_120mM_plus.9617.9617.3	3	9.05	0	2.25E+05		(K)SYCAEIA	(K)S Y/C/A E/I A H N V S/S K(N)	C:Carbamidomethylation	103.95	489.236	1465.674	0.0194	13.3	6.47	15730.4	11.67	HUMAN	D3YTB1	60S ribosomal protein L32 (Fragment)
12339	dirMS_041712_NAR_20mM_plus.12347.12347.2	2	9.05	0	2.26E+05		(K)LLQLVE	(K)L L/Q|L/V\E D R(G)		158.35	493.2863	985.568	-0.0023	-2.4	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
12340	dirMS_041712_NAR_20mM_plus.12352.12352.2	2	9.05	0	6.99E+04		(R)DLAPIGI	(R)D L|A/P/I G I R(V)		158.1	427.7587	854.509	0.0007	0.8	5.84	27150.8	7.95	HUMAN	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2
12341	dirMS_041712_NAR_20mM_plus.17034.17034.2	2	9.05	0	9.54E+04		(R)AIVAIEN	(R)A I V/A\I|E|N/P/A D V/S V I S S R(N)		188.95	870.9764	1740.949	-0.0035	-2	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
12342	dirMS_041712_NAR_20mM_plus.18122.18122.2	2	9.05	0	1.70E+05		(R)LTGQLFI	(R)L T\G Q|L|F/L G/G S I V K(G)		197.02	666.8962	1332.789	-0.0034	-2.6	8.75	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
12343	dirMS_041712_NAR_20mM_plus.8141.8141.2	2	9.05	0	3.71E+03		(R)GLANPE	(R)G L A N/P E/P A/P E P K(V)		126.05	610.3183	1219.632	-0.0024	-2	4.53	54333.1	6.51	HUMAN	H0Y5S1	Protein transport protein Sec16A (Fragment)
12344	dirMS_041712_NAR_30mM_plus2.11703.11703.2	2	9.05	0	9.40E+05		(K)YGDGIQ	(K)Y/G|D|G I/Q/L/T R(S)		114.05	511.766	1022.527	-0.0018	-1.8	5.83	334221.3	6.44	HUMAN	P15924	Desmoplakin
12345	dirMS_041712_NAR_30mM_plus2.16456.16456.3	3	9.05	0	4.35E+05		(K)LLDLVQ	(K)L L D L\V Q|Q/S C N/Y K(Q)	C:Carbamidomethylation	139.05	494.2566	1480.746	0.0088	5.9	5.83	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
12346	dirMS_041712_NAR_40mM_plus2.14161.14161.3	3	9.05	0	1.15E+05		(R)LVLEVA	(R)L V/L/E/V A Q/H L/G E S T V R(T)		149.32	550.9762	1650.917	-0.0033	-2	5.4	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
12347	dirMS_041712_NAR_40mM_plus2.9144.9144.2	2	9.05	0	9.56E+04		(R)LSIYEAR	(R)L/S/I/Y/E A R(C)		116.12	426.2316	851.462	-0.0062	-7.3	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
12348	dirMS_041712_NAR_50mM_plus2.15047.15047.3	3	9.05	1	4.77E+05		(R)LSQELEY	(R)L/S|Q/E/L E Y L/T E D V K/R(L)		147	574.9669	1722.891	-0.0047	-2.7	4.41	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
12349	dirMS_041712_NAR_50mM_plus2.15474.15474.3	3	9.05	1	9.88E+05		(R)KVPGVT	(R)K\V P G V T A I E|L/D/E/D T/G T F R(I)		149.83	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
12350	dirMS_041712_NAR_50mM_plus2.18759.18759.3	3	9.05	0	1.81E+05		(K)ASVITQ	(K)A S|V/I/T/Q V F H V|P L E E R(K)		166.42	575.6533	1724.933	0.0124	7.2	5.4	24511.6	6.62	HUMAN	C9J5E5	Vigilin (Fragment)
12351	dirMS_041712_NAR_50mM_plus2.19176.19177.3	3	9.05	1	4.00E+05		(K)GVPTGF	(K)G V/P/T/G F/I L P I\R D/I|R(A)		169.6	518.6453	1553.916	0.0051	3.3	9.6	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
12352	dirMS_041712_NAR_50mM_plus2.8314.8314.3	3	9.05	0	1.40E+05		(R)IYDLNKF	(R)I/Y/D|L N K/P E A E/P K(E)		110.27	472.917	1416.737	-0.0005	-0.3	4.68	28733.7	4.82	HUMAN	B0AZV0	Serine-threonine kinase receptor-associated protein
12353	dirMS_041712_NAR_50mM_plus2.8681.8681.3	3	9.05	1	9.99E+04		(R)SCMLTG	(R)S C|M/L/T G T/P E S V Q S A K R(L)	C:Carbamidomethylation	112.52	584.6157	1751.842	-0.0089	-5.1	8.46	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
12354	dirMS_041712_NAR_120mM_minus.8243.8243.3	3	9.04	1	1.08E+06	N1313n	(K)RAAVGC	(K)R A|A/V G\Q E S P/G G L E A G n|A\K(A)	n:N-acetylglucosamine (N)	99.27	638.9836	1711.872	203.0641	-8	6.14	152367.9	8.58	HUMAN	Q29RF7	Sister chromatid cohesion protein PDS5 homolog A
12355	dirMS_041712_NAR_120mM_minus.9389.9389.3	3	9.04	0	1.64E+06		(K)EFHLNES	(K)E F H\L N\E|S/G D/P/S S K(S)		106.15	482.8881	1446.65	0.0002	0.1	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
12356	dirMS_041712_NAR_20mM_minus.9473.9473.2	2	9.04	0	1.29E+05	M61m	(K)NQVAm	(K)N Q|V A m/N/P T N/T V F D/A/K(R)	m:Oxidized methionine	145.03	833.398	1649.795	15.9935	-0.8	5.84	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
12357	dirMS_041712_NAR_30mM_minus2.19566.19566.2	2	9.04	0	4.70E+05		(R)ASLSLW	(R)A S L/S\L/W Q/A/M/E/K(G)		162.73	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
12358	dirMS_041712_NAR_50mM_minus2.10659.10659.3	3	9.04	1	3.29E+05		(K)NQVAM	(K)N\Q/V/A/M/N P T N T V/F D/A/K R(L)		128.83	602.6379	1805.896	0.0029	1.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
12359	dirMS_041712_NAR_50mM_minus2.14902.14902.3	3	9.04	1	1.53E+05		(R)LELGLGF	(R)L E/L/G L G R E R P A/K(A)		152.9	446.931	1338.785	-0.0068	-5.1	8.75	56025.3	10.24	HUMAN	G5E9N1	MON1 homolog A (Yeast), isoform CRA_a
12360	dirMS_041712_NAR_50mM_minus2.16955.16955.3	3	9.04	0	1.02E+05		(K)LILPHVD	(K)L I/L/P H V/D/I Q L K(Y)		164.9	430.2702	1288.799	-0.0027	-2.1	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
12361	dirMS_041712_NAR_60mM_minus.17241.17241.3	3	9.04	1	3.68E+05		(R)KAPSDL	(R)K A P S D\L|Y/Q I/I/L K(A)		156.28	463.6095	1388.815	-0.0008	-0.6	8.5	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
12362	dirMS_041712_NAR_120mM_plus.13415.13415.4	4	9.04	1	1.27E+06		(K)DKFNEC	(K)D K F N E/C G H/V\L/Y/A D/I K(M)	C:Carbamidomethylation	123.87	452.9713	1808.864	-0.0002	-0.1	5.38	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
12363	dirMS_041712_NAR_120mM_plus.14789.14789.4	4	9.04	2	1.65E+06		(R)YLYTLVI	(R)Y L|Y T\L/V/I/T D K E K A E/K(L)		131.07	454.2533	1813.995	-0.0032	-1.8	6.18	7621.9	10.1	HUMAN	J3KT73	60S ribosomal protein L38
12364	dirMS_041712_NAR_120mM_plus.15745.15745.3	3	9.04	0	2.52E+05		(R)HTMMF	(R)H T\M\M F|S A T/F/P K(E)		136.05	433.2091	1297.607	0.006	4.6	8.76	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
12365	dirMS_041712_NAR_120mM_plus.17179.17179.4	4	9.04	2	1.57E+06		(R)GFCFITF	(R)G F\C F I T/F K E E E/P V K K(I)	C:Carbamidomethylation	142.82	465.4906	1858.941	-0.0002	-0.1	6.23	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
12366	dirMS_041712_NAR_20mM_plus.10939.10939.2	2	9.04	0	1.17E+05		(K)EITALAP	(K)E/I|T A\L/A P S/T M K(I)		148.15	581.3129	1161.618	0.0001	0.1	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
12367	dirMS_041712_NAR_20mM_plus.17932.17932.2	2	9.04	0	7.99E+04		(K)VNIIPIIA	(K)V/N I/I/P I I A K(A)		194.77	490.8283	980.65	-0.001	-1	8.72	51212	5.84	HUMAN	A6NFQ9	Septin-8
12368	dirMS_041712_NAR_20mM_plus.18073.18073.2	2	9.04	0	9.96E+04		(K)VDFPQD	(K)V D/F/P/Q/D Q L T A\L\T G R(I)		195.73	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
12369	dirMS_041712_NAR_30mM_plus2.11222.11222.2	2	9.04	0	6.41E+05		(R)QVPFNE	(R)Q\V/P/F N/E V/R(L)		111.43	494.7669	988.521	0.0055	5.5	6	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
12370	dirMS_041712_NAR_30mM_plus2.11321.11321.2	2	9.04	0	4.30E+05		(K)TTDGYLI	(K)T\T|D/G Y/L/L R(L)		112.62	469.75	938.494	-0.0014	-1.5	5.5	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
12371	dirMS_041712_NAR_30mM_plus2.17945.17945.2	2	9.04	0	3.97E+05		(R)QDVYDL	(R)Q D/V/Y D/L/L/K(T)		147.17	497.2641	993.525	-0.0042	-4.2	4.21	106861.4	5.24	HUMAN	Q99460	26S proteasome non-ATPase regulatory subunit 1
12372	dirMS_041712_NAR_30mM_plus2.22216.22216.2	2	9.04	0	3.61E+05		(R)VGNLGL	(R)V G/N/L\G L/A/T S F/F N E R(N)		172.77	762.8926	1524.781	-0.0026	-1.7	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
12373	dirMS_041712_NAR_30mM_plus2.4893.4893.2	2	9.04	0	1.89E+05		(K)NCSETQ	(K)N C|S\E/T\Q/Y E S/K(V)	C:Carbamidomethylation	76.98	623.256	1245.505	-0.0005	-0.4	4.53	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
12374	dirMS_041712_NAR_30mM_plus2.5757.5757.2	2	9.04	0	1.83E+05	M57m	(K)EmGTPD	(K)E m/G T/P D/V/R(I)	m:Oxidized methionine	84.58	460.7158	904.419	16.005	11	4.37	15175.4	10.46	HUMAN	B7Z4C8	60S ribosomal protein L31
12375	dirMS_041712_NAR_40mM_plus2.12299.12299.3	3	9.04	0	3.63E+04		(R)VLTEDE	(R)V L/T E D E M/G H P E I G/D/A I A R(L)		138.75	651.6493	1952.938	-0.0049	-2.5	4.17	40874	5.06	HUMAN	E9PCI9	Farnesyl pyrophosphate synthase
12376	dirMS_041712_NAR_40mM_plus2.16100.16101.2	2	9.04	0	1.43E+05		(R)YLTVAA	(R)Y L|T/V|A/A V F R(G)		162	520.2997	1039.593	-0.0014	-1.3	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
12377	dirMS_041712_NAR_50mM_plus2.11582.11582.3	3	9.04	1	5.26E+05		(K)LIPDSIGI	(K)L I|P D S I/G/K D/I E K(A)		128.77	443.2514	1327.747	-0.0071	-5.4	4.56	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
12378	dirMS_041712_NAR_50mM_plus2.13355.13355.3	3	9.04	0	4.70E+05		(K)QLTEED	(K)Q L/T/E/E D G V/H S V/I E E N I K(C)		138.32	647.3311	1939.961	0.018	9.3	4.25	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
12379	dirMS_041712_NAR_50mM_plus2.14835.14835.3	3	9.04	1	3.12E+04		(R)ARLGGII	(R)A R L G G I P\V/G\V|V|A/V E T R(T)		147.18	531.9842	1593.944	-0.0055	-3.4	9.64	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
12380	dirMS_041712_NAR_60mM_plus.19147.19147.3	3	9.04	0	5.07E+03		(R)HNIAYFI	(R)H N I A Y\F|P Q|I/V S V A A\R(M)		158.1	562.6339	1685.912	-0.0251	-14.9	8.75	19693.7	9.29	HUMAN	K7EKW4	Isochorismatase domain-containing protein 2, mitochondrial (Fragment)
12381	dirMS_041712_NAR_60mM_plus.19545.19545.3	3	9.04	1	4.98E+05		(R)TRIEGLL	(R)T R I E\G L|L A|A/F/P K(L)		160.15	439.262	1315.773	-0.0018	-1.4	8.41	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
12382	dirMS_041712_NAR_60mM_plus.20505.20505.3	3	9.04	1	3.02E+05		(R)AQFEGI	(R)A Q|F/E/G I V T D L I R R(T)		167.4	506.6178	1517.843	-0.0046	-3	6.12	18505.2	10.14	HUMAN	H0YBG6	Stress-70 protein, mitochondrial (Fragment)
12383	dirMS_041712_NAR_120mM_minus.20836.20836.4	4	9.03	1	5.83E+05		(R)SLHDAL	(R)S L H D A L\C|V/L/A Q T V K/D S/R(T)	C:Carbamidomethylation	173.1	479.0049	1912.991	0.0068	3.6	6.47	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
12384	dirMS_041712_NAR_30mM_minus2.12845.12845.2	2	9.03	0	5.66E+05		(R)VNFAMI	(R)V/N|F/A\M N V/G K(A)		124.17	490.2513	979.503	-0.0076	-7.8	8.72	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
12385	dirMS_041712_NAR_30mM_minus2.17135.17135.2	2	9.03	0	1.15E+04		(K)VIVPNM	(K)V I|V/P/N M E F R(A)		147.4	552.7932	1104.587	-0.0079	-7.2	5.97	86098.8	5.31	HUMAN	B4DUC5	Exportin-2
12386	dirMS_041712_NAR_50mM_minus2.16040.16040.3	3	9.03	1	1.21E+05		(R)NTISLLV	(R)N/T I/S L/L\V A G/L K K(E)		159.28	419.5997	1256.794	-0.0091	-7.2	10	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
12387	dirMS_041712_NAR_60mM_minus.14055.14055.3	3	9.03	1	3.79E+05		(R)SLIANLA	(R)S L|I/A N L/A/A/A N C Y K K(E)	C:Carbamidomethylation	138.5	512.9419	1536.82	-0.0091	-5.9	9.7	36978.6	6.33	HUMAN	B7Z800	Adenosine kinase
12388	dirMS_041712_NAR_60mM_minus.17861.17861.3	3	9.03	0	1.37E+05		(R)LFGHSS	(R)L F G H S S T S A\L/S/A I/L R(S)		160.07	520.6207	1559.854	-0.0065	-4.1	9.75	376926.5	4.99	HUMAN	H0Y5W0	E3 ubiquitin-protein ligase HUWE1 (Fragment)
12389	dirMS_041712_NAR_60mM_minus.18599.18599.3	3	9.03	0	2.87E+05		(K)TFLVWV	(K)T F/L/V/W V/N E E D H/L R(V)		165.77	553.2818	1657.833	-0.0024	-1.5	4.65	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
12390	dirMS_041712_NAR_60mM_minus.6890.6890.3	3	9.03	1	6.14E+04		(R)DSGRGD	(R)D S G R/G D S V|S|D S/G S/D A L R(S)		97.03	560.916	1680.742	-0.0085	-5.1	4.14	50974.6	5.31	HUMAN	B5ME91	Programmed cell death protein 4
12391	dirMS_041712_NAR_20mM_plus.16543.16543.2	2	9.03	0	1.35E+05		(K)TVDNFV	(K)T V/D\N F|V/A L A/T G E K(G)		185.85	682.8565	1364.706	0.0001	0.1	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
12392	dirMS_041712_NAR_30mM_plus2.11224.11224.2	2	9.03	0	1.77E+05		(R)LTWHSC	(R)L T W H/S C P E\D\E|A|Q(-)	C:Carbamidomethylation	112.45	736.8094	1472.611	0.0005	0.3	4.13	20982.2	5.23	HUMAN	Q13185	Chromobox protein homolog 3
12393	dirMS_041712_NAR_30mM_plus2.13271.13271.2	2	9.03	0	8.79E+05		(K)NSGVLM	(K)N\S|G/V/L M V V/K(C)		123	473.7749	946.539	0.0035	3.7	8.75	9148.5	9.4	HUMAN	C9JES7	COX assembly mitochondrial protein homolog
12394	dirMS_041712_NAR_30mM_plus2.15394.15394.2	2	9.03	0	6.18E+05		(R)YPVNSV	(R)Y/P/V|N S V N I L/K(A)		133.52	573.8278	1146.652	-0.0034	-3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
12395	dirMS_041712_NAR_30mM_plus2.16749.16749.2	2	9.03	0	3.00E+05		(R)DFFLAN	(R)D F|F|L A/N/A S R(A)		141.18	520.7632	1040.516	0.0032	3	5.84	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
12396	dirMS_041712_NAR_30mM_plus2.19783.19783.2	2	9.03	0	3.53E+05		(K)SNNVEM	(K)S N|N/V|E/M D W V/L K(H)		156.98	667.8205	1334.641	-0.0072	-5.4	4.37	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
12397	dirMS_041712_NAR_30mM_plus2.21012.21102.2	2	9.03	0	4.37E+05		(K)AIDLFTD	(K)A I|D|L|F T D/A/I K(L)		164.72	553.8012	1106.609	-0.0141	-12.7	4.21	18141.9	4.7	HUMAN	F6VDH7	Hsc70-interacting protein (Fragment)
12398	dirMS_041712_NAR_30mM_plus2.9505.9505.2	2	9.03	0	2.76E+05		(R)LLTYNA	(R)L/L|T/Y N A/A R(L)		103.95	461.2586	921.515	-0.0053	-5.8	8.75	36309.7	5.86	HUMAN	B4DQ51	Short/branched chain-specific acyl-CoA dehydrogenase, mitochondrial
12399	dirMS_041712_NAR_40mM_plus2.9489.9489.2	2	9.03	0	7.31E+04		(R)GGGGNI	(R)G G G G N/F/G P G/P G S/N F/R(G)		119.27	689.3182	1377.629	-0.0003	-0.2	9.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
12400	dirMS_041712_NAR_50mM_plus2.8196.8196.3	3	9.03	1	5.51E+04		(R)QAVTNF	(R)Q/A V/T N/P\N N T/F Y A T K R(L)		109.77	575.628	1724.872	-0.002	-1.2	9.99	6809.6	9.69	HUMAN	D6RA73	Stress-70 protein, mitochondrial (Fragment)
12401	dirMS_041712_NAR_60mM_plus.19275.19275.3	3	9.03	1	5.03E+05		(K)WNLDEL	(K)W|N/L D/E|L/P K F E K(N)		158.63	473.5847	1418.731	0.0081	5.7	4.68	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
12402	dirMS_041712_NAR_20mM_minus.9209.9209.2	2	9.02	0	5.95E+03		(K)ATISND	(K)A T|I|S/N D G A T\I/L K(L)		141.77	602.3306	1203.658	-0.004	-3.3	5.88	55284.8	7.77	HUMAN	B8ZZC9	T-complex protein 1 subunit eta
12403	dirMS_041712_NAR_30mM_minus2.11819.11819.2	2	9.02	0	3.64E+04		(R)SPEVLL	(R)S P\E/V|L|L/G S A R(Y)		117.67	514.79	1028.574	-0.0008	-0.7	5.72	21780.9	8.65	HUMAN	E5RIU6	Cyclin-dependent kinase 1 (Fragment)
12404	dirMS_041712_NAR_30mM_minus2.16372.16372.2	2	9.02	0	1.54E+05		(R)GLGLDD	(R)G L|G/L/D/D/A L/E P R(Q)		142.03	578.299	1155.6	-0.0097	-8.4	4.03	51326.8	5.49	HUMAN	Q9Y230	RuvB-like 2
12405	dirMS_041712_NAR_30mM_minus2.19748.19748.2	2	9.02	0	3.53E+04		(K)EGLLLW	(K)E G\L/L/L/W|C Q R(K)	C:Carbamidomethylation	164.27	587.8058	1174.604	0.0006	0.5	6.1	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
12406	dirMS_041712_NAR_40mM_minus2.14332.14332.3	3	9.02	0	6.10E+05		(R)IHFPLAT	(R)I H F P L\A\T Y A/P V I/S/A\E K(A)		167.93	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
12407	dirMS_041712_NAR_50mM_minus2.13244.13244.3	3	9.02	0	1.66E+05		(K)MLDAED	(K)M/L|D/A E D/I/V G/T A R P D E K(A)		143.5	587.2894	1759.853	0.0006	0.3	4.1	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
12408	dirMS_041712_NAR_60mM_minus.10941.10941.3	3	9.02	0	2.65E+05		(R)ALPESL	(R)A L/P E/S/L/G/Q H A L R(S)		121.25	431.2376	1291.712	-0.0135	-10.4	6.79	31463.6	5.53	HUMAN	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1
12409	dirMS_041712_NAR_60mM_minus.19798.19798.3	3	9.02	1	1.61E+06		(K)EIIDLVL	(K)E I/I/D/L/V L D R I R(K)		179.72	452.2739	1354.805	0.0019	1.4	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
12410	dirMS_041712_NAR_120mM_plus.13194.13242.3	3	9.02	1	2.76E+06		(K)VKLEAEI	(K)V K\L E A E\I|A/T/Y/R(R)		121.77	431.5774	1292.721	-0.0032	-2.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
12411	dirMS_041712_NAR_120mM_plus.18065.18065.3	3	9.02	1	3.70E+05		(R)ARFEELN	(R)A R F E E\L\N|A/D|L F R(G)		147.85	494.2571	1480.754	0.0024	1.7	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
12412	dirMS_041712_NAR_120mM_plus.20785.20785.4	4	9.02	1	5.00E+05		(R)GIEKPPF	(R)G I/E/K/P\P\F E L/P D/F I K R(T)		162.38	447.2518	1785.99	-0.0044	-2.5	6.18	98282.7	5.49	HUMAN	E9PPJ0	Splicing factor 3B subunit 2
12413	dirMS_041712_NAR_120mM_plus.9263.9328.3	3	9.02	1	6.06E+05		(R)ALSTGE	(R)A L|S/T/G\E K G F G Y K(G)		102.35	419.8851	1257.647	-0.0066	-5.3	8.54	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
12414	dirMS_041712_NAR_20mM_plus.16816.16816.2	2	9.02	0	3.15E+05		(K)LGGSAV	(K)L G G S A\V|I/S L/E/G K|P L(-)		186.2	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
12415	dirMS_041712_NAR_20mM_plus.7814.7814.2	2	9.02	0	8.55E+04		(K)AQAAAF	(K)A Q/A|A/A|P A S/V P A Q A P K(R)		123.6	689.3745	1377.748	-0.0068	-4.9	8.8	17808.8	11.77	HUMAN	P47914	60S ribosomal protein L29
12416	dirMS_041712_NAR_30mM_plus2.11872.11872.2	2	9.02	0	7.29E+05		(R)SSTDSLP	(R)S S T/D\S|L/P G\P I\S/R(Q)		115.23	608.8101	1216.617	-0.0039	-3.2	5.55	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
12417	dirMS_041712_NAR_30mM_plus2.13379.13549.2	2	9.02	0	1.12E+06		(K)ELSDIAL	(K)E L|S/D/I/A/L/R(I)		123.73	458.7641	916.51	0.0111	12.1	4.37	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
12418	dirMS_041712_NAR_30mM_plus2.14378.14378.2	2	9.02	0	2.68E+05		(K)DSNFAG	(K)D S N\F|A/G/D L V R(N)		128.37	547.2595	1093.527	-0.0155	-14.2	4.21	103258.6	6.54	HUMAN	Q86XP3	ATP-dependent RNA helicase DDX42
12419	dirMS_041712_NAR_30mM_plus2.16953.16973.2	2	9.02	0	2.83E+05		(K)GAVEIIF	(K)G A|V/E/I\I/F K(G)		141.62	438.7625	876.519	-0.0012	-1.4	6	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
12420	dirMS_041712_NAR_40mM_plus2.6709.6709.2	2	9.02	0	1.68E+04		(K)SLAAEEE	(K)S L|A/A/E/E E A A R(Q)		99.53	523.7589	1046.511	-0.0008	-0.7	4.25	533778	5.74	HUMAN	Q15149	Plectin
12421	dirMS_041712_NAR_50mM_plus2.18781.18862.3	3	9.02	1	2.94E+05		(R)DSIVAEL	(R)D S/I/V/A/E L D R E M S/R(S)		167.32	507.5872	1520.737	0.0097	6.4	4.32	34709.6	4.98	HUMAN	O14579	Coatomer subunit epsilon

12422	dirMS_041712_NAR_50mM_plus2.7691.7691.3	3	9.02	1	1.36E+05		(R)LGTPELS	(R)L/G/T/P/E L/S T A E R K(E)		106.72	434.5738	1301.706	0.0009	0.7	6.14	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
12423	dirMS_041712_NAR_120mM_minus.10996.10997.3	3	9.01	0	1.18E+05		(K)IHPTSVI	(K)I H\P T S\V|I/S G Y/R(L)		113.68	410.556	1229.664	-0.0103	-8.3	8.75	47423	5.43	HUMAN	E7ERF2	T-complex protein 1 subunit alpha
12424	dirMS_041712_NAR_120mM_minus.17113.17113.3	3	9.01	1	7.58E+04		(R)IRGETLG	(R)I R G E T L G\I|I|G L/G R(V)		148.32	452.2751	1354.816	-0.0058	-4.3	9.6	20631.5	6.98	HUMAN	D6RAX2	C-terminal-binding protein 1 (Fragment)
12425	dirMS_041712_NAR_20mM_minus.13118.13118.2	2	9.01	0	2.31E+05		(R)GVVDSE	(R)G V/V D S E D|I/P/L N L S\R(E)		183.02	757.3944	1513.786	-0.0041	-2.7	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
12426	dirMS_041712_NAR_20mM_minus.7097.7097.2	2	9.01	0	1.68E+05		(R)AAQVA	(R)A A Q|V|A Q D E E I A R(L)		118.77	650.8255	1300.649	-0.0054	-4.2	4.14	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
12427	dirMS_041712_NAR_40mM_minus2.11008.11008.3	3	9.01	1	1.14E+05	M362m	(R)EGSVmL	(R)E G S V/m/L Q/V D/V D T V K G G L/K(L)	m:Oxidized methionine	147.85	630.9989	1874.989	15.993	-1	4.56	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
12428	dirMS_041712_NAR_50mM_minus2.14249.14249.3	3	9.01	0	1.56E+05	M13m	(R)DLISHDE	(R)D L|I/S/H D E m F/S D I Y K(I)	m:Oxidized methionine	149.13	576.9343	1712.784	16.0047	5.7	4.22	19709.1	4.83	HUMAN	P13693	Translationally-controlled tumor protein
12429	dirMS_041712_NAR_60mM_minus.15481.15481.3	3	9.01	0	3.72E+05		(K)THLPGF	(K)T H L P G F\V|E|Q/A E A L K(A)		146.35	513.947	1539.817	0.0099	6.4	5.37	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
12430	dirMS_041712_NAR_120mM_plus.13428.13428.4	4	9.01	1	1.27E+06		(K)DKFNEC	(K)D K F N E/C/G H\V L/Y/A D/I K(M)	C:Carbamidomethylation	123.87	452.9713	1808.864	-0.0002	-0.1	5.38	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
12431	dirMS_041712_NAR_120mM_plus.6433.6433.3	3	9.01	1	1.74E+04		(K)DSYVGD	(K)D S/Y/V/G D E/A/Q S K/R(G)		87.23	452.2133	1354.623	0.002	1.5	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
12432	dirMS_041712_NAR_20mM_plus.15527.15527.3	3	9.01	0	1.81E+05		(R)GVVDSE	(R)G V\V D S E D I|P/L N/L S R(E)		179.22	505.2667	1513.786	-0.0001	-0.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
12433	dirMS_041712_NAR_20mM_plus.18377.18377.3	3	9.01	0	8.80E+04	M36m	(K)NIPmTL	(K)N I/P/m T L E\L|L/Q S T R(I)	m:Oxidized methionine	197.85	511.28	1515.82	16.0055	6.9	6	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
12434	dirMS_041712_NAR_30mM_plus2.22308.22308.3	3	9.01	0	5.24E+05		(R)VGNLGL	(R)V G N L G L A|T S/F/F/N E R(N)		172.8	508.9306	1524.781	-0.0033	-2.1	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
12435	dirMS_041712_NAR_40mM_plus2.7589.7589.2	2	9.01	0	8.64E+03		(R)INISEGN	(R)I N|I/S/E/G N C\P E R(I)	C:Carbamidomethylation	104.55	644.7998	1288.595	-0.0027	-2.1	4.53	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
12436	dirMS_041712_NAR_40mM_plus2.9132.9132.2	2	9.01	0	8.93E+04		(K)GSDFDC	(K)G S D/F/D/C E/L|R(L)	C:Carbamidomethylation	115.47	549.7296	1098.452	-0.0001	-0.1	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
12437	dirMS_041712_NAR_50mM_plus2.7782.7782.3	3	9.01	1	9.77E+04		(R)EFEDPRI	(R)E F E D P/R/D A/P/P P T R(A)		106.6	509.5779	1526.723	-0.0042	-2.8	4.32	51612.9	9.98	HUMAN	P08621	U1 small nuclear ribonucleoprotein 70 kDa
12438	dirMS_041712_NAR_120mM_minus.11961.11961.3	3	9	0	5.63E+05		(R)IVNHW	(R)I/V/N H W/A S/P E/L R(Q)		118.8	441.2372	1321.701	-0.0041	-3.1	6.75	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
12439	dirMS_041712_NAR_120mM_minus.12013.12013.3	3	9	1	2.38E+06		(K)MKEIAE	(K)M K E\I\A E\A/Y/L/G K(T)		119.63	418.2252	1252.661	0.0005	0.4	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
12440	dirMS_041712_NAR_120mM_minus.7027.7027.2	2	9	0	1.93E+05	M46m	(R)HQGVm	(R)H/Q|G\V m V G\M G\Q\K(D)	m:Oxidized methionine	92.85	594.2863	1171.571	15.9943	-0.5	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
12441	dirMS_041712_NAR_20mM_minus.10113.10113.2	2	9	0	8.14E+04		(K)STGGAP	(K)S T G G A|P T F N V/T/V T/K(T)		150.73	690.3599	1379.717	-0.004	-2.9	8.47	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
12442	dirMS_041712_NAR_40mM_minus2.6401.6401.2	2	9	0	6.89E+03		(R)SFDACV	(R)S/F/D A C V/K(A)	C:Carbamidomethylation	104.1	413.6882	826.376	-0.0072	-8.8	5.55	120358.9	6.28	HUMAN	Q9Y666	Solute carrier family 12 member 7
12443	dirMS_041712_NAR_50mM_minus2.13049.13049.3	3	9	1	1.05E+06	M320m	(K)YmACCL	(K)Y m|A C/C L L Y R G D V V|P K(E)	C:Carbamidomethylation m:Oxid	141.47	620.9644	1844.886	15.9931	-1	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
12444	dirMS_041712_NAR_50mM_minus2.15973.15973.3	3	9	0	5.46E+05		(K)GSDHSA	(K)G S/D H S A S L\E|P\G E\L A E L/V R(S)		159.35	622.978	1866.919	0.0003	0.1	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
12445	dirMS_041712_NAR_50mM_minus2.16758.16758.3	3	9	0	4.18E+05		(K)NILFVIT	(K)N I/L/F/V/I/T K/P D V Y K(S)		164.02	517.2991	1549.899	-0.0161	-10.4	8.5	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
12446	dirMS_041712_NAR_60mM_minus.16643.16643.3	3	9	0	1.51E+06		(R)DGLAFN	(R)D G L/A/F N A L/I H R(H)		153.73	409.5576	1226.664	-0.0058	-4.7	6.74	146974	5.55	HUMAN	C9JRP8	Spectrin beta chain, non-erythrocytic 4
12447	dirMS_041712_NAR_120mM_plus.21192.21192.3	3	9	2	5.22E+05		(R)TLAEIAK	(R)T L|A|E/I|A K V E L D N M P L R G K(Q)		163.83	666.7047	1998.105	-0.0057	-2.8	5.85	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
12448	dirMS_041712_NAR_120mM_plus.4093.4243.3	3	9	1	1.73E+07	M310m	(R)TKTEISE	(R)T K\T E|I/S/E/m N/R(N)	m:Oxidized methionine	69.83	408.8687	1208.594	15.9976	2.2	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
12449	dirMS_041712_NAR_120mM_plus.7273.7273.3	3	9	1	3.21E+05	M462m	(R)KAYGGA	(R)K A Y G G\A|Y/D/V/m S/S K(H)	m:Oxidized methionine	91.37	464.8863	1376.651	15.9929	-1.5	8.43	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
12450	dirMS_041712_NAR_20mM_plus.13303.13372.2	2	9	0	4.59E+05	M148m	(R)DLTDYL	(R)D L|T/D Y L m/K(I)	m:Oxidized methionine	164.65	507.7439	998.486	15.9942	-0.7	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
12451	dirMS_041712_NAR_20mM_plus.13808.13808.2	2	9	0	2.53E+05		(R)GDLGIEI	(R)G D/L/G\I\E\I/P/A E K(V)		166.85	571.3075	1141.61	-0.0022	-1.9	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
12452	dirMS_041712_NAR_20mM_plus.16437.16437.3	3	9	0	1.35E+05		(R)QAQEYE	(R)Q A\Q E\Y E|A L/L N/I K(V)		184.45	473.9191	1419.748	-0.0051	-3.6	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
12453	dirMS_041712_NAR_20mM_plus.18913.18913.3	3	9	0	1.01E+05		(R)AAVPSG	(R)A A V|P S G A S T G\I/Y E A L/E/L/R(D)		201.5	602.3183	1804.944	-0.0036	-2	4.53	43048.9	4.99	HUMAN	B7Z2X9	Enolase
12454	dirMS_041712_NAR_20mM_plus.19074.19074.2	2	9	0	2.19E+05		(K)ILTFDQL	(K)I L/T F/D\Q L/A L\D S P K(G)		202.92	730.9063	1460.8	0.0058	4	4.21	14643	11.93	HUMAN	F8VUA6	60S ribosomal protein L18 (Fragment)
12455	dirMS_041712_NAR_30mM_plus2.17775.17775.2	2	9	0	3.03E+05		(K)SLEDQV	(K)S L/E/D Q|V/E M/L R(T)		145.92	610.3003	1219.599	-0.0054	-4.4	4.14	61161.1	4.34	HUMAN	K7ELL7	Glucosidase 2 subunit beta
12456	dirMS_041712_NAR_40mM_plus2.15695.15695.3	3	9	1	3.51E+04	S53s	(R)LLIYGAS	(R)L L\I/Y G A s S R A/T G I/P D R(F)	s:N-acetylglucosamine (S)	158.55	631.6874	1689.928	203.1194	21.1	8.75	11889	9.11	HUMAN	P01620	Ig kappa chain V-III region SIE
12457	dirMS_041712_NAR_50mM_plus2.14131.14131.3	3	9	1	6.91E+04		(K)VVSSSIV	(K)V V|S S S I V D K/Y\I/G E S A R(L)		142.2	570.6392	1709.907	-0.0038	-2.2	6.04	29938.9	6.07	HUMAN	H0YJC0	26S protease regulatory subunit 10B (Fragment)
12458	dirMS_041712_NAR_50mM_plus2.18212.18468.3	3	9	0	3.22E+05		(R)VFITDDF	(R)V/F|I/T/D D F H D M M/P K(Y)		164.5	532.581	1595.723	0.0052	3.2	4.41	92752.5	4.76	HUMAN	P14625	Endoplasmin
12459	dirMS_041712_NAR_60mM_plus.11310.11394.3	3	9	0	5.16E+05		(K)YQYGGL	(K)Y/Q|Y/G/G L/N S G R P V T P P R(T)		116.58	587.9675	1761.903	-0.0151	-8.6	9.99	37984.9	5.84	HUMAN	P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit
12460	dirMS_041712_NAR_60mM_plus.11908.11909.3	3	9	0	9.79E+05		(K)FYEEVHI	(K)F Y/E E/V/H D L E R(K)		119.13	446.2162	1336.617	0.0172	12.9	4.4	18209.2	5.03	HUMAN	A8MXH2	Nucleosome assembly protein 1-like 4 (Fragment)
12461	dirMS_041712_NAR_60mM_plus.15016.15016.3	3	9	1	7.66E+04		(R)ELNITAA	(R)E L N I/T A A K\E I E/V/G G G R(K)		134.78	552.9655	1656.892	-0.0096	-5.8	4.79	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
12462	dirMS_041712_NAR_60mM_plus.7809.7851.3	3	9	0	1.06E+06		(R)SAHATA	(R)S A H A\T A\P\V/N|I|A/G S R(T)		99.03	451.2397	1351.708	-0.0031	-2.3	9.49	300351.7	12.1	HUMAN	Q9UQ35	Serine/arginine repetitive matrix protein 2
12463	dirMS_041712_NAR_120mM_minus.9517.9517.2	2	8.99	0	5.89E+05		(K)HVVFIA	(K)H/V|V/F I A Q/R(R)		105.95	485.2837	969.563	-0.0027	-2.8	9.75	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
12464	dirMS_041712_NAR_20mM_minus.9448.9448.3	3	8.99	0	1.18E+04	M175m	(R)LEQGQA	(R)L E Q G Q A I/D/D L/m/P A Q K(-)	m:Oxidized methionine	144.5	558.2794	1656.826	15.9975	1.5	4.03	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
12465	dirMS_041712_NAR_30mM_minus2.15299.15299.2	2	8.99	0	6.30E+05		(R)YPVNSV	(R)Y/P/V/N/S V N I L/K(A)		136.83	573.8282	1146.652	-0.0026	-2.3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
12466	dirMS_041712_NAR_50mM_minus2.14311.14311.3	3	8.99	0	4.31E+05		(R)QIFHPE	(R)Q I/F/H/P E Q L I T/G/K(E)		149.72	470.9286	1410.774	-0.0027	-1.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
12467	dirMS_041712_NAR_60mM_minus.5300.5300.3	3	8.99	0	2.93E+05		(R)AEAEAG	(R)A E|A\E A/G S\P R P D/P R(E)		84.6	451.5562	1352.655	-0.0013	-0.9	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
12468	dirMS_041712_NAR_60mM_minus.9069.9069.3	3	8.99	0	2.42E+05		(K)SVIHSGF	(K)S V/I H\S G|P F|T E/S\Q K(S)		110.93	472.9099	1416.712	0.0034	2.4	6.47	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
12469	dirMS_041712_NAR_60mM_minus.9790.9902.3	3	8.99	1	6.93E+06	S303s	(R)DHHMs	(R)D H/H M s G W S|Y/K R V E K(S)	s:N-acetylglucosamine (S)	114.9	654.9721	1759.833	203.0684	-5.6	8.51	51648.4	5.55	HUMAN	B7XGB9	Protein phosphatase 1M
12470	dirMS_041712_NAR_20mM_plus.18944.18944.2	2	8.99	0	5.15E+04		(R)NLTALGI	(R)N L T A/L|G/L N L V/A/S G G T A K(A)		201.48	800.4534	1599.906	-0.0069	-4.3	8.75	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
12471	dirMS_041712_NAR_20mM_plus.18963.18963.3	3	8.99	0	6.34E+04		(K)DTSYLFI	(K)D T S Y\L/F\I/T/G/P D V V K(S)		201.93	518.9378	1554.805	-0.0062	-4	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
12472	dirMS_041712_NAR_30mM_plus2.18968.18968.2	2	8.99	0	5.46E+05		(R)LSNIFVI	(R)L S\N|I/F V/I/G K(G)		152.27	495.8019	990.598	-0.0017	-1.7	8.75	29825.4	10.37	HUMAN	P62701	40S ribosomal protein S4, X isoform
12473	dirMS_041712_NAR_30mM_plus2.21804.21804.2	2	8.99	0	2.29E+05		(R)TTNFAG	(R)T T/N F/A/G/I\L/S Q|G L R(I)		169.4	689.3749	1377.748	-0.006	-4.3	9.41	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
12474	dirMS_041712_NAR_50mM_plus2.11710.11953.3	3	8.99	1	4.35E+05		(K)QIDLSTV	(K)Q I/D L S/T/V/D/L K K(L)		130.47	420.5781	1259.72	-0.0008	-0.6	5.96	21156.2	9.41	HUMAN	P55145	Mesencephalic astrocyte-derived neurotrophic factor
12475	dirMS_041712_NAR_60mM_plus.13778.13778.3	3	8.99	1	4.71E+05		(R)KYEMFA	(R)K\Y\E M F A Q/T|L/Q/Q S R(G)		128.72	543.9389	1629.805	-0.0032	-2	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
12476	dirMS_041712_NAR_60mM_plus.18077.18077.3	3	8.99	1	4.10E+05		(K)ESQAKD	(K)E S Q/A/K/D V/I/E/E Y F K(C)		151.17	529.2635	1585.774	0.0015	1	4.41	14914.1	6.84	HUMAN	P25398	40S ribosomal protein S12
12477	dirMS_041712_NAR_60mM_plus.20641.20641.3	3	8.99	0	7.27E+05		(R)LGFHLPI	(R)L G F H L\P L E\V|A\Y Q/R(G)		168.62	514.9568	1542.843	0.0131	8.5	6.75	533778	5.74	HUMAN	Q15149	Plectin
12478	dirMS_041712_NAR_60mM_plus.21118.21118.3	3	8.99	1	1.05E+05		(K)AKINEA	(K)A K I N E A|V|E|C L L/S L K(A)	C:Carbamidomethylation	173.75	529.9643	1587.878	0.0009	0.6	6.18	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
12479	dirMS_041712_NAR_60mM_plus.5665.5665.3	3	8.99	0	7.68E+04		(R)TAEHEA	(R)T A E H E A\A\Q|Q/D L/Q/S K(F)		87.8	519.2487	1555.735	-0.0031	-2	4.65	156557.7	5.52	HUMAN	Q86UP2	Kinectin
12480	dirMS_041712_NAR_120mM_minus.5409.5409.2	2	8.98	1	5.63E+04		(K)AAQEEY	(K)A A/Q/E/E Y\V K R(A)		82.85	547.2876	1093.564	0.0043	3.9	6.19	39795.8	9.08	HUMAN	H3BQN4	Fructose-bisphosphate aldolase
12481	dirMS_041712_NAR_30mM_minus2.18199.18199.2	2	8.98	0	1.96E+05		(K)VADIGL	(K)V A|D\I/G/L A/A/W G R(K)		152.82	564.8076	1128.616	-0.0081	-7.2	5.81	48285.8	5.93	HUMAN	P23526	Adenosylhomocysteinase
12482	dirMS_041712_NAR_30mM_minus2.4713.4713.2	2	8.98	0	1.22E+05		(K)AAQASD	(K)A/A Q/A/S D L E K(I)		77.57	466.7386	932.468	0.0016	1.7	4.37	37710.6	6.36	HUMAN	P37837	Transaldolase
12483	dirMS_041712_NAR_30mM_minus2.7157.7157.2	2	8.98	0	1.16E+05		(K)MQAVQ	(K)M Q|A/V/Q/E A T R(L)		94	517.257	1033.509	-0.0028	-2.7	5.75	533778	5.74	HUMAN	Q15149	Plectin
12484	dirMS_041712_NAR_30mM_minus2.7188.7188.2	2	8.98	0	2.82E+05		(K)EGIPPD	(K)E\G I/P|P D Q Q R(L)		93.73	520.2591	1039.517	-0.0058	-5.6	4.37	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
12485	dirMS_041712_NAR_40mM_minus2.15607.15607.3	3	8.98	1	4.96E+05		(K)ALFEEVF	(K)A L/F/E/E/V/P E L L T E A E K K(E)		181.8	615.9988	1845.984	-0.0026	-1.4	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
12486	dirMS_041712_NAR_40mM_minus2.6241.6241.2	2	8.98	0	1.26E+05		(K)VIDDTNI	(K)V I|D/D/T N/I T/R(L)		102.3	523.7749	1046.548	-0.0051	-4.9	4.21	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
12487	dirMS_041712_NAR_50mM_minus2.12249.12249.3	3	8.98	1	1.53E+05		(K)ASLAETI	(K)A S|L/A E/T D K I T L E V/A K(L)		137.92	530.2953	1588.879	-0.0079	-5	4.68	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
12488	dirMS_041712_NAR_50mM_minus2.13661.13661.3	3	8.98	0	2.19E+04		(R)DLSHIGI	(R)D L S H I G D A\V|V|I/S C A/K(D)	C:Carbamidomethylation	145.88	528.9397	1584.805	-0.0005	-0.3	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
12489	dirMS_041712_NAR_60mM_minus.11020.11062.3	3	8.98	1	5.49E+05	M112m	(R)EmDRET	(R)E/m D R E T\L|I/D V A/R(T)	m:Oxidized methionine	121.17	488.5781	1447.721	15.9988	2.6	4.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
12490	dirMS_041712_NAR_120mM_plus.21020.21020.3	3	8.98	2	1.37E+06		(R)TLAEIAK	(R)T L|A/E I/A K\V/E L D/N\M P L R G K(Q)		162.93	666.7047	1998.105	-0.0057	-2.8	5.85	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
12491	dirMS_041712_NAR_120mM_plus.8635.8635.3	3	8.98	0	1.25E+06		(R)RPELEDS	(R)R P\E\L\E/D|S/T/L/R(Y)		98.35	405.8796	1215.633	-0.0085	-7	4.68	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
12492	dirMS_041712_NAR_120mM_plus.9056.9056.3	3	8.98	1	2.52E+05	S141s	(R)DPQGsS	(R)D P Q G/s/S L|P G G R R(Q)	s:N-acetylglucosamine (S)	100.88	477.2447	1226.624	203.0959	11.6	9.6	39931.9	4.74	HUMAN	E9PBI0	Zinc finger and SCAN domain-containing protein 18
12493	dirMS_041712_NAR_20mM_plus.10727.10727.2	2	8.98	0	2.38E+04		(K)YEELQIT	(K)Y E/E/L/Q/I/T/A G R(H)		145.37	590.304	1179.6	0.0003	0.3	4.53	60351.2	8.36	HUMAN	P04259	Keratin, type II cytoskeletal 6B
12494	dirMS_041712_NAR_20mM_plus.11941.11941.2	2	8.98	0	6.74E+04		(K)VLIANN	(K)V L I|A/N N/G I A/A V/K(C)		155.83	591.8632	1182.72	-0.0014	-1.2	8.72	269989.9	5.92	HUMAN	F8W8T8	Acetyl-CoA carboxylase 2
12495	dirMS_041712_NAR_20mM_plus.13696.13811.2	2	8.98	0	1.24E+05		(R)LVVPAT	(R)L V|V|P A\T Q C G S L\I/G K(G)	C:Carbamidomethylation	167.17	721.9033	1442.804	-0.0042	-2.9	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
12496	dirMS_041712_NAR_20mM_plus.15994.15994.2	2	8.98	0	2.04E+05		(K)VVDLLAI	(K)V V/D L\L/A/P Y A K(G)		181.53	544.8228	1088.635	0.0033	3	5.8	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
12497	dirMS_041712_NAR_20mM_plus.16261.16261.3	3	8.98	0	1.06E+04		(K)TIIPLISQ	(K)T I/I P L/I/S Q C T/P K(V)	C:Carbamidomethylation	183.5	457.5916	1370.771	-0.011	-8	8.41	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
12498	dirMS_041712_NAR_30mM_plus2.14711.14711.2	2	8.98	0	3.22E+05		(R)YQETFN	(R)Y Q|E/T/F N V I/E R(C)		129.92	649.8225	1298.638	0.0002	0.1	4.53	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
12499	dirMS_041712_NAR_30mM_plus2.7224.7224.2	2	8.98	0	1.58E+05		(K)TGEGFYI	(K)T/G|E/G/F Y/K(Y)		92.13	401.1973	801.378	0.0096	12	5.66	35407.1	6.73	HUMAN	E9PF18	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial
12500	dirMS_041712_NAR_50mM_plus2.17903.17903.3	3	8.98	1	3.12E+05		(K)AKIGLIQ	(K)A K I G L\I/Q/F/C L/S/A P K(T)	C:Carbamidomethylation	162.22	515.9649	1545.882	-0.002	-1.3	10	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
12501	dirMS_041712_NAR_50mM_plus2.18440.18440.3	3	8.98	1	3.49E+05		(R)GDSVIV	(R)G D\S V|I/V V L R N P L/I/A G K(-)		165.37	550.9999	1650.99	-0.005	-3	8.75	6144.3	10.23	HUMAN	K7EJB5	Small nuclear ribonucleoprotein Sm D2
12502	dirMS_041712_NAR_50mM_plus2.19483.19483.3	3	8.98	0	2.87E+06		(K)ISSIQSIV	(K)I S S I/Q S I V/P A L E I/A/N A H R(K)		170.32	640.3623	1919.071	0.0015	0.8	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
12503	dirMS_041712_NAR_60mM_plus.7163.7163.2	2	8.98	0	3.11E+05		(K)TIEAEAA	(K)T I E|A/E A|A H/G T V T/R(H)		95.57	678.3494	1355.691	0.0002	0.1	5.37	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
12504	dirMS_041712_NAR_120mM_minus.14728.14728.2	2	8.97	0	6.49E+05		(R)HSLVSF	(R)H/S|L V/S F V V/R(I)		134.32	522.3023	1043.6	-0.0023	-2.2	9.75	36359.2	5.35	HUMAN	Q9BUD6	Spondin-2
12505	dirMS_041712_NAR_20mM_minus.13740.13740.2	2	8.97	0	3.90E+05		(K)LGGSAV	(K)L G G\S A V/I S/L/E G K|P L(-)		188.65	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
12506	dirMS_041712_NAR_50mM_minus2.17771.17887.3	3	8.97	0	4.27E+05	M203m	(R)DTGIFLI	(R)D T|G I/F/L/D L m H L K(K)	m:Oxidized methionine	170.33	473.5826	1402.74	15.9933	-1.1	5.21	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
12507	dirMS_041712_NAR_50mM_minus2.6769.6769.3	3	8.97	1	2.55E+04		(K)LAQYEPI	(K)L A/Q|Y E/P P Q E E K R/A E(-)		104.98	563.2743	1687.829	-0.0202	-12	4.69	11966.5	5.71	HUMAN	Q99417	C-Myc-binding protein
12508	dirMS_041712_NAR_60mM_minus.16855.16855.3	3	8.97	1	2.46E+05		(R)KGFSEGI	(R)K G F S E G L\W\E|I/E N/N P\T V/K(A)		153.75	649.9986	1947.981	0.0002	0.1	4.79	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
12509	dirMS_041712_NAR_60mM_minus.19040.19040.3	3	8.97	1	2.48E+05		(R)DSIVAEL	(R)D S/I|V/A E L D/R E M\S R(S)		168.02	507.5858	1520.737	0.0055	3.6	4.32	34709.6	4.98	HUMAN	O14579	Coatomer subunit epsilon
12510	dirMS_041712_NAR_120mM_plus.15297.15297.4	4	8.97	2	7.99E+05		(R)AGEVER	(R)A/G|E/V E R D L D K/A D/S M I R(L)		133.18	451.9773	1804.886	0.0016	0.9	4.44	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
12511	dirMS_041712_NAR_20mM_plus.16229.16229.3	3	8.97	0	1.32E+05		(R)LLDAQL	(R)L L D A Q\L A T/G/G\I V D/P R(L)		183.53	513.6218	1538.854	-0.0028	-1.8	4.21	533778	5.74	HUMAN	Q15149	Plectin
12512	dirMS_041712_NAR_20mM_plus.17789.17789.2	2	8.97	0	7.89E+04		(K)VNIIPIIA	(K)V/N|I/I/P I I A K(A)		194.57	490.8283	980.65	-0.001	-1	8.72	51212	5.84	HUMAN	A6NFQ9	Septin-8
12513	dirMS_041712_NAR_20mM_plus.8243.8243.3	3	8.97	0	2.17E+05	M346m M	(K)mGGmE	(K)m G G m E G P F|G/G/G m E/N m/G R(F)	m:Oxidized methionine	126.37	593.558	1714.68	63.979	-0.4	4.53	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
12514	dirMS_041712_NAR_30mM_plus2.21337.21337.2	2	8.97	0	2.64E+05		(R)GVVQEL	(R)G V/V/Q/E L/Q Q A/I/S K(L)		166.05	650.3632	1299.727	-0.0076	-5.8	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
12515	dirMS_041712_NAR_40mM_plus2.18446.18446.3	3	8.97	0	3.62E+04		(K)ALESPEI	(K)A L|E/S/P E R P\F L/A I L G G A K(V)		174.68	590.3359	1768.996	-0.0024	-1.4	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
12516	dirMS_041712_NAR_40mM_plus2.6789.6789.2	2	8.97	0	4.44E+04		(K)SFQQSSI	(K)S F/Q|Q/S/S L/S R(D)		100.17	520.2619	1039.517	-0.0002	-0.2	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
12517	dirMS_041712_NAR_40mM_plus2.6950.6950.2	2	8.97	0	2.64E+04		(R)DYDDM	(R)D Y|D/D M/S/P R(R)		100.75	499.6964	998.388	-0.0029	-2.9	3.93	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
12518	dirMS_041712_NAR_50mM_plus2.20828.20828.3	3	8.97	0	2.40E+05		(K)HSQFIG	(K)H S Q F\I\G\Y|P I T L F V E K(E)		178.95	593.6536	1778.948	-0.0013	-0.8	6.75	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
12519	dirMS_041712_NAR_60mM_plus.16107.16416.3	3	8.97	0	1.53E+06		(K)SLTNDW	(K)S L|T N/D W/E D H L A/V K(H)		141.98	509.919	1527.744	-0.0014	-0.9	4.53	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
12520	dirMS_041712_NAR_60mM_plus.17237.17237.3	3	8.97	0	1.05E+06		(R)QIFHPE	(R)Q I F H/P E\Q L/I/T G/K(E)		146.97	470.9225	1410.774	-0.021	-14.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
12521	dirMS_041712_NAR_60mM_plus.20718.20718.3	3	8.97	0	7.21E+05		(R)LGFHLPI	(R)L G F H L P L E\V|A|Y/Q R(G)		168.63	514.9568	1542.843	0.0131	8.5	6.75	533778	5.74	HUMAN	Q15149	Plectin
12522	dirMS_041712_NAR_60mM_plus.9412.9412.2	2	8.97	0	5.11E+05		(K)QEYDES	(K)Q E Y/D|E|S/G\P/S I/V H/R(K)		107.15	758.8546	1516.703	-0.0007	-0.5	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
12523	dirMS_041712_NAR_120mM_minus.13307.13307.4	4	8.96	0	3.25E+05		(R)VLSAPPI	(R)V L S A/P/P/H F H F/G Q T N R(T)		126.85	427.7219	1707.871	-0.0056	-3.3	9.74	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
12524	dirMS_041712_NAR_120mM_minus.18108.18108.3	3	8.96	1	2.86E+05		(R)ARFEEL	(R)A R F E E\L/N/A/D/L F R(G)		153.08	494.2561	1480.754	-0.0006	-0.4	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
12525	dirMS_041712_NAR_120mM_minus.7885.7885.2	2	8.96	1	1.08E+06		(R)AQYDEL	(R)A Q|Y|D/E L A R/K(N)		96.87	547.2876	1093.564	0.0043	3.9	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
12526	dirMS_041712_NAR_20mM_minus.14482.14482.3	3	8.96	0	2.19E+05		(K)LAAELS	(K)L A\A E L S A T L/E|Q A/A/A T A R(V)		198.9	562.9713	1686.902	-0.0027	-1.6	4.53	558007.1	5.44	HUMAN	P58107	Epiplakin
12527	dirMS_041712_NAR_30mM_minus2.16262.16262.2	2	8.96	0	5.16E+05		(K)LIINSLYK	(K)L I|I/N S L Y K(N)		141.27	482.2955	963.587	-0.0036	-3.8	8.59	5582.4	4.81	HUMAN	F8W026	Endoplasmin (Fragment)
12528	dirMS_041712_NAR_50mM_minus2.12822.12822.3	3	8.96	0	1.53E+05		(K)ASLASLP	(K)A S/L\A S L/P P L/H V/A K(L)		141.37	435.2622	1303.773	-0.0012	-0.9	8.8	141626	5.5	HUMAN	A8MY36	Dynactin subunit 1
12529	dirMS_041712_NAR_50mM_minus2.17872.17872.3	3	8.96	0	2.97E+05		(K)HNQLPL	(K)H N Q L P\L\V|I|E\F/T E Q T A P/K(I)		170.05	655.6843	1965.044	-0.0057	-2.9	5.4	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
12530	dirMS_041712_NAR_50mM_minus2.9427.9427.2	2	8.96	1	7.15E+05		(R)DGKLVS	(R)D/G K L|V|S E S S D/V L|P K(-)		121.97	737.3927	1473.78	-0.0014	-0.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8

12531	dirMS_041712_NAR_60mM_minus.10088.10088.3	3	8.96	1	1.34E+04		(R)VAIEPG	(R)V/A|I/E/P/G A P R E N D E F C K(M)	C:Carbamidomethylation	115.98	611.2977	1831.864	0.0142	7.8	4.41	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
12532	dirMS_041712_NAR_60mM_minus.7527.7527.3	3	8.96	0	1.58E+05		(R)AAHSEG	(R)A A H S E G N\T/T/A/G/L D/M R(E)		101.22	510.9003	1530.697	-0.0102	-6.7	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
12533	dirMS_041712_NAR_120mM_plus.5294.5294.3	3	8.96	1	1.54E+05		(R)NDDDEE	(R)N/D/D/D|E/E/E A A|R E R(R)		81.02	483.5401	1448.588	0.0173	12	3.95	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
12534	dirMS_041712_NAR_120mM_plus.7883.7883.2	2	8.96	0	5.08E+05		(K)STTTGH	(K)S T|T/T/G H L\I|Y|K(C)		95.33	560.8014	1120.6	-0.0042	-3.7	8.34	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
12535	dirMS_041712_NAR_120mM_plus.8049.8147.2	2	8.96	0	7.58E+05		(K)HYEMLA	(K)H/Y|E|M L/A N\R(T)		96.27	517.2485	1033.488	0.0013	1.3	6.75	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
12536	dirMS_041712_NAR_20mM_plus.8671.8671.2	2	8.96	0	1.87E+05	M224m	(K)GGKPEP	(K)G G K P E/P P A m|P Q\P V|P T A(-)	m:Oxidized methionine	130.62	795.402	1573.804	15.9924	-1.6	6	25541.5	9.92	HUMAN	E9PL09	40S ribosomal protein S3
12537	dirMS_041712_NAR_30mM_plus2.16777.16777.2	2	8.96	0	4.32E+05		(K)GCSFLP	(K)G C/S|F/L|P D/P Y Q K(Q)	C:Carbamidomethylation	140.87	656.306	1311.604	0.0009	0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
12538	dirMS_041712_NAR_30mM_plus2.17401.17401.2	2	8.96	0	1.64E+05		(R)ASLEAA	(R)A S L/E A/A/I/A D A|E/Q R(G)		145.03	672.8406	1344.675	-0.0015	-1.1	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
12539	dirMS_041712_NAR_30mM_plus2.20334.20334.2	2	8.96	0	1.62E+04		(R)ILLLGLD	(R)I L\L/L/G/L\D/N A G K(T)		161.8	563.8448	1126.683	-0.0007	-0.6	5.84	20626.3	6.76	HUMAN	P36405	ADP-ribosylation factor-like protein 3
12540	dirMS_041712_NAR_30mM_plus2.9940.9940.2	2	8.96	0	7.22E+05		(R)GTDLTD	(R)G T D\L/T/D E Q I\R(F)		105.63	574.288	1147.559	0.0098	8.5	4.03	103045.5	7.1	HUMAN	B9ZVT1	RNA-binding protein 12B
12541	dirMS_041712_NAR_40mM_plus2.15653.15653.3	3	8.96	0	1.01E+04		(R)LQVIVC	(R)L Q|V\I V/C S A T L H S F D|V K(K)	C:Carbamidomethylation	158.6	606.3237	1816.963	-0.006	-3.3	6.74	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
12542	dirMS_041712_NAR_40mM_plus2.17210.17210.3	3	8.96	1	3.36E+05		(K)VIAATN	(K)V I/A|A T N R V D I\L D/P\A L L\R(S)		168.1	617.3636	1850.086	-0.0096	-5.2	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
12543	dirMS_041712_NAR_40mM_plus2.9873.9873.2	2	8.96	0	8.87E+04		(K)FFDQYR	(K)F/F/D Q/Y/R(S)		122.05	438.2084	875.405	0.0049	5.6	5.83	334221.3	6.44	HUMAN	P15924	Desmoplakin
12544	dirMS_041712_NAR_50mM_plus2.13838.13838.3	3	8.96	0	1.48E+06		(K)DLAGC	(K)D L/A/G C I/H/G L S N V K(L)	C:Carbamidomethylation	140.47	461.9061	1383.705	-0.0012	-0.8	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
12545	dirMS_041712_NAR_50mM_plus2.17012.17012.3	3	8.96	0	7.43E+05		(R)QYYTLL	(R)Q Y Y T L/L\N/Q A/P D M L H R(K)		156.98	621.6447	1862.922	-0.0022	-1.2	6.74	4335.1	9.82	HUMAN	E5RH00	Ras GTPase-activating protein-binding protein 1
12546	dirMS_041712_NAR_50mM_plus2.19007.19007.3	3	8.96	1	2.87E+05		(K)LALFQA	(K)L A/L/F/Q/A I/G/K E V V D R(A)		168.12	520.3019	1558.895	-0.004	-2.6	6.07	266161	5.68	HUMAN	E9PPU0	Epiplakin
12547	dirMS_041712_NAR_60mM_plus.16593.16593.3	3	8.96	0	1.92E+05		(R)LSQYQE	(R)L/S|Q/Y Q E P L/H L/P G V R(V)		143.7	546.297	1636.881	-0.0041	-2.5	6.75	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
12548	dirMS_041712_NAR_60mM_plus.7983.7983.3	3	8.96	1	5.81E+05		(K)ALSRQE	(K)A L|S R Q E\M Q/E V/Q/S S R(S)		100.27	550.2735	1648.807	-0.0012	-0.7	6.19	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
12549	dirMS_041712_NAR_120mM_minus.11012.11012.3	3	8.95	1	2.18E+05	S303s	(R)DHHMs	(R)D H H M/s G W S|Y/K R V E K(S)	s:N-acetylglucosamine (S)	114.47	654.9729	1759.833	203.0708	-4.3	8.51	51648.4	5.55	HUMAN	B7XGB9	Protein phosphatase 1M
12550	dirMS_041712_NAR_120mM_minus.9290.9290.3	3	8.95	1	1.47E+05		(R)EQAEEE	(R)E Q/A/E E/E/R Y F R(A)		104.9	452.8778	1356.618	0.001	0.7	4.5	12248.6	9.34	HUMAN	Q9UII2	ATPase inhibitor, mitochondrial
12551	dirMS_041712_NAR_30mM_minus2.5834.5834.2	2	8.95	0	4.20E+04		(R)VSTEVD	(R)V/S/T E/V/D/A R(L)		86.07	438.7245	876.442	-0.0004	-0.5	4.37	35556.4	9.3	HUMAN	F2Z393	Transaldolase
12552	dirMS_041712_NAR_40mM_minus2.11654.11654.3	3	8.95	1	1.33E+04		(R)DLAALG	(R)D L/A\A|L/G D K V/N S L/G E T\A E R(L)		151.8	620.3199	1858.95	-0.0053	-2.9	4.32	285798.6	5.23	HUMAN	A6NG51	Spectrin alpha chain, non-erythrocytic 1
12553	dirMS_041712_NAR_50mM_minus2.11600.11600.3	3	8.95	1	1.92E+05		(K)IEVEKPF	(K)I/E/V E K/P F A I A K E(-)		134.38	458.5927	1373.767	-0.0039	-2.9	5.01	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
12554	dirMS_041712_NAR_50mM_minus2.11738.11738.3	3	8.95	0	2.43E+05	M291m	(K)TGEEIFG	(K)T G\E|E\I/F|G T I G m R P N A K(N)	m:Oxidized methionine	134.33	579.6239	1720.869	15.9885	-3.7	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
12555	dirMS_041712_NAR_50mM_minus2.14773.14773.3	3	8.95	0	4.12E+05		(K)QLEAID	(K)Q L/E/A I D/Q L/H/L E Y A/K(R)		152.43	557.6327	1670.875	0.0087	5.2	4.65	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
12556	dirMS_041712_NAR_50mM_minus2.17789.17789.3	3	8.95	1	2.31E+05		(K)LALFQA	(K)L/A|L/F Q A I/G K E V V D R(A)		170.53	520.3043	1558.895	0.0032	2	6.07	266161	5.68	HUMAN	E9PPU0	Epiplakin
12557	dirMS_041712_NAR_50mM_minus2.18203.18203.3	3	8.95	1	2.31E+05		(K)LKEAELL	(K)L K\E A E L\L|E|P L/M/P A I R(A)		172.78	574.9957	1722.982	-0.0097	-5.6	4.79	56164.6	6.01	HUMAN	E9PP73	Coatomer subunit beta (Fragment)
12558	dirMS_041712_NAR_50mM_minus2.7856.7856.3	3	8.95	0	4.58E+04		(R)QLSQAG	(R)Q L S Q A/G/S/F/S D G T/H G G L R(Y)		111.92	573.2875	1717.825	0.0227	13.2	6.74	266161	5.68	HUMAN	E9PPU0	Epiplakin
12559	dirMS_041712_NAR_60mM_minus.12676.12676.3	3	8.95	1	1.29E+05		(R)TPSDVK	(R)T\P/S D V K E L/V/L/D/N S R(S)		131.18	524.9451	1572.823	-0.002	-1.3	4.55	20111	4.47	HUMAN	H0YN26	Acidic leucine-rich nuclear phosphoprotein 32 family member A
12560	dirMS_041712_NAR_60mM_minus.18186.18186.3	3	8.95	1	1.37E+05		(R)SELELTL	(R)S E|L/E/L/T|L G K L E/Q V R(S)		163.05	538.9724	1614.906	-0.0035	-2.1	4.78	533778	5.74	HUMAN	Q15149	Plectin
12561	dirMS_041712_NAR_120mM_plus.8528.8549.3	3	8.95	0	1.29E+04		(K)MADHW	(K)M/A D/H/W E/T A P/R(H)		97.3	405.188	1213.542	0.0076	6.2	5.3	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
12562	dirMS_041712_NAR_20mM_plus.12474.12474.2	2	8.95	0	2.52E+05		(K)LLQLVE	(K)L/L/Q/L/V/E/D R(G)		159.55	493.2863	985.568	-0.0023	-2.4	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
12563	dirMS_041712_NAR_30mM_plus2.21223.21223.2	2	8.95	0	1.88E+05		(R)QTLMW	(R)Q T|L/M/W S A T/W/P K(E)		165.88	674.8389	1348.672	-0.0013	-1	8.75	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
12564	dirMS_041712_NAR_40mM_plus2.9266.9267.3	3	8.95	0	7.25E+03	M115m	(R)VmLGET	(R)V m|L/G E/T N/P A/D/S K/P G T I R(G)	m:Oxidized methionine	117.13	601.3077	1785.916	15.9922	-1.5	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
12565	dirMS_041712_NAR_50mM_plus2.17361.17361.3	3	8.95	1	9.11E+05		(R)VYAEDP	(R)V/Y|A E D/P Y K S F G L/P S I G R(L)		159.33	633.6509	1898.965	-0.0265	-14	6.04	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
12566	dirMS_041712_NAR_50mM_plus2.20223.20223.3	3	8.95	0	3.21E+05		(R)NEVSFV	(R)N E/V/S/F V I H/N L P\V L A K(M)		174.43	560.6531	1679.948	-0.0032	-1.9	6.75	35663.7	5.91	HUMAN	B4DWK0	Selenide, water dikinase 1
12567	dirMS_041712_NAR_50mM_plus2.5695.5695.3	3	8.95	1	1.06E+06		(K)TAGPIA	(K)T/A/G\P I/A S A Q K Q/P A G K(V)		91.9	475.5987	1424.786	-0.0041	-2.8	10	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
12568	dirMS_041712_NAR_50mM_plus2.9808.9808.3	3	8.95	1	5.18E+04		(R)VSSDNV	(R)V/S|S D N|V\A/D/L/H E K Y S G S T/P(-)		118.8	635.9661	1905.882	0.0013	0.7	4.54	17952.8	6.73	HUMAN	E9PAV2	Proteasome subunit beta type-5
12569	dirMS_041712_NAR_60mM_plus.10829.10829.3	3	8.95	1	3.23E+04		(K)KGENYV	(K)K G/E N Y V|Y|I/N E/A/T R(H)		114.25	519.5996	1556.77	0.0139	8.9	6.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
12570	dirMS_041712_NAR_60mM_plus.17347.17347.3	3	8.95	0	2.00E+05	S159s	(K)LsPSQH	(K)L s P S Q/H|L/A V L T K(Q)	s:N-acetylglucosamine (S)	147.5	499.6156	1293.753	203.0797	0.2	8.76	41560.9	5.97	HUMAN	B7Z6X4	Cyclin-I
12571	dirMS_041712_NAR_60mM_plus.19451.19612.3	3	8.95	1	4.46E+04		(R)SLADIA	(R)S L|A/D|I/A R/E E A S N F R(S)		159.53	526.9346	1578.787	0.0022	1.4	4.68	20458.8	4.99	HUMAN	G3V4X5	Proteasome subunit alpha type-3
12572	dirMS_041712_NAR_60mM_plus.6519.6519.2	2	8.95	1	1.43E+05		(K)LAQKNP	(K)L/A/Q K/N/P M/Y/Q\K(E)		92.67	610.8257	1220.646	-0.0015	-1.2	9.7	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
12573	dirMS_041712_NAR_120mM_minus.20158.20158.3	3	8.94	0	2.08E+05		(K)KPGGFD	(K)K P G G F D\I|S\L/F/Y/R(D)		166.23	467.2504	1399.737	-0.0002	-0.2	8.59	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
12574	dirMS_041712_NAR_120mM_minus.4379.4379.2	2	8.94	0	3.95E+05		(K)HYAMQ	(K)H/Y|A\M\Q|E\A K(Q)		72.92	489.2307	977.451	0.0032	3.3	6.75	39309.6	4.32	HUMAN	F8WCY5	Reticulocalbin-2
12575	dirMS_041712_NAR_20mM_minus.7053.7053.2	2	8.94	0	4.77E+05	M281m	(R)AEAESm	(R)A/E|A|E/S m Y Q/I K(Y)	m:Oxidized methionine	117.9	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
12576	dirMS_041712_NAR_50mM_minus2.10412.10412.3	3	8.94	0	3.38E+04		(R)GITINAA	(R)G I/T/I/N A A H/V/E Y S T A A R(H)		127.28	558.6229	1673.861	-0.0064	-3.8	6.75	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
12577	dirMS_041712_NAR_50mM_minus2.15641.15641.3	3	8.94	0	1.81E+05		(R)QVVQGI	(R)Q/V|V/Q\G L\L S E T/Y/L E A/H R(I)		156.92	614.9953	1842.971	0.0005	0.3	5.4	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
12578	dirMS_041712_NAR_50mM_minus2.7707.7707.3	3	8.94	1	1.66E+04	M26m	(K)LAEQAE	(K)L A|E Q A/E R Y D|D\M/A/A/C m K(S)	C:Carbamidomethylation m:Oxid	111.05	639.9511	1901.819	16.0197	12.9	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
12579	dirMS_041712_NAR_60mM_minus.14258.14258.3	3	8.94	1	8.82E+05		(R)MSMKE	(R)M S M K E V D E\Q|M|L/N V Q N K(N)		140.17	641.9701	1923.897	-0.0015	-0.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
12580	dirMS_041712_NAR_60mM_minus.18979.18979.3	3	8.94	0	4.77E+05		(R)LGFHLP	(R)L/G F H L\P\L/E|V/A/Y Q R(G)		168.4	514.9512	1542.843	-0.0037	-2.4	6.75	533778	5.74	HUMAN	Q15149	Plectin
12581	dirMS_041712_NAR_120mM_plus.10206.10353.4	4	8.94	0	2.30E+06		(K)NLPLAD	(K)N L\P/L A D Q/G S S H H I T/V/K(I)		107.22	429.9809	1716.903	-0.001	-0.6	6.92	334221.3	6.44	HUMAN	P15924	Desmoplakin
12582	dirMS_041712_NAR_120mM_plus.12179.12179.4	4	8.94	1	2.49E+06		(K)TLTTVQ	(K)T L|T\T V Q/G I/A/D D Y D K K K(L)		117.18	449.7412	1795.944	-0.0006	-0.4	5.71	13778.5	7.96	HUMAN	K7EM18	Eukaryotic translation initiation factor 1
12583	dirMS_041712_NAR_120mM_plus.14734.14734.3	3	8.94	1	4.93E+05		(R)KLDELY	(R)K\L/D E L|Y/G/T W R(K)		130.97	427.5607	1280.663	0.0042	3.3	6.07	37884.5	11.27	HUMAN	H3BM89	60S ribosomal protein L4
12584	dirMS_041712_NAR_120mM_plus.8654.8654.3	3	8.94	0	1.22E+06		(R)RPELED	(R)R P\E\L E/D/S/T/L/R(Y)		98.42	405.8796	1215.633	-0.0085	-7	4.68	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
12585	dirMS_041712_NAR_20mM_plus.13963.13963.2	2	8.94	0	3.83E+04		(R)TPAIPTA	(R)T/P A\I|P T/A/V N L A D S R(T)		167.85	713.3863	1425.77	-0.0043	-3	5.5	300351.7	12.1	HUMAN	Q9UQ35	Serine/arginine repetitive matrix protein 2
12586	dirMS_041712_NAR_20mM_plus.18881.18881.3	3	8.94	0	1.01E+05		(R)AAVPSG	(R)A A V/P S G A/S T G\I|Y E A/L/E L R(D)		201.5	602.3183	1804.944	-0.0036	-2	4.53	43048.9	4.99	HUMAN	B7Z2X9	Enolase
12587	dirMS_041712_NAR_30mM_plus2.20036.20036.2	2	8.94	0	2.43E+05		(K)LYNLFLK	(K)L/Y|N/L/F L/K(I)		159.32	455.7738	910.54	0.0007	0.7	8.59	41666	7.73	HUMAN	E9PDQ8	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial
12588	dirMS_041712_NAR_30mM_plus2.21647.21647.2	2	8.94	0	2.01E+05		(R)TTNFAG	(R)T T N F/A/G I L/S Q G L/R(I)		169.25	689.3749	1377.748	-0.006	-4.3	9.41	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
12589	dirMS_041712_NAR_30mM_plus2.22013.22211.2	2	8.94	0	2.42E+05		(R)AFITNIP	(R)A F|I/T/N/I|P F D V/K(W)		171.38	632.8481	1264.694	-0.0047	-3.7	5.88	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
12590	dirMS_041712_NAR_30mM_plus2.4930.4930.2	2	8.94	0	7.01E+05		(R)MGQTM	(R)M/G/Q|T M E/R(I)		77.38	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
12591	dirMS_041712_NAR_30mM_plus2.6832.6832.2	2	8.94	0	2.79E+04		(R)VLADPS	(R)V/L|A/D/P S D D\T K(G)		90.25	530.7617	1060.516	0.0004	0.4	3.93	266161	5.68	HUMAN	E9PPU0	Epiplakin
12592	dirMS_041712_NAR_30mM_plus2.8110.8110.2	2	8.94	0	1.34E+06		(K)QGGGG	(K)Q/G/G G/G/G\G G S V/P G I E R(M)		97.15	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
12593	dirMS_041712_NAR_40mM_plus2.9527.9527.3	3	8.94	0	3.47E+04		(R)GGGGN	(R)G G\G G\N F\G|P/G/P G S N F/R(G)		119.3	459.8801	1377.629	-0.0037	-2.7	9.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
12594	dirMS_041712_NAR_50mM_plus2.13501.13501.3	3	8.94	0	1.48E+06		(R)VLVVHD	(R)V/L/V/V/H D G F E G L/A K(G)		139.78	461.9229	1383.763	-0.0089	-6.5	5.32	18719.9	6.91	HUMAN	F8VP00	6-phosphofructokinase, muscle type (Fragment)
12595	dirMS_041712_NAR_50mM_plus2.17383.17383.3	3	8.94	1	9.75E+05		(K)DNNGVI	(K)D N|N G V/I G/L/L E/P M/K K(S)		159.12	509.9448	1527.82	-0.0001	-0.1	6.07	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
12596	dirMS_041712_NAR_60mM_plus.5161.5161.3	3	8.94	0	2.14E+04		(R)LENNEN	(R)L/E|N/N E/N K/P V T N S R(D)		85.37	505.5852	1514.756	-0.0147	-9.7	6.14	62504.2	9.01	HUMAN	Q9Y5A9	YTH domain family protein 2
12597	dirMS_041712_NAR_120mM_minus.7360.7360.2	2	8.93	1	9.63E+04		(R)LSVDYG	(R)L/S|V/D Y/G/K/K(S)		94.15	455.2555	909.504	-0.0003	-0.3	8.5	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
12598	dirMS_041712_NAR_20mM_minus.11533.11533.2	2	8.93	0	1.40E+05	M98m	(R)TLTIVDT	(R)T L/T/I|V D T\G I/G m/T K(A)	m:Oxidized methionine	163.17	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
12599	dirMS_041712_NAR_20mM_minus.13063.13063.2	2	8.93	0	1.03E+06	M73m	(R)AILVDLE	(R)A I/L\V|D\L/E|P/G T m D S V R(S)	m:Oxidized methionine	182.62	816.4184	1615.836	15.9935	-0.8	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
12600	dirMS_041712_NAR_20mM_minus.7083.7083.2	2	8.93	0	4.77E+05	M281m	(R)AEAESm	(R)A E|A\E/S/m/Y/Q I K(Y)	m:Oxidized methionine	117.9	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
12601	dirMS_041712_NAR_30mM_minus2.10378.10378.2	2	8.93	0	1.07E+05		(R)GGPISFS	(R)G G|P|I/S/F/S/S S/R(S)		109.98	497.7529	994.495	0.0033	3.3	9.75	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
12602	dirMS_041712_NAR_30mM_minus2.13955.13955.2	2	8.93	0	2.05E+05		(R)AFFSEVE	(R)A F|F/S/E V E/R(R)		129.48	492.7447	984.479	0.0036	3.7	4.53	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
12603	dirMS_041712_NAR_30mM_minus2.15823.15838.2	2	8.93	0	2.72E+05		(K)EGALDL	(K)E G A|L/D|L/S/G L R(A)		139.13	515.7847	1030.553	0.0094	9.1	4.37	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
12604	dirMS_041712_NAR_30mM_minus2.8625.8625.2	2	8.93	0	3.56E+04		(K)VLTPTQ	(K)V/L/T|P T Q V/K(N)		101.47	443.2733	885.54	-0.0011	-1.2	8.72	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
12605	dirMS_041712_NAR_60mM_minus.18418.18418.3	3	8.93	0	2.38E+05		(K)SQLDIII	(K)S Q|L/D I/I I H S L K(K)		164.08	422.9181	1266.742	-0.0019	-1.5	6.46	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
12606	dirMS_041712_NAR_60mM_minus.5632.5632.3	3	8.93	1	2.78E+05		(K)EAEGAP	(K)E\A E/G A P/Q/V E A G/K R(L)		87.38	447.8959	1341.676	-0.0026	-1.9	4.79	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
12607	dirMS_041712_NAR_60mM_minus.6481.6481.3	3	8.93	1	8.87E+04		(K)SESPKEP	(K)S E/S/P/K E|P E/Q L R(K)		94.9	433.8887	1299.654	-0.0024	-1.8	4.78	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
12608	dirMS_041712_NAR_60mM_minus.6621.6621.3	3	8.93	0	5.20E+04		(R)ATAPQT	(R)A T/A/P Q T Q/H V S P M R(Q)		95.48	475.2404	1423.711	-0.0044	-3.1	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
12609	dirMS_041712_NAR_20mM_plus.10011.10011.2	2	8.93	0	3.93E+05		(K)LVSESSD	(K)L/V/S E/S S D V/L P K(-)		140.85	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
12610	dirMS_041712_NAR_20mM_plus.15894.15894.2	2	8.93	0	2.02E+05		(R)GVVDSE	(R)G V|V|D S E D\I/P L N/L S\R(E)		180.07	757.3956	1513.786	-0.0017	-1.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
12611	dirMS_041712_NAR_20mM_plus.16247.16247.3	3	8.93	0	1.32E+05		(R)LLDAQL	(R)L/L D A Q L\A/T/G G I/V D/P/R(L)		183.53	513.6218	1538.854	-0.0028	-1.8	4.21	533778	5.74	HUMAN	Q15149	Plectin
12612	dirMS_041712_NAR_20mM_plus.16343.16343.3	3	8.93	0	1.29E+05		(R)LLDAQL	(R)L L D A Q L A\T G/G I/V/D/P R(L)		183.55	513.6218	1538.854	-0.0028	-1.8	4.21	533778	5.74	HUMAN	Q15149	Plectin
12613	dirMS_041712_NAR_20mM_plus.16925.16925.2	2	8.93	0	1.62E+05		(K)LGGSAV	(K)L G/G S A V/I/S L E G K|P L(-)		187.15	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
12614	dirMS_041712_NAR_20mM_plus.9177.9177.2	2	8.93	0	4.54E+04		(R)IIYGGSV	(R)I I|Y G G/S/V T G A/T C K(E)	C:Carbamidomethylation	135.4	663.8412	1326.672	0.0029	2.2	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
12615	dirMS_041712_NAR_30mM_plus2.13491.13491.2	2	8.93	0	7.08E+04		(R)WEYENE	(R)W/E|Y\E N E/L S K(V)		124.18	599.2758	1197.542	0.0021	1.7	4.25	334221.3	6.44	HUMAN	P15924	Desmoplakin
12616	dirMS_041712_NAR_30mM_plus2.5169.5169.2	2	8.93	0	1.16E+05		(K)SACGVC	(K)S A C/G|V/C P G R(L)	C:Carbamidomethylation	80.07	482.2128	963.414	0.0048	5	9.47	13520.9	11.92	HUMAN	P49207	60S ribosomal protein L34
12617	dirMS_041712_NAR_50mM_plus2.10052.10237.3	3	8.93	0	6.15E+05		(K)VGQEIE	(K)V/G Q|E/I E V R P G I\V/S/K(D)		121.05	504.2907	1510.859	-0.0012	-0.8	6.11	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
12618	dirMS_041712_NAR_50mM_plus2.10990.10990.3	3	8.93	0	1.82E+05		(K)GYAEVV	(K)G Y|A/E/V V/V A S/E N S V H K(L)		124.73	530.2702	1588.797	-0.0005	-0.3	5.4	16170.5	4.37	HUMAN	C9J286	Cleavage and polyadenylation-specificity factor subunit 7 (Fragment)
12619	dirMS_041712_NAR_50mM_plus2.16827.16827.3	3	8.93	0	7.42E+05		(R)QYYTLL	(R)Q Y\Y T L L\N Q/A/P/D M L H R(K)		156.87	621.6447	1862.922	-0.0022	-1.2	6.74	4335.1	9.82	HUMAN	E5RH00	Ras GTPase-activating protein-binding protein 1
12620	dirMS_041712_NAR_50mM_plus2.7469.7469.3	3	8.93	1	5.04E+04		(K)ALAAAG	(K)A L|A A/A G Y D V/E K\N N S R(I)		105.45	526.9339	1578.787	0.0001	0.1	6.11	21864.9	11.03	HUMAN	P10412	Histone H1.4
12621	dirMS_041712_NAR_50mM_plus2.9037.9037.3	3	8.93	1	2.24E+05		(K)LLDGPS	(K)L L|D/G/P S/T E K D L D/E/K(K)		115.05	520.5958	1559.78	-0.0071	-4.5	4.11	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
12622	dirMS_041712_NAR_60mM_plus.11890.11988.3	3	8.93	1	1.21E+06		(K)LKQSLP	(K)L K Q S L|P/P G L A V K(E)		119.55	417.5978	1250.783	-0.0042	-3.4	10	8274.8	10.19	HUMAN	P63173	60S ribosomal protein L38
12623	dirMS_041712_NAR_60mM_plus.5714.5714.3	3	8.93	1	1.91E+05		(R)SGGGYG	(R)S G/G/G/Y/G/G D R\S S G G G Y S G D\R(S)		88.07	583.5777	1748.722	-0.0033	-1.9	5.68	21563.9	10.01	HUMAN	K7EKB2	TATA-binding protein-associated factor 2N (Fragment)
12624	dirMS_041712_NAR_60mM_plus.6621.6621.3	3	8.93	0	7.55E+05		(K)LVDQSG	(K)L/V D Q/S/G|P P H E P K(F)		93.77	435.2257	1303.664	-0.0015	-1.2	5.32	142137.5	9.17	HUMAN	E7ENU4	Double-stranded RNA-specific adenosine deaminase
12625	dirMS_041712_NAR_60mM_plus.7189.7326.3	3	8.93	1	1.05E+06		(K)EMDEE	(K)E M/D E E/D K/A F/K(Q)		96.05	414.5175	1241.535	0.0025	2	4.18	7066.2	10	HUMAN	Q9Y2S6	Translation machinery-associated protein 7
12626	dirMS_041712_NAR_120mM_minus.16421.16421.3	3	8.92	1	1.67E+04	M1888m S	(K)KmFHD	(K)K m F H D D E|L E/E s E K(F)	m:Oxidized methionine s:N-a	144.07	619.2763	1636.716	219.0984	13	4.35	320853.7	5.82	HUMAN	Q9H5I5	Piezo-type mechanosensitive ion channel component 2
12627	dirMS_041712_NAR_30mM_minus2.11340.11340.2	2	8.92	0	2.37E+05		(R)QPSQGF	(R)Q P/S/Q|G|P T F/G I K(G)		115.4	580.3084	1159.611	-0.0011	-0.9	8.75	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
12628	dirMS_041712_NAR_30mM_minus2.11439.11439.2	2	8.92	0	3.26E+05		(R)VQELPL	(R)V Q|E/L P L A/R(I)		115.7	463.2738	925.547	-0.0062	-6.7	5.97	16202.4	6.61	HUMAN	E9PI99	Nuclear transcription factor Y subunit gamma (Fragment)
12629	dirMS_041712_NAR_30mM_minus2.19810.19810.2	2	8.92	0	1.11E+06		(K)FLPLFDR	(K)F L|P/L F D R(V)		164.83	454.2604	907.504	0.0099	10.9	5.84	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
12630	dirMS_041712_NAR_50mM_minus2.17689.17689.3	3	8.92	1	1.01E+05		(K)ITQDIFQ	(K)I/T/Q/D/I\F/Q/Q L L K R(G)		169.85	501.6277	1502.869	-0.0004	-0.3	8.75	72796.9	6.75	HUMAN	A6NC17	Methionine--tRNA ligase, cytoplasmic
12631	dirMS_041712_NAR_60mM_minus.15686.15686.3	3	8.92	1	1.72E+05		(R)GRLPLL	(R)G R L\P\L\L/A/V C D/Y K(Q)	C:Carbamidomethylation	146.87	468.9273	1404.767	0.0006	0.4	8.59	533778	5.74	HUMAN	Q15149	Plectin
12632	dirMS_041712_NAR_60mM_minus.19409.19409.3	3	8.92	1	6.95E+05		(K)LASDLLE	(K)L/A/S/D L L E W I R/R(T)		172.9	457.9288	1371.774	-0.0025	-1.8	6.07	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
12633	dirMS_041712_NAR_60mM_minus.5152.5152.3	3	8.92	1	6.90E+04		(K)EEASGS	(K)E E A/S/G S/S/V T A E E A K K(F)		83.3	508.2453	1522.723	-0.0018	-1.2	4.49	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
12634	dirMS_041712_NAR_20mM_plus.10324.10324.2	2	8.92	0	1.17E+05	M189m M	(K)SLAmEm	(K)S L/A m/E/m V/L/T G/D R(I)	m:Oxidized methionine	144.1	677.8126	1322.644	31.9736	-12	4.37	31843.3	8.87	HUMAN	P30084	Enoyl-CoA hydratase, mitochondrial
12635	dirMS_041712_NAR_20mM_plus.14502.14502.2	2	8.92	0	1.80E+05		(K)VSTLPA	(K)V S|T|L/P A I T L K(L)		172.07	521.8283	1042.651	-0.0013	-1.3	8.72	20599.3	9.19	HUMAN	H7C1V0	Cathepsin D light chain (Fragment)
12636	dirMS_041712_NAR_20mM_plus.16665.16665.2	2	8.92	0	1.54E+05		(R)LLEAQIA	(R)L L\E\A\Q\I|A\T\G G I I D/P K(E)		185.72	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
12637	dirMS_041712_NAR_20mM_plus.6955.6955.2	2	8.92	0	9.56E+04		(K)AAAAAA	(K)A A/A\A/A|A/A\L\Q A K(S)		114.28	478.7792	956.552	-0.0012	-1.3	8.8	37884.5	11.27	HUMAN	H3BM89	60S ribosomal protein L4
12638	dirMS_041712_NAR_20mM_plus.8153.8153.2	2	8.92	0	5.54E+04		(K)AQLEPV	(K)A Q|L/E/P V/A S P A K(K)		126.37	555.8092	1110.615	-0.0042	-3.8	6.05	533778	5.74	HUMAN	Q15149	Plectin
12639	dirMS_041712_NAR_40mM_plus2.7714.7714.2	2	8.92	0	8.63E+04		(R)FGQGG	(R)F/G\Q|G/G A\G|P V/G G/Q G P R(G)		105.47	671.3368	1341.666	0.0005	0.4	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich

12640	dirMS_041712_NAR_50mM_plus2.10723.10723.3	3	8.92	1	4.93E+05		(R)DGKLVS	(R)D G K L V S E|S S/D V L/P/K(-)		124.1	491.9313	1473.78	-0.0002	-0.1	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
12641	dirMS_041712_NAR_50mM_plus2.11799.11799.3	3	8.92	1	7.42E+05		(R)INVYYN	(R)I/N|V/Y/Y N E A T G G K Y/V P R(A)		130.43	615.3151	1843.934	-0.003	-1.6	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
12642	dirMS_041712_NAR_50mM_plus2.14498.14515.3	3	8.92	0	5.58E+05		(R)LINANM	(R)L I/N A/N M M V L/G/H E/P R(Q)		145.02	532.2775	1594.819	-0.0013	-0.8	6.75	34747.6	6.06	HUMAN	O00487	26S proteasome non-ATPase regulatory subunit 14
12643	dirMS_041712_NAR_50mM_plus2.16447.16447.3	3	8.92	0	7.49E+05		(K)ANIVHL	(K)A N\I V H L M/L/S S/P E/Q I Q K(Q)		154.68	603.3265	1807.974	-0.0085	-4.7	6.79	104619	5.75	HUMAN	F8W904	Exportin-2
12644	dirMS_041712_NAR_50mM_plus2.22163.22163.3	3	8.92	1	1.16E+04		(K)EGGLGP	(K)E G/G/L|G/P L N I/P L L A D V T R R(L)		190.08	631.029	1891.076	-0.0035	-1.9	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
12645	dirMS_041712_NAR_50mM_plus2.9921.9921.3	3	8.92	1	9.24E+05	M227m	(R)mQKEIT	(R)m Q K E I T/A\L/A/P S T M/K(I)	m:Oxidized methionine	119.38	522.2726	1548.812	15.9908	-2.6	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
12646	dirMS_041712_NAR_60mM_plus.8072.8260.3	3	8.92	1	6.10E+05		(K)ALSRQE	(K)A L/S R Q E\M\Q/E/V/Q/S S/R(S)		100.33	550.2735	1648.807	-0.0012	-0.7	6.19	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
12647	dirMS_041712_NAR_120mM_minus.13524.13524.3	3	8.91	0	4.86E+05		(K)YNPTW	(K)Y N|P T W/H/C I/V G R(N)	C:Carbamidomethylation	128.35	468.2346	1402.669	0.0208	14.8	8.75	10536.9	6.9	HUMAN	P63167	Dynein light chain 1, cytoplasmic
12648	dirMS_041712_NAR_20mM_minus.12352.12352.3	3	8.91	0	7.61E+05	M73m	(R)AVLVDL	(R)A V\L\V D L\E/P G/T/m/D S V R(S)	m:Oxidized methionine	172.45	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
12649	dirMS_041712_NAR_20mM_minus.12357.12357.3	3	8.91	0	7.85E+05	M73m	(R)AVLVDL	(R)A V L\V D L/E/P G T m/D S V R(S)	m:Oxidized methionine	172.48	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
12650	dirMS_041712_NAR_30mM_minus2.17762.17762.2	2	8.91	0	6.65E+04		(K)IFFAGDT	(K)I F/F/A/G D T I P K(S)		151.17	554.8038	1108.604	-0.0034	-3.1	5.84	258215.9	5.48	HUMAN	E7EN95	Filamin-B
12651	dirMS_041712_NAR_30mM_minus2.7068.7068.2	2	8.91	0	3.32E+05		(R)TYDETY	(R)T Y|D/E/T Y Q R(Y)		92.9	538.2398	1075.469	0.0032	3	4.37	40616.6	9.46	HUMAN	H0YHI8	Protein phosphatase 1 regulatory subunit 12A (Fragment)
12652	dirMS_041712_NAR_30mM_minus2.9512.9512.2	2	8.91	0	1.22E+05		(K)IIDIQEK	(K)I/I/D/I Q/E/K(V)		106.07	429.7546	858.493	0.0088	10.3	4.37	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
12653	dirMS_041712_NAR_50mM_minus2.12136.12136.3	3	8.91	0	9.91E+04		(R)LAILGIH	(R)L A|I L/G I/H/N E V S K(I)		137.17	431.9219	1293.753	-0.0014	-1.1	6.75	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
12654	dirMS_041712_NAR_50mM_minus2.17826.17826.3	3	8.91	1	2.31E+05		(K)LALFQAI	(K)L A|L/F Q/A I/G K E V V D R(A)		170.53	520.3043	1558.895	0.0032	2	6.07	266161	5.68	HUMAN	E9PPU0	Epiplakin
12655	dirMS_041712_NAR_60mM_minus.18734.18734.3	3	8.91	0	2.88E+05		(K)TFLVWV	(K)T F|L/V/W/V N E E D H L R(V)		165.82	553.2818	1657.833	-0.0024	-1.5	4.65	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
12656	dirMS_041712_NAR_60mM_minus.18854.18854.3	3	8.91	0	1.43E+05		(K)VAHALA	(K)V A H A L A E\G\L\G\V/I|A C I G E K(L)	C:Carbamidomethylation	166.95	603.3262	1807.974	-0.0094	-5.2	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
12657	dirMS_041712_NAR_120mM_plus.11271.11271.3	3	8.91	1	2.23E+05		(K)FGQYNK	(K)F/G/Q/Y N K E D|P T S F R(L)		112.6	530.2516	1588.739	0.0012	0.8	6.07	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
12658	dirMS_041712_NAR_120mM_plus.7203.7203.2	2	8.91	1	1.06E+06		(R)LSVDYG	(R)L/S|V D/Y G K/K(S)		90.95	455.2548	909.504	-0.0017	-1.9	8.5	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
12659	dirMS_041712_NAR_20mM_plus.12339.12339.2	2	8.91	0	1.17E+05		(K)VNQIGS	(K)V N/Q\I/G/S V/T E S I/Q A C/K(L)	C:Carbamidomethylation	157.67	817.4114	1633.821	-0.0059	-3.6	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
12660	dirMS_041712_NAR_20mM_plus.17516.17516.3	3	8.91	0	1.38E+04	M199m	(K)SmVPV	(K)S m V P V Q V/Q/L/D\V/P V V K(V)	m:Oxidized methionine	192.58	551.9759	1637.93	15.9837	-6.8	5.55	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
12661	dirMS_041712_NAR_30mM_plus2.16687.16687.2	2	8.91	0	3.12E+05		(R)SIQADG	(R)S I|Q A/D G L\V/W/G S S K(L)		140.42	674.3475	1347.69	-0.0026	-1.9	5.55	24934.4	4.5	HUMAN	P24534	Elongation factor 1-beta
12662	dirMS_041712_NAR_30mM_plus2.20362.20362.2	2	8.91	0	6.67E+04		(K)LAVNM	(K)L/A|V/N M/V/P F P R(L)		160.6	572.32	1143.634	-0.0016	-1.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
12663	dirMS_041712_NAR_30mM_plus2.21507.21507.2	2	8.91	0	2.83E+05		(R)EADDIV	(R)E A/D/D I/V/N W L K(K)		167.57	601.81	1202.605	0.0075	6.3	4.03	26363.4	4.91	HUMAN	I3L312	Protein disulfide-isomerase (Fragment)
12664	dirMS_041712_NAR_40mM_plus2.10460.10460.2	2	8.91	0	9.40E+04		(K)IGGIGTV	(K)I/G|G I|G/T V/P V G R(V)		125.75	513.3081	1025.61	-0.0013	-1.2	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
12665	dirMS_041712_NAR_40mM_plus2.17507.17507.3	3	8.91	0	2.47E+04		(R)GTEDITS	(R)G T E/D\I/T S P/H G I/P L D\L/L D R(V)		169.42	650.3372	1948.997	-0.0004	-0.2	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
12666	dirMS_041712_NAR_40mM_plus2.6309.6309.2	2	8.91	0	5.99E+04		(R)ISSSSFS	(R)I/S/S/S/S/F S R(V)		96.4	435.7189	870.432	-0.001	-1.2	9.75	19288.4	10.19	HUMAN	F8VQY3	Keratin, type II cytoskeletal 8 (Fragment)
12667	dirMS_041712_NAR_50mM_plus2.13696.13696.3	3	8.91	0	4.46E+05		(K)FLSDPQ	(K)F L/S/D/P Q/V H T V L V E/R(S)		140.13	547.2984	1639.88	0.0004	0.3	5.32	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
12668	dirMS_041712_NAR_50mM_plus2.7576.7576.3	3	8.91	0	8.41E+04		(R)AGAISA	(R)A G\A|I|S/A S G/P E L Q/G A G H S K(L)		105.87	546.6129	1637.824	0	0	6.79	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
12669	dirMS_041712_NAR_60mM_plus.21292.21292.3	3	8.91	1	1.34E+05		(R)TLAEIAK	(R)T L|A E I/A K V E L D N/M P L R(G)		175.47	604.9996	1812.989	-0.0045	-2.5	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
12670	dirMS_041712_NAR_60mM_plus.9160.9160.3	3	8.91	0	1.59E+06		(K)EFHLNE	(K)E F/H L N E|S/G D/P S S K(S)		105.52	482.8882	1446.65	0.0005	0.3	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
12671	dirMS_041712_NAR_20mM_minus.8930.8930.2	2	8.9	0	2.76E+05		(R)ALGQN	(R)A L G Q|N/P T N/A/E V/L/K(V)		138.8	677.871	1354.733	0.0022	1.6	6.05	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
12672	dirMS_041712_NAR_30mM_minus2.14058.14058.2	2	8.9	0	2.61E+05		(K)CDFPIM	(K)C D|F/P\I/M/K(F)	C:Carbamidomethylation	129.72	455.7144	910.416	0.0054	5.9	5.84	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
12673	dirMS_041712_NAR_30mM_minus2.15676.15676.2	2	8.9	0	2.34E+05	M213m M	(R)FLEImm	(R)F|L|E I m m H E G\K(C)	m:Oxidized methionine	138.42	633.8048	1234.596	32.0064	13.1	5.4	31077.7	6.05	HUMAN	A0PJE2-3	Isoform 3 of Dehydrogenase/reductase SDR family member 12
12674	dirMS_041712_NAR_40mM_minus2.11814.11814.3	3	8.9	0	1.13E+05		(R)LASTLV	(R)L A|S T L V H L G E Y/Q A A/V D/G A R(K)		152.88	657.6842	1971.029	0.0086	4.4	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
12675	dirMS_041712_NAR_50mM_minus2.11230.11230.3	3	8.9	1	1.29E+05		(K)NQVAL	(K)N Q|V/A L/N/P\Q N T V F D\A K/R(L)		132.68	605.6545	1814.951	-0.0018	-1	8.75	70336.2	5.48	HUMAN	P08107	Heat shock 70 kDa protein 1A/1B
12676	dirMS_041712_NAR_50mM_minus2.18104.18104.3	3	8.9	0	2.77E+05		(R)SLHDAL	(R)S L H D A\L C|V|L/A/Q T\V K(D)	C:Carbamidomethylation	171.77	518.9488	1554.831	0.001	0.6	6.46	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
12677	dirMS_041712_NAR_60mM_minus.17239.17239.3	3	8.9	1	3.68E+05		(R)KAPSDL	(R)K A P S D\L|Y\Q/I/I L K(A)		156.28	463.6095	1388.815	-0.0008	-0.6	8.5	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
12678	dirMS_041712_NAR_60mM_minus.8784.8784.3	3	8.9	1	5.81E+03		(K)AQAEVE	(K)A Q\A E/V/E G L G K/G/V A R(L)		108.32	462.2579	1384.754	0.0048	3.5	6.19	533778	5.74	HUMAN	Q15149	Plectin
12679	dirMS_041712_NAR_120mM_plus.11045.11045.4	4	8.9	0	8.23E+05		(R)GAIQFV	(R)G A I Q/F V/T H/Y Q/H/S S T Q R(R)		111.1	465.7339	1859.915	-0.0009	-0.5	8.76	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
12680	dirMS_041712_NAR_20mM_plus.18070.18070.2	2	8.9	0	1.74E+05		(K)VANVSL	(K)V A/N|V/S/L L A L Y K(G)		195.47	595.8558	1190.714	-0.01	-8.4	8.56	15978.4	10.84	HUMAN	P62266	40S ribosomal protein S23
12681	dirMS_041712_NAR_30mM_plus2.12709.12709.2	2	8.9	0	3.39E+05		(K)IGVTVLS	(K)I/G|V/T V L S/R(I)		120	422.7657	844.525	-0.001	-1.1	9.75	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
12682	dirMS_041712_NAR_30mM_plus2.14373.14373.2	2	8.9	0	2.16E+05		(K)ASEGPA	(K)A/S\E G/P A/F/F\P G R(C)		127.95	568.2831	1135.553	0.0058	5.1	6.05	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
12683	dirMS_041712_NAR_30mM_plus2.20228.20228.2	2	8.9	0	1.14E+05		(K)TNVAL	(K)T N\V/A/L/M/C M L/R(E)	C:Carbamidomethylation	159.72	604.8021	1208.595	0.0021	1.7	9.41	71929.1	5.1	HUMAN	C9JAQ9	U5 small nuclear ribonucleoprotein 200 kDa helicase
12684	dirMS_041712_NAR_40mM_plus2.13502.13502.3	3	8.9	0	1.42E+04		(K)LTEVPV	(K)L T\E\V/P V E P V/L T V/H/P E/S K(S)		146.12	625.3454	1874.027	-0.0053	-2.8	4.75	81726.4	6.71	HUMAN	Q9H307	Pinin
12685	dirMS_041712_NAR_40mM_plus2.16818.16818.3	3	8.9	1	1.02E+05		(R)ALGTEV	(R)A L/G/T/E V/I/Q L/F P E K G N M G K(I)		165.6	644.6779	1932.026	-0.0068	-3.5	6.18	67184.7	9.24	HUMAN	O95831	Apoptosis-inducing factor 1, mitochondrial
12686	dirMS_041712_NAR_40mM_plus2.17469.17469.3	3	8.9	0	1.58E+05		(R)VYAILTH	(R)V/Y|A I L/T/H G\I/F S G P A I S R(I)		169.33	601.3376	1801.996	0.0023	1.3	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
12687	dirMS_041712_NAR_50mM_plus2.5578.5578.3	3	8.9	1	1.11E+05		(K)DSYVGD	(K)D S/Y/V|G D/E/A/Q S K/R(G)		90.6	452.2114	1354.623	-0.0037	-2.7	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
12688	dirMS_041712_NAR_60mM_plus.13920.13920.3	3	8.9	1	9.60E+05		(K)TTVKDL	(K)T T V/K D L S\E|L/G|S V/R(T)		129.52	468.9268	1404.769	-0.0034	-2.4	5.74	533778	5.74	HUMAN	Q15149	Plectin
12689	dirMS_041712_NAR_60mM_plus.17551.17551.3	3	8.9	1	8.36E+05		(R)DKLNNL	(R)D K\L N N\L/V/L/F/D K(A)		148.42	440.2499	1318.737	-0.0014	-1	5.96	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
12690	dirMS_041712_NAR_120mM_minus.16726.16726.3	3	8.89	1	4.41E+05		(R)ISEQFTA	(R)I/S/E/Q F\T A M F R/R(K)		145.63	462.5714	1385.699	0.0002	0.2	9.6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
12691	dirMS_041712_NAR_20mM_minus.11247.11247.2	2	8.89	0	2.79E+05		(K)LSELEAA	(K)L S E|L|E A/A/L Q/R(A)		159.5	565.3134	1129.621	-0.0016	-1.5	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
12692	dirMS_041712_NAR_20mM_minus.12290.12290.2	2	8.89	0	1.74E+05		(R)AAVIGP	(R)A A\V|I/G/P D V F\A K(L)		171.48	544.3103	1087.615	-0.0013	-1.2	5.88	266161	5.68	HUMAN	E9PPU0	Epiplakin
12693	dirMS_041712_NAR_20mM_minus.14693.14693.3	3	8.89	0	3.68E+05		(K)LAVEAL	(K)L A V E A\L S S L/D/G D L A G R(Y)		201.3	529.6163	1586.838	-0.0041	-2.6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
12694	dirMS_041712_NAR_30mM_minus2.12490.12490.2	2	8.89	0	2.66E+05		(R)TLSGME	(R)T L|S G M/E/S/Y/C V R(A)	C:Carbamidomethylation	122.02	651.795	1302.582	0.001	0.8	5.66	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
12695	dirMS_041712_NAR_50mM_minus2.14979.14979.3	3	8.89	1	8.94E+05		(R)IINEPTA	(R)I I|N E/P T A A A I/A Y G L D K R(E)		152.67	606.0022	1815.996	-0.0043	-2.4	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
12696	dirMS_041712_NAR_60mM_minus.12760.12760.3	3	8.89	1	1.93E+05		(K)LSAEKV	(K)L/S\A E K V/E/I/A T/L T R(E)		130.95	477.6112	1430.821	-0.0023	-1.6	6.14	26661.1	7.81	HUMAN	H0YL69	Proteasome subunit alpha type (Fragment)
12697	dirMS_041712_NAR_60mM_minus.17897.17897.3	3	8.89	1	3.70E+05		(K)NLRDID	(K)N L R D I D\E\V|S/S L L/R(T)		160.93	510.6099	1529.828	-0.013	-8.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
12698	dirMS_041712_NAR_120mM_plus.10884.10884.3	3	8.89	0	1.18E+06		(R)GSAVH	(R)G S|A/V/H/Q/L/S E E L R(C)		110.8	442.5657	1325.681	0.0017	1.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
12699	dirMS_041712_NAR_20mM_plus.10821.10821.2	2	8.89	0	7.09E+03	M142m	(R)VVNVSS	(R)V V|N|V/S S I\m S V/R(A)	m:Oxidized methionine	146.97	603.8291	1190.656	15.9948	-0.1	9.72	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
12700	dirMS_041712_NAR_20mM_plus.15996.15996.2	2	8.89	0	3.61E+05		(R)GNPTVE	(R)G N/P/T V/E/V D L F/T/S K(G)		180.82	703.861	1406.716	-0.0015	-1	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
12701	dirMS_041712_NAR_20mM_plus.17038.17038.2	2	8.89	0	8.06E+04		(K)VNIIPIIA	(K)V/N/I/I/P I I A/K(A)		189.2	490.8283	980.65	-0.001	-1	8.72	51212	5.84	HUMAN	A6NFQ9	Septin-8
12702	dirMS_041712_NAR_20mM_plus.19318.19318.2	2	8.89	0	8.40E+04		(R)ALIAGG	(R)A L I/A|G/G G/A|P E I\E L A L R(L)		205.1	775.9467	1550.89	-0.0039	-2.5	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
12703	dirMS_041712_NAR_20mM_plus.9300.9300.2	2	8.89	0	9.62E+03		(K)AEPVEV	(K)A E|P V/E V/V\A P R(G)		135.58	533.798	1066.589	-0.0004	-0.4	4.53	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
12704	dirMS_041712_NAR_30mM_plus2.11996.11996.2	2	8.89	0	6.83E+05		(K)CGDLVF	(K)C G\D|L/V/F A/K(M)	C:Carbamidomethylation	116.12	455.2298	909.45	0.0025	2.7	5.84	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
12705	dirMS_041712_NAR_30mM_plus2.12296.12296.2	2	8.89	0	9.10E+05		(K)EVDEQ	(K)E/V/D/E Q\M L\N V/Q/N/K(N)		117.03	723.8478	1446.689	-0.001	-0.7	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
12706	dirMS_041712_NAR_30mM_plus2.12711.12711.2	2	8.89	0	3.63E+05		(R)ELAEDG	(R)E L/A|E/D G/Y|S|G V\E V R(V)		120.58	712.3382	1423.67	-0.0008	-0.6	4	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
12707	dirMS_041712_NAR_30mM_plus2.21870.21870.2	2	8.89	0	4.06E+05		(R)FSWNV	(R)F S|W/N/V W|P S S R(L)		169.8	633.3085	1265.606	0.0035	2.8	9.75	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
12708	dirMS_041712_NAR_30mM_plus2.5897.5968.2	2	8.89	0	4.28E+05		(K)MIYASS	(K)M/I|Y A/S/S/K(D)		85.65	400.2035	799.402	-0.0021	-2.7	8.34	22956	8.8	HUMAN	E9PK25	Cofilin-1
12709	dirMS_041712_NAR_40mM_plus2.15537.15537.3	3	8.89	0	1.01E+04		(R)LQVIVC	(R)L Q/V|I V C S A T L H S F D|V/K(K)	C:Carbamidomethylation	158.6	606.3237	1816.963	-0.006	-3.3	6.74	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
12710	dirMS_041712_NAR_40mM_plus2.7149.7149.2	2	8.89	0	1.60E+04		(R)VGFAEA	(R)V/G|F/A E/A A R(L)		101.97	410.7186	820.431	-0.0013	-1.5	5.97	20599.3	9.19	HUMAN	H7C1V0	Cathepsin D light chain (Fragment)
12711	dirMS_041712_NAR_50mM_plus2.15628.15628.3	3	8.89	0	1.49E+06		(R)LASTLV	(R)L A|S T/L V H L G E Y Q A/A/V D G A R(K)		149.7	657.6802	1971.029	-0.0034	-1.7	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
12712	dirMS_041712_NAR_60mM_plus.12833.12833.3	3	8.89	1	9.04E+05	M232m	(R)MSmKE	(R)M S m K E V D\E Q|M|L/N V Q/N K(N)	m:Oxidized methionine	123.57	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
12713	dirMS_041712_NAR_60mM_plus.16983.16983.3	3	8.89	1	6.61E+06		(K)LKVPEW	(K)L K/V P E/W/V/D T/V K(L)		145.77	438.5872	1313.746	0.0007	0.5	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
12714	dirMS_041712_NAR_60mM_plus.18238.18238.3	3	8.89	1	5.89E+04		(R)STVRDI	(R)S T V\R D I\D|P Q/N D/L T F/L R(I)		152.85	630.661	1889.972	-0.0031	-1.7	4.43	16537.8	6.59	HUMAN	B1AKR6	Dynein light chain roadblock-type 1
12715	dirMS_041712_NAR_120mM_minus.10070.10070.4	4	8.88	1	1.65E+05		(R)AQGEP	(R)A/Q/G E/P V/A G H E S P K I/P Y E/K(Q)		109.07	484.9989	1936.976	-0.0025	-1.3	5.5	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
12716	dirMS_041712_NAR_40mM_minus2.12739.12739.3	3	8.88	0	1.40E+05		(K)IEVIKPG	(K)I/E|V I/K/P G D L/G V D\L T S K(L)		159.02	561.989	1683.953	-0.0003	-0.2	4.56	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
12717	dirMS_041712_NAR_50mM_minus2.11589.11589.3	3	8.88	0	1.03E+05		(R)VTCPNH	(R)V T|C/P N H P D A I\L\V/E D Y/R(A)	C:Carbamidomethylation	134.67	633.641	1898.907	0.0019	1	4.54	25558.6	9.3	HUMAN	B1APE1	General transcription factor IIB (Fragment)
12718	dirMS_041712_NAR_50mM_minus2.7845.7845.3	3	8.88	1	1.10E+05		(K)VLLQSK	(K)V L|L/Q/S K D Q\I/T A G N A A R(K)		111.77	562.3158	1684.934	-0.0012	-0.7	8.72	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
12719	dirMS_041712_NAR_60mM_minus.10727.11060.3	3	8.88	1	2.04E+06		(R)FPGQLN	(R)F/P G Q/L/N|A D L R K(L)		121.02	420.2346	1258.69	-0.001	-0.8	8.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
12720	dirMS_041712_NAR_60mM_minus.6046.6046.3	3	8.88	1	2.59E+06		(K)DSYVGD	(K)D S|Y/V/G D E A Q S K/R(G)		90.6	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
12721	dirMS_041712_NAR_120mM_plus.4397.4397.3	3	8.88	1	2.63E+05		(R)AAEEED	(R)A/A/E\E E/D E A D/P K R(Q)		72.22	453.8721	1359.602	-0.0005	-0.4	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
12722	dirMS_041712_NAR_20mM_plus.14950.14950.2	2	8.88	0	1.45E+05		(K)VLEQLT	(K)V L/E Q L|T/G Q/T P V|F S K(A)		174.65	773.9244	1546.848	-0.006	-3.9	5.97	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
12723	dirMS_041712_NAR_20mM_plus.15160.15160.2	2	8.88	0	5.88E+04		(R)EQLAIA	(R)E Q|L/A/I/A/E F A R(S)		176.1	574.312	1147.611	0.0061	5.3	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
12724	dirMS_041712_NAR_20mM_plus.16276.16276.2	2	8.88	0	6.43E+04		(R)LSNIFV	(R)L S N I|F V/I G K(G)		183.62	495.8022	990.598	-0.0011	-1.1	8.75	29825.4	10.37	HUMAN	P62701	40S ribosomal protein S4, X isoform
12725	dirMS_041712_NAR_20mM_plus.7307.7307.2	2	8.88	0	3.27E+05	M281m	(R)AEAESm	(R)A E|A E/S m Y Q/I/K(Y)	m:Oxidized methionine	118.62	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
12726	dirMS_041712_NAR_30mM_plus2.12564.12564.2	2	8.88	0	6.78E+05		(R)SGYLLP	(R)S G Y/L/L/P D/T K(A)		118.08	497.2641	993.525	-0.0042	-4.2	5.55	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
12727	dirMS_041712_NAR_30mM_plus2.4856.4856.2	2	8.88	1	2.37E+05		(R)NTKGG	(R)N T/K G G D/A\P A\A\G\E|D A(-)		76.98	637.286	1273.565	-0.0008	-0.6	4.03	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
12728	dirMS_041712_NAR_40mM_plus2.6384.6384.2	2	8.88	0	4.15E+03		(R)IYVSAN	(R)I/Y|V/S A N S G A R(I)		96.6	519.2719	1037.537	-0.0009	-0.9	8.75	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
12729	dirMS_041712_NAR_40mM_plus2.9574.9574.2	2	8.88	0	7.31E+04		(R)GGGGN	(R)G G G/G N F/G|P G P G S N/F R(G)		119.27	689.3182	1377.629	-0.0003	-0.2	9.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
12730	dirMS_041712_NAR_50mM_plus2.21775.21775.3	3	8.88	1	1.20E+05		(K)ESLCQA	(K)E S/L/C/Q A/A/L/G L/I L K E K(A)	C:Carbamidomethylation	185.33	558.3196	1672.93	0.014	8.4	6.24	66923.1	6.88	HUMAN	E9PG35	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (Fragment)
12731	dirMS_041712_NAR_50mM_plus2.6233.6233.3	3	8.88	0	4.48E+04	M437m	(R)LESGM	(R)L/E/S G/M Q/N/m S I H T K(T)	m:Oxidized methionine	97.02	497.9026	1475.698	15.9951	0.1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
12732	dirMS_041712_NAR_60mM_plus.18973.18973.3	3	8.88	0	1.68E+05		(R)NHPGLL	(R)N H/P G L L\L/M/D/T T F/R(D)		156.75	505.6001	1514.778	0.0073	4.8	6.74	130372.9	6.37	HUMAN	P11498	Pyruvate carboxylase, mitochondrial
12733	dirMS_041712_NAR_30mM_minus2.13037.13037.2	2	8.87	2	3.55E+05		(K)KSFKSPE	(K)K S/F|K S P E P R(L)		124.82	538.2931	1075.59	-0.0105	-9.8	9.99	31183.3	5.86	HUMAN	P21583	Kit ligand
12734	dirMS_041712_NAR_30mM_minus2.15705.15705.2	2	8.87	1	4.79E+03		(K)LFSAAE	(K)L F/S A A E A R Q K(F)		139.85	560.8108	1120.611	0.0034	3	8.75	22297.1	5.98	HUMAN	A6NL66	Leucine-rich repeat-containing protein 42 (Fragment)
12735	dirMS_041712_NAR_30mM_minus2.16988.16988.2	2	8.87	0	1.94E+05		(R)IYNVIGT	(R)I/Y|N/V|I G T L/R(G)		146.9	524.8092	1048.615	-0.0038	-3.7	8.75	84557.3	6.5	HUMAN	Q04609	Glutamate carboxypeptidase 2
12736	dirMS_041712_NAR_30mM_minus2.7246.7246.2	2	8.87	0	2.65E+05		(K)SAVLQE	(K)S A|V/L/Q\E A R(I)		94.4	437.2408	873.479	-0.0045	-5.2	5.72	28218.2	9.35	HUMAN	F6X838	Coatomer subunit gamma-2
12737	dirMS_041712_NAR_50mM_minus2.12738.12738.3	3	8.87	0	2.86E+05		(K)EGKPTIV	(K)E G K P T I|V\E E/D|D/P E L/F K(Q)		140.9	615.9772	1845.912	0.0054	2.9	4.08	29841.1	9.04	HUMAN	O75937	DnaJ homolog subfamily C member 8
12738	dirMS_041712_NAR_60mM_minus.14586.14586.3	3	8.87	0	3.84E+05		(K)AVGHPF	(K)A V/G H/P/F\V|I Q|L G/R(I)		141.82	431.9182	1293.743	-0.0026	-2	9.8	124524.8	5.71	HUMAN	O14980	Exportin-1
12739	dirMS_041712_NAR_120mM_plus.16184.16184.4	4	8.87	2	2.64E+05		(R)EDLRLP	(R)E D L R L|P/E/G D L/G/K E I E Q/K(Y)		138.37	493.0097	1969.024	-0.0067	-3.4	4.36	16346.3	4.85	HUMAN	I3L397	Eukaryotic translation initiation factor 5A-1 (Fragment)
12740	dirMS_041712_NAR_20mM_plus.10075.10075.2	2	8.87	0	1.95E+05		(K)GEATVS	(K)G E\A T V/S/F/D D/P P S/A K(A)		141.13	710.8324	1420.659	-0.0015	-1.1	4.03	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
12741	dirMS_041712_NAR_20mM_plus.15344.15344.2	2	8.87	0	1.68E+04	M73m	(R)AILVDLE	(R)A I\L V/D/L/E|P G T/m D S V R(S)	m:Oxidized methionine	177.98	816.4181	1615.836	15.9929	-1.2	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
12742	dirMS_041712_NAR_20mM_plus.17499.17499.2	2	8.87	0	1.61E+05	M74m	(R)mIAGQ	(R)m I A\G/Q|V|L/D I N L A A E|P K(V)	m:Oxidized methionine	192.85	849.9568	1682.915	15.9918	-1.9	4.37	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
12743	dirMS_041712_NAR_30mM_plus2.4907.4907.2	2	8.87	0	3.08E+05	M71m	(K)ETmQSL	(K)E T/m/Q/S/L/N D R(L)	m:Oxidized methionine	77.52	555.2469	1093.494	15.9923	-2.4	4.37	48845.9	4.72	HUMAN	C4AM86	Keratin, type I cuticular Ha5
12744	dirMS_041712_NAR_30mM_plus2.5467.5467.3	3	8.87	0	6.70E+04		(R)GGSGG	(R)G G S G G S/Y/G G G G S G\G G/Y G/G G S/G S R(G)		82.82	597.9128	1791.728	-0.0039	-2.2	8.59	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
12745	dirMS_041712_NAR_40mM_plus2.13576.13576.3	3	8.87	0	1.42E+04		(K)LTEVPV	(K)L T E V/P V E P V L/T V H/P E S K(S)		146.12	625.3454	1874.027	-0.0053	-2.8	4.75	81726.4	6.71	HUMAN	Q9H307	Pinin
12746	dirMS_041712_NAR_40mM_plus2.6244.6244.2	2	8.87	0	4.33E+05		(K)NAGFTP	(K)N A|G\F/T/P Q E R(Q)		96.22	510.2487	1019.491	-0.0004	-0.4	6	29474.8	6.94	HUMAN	G3V3M6	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
12747	dirMS_041712_NAR_50mM_plus2.11675.11675.3	3	8.87	1	1.31E+05		(K)IGRIEDV	(K)I G R I E D V T\P I|P/S D S T/R(R)		128.73	585.9784	1755.924	-0.0029	-1.7	4.56	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
12748	dirMS_041712_NAR_50mM_plus2.18439.18439.3	3	8.87	1	3.49E+05		(R)GDSVIV	(R)G D|S\V/I/V V L R N P L/I A G K(-)		165.37	550.9999	1650.99	-0.005	-3	8.75	6144.3	10.23	HUMAN	K7EJB5	Small nuclear ribonucleoprotein Sm D2

12749	dirMS_041712_NAR_50mM_plus2.9033.9033.3	3	8.87	1	3.78E+05		(K)TAVCDIF	(K)T A/V\C/D I/P P R G L K(M)	C:Carbamidomethylation	114.98	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
12750	dirMS_041712_NAR_50mM_plus2.9329.9329.3	3	8.87	0	1.33E+05		(K)AEITLVA	(K)A E/I/T L\V/A T K P E K(L)		116.23	433.922	1299.752	-0.0004	-0.3	6.18	98761.7	5.56	HUMAN	Q9UBF2	Coatomer subunit gamma-2
12751	dirMS_041712_NAR_60mM_plus.14721.14721.3	3	8.87	1	5.21E+05		(K)NKDQGT	(K)N K\D Q G T Y E/D Y|V/E/G L R(V)		133.53	596.2816	1786.824	0.006	3.4	4.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
12752	dirMS_041712_NAR_60mM_plus.16111.16111.3	3	8.87	1	5.67E+05		(R)IKIGDPL	(R)I K I G D/P L/L/E D/T R(M)		141.5	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
12753	dirMS_041712_NAR_60mM_plus.17184.17184.3	3	8.87	0	2.04E+05		(K)THLPGF	(K)T\H\L\P G F\V|E/Q A E\A L/K(A)		147.35	513.9442	1539.817	0.0015	1	5.37	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
12754	dirMS_041712_NAR_120mM_minus.14751.14751.2	2	8.86	0	6.49E+05		(R)HSLVSF	(R)H/S|L/V/S F V V R(I)		134.32	522.3023	1043.6	-0.0023	-2.2	9.75	36359.2	5.35	HUMAN	Q9BUD6	Spondin-2
12755	dirMS_041712_NAR_20mM_minus.10334.10334.3	3	8.86	0	3.90E+03		(R)ELIQEYG	(R)E L I Q E Y/G A|Q/S/G G/L E K(L)		152.13	541.2755	1621.807	0.0052	3.2	4.25	266161	5.68	HUMAN	E9PPU0	Epiplakin
12756	dirMS_041712_NAR_30mM_minus2.10817.10817.2	2	8.86	0	1.30E+06		(R)GYSFTTT	(R)G Y|S F/T/T T A E R(E)		111.8	566.7699	1132.527	0.0056	4.9	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
12757	dirMS_041712_NAR_30mM_minus2.16158.16158.2	2	8.86	1	1.55E+05		(R)FVLSQAI	(R)F V|L/S/Q A/K D\E L(-)		141.43	575.3113	1149.615	0.0003	0.3	4.37	41053.3	5.58	HUMAN	Q86UY0	TXNDC5 protein
12758	dirMS_041712_NAR_30mM_minus2.17028.17028.2	2	8.86	0	8.36E+03		(K)FAEAFE	(K)F A|E A/F/E A I P R(A)		146.13	575.7971	1150.589	-0.0022	-1.9	4.53	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
12759	dirMS_041712_NAR_30mM_minus2.7259.7259.2	2	8.86	0	1.16E+05		(K)MQAVQ	(K)M Q|A/V|Q E/A T\R(L)		94	517.257	1033.509	-0.0028	-2.7	5.75	533778	5.74	HUMAN	Q15149	Plectin
12760	dirMS_041712_NAR_40mM_minus2.15031.15031.3	3	8.86	0	1.44E+05		(K)LFLFHTS	(K)L/F\L/F H T S L/P\I A E A P G K(L)		173.92	580.9924	1740.968	-0.0057	-3.3	6.75	108105.4	6.57	HUMAN	E7EP00	Protein transport protein Sec24C
12761	dirMS_041712_NAR_50mM_minus2.7187.7210.3	3	8.86	0	1.54E+05	M378m M	(K)mIVDPV	(K)m I\V/D/P\V E/P H G E m K(F)	m:Oxidized methionine	107.92	505.2416	1481.713	31.9975	5.1	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
12762	dirMS_041712_NAR_60mM_minus.11295.11295.3	3	8.86	1	7.95E+05		(K)MKEIAE	(K)M/K E\I A\E/A Y/L/G K(T)		122.48	418.226	1252.661	0.0029	2.3	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
12763	dirMS_041712_NAR_60mM_minus.11318.11318.3	3	8.86	1	9.28E+05	M232m	(R)MSmKE	(R)M/S m K E V D E Q|M|L/N V/Q N K(N)	m:Oxidized methionine	122.78	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
12764	dirMS_041712_NAR_20mM_plus.9893.9893.2	2	8.86	0	6.91E+04		(R)ALGQNF	(R)A L G Q/N/P T N A E V|L K(V)		140.02	677.8702	1354.733	0.0006	0.5	6.05	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
12765	dirMS_041712_NAR_50mM_plus2.21515.21531.3	3	8.86	0	1.01E+05		(K)THLPLAL	(K)T H L\P L A\L\L|P Q/T L/L D Q K(V)		183.97	601.0191	1801.058	-0.0154	-8.6	6.41	22243.5	7.91	HUMAN	E9PKR8	Sulfotransferase 1A2 (Fragment)
12766	dirMS_041712_NAR_60mM_plus.10794.10794.3	3	8.86	1	2.00E+06		(R)KLDPGSI	(R)K L D\P G S/E\E|T\Q/T/L V/R(E)		114.85	524.9456	1572.823	-0.0005	-0.3	4.68	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
12767	dirMS_041712_NAR_60mM_plus.13262.13262.3	3	8.86	1	1.19E+05		(R)SEADSD	(R)S E|A D/S D K N A/T I/L/E L|R(S)		126.82	554.615	1661.834	-0.0036	-2.2	4.32	334221.3	6.44	HUMAN	P15924	Desmoplakin
12768	dirMS_041712_NAR_60mM_plus.7069.7069.3	3	8.86	0	4.98E+05		(R)VSSDNV	(R)V/S/S D N|V/A/D/L H E K(Y)		95.33	438.55	1313.633	0.0023	1.7	4.54	17952.8	6.73	HUMAN	E9PAV2	Proteasome subunit beta type-5
12769	dirMS_041712_NAR_20mM_minus.13745.13745.2	2	8.85	0	3.96E+05		(K)LGGSAV	(K)L G G S A V/I/S L/E G K/P L(-)		188.67	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
12770	dirMS_041712_NAR_30mM_minus2.16214.16214.2	2	8.85	0	5.86E+05		(R)DFFLAN	(R)D F|F|L A N A/S R(A)		142.07	520.763	1040.516	0.0028	2.6	5.84	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
12771	dirMS_041712_NAR_30mM_minus2.18027.18027.3	3	8.85	0	6.94E+04		(R)SSFYVN	(R)S S F Y V N G L/T/L G G Q K(C)		152.48	490.9238	1470.759	-0.0019	-1.3	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
12772	dirMS_041712_NAR_30mM_minus2.18137.18137.2	2	8.85	0	8.93E+04		(R)NVVIWS	(R)N/V/V I W/S/I/K(S)		152.87	479.7891	958.572	-0.0011	-1.2	8.75	14660.6	9.23	HUMAN	K7EL08	AP-1 complex subunit mu-2 (Fragment)
12773	dirMS_041712_NAR_40mM_minus2.14508.14508.3	3	8.85	0	1.74E+04		(K)SLCIPFKI	(K)S L/C|I/P F K P L C E L Q/P G A K(C)	C:Carbamidomethylation	170.4	653.3446	1958.024	-0.0046	-2.3	8.31	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
12774	dirMS_041712_NAR_50mM_minus2.14486.14486.3	3	8.85	0	1.56E+04		(R)IDQVNQ	(R)I/D\Q/V/N Q L/L/E L D H Q K(R)		150.7	564.9709	1692.892	0.0066	3.9	4.54	44513	5.59	HUMAN	B4DIH5	COP9 signalosome complex subunit 2
12775	dirMS_041712_NAR_50mM_minus2.17717.17717.3	3	8.85	0	3.07E+05		(K)HNQLPL	(K)H N Q L P L\V|I E/F/T E Q T/A/P K(I)		170.02	655.6843	1965.044	-0.0057	-2.9	5.4	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
12776	dirMS_041712_NAR_50mM_minus2.6663.6663.3	3	8.85	1	6.32E+04		(R)AVASQP	(R)A V|A/S Q/P D/S V D/A A E R A E K(F)		105	581.9591	1743.851	0.012	6.9	4.32	81955.5	5.78	HUMAN	E9PHT6	Pantothenate kinase 4
12777	dirMS_041712_NAR_60mM_minus.16306.16324.3	3	8.85	1	6.39E+05		(K)EIIDPVLI	(K)E I/I/D P V L D R I/R(K)		151.22	446.9287	1338.774	-0.0024	-1.8	4.56	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
12778	dirMS_041712_NAR_120mM_plus.7851.7851.2	2	8.85	0	4.86E+05		(K)STTTGHI	(K)S/T/T/T/G H L\I/Y/K(C)		95.28	560.8014	1120.6	-0.0042	-3.7	8.34	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
12779	dirMS_041712_NAR_30mM_plus2.18972.19198.2	2	8.85	0	4.13E+05		(K)AVVMDI	(K)A V|V/M/D\L L/R(Q)		153.57	458.7641	916.528	-0.0075	-8.2	5.88	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
12780	dirMS_041712_NAR_30mM_plus2.4129.4129.2	2	8.85	0	1.20E+06	M299m M	(K)NmmAA	(K)N m/m/A|A C D|P/R(H)	C:Carbamidomethylation m:Oxid	69.07	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
12781	dirMS_041712_NAR_30mM_plus2.4200.4200.2	2	8.85	0	1.17E+06	M299m M	(K)NmmAA	(K)N m\m/A/A C D|P R(H)	C:Carbamidomethylation m:Oxid	69.63	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
12782	dirMS_041712_NAR_30mM_plus2.5805.5805.2	2	8.85	0	6.56E+04		(K)NTCTSV	(K)N T|C/T S V Y/T K(D)	C:Carbamidomethylation	84.92	537.2502	1073.493	-0.0001	-0.1	8.59	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
12783	dirMS_041712_NAR_40mM_plus2.16142.16264.2	2	8.85	0	1.50E+05		(R)YLTVAA	(R)Y L|T|V/A/A/V F R(G)		162.03	520.2997	1039.593	-0.0014	-1.3	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
12784	dirMS_041712_NAR_60mM_plus.11185.11185.3	3	8.85	0	3.61E+05		(R)LVKPGN	(R)L V/K/P G N Q N\T/Q/V/T E/A W N K(V)		116.13	643.0039	1927.003	-0.0061	-3.1	8.59	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
12785	dirMS_041712_NAR_60mM_plus.16595.16595.3	3	8.85	1	5.78E+05		(K)AAVEWI	(K)A A|V/E/W F D G K/D F Q/G S K(L)		143.15	562.2762	1684.797	0.0175	10.4	4.56	65213.5	9.57	HUMAN	B0QYK0	Ewing sarcoma breakpoint region 1
12786	dirMS_041712_NAR_60mM_plus.18041.18041.3	3	8.85	1	4.02E+04		(K)MFGIDR	(K)M/F/G I/D R D A/I\A Q/A V R(G)		152.52	521.6038	1562.811	-0.0139	-8.9	5.71	63448.4	7.29	HUMAN	B4E022	Transketolase
12787	dirMS_041712_NAR_60mM_plus.20149.20149.3	3	8.85	1	1.54E+05		(R)ELIKVLEI	(R)E L/I K V L/E E A/N Q/A|I N/P K(L)		165.17	603.6768	1809.012	0.0042	2.3	4.79	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
12788	dirMS_041712_NAR_120mM_minus.16558.16558.4	4	8.84	0	4.90E+05		(K)HLEINPD	(K)H L E\I\N P/D H S/I I E/T L R(Q)		145.22	447.4904	1786.945	-0.0049	-2.7	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
12789	dirMS_041712_NAR_120mM_minus.8431.8431.2	2	8.84	0	5.91E+05		(-)DLDVGN	(-)D/L|D V G N W R(E)		100.4	487.7332	974.469	-0.0099	-10.2	4.21	38133.9	4.64	HUMAN	H7C026	Bromodomain-containing protein 8 (Fragment)
12790	dirMS_041712_NAR_30mM_minus2.11381.11397.2	2	8.84	0	3.32E+05		(R)VQELPL	(R)V Q|E|L\P L A/R(I)		115.55	463.2738	925.547	-0.0062	-6.7	5.97	16202.4	6.61	HUMAN	E9PI99	Nuclear transcription factor Y subunit gamma (Fragment)
12791	dirMS_041712_NAR_40mM_minus2.14517.14517.3	3	8.84	0	2.26E+05		(R)DIKPQN	(R)D I K P Q N L\L|L/D/P D T A V L K(L)		169.68	631.6945	1893.069	-0.0002	-0.1	4.43	47257	9.38	HUMAN	P49841	Glycogen synthase kinase-3 beta
12792	dirMS_041712_NAR_50mM_minus2.10990.10990.3	3	8.84	1	4.01E+05		(R)INVYYNI	(R)I N|V|Y/Y\N E A/T G G K Y/V P R(A)		131.28	615.3184	1843.934	0.0069	3.8	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
12793	dirMS_041712_NAR_50mM_minus2.12885.12885.3	3	8.84	0	3.05E+05		(K)EGKPTIV	(K)E G K P T I\V E/E/D/D/P E L/F K(Q)		141.07	615.9772	1845.912	0.0054	2.9	4.08	29841.1	9.04	HUMAN	O75937	DnaJ homolog subfamily C member 8
12794	dirMS_041712_NAR_50mM_minus2.14958.14958.3	3	8.84	0	4.48E+05		(R)LQQELD	(R)L Q|Q E L D D/L T/V/D L D H Q\R(Q)		153.03	646.6559	1937.956	-0.0032	-1.6	4.03	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
12795	dirMS_041712_NAR_50mM_minus2.15495.15495.3	3	8.84	1	2.25E+04		(K)CEFQDA	(K)C E|F Q D A Y V/L L/S E K K(I)	C:Carbamidomethylation	156.05	577.2917	1729.847	0.014	8.1	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
12796	dirMS_041712_NAR_50mM_minus2.16370.16370.3	3	8.84	0	4.08E+05		(R)VLDPFTI	(R)V L/D/P/F T I K/P L D R(K)		161.9	471.9411	1413.81	-0.0013	-0.9	5.93	63448.4	7.29	HUMAN	B4E022	Transketolase
12797	dirMS_041712_NAR_60mM_minus.11693.11693.3	3	8.84	1	4.83E+05	M57m	(K)VAmRAL	(K)V A m R A L/G F/E|P K(K)	m:Oxidized methionine	125.12	412.2311	1218.666	16.0124	14.2	8.72	19738.1	4.91	HUMAN	P41208	Centrin-2
12798	dirMS_041712_NAR_60mM_minus.16796.16796.3	3	8.84	1	2.46E+05		(R)KGFSEGI	(R)K G F S E G L\W E|I/E/N N P\T V K(A)		153.75	649.9986	1947.981	0.0002	0.1	4.79	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
12799	dirMS_041712_NAR_60mM_minus.17901.17901.3	3	8.84	1	4.20E+05	M148m	(R)LDLAGR	(R)L/D/L/A G R D L T D Y L m K(I)	m:Oxidized methionine	159.92	547.2829	1623.841	15.9931	-1.1	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
12800	dirMS_041712_NAR_120mM_plus.10608.10608.3	3	8.84	1	7.58E+05		(K)IKGEHP	(K)I/K/G/E H|P G L S I G D\V A K(K)		108.45	507.6167	1520.843	-0.0076	-5	6.75	24408.7	5.92	HUMAN	B2RPK0	Putative high mobility group protein B1-like 1
12801	dirMS_041712_NAR_120mM_plus.13601.13601.3	3	8.84	0	1.10E+06		(K)THINIVV	(K)T H|I N I\V/V I G/H/V D S G/K(S)		124.05	530.2975	1588.881	-0.0026	-1.6	6.61	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
12802	dirMS_041712_NAR_120mM_plus.15963.15963.4	4	8.84	1	3.61E+05	M108m	(K)FLSDVYF	(K)F L S D\V Y/P D G F K G H m L T/K(S)	m:Oxidized methionine	137.13	493.498	1954.973	15.997	1.1	6.74	15838.9	7.03	HUMAN	H0Y5U0	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
12803	dirMS_041712_NAR_120mM_plus.6412.6412.2	2	8.84	0	1.01E+05	M419m	(R)mGAGL	(R)m/G/A|G L/G/H|G M D R(V)	m:Oxidized methionine	86.92	559.2491	1101.493	15.9981	2.9	6.49	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
12804	dirMS_041712_NAR_20mM_plus.10374.10374.2	2	8.84	0	7.50E+04		(R)IEDVTPI	(R)I E\D\V/T/P I/P S D/S T R(R)		144.38	715.3607	1429.717	-0.0028	-2	4.03	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
12805	dirMS_041712_NAR_20mM_plus.13874.13874.2	2	8.84	0	1.26E+05	M62m	(R)DASLmV	(R)D A/S|L/m|V/T/N D G A\T I/L K(N)	m:Oxidized methionine	167.72	782.8922	1548.794	15.9833	-7.4	4.21	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
12806	dirMS_041712_NAR_20mM_plus.14287.14287.2	2	8.84	0	8.76E+04		(K)GVVDSD	(K)G V V|D S D D\L|P L/N/V/S R(E)		170.28	743.3789	1485.754	-0.0038	-2.6	3.93	92752.5	4.76	HUMAN	P14625	Endoplasmin
12807	dirMS_041712_NAR_20mM_plus.14651.14651.2	2	8.84	0	1.45E+05		(K)LVILANN	(K)L V|I/L/A/N N C P A L R(K)	C:Carbamidomethylation	172.52	677.3851	1353.767	-0.0042	-3.1	9.75	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
12808	dirMS_041712_NAR_20mM_plus.17068.17068.3	3	8.84	0	2.36E+05		(R)AIVAIEN	(R)A I\V\A\I E N P A/D V/S/V I/S S R(N)		188.88	580.9864	1740.949	-0.0044	-2.5	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
12809	dirMS_041712_NAR_20mM_plus.18594.18594.2	2	8.84	0	2.99E+05		(K)TAVETA	(K)T A\V/E/T/A/V L\L L R(I)		199.78	593.3625	1185.72	-0.0024	-2	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
12810	dirMS_041712_NAR_30mM_plus2.17654.17654.2	2	8.84	0	2.06E+05		(K)LFDFPGI	(K)L/F|D/F/P G R(G)		146.18	426.2291	851.441	0.0099	11.6	5.84	56825.2	9.49	HUMAN	Q9P258	Protein RCC2
12811	dirMS_041712_NAR_50mM_plus2.17564.17564.3	3	8.84	1	2.05E+05		(K)TLEEDEE	(K)T L|E/E\D E E E/L F/K M R(A)		160.38	556.9323	1668.778	0.0038	2.3	4.14	19157.5	10.04	HUMAN	C9JDM3	Ran-specific GTPase-activating protein (Fragment)
12812	dirMS_041712_NAR_60mM_plus.11903.11903.3	3	8.84	1	1.21E+06		(K)LKQSLPF	(K)L/K Q S L/P/P G L A V/K(E)		119.55	417.5978	1250.783	-0.0042	-3.4	10	8274.8	10.19	HUMAN	P63173	60S ribosomal protein L38
12813	dirMS_041712_NAR_60mM_plus.18192.18192.3	3	8.84	1	3.37E+05		(R)IRIDSLS	(R)I R I/D S|L S A Q|L/S Q L Q K(Q)		153.28	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
12814	dirMS_041712_NAR_20mM_minus.12329.12329.3	3	8.83	0	7.09E+05	M73m	(R)AVLVDLI	(R)A V L V D L/E/P G T m/D S V R(S)	m:Oxidized methionine	172.37	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
12815	dirMS_041712_NAR_30mM_minus2.18786.18786.2	2	8.83	0	1.61E+05		(K)GWPLYL	(K)G W|P L Y/L/S T K(N)		157.23	532.7918	1064.578	-0.0012	-1.1	8.59	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
12816	dirMS_041712_NAR_40mM_minus2.14639.14639.3	3	8.83	1	1.37E+05		(K)GTVPDD	(K)G T V/P D D A V/E A L/A D/S L G K K(E)		170.37	595.9791	1785.923	-0.0001	-0.1	4.23	81397.3	4.99	HUMAN	B7Z468	Calpastatin
12817	dirMS_041712_NAR_50mM_minus2.12796.12796.3	3	8.83	1	2.33E+05		(R)QATKDA	(R)Q A\T K D A G T/I/A/G/L/N V L R(I)		140.57	543.3085	1627.913	-0.0016	-1	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
12818	dirMS_041712_NAR_50mM_minus2.17824.17824.3	3	8.83	0	3.07E+05		(K)HNQLPL	(K)H N Q\L\P L\V\I/E|F/T E Q T A/P K(I)		170.02	655.6843	1965.044	-0.0057	-2.9	5.4	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
12819	dirMS_041712_NAR_50mM_minus2.17859.17859.3	3	8.83	1	2.28E+05	M116m	(R)ELAILLG	(R)E L\A\I|L/L/G m L D/P A E K D E K(G)	m:Oxidized methionine	170.82	634.3353	1884.999	15.9927	-1.2	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
12820	dirMS_041712_NAR_60mM_minus.10368.10368.3	3	8.83	1	6.05E+05	M88m	(K)DVDEAY	(K)D V|D/E/A/Y m N K V E/L E S R(L)	m:Oxidized methionine	118.37	605.2791	1797.832	15.9904	-2.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
12821	dirMS_041712_NAR_60mM_minus.18374.18374.3	3	8.83	1	1.43E+05		(R)TLLLDGI	(R)T L|L/L/D/G N P F R/V P R(A)		163.85	499.9563	1497.854	0.0007	0.5	9.26	68762.2	6.04	HUMAN	Q9H9A6	Leucine-rich repeat-containing protein 40
12822	dirMS_041712_NAR_30mM_plus2.4881.4881.2	2	8.83	0	3.09E+05	M71m	(K)ETmQSL	(K)E T/m/Q/S L N/D/R(L)	m:Oxidized methionine	77.4	555.2469	1093.494	15.9923	-2.4	4.37	48845.9	4.72	HUMAN	C4AM86	Keratin, type I cuticular Ha5
12823	dirMS_041712_NAR_30mM_plus2.6747.6747.2	2	8.83	0	2.45E+05		(R)SPDNPN	(R)S/P|D N|P M/N Q R(A)		89.27	529.7357	1058.468	-0.0042	-4	5.55	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
12824	dirMS_041712_NAR_50mM_plus2.18611.18635.3	3	8.83	1	1.68E+05		(R)GLFIIDD	(R)G L/F I/I/D/D K G I L R(Q)		166.17	453.9379	1359.8	-0.0003	-0.2	5.96	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
12825	dirMS_041712_NAR_50mM_plus2.6627.6627.3	3	8.83	1	3.80E+05		(R)IVDGKV	(R)I V/D G K/V/V/S E T N D T K(V)		100.3	502.2651	1504.785	-0.0046	-3	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
12826	dirMS_041712_NAR_50mM_plus2.9553.9553.3	3	8.83	1	3.51E+05	M61m	(K)NQVAm	(K)N\Q/V/A/m N/P T/N T V F D A K\R(L)	m:Oxidized methionine	117.07	607.9678	1805.896	15.9926	-1.3	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
12827	dirMS_041712_NAR_50mM_plus2.9590.9590.3	3	8.83	0	2.45E+05		(R)LVKPGN	(R)L V/K P G N Q N T/Q/V/T E/A/W N K(V)		117.08	643.0046	1927.003	-0.004	-2.1	8.59	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
12828	dirMS_041712_NAR_60mM_plus.11970.11970.3	3	8.83	1	6.23E+05		(K)SVSDYD	(K)S V/S D Y D G K/L/S N F K(T)		119.6	487.2426	1459.706	0.0069	4.7	5.68	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
12829	dirMS_041712_NAR_60mM_plus.15057.15057.3	3	8.83	0	5.66E+05		(K)LSMKPE	(K)L/S M/K/P E P L F R(S)		135.85	406.5616	1217.671	-0.0008	-0.7	8.75	75482.2	6.34	HUMAN	D6RA32	Microtubule-associated protein 1B (Fragment)
12830	dirMS_041712_NAR_120mM_minus.17859.17859.3	3	8.82	1	7.72E+05		(R)RAPFDLI	(R)R A P F\D|L|F E/N R(K)		152.67	422.2193	1264.643	0.0001	0	6.07	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
12831	dirMS_041712_NAR_120mM_minus.5116.5116.3	3	8.82	0	1.86E+05		(R)YINTEH	(R)Y/I|N T E/H/G G S Q A R(F)		80.6	444.8813	1332.629	0.0002	0.2	6.75	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
12832	dirMS_041712_NAR_20mM_minus.8284.8284.2	2	8.82	0	1.25E+05		(K)VTADVII	(K)V T/A D/V I\N A A E/K(L)		132.47	565.8065	1130.605	0.0005	0.5	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
12833	dirMS_041712_NAR_30mM_minus2.13640.13640.2	2	8.82	0	2.30E+05		(K)FAFQAE	(K)F/A|F/Q/A/E/V N R(M)		127.28	541.2823	1081.543	0.0148	13.7	6	92752.5	4.76	HUMAN	P14625	Endoplasmin
12834	dirMS_041712_NAR_30mM_minus2.6564.6564.2	2	8.82	0	2.34E+05		(R)QQYESV	(R)Q\Q|Y E S V/A/A\K(N)		89.95	512.2534	1023.511	-0.011	-10.8	6	49709.6	5.19	HUMAN	B0YJC4	Vimentin
12835	dirMS_041712_NAR_50mM_minus2.11771.11771.3	3	8.82	0	6.96E+04	M425m M	(R)VFITDDF	(R)V/F|I T/D D\F H D m m P K(Y)	m:Oxidized methionine	135.23	543.2416	1595.723	31.987	-1.7	4.41	92752.5	4.76	HUMAN	P14625	Endoplasmin
12836	dirMS_041712_NAR_50mM_minus2.16414.16414.3	3	8.82	1	6.81E+04		(R)CITDPQ	(R)C I|T/D/P Q T/G L/C L L P L K E K(K)	C:Carbamidomethylation	161.65	662.6828	1986.04	-0.006	-3	6.07	533778	5.74	HUMAN	Q15149	Plectin
12837	dirMS_041712_NAR_50mM_minus2.6239.6239.3	3	8.82	0	2.41E+05	M434m	(R)LESGmC	(R)L E|S G m Q N/M/S I H T K(T)	m:Oxidized methionine	98.83	497.9018	1475.698	15.9927	-1.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
12838	dirMS_041712_NAR_50mM_minus2.7427.7427.3	3	8.82	1	9.46E+04		(K)ATQPET	(K)A T/Q|P E T/T\E E V T D L K R(Q)		109.53	573.2875	1717.86	-0.0123	-7.2	4.41	72152.1	5.27	HUMAN	A0MZ66	Shootin-1
12839	dirMS_041712_NAR_60mM_minus.14910.14910.3	3	8.82	0	2.66E+05		(K)YYITIIDA	(K)Y Y I\T I/I/D A/P G H R(D)		142.87	473.5815	1418.743	-0.0127	-9	6.74	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
12840	dirMS_041712_NAR_60mM_minus.9056.9056.3	3	8.82	0	5.27E+04		(K)LPANHP	(K)L/P A N/H/P L/L/T G Q R(V)		110.58	439.5833	1316.743	-0.008	-6.1	9.75	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
12841	dirMS_041712_NAR_120mM_plus.17264.17264.4	4	8.82	1	1.28E+06		(K)FLSDVYF	(K)F L\S D V/Y/P/D/G F K G H M L T K(S)		143.43	489.4962	1954.973	-0.0102	-5.2	6.74	15838.9	7.03	HUMAN	H0Y5U0	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
12842	dirMS_041712_NAR_20mM_plus.16714.16714.2	2	8.82	0	1.65E+05		(K)TVDNFV	(K)T/V/D/N/F/V/A L/A T G E K(G)		186.22	682.8565	1364.706	0.0001	0.1	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
12843	dirMS_041712_NAR_20mM_plus.8952.8952.2	2	8.82	0	2.02E+05		(K)VTADVII	(K)V/T|A/D\V/I N A A E K(L)		132.53	565.806	1130.605	-0.0005	-0.4	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
12844	dirMS_041712_NAR_50mM_plus2.13676.13676.3	3	8.82	1	3.50E+05		(R)VVLELK	(R)V V|L/E L K A D V V P K(T)		140.18	437.2744	1309.809	-0.0003	-0.2	6.04	17888.9	8.97	HUMAN	H0Y548	Peptidyl-prolyl cis-trans isomerase (Fragment)
12845	dirMS_041712_NAR_50mM_plus2.21448.21448.3	3	8.82	0	1.01E+05		(K)THLPLAL	(K)T H L\P L A\L|L|P Q T L L D Q K(V)		183.97	601.0191	1801.058	-0.0154	-8.6	6.41	22243.5	7.91	HUMAN	E9PKR8	Sulfotransferase 1A2 (Fragment)
12846	dirMS_041712_NAR_60mM_plus.19383.19555.3	3	8.82	1	7.03E+05		(K)TVTAMD	(K)T V/T/A/M/D V/V/Y A L K R(Q)		160.7	489.6071	1466.804	0.0032	2.2	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
12847	dirMS_041712_NAR_30mM_minus2.11056.11056.2	2	8.81	0	1.20E+06		(R)TSASIILF	(R)T/S|A/S\I I L R(G)		113.7	430.7619	860.52	-0.0035	-4	9.41	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
12848	dirMS_041712_NAR_30mM_minus2.12989.12989.2	2	8.81	0	3.15E+05		(K)FASFIDK	(K)F/A/S F/I/D/K(V)		124.38	414.2189	827.43	0.0007	0.9	5.84	54364	5.73	HUMAN	F5H8K9	Keratin, type II cytoskeletal 4
12849	dirMS_041712_NAR_30mM_minus2.14348.14348.2	2	8.81	0	2.40E+05		(K)CCSGAI	(K)C/C|S|G A|I\I V L/T K(S)	C:Carbamidomethylation	131.97	611.3188	1221.633	-0.0027	-2.2	8.75	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
12850	dirMS_041712_NAR_30mM_minus2.8011.8011.2	2	8.81	0	1.83E+05		(K)GSGTAE	(K)G S|G T/A/E V E L/K(K)		98.32	495.7528	990.51	-0.0119	-12	4.53	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
12851	dirMS_041712_NAR_50mM_minus2.11790.11790.3	3	8.81	0	1.91E+05	M221m	(K)mLDAED	(K)m L/D A/E D I/V G T A R P D/E\K(A)	m:Oxidized methionine	134.97	592.6214	1759.853	15.9966	0.9	4.1	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
12852	dirMS_041712_NAR_50mM_minus2.14297.14297.3	3	8.81	1	8.33E+04		(R)LSQELEY	(R)L S/Q E L E Y/L/T E/D V/K/R(L)		149.87	574.9724	1722.891	0.0118	6.8	4.41	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
12853	dirMS_041712_NAR_50mM_minus2.16520.16520.3	3	8.81	1	1.59E+05		(K)TVTAMD	(K)T V/T A/M D V/V Y A L K/R(Q)		162.77	489.6051	1466.804	-0.0028	-1.9	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
12854	dirMS_041712_NAR_60mM_minus.10719.10719.3	3	8.81	0	2.54E+05		(R)GISEETT	(R)G I/S E/E T T T/G V H N/L Y K(M)		119.3	550.2838	1648.818	0.0192	11.6	5.4	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
12855	dirMS_041712_NAR_60mM_minus.13981.13981.3	3	8.81	0	3.32E+05		(K)LHLGTT	(K)L H\L G T T Q\N S/L/T\E/A D/F/R(E)		137.52	601.6438	1802.903	0.0137	7.6	5.32	49472.3	6.75	HUMAN	O75351	Vacuolar protein sorting-associated protein 4B
12856	dirMS_041712_NAR_60mM_minus.15002.15002.3	3	8.81	0	2.16E+05		(K)MLDAED	(K)M/L|D|A E D I/V N T A R P D E K(A)		143.72	606.2986	1816.875	0.0067	3.7	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
12857	dirMS_041712_NAR_60mM_minus.8856.8856.3	3	8.81	1	1.14E+05		(K)YAGKDG	(K)Y|A|G K D G Y/N Y T L S/K(T)		109.12	493.9126	1479.711	0.0118	8	8.38	11854.4	6.57	HUMAN	P31949	Protein S100-A11

12858	dirMS_041712_NAR_60mM_minus.9763.9763.3	3	8.81	1	1.01E+06		(K)TAVCDIF	(K)T A|V C D/I/P P R/G L K(M)	C:Carbamidomethylation	114.77	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
12859	dirMS_041712_NAR_20mM_plus.15281.15281.2	2	8.81	0	7.05E+03		(K)DVLSVAI	(K)D V L/S V/A/F S S D N R(Q)		176.72	655.3293	1309.638	0.0131	10	4.21	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
12860	dirMS_041712_NAR_20mM_plus.16210.16210.2	2	8.81	0	8.34E+04		(R)AYILNLV	(R)A/Y|I L/N L V/K(Q)		183.75	467.2905	933.577	-0.0031	-3.3	8.63	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
12861	dirMS_041712_NAR_20mM_plus.7337.7337.2	2	8.81	0	2.01E+05		(K)VTLTSEE	(K)V T|L/T/S E/E E A R(L)		119.8	567.7865	1134.564	0.002	1.8	4.25	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
12862	dirMS_041712_NAR_30mM_plus2.18763.18763.2	2	8.81	0	2.71E+05		(R)QFLTQLI	(R)Q F/L/T/Q/L/M Q/K(E)		151.42	568.8061	1136.613	-0.0083	-7.3	8.75	81733.5	5.24	HUMAN	E9PAW1	Splicing factor 3A subunit 1
12863	dirMS_041712_NAR_30mM_plus2.21577.21577.2	2	8.81	0	3.32E+05		(K)FDGILGM	(K)F D|G\I/L/G/M A Y P R(I)		167.47	620.3199	1239.619	0.0135	10.9	5.83	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
12864	dirMS_041712_NAR_40mM_plus2.7024.7024.2	2	8.81	0	5.19E+04		(R)SYSDPPL	(R)S Y|S/D P P/L K(F)		101.4	453.7354	906.457	0.0068	7.5	5.55	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
12865	dirMS_041712_NAR_50mM_plus2.10307.10307.3	3	8.81	1	2.19E+05		(R)TGLIKGS	(R)T/G|L I/K G S G T A E V E L K(K)		121.85	501.6143	1502.842	-0.0141	-9.4	5.81	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
12866	dirMS_041712_NAR_50mM_plus2.16148.16148.3	3	8.81	1	1.29E+06		(K)GADFLV	(K)G A/D\F/L/V/T E V/E N G G S L G S K K(G)		152.28	636.6618	1907.971	-0.0001	0	4.68	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
12867	dirMS_041712_NAR_50mM_plus2.16978.16978.3	3	8.81	1	4.54E+05		(K)VLDSGA	(K)V L/D S G/A/P I K I|P V G P E T L G R(I)		156.95	640.3623	1919.096	-0.0237	-12.3	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
12868	dirMS_041712_NAR_50mM_plus2.5212.5212.3	3	8.81	0	2.68E+05	M21m	(R)SGSmDF	(R)S G S m|D P S G A/H/P S V R(Q)	m:Oxidized methionine	86.13	467.5461	1384.627	15.9964	1	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
12869	dirMS_041712_NAR_50mM_plus2.7715.7715.3	3	8.81	1	9.26E+04		(R)FNEVAA	(R)F/N|E/V A A Q Y S/E D K A R(Q)		106.63	543.2611	1627.771	-0.0023	-1.4	4.68	14236.2	10.25	HUMAN	F5H1P5	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4
12870	dirMS_041712_NAR_60mM_plus.10846.10846.3	3	8.81	1	6.35E+05		(R)AVDERF	(R)A V|D/E R F/P G/C M Q G R(T)	C:Carbamidomethylation	114.63	508.237	1522.689	0.0075	4.9	6.12	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
12871	dirMS_041712_NAR_60mM_plus.13921.13921.3	3	8.81	1	9.47E+05		(K)TTVKDLS	(K)T T V/K D L S\E|L/G S V/R(T)		129.53	468.9268	1404.769	-0.0034	-2.4	5.74	533778	5.74	HUMAN	Q15149	Plectin
12872	dirMS_041712_NAR_60mM_plus.14722.14722.3	3	8.81	1	5.21E+05		(K)NKDQGT	(K)N K D\Q G T Y/E D|Y|V/E/G L R(V)		133.53	596.2816	1786.824	0.006	3.4	4.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
12873	dirMS_041712_NAR_60mM_plus.16400.16400.3	3	8.81	0	7.59E+05		(K)SPYQEFT	(K)S P/Y/Q/E|F/T|D H L V\K(T)		142.53	488.5776	1463.717	0.0017	1.2	5.3	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
12874	dirMS_041712_NAR_120mM_minus.9732.9732.3	3	8.8	0	4.13E+05		(K)NCPHIV	(K)N C P H I|V|V G T/P G R(I)	C:Carbamidomethylation	107.6	436.2293	1306.669	0.0049	3.7	9.75	28185.1	10.76	HUMAN	B4DIJ6	Spliceosome RNA helicase DDX39B
12875	dirMS_041712_NAR_20mM_minus.8523.8578.2	2	8.8	0	2.54E+05		(K)TIAPALV	(K)T I|A|P A L V S K(K)		135.52	450.2808	899.556	-0.0017	-1.9	8.41	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
12876	dirMS_041712_NAR_20mM_minus.8748.8748.2	2	8.8	0	2.15E+04		(K)VAGQDC	(K)V A|G Q D/G/S V V/Q F/K(I)		136.87	617.823	1234.643	-0.0039	-3.2	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
12877	dirMS_041712_NAR_30mM_minus2.17930.17930.2	2	8.8	0	9.97E+04		(R)LNLWISI	(R)L/N|L W I/S/R(T)		152.05	451.2694	901.525	0.0061	6.8	9.75	58791	9.93	HUMAN	E9PDI4	Ladinin-1
12878	dirMS_041712_NAR_30mM_minus2.9403.9419.2	2	8.8	0	1.50E+06		(R)LAVAGE	(R)L/A|V A/G E D A/R(I)		105.8	451.242	901.474	0.003	3.3	4.37	77459.4	5.04	HUMAN	B3KSY4	Coronin
12879	dirMS_041712_NAR_30mM_minus2.9422.9423.2	2	8.8	0	2.50E+05		(R)EGLEND	(R)E G/L/E/N/D/L/K(S)		105.3	459.2338	917.457	0.0029	3.1	4.14	96649	6.13	HUMAN	Q8WUM4	Programmed cell death 6-interacting protein
12880	dirMS_041712_NAR_40mM_minus2.9520.9520.3	3	8.8	0	2.03E+04		(R)IIPSEKPS	(R)I I/P/S E K P S S T L Q Y F/P K(S)		138.47	612.3321	1834.995	-0.0132	-7.2	8.5	78759	9.49	HUMAN	E9PIW0	B-cell CLL/lymphoma 9-like protein (Fragment)
12881	dirMS_041712_NAR_50mM_minus2.13349.13349.3	3	8.8	1	1.91E+05		(K)TITLEVEI	(K)T I|T/L E V E/P S D T I E N V K\A K(I)		144.63	663.0226	1987.059	-0.0061	-3.1	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
12882	dirMS_041712_NAR_50mM_minus2.14485.14485.3	3	8.8	0	1.56E+04		(R)IDQVNQ	(R)I/D|Q/V/N\Q L/L E L D H Q K(R)		150.7	564.9709	1692.892	0.0066	3.9	4.54	44513	5.59	HUMAN	B4DIH5	COP9 signalosome complex subunit 2
12883	dirMS_041712_NAR_50mM_minus2.15672.15672.3	3	8.8	0	2.54E+05	M460m	(R)ISIEmNG	(R)I S|I/E m/N G T L E/D Q/L S H L K(Q)	m:Oxidized methionine	157.28	648.6635	1927.979	15.9966	0.9	4.65	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
12884	dirMS_041712_NAR_50mM_minus2.6751.6751.3	3	8.8	1	8.76E+04	M22m M2(	(K)LAEQAE	(K)L/A|E/Q/A/E R Y D D/m A A C m K(S)	C:Carbamidomethylation m:Oxid	104.8	645.2741	1901.819	31.9887	-0.6	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
12885	dirMS_041712_NAR_60mM_minus.19789.19897.3	3	8.8	1	1.81E+06		(K)EIIDLVLI	(K)E I/I/D/L/V\L D/R I R(K)		179.88	452.2739	1354.805	0.0019	1.4	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
12886	dirMS_041712_NAR_60mM_minus.8011.8011.3	3	8.8	1	8.24E+05		(R)LREDEN	(R)L R E D E\N\A\E|P V/G T T/Y Q K(T)		104.68	617.3015	1849.893	-0.0027	-1.5	4.41	76925.9	4.46	HUMAN	A8MV58	Drebrin
12887	dirMS_041712_NAR_60mM_minus.8221.8221.3	3	8.8	0	1.27E+04	M354m	(R)LSNRPAI	(R)L/S N R P A/F\m|P/S E/G/R(M)	m:Oxidized methionine	105.97	493.2448	1461.727	15.9931	-1.2	9.6	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
12888	dirMS_041712_NAR_20mM_plus.16896.16896.2	2	8.8	0	1.89E+05		(K)LGGSAV	(K)L G G S A V|I/S\L E G\K|P L(-)		187.03	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
12889	dirMS_041712_NAR_20mM_plus.7761.7761.2	2	8.8	0	1.95E+05		(R)ALANSL	(R)A L|A\N|S/L\A C Q G K(Y)	C:Carbamidomethylation	123.77	566.7967	1132.578	0.0082	7.2	8.8	13951.6	9.48	HUMAN	H3BR68	Fructose-bisphosphate aldolase A (Fragment)
12890	dirMS_041712_NAR_20mM_plus.9907.9907.2	2	8.8	0	2.39E+05		(K)VASGCLI	(K)V/A/S\G/C|L/D I N S S V/K(G)	C:Carbamidomethylation	139.65	675.3376	1349.673	-0.005	-3.7	5.81	56837	7.19	HUMAN	E7ETT1	Propionyl-CoA carboxylase beta chain, mitochondrial
12891	dirMS_041712_NAR_30mM_plus2.16950.16950.2	2	8.8	0	3.50E+05		(K)SNQQLV	(K)S N/Q|Q/L|V\D I I E K(V)		141.35	643.8504	1286.695	-0.0015	-1.2	4.37	22568.6	6.35	HUMAN	B3KQ25	Proteasome activator complex subunit 3
12892	dirMS_041712_NAR_30mM_plus2.21497.21497.2	2	8.8	0	8.15E+03		(R)VNQAIW	(R)V N Q/A I/W/L|L C T G/A R(E)	C:Carbamidomethylation	167.72	751.3976	1501.794	-0.0065	-4.3	9.72	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
12893	dirMS_041712_NAR_30mM_plus2.7647.7706.2	2	8.8	0	1.34E+06		(R)SYSDPPL	(R)S Y|S/D P/P L/K(F)		94.35	453.7343	906.457	0.0046	5.1	5.55	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
12894	dirMS_041712_NAR_50mM_plus2.20667.20667.3	3	8.8	1	2.19E+05		(K)VKIPEGT	(K)V K I P E G\T I|L/T/M/D|M L T V/K(V)		177.23	630.3524	1889.049	-0.006	-3.2	6.04	40763.2	6.29	HUMAN	Q9NR45	Sialic acid synthase
12895	dirMS_041712_NAR_60mM_plus.5675.5675.3	3	8.8	1	1.53E+05	M131m	(R)QmGQP	(R)Q m|G\Q/P C/D A/Y Q K R(L)	C:Carbamidomethylation m:Oxid	87.98	499.8898	1481.662	15.9925	-1.6	8.59	334221.3	6.44	HUMAN	P15924	Desmoplakin
12896	dirMS_041712_NAR_20mM_minus.8684.8684.3	3	8.79	0	6.96E+04		(R)SPSDSST	(R)S P S D S S T A S T/P/V/A/E Q I E\R(A)		136.63	621.2935	1861.877	-0.0114	-6.1	4.14	76925.9	4.46	HUMAN	A8MV58	Drebrin
12897	dirMS_041712_NAR_20mM_plus.14324.14324.2	2	8.79	0	8.58E+04		(R)VFSGLVS	(R)V/F|S/G L V/S T G L K(V)		170.27	554.3224	1107.641	-0.0033	-3	8.72	96306.4	6.41	HUMAN	P13639	Elongation factor 2
12898	dirMS_041712_NAR_20mM_plus.16205.16205.3	3	8.79	0	1.08E+06	M221m	(R)ALTVPEL	(R)A L T V/P E L T Q/Q m F/D/A/K(N)	m:Oxidized methionine	184.28	569.9583	1691.867	15.9931	-1.1	4.37	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
12899	dirMS_041712_NAR_20mM_plus.16311.16337.2	2	8.79	0	1.11E+05		(K)TIIPLISQ	(K)T I|I|P L/I|S Q C T P K(V)	C:Carbamidomethylation	184.03	685.8877	1370.771	-0.0031	-2.2	8.41	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
12900	dirMS_041712_NAR_20mM_plus.17579.17579.3	3	8.79	0	1.96E+05		(K)SYELPDG	(K)S Y E|L/P D G\Q|V\I/T I G N/E R(F)		193.17	597.6357	1790.892	0.0006	0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
12901	dirMS_041712_NAR_20mM_plus.6876.6876.2	2	8.79	0	4.12E+05	M132m	(R)DmVGIA	(R)D m|V|G|I|A Q T G S G K(T)	m:Oxidized methionine	112.87	590.2864	1163.573	15.993	-1.6	5.84	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
12902	dirMS_041712_NAR_20mM_plus.9964.9964.2	2	8.79	0	1.64E+05		(K)YQAVTA	(K)Y Q|A/V/T/A T L E E K(R)		139.78	626.8223	1252.642	-0.0046	-3.7	4.53	23633.9	11.02	HUMAN	P40429	60S ribosomal protein L13a
12903	dirMS_041712_NAR_30mM_plus2.19030.19030.2	2	8.79	0	1.87E+05		(K)LNLGTV	(K)L N|L/G T/V/G F Y R(T)		152.8	570.3123	1139.621	-0.0034	-3	8.75	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
12904	dirMS_041712_NAR_40mM_plus2.6993.6993.2	2	8.79	0	1.27E+05		(R)MGPVM	(R)M/G/P V/M D R(M)		100.62	403.1892	805.37	0.0016	2	5.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
12905	dirMS_041712_NAR_40mM_plus2.8042.8042.2	2	8.79	0	3.33E+04		(R)SGQGAF	(R)S G Q|G/A/F|G N M C/R(G)	C:Carbamidomethylation	107.53	592.7523	1184.494	0.0038	3.2	9.47	18988.7	11.2	HUMAN	H3BTP7	60S ribosomal protein L4 (Fragment)
12906	dirMS_041712_NAR_50mM_plus2.15193.15193.3	3	8.79	0	2.43E+04		(K)VALLLLD	(K)V A\L\L/L/L/D Q G A S P H/A/A A K(N)		147.53	558.9877	1674.954	-0.0052	-3.1	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
12907	dirMS_041712_NAR_50mM_plus2.17044.17044.3	3	8.79	1	1.53E+07		(R)VSFELFA	(R)V/S/F\E L F/A D K V P K(T)		156.88	460.5906	1379.757	0.0003	0.2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
12908	dirMS_041712_NAR_50mM_plus2.18992.18992.3	3	8.79	0	3.02E+05		(K)LAKPLSS	(K)L A K/P L S\S\L T/P L I M A A/K(E)		167.95	552.004	1653.997	0.0003	0.2	10	24711.4	5.19	HUMAN	H7C1X3	PAK-2p34 (Fragment)
12909	dirMS_041712_NAR_50mM_plus2.7186.7186.3	3	8.79	1	4.90E+04	M170m	(R)SCmLTG	(R)S C/m|L/T G T/P E/S V Q S A K R(L)	C:Carbamidomethylation m:Oxid	103.42	589.9509	1751.842	15.9967	1	8.46	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
12910	dirMS_041712_NAR_120mM_minus.6817.6817.2	2	8.78	0	4.89E+05		(K)HQPTAII	(K)H Q|P\T A\I I|A K(T)		91.83	489.7898	978.573	-0.0008	-0.8	8.76	63448.4	7.29	HUMAN	B4E022	Transketolase
12911	dirMS_041712_NAR_20mM_minus.14502.14502.3	3	8.78	0	1.37E+05		(R)LSVEEA	(R)L S V E E A V A\A/G\V|V/G/G E I Q E K(L)		199.57	629.0005	1884.991	-0.0044	-2.3	4.09	266161	5.68	HUMAN	E9PPU0	Epiplakin
12912	dirMS_041712_NAR_30mM_minus2.6317.6317.2	2	8.78	0	1.62E+05		(K)MQASIE	(K)M/Q/A S|I/E/K(G)		88.65	403.7074	806.408	-0.0001	-0.2	5.75	32745.6	4.64	HUMAN	P06748	Nucleophosmin
12913	dirMS_041712_NAR_40mM_minus2.11982.11982.3	3	8.78	0	2.73E+05		(K)DAGEGL	(K)D A|G\E/G L/L A/V Q I T D/P E\G\K P K(K)		154	646.6785	1938.018	0.0031	1.6	4.32	283472.4	5.71	HUMAN	P21333	Filamin-A
12914	dirMS_041712_NAR_40mM_minus2.14522.14522.3	3	8.78	1	1.04E+06	M116m	(R)ELAILLG	(R)E L\A/I/L/L/G m L D P A E K D E K(G)	m:Oxidized methionine	170.97	634.338	1884.999	16.0008	3.1	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
12915	dirMS_041712_NAR_50mM_minus2.13960.13960.3	3	8.78	1	3.85E+05		(K)ITDIIGKE	(K)I T|D I|I/G/K E E G I/G P/E N L R(G)		146.92	618.665	1853.997	-0.0163	-8.8	4.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
12916	dirMS_041712_NAR_50mM_minus2.16978.16978.3	3	8.78	0	1.55E+05		(R)LLEVLSG	(R)L L/E/V/L S G E/I/L P K P T K(G)		165.35	546.3329	1636.988	-0.0042	-2.6	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
12917	dirMS_041712_NAR_50mM_minus2.9449.9449.2	2	8.78	1	7.15E+05		(R)DGKLVS	(R)D/G/K L|V|S E S S D V L|P K(-)		121.97	737.3927	1473.78	-0.0014	-0.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
12918	dirMS_041712_NAR_60mM_minus.8904.8904.3	3	8.78	1	3.60E+05	M230m M:	(R)mSMKE	(R)m S M K E V D\E Q\m|L N/V/Q/N K(N)	m:Oxidized methionine	110.3	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
12919	dirMS_041712_NAR_120mM_plus.11711.11711.3	3	8.78	0	2.30E+05		(K)VYNYNH	(K)V/Y/N Y/N H L/M P T R(Y)		114.35	469.8997	1407.684	0.0008	0.5	8.57	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
12920	dirMS_041712_NAR_120mM_plus.21689.21689.4	4	8.78	1	2.41E+05		(R)KVDIIAD	(R)K V D I\I A D/A A Y/S I/F\Q/K/P K(S)		166.97	477.5186	1907.064	-0.0111	-5.8	8.43	23634.7	4.93	HUMAN	B4DWC7	Hydroxysteroid dehydrogenase-like protein 2
12921	dirMS_041712_NAR_20mM_plus.10635.10635.2	2	8.78	0	6.78E+04		(K)VLQLYPI	(K)V L|Q|L/Y|P N N K(A)		145.98	544.8057	1088.61	-0.0057	-5.3	8.56	9740.1	10.08	HUMAN	H0YFG2	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed (Fragment)
12922	dirMS_041712_NAR_30mM_plus2.19370.19370.2	2	8.78	0	1.35E+05		(K)IIGNLLY	(K)I I|G N L/L/Y Y R(Y)		155.28	562.8247	1124.646	-0.0041	-3.7	8.59	125076	8.92	HUMAN	H0YLE8	Ras GTPase-activating-like protein IQGAP1
12923	dirMS_041712_NAR_30mM_plus2.7484.7484.2	2	8.78	0	2.71E+05		(R)AAMGP	(R)A A|M|G/P G I S R(M)		93.57	430.2276	859.445	0.0025	2.9	9.79	22167.3	10.15	HUMAN	E7ENQ8	Phosphoglucomutase-2
12924	dirMS_041712_NAR_40mM_plus2.6265.6265.2	2	8.78	0	1.87E+05		(K)TEISEMI	(K)T\E|I/S/E/M N R(N)		96.22	490.2292	979.451	-0.0002	-0.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
12925	dirMS_041712_NAR_40mM_plus2.6887.6887.2	2	8.78	0	5.95E+04		(K)CCTESLV	(K)C C|T|E/S L V/N R(R)	C:Carbamidomethylation	100.58	569.7569	1138.498	0.0086	7.5	6	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
12926	dirMS_041712_NAR_50mM_plus2.14107.14107.3	3	8.78	0	1.78E+06	M457m	(R)mGPLGL	(R)m/G/P/L/G L/D/H M A S S I E R(M)	m:Oxidized methionine	142.8	543.9304	1613.777	15.9992	2.6	5.3	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
12927	dirMS_041712_NAR_50mM_plus2.16361.16361.3	3	8.78	1	1.22E+05		(R)EGIVTAT	(R)E G I/V/T/A/T E Q E V K E D I/A K(L)		154.88	620.658	1859.96	-0.0002	-0.1	4.25	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
12928	dirMS_041712_NAR_50mM_plus2.6015.6028.3	3	8.78	0	8.84E+04		(R)ITPPAAK	(R)I T|P/P A A K/P G S P Q A K(S)		95.85	454.9298	1362.774	0.0009	0.6	10	214357.5	7.19	HUMAN	P35658	Nuclear pore complex protein Nup214
12929	dirMS_041712_NAR_50mM_plus2.8697.8697.3	3	8.78	0	1.95E+04		(R)TVAIYSE	(R)T V/A I/Y/S/E Q D T G Q M H R(Q)		113.87	579.2737	1735.807	-0.0003	-0.2	5.29	58266.4	9.46	HUMAN	B4DN00	Pyruvate carboxylase, mitochondrial
12930	dirMS_041712_NAR_50mM_plus2.9987.9987.3	3	8.78	1	2.46E+06		(K)ATAVVD	(K)A T|A/V|V D/G A\F K E V K(L)		120.07	445.5822	1334.731	0.0006	0.5	6.11	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
12931	dirMS_041712_NAR_60mM_plus.15079.15079.3	3	8.78	1	2.51E+05		(R)LVDYLEC	(R)L/V/D/Y/L/E/G I R K(N)		135.35	402.5673	1205.689	-0.0015	-1.2	6.07	26450.3	5.66	HUMAN	Q96BR5	Sel1 repeat-containing protein 1
12932	dirMS_041712_NAR_60mM_plus.15227.15227.3	3	8.78	1	2.48E+05		(-)MKVELCS	(-)M K V E L|C/S|F S/G Y K(I)	C:Carbamidomethylation	136.28	483.5686	1448.691	0	0	8.26	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
12933	dirMS_041712_NAR_60mM_plus.18480.18480.3	3	8.78	1	2.24E+05		(R)GMLKDI	(R)G M/L|K D N A/M/L/E\Y L K(I)		153.68	509.2606	1525.775	-0.0081	-5.3	6.07	65692.2	5.7	HUMAN	E7EQR4	Ezrin
12934	dirMS_041712_NAR_120mM_minus.10940.10940.3	3	8.77	1	2.36E+05		(R)TNEKVE	(R)T N/E K V E\L|Q|E L/N D/R(F)		114.1	529.9368	1587.797	-0.0014	-0.9	4.41	49709.6	5.19	HUMAN	B0YJC4	Vimentin
12935	dirMS_041712_NAR_50mM_minus2.12713.12713.3	3	8.77	0	1.03E+06	M114m M:	(R)AGKPVI	(R)A G K\P V I|C A T|Q/m L E S m I K(K)	C:Carbamidomethylation m:Oxid	139.93	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
12936	dirMS_041712_NAR_50mM_minus2.6143.6160.3	3	8.77	1	1.78E+05		(R)IVDGKV	(R)I/V|D G K/V V/S E T N D T K(V)		97.65	502.2662	1504.785	-0.0013	-0.9	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
12937	dirMS_041712_NAR_60mM_minus.16977.16977.3	3	8.77	1	3.56E+05		(R)ARFEELI	(R)A R\F E E\L|N|A/D/L F/R(G)		154.08	494.2594	1480.754	0.0093	6.3	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
12938	dirMS_041712_NAR_60mM_minus.19952.19952.3	3	8.77	1	8.17E+05		(R)LIALLEVI	(R)L I/A L/L/E V L S Q K R(M)		182.02	461.6287	1382.873	-0.0014	-1	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
12939	dirMS_041712_NAR_60mM_minus.6523.6523.3	3	8.77	1	4.07E+04		(K)SPPREGS	(K)S P\P R E G S Q\G E\L|T/P A\N S Q S R(M)		95.02	666.6591	1997.964	-0.0008	-0.4	5.87	53941.6	6.3	HUMAN	C9JFE4	COP9 signalosome complex subunit 1
12940	dirMS_041712_NAR_60mM_minus.7924.7924.3	3	8.77	1	8.24E+05		(R)LREDEN	(R)L R E D E N\A E|P V/G T T Y/Q K(T)		104.68	617.3015	1849.893	-0.0027	-1.5	4.41	76925.9	4.46	HUMAN	A8MV58	Drebrin
12941	dirMS_041712_NAR_120mM_plus.5800.5800.3	3	8.77	1	1.53E+05		(K)AMKEYE	(K)A/M/K/E\Y/E/E E/E R(K)		84.07	438.5281	1313.568	0.0019	1.5	4.32	11829.2	4.96	HUMAN	K7EIU0	Hsp90 co-chaperone Cdc37 (Fragment)
12942	dirMS_041712_NAR_20mM_plus.17033.17033.2	2	8.77	0	9.54E+04		(R)AIVAIEN	(R)A I V A|I/E N/P A D/V\S|V I S S R(N)		188.95	870.9764	1740.949	-0.0035	-2	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
12943	dirMS_041712_NAR_20mM_plus.17904.17954.2	2	8.77	0	2.01E+05		(K)VANVSL	(K)V A|N\V/S/L L A\L Y K(G)		195.28	595.8558	1190.714	-0.01	-8.4	8.56	15978.4	10.84	HUMAN	P62266	40S ribosomal protein S23
12944	dirMS_041712_NAR_20mM_plus.8763.8763.2	2	8.77	0	6.19E+04		(K)EQVANS	(K)E Q/V/A/N S A F V E/R(C)		130.78	625.3102	1249.617	-0.004	-3.2	4.53	17664	8.77	HUMAN	H0Y6E4	Heat shock protein HSP 90-beta (Fragment)
12945	dirMS_041712_NAR_30mM_plus2.16579.16579.2	2	8.77	0	3.17E+05		(R)FLICTDV	(R)F/L|I/C/T/D V A A R(G)	C:Carbamidomethylation	139.77	583.3055	1165.603	0.0003	0.3	5.84	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
12946	dirMS_041712_NAR_40mM_plus2.10873.10873.3	3	8.77	1	1.50E+04		(R)DVVICPI	(R)D V|V I/C/P D A S L E D A K K(E)	C:Carbamidomethylation	130.32	553.9465	1659.826	-0.0009	-0.5	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
12947	dirMS_041712_NAR_40mM_plus2.19025.19025.3	3	8.77	0	1.41E+05		(R)ETSSDV	(R)E T/S S/D/V/A\L A S H/I L T A L R(E)		178.63	595.3161	1783.955	-0.0211	-11.8	5.32	36920.6	4.68	HUMAN	O00273	DNA fragmentation factor subunit alpha
12948	dirMS_041712_NAR_40mM_plus2.6152.6194.2	2	8.77	0	2.30E+05		(K)CNLCYR	(K)C/N|L/C/Y/R(V)	C:Carbamidomethylation	95.28	443.1854	885.371	-0.007	-8	8.75	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
12949	dirMS_041712_NAR_40mM_plus2.7306.7306.2	2	8.77	0	9.67E+04		(R)STFSTNY	(R)S T|F/S T/N Y R(S)		102.65	488.2297	975.453	-0.0009	-0.9	8.46	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
12950	dirMS_041712_NAR_40mM_plus2.7432.7432.2	2	8.77	0	8.07E+04		(K)EEYGPG	(K)E E/Y/G P G V Q G K(E)		103.3	532.252	1063.506	-0.0087	-8.2	4.53	60692.5	7.44	HUMAN	D6RDG4	Centrosomal protein POC5
12951	dirMS_041712_NAR_50mM_plus2.7399.7399.3	3	8.77	1	3.36E+05	M2747m	(K)TLQEVTI	(K)T L/Q|E/V T E/m/D S V K R(Y)	m:Oxidized methionine	105.03	517.9284	1535.773	15.9973	1.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
12952	dirMS_041712_NAR_30mM_minus2.12388.12388.2	2	8.76	0	1.83E+05		(R)TLSGME	(R)T L/S G M/E S Y C V R(A)	C:Carbamidomethylation	121.77	651.795	1302.582	0.001	0.8	5.66	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
12953	dirMS_041712_NAR_40mM_minus2.8202.8202.3	3	8.76	1	3.18E+05		(R)DGKLVS	(R)D G K L V S\E/S/S D V\L/P K(-)		128.2	491.9311	1473.78	-0.0008	-0.5	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
12954	dirMS_041712_NAR_50mM_minus2.11191.11191.3	3	8.76	0	1.66E+04		(R)VVVLMC	(R)V V|V L/M|G S T S D L/G H C E K(I)	C:Carbamidomethylation	132.28	577.9535	1731.84	0.0055	3.2	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
12955	dirMS_041712_NAR_50mM_minus2.13613.13613.3	3	8.76	0	5.30E+05		(K)LQMEAF	(K)L Q|M E/A/P H I\I/V G T P\G R(V)		145.55	540.2947	1618.873	-0.0038	-2.4	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
12956	dirMS_041712_NAR_50mM_minus2.14676.14676.3	3	8.76	0	1.16E+04		(K)GILADEI	(K)G I|L/A/D/E D S S R P V\W L K(A)		150.35	562.6354	1685.886	0.0059	3.5	4.56	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
12957	dirMS_041712_NAR_50mM_minus2.16893.16910.3	3	8.76	0	1.44E+05		(K)TVSGVN	(K)T V|S G/V/N G/P L/V I L D H V K(V)		164.98	549.9835	1647.943	-0.0069	-4.2	6.41	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
12958	dirMS_041712_NAR_50mM_minus2.17615.17615.3	3	8.76	1	1.24E+05		(K)NAAGAL	(K)N A|A/G A L D\L L K/E/L K(N)		168.68	452.601	1355.789	-0.0008	-0.6	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
12959	dirMS_041712_NAR_50mM_minus2.9047.9047.3	3	8.76	1	7.92E+05		(K)ATAVVD	(K)A/T/A/V V/D G A F K E V K(L)		119.97	445.5821	1334.731	0.0003	0.2	6.11	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
12960	dirMS_041712_NAR_60mM_minus.14449.14449.3	3	8.76	1	2.64E+05		(R)VEVERD	(R)V/E/V E R D N L/A E D/I M R(L)		139.98	563.6139	1688.827	-0.0001	0	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
12961	dirMS_041712_NAR_60mM_minus.14605.14605.3	3	8.76	0	4.00E+05		(K)AVGHPF	(K)A V/G H/P F V|I Q/L/G/R(I)		141.87	431.9182	1293.743	-0.0026	-2	9.8	124524.8	5.71	HUMAN	O14980	Exportin-1
12962	dirMS_041712_NAR_60mM_minus.6101.6101.3	3	8.76	1	1.53E+06		(K)DSYVGD	(K)D/S/Y/V/G D E A Q S K/R(G)		90.97	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
12963	dirMS_041712_NAR_60mM_minus.7498.7498.3	3	8.76	0	6.22E+04		(K)ITPAHDC	(K)I T|P A/H D Q N/D/Y/E V G Q R(H)		101.22	581.6072	1742.809	-0.0022	-1.3	4.54	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
12964	dirMS_041712_NAR_120mM_plus.15427.15427.4	4	8.76	1	9.61E+04		(K)LDKAQII	(K)L D K A Q I/H D\L V\L\V/G G S T/R(I)		134.05	456.259	1822.018	-0.004	-2.2	6.75	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
12965	dirMS_041712_NAR_120mM_plus.6681.6681.3	3	8.76	1	8.63E+05		(R)SKEQAE	(R)S K E Q A E|L/E/A/A/R(Q)		88.25	411.2137	1231.628	-0.0012	-0.9	4.78	533778	5.74	HUMAN	Q15149	Plectin
12966	dirMS_041712_NAR_120mM_plus.8128.8173.2	2	8.76	0	7.58E+05		(K)HYEMLA	(K)H|Y|E/M\L\A N/R(T)		96.27	517.2485	1033.488	0.0013	1.3	6.75	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B

12967	dirMS_041712_NAR_20mM_plus.9481.9614.2	2	8.76	0	3.16E+05		(K)LVLVGD(	(K)L V|L|V/G D/G G T G K(T)		137.4	508.292	1015.578	-0.0015	-1.5	5.84	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
12968	dirMS_041712_NAR_30mM_plus2.14143.14143.3	3	8.76	0	2.76E+05		(R)LNDSILC	(R)L N D\S\I\L/Q/A/T/E\Q R(R)		127.3	463.2439	1387.718	-0.0004	-0.3	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
12969	dirMS_041712_NAR_30mM_plus2.17061.17329.2	2	8.76	0	6.04E+05		(K)NAAGAL	(K)N A|A|G A/L D L L/K(E)		143.22	493.2867	985.568	-0.0015	-1.6	5.84	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
12970	dirMS_041712_NAR_40mM_plus2.12841.12841.3	3	8.76	1	1.22E+04		(K)SGEISLP	(K)S/G\E\I/S L P I/K E E P S P I S K(M)		142.55	604.3276	1810.98	-0.0114	-6.3	4.78	119334.1	5.73	HUMAN	B4DGT8	MKL/myocardin-like 2, isoform CRA_a
12971	dirMS_041712_NAR_50mM_plus2.16555.16555.3	3	8.76	1	2.21E+05		(R)STVRDID	(R)S T V R D I D|P/Q/N D|L T F L R(I)		154.87	630.6609	1889.972	-0.0034	-1.8	4.43	16537.8	6.59	HUMAN	B1AKR6	Dynein light chain roadblock-type 1
12972	dirMS_041712_NAR_60mM_plus.12141.12141.2	2	8.76	1	1.52E+06		(R)DGKLVS	(R)D G K L/V|S/E S S D\V/L|P K(-)		120.25	737.3869	1473.78	-0.013	-8.8	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
12973	dirMS_041712_NAR_60mM_plus.12835.12835.3	3	8.76	1	9.04E+05	M232m	(R)MSmKE\	(R)M S m K E V D E Q\M|L/N/V Q N K(N)	m:Oxidized methionine	123.57	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
12974	dirMS_041712_NAR_60mM_plus.17638.17638.3	3	8.76	1	4.69E+05		(R)KVNNAD	(R)K\V N N A D D\F|P/N L F R(Q)		149.22	517.2632	1549.776	-0.0007	-0.5	5.96	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
12975	dirMS_041712_NAR_60mM_plus.19742.19742.3	3	8.76	0	3.39E+05		(R)NSVSNF	(R)N/S/V/S N/F/L/H/S L E R(G)		162.58	468.2401	1402.707	-0.0016	-1.1	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
12976	dirMS_041712_NAR_60mM_plus.20623.20623.3	3	8.76	1	7.00E+05		(K)IKYPENF	(K)I/K Y P E N|F/F L/L R(G)		167.98	480.6056	1439.805	-0.0023	-1.6	8.59	33222.3	5.74	HUMAN	A6NNR3	Serine/threonine-protein phosphatase
12977	dirMS_041712_NAR_120mM_minus.15201.15201.4	4	8.75	1	2.55E+05		(R)EALLSSA	(R)E A\L/L/S S A V/D H G/S D E/V K F R(Q)		136.03	490.7539	1959.977	0.0167	8.5	4.75	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
12978	dirMS_041712_NAR_20mM_minus.7973.7973.2	2	8.75	0	8.30E+04		(R)DQVTYC	(R)D Q/V|T|Y Q Q L/R(E)		129.75	575.7953	1150.585	-0.0018	-1.6	5.83	266161	5.68	HUMAN	E9PPU0	Epiplakin
12979	dirMS_041712_NAR_30mM_minus2.16805.16824.2	2	8.75	0	5.82E+05		(K)MIFVGIK	(K)M/I|F/V/G I/K(K)		145.68	404.2383	807.48	-0.0104	-12.9	8.5	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
12980	dirMS_041712_NAR_30mM_minus2.18031.18031.2	2	8.75	0	1.04E+05		(R)TFPVLLR	(R)T F/P V L/L R(L)		152.87	423.2631	845.524	-0.0054	-6.4	9.41	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
12981	dirMS_041712_NAR_30mM_minus2.18684.18684.2	2	8.75	0	1.04E+05		(K)GFGGIG(	(K)G F/G/G I|G/G I L R(Y)		156.73	473.7762	946.547	-0.0018	-1.9	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
12982	dirMS_041712_NAR_30mM_minus2.18709.18709.2	2	8.75	0	7.71E+04		(R)SSIAGLL	(R)S S/I/A/G L/L L/K(A)		155.72	451.2891	901.572	-0.0008	-0.9	8.47	533778	5.74	HUMAN	Q15149	Plectin
12983	dirMS_041712_NAR_30mM_minus2.5422.5422.2	2	8.75	0	4.31E+05		(R)TDTGEP	(R)T D|T|G E P M\G R(G)		82.83	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
12984	dirMS_041712_NAR_40mM_minus2.12029.12029.3	3	8.75	0	1.48E+05		(K)AAPEAS:	(K)A A/P E A/S S/P P A S P L Q H L L/P G K(A)		154.52	656.6876	1968.055	-0.0067	-3.4	6.79	84649.8	5.82	HUMAN	Q96TA1	Niban-like protein 1
12985	dirMS_041712_NAR_40mM_minus2.15000.15000.3	3	8.75	0	1.44E+05		(K)LFLFHTS	(K)L F|L F H T S\L|P I\A E A/P G K(L)		173.92	580.9924	1740.968	-0.0057	-3.3	6.75	108105.4	6.57	HUMAN	E7EP00	Protein transport protein Sec24C
12986	dirMS_041712_NAR_50mM_minus2.14438.14438.3	3	8.75	1	1.40E+05		(R)GDVVPK	(R)G D V|V/P K/D V/N A A/I A T I K(T)		150.42	537.6375	1610.911	-0.0133	-8.2	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
12987	dirMS_041712_NAR_50mM_minus2.15131.15131.3	3	8.75	0	2.63E+05	M118m	(R)AGKPVI(	(R)A G K\P V I\C A\T Q|M/L/E S m I/K(K)	C:Carbamidomethylation m:Oxid	154.53	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
12988	dirMS_041712_NAR_60mM_minus.8446.8446.3	3	8.75	1	5.51E+04		(R)FEEEIKA	(R)F/E|E E I/K/A E Q E/E R(K)		107.07	512.9085	1536.718	-0.0067	-4.4	4.2	26810.9	5.15	HUMAN	Q96C19	EF-hand domain-containing protein D2
12989	dirMS_041712_NAR_20mM_plus.14749.14749.2	2	8.75	0	1.13E+05		(K)LVILANN	(K)L V|I/L|A/N/N C|P A L R(K)	C:Carbamidomethylation	172.83	677.3851	1353.767	-0.0042	-3.1	9.75	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
12990	dirMS_041712_NAR_30mM_plus2.14206.14439.2	2	8.75	0	5.63E+05		(K)IEDFLER	(K)I/E|D/F/L E/R(R)		128	461.2413	921.468	0.0077	8.4	4.14	16684.5	11.19	HUMAN	B5MCT8	40S ribosomal protein S9
12991	dirMS_041712_NAR_30mM_plus2.14465.14465.2	2	8.75	0	5.73E+05		(K)CCSGAII'	(K)C/C|S G\A I I/V/L T K(S)	C:Carbamidomethylation	128.2	611.3189	1221.633	-0.0025	-2	8.75	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
12992	dirMS_041712_NAR_30mM_plus2.18061.18061.3	3	8.75	0	1.41E+05		(R)VNPALA	(R)V N|P\A\L\A/E L N L/R(S)		147.58	403.9019	1209.695	-0.0039	-3.2	5.97	20026.6	4.67	HUMAN	E9PIK5	Ribonuclease inhibitor (Fragment)
12993	dirMS_041712_NAR_30mM_plus2.20460.20460.2	2	8.75	0	6.67E+04		(K)LAVNM\	(K)L A\V|N/M V/P F P R(L)		160.6	572.32	1143.634	-0.0016	-1.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
12994	dirMS_041712_NAR_30mM_plus2.6976.6976.2	2	8.75	0	1.34E+05		(K)YTQSNS'	(K)Y/T|Q/S N/S V/C Y\A K(N)	C:Carbamidomethylation	91.15	660.7963	1320.589	-0.0036	-2.7	8.5	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
12995	dirMS_041712_NAR_40mM_plus2.13985.13985.3	3	8.75	0	2.92E+05		(R)LASTLVH	(R)L A|S/T L|V H L G E Y Q A|A V D G A R(K)		148.43	657.6841	1971.029	0.0083	4.2	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
12996	dirMS_041712_NAR_40mM_plus2.17435.17435.3	3	8.75	0	1.53E+05		(R)VYAILTH	(R)V Y/A/I L T/H/G\I/F/S G P A I\S R(I)		169.28	601.3376	1801.996	0.0023	1.3	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
12997	dirMS_041712_NAR_50mM_plus2.12720.12720.3	3	8.75	0	5.15E+05		(R)IMDPNI\	(R)I/M/D/P N/I V G S E H/Y D V A R(G)		134.6	605.9694	1815.869	0.0242	13.3	4.54	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
12998	dirMS_041712_NAR_50mM_plus2.18148.18148.3	3	8.75	1	1.09E+05		(K)DLEIKIP\	(K)D L\E|I K/I/P V/V V R(L)		163.5	427.6021	1280.794	-0.0019	-1.5	6.07	44183.5	5.64	HUMAN	F5GXC8	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial
12999	dirMS_041712_NAR_50mM_plus2.8798.8798.3	3	8.75	0	1.55E+06		(R)LESGMC	(R)L/E|S G/M Q N M/S I H T K(T)		113.23	492.5704	1475.698	-0.0015	-1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
13000	dirMS_041712_NAR_60mM_plus.17477.17477.3	3	8.75	1	6.41E+05		(R)IFDSEEIL	(R)I/F/D/S E E I/L/A G Y K R(E)		149	514.2744	1540.801	0.0081	5.2	4.68	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
13001	dirMS_041712_NAR_120mM_minus.8012.8032.3	3	8.74	1	5.67E+05		(K)LDEREA(	(K)L/D/E R E\A G\I/T E/K(V)		97.85	420.8858	1260.643	-0.0002	-0.1	4.41	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
13002	dirMS_041712_NAR_20mM_minus.8701.8701.3	3	8.74	0	6.96E+04		(R)SPSDSST	(R)S P S D S S T A S T/P/V/A\E Q I E|R(A)		136.63	621.2935	1861.877	-0.0114	-6.1	4.14	76925.9	4.46	HUMAN	A8MV58	Drebrin
13003	dirMS_041712_NAR_30mM_minus2.11233.11233.2	2	8.74	0	3.89E+05		(R)NTDEM\	(R)N|T/D/E/M V/E/L R(I)		115.05	553.7611	1106.515	0.0003	0.2	4.14	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
13004	dirMS_041712_NAR_40mM_minus2.8075.8075.3	3	8.74	0	1.70E+05	M35m	(K)AASDIAr	(K)A A|S D I/A m T E L/P/P T H/P I R(L)	m:Oxidized methionine	128.2	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
13005	dirMS_041712_NAR_50mM_minus2.11023.11023.3	3	8.74	1	2.84E+04		(R)AGPGTL	(R)A G/P/G/T/L S V T I/E G/P S K V K(M)		131.03	547.6439	1640.922	-0.0046	-2.8	8.64	258215.9	5.48	HUMAN	E7EN95	Filamin-B
13006	dirMS_041712_NAR_50mM_minus2.16911.16911.3	3	8.74	0	1.44E+05		(K)TVSGVN	(K)T V/S G V N G P L/V I/L D H V K(V)		164.98	549.9835	1647.943	-0.0069	-4.2	6.41	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
13007	dirMS_041712_NAR_50mM_minus2.17266.17266.3	3	8.74	1	1.35E+05		(K)VIAATNI	(K)V/I/A/A T N R V D I L D/P A L L R(S)		166.88	617.366	1850.086	-0.0024	-1.3	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
13008	dirMS_041712_NAR_60mM_minus.14054.14054.3	3	8.74	1	2.40E+05		(R)VVISLQL	(R)V V|I/S L/Q L/T A E K R(V)		138.07	452.9408	1356.821	-0.0131	-9.6	8.72	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
13009	dirMS_041712_NAR_60mM_minus.15331.15331.3	3	8.74	0	1.17E+05		(R)QIFHPE(	(R)Q I/F H/P E Q L/I/T/G K(E)		145.13	470.9285	1410.774	-0.003	-2.1	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
13010	dirMS_041712_NAR_60mM_minus.16452.16452.3	3	8.74	1	3.17E+05		(K)LKLSILYF	(K)L K L S I L Y|P/A T T\G R(N)		151.1	478.2883	1432.852	-0.0019	-1.3	9.99	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
13011	dirMS_041712_NAR_60mM_minus.16838.16838.3	3	8.74	1	2.46E+05		(R)KGFSEGI	(R)K G F S E\G L W E|I|E/N\N P\T V/K(A)		153.75	649.9986	1947.981	0.0002	0.1	4.79	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
13012	dirMS_041712_NAR_30mM_plus2.19276.19276.2	2	8.74	0	1.99E+06		(R)QAQEYE	(R)Q A Q|E Y/E/A L L/N I\K(V)		153.75	710.3766	1419.748	-0.0019	-1.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13013	dirMS_041712_NAR_30mM_plus2.4905.4905.2	2	8.74	0	7.38E+05		(R)MGQTN	(R)M/G/Q/T M E R(I)		77.27	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
13014	dirMS_041712_NAR_50mM_plus2.20930.20930.3	3	8.74	0	3.39E+05		(K)HSQFIG\	(K)H S Q F\I/G\Y/P/I/T/L F V E K(E)		179.37	593.6536	1778.948	-0.0013	-0.8	6.75	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
13015	dirMS_041712_NAR_60mM_plus.20290.20290.3	3	8.74	1	4.21E+05		(K)NAAGAL	(K)N/A|A|G A/L D L L K\E/L K(N)		166.93	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
13016	dirMS_041712_NAR_60mM_plus.6578.6578.3	3	8.74	0	7.03E+05		(K)LVDQSG	(K)L/V/D Q/S\G P P H E/P K(F)		93.72	435.2257	1303.664	-0.0015	-1.2	5.32	142137.5	9.17	HUMAN	E7ENU4	Double-stranded RNA-specific adenosine deaminase
13017	dirMS_041712_NAR_60mM_plus.7437.7437.2	2	8.74	1	1.58E+06		(R)AAPGAE	(R)A A/P G A E|F A/P N K R(R)		96.2	614.8248	1228.643	-0.001	-0.8	8.79	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
13018	dirMS_041712_NAR_30mM_minus2.18412.18412.2	2	8.73	0	3.02E+04		(R)GLFIIDG	(R)G/L/F/I I D/G K(G)		154.33	431.7497	862.503	-0.0112	-12.9	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
13019	dirMS_041712_NAR_30mM_minus2.19244.19244.2	2	8.73	0	1.22E+06		(K)LAVNM\	(K)L A|V/N\M V|P F P/R(L)		159.22	572.3143	1143.634	-0.013	-11.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
13020	dirMS_041712_NAR_30mM_minus2.7662.7677.2	2	8.73	0	4.76E+05		(R)STLEPVE	(R)S/T|L/E/P V E/K(A)		96.18	451.7442	902.483	-0.0018	-2	4.53	25598.3	6.45	HUMAN	E7EP11	Heat shock 70 kDa protein 1A/1B
13021	dirMS_041712_NAR_40mM_minus2.13416.13416.3	3	8.73	1	1.96E+05		(K)LGVQVV	(K)L/G\V/Q/V/V/I T D P E K L D/Q I R(Q)		163.38	641.7007	1923.091	-0.0034	-1.8	4.56	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
13022	dirMS_041712_NAR_50mM_minus2.12164.12164.3	3	8.73	1	2.39E+05		(K)LIADVAF	(K)L/I|A D/V/A/P S A I R E N D I K(S)		137.7	575.6545	1724.954	-0.0052	-3	4.56	18388.8	6.85	HUMAN	F5H1Y3	Flap endonuclease 1 (Fragment)
13023	dirMS_041712_NAR_50mM_minus2.7439.7439.3	3	8.73	0	6.77E+04		(K)STAGDT	(K)S T|A/G D T/H L G G E D F D/N R(M)		108.82	564.5808	1691.726	0.0023	1.3	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
13024	dirMS_041712_NAR_60mM_minus.12891.12891.3	3	8.73	1	1.86E+05		(K)LSAEKVE	(K)L/S/A E K V E/I A/T L/T R(E)		131.38	477.6112	1430.821	-0.0023	-1.6	6.14	26661.1	7.81	HUMAN	H0YL69	Proteasome subunit alpha type (Fragment)
13025	dirMS_041712_NAR_60mM_minus.19000.19000.3	3	8.73	0	2.76E+05		(R)CRPDQL	(R)C R P D Q L|T|G\L|S L/L/P L S E K(A)	C:Carbamidomethylation	168.15	643.0129	1927.032	-0.0076	-3.9	6.07	533778	5.74	HUMAN	Q15149	Plectin
13026	dirMS_041712_NAR_60mM_minus.8593.8593.3	3	8.73	0	7.13E+04		(R)IFHELTQ	(R)I/F H/E L T Q/T\D K(A)		107.83	411.2127	1231.632	-0.0082	-6.6	5.32	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
13027	dirMS_041712_NAR_120mM_plus.5611.5611.3	3	8.73	0	9.60E+04		(K)IAGHPL/	(K)I/A G H/P/L\A Q N E R(C)		82.47	402.5461	1205.639	-0.0148	-12.3	6.75	18455.6	6.76	HUMAN	F8W8K5	Sorting nexin-12
13028	dirMS_041712_NAR_120mM_plus.6473.6473.2	2	8.73	0	4.57E+05		(K)HQPTAII	(K)H/Q|P T A\I\I\A K(T)		87.75	489.7897	978.573	-0.001	-1	8.76	63448.4	7.29	HUMAN	B4E022	Transketolase
13029	dirMS_041712_NAR_20mM_plus.12808.12808.2	2	8.73	0	1.23E+05	M137m	(K)IEVIEIm1	(K)I E\V|I|E I/m T/D R(G)	m:Oxidized methionine	160.97	617.8225	1218.64	15.9979	2.4	4.14	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
13030	dirMS_041712_NAR_20mM_plus.14439.14439.2	2	8.73	0	1.31E+05		(R)FIDTTLA	(R)F I|D T T/L/A/I T S R(F)		171.47	619.3413	1237.679	-0.0034	-2.7	5.84	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
13031	dirMS_041712_NAR_20mM_plus.16668.16668.2	2	8.73	0	7.50E+04		(R)SSIAGLL	(R)S/S|I/A/G L\L L K(A)		186.4	451.2885	901.572	-0.002	-2.2	8.47	533778	5.74	HUMAN	Q15149	Plectin
13032	dirMS_041712_NAR_20mM_plus.7263.7263.2	2	8.73	0	2.87E+05	M281m	(R)AEAESm	(R)A E|A E/S m/Y Q I/K(Y)	m:Oxidized methionine	118.4	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
13033	dirMS_041712_NAR_30mM_plus2.15734.15734.2	2	8.73	0	2.11E+05		(K)LLPPYLR	(K)L L/P/P/Y L R(V)		135.32	436.2709	871.54	-0.0055	-6.3	8.75	55805.4	6.7	HUMAN	P43490	Nicotinamide phosphoribosyltransferase
13034	dirMS_041712_NAR_30mM_plus2.9029.9029.2	2	8.73	0	5.36E+05		(K)QADVNI	(K)Q A\D V/N/L/V/N/A/K(L)		100.82	536.2922	1071.579	-0.0022	-2	5.84	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
13035	dirMS_041712_NAR_40mM_plus2.13848.13848.3	3	8.73	0	2.23E+05		(K)VALLLLD	(K)V A L/L|L/L/D Q/G/A S P H A A A K(N)		148.13	558.9886	1674.954	-0.0025	-1.5	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
13036	dirMS_041712_NAR_40mM_plus2.13993.13993.3	3	8.73	1	8.78E+04		(R)STGLELE	(R)S T|G/L/E L E T/P S L V/P V/K K(N)		148.73	566.6552	1697.968	-0.0173	-10.2	5.86	34828	9.96	HUMAN	F5H5K4	Serine/threonine-protein phosphatase 1 regulatory subunit 10
13037	dirMS_041712_NAR_40mM_plus2.17163.17163.3	3	8.73	0	6.64E+04		(R)IHFPLAT	(R)I H F P L A T Y/A|P V/I S A E K(A)		166.77	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
13038	dirMS_041712_NAR_50mM_plus2.11384.11384.3	3	8.73	1	1.53E+05		(R)VQSVEQ	(R)V Q|S V/E Q I R E V/A S G A A R(I)		127.38	567.3075	1699.909	-0.0006	-0.4	6.11	20631.5	6.98	HUMAN	D6RAX2	C-terminal-binding protein 1 (Fragment)
13039	dirMS_041712_NAR_50mM_plus2.9581.9581.3	3	8.73	1	3.39E+05		(R)AGTGVD	(R)A G T/G/V/D N V/D/L/E A A T R\K(G)		117.4	539.6108	1616.824	-0.006	-3.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
13040	dirMS_041712_NAR_60mM_plus.7000.7000.3	3	8.73	0	1.83E+05		(K)TQAYQD	(K)T Q|A/Y Q D Q K/P G T S G L R(K)		94.9	550.6115	1649.824	-0.0042	-2.6	8.25	61733.3	6.3	HUMAN	P36871	Phosphoglucomutase-1
13041	dirMS_041712_NAR_60mM_plus.8600.8600.3	3	8.73	1	4.16E+05		(K)QGIETPE	(K)Q G/I E T/P E/D Q N D L R K(M)		102.63	548.2719	1642.803	-0.002	-1.2	4.32	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
13042	dirMS_041712_NAR_120mM_minus.10699.10699.3	3	8.72	1	2.17E+05	M86m	(K)mKEIAE/	(K)m K E I A/E/A/Y/L/G K(T)	m:Oxidized methionine	111.63	423.557	1252.661	15.9959	0.7	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
13043	dirMS_041712_NAR_120mM_minus.15204.15204.3	3	8.72	1	5.42E+04		(R)LSAEERD	(R)L/S/A\E E R D Q L\L/P N L R(A)		136.85	551.9677	1653.892	-0.0033	-2	4.68	12056.4	6.28	HUMAN	P61457	Pterin-4-alpha-carbinolamine dehydratase
13044	dirMS_041712_NAR_40mM_minus2.13200.13200.3	3	8.72	0	2.48E+04		(K)SYELPD(	(K)S Y E L\P D G Q V/I/T I/G/N E R(F)		161.1	597.6327	1790.892	-0.0084	-4.7	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
13045	dirMS_041712_NAR_50mM_minus2.10832.10832.3	3	8.72	0	1.65E+05		(R)LLELGPK	(R)L L|E/L G P/K/P E V\A/Q Q T R(K)		129.83	560.3182	1678.949	-0.0086	-5.1	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
13046	dirMS_041712_NAR_50mM_minus2.17407.17407.3	3	8.72	0	3.09E+05		(K)VAHALA	(K)V A H A L A E G L|G\V|I/A/C I G/E/K(L)	C:Carbamidomethylation	168.5	603.3247	1807.974	-0.0139	-7.7	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
13047	dirMS_041712_NAR_50mM_minus2.7811.7811.3	3	8.72	0	3.55E+04		(R)VILGSEA	(R)V I|L|G S/E A A Q Q H P E E/V R(G)		111.43	588.3055	1762.908	-0.0063	-3.6	4.75	19458.5	4.89	HUMAN	E9PKK8	Dipeptidyl peptidase 3 (Fragment)
13048	dirMS_041712_NAR_60mM_minus.13398.13398.3	3	8.72	1	1.86E+05		(R)LATALQI	(R)L/A/T/A\L Q K/L\E E A E K(A)		134.07	481.9376	1443.805	-0.0071	-4.9	4.79	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
13049	dirMS_041712_NAR_60mM_minus.6885.6885.3	3	8.72	1	2.94E+05		(R)VKVEPA'	(R)V/K V E/P A|V/D T/S R(I)		97.32	400.8938	1200.658	0.0086	7.1	6.04	258215.9	5.48	HUMAN	E7EN95	Filamin-B
13050	dirMS_041712_NAR_120mM_plus.14897.15020.4	4	8.72	2	1.54E+06		(R)YLYTLVI'	(R)Y L/Y/T/L V/I/T D K E K A E K(L)		131.28	454.2533	1813.995	-0.0032	-1.8	6.18	7621.9	10.1	HUMAN	J3KT73	60S ribosomal protein L38
13051	dirMS_041712_NAR_120mM_plus.4630.4630.3	3	8.72	1	1.96E+05		(R)LKQSAEI	(R)L/K\Q S A E E Q/A/Q/A/R(A)		74.5	453.5701	1358.702	-0.0065	-4.8	6.14	533778	5.74	HUMAN	Q15149	Plectin
13052	dirMS_041712_NAR_120mM_plus.7179.7179.2	2	8.72	1	4.20E+05		(K)GANPVE	(K)G/A/N|P V E/I R/R(G)		91.22	506.287	1011.569	-0.0027	-2.6	9.6	17213.7	10.05	HUMAN	B7Z712	60 kDa heat shock protein, mitochondrial
13053	dirMS_041712_NAR_20mM_plus.16763.16763.2	2	8.72	0	1.17E+05		(R)LLEAQIA	(R)L L\E/A Q/I A T G G I\I\D/P K(E)		185.97	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
13054	dirMS_041712_NAR_20mM_plus.19143.19143.2	2	8.72	0	1.44E+05		(R)EGDVLT	(R)E G D/V L/T L/L/E\S E/R(E)		203.47	680.8536	1360.696	0.0045	3.3	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
13055	dirMS_041712_NAR_30mM_plus2.11788.11788.2	2	8.72	0	9.24E+04		(R)GCTATL(	(R)G C|T A|T/L/G N/F\A K(A)	C:Carbamidomethylation	114.95	570.2807	1139.551	0.0028	2.4	8.75	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
13056	dirMS_041712_NAR_40mM_plus2.13262.13299.3	3	8.72	0	1.97E+05		(R)DLSHIGI	(R)D L S H I\G D\A\V|V|I/S C A K(D)	C:Carbamidomethylation	144.35	528.9395	1584.805	-0.0011	-0.7	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
13057	dirMS_041712_NAR_40mM_plus2.16037.16037.3	3	8.72	0	3.15E+05		(K)VAIVKP(	(K)V A/I V K P G V|P/M/E I V L/N K(E)		161.13	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
13058	dirMS_041712_NAR_40mM_plus2.17887.17887.3	3	8.72	0	1.42E+05		(R)DIKPQN	(R)D I K P Q N L\L/L/D/P/D/T A V L K(L)		170.92	631.6874	1893.069	-0.0215	-11.4	4.43	47257	9.38	HUMAN	P49841	Glycogen synthase kinase-3 beta
13059	dirMS_041712_NAR_40mM_plus2.6197.6197.2	2	8.72	1	2.84E+05		(R)YSGGNY	(R)Y S|G\G N/Y R D N Y|D\N(-)		95.58	719.2857	1437.567	-0.0024	-1.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
13060	dirMS_041712_NAR_60mM_plus.15100.15100.3	3	8.72	1	1.45E+05		(R)VFDKDG	(R)V F D K D\G N G Y|I/S/A/A E L R(H)		135.57	585.6281	1754.871	-0.001	-0.6	4.56	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
13061	dirMS_041712_NAR_60mM_plus.20525.20686.3	3	8.72	1	4.98E+05		(R)DSIVAEL	(R)D S/I/V/A/E L D/R E M S/R(S)		168.35	507.5883	1520.737	0.013	8.6	4.32	34709.6	4.98	HUMAN	O14579	Coatomer subunit epsilon
13062	dirMS_041712_NAR_60mM_plus.21461.21461.3	3	8.72	0	1.06E+06		(R)LHFFMP	(R)L H F\F\M P G\F/A|P\L T S R(G)		178.98	540.9492	1620.835	-0.0025	-1.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
13063	dirMS_041712_NAR_60mM_plus.9492.9492.2	2	8.72	0	4.97E+05		(K)SYCAEIA	(K)S Y/C A E|I/A/H N/V/S S K(N)	C:Carbamidomethylation	107.47	733.3425	1465.674	0.0037	2.5	6.47	15730.4	11.67	HUMAN	D3YTB1	60S ribosomal protein L32 (Fragment)
13064	dirMS_041712_NAR_20mM_minus.13134.13134.2	2	8.71	0	4.63E+05		(K)TITLEVEI	(K)T I\T\L E|V/E|P/S D T I E N V K(A)		183.05	894.4654	1787.927	-0.0038	-2.1	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
13065	dirMS_041712_NAR_30mM_minus2.16147.16147.2	2	8.71	0	2.52E+04		(R)VFSGLV!	(R)V/F|S G L/V S T G L/K(V)		141.38	554.3215	1107.641	-0.0051	-4.6	8.72	96306.4	6.41	HUMAN	P13639	Elongation factor 2
13066	dirMS_041712_NAR_30mM_minus2.16620.16620.2	2	8.71	0	2.62E+05	M2243m	(K)mSIYQA	(K)m S/I|Y Q/A M W/K(G)	m:Oxidized methionine	144.13	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
13067	dirMS_041712_NAR_30mM_minus2.18229.18229.3	3	8.71	0	3.69E+05		(R)QAQEYE	(R)Q A Q\E\Y E/A/L/L/N I K(V)		154.4	473.9196	1419.748	-0.0036	-2.5	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13068	dirMS_041712_NAR_50mM_minus2.12651.12651.3	3	8.71	1	3.93E+05		(K)NTVELL\	(K)N T|V|E/L/L/V E D K/G N Q V Y R(C)		140.42	626.3309	1876.976	0.0018	1	4.68	258215.9	5.48	HUMAN	E7EN95	Filamin-B
13069	dirMS_041712_NAR_50mM_minus2.16837.16837.3	3	8.71	0	4.60E+05		(K)NILFVITI	(K)N/I/L/F V I/T K P D/V Y K(S)		164.12	517.2991	1549.899	-0.0161	-10.4	8.5	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
13070	dirMS_041712_NAR_50mM_minus2.8452.8452.3	3	8.71	1	2.40E+05		(R)AGTGVD	(R)A G T/G/V/D N V/D/L E A A T R\K(G)		116.53	539.6119	1616.824	-0.0027	-1.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
13071	dirMS_041712_NAR_60mM_minus.11843.11843.3	3	8.71	1	4.61E+05	M230m	(R)mSMKE\	(R)m S M K E V D\E\Q|M/L|N V Q N K(N)	m:Oxidized methionine	125.58	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13072	dirMS_041712_NAR_120mM_plus.9100.9100.3	3	8.71	1	2.52E+05		(R)LRECELS	(R)L R E C E\L/S|P G V N R(D)	C:Carbamidomethylation	100.88	477.2447	1429.722	-0.0021	-1.5	6.14	57188.9	5.97	HUMAN	H7C3A1	Serrate RNA effector molecule homolog (Fragment)
13073	dirMS_041712_NAR_20mM_plus.14828.14828.2	2	8.71	0	1.28E+05		(K)FANPFP/	(K)F A|N|P/F/P A A V R(G)		173.88	545.2958	1089.584	0.0003	0.3	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
13074	dirMS_041712_NAR_30mM_plus2.13450.13450.2	2	8.71	0	1.65E+05		(K)TGCNVL	(K)T G/C|N/V|L/L/I Q K(S)	C:Carbamidomethylation	123.63	573.3212	1145.635	0.0004	0.4	8.41	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
13075	dirMS_041712_NAR_30mM_plus2.20275.20275.2	2	8.71	2	2.51E+04	T159t	(R)YLLSARE	(R)Y L/L S/A R/E R\t G G(-)	t:N-acetylglucosamine (T)	160.07	713.3669	1222.654	203.0727	-4.7	8.75	18176.8	9.92	HUMAN	B0QY93	Beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase (Fragment)

13076	dirMS_041712_NAR_30mM_plus2.22317.22317.3	3	8.71	0	5.24E+05		(R)VGNLGL	(R)V G N L G L A T/S/F/F N E\R(N)		172.8	508.9306	1524.781	-0.0033	-2.1	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
13077	dirMS_041712_NAR_40mM_plus2.11774.11774.2	2	8.71	0	2.67E+05		(R)NLLSVA	(R)N/L|L S/V/A/Y|K(N)		135.22	454.2649	907.525	-0.0022	-2.4	8.59	18789.1	6.77	HUMAN	A2IDB2	14-3-3 protein eta (Fragment)
13078	dirMS_041712_NAR_60mM_plus.10437.10437.3	3	8.71	0	1.69E+06		(K)VFEHDS	(K)V/F/E H D S V/E/L/N C K(M)	C:Carbamidomethylation	111.72	492.8967	1476.679	-0.0032	-2.2	4.65	31975.7	6.55	HUMAN	P10768	S-formylglutathione hydrolase
13079	dirMS_041712_NAR_60mM_plus.19476.19476.3	3	8.71	1	4.46E+04		(R)SLADIAR	(R)S L|A/D/I/A R E/E A S N F R(S)		159.53	526.9346	1578.787	0.0022	1.4	4.68	20458.8	4.99	HUMAN	G3V4X5	Proteasome subunit alpha type-3
13080	dirMS_041712_NAR_30mM_minus2.12824.12824.2	2	8.7	0	4.06E+04		(R)GGEPQC	(R)G G E/P Q/G P/P\F I K(Y)		122.6	563.7964	1126.589	-0.0036	-3.2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
13081	dirMS_041712_NAR_30mM_minus2.13939.13939.2	2	8.7	0	2.70E+05		(R)LDLLEDF	(R)L/D|L|L E D R(S)		129.48	437.2408	873.468	0.0067	7.7	4.03	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
13082	dirMS_041712_NAR_30mM_minus2.15781.15781.2	2	8.7	0	1.24E+05		(K)APGFAQ	(K)A/P|G F/A Q M L/K(E)		139.2	481.7625	962.513	0.0049	5.1	8.8	60047.9	5.54	HUMAN	G5E9B2	Chaperonin containing TCP1, subunit 8 (Theta), isoform CRA_a
13083	dirMS_041712_NAR_30mM_minus2.16763.16763.2	2	8.7	0	3.01E+05	M2243m	(K)mSIYQA	(K)m S\I/Y Q\A M\W|K(G)	m:Oxidized methionine	144.85	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
13084	dirMS_041712_NAR_30mM_minus2.7799.7799.2	2	8.7	0	1.61E+05		(K)IFAQDG	(K)I F|A Q/D G E/G/Q R(I)		96.53	560.7727	1120.538	0	0	4.37	258215.9	5.48	HUMAN	E7EN95	Filamin-B
13085	dirMS_041712_NAR_50mM_minus2.11642.11642.3	3	8.7	1	1.90E+05		(K)IEVEKPF	(K)I E\V E K/P F A I A/K E(-)		134.4	458.5927	1373.767	-0.0039	-2.9	5.01	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
13086	dirMS_041712_NAR_50mM_minus2.12574.12574.3	3	8.7	2	2.89E+05		(K)SDLKAAI	(K)S D L/K A A R S I/P A G A E P E/K(S)		138.9	580.6487	1739.929	0.0029	1.7	5.9	20743.6	7.96	HUMAN	H3BMV3	Hematological and neurological-expressed 1-like protein (Fragment)
13087	dirMS_041712_NAR_50mM_minus2.16928.16928.3	3	8.7	0	4.31E+05		(K)NILFVITI	(K)N I|L/F/V I T K/P D V Y K(S)		164.18	517.2991	1549.899	-0.0161	-10.4	8.5	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
13088	dirMS_041712_NAR_50mM_minus2.8018.8018.3	3	8.7	0	1.06E+05		(K)AEITLVA	(K)A E/I/T/L/V/A T K P E K(L)		113.17	433.9205	1299.752	-0.0049	-3.8	6.18	98761.7	5.56	HUMAN	Q9UBF2	Coatomer subunit gamma-2
13089	dirMS_041712_NAR_50mM_minus2.8912.8912.3	3	8.7	1	1.13E+04		(K)TLQEVTE	(K)T L\Q/E/V/T E M D S V K R(Y)		119.4	512.5962	1535.773	0.0007	0.4	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
13090	dirMS_041712_NAR_60mM_minus.6495.6495.3	3	8.7	1	1.99E+05		(R)AIEAAPC	(R)A I/E/A/A/P Q/E P E Q K R(S)		95.33	489.5907	1466.76	-0.0022	-1.5	4.79	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
13091	dirMS_041712_NAR_120mM_plus.20363.20363.4	4	8.7	2	5.54E+05		(K)LTVEDLE	(K)L T V/E/D/L/E K E R D/F Y F G K(L)		160.7	498.0043	1988.996	-0.001	-0.5	4.51	30169.7	5.02	HUMAN	Q15691	Microtubule-associated protein RP/EB family member 1
13092	dirMS_041712_NAR_20mM_plus.8944.9136.2	2	8.7	0	4.88E+05		(K)VIPELNG	(K)V I|P E L/N/G/K(L)		133.33	435.2573	869.509	-0.0018	-2	5.97	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
13093	dirMS_041712_NAR_30mM_plus2.6191.6219.2	2	8.7	0	9.50E+04		(K)MQAVQ	(K)M/Q|A|V/Q/E A T R(L)		86.72	517.2613	1033.509	0.0058	5.6	5.75	533778	5.74	HUMAN	Q15149	Plectin
13094	dirMS_041712_NAR_40mM_plus2.6354.6389.2	2	8.7	0	4.41E+05		(K)NAGFTP	(K)N A|G|F/T/P Q E/R(Q)		96.23	510.2487	1019.491	-0.0004	-0.4	6	29474.8	6.94	HUMAN	G3V3M6	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
13095	dirMS_041712_NAR_50mM_plus2.12933.12933.3	3	8.7	1	3.18E+05		(R)ELAVQIY	(R)E L A/V/Q/I/Y/E E A R K(F)		135.6	483.5916	1448.774	-0.0141	-9.7	4.79	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
13096	dirMS_041712_NAR_50mM_plus2.5957.5957.3	3	8.7	1	7.67E+04		(K)IQDKEGI	(K)I Q D K E G I|P/P D/Q Q R(L)		95.88	508.5966	1523.781	-0.006	-3.9	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
13097	dirMS_041712_NAR_60mM_plus.16222.16222.3	3	8.7	0	2.86E+05		(R)DVRPYIV	(R)D V R P Y\I|V/G A/V V/R(G)		141.5	448.5963	1343.779	-0.005	-3.8	8.75	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
13098	dirMS_041712_NAR_60mM_plus.7141.7141.2	2	8.7	0	3.11E+05		(K)TIEAEAA	(K)T I/E/A/E A/A H\G T V T R(H)		95.57	678.3494	1355.691	0.0002	0.1	5.37	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
13099	dirMS_041712_NAR_60mM_plus.8150.8150.3	3	8.7	1	4.99E+05		(R)LSQIGVE	(R)L/S Q|I/G V E N\T E E N R R(L)		100.98	548.9468	1644.83	-0.0041	-2.5	4.79	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
13100	dirMS_041712_NAR_120mM_minus.7702.7702.3	3	8.69	1	2.33E+05		(R)EVQQGE	(R)E V/Q/Q/G E E F E R R(I)		96.3	469.5586	1406.666	-0.0046	-3.3	4.49	15567.5	8.13	HUMAN	H0Y4J6	Adenylate kinase isoenzyme 1 (Fragment)
13101	dirMS_041712_NAR_20mM_minus.12316.12316.2	2	8.69	0	1.64E+05		(R)AAVIGPI	(R)A A V|I/G/P D V F A K(L)		171.57	544.3103	1087.615	-0.0013	-1.2	5.88	266161	5.68	HUMAN	E9PPU0	Epiplakin
13102	dirMS_041712_NAR_30mM_minus2.12355.12355.2	2	8.69	0	3.54E+05		(K)DISLSDY	(K)D I|S/L/S D/Y K(G)		120.72	470.7357	940.462	0.0019	2	4.21	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
13103	dirMS_041712_NAR_30mM_minus2.16220.16311.2	2	8.69	0	1.52E+05		(R)SLVSGLI	(R)S/L|V|S/G/L I R(L)		142.02	422.7649	844.525	-0.0026	-3	9.47	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
13104	dirMS_041712_NAR_50mM_minus2.16334.16334.3	3	8.69	0	1.52E+04	M1206m	(K)GCDDGF	(K)G C/D/D G F I A L/L/P m K P R(R)	C:Carbamidomethylation m:Oxid	160.9	569.2841	1689.845	15.9926	-1.3	5.96	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
13105	dirMS_041712_NAR_50mM_minus2.18783.18783.3	3	8.69	0	2.24E+05		(K)GAEILEV	(K)G A|E/I/L E V L H/S L/P A V R(Q)		183.15	535.3101	1603.917	-0.0009	-0.5	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
13106	dirMS_041712_NAR_50mM_minus2.5278.5278.3	3	8.69	0	8.24E+05		(K)TATPQQ	(K)T/A|T/P Q Q A Q E V H E K(L)		88.02	489.5768	1466.723	-0.0075	-5.1	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
13107	dirMS_041712_NAR_120mM_plus.14902.14902.2	2	8.69	1	7.19E+05		(R)KFLDGIY	(R)K|F/L/D/G I Y V|S\E K(G)		131.43	649.8522	1298.699	-0.002	-1.5	6.07	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
13108	dirMS_041712_NAR_20mM_plus.12117.12117.2	2	8.69	0	3.94E+04	M234m	(K)mVVESA	(K)m V|V/E S/A Y E V I/K(L)	m:Oxidized methionine	156.78	642.3228	1267.66	15.9781	-13.1	4.53	36923.1	5.71	HUMAN	P07195	L-lactate dehydrogenase B chain
13109	dirMS_041712_NAR_20mM_plus.12854.12854.2	2	8.69	0	5.96E+04		(R)LLAEPVF	(R)L L|A E\P V/P G I K(A)		161.4	518.823	1036.64	-0.0014	-1.3	6	12039.9	9.34	HUMAN	F8VSD4	Ubiquitin-conjugating enzyme E2 N
13110	dirMS_041712_NAR_20mM_plus.18448.18448.3	3	8.69	0	2.24E+05		(R)LSVEEA	(R)L S V E\E A V A A\G\V V/G/G E I Q E K(L)		198.52	629.0001	1884.991	-0.0056	-2.9	4.09	266161	5.68	HUMAN	E9PPU0	Epiplakin
13111	dirMS_041712_NAR_20mM_plus.8271.8271.2	2	8.69	0	5.19E+04		(R)AVVIVDI	(R)A V|V/I V/D/D/R(G)		127.05	443.7527	886.499	-0.0011	-1.3	4.21	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
13112	dirMS_041712_NAR_30mM_plus2.10912.10912.2	2	8.69	0	4.80E+05		(K)LTAQFV	(K)L/T|A/Q F V A R(N)		110.72	453.2619	905.52	-0.0038	-4.2	9.75	88941.6	5.15	HUMAN	Q15459	Splicing factor 3A subunit 1
13113	dirMS_041712_NAR_30mM_plus2.18995.18995.2	2	8.69	0	3.39E+05		(R)LTAEDLF	(R)L/T/A/E D/L F/E A R(I)		153.2	582.796	1164.59	-0.0048	-4.1	4.14	533778	5.74	HUMAN	Q15149	Plectin
13114	dirMS_041712_NAR_30mM_plus2.19934.19934.3	3	8.69	0	2.45E+05		(R)IIPGFMC	(R)I I/P G F M C Q/G G D/F T/R(H)	C:Carbamidomethylation	157.77	533.5865	1598.745	-0.0004	-0.3	5.84	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
13115	dirMS_041712_NAR_40mM_plus2.16240.16240.3	3	8.69	0	5.88E+05		(R)FGVPVI	(R)F G\V/P V/I A D/G G I/Q N V G H I A K(A)		162.43	631.3436	1892.039	-0.0226	-12	6.74	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
13116	dirMS_041712_NAR_50mM_plus2.6869.6869.3	3	8.69	1	8.09E+05		(K)IVADKD	(K)I V|A D K D/Y S V/T A N S K(I)		101.35	504.2628	1510.775	-0.0009	-0.6	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
13117	dirMS_041712_NAR_50mM_plus2.8541.8541.3	3	8.69	0	3.95E+03		(K)IAVAHN	(K)I A/V A H/N/G E L V N/A A R(L)		111.67	478.9337	1434.781	0.0054	3.7	6.75	21375	6.37	HUMAN	D6RCC8	Amidophosphoribosyltransferase
13118	dirMS_041712_NAR_60mM_plus.12183.12183.3	3	8.69	1	1.01E+06	M232m	(R)MSmKE	(R)M S m K E V D E Q|M/L/N V Q N K(N)	m:Oxidized methionine	120.57	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13119	dirMS_041712_NAR_60mM_plus.5221.5221.3	3	8.69	0	2.64E+04		(R)TATEKP	(R)T A/T/E/K/P/G/P A E A A R(Q)		84.77	433.5671	1298.67	0.0168	13	5.81	49823.3	9.39	HUMAN	B4DQQ4	NADPH:adrenodoxin oxidoreductase, mitochondrial
13120	dirMS_041712_NAR_60mM_plus.9065.9065.3	3	8.69	1	6.48E+05	M118m	(K)LVDPERI	(K)L/V/D/P E R D m S L R(L)	m:Oxidized methionine	105.38	449.5594	1330.678	15.9853	-7.1	4.56	70523.3	4.94	HUMAN	G3V153	Caprin-1
13121	dirMS_041712_NAR_120mM_minus.11188.11188.3	3	8.68	1	2.09E+04		(K)KYEFGES	(K)K Y\E\F\G\E/S\D/L/R(S)		116.38	415.2091	1243.595	0.0174	14	4.68	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
13122	dirMS_041712_NAR_120mM_minus.13199.13199.4	4	8.68	0	2.35E+05		(R)VLSAPPH	(R)V L S A/P/P H F H/F/G Q T N R(T)		126.22	427.7219	1707.871	-0.0056	-3.3	9.74	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
13123	dirMS_041712_NAR_120mM_minus.14556.14556.3	3	8.68	1	1.51E+05		(R)KFNALF	(R)K\F N A L F\A/Q/G N Y S E A A/K(V)		133.17	586.9656	1758.881	0.0013	0.7	8.5	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
13124	dirMS_041712_NAR_120mM_minus.8581.8581.3	3	8.68	1	5.01E+04		(R)LKVTEG	(R)L K V T E G G E/P/Y/R(L)		101.15	416.885	1248.658	-0.0178	-14.3	6.14	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
13125	dirMS_041712_NAR_40mM_minus2.8248.8248.3	3	8.68	1	3.04E+05	M119m	(R)SNTPILV	(R)S N/T/P I/L/V/D/G K D V m P E V N K(V)	m:Oxidized methionine	128.4	658.0032	1956.011	15.9844	-5.3	4.56	18405.7	9.81	HUMAN	K7EP41	Glucose-6-phosphate isomerase (Fragment)
13126	dirMS_041712_NAR_50mM_minus2.13086.13086.3	3	8.68	0	3.53E+05		(R)ETNLDSI	(R)E T\N L/D/S L/P L/V D T/H S K(R)		142.43	556.9529	1668.844	0.0002	0.1	4.53	53707.8	5.06	HUMAN	P08670	Vimentin
13127	dirMS_041712_NAR_50mM_minus2.15766.15766.3	3	8.68	0	9.31E+04		(K)SLLSSAS	(K)S L/L/S/S A/S A T V/G H/G L T A V K(E)		158.05	566.9809	1698.939	-0.0103	-6.1	8.49	61083	4.61	HUMAN	Q8IWE2	Protein NOXP20
13128	dirMS_041712_NAR_50mM_minus2.17745.17745.3	3	8.68	1	2.31E+05		(K)LALFQAI	(K)L|A/L/F/Q A I G K E\V V D R(A)		170.53	520.3043	1558.895	0.0032	2	6.07	266161	5.68	HUMAN	E9PPU0	Epiplakin
13129	dirMS_041712_NAR_60mM_minus.10369.10369.3	3	8.68	1	6.05E+05	M88m	(K)DVDEAY	(K)D V/D\E A/Y m N K V E/L E/S R(L)	m:Oxidized methionine	118.37	605.2791	1797.832	15.9904	-2.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
13130	dirMS_041712_NAR_60mM_minus.10851.10851.3	3	8.68	1	5.44E+05	M239m	(R)MSMKE	(R)M S M K E V/D E\Q\m|L|N V Q N K(N)	m:Oxidized methionine	119.9	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13131	dirMS_041712_NAR_60mM_minus.11910.11910.3	3	8.68	1	4.95E+04		(R)RALEAE	(R)R A L E A\E Q|V/E I/T V/G R(F)		126.3	524.2879	1570.855	-0.0056	-3.6	4.79	266161	5.68	HUMAN	E9PPU0	Epiplakin
13132	dirMS_041712_NAR_60mM_minus.6874.6874.3	3	8.68	1	1.09E+05	M281m	(R)SRAEAES	(R)S R\A E\A E/S m/Y/Q/I K(Y)	m:Oxidized methionine	96.73	476.895	1412.684	15.9866	-5.8	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
13133	dirMS_041712_NAR_60mM_minus.7341.7462.3	3	8.68	1	6.21E+05	M136m M	(K)VKEGmN	(K)V K E G m\N\I|V|E A/m E R(F)	m:Oxidized methionine	100.3	513.25	1505.745	31.9904	0.4	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
13134	dirMS_041712_NAR_120mM_plus.12207.12207.3	3	8.68	0	6.37E+05		(R)SSHYDEI	(R)S S\H Y D E\L\L/A/A/E/A R(A)		117.62	487.9048	1461.697	0.003	2.1	4.65	26398.4	5.21	HUMAN	H7C597	Staphylococcal nuclease domain-containing protein 1 (Fragment)
13135	dirMS_041712_NAR_120mM_plus.12855.12855.3	3	8.68	1	1.80E+06		(R)GYVKEQ	(R)G Y|V/K/E/Q F A W R(H)		121.68	428.5561	1283.653	0.0006	0.5	8.59	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
13136	dirMS_041712_NAR_120mM_plus.16355.16451.4	4	8.68	1	6.42E+05		(K)LITKPSE	(K)L/I T K/P S E G T T L R V\E\D L/V/K(Q)		138.93	500.5387	1999.143	-0.0104	-5.2	6.18	81410.7	5.8	HUMAN	B3KTC7	Double-strand break repair protein MRE11A
13137	dirMS_041712_NAR_20mM_plus.11259.11259.2	2	8.68	0	1.33E+05		(R)YALYDA	(R)Y A|L/Y/D/A T Y E T K(E)		150.25	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
13138	dirMS_041712_NAR_20mM_plus.12875.12875.2	2	8.68	0	1.21E+05		(K)IDIIPNP	(K)I D|I|I|P N/P Q E R(T)		160.65	597.8227	1194.648	-0.0096	-8	4.37	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
13139	dirMS_041712_NAR_30mM_plus2.17083.17083.2	2	8.68	0	2.83E+05		(R)ISWYLR(	(R)I/S|W Y/L R(D)		142.57	419.2286	837.462	-0.0118	-14.1	8.75	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
13140	dirMS_041712_NAR_30mM_plus2.18366.18366.2	2	8.68	0	2.39E+05		(K)TTFEDLI	(K)T T|F/E/D L I Q/R(C)		149.22	561.7934	1122.579	0.0006	0.5	4.37	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
13141	dirMS_041712_NAR_30mM_plus2.19555.19555.2	2	8.68	0	2.26E+05		(K)TVDNFV	(K)T V/D N F/V/A/L/A T G E K(G)		155.53	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
13142	dirMS_041712_NAR_30mM_plus2.9574.9574.2	2	8.68	0	7.52E+05		(R)MGYMD	(R)M/G\Y/M D|P/R(E)		103.33	435.186	869.364	0.0003	0.3	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
13143	dirMS_041712_NAR_50mM_plus2.12139.12281.3	3	8.68	1	1.20E+06		(K)ASLENSL	(K)A/S/L/E/N S L R E V E/A R(Y)		132.27	491.9313	1473.766	0.0138	9.3	4.79	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13144	dirMS_041712_NAR_50mM_plus2.12594.12594.3	3	8.68	1	5.35E+05		(K)FSIEDLK	(K)F/S/I/E D/L K/A Q/P K(Q)		134.4	425.8966	1275.694	-0.0191	-15	6.07	13579.2	9.99	HUMAN	E9PPQ6	Thymocyte nuclear protein 1 (Fragment)
13145	dirMS_041712_NAR_50mM_plus2.15065.15065.3	3	8.68	1	3.19E+04		(R)GSVLEPE	(R)G S V/L/E/P E/G T V E I K F R(R)		147.18	554.3005	1660.891	-0.0035	-2.1	4.79	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
13146	dirMS_041712_NAR_50mM_plus2.20794.20794.3	3	8.68	1	7.61E+04		(K)TSAQVV	(K)T S/A Q|V V L/D G L V\D K/I G D V/K(C)		178.37	619.6814	1857.033	-0.0031	-1.7	4.43	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
13147	dirMS_041712_NAR_60mM_plus.12790.12790.3	3	8.68	0	3.02E+05		(R)ILHLLGC	(R)I/L H\L\L G/Q/E/G/P K(T)		123.6	402.2397	1204.705	-0.0003	-0.2	6.75	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
13148	dirMS_041712_NAR_60mM_plus.15956.15956.3	3	8.68	1	2.52E+05		(R)TSFLDD	(R)T S|F/L/D/D/A F R K(N)		139.92	400.5399	1199.605	-0.0004	-0.3	5.62	21195.7	6.97	HUMAN	H0YJ21	Cytoplasmic dynein 1 heavy chain 1 (Fragment)
13149	dirMS_041712_NAR_60mM_plus.5987.5987.3	3	8.68	1	1.32E+05		(K)AQQELE	(K)A Q/Q E/L E E/Q T R/R(A)		89.23	463.233	1387.692	-0.008	-5.8	4.79	67933	6.08	HUMAN	P26038	Moesin
13150	dirMS_041712_NAR_120mM_minus.10469.10469.3	3	8.67	1	4.00E+04	M86m	(K)mKEIAE	(K)m K E I A|E/A/Y/L/G/K(T)	m:Oxidized methionine	109.95	423.557	1252.661	15.9959	0.7	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
13151	dirMS_041712_NAR_20mM_minus.12177.12177.2	2	8.67	0	5.16E+05	M185m	(K)LAVNm\	(K)L A V/N\m V/P/F/P R(L)	m:Oxidized methionine	171.07	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
13152	dirMS_041712_NAR_30mM_minus2.15560.15560.2	2	8.67	0	3.35E+04	M1342m	(R)ASLSLW	(R)A S L/S|L|W Q|A m E K(G)	m:Oxidized methionine	138.07	640.3185	1263.64	15.9895	-4.2	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
13153	dirMS_041712_NAR_30mM_minus2.17695.17695.2	2	8.67	0	1.24E+05		(K)TTFEDLI	(K)T T/F/E/D L/I Q/R(C)		150.5	561.7944	1122.579	0.0026	2.3	4.37	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
13154	dirMS_041712_NAR_40mM_minus2.9193.9193.3	3	8.67	0	1.57E+05	M26m	(R)LSAmLV	(R)L S/A m L V\P\V/T/P E V K P K(R)	m:Oxidized methionine	136.37	542.315	1608.939	15.9911	-2.3	8.59	31524.1	4.5	HUMAN	P82970	High mobility group nucleosome-binding domain-containing protein 5
13155	dirMS_041712_NAR_50mM_minus2.12035.12035.3	3	8.67	1	2.49E+04		(R)ELISNSSI	(R)E L/I/S/N/S/S D A\L D K I R(Y)		137.62	520.9445	1560.823	-0.0038	-2.5	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
13156	dirMS_041712_NAR_50mM_minus2.14353.14353.3	3	8.67	1	1.08E+06		(K)EAFSLFD	(K)E A\F/S L/F D K/D G D G T I T/T K(E)		149.88	615.6336	1844.891	-0.005	-2.7	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
13157	dirMS_041712_NAR_50mM_minus2.15155.15155.3	3	8.67	0	3.46E+05		(R)DGLAFN	(R)D G L/A/F/N/A L/I H/R(H)		155.13	409.5594	1226.664	-0.0004	-0.3	6.74	146974	5.55	HUMAN	C9JRP8	Spectrin beta chain, non-erythrocytic 4
13158	dirMS_041712_NAR_50mM_minus2.8632.8676.3	3	8.67	1	2.14E+05		(R)VAIEPG	(R)V/A|I|E|P G A P R E N D E F C K(M)	C:Carbamidomethylation	117.37	611.2923	1831.864	-0.002	-1.1	4.41	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
13159	dirMS_041712_NAR_60mM_minus.16956.16956.3	3	8.67	1	2.92E+05		(R)LKLPAV	(R)L K L P A V/V/T/A/D/L R(L)		154.1	432.6056	1295.805	-0.0023	-1.8	8.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
13160	dirMS_041712_NAR_120mM_plus.16346.16346.4	4	8.67	1	1.30E+06		(R)YAEIVHL	(R)Y A/E I V/H L T/L/P\D/G T K/R(S)		138.97	428.9885	1712.933	-0.0008	-0.5	6.75	21230	6.36	HUMAN	H0YC04	V-type proton ATPase subunit B, brain isoform (Fragment)
13161	dirMS_041712_NAR_30mM_plus2.21852.21852.2	2	8.67	0	1.55E+05		(K)ANFLQN	(K)A N\F|L|Q/N M|I/E D R(T)		170.25	675.8282	1350.647	0.0021	1.5	4.37	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
13162	dirMS_041712_NAR_30mM_plus2.6250.6250.2	2	8.67	0	6.85E+04		(R)ETPENL	(R)E T/P E N L/A K(L)		87.08	451.239	901.462	0.0082	9.1	4.53	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
13163	dirMS_041712_NAR_30mM_plus2.6721.6722.2	2	8.67	0	2.64E+05		(R)FQTMEE	(R)F Q|T|M/E|E K(K)		89.95	456.7106	912.413	0.0008	0.9	4.53	40551.6	10.15	HUMAN	G5E9G0	60S ribosomal protein L3
13164	dirMS_041712_NAR_40mM_plus2.11277.11277.3	3	8.67	0	1.21E+05		(K)EAGELKI	(K)E/A G E/L K P E E E|I T/V/G/P V Q K(L)		132.8	651.6782	1953.017	0.0025	1.3	4.32	108281.4	5.72	HUMAN	P53618	Coatomer subunit beta
13165	dirMS_041712_NAR_50mM_plus2.12721.12721.3	3	8.67	1	5.93E+05		(K)AVLFCLS	(K)A/V/L F C L S E D/K K(N)	C:Carbamidomethylation	134.23	437.2325	1309.682	0.0009	0.7	6.11	22956	8.8	HUMAN	E9PK25	Cofilin-1
13166	dirMS_041712_NAR_50mM_plus2.15046.15046.3	3	8.67	1	3.37E+05		(R)LSQELEY	(R)L/S/Q E L E Y/L/T E D V K\R(L)		147.32	574.9669	1722.891	-0.0047	-2.7	4.41	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
13167	dirMS_041712_NAR_60mM_plus.17731.17731.3	3	8.67	1	9.22E+04		(R)SKGIYQS	(R)S K G I Y Q S L E/G/A V/Q/A|G Q L K(V)		149.95	626.3401	1877.013	-0.007	-3.7	8.22	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
13168	dirMS_041712_NAR_120mM_minus.16478.16686.3	3	8.66	1	6.08E+05		(R)ISEQFTA	(R)I/S/E/Q F T A M F R/R(K)		145.08	462.5714	1385.699	0.0002	0.2	9.6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
13169	dirMS_041712_NAR_20mM_minus.11148.11148.2	2	8.66	0	6.82E+04		(R)DFTPVC	(R)D F|T/P/V/C T T E L G R(A)	C:Carbamidomethylation	159.28	698.3303	1395.657	-0.004	-2.8	4.37	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
13170	dirMS_041712_NAR_30mM_minus2.16306.16306.2	2	8.66	0	1.09E+05		(K)FGVIFAC	(K)F G/V|I|F A G A Q K(N)		141.95	519.2901	1037.578	-0.0049	-4.7	8.75	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
13171	dirMS_041712_NAR_30mM_minus2.19482.19482.2	2	8.66	0	3.18E+05		(R)ASLSLW	(R)A S|L S L/W/Q A M E K(G)		162.37	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
13172	dirMS_041712_NAR_30mM_minus2.6213.6213.2	2	8.66	0	1.72E+05		(R)AQAEQ	(R)A Q|A/E/Q/A A L/R(Q)		88.18	479.2592	957.511	-0.0001	-0.1	6.05	533778	5.74	HUMAN	Q15149	Plectin
13173	dirMS_041712_NAR_40mM_minus2.14568.14568.3	3	8.66	0	2.20E+04		(K)SLCIPFKI	(K)S L/C\I/P F K P L C/E L Q P G A K(C)	C:Carbamidomethylation	169.72	653.3446	1958.024	-0.0046	-2.3	8.31	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
13174	dirMS_041712_NAR_50mM_minus2.13048.13048.3	3	8.66	1	1.05E+06	M320m	(K)YmACCL	(K)Y/m/A/C C L L Y R G D V V/P K(E)	C:Carbamidomethylation m:Oxid	141.47	620.9644	1844.886	15.9931	-1	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
13175	dirMS_041712_NAR_50mM_minus2.13217.13217.3	3	8.66	0	2.72E+04		(R)IYDAQN	(R)I/Y/D A Q N E/L S A A T H L T S K(L)		141.85	621.3116	1861.929	-0.0088	-4.7	5.32	15355.1	5.12	HUMAN	C9JAB0	DCC-interacting protein 13-alpha (Fragment)
13176	dirMS_041712_NAR_50mM_minus2.15452.15452.3	3	8.66	1	1.32E+05		(R)EIISFGSC	(R)E I/I/S/F/G S G Y G G N/S L L G/K K(C)		155.88	609.6545	1826.965	-0.0157	-8.6	8.59	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
13177	dirMS_041712_NAR_50mM_minus2.17930.18000.3	3	8.66	1	9.88E+04		(K)ILDVASL	(K)I/L|D|V/A/S L E V L N E V N R R(S)		171.25	614.0139	1840.029	-0.0015	-0.8	4.68	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
13178	dirMS_041712_NAR_60mM_minus.12115.12115.3	3	8.66	0	1.57E+05		(R)QQLQQ	(R)Q Q L Q Q\V|P/G L L H R(M)		127.5	472.941	1416.807	0.0014	1	9.75	74230.8	5.34	HUMAN	B1AH89	Tubulin tyrosine ligase-like family, member 12
13179	dirMS_041712_NAR_60mM_minus.7641.7641.3	3	8.66	1	5.65E+05		(R)YLAEVA	(R)Y/L|A E/V/A/A G D D K K(G)		102.07	427.222	1279.653	-0.0014	-1.1	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
13180	dirMS_041712_NAR_120mM_plus.16690.16729.4	4	8.66	2	3.52E+05		(R)VITEEEK	(R)V I|T E|E E K N F K/A/F A S L R(M)		140.75	471.2558	1882.007	-0.0055	-2.9	6.2	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
13181	dirMS_041712_NAR_120mM_plus.8137.8137.3	3	8.66	1	4.76E+05		(R)SSDVSW	(R)S/S/D/V/S W S D/T R\R(T)		95.73	432.5393	1295.598	0.0059	4.5	5.68	116336.3	8.59	HUMAN	G3V220	Transcription elongation regulator 1
13182	dirMS_041712_NAR_20mM_plus.15696.15696.2	2	8.66	0	2.37E+05		(K)TITLEVEI	(K)T I T L E/V/E|P S D T I/E N V K(A)		179.03	894.4658	1787.927	-0.003	-1.7	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
13183	dirMS_041712_NAR_20mM_plus.7815.7815.3	3	8.66	0	1.06E+05		(K)AQAAAF	(K)A Q A A A P A S\V/P A Q/A P K(R)		123.6	459.9204	1377.748	-0.0018	-1.3	8.8	17808.8	11.77	HUMAN	P47914	60S ribosomal protein L29
13184	dirMS_041712_NAR_20mM_plus.8063.8063.2	2	8.66	0	4.38E+03		(R)GLANPE	(R)G L A N|P E/P/A/P E P K(V)		124.33	610.3183	1219.632	-0.0024	-2	4.53	54333.1	6.51	HUMAN	H0Y5S1	Protein transport protein Sec16A (Fragment)

13185	dirMS_041712_NAR_30mM_plus2.10829.10848.2	2	8.66	0	5.84E+05		(-)MIEVVCN	(-)M/I|E|V/V C/N D R(L)	C:Carbamidomethylation	109.77	568.2669	1135.523	0.0031	2.7	4.37	4334.2	11.58	HUMAN	K7EQ43	Ubiquitin-like protein 5
13186	dirMS_041712_NAR_30mM_plus2.10933.10933.2	2	8.66	0	1.36E+05		(K)FMGTEL	(K)F/M|G/T E L/N G K(T)		111.22	498.7455	996.482	0.0018	1.8	6	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
13187	dirMS_041712_NAR_30mM_plus2.17537.17537.2	2	8.66	0	6.53E+05		(R)MNVLAD	(R)M/N|V|L/A D A L K(S)		144.57	487.7743	974.534	0.0074	7.6	5.59	27396	9.9	HUMAN	H3BN98	Uncharacterized protein (Fragment)
13188	dirMS_041712_NAR_30mM_plus2.17591.17831.3	3	8.66	0	6.77E+05		(R)SIQEELQ	(R)S I\Q/E\E\L/Q Q/L R(Q)		146.32	415.225	1243.664	-0.0036	-2.9	4.53	533778	5.74	HUMAN	Q15149	Plectin
13189	dirMS_041712_NAR_30mM_plus2.22298.22298.3	3	8.66	0	2.88E+05		(K)NSSYFVE	(K)N S S Y F V E/W/I/P N N V K(V)		172	566.2872	1696.833	0.0141	8.3	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
13190	dirMS_041712_NAR_30mM_plus2.8602.8602.2	2	8.66	0	2.70E+05		(K)IANPVEG	(K)I/A/N/P V E/G S/T D R(Q)		98.27	579.7908	1158.575	-0.0006	-0.5	4.37	34267.8	9.05	HUMAN	B4DXP5	Poly(rC)-binding protein 2
13191	dirMS_041712_NAR_40mM_plus2.17734.17734.3	3	8.66	0	2.53E+05		(R)DIKPQN	(R)D I\K\P Q N L\L|L/D/P D T A V L K(L)		170.78	631.6874	1893.069	-0.0215	-11.4	4.43	47257	9.38	HUMAN	P49841	Glycogen synthase kinase-3 beta
13192	dirMS_041712_NAR_50mM_plus2.10375.10375.3	3	8.66	0	1.38E+05	M277m	(R)GLGHQV	(R)G L\G H Q\V A T D A L|V/A/m E K(A)	m:Oxidized methionine	120.62	552.6181	1639.847	15.9925	-1.4	5.32	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
13193	dirMS_041712_NAR_50mM_plus2.10811.10811.3	3	8.66	1	2.12E+05		(K)AQALRD	(K)A Q/A|L R D N S T/M/G Y M M A K(K)		123.72	596.6125	1787.824	-0.0008	-0.4	8.63	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
13194	dirMS_041712_NAR_50mM_plus2.13318.13318.3	3	8.66	0	2.15E+05		(K)KPMSLA	(K)K P M S L A S G\L|V|P A A P P K(R)		138.13	521.9673	1563.893	-0.0054	-3.4	10	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
13195	dirMS_041712_NAR_50mM_plus2.16354.16354.3	3	8.66	0	2.89E+05		(K)ACQSIYP	(K)A C|Q/S I/Y/P/L H D V F V R(K)	C:Carbamidomethylation	154.4	568.9562	1704.853	0.0014	0.8	6.79	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
13196	dirMS_041712_NAR_60mM_plus.20407.20407.3	3	8.66	1	3.02E+05		(R)AQFEGIV	(R)A Q|F/E/G I V T D\L I R R(T)		167.4	506.6178	1517.843	-0.0046	-3	6.12	18505.2	10.14	HUMAN	H0YBG6	Stress-70 protein, mitochondrial (Fragment)
13197	dirMS_041712_NAR_60mM_plus.9467.9467.2	2	8.66	0	1.27E+06		(K)STAGDT	(K)S/T/A G D/T H L|G G E D|F D|N R(M)		107.4	846.3654	1691.726	-0.0021	-1.2	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
13198	dirMS_041712_NAR_120mM_minus.13660.13660.2	2	8.65	1	2.18E+05	N245n	(K)HLRIHnG	(K)H/L|R I H n G E K(R)	n:N-acetylglucosamine (N)	129.08	653.8514	1103.607	203.0887	7.1	8.76	65447.9	9.43	HUMAN	B4DRP8	Zinc finger protein 461
13199	dirMS_041712_NAR_120mM_minus.15410.15410.3	3	8.65	2	9.57E+05		(R)ALKDEEK	(R)A/L/K|D E E K M E\L/Q E/I Q L K(E)		137.72	649.0139	1945.031	-0.0039	-2	4.58	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
13200	dirMS_041712_NAR_20mM_minus.11597.11597.2	2	8.65	0	3.28E+05		(R)GALQNI	(R)G A/L|Q N/I|I\P A S T G A A K(A)		164.48	706.3976	1411.79	-0.0024	-1.7	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
13201	dirMS_041712_NAR_30mM_minus2.9860.9901.2	2	8.65	0	4.95E+05		(K)SIEVIEN	(K)S I|E|V/I E/N/R(M)		108.45	480.2603	959.516	-0.0023	-2.4	4.53	30121.3	4.2	HUMAN	E9PRH9	Nuclear autoantigenic sperm protein (Fragment)
13202	dirMS_041712_NAR_40mM_minus2.14624.14624.3	3	8.65	1	1.07E+06		(K)TFVNITP	(K)T F|V/N|I/T/P A E V/G V L V G K D R(S)		171.58	639.0252	1915.065	-0.0037	-1.9	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
13203	dirMS_041712_NAR_50mM_minus2.15455.15455.3	3	8.65	0	1.49E+05		(K)ICDQWD	(K)I/C/D Q W/D A/L/G/S L/T H S R(R)	C:Carbamidomethylation	156.35	586.9489	1758.823	0.0094	5.3	5.21	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
13204	dirMS_041712_NAR_50mM_minus2.7803.7803.3	3	8.65	0	2.44E+05		(R)LESGMQ	(R)L/E|S G M Q N\M S I/H T K(T)		111.27	492.5712	1475.698	0.0009	0.6	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
13205	dirMS_041712_NAR_60mM_minus.14179.14179.3	3	8.65	0	4.39E+05	M84m	(K)YPIEHGI	(K)Y/P/I E H G I I/T|N|W/D D m E K(I)	m:Oxidized methionine	139.23	659.6373	1960.911	15.9864	-4.3	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
13206	dirMS_041712_NAR_60mM_minus.14203.14203.3	3	8.65	0	4.39E+05	M84m	(K)YPIEHGI	(K)Y P/I E H G I I/T\N/W/D D m E/K(I)	m:Oxidized methionine	139.23	659.6373	1960.911	15.9864	-4.3	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
13207	dirMS_041712_NAR_60mM_minus.4706.4706.3	3	8.65	0	6.11E+05	M46m M49	(R)HQGVm	(R)H Q G V\m|V/G\m G Q/K(D)	m:Oxidized methionine	77.87	401.8579	1171.571	31.9881	-1.4	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
13208	dirMS_041712_NAR_60mM_minus.8250.8250.3	3	8.65	1	3.21E+05		(K)TVDDVIK	(K)T/V/D/D V I/K/E Q N/R(E)		105.72	439.5636	1316.68	-0.0042	-3.2	4.55	20828.6	6.05	HUMAN	C9J0A7	Charged multivesicular body protein 2b
13209	dirMS_041712_NAR_60mM_minus.8720.8720.3	3	8.65	1	1.12E+05		(K)SAVGFD	(K)S A/V/G F D/Y Q G K T E K(H)		108.63	477.2381	1429.696	0.004	2.8	5.79	25153.2	6.6	HUMAN	H7C314	Src substrate cortactin (Fragment)
13210	dirMS_041712_NAR_120mM_plus.10736.10736.4	4	8.65	2	5.03E+05		(K)SKGCGV	(K)S K G C G V\V K F E S\P E|V/A\E R(A)	C:Carbamidomethylation	109.53	470.4895	1878.938	-0.0017	-0.9	5.95	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
13211	dirMS_041712_NAR_120mM_plus.6116.6116.3	3	8.65	0	6.89E+05		(K)QRPQAT	(K)Q R\P Q\A|T/A/E Q/I/R(L)		85.9	433.2367	1297.697	-0.0016	-1.2	9.6	113668.7	6.2	HUMAN	F8W726	Ubiquitin-associated protein 2-like
13212	dirMS_041712_NAR_120mM_plus.8514.8514.2	2	8.65	1	1.39E+05		(K)SGKYVLG	(K)S G/K/Y/V L/G/Y K(Q)		97.87	507.7834	1014.562	-0.0023	-2.3	9.52	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
13213	dirMS_041712_NAR_20mM_plus.10868.10868.2	2	8.65	0	2.06E+04		(K)DVNAAI	(K)D V/N|A A/I A T I K(T)		147.28	508.292	1015.578	-0.0015	-1.5	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
13214	dirMS_041712_NAR_20mM_plus.13508.13508.2	2	8.65	0	1.03E+05		(K)IFVGGLS	(K)I F|V/G G L S|P D T/P E E K(I)		165.22	744.8731	1488.758	-0.0191	-12.8	4.14	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
13215	dirMS_041712_NAR_30mM_plus2.16559.16559.3	3	8.65	0	4.10E+05		(K)LLDLVQQ	(K)L\L D\L\V/Q/Q/S C N/Y K(Q)	C:Carbamidomethylation	139.15	494.2566	1480.746	0.0088	5.9	5.83	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
13216	dirMS_041712_NAR_40mM_plus2.12253.12269.2	2	8.65	0	8.58E+04		(K)NIIVGFA	(K)N I|I|V/G F/A R(M)		138.62	445.2651	889.525	-0.0025	-2.8	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
13217	dirMS_041712_NAR_40mM_plus2.16116.16116.3	3	8.65	0	2.04E+04		(R)ALSTPYI	(R)A L|S T/P Y I H/S L A P I V V E K(L)		161.45	613.3524	1838.042	0.0004	0.2	6.79	12597.4	8.27	HUMAN	H7C2X3	HEAT repeat-containing protein 5B (Fragment)
13218	dirMS_041712_NAR_50mM_plus2.11595.11595.3	3	8.65	1	8.59E+04		(R)SEADSD	(R)S E/A D S D K N\A\T|I L E L/R(S)		129.12	554.6155	1661.834	-0.0021	-1.3	4.32	334221.3	6.44	HUMAN	P15924	Desmoplakin
13219	dirMS_041712_NAR_60mM_plus.11290.11290.2	2	8.65	0	6.36E+05		(K)NFYVEH	(K)N F/Y|V/E/H|P E V A R(L)		116.55	680.8363	1360.664	0.0009	0.7	5.4	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
13220	dirMS_041712_NAR_60mM_plus.21109.21109.3	3	8.65	1	1.84E+04		(K)LKEAELL	(K)L K E A E L\L\E/P L/M/P A I/R(A)		173.6	574.9975	1722.982	-0.0043	-2.5	4.79	56164.6	6.01	HUMAN	E9PP73	Coatomer subunit beta (Fragment)
13221	dirMS_041712_NAR_60mM_plus.21442.21442.3	3	8.65	1	3.68E+05		(R)ARDDLIT	(R)A R D D\L\I|T/D|L L/N E/A K(Q)		177.42	529.6165	1586.838	-0.0035	-2.2	4.23	23653.1	9.28	HUMAN	C9J8H1	V-type proton ATPase subunit E 1 (Fragment)
13222	dirMS_041712_NAR_60mM_plus.6891.7505.3	3	8.65	1	1.65E+06		(R)VVSSIEQ	(R)V/V|S/S I E Q K T E G A E/K(K)		95.08	502.2639	1504.785	-0.0082	-5.4	4.79	8491.4	6.28	HUMAN	E5RIR4	14-3-3 protein zeta/delta (Fragment)
13223	dirMS_041712_NAR_60mM_plus.7850.7850.3	3	8.65	1	2.85E+06		(R)LKSTCIYG	(R)L K S\T C\I/Y G G A/P K(G)	C:Carbamidomethylation	98.97	432.2316	1294.682	-0.0021	-1.7	9.7	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
13224	dirMS_041712_NAR_120mM_minus.14672.14689.2	2	8.64	0	6.49E+05		(R)HSLVSFV	(R)H/S|L|V/S F/V V/R(I)		134.32	522.3023	1043.6	-0.0023	-2.2	9.75	36359.2	5.35	HUMAN	Q9BUD6	Spondin-2
13225	dirMS_041712_NAR_120mM_minus.15274.15274.4	4	8.64	2	5.06E+06		(R)ALKDEEK	(R)A L K D E E/K M E\L\Q/E|I Q L K(E)		137.65	487.0126	1945.031	-0.0025	-1.3	4.58	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
13226	dirMS_041712_NAR_20mM_minus.10930.10930.2	2	8.64	0	1.01E+05		(K)GTIQVIT	(K)G T I Q/V/I/T Q\G T|S L K(N)		157.17	673.3789	1345.769	-0.018	-13.4	8.75	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
13227	dirMS_041712_NAR_30mM_minus2.16142.16142.2	2	8.64	0	7.79E+04		(R)SETDLLD	(R)S E|T D/L/L D/I\R(S)		141.05	531.2806	1061.547	0.0066	6.2	4.03	51583.6	7.73	HUMAN	B4DVE7	Annexin
13228	dirMS_041712_NAR_30mM_minus2.5039.5039.2	2	8.64	0	3.48E+05		(R)TDTGEP	(R)T D|T|G E\P M G R(G)		81.07	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
13229	dirMS_041712_NAR_40mM_minus2.11371.11371.3	3	8.64	0	1.95E+05		(K)LVTSIGD	(K)L V|T S/I/G D V V N H D/P V V G D R(L)		150.32	631.3335	1891.987	-0.0013	-0.7	4.41	27786.2	5.93	HUMAN	H0Y4Z6	Phosphorylase (Fragment)
13230	dirMS_041712_NAR_40mM_minus2.12488.12488.3	3	8.64	1	2.48E+05		(K)DVAIKEP	(K)D V/A I K\E P L\V/D V\V D/P K(Q)		156.3	546.3068	1636.916	-0.0098	-6	4.23	24376.8	6.08	HUMAN	E9PIX6	Protein arginine N-methyltransferase 1 (Fragment)
13231	dirMS_041712_NAR_40mM_minus2.9084.9084.3	3	8.64	0	1.57E+05	M26m	(R)LSAmLV	(R)L S/A m L V/P V/T/P E/V K P K(R)	m:Oxidized methionine	136.37	542.315	1608.939	15.9911	-2.3	8.59	31524.1	4.5	HUMAN	P82970	High mobility group nucleosome-binding domain-containing protein 5
13232	dirMS_041712_NAR_50mM_minus2.12766.12766.3	3	8.64	0	2.74E+05		(K)AASDIAM	(K)A A S/D/I/A/M T E/L/P P T H P I R(L)		140.63	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
13233	dirMS_041712_NAR_50mM_minus2.13533.13533.3	3	8.64	1	1.91E+05		(K)TITLEVE	(K)T I/T\L/E V/E/P S D T I E N V K A K(I)		144.63	663.0226	1987.059	-0.0061	-3.1	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
13234	dirMS_041712_NAR_50mM_minus2.13550.13550.3	3	8.64	0	2.79E+05		(K)VIQYLAY	(K)V/I/Q Y L A Y/V/A S/S H K(S)		144.68	493.6043	1478.8	-0.0018	-1.2	8.48	227783.5	5.5	HUMAN	P35579	Myosin-9
13235	dirMS_041712_NAR_50mM_minus2.15371.15371.3	3	8.64	1	8.63E+04		(R)YRVPDV	(R)Y R V\P D V L|V/A/D|P P I A R(L)		155.97	560.9824	1680.943	-0.0105	-6.3	5.96	96499.9	5.43	HUMAN	F5H6X6	Neutral alpha-glucosidase AB
13236	dirMS_041712_NAR_50mM_minus2.15939.15939.3	3	8.64	1	2.34E+04	M132m	(R)TLAEIAK	(R)T L|A|E I/A K V E L D N m/P L R(G)	m:Oxidized methionine	158.85	610.3273	1812.989	15.9786	-8.9	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
13237	dirMS_041712_NAR_60mM_minus.8247.8247.3	3	8.64	1	1.32E+05		(R)KQSTDE	(R)K Q S T/D\E E/V/T/S L A/K(S)		105.82	479.2451	1435.728	-0.0067	-4.7	4.68	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
13238	dirMS_041712_NAR_120mM_plus.14873.14873.2	2	8.64	1	7.27E+05		(R)KFLDGIY	(R)K|F/L/D/G I Y/V/S\E K(G)		131.42	649.8522	1298.699	-0.002	-1.5	6.07	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
13239	dirMS_041712_NAR_20mM_plus.17200.17200.2	2	8.64	0	9.17E+04		(R)AVLVDLE	(R)A V\L V/D L E/P/G T M D/S V R(S)		189.58	801.414	1601.82	0.0004	0.2	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
13240	dirMS_041712_NAR_30mM_plus2.19341.19341.2	2	8.64	0	1.50E+05		(K)TLGILGL	(K)T L/G|I/L/G L G R(I)		154.73	450.2857	899.567	-0.0032	-3.5	9.41	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
13241	dirMS_041712_NAR_30mM_plus2.4882.4882.2	2	8.64	1	2.23E+05		(R)NTKGGD	(R)N T K G G D A\P A|A G E/D A(-)		77.07	637.286	1273.565	-0.0008	-0.6	4.03	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
13242	dirMS_041712_NAR_40mM_plus2.9818.9818.3	3	8.64	0	1.23E+05		(R)VMLGET	(R)V M/L G E/T N/P A D/S K P G T I/R(G)		122.05	595.9778	1785.916	0.0025	1.4	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
13243	dirMS_041712_NAR_50mM_plus2.17221.17221.3	3	8.64	1	8.65E+05		(R)VYAEDPY	(R)V Y/A E/D/P Y K/S F G L|P S I G R(L)		159.17	633.6509	1898.965	-0.0265	-14	6.04	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
13244	dirMS_041712_NAR_50mM_plus2.20104.20104.3	3	8.64	0	2.68E+05		(R)LQSLPFA	(R)L Q/S L/P F/A/L T\H L N/L K(A)		173.9	532.3178	1594.931	0.0073	4.6	8.76	175851.7	5.01	HUMAN	Q14160	Protein scribble homolog
13245	dirMS_041712_NAR_50mM_plus2.20450.20450.3	3	8.64	1	1.87E+05		(K)SYLNMD	(K)S Y|L/N M D A I/M E A I K/K(T)		176.7	542.9473	1626.823	0.0044	2.7	5.79	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
13246	dirMS_041712_NAR_50mM_plus2.21305.21305.3	3	8.64	0	1.08E+06		(R)AGKPVIC	(R)A G K P V I C A\T Q|M/L/E/S M I K(K)	C:Carbamidomethylation	181.15	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
13247	dirMS_041712_NAR_50mM_plus2.5183.5183.3	3	8.64	0	2.68E+05	M21m	(R)SGSmDP	(R)S G\S/m/D P S G/A/H/P S V R(Q)	m:Oxidized methionine	86.13	467.5461	1384.627	15.9964	1	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
13248	dirMS_041712_NAR_50mM_plus2.5985.5985.3	3	8.64	0	1.14E+05		(R)AGAAGG	(R)A/G\A|A/G/G/P E E E/A E K P V K(T)		95.73	513.9259	1539.765	-0.0018	-1.2	4.49	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
13249	dirMS_041712_NAR_60mM_plus.11650.11650.3	3	8.64	1	2.93E+06		(K)KAEAGA	(K)K A\E A G A G S\A|T/E/F/Q F R(G)		118.23	523.9277	1569.766	0.003	1.9	6.14	18897.4	10.15	HUMAN	P46783	40S ribosomal protein S10
13250	dirMS_041712_NAR_60mM_plus.16460.16460.3	3	8.64	0	7.52E+05		(K)MTHLPE	(K)M T H\L P E\L|D/T|L/S/S E R(A)		142.2	543.6023	1628.795	-0.0025	-1.5	4.65	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
13251	dirMS_041712_NAR_60mM_plus.19340.19340.3	3	8.64	1	4.39E+05		(K)WNLDEL	(K)W|N\L D E L/P K F E K(N)		158.8	473.5847	1418.731	0.0081	5.7	4.68	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
13252	dirMS_041712_NAR_60mM_plus.5568.5568.3	3	8.64	0	3.12E+05	M111m	(R)MEELHN	(R)M/E|E/L H N Q E m Q K(R)	m:Oxidized methionine	87.4	478.2118	1416.625	15.9962	0.9	4.75	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
13253	dirMS_041712_NAR_120mM_minus.10065.10065.2	2	8.63	0	5.19E+05		(K)HIYYITG	(K)H/I|Y\Y I T G E/T K(D)		109.03	612.8167	1224.626	0.0002	0.2	6.75	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
13254	dirMS_041712_NAR_120mM_minus.19503.19503.3	3	8.63	0	7.14E+05		(R)NSVSNF	(R)N S|V/S N F/L/H/S L E R(G)		162.22	468.2346	1402.707	-0.0181	-12.9	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
13255	dirMS_041712_NAR_20mM_minus.13165.13165.3	3	8.63	0	2.65E+05		(K)VGINYQ	(K)V G I N Y\Q/P\P T V/V/P G G D L A K(V)		183.15	608.9971	1824.985	-0.0087	-4.8	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
13256	dirMS_041712_NAR_20mM_minus.13608.13608.2	2	8.63	0	1.30E+05		(K)ALQQGL	(K)A L/Q/Q|G L/V/G L/E L K(E)		187.4	634.8811	1268.757	-0.0023	-1.8	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
13257	dirMS_041712_NAR_20mM_minus.13797.13797.2	2	8.63	0	4.04E+05		(K)LGGSAV	(K)L/G G S A V I/S L E\G K|P L(-)		188.7	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
13258	dirMS_041712_NAR_40mM_minus2.10924.10924.3	3	8.63	0	1.05E+05	M56m	(K)VAIVKPG	(K)V A|I/V K/P G V\P m E/I V L N K(E)	m:Oxidized methionine	147.12	575.0112	1707.024	15.9953	0.2	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
13259	dirMS_041712_NAR_40mM_minus2.15020.15020.3	3	8.63	0	1.44E+05		(K)LFLFHTS	(K)L F/L F H T S\L|P\I A E A P G K(L)		173.92	580.9924	1740.968	-0.0057	-3.3	6.75	108105.4	6.57	HUMAN	E7EP00	Protein transport protein Sec24C
13260	dirMS_041712_NAR_50mM_minus2.13555.13555.3	3	8.63	1	2.80E+05		(K)ITDIIGKE	(K)I/T/D I|I G K/E E G\I/G/P E N L R(G)		145.55	618.665	1853.997	-0.0163	-8.8	4.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
13261	dirMS_041712_NAR_50mM_minus2.16394.16394.3	3	8.63	1	9.61E+04		(K)VKLAAV	(K)V K/L A A V D A T V/N|Q|V|L/A S R(Y)		161.62	585.6709	1755.012	-0.0142	-8.1	8.72	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
13262	dirMS_041712_NAR_50mM_minus2.16851.16851.3	3	8.63	0	4.60E+05		(K)NILFVITK	(K)N I/L F V I/T/K/P D V Y K(S)		164.12	517.2991	1549.899	-0.0161	-10.4	8.5	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
13263	dirMS_041712_NAR_50mM_minus2.17054.17054.3	3	8.63	1	5.94E+04		(R)EFTRLEIC	(R)E F/T R L E/I|C/N/L T/P D A L K(S)	C:Carbamidomethylation	164.93	640.6675	1919.989	-0.0016	-0.8	4.68	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
13264	dirMS_041712_NAR_50mM_minus2.8926.8926.3	3	8.63	0	2.36E+05		(R)VMLGET	(R)V/M/L/G E T N/P A D S K P G T I R(G)		118.3	595.9744	1785.916	-0.0077	-4.3	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
13265	dirMS_041712_NAR_60mM_minus.18889.18889.3	3	8.63	0	1.36E+06		(R)IHFPLAT	(R)I H\F P L A\T Y|A|P/V I S A E K(A)		166.23	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
13266	dirMS_041712_NAR_60mM_minus.19264.19264.3	3	8.63	0	3.35E+05		(K)HGATVL	(K)H G A T\V L/T\A/L/G/G I/L/K(K)		170.82	450.939	1350.81	-0.0079	-5.9	8.76	8125.3	9.3	HUMAN	B0QYF7	Myoglobin (Fragment)
13267	dirMS_041712_NAR_120mM_plus.22857.22881.3	3	8.63	1	4.64E+05		(K)GLAPDLI	(K)G L|A\P/D/L/P E D L/Y H L I K K(A)		173.95	608.0076	1822.011	-0.0027	-1.5	5.38	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
13268	dirMS_041712_NAR_20mM_plus.10568.10588.2	2	8.63	0	4.42E+04	M222m	(K)VVPEmT	(K)V V|P E/m T E/I L K(K)	m:Oxidized methionine	144.23	587.8225	1158.644	15.9939	-0.9	4.53	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
13269	dirMS_041712_NAR_20mM_plus.11082.11082.2	2	8.63	0	9.89E+04	M196m	(K)DAGTIAG	(K)D A G T\I|A|G/L/N V m R(I)	m:Oxidized methionine	148.72	617.3237	1217.631	16.0094	11.8	5.84	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
13270	dirMS_041712_NAR_20mM_plus.16980.16980.2	2	8.63	0	2.55E+05		(K)VQIAVA	(K)V Q/I|A\V/A|N A Q\E L L/Q R(M)		188.03	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
13271	dirMS_041712_NAR_20mM_plus.18516.18516.2	2	8.63	0	1.58E+04		(K)LLDEVFF	(K)L/L/D|E V/F F S E/K(I)		198.55	613.8195	1226.63	0.0014	1.1	4.14	20360.1	6.3	HUMAN	H0YKT8	Proteasome subunit beta type (Fragment)
13272	dirMS_041712_NAR_20mM_plus.8148.8148.3	3	8.63	0	2.31E+05	M346m M3	(K)mGGmE	(K)m G G m/E G P F/G/G\G|m/E/N m G R(F)	m:Oxidized methionine	126.28	593.558	1714.68	63.979	-0.4	4.53	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
13273	dirMS_041712_NAR_30mM_plus2.14464.14464.2	2	8.63	0	3.64E+05		(R)ELAFQIS	(R)E L|A/F Q I/S/K(E)		128.67	468.2629	935.52	-0.0011	-1.2	6.1	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
13274	dirMS_041712_NAR_30mM_plus2.5575.5575.2	2	8.63	0	2.10E+05		(R)ENPVYE	(R)E N|P V Y/E/K(K)		83.58	439.717	878.425	0.0013	1.5	4.53	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
13275	dirMS_041712_NAR_30mM_plus2.6873.6873.2	2	8.63	0	2.73E+05		(K)AEYLCR	(K)A E|Y/L/C/R(I)	C:Carbamidomethylation	90.82	406.1945	811.377	0.005	6.2	6.04	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
13276	dirMS_041712_NAR_40mM_plus2.13373.13373.3	3	8.63	0	1.40E+05		(R)LTIIVSDP	(R)L T|I/I/V/S D/P S H C N V L R(A)	C:Carbamidomethylation	144.63	575.31	1723.916	-0.0005	-0.3	6.74	35906.1	9.96	HUMAN	E9PB02	Ribonuclease P protein subunit p30
13277	dirMS_041712_NAR_40mM_plus2.16222.16222.3	3	8.63	1	1.95E+05		(K)LGVQVV	(K)L G/V Q|V/V/I T/D P E K L D/Q I R(Q)		161.88	641.701	1923.091	-0.0025	-1.3	4.56	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
13278	dirMS_041712_NAR_40mM_plus2.5416.5416.2	2	8.63	0	2.45E+05	M300m	(K)NMmAA	(K)N M/m A/A C D|P/R(H)	C:Carbamidomethylation m:Oxid	89.2	541.2145	1065.427	15.9943	-0.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
13279	dirMS_041712_NAR_50mM_plus2.12040.12040.3	3	8.63	0	3.79E+05		(K)FSVCVLG	(K)F S/V/C V\L/G/D Q Q H C/D/E A K(A)	C:Carbamidomethylation	131.38	631.6129	1892.827	-0.0024	-1.3	4.54	25002	10.06	HUMAN	P62906	60S ribosomal protein L10a
13280	dirMS_041712_NAR_50mM_plus2.12479.12479.3	3	8.63	1	3.56E+04		(K)LLQAQG	(K)L L/Q/A Q/G V/E V/P S K D S L|P K(K)		133.63	603.6741	1809.012	-0.0039	-2.2	6.07	139280.8	5.39	HUMAN	O60841	Eukaryotic translation initiation factor 5B
13281	dirMS_041712_NAR_50mM_plus2.15603.15603.3	3	8.63	1	1.01E+06		(R)KVPGVT	(R)K\V/P G V T A\I\E\L D E D/T G/T F/R(I)		149.87	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
13282	dirMS_041712_NAR_50mM_plus2.16803.16803.3	3	8.63	1	1.87E+05	M132m	(R)TLAEIAK	(R)T L|A/E I/A K V E L/D N m|P L R(G)	m:Oxidized methionine	155.92	610.3302	1812.989	15.9873	-4.2	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
13283	dirMS_041712_NAR_50mM_plus2.17158.17158.3	3	8.63	1	4.95E+04		(K)LLVYEAL	(K)L L/V/Y E/A/L/E Y A K R(A)		159.43	489.9441	1467.821	-0.0028	-1.9	6.14	32535.6	9.19	HUMAN	B4DZW6	Regulator of microtubule dynamics protein 1
13284	dirMS_041712_NAR_50mM_plus2.17657.17658.3	3	8.63	1	8.31E+05		(R)DSEQVA	(R)D S/E/Q|V/A E/L K Q E L A T L K(S)		161.07	601.322	1801.954	-0.0027	-1.5	4.41	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
13285	dirMS_041712_NAR_50mM_plus2.20241.20262.3	3	8.63	1	5.58E+05		(R)SKALGSD	(R)S K A L\G S D H C P I T\L\Y\L|A|L(-)	C:Carbamidomethylation	174.68	620.3259	1858.973	-0.01	-5.4	6.46	5634.5	9.82	HUMAN	G3V574	DNA-(apurinic or apyrimidinic site) lyase
13286	dirMS_041712_NAR_120mM_minus.12273.12273.4	4	8.62	2	4.00E+05		(K)KGTVEG	(K)K\G T V\E/G F E/P A D N K C L L R(A)	C:Carbamidomethylation	120.57	484.251	1933.98	0.0021	1.1	6.18	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
13287	dirMS_041712_NAR_20mM_minus.14444.14444.2	2	8.62	0	2.52E+05		(R)APGSGL	(R)A/P|G S G L/A L L|P L K(I)		198.32	568.8551	1136.704	-0.0008	-0.7	8.8	266161	5.68	HUMAN	E9PPU0	Epiplakin
13288	dirMS_041712_NAR_30mM_minus2.13935.13975.2	2	8.62	0	2.05E+05		(R)AFFSEVE	(R)A F|F|S/E/V E R(R)		129.48	492.7447	984.479	0.0036	3.7	4.53	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
13289	dirMS_041712_NAR_30mM_minus2.14925.14947.2	2	8.62	0	2.26E+05		(K)NMVLFT	(K)N M|V|L F/T R(Q)		134.87	440.7384	880.471	-0.0014	-1.6	9.75	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1
13290	dirMS_041712_NAR_50mM_minus2.11157.11157.3	3	8.62	1	1.86E+05		(R)DNKQAG	(R)D N/K Q A\G\V|F/E/P T I V K(V)		132.05	515.9485	1545.827	0.0038	2.5	6.07	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
13291	dirMS_041712_NAR_50mM_minus2.13111.13111.3	3	8.62	0	3.56E+05		(R)ETNLDSI	(R)E\T N/L/D S L/P L/V D/T H\S K(R)		142.45	556.9529	1668.844	0.0002	0.1	4.53	53707.8	5.06	HUMAN	P08670	Vimentin
13292	dirMS_041712_NAR_50mM_minus2.16599.16599.3	3	8.62	1	9.23E+04		(R)DSEQVA	(R)D S/E/Q/V/A E/L K/Q E L A T L K(S)		163.05	601.3217	1801.954	-0.0036	-2	4.41	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
13293	dirMS_041712_NAR_50mM_minus2.8503.8503.3	3	8.62	1	1.43E+04		(K)ALIEMEK	(K)A L/I/E|M E K Q Q Q D/Q/V D R(N)		116.15	610.9698	1830.901	-0.0066	-3.6	4.32	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)

13294	dirMS_041712_NAR_60mM_minus.11883.11883.3	3	8.62	0	1.92E+05		(R)ILHLLGQ	(R)I L/H/L L/G\Q/E\G P K(T)		126.37	402.2384	1204.705	-0.0042	-3.5	6.75	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
13295	dirMS_041712_NAR_60mM_minus.9095.9095.3	3	8.62	1	1.62E+05	M232m M	(R)MSmKEV	(R)M/S m K E V D E\Q/m|L|N/V|Q\N K(N)	m:Oxidized methionine	110.57	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13296	dirMS_041712_NAR_120mM_plus.5642.5642.3	3	8.62	1	1.89E+05		(R)SGGGYG	(R)S G|G/G/Y/G G D R G G G Y G G D/R(G)		82.35	515.5539	1544.647	-0.0001	-0.1	5.68	21563.9	10.01	HUMAN	K7EKB2	TATA-binding protein-associated factor 2N (Fragment)
13297	dirMS_041712_NAR_20mM_plus.15950.15963.2	2	8.62	0	3.17E+05	M81m	(K)SFYPEEV	(K)S F|Y/P E E\V/S/S m V L T K(M)	m:Oxidized methionine	181.02	816.8988	1616.788	16.0027	4.8	4.53	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
13298	dirMS_041712_NAR_30mM_plus2.20205.20205.2	2	8.62	0	1.13E+05		(K)TNVALM	(K)T N|V/A/L/M\C/M L R(E)	C:Carbamidomethylation	159.65	604.8021	1208.595	0.0021	1.7	9.41	71929.1	5.1	HUMAN	C9JAQ9	U5 small nuclear ribonucleoprotein 200 kDa helicase
13299	dirMS_041712_NAR_30mM_plus2.7929.7929.2	2	8.62	0	2.20E+05		(K)IAVAAQ	(K)I/A|V/A/A/Q N C Y K(V)	C:Carbamidomethylation	96.05	569.2905	1137.572	0.0016	1.4	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
13300	dirMS_041712_NAR_30mM_plus2.8737.8862.3	3	8.62	0	1.43E+06		(R)FGQGGA	(R)F G Q G\G A G|P|V|G G Q/G P R(G)		99.68	447.893	1341.666	-0.0014	-1	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
13301	dirMS_041712_NAR_40mM_plus2.11918.11918.2	2	8.62	0	9.27E+04		(R)NFDEILR	(R)N F/D|E/I L R(V)		136.5	453.7354	906.468	-0.0044	-4.9	4.37	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
13302	dirMS_041712_NAR_50mM_plus2.16250.16250.3	3	8.62	0	2.89E+05		(K)ACQSIYP	(K)A C/Q/S I Y/P L/H/D V F V R(K)	C:Carbamidomethylation	154.4	568.9562	1704.853	0.0014	0.8	6.79	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
13303	dirMS_041712_NAR_50mM_plus2.17020.17020.3	3	8.62	1	3.71E+05		(K)LSKNEVL	(K)L S K N E V\L M V|N\I/G S L\S T G G R(V)		157	659.0229	1975.064	-0.0099	-5	8.75	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
13304	dirMS_041712_NAR_50mM_plus2.17961.18027.3	3	8.62	1	2.19E+05		(R)IGFDVVT	(R)I/G/F/D/V/V/T L S G T R G P L S R(V)		162.87	592.331	1774.981	-0.0026	-1.4	9.6	25356.9	9.94	HUMAN	Q5TDF0	Cancer-related nucleoside-triphosphatase
13305	dirMS_041712_NAR_50mM_plus2.8948.8948.3	3	8.62	0	6.04E+05		(R)AALAHS	(R)A A L A H S/E E\V\T/A/S/Q/V/A A/T K(T)		113.75	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
13306	dirMS_041712_NAR_60mM_plus.18004.18004.3	3	8.62	1	2.30E+05		(R)YRVPDV	(R)Y R V P D V\L|V|A/D/P\P I A R(L)		150.93	560.9839	1680.943	-0.006	-3.6	5.96	96499.9	5.43	HUMAN	F5H6X6	Neutral alpha-glucosidase AB
13307	dirMS_041712_NAR_120mM_minus.11036.11036.3	3	8.61	0	5.83E+05		(R)GLHQSIE	(R)G L/H\Q S\I/E/E/F/R(A)		114.27	405.8796	1215.612	0.0126	10.4	5.4	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
13308	dirMS_041712_NAR_20mM_minus.14654.14654.2	2	8.61	0	8.83E+04		(R)IITLTGPT	(R)I I|T L/T|G/P T N A I F K(A)		201.33	694.9107	1388.815	-0.0007	-0.5	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
13309	dirMS_041712_NAR_30mM_minus2.10685.10849.2	2	8.61	0	1.06E+06	M950m	(R)LSLYQAm	(R)L S|L/Y/Q/A m R(Q)	m:Oxidized methionine	112.02	499.2567	981.519	15.9875	-7.4	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
13310	dirMS_041712_NAR_30mM_minus2.11591.11591.2	2	8.61	0	1.58E+05		(R)TPCEEIL	(R)T/P/C E E/I/L|V K(H)	C:Carbamidomethylation	118.02	544.7899	1088.566	0.0069	6.3	4.53	83264.1	6.04	HUMAN	E9PHF0	Filamin-A
13311	dirMS_041712_NAR_30mM_minus2.15298.15298.2	2	8.61	0	6.42E+05		(R)YPVNSV	(R)Y/P\V/N\S V N I|L K(A)		136.8	573.8282	1146.652	-0.0026	-2.3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
13312	dirMS_041712_NAR_40mM_minus2.8134.8134.3	3	8.61	0	1.18E+04	M33m	(R)VLTEDEm	(R)V L/T/E/D E m/G H/P E/I/G D A I A\R(L)	m:Oxidized methionine	127.97	656.9824	1952.938	15.9944	-0.2	4.17	40874	5.06	HUMAN	E9PCI9	Farnesyl pyrophosphate synthase
13313	dirMS_041712_NAR_50mM_minus2.15930.15930.3	3	8.61	1	8.21E+04		(K)DANAKL	(K)D A/N A K L S E\L/E|A|A L Q R(A)		158.97	543.6248	1628.86	-0.0004	-0.2	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
13314	dirMS_041712_NAR_60mM_minus.13527.13527.3	3	8.61	1	1.16E+05	M160m	(K)FRQDLm	(K)F R Q D\L m\N\I|A/G T T L S S K(L)	m:Oxidized methionine	135.43	599.9744	1781.921	15.9872	-4.3	8.75	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
13315	dirMS_041712_NAR_60mM_minus.16215.16215.3	3	8.61	1	5.68E+05		(K)LKLSILYP	(K)L K L S I L\Y|P A/T T G R(N)		150.5	478.2883	1432.852	-0.0019	-1.3	9.99	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
13316	dirMS_041712_NAR_20mM_plus.12172.12172.2	2	8.61	0	1.46E+04	M66m	(R)GGGVGG	(R)G G G V/G|G F L/P A m/K(Q)	m:Oxidized methionine	156.62	553.7889	1090.571	15.9991	3.8	8.75	19338.9	5.33	HUMAN	E7EQS9	tRNA-splicing ligase RtcB homolog
13317	dirMS_041712_NAR_20mM_plus.18746.18746.2	2	8.61	0	2.32E+05		(R)IITLAGPT	(R)I I/T L/A/G P T N A I F K(A)		200.97	679.9039	1358.804	-0.0037	-2.7	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
13318	dirMS_041712_NAR_20mM_plus.7399.7399.2	2	8.61	0	8.16E+04		(K)SNVSDA	(K)S N V|S D A/V/A/Q S T R(I)		119.4	617.8019	1234.602	-0.0057	-4.6	5.55	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
13319	dirMS_041712_NAR_20mM_plus.7916.7916.2	2	8.61	0	3.59E+05	M239m	(K)EVDEQm	(K)E V/D E/Q/m L\N|V/Q/N K(N)	m:Oxidized methionine	124.95	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13320	dirMS_041712_NAR_30mM_plus2.12524.12524.2	2	8.61	0	2.56E+05		(R)NCSSFLI	(R)N/C/S S/F/L/I/K(R)	C:Carbamidomethylation	118.62	484.7469	968.487	-0.0005	-0.5	8.75	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
13321	dirMS_041712_NAR_30mM_plus2.14546.14546.2	2	8.61	0	3.61E+05		(R)ELAFQIS	(R)E L/A F/Q|I/S/K(E)		129	468.2629	935.52	-0.0011	-1.2	6.1	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
13322	dirMS_041712_NAR_30mM_plus2.4132.4184.2	2	8.61	0	1.42E+06	M299m M	(K)NmmAA	(K)N m/m|A A C/D|P/R(H)	C:Carbamidomethylation m:Oxid	69.3	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
13323	dirMS_041712_NAR_50mM_plus2.18948.18948.3	3	8.61	1	2.79E+05		(K)LALFQAI	(K)L/A|L/F/Q A I/G K E V V D/R(A)		167.97	520.3019	1558.895	-0.004	-2.6	6.07	266161	5.68	HUMAN	E9PPU0	Epiplakin
13324	dirMS_041712_NAR_50mM_plus2.6587.6587.3	3	8.61	1	4.18E+04		(R)TAEEPPQ	(R)T A\E/E|P P Q E K A P E/P T D A R(K)		99.48	622.6353	1865.888	0.0038	2	4.25	86421.8	4.29	HUMAN	O43719	HIV Tat-specific factor 1
13325	dirMS_041712_NAR_50mM_plus2.7375.7375.3	3	8.61	0	6.94E+04		(K)TTAPVPE	(K)T T|A|P V/P E P T K/P G D|P R(E)		104.75	521.6042	1562.817	-0.0193	-12.3	5.74	109165.8	8.64	HUMAN	E7ERS3	Zinc finger CCCH domain-containing protein 18
13326	dirMS_041712_NAR_50mM_plus2.8354.8354.3	3	8.61	1	3.09E+05		(K)ATQPET	(K)A T/Q/P E T T E E V T D\L K/R(Q)		110.27	573.2915	1717.86	-0.0003	-0.2	4.41	72152.1	5.27	HUMAN	A0MZ66	Shootin-1
13327	dirMS_041712_NAR_60mM_plus.11469.11469.3	3	8.61	1	1.22E+06		(R)GASKEIL	(R)G A/S K E I\L|S/E/V E/R(N)		117.7	439.9069	1317.701	0.0053	4	4.79	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
13328	dirMS_041712_NAR_60mM_plus.17354.17354.3	3	8.61	0	1.75E+04		(R)IYSHSLLI	(R)I/Y S H S\L\L/P V/L/R(S)		147.6	433.2569	1297.763	-0.0065	-5	8.75	60871.9	6.3	HUMAN	B4DJ93	Phosphoribosylformylglycinamidine cyclo-ligase
13329	dirMS_041712_NAR_60mM_plus.8112.8112.3	3	8.61	1	6.93E+05		(K)ALSRQEI	(K)A L\S R Q E M\Q/E/V/Q S S R(S)		100.48	550.2735	1648.807	-0.0012	-0.7	6.19	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
13330	dirMS_041712_NAR_60mM_plus.8734.8734.3	3	8.61	1	3.99E+04		(R)LLEEEDS	(R)L/L E E/E/D/S K L K(G)		103.8	401.8861	1203.647	-0.003	-2.5	4.41	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
13331	dirMS_041712_NAR_120mM_minus.16672.16672.3	3	8.6	0	3.08E+05		(K)HLEINPD	(K)H L|E I N\P D/H|S/I I/E T L/R(Q)		146.27	596.3176	1786.945	-0.0064	-3.6	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
13332	dirMS_041712_NAR_30mM_minus2.12743.12743.2	2	8.6	0	2.37E+05		(R)CGYFDE	(R)C G|Y|F/D/E E/M N R(I)	C:Carbamidomethylation	122.97	660.7538	1320.498	0.002	1.5	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
13333	dirMS_041712_NAR_30mM_minus2.17352.17352.2	2	8.6	0	2.79E+05		(K)FEDENFI	(K)F E|D E\N F/I L K(H)		148.07	577.7894	1154.573	-0.0013	-1.1	4.14	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
13334	dirMS_041712_NAR_30mM_minus2.18804.18804.2	2	8.6	0	1.73E+05		(R)AIGIGAY	(R)A/I|G|I|G/A Y L V R(L)		157.37	516.8122	1032.62	-0.0029	-2.8	8.79	9731	5.19	HUMAN	E9PEW7	Acetyl-CoA carboxylase 2
13335	dirMS_041712_NAR_40mM_minus2.10752.10752.3	3	8.6	0	1.98E+05		(R)DLSHIGD	(R)D L S\H I|G D\A\V|V/I S C A/K(D)	C:Carbamidomethylation	146.93	528.9384	1584.805	-0.0044	-2.8	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
13336	dirMS_041712_NAR_50mM_minus2.10497.10497.3	3	8.6	0	2.90E+05	M35m	(K)AASDIAm	(K)A A\S D\I/A/m T/E L/P P T H P I R(L)	m:Oxidized methionine	127.85	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
13337	dirMS_041712_NAR_50mM_minus2.13499.13499.3	3	8.6	1	1.72E+05		(R)LAIKLPD	(R)L/A/I K L|P D D Q I/P/K(T)		145.38	450.9376	1350.799	-0.0009	-0.7	5.96	26413	9.18	HUMAN	B1APP6	6-phosphofructokinase type C (Fragment)
13338	dirMS_041712_NAR_60mM_minus.10058.10058.3	3	8.6	1	1.94E+05		(R)VEVGKD	(R)V/E/V/G K D Q E F T V D/T R(G)		115.57	541.6051	1622.802	-0.0013	-0.8	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
13339	dirMS_041712_NAR_60mM_minus.9370.9370.3	3	8.6	1	1.46E+05		(R)KIQVLQQ	(R)K I Q V L|Q/Q Q|A/D/D A E\E R(A)		112	590.9696	1770.898	-0.0038	-2.2	4.32	11017	4.8	HUMAN	D6R904	Tropomyosin alpha-3 chain
13340	dirMS_041712_NAR_60mM_minus.9741.9741.3	3	8.6	1	4.56E+04		(K)TAVCDIP	(K)T/A/V C D I/P P/R G L K(M)	C:Carbamidomethylation	112.72	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
13341	dirMS_041712_NAR_120mM_plus.10681.10681.3	3	8.6	0	9.41E+05		(R)YYDSRPG	(R)Y/Y|D/S R/P G G Y G Y G Y G R(S)		108.63	577.5892	1730.756	-0.0027	-1.6	8.38	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
13342	dirMS_041712_NAR_120mM_plus.15312.15312.4	4	8.6	1	1.45E+06		(R)VKPAPD	(R)V K/P A P D E/T/S F/S/E A L L K R(N)		133.42	472.7599	1888.017	0.0003	0.2	6.15	43289.6	5.19	HUMAN	Q12905	Interleukin enhancer-binding factor 2
13343	dirMS_041712_NAR_120mM_plus.4152.4152.3	3	8.6	1	1.96E+06	M54m	(K)SLDEmE	(K)S\L|D E m/E/K Q/Q R(E)	m:Oxidized methionine	70.17	427.2032	1263.6	15.9953	0.3	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
13344	dirMS_041712_NAR_20mM_plus.19132.19132.2	2	8.6	0	9.41E+04		(R)DLLFQAL	(R)D L|L/F/Q A/L/G R(T)		203.32	516.7952	1032.584	-0.0005	-0.5	5.84	66742	6.4	HUMAN	Q9NSD9	Phenylalanine--tRNA ligase beta subunit
13345	dirMS_041712_NAR_30mM_plus2.15380.15380.2	2	8.6	0	2.68E+05		(R)LLCNFM	(R)L/L/C N/F M R(Q)	C:Carbamidomethylation	132.98	477.2409	953.47	0.005	5.2	9.75	18685.5	9.45	HUMAN	B4DEV8	Proteasome subunit alpha type
13346	dirMS_041712_NAR_30mM_plus2.20169.20169.2	2	8.6	0	1.22E+04		(R)ALDTMN	(R)A/L/D\T M/N F D/V I/K(G)		159.3	633.8315	1266.64	0.0159	12.5	4.21	68197.9	9.58	HUMAN	B1ANR0	Poly(A) binding protein, cytoplasmic 4 (Inducible form)
13347	dirMS_041712_NAR_30mM_plus2.22158.22158.2	2	8.6	0	1.55E+05		(R)WQFLTL	(R)W/Q|F/L/T/L R(E)		171.02	482.2695	963.541	-0.0093	-9.7	9.75	132493.1	6.53	HUMAN	B4DER1	Leucine--tRNA ligase, cytoplasmic
13348	dirMS_041712_NAR_30mM_plus2.8422.8422.2	2	8.6	0	7.55E+04		(K)QGGGGG	(K)Q/G G G/G/G G G S V/P G I E/R(M)		98.27	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
13349	dirMS_041712_NAR_40mM_plus2.16000.16000.2	2	8.6	0	1.03E+05		(R)YLTVAAV	(R)Y L/T|V/A/A V F R(G)		161.77	520.2997	1039.593	-0.0014	-1.3	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13350	dirMS_041712_NAR_40mM_plus2.19476.19476.3	3	8.6	1	4.58E+05		(K)ALFEEVP	(K)A L/F\E E/V/P E L L T E/A E/K/K(E)		181.77	615.9991	1845.984	-0.0017	-0.9	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
13351	dirMS_041712_NAR_40mM_plus2.9018.9018.2	2	8.6	0	3.90E+04		(R)INVELST	(R)I/N/V/E L S T K(G)		114.85	452.2587	903.515	-0.0044	-4.9	6	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
13352	dirMS_041712_NAR_50mM_plus2.6701.6701.3	3	8.6	0	2.44E+04		(R)DSSESQL	(R)D S/S E/S Q/L|A/S T E S D K P T T G R(V)		100.1	665.9753	1995.91	0.0012	0.6	4.32	15625.6	4.4	HUMAN	K7EQH1	Uncharacterized protein C18orf25 (Fragment)
13353	dirMS_041712_NAR_60mM_plus.10689.10689.2	2	8.6	1	1.68E+06		(R)VKYETEL	(R)V|K|Y|E T E/L A M R(Q)		113.15	620.326	1239.64	0.0045	3.7	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13354	dirMS_041712_NAR_60mM_plus.11225.11225.2	2	8.6	0	7.25E+05		(R)DNIQGIT	(R)D N I|Q/G/I/T K/P A I/R(R)		116.43	663.3768	1325.754	-0.0073	-5.5	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
13355	dirMS_041712_NAR_60mM_plus.13691.13691.3	3	8.6	1	5.96E+05		(R)FKIPGSP	(R)F K|I P G S|P/P E S M G R(G)		128.43	468.2401	1402.715	-0.009	-6.4	8.75	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
13356	dirMS_041712_NAR_60mM_plus.17213.17213.3	3	8.6	1	4.96E+06		(K)LKVPEW	(K)L K/V|P E W V/D T V K(L)		146.07	438.5872	1313.746	0.0007	0.5	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
13357	dirMS_041712_NAR_120mM_minus.10056.10056.3	3	8.59	1	9.65E+04		(K)LLKDAEA	(K)L L K D A E/A L/S/Q/R(L)		109.18	415.2365	1243.7	-0.0055	-4.4	6.07	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
13358	dirMS_041712_NAR_20mM_minus.13910.13916.2	2	8.59	0	8.11E+05		(K)VLTPELY	(K)V/L|T|P E/L Y A E L R(A)		191.32	652.3653	1303.726	-0.0023	-1.8	4.53	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
13359	dirMS_041712_NAR_20mM_minus.7608.7608.2	2	8.59	0	8.60E+05	M239m	(K)EVDEQm	(K)E V/D\E/Q m L/N\V/Q|N K(N)	m:Oxidized methionine	124.65	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13360	dirMS_041712_NAR_20mM_minus.9970.9970.2	2	8.59	0	3.05E+05	Y224y	(R)ADLTEYL	(R)A D L T/E Y L/S/T H y K(A)	y:Phosphorylated Y	150.25	760.8343	1440.7	79.9608	-3.6	5.32	53329.5	5.94	HUMAN	P31930	Cytochrome b-c1 complex subunit 1, mitochondrial
13361	dirMS_041712_NAR_30mM_minus2.15119.15119.2	2	8.59	0	3.04E+05		(R)GGYIGST	(R)G G Y|I/G/S/T Y F E R(C)		135.45	625.2953	1249.585	-0.0015	-1.2	6	21184.9	7.82	HUMAN	P61081	NEDD8-conjugating enzyme Ubc12
13362	dirMS_041712_NAR_30mM_minus2.16119.16119.2	2	8.59	0	2.24E+04		(K)SEGGFIW	(K)S E|G/G F I W A/C/K(N)	C:Carbamidomethylation	141.03	577.7702	1154.53	0.0032	2.8	5.72	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
13363	dirMS_041712_NAR_30mM_minus2.19031.19131.2	2	8.59	1	2.15E+05		(K)SKLEFSIY	(K)S K\L E\F S I|Y|P/A|P(-)		158.93	626.334	1251.662	-0.0012	-1	5.72	21962.5	5.85	HUMAN	C9JJQ8	Tubulin alpha-4A chain (Fragment)
13364	dirMS_041712_NAR_50mM_minus2.15911.15911.3	3	8.59	0	9.69E+04		(K)INLEAAE	(K)I/N L|E A A E/L G E I S D I/H T K(L)		158.72	618.326	1852.965	-0.0016	-0.9	4.4	84268.2	6.32	HUMAN	Q9UHD2	Serine/threonine-protein kinase TBK1
13365	dirMS_041712_NAR_50mM_minus2.17102.17102.3	3	8.59	1	8.54E+04		(K)ASIAQAV	(K)A S I/A/Q\A V R D G\L\L|P T G/L G Q R(L)		165.25	641.6908	1923.077	-0.0192	-10	9.64	266161	5.68	HUMAN	E9PPU0	Epiplakin
13366	dirMS_041712_NAR_60mM_minus.9653.9653.2	2	8.59	1	4.41E+05		(R)LQAEIEG	(R)L/Q/A E I/E/G/L/K G Q R(A)		114.13	671.3768	1341.748	-0.0022	-1.6	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
13367	dirMS_041712_NAR_120mM_plus.20625.20625.4	4	8.59	1	2.15E+05		(K)AAIDWF	(K)A A|I D/W/F/D G K E F H G N I I K(V)		161.23	491.0027	1960.992	-0.0026	-1.3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
13368	dirMS_041712_NAR_120mM_plus.8949.9089.3	3	8.59	1	1.06E+06		(R)EQAEEE	(R)E/Q A/E E/E R Y F/R(A)		101.13	452.8785	1356.618	0.0031	2.3	4.5	12248.6	9.34	HUMAN	Q9UII2	ATPase inhibitor, mitochondrial
13369	dirMS_041712_NAR_20mM_plus.12686.12686.3	3	8.59	0	4.87E+04	M17m M2	(K)GAEEmE	(K)G A E E m E T V\I/P V D/V m R(R)	m:Oxidized methionine	160.27	569.9346	1675.803	31.9863	-2.1	4	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
13370	dirMS_041712_NAR_20mM_plus.16812.16812.2	2	8.59	0	1.05E+05		(K)VLTPELY	(K)V L/T|P E|L Y A E/L R(A)		187.53	652.3664	1303.726	-0.0001	-0.1	4.53	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
13371	dirMS_041712_NAR_20mM_plus.8969.9054.2	2	8.59	0	4.46E+05	M161m	(K)LLIEmEQ	(K)L/L|I/E/m E Q/R(L)	m:Oxidized methionine	132.82	524.278	1031.555	15.9933	-1.5	4.53	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
13372	dirMS_041712_NAR_30mM_plus2.17080.17096.2	2	8.59	0	3.20E+05		(K)SQLLSYII	(K)S Q|L|L|S/Y I D/R(L)		142.62	547.7952	1094.584	-0.0009	-0.8	5.55	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
13373	dirMS_041712_NAR_30mM_plus2.20939.21145.2	2	8.59	0	3.51E+05		(K)TIFAYFT	(K)T\I|F/A\Y/F/T G S K(D)		165.17	567.7949	1134.583	-0.0005	-0.4	8.26	8599.5	5.51	HUMAN	I3L0K2	Thioredoxin domain-containing protein 17
13374	dirMS_041712_NAR_50mM_plus2.15186.15186.3	3	8.59	1	7.22E+05		(R)GFPTIYF	(R)G F/P T/I/Y/F S/P A N K K(L)		148.57	490.5973	1469.779	-0.0014	-0.9	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
13375	dirMS_041712_NAR_50mM_plus2.21350.21350.3	3	8.59	0	6.47E+05		(R)AGKPVIC	(R)A/G K\P V I C|A/T\Q/M L E S M I K(K)	C:Carbamidomethylation	181.43	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
13376	dirMS_041712_NAR_50mM_plus2.22118.22118.3	3	8.59	1	5.56E+05		(K)AGFLDLK	(K)A/G|F L/D L K/D F L/P K(E)		188.95	455.2587	1363.762	-0.0005	-0.3	6	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
13377	dirMS_041712_NAR_50mM_plus2.9743.9743.3	3	8.59	0	2.98E+04		(K)GAVDGG	(K)G A|V|D G/G L/S I/P H S T K(R)		119.98	446.9057	1338.701	0.0013	1	6.74	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
13378	dirMS_041712_NAR_50mM_plus2.9916.9916.3	3	8.59	1	4.84E+05		(K)TAVCDIP	(K)T A|V/C D/I/P/P R G L K(M)	C:Carbamidomethylation	119.48	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
13379	dirMS_041712_NAR_20mM_minus.13251.13251.3	3	8.58	0	7.44E+04		(R)GNPTVE	(R)G N P T/V E V/D L F T S K(G)		183.13	469.5754	1406.716	-0.0045	-3.2	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
13380	dirMS_041712_NAR_30mM_minus2.7239.7239.2	2	8.58	0	1.16E+05		(K)MQAVQ	(K)M Q/A|V|Q E A T\R(L)		94	517.257	1033.509	-0.0028	-2.7	5.75	533778	5.74	HUMAN	Q15149	Plectin
13381	dirMS_041712_NAR_50mM_minus2.7233.7233.3	3	8.58	1	1.49E+05		(R)IAECSSQ	(R)I/A|E C/S S Q L A E E E E K A K(N)	C:Carbamidomethylation	108.03	607.9557	1821.853	-0.0009	-0.5	4.32	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
13382	dirMS_041712_NAR_50mM_minus2.9603.9603.3	3	8.58	0	1.73E+05	M329m	(K)SNmGHP	(K)S N|m G H/P E/P\A|S G L A A L A K(V)	m:Oxidized methionine	122.73	556.279	1650.827	15.9956	0.4	6.47	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
13383	dirMS_041712_NAR_60mM_minus.15289.15289.3	3	8.58	1	2.01E+05		(R)LYSILGT	(R)L Y|S\I/L G T T/L K D E G K(L)		144.85	513.2854	1537.847	-0.0056	-3.6	6.07	66876.9	6.17	HUMAN	O75083	WD repeat-containing protein 1
13384	dirMS_041712_NAR_60mM_minus.15630.15630.3	3	8.58	1	2.57E+04		(K)SFEERVE	(K)S/F/E E R V E/T T V T S L K(V)		146.95	542.6247	1625.838	0.0215	13.2	4.78	18660.8	5.58	HUMAN	E9PNK6	Tumor protein D53
13385	dirMS_041712_NAR_120mM_plus.9165.9165.3	3	8.58	0	1.54E+05		(R)VTAIHID	(R)V/T A\I/H I D/P A/T H/R(Q)		101.28	444.2411	1330.723	-0.0139	-10.4	6.89	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
13386	dirMS_041712_NAR_20mM_plus.14864.14864.2	2	8.58	0	6.30E+04		(K)LLIIGDSG	(K)L L/I\I/G/D/S G V G/K(S)		173.82	536.3211	1071.641	-0.0059	-5.5	5.84	21499.1	9.02	HUMAN	F5H157	Ras-related protein Rab-35 (Fragment)
13387	dirMS_041712_NAR_20mM_plus.18275.18275.3	3	8.58	0	3.15E+05		(R)AAVEEG	(R)A A\V E E G I/V L/G|G G/C/A/L L R(C)	C:Carbamidomethylation	198.02	562.3058	1684.905	-0.0022	-1.3	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
13388	dirMS_041712_NAR_20mM_plus.19062.19062.3	3	8.58	0	2.07E+05		(K)TLETQSA	(K)T L E T Q S\A L/G/P/A/L Q/A A F/K(L)		202.57	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
13389	dirMS_041712_NAR_20mM_plus.9324.9324.2	2	8.58	0	1.86E+05		(K)SVTNED	(K)S V/T N/E/D V/T Q/E E L G G A K(T)		136	838.9014	1676.797	-0.0018	-1.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
13390	dirMS_041712_NAR_20mM_plus.9517.9530.2	2	8.58	0	3.05E+05		(K)LVLVGDG	(K)L V|L|V|G D/G G T G K(T)		137.35	508.292	1015.578	-0.0015	-1.5	5.84	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
13391	dirMS_041712_NAR_30mM_plus2.13202.13222.2	2	8.58	0	6.34E+05		(K)QSLPPG	(K)Q S|L/P/P G L A V/K(E)		122.8	505.3008	1009.604	-0.0097	-9.6	8.75	8274.8	10.19	HUMAN	P63173	60S ribosomal protein L38
13392	dirMS_041712_NAR_30mM_plus2.20468.20468.2	2	8.58	0	9.51E+04		(K)TENLLGS	(K)T E/N\L|L/G/S Y F/P K(K)		161.23	634.8311	1268.652	0.0028	2.2	5.66	28772.3	6.28	HUMAN	A6NJG9	Proteasome activator complex subunit 1
13393	dirMS_041712_NAR_30mM_plus2.21155.21155.2	2	8.58	0	1.02E+05		(K)VFSIGPV	(K)V F|S I/G/P\V F R(A)		164.3	511.2941	1021.583	-0.002	-2	9.72	57534.6	6.11	HUMAN	P14868	Aspartate--tRNA ligase, cytoplasmic
13394	dirMS_041712_NAR_30mM_plus2.7567.7567.2	2	8.58	0	6.31E+05		(K)SFQQSSL	(K)S F/Q|Q S/S L/S/R(D)		93.8	520.2659	1039.517	0.0078	7.5	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
13395	dirMS_041712_NAR_40mM_plus2.10773.10773.3	3	8.58	0	1.77E+05		(K)MAPVPL	(K)M A|P V/P/L D D S N R P A/S L T K(D)		128.32	604.6467	1811.932	-0.0065	-3.6	5.71	53030.7	11.3	HUMAN	E9PJA7	Bcl-2-associated transcription factor 1
13396	dirMS_041712_NAR_50mM_plus2.10224.10327.3	3	8.58	0	3.78E+05		(R)MVQVH	(R)M/V\Q V H E/L/S C E/G I S K(S)	C:Carbamidomethylation	121.6	539.5992	1616.777	0.006	3.7	5.38	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
13397	dirMS_041712_NAR_60mM_plus.11159.11159.3	3	8.58	1	4.49E+05	M230m M	(R)mSmKEV	(R)m S m K E V D\E\Q|M/L/N/V Q N K(N)	m:Oxidized methionine	115.73	652.6326	1923.897	31.986	-2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13398	dirMS_041712_NAR_120mM_minus.4537.4537.2	2	8.57	0	7.49E+05		(R)HSDGNL	(R)H/S|D G N L\C/V|K(V)	C:Carbamidomethylation	73.97	515.2423	1029.478	-0.0009	-0.9	6.74	7781.8	6.82	HUMAN	E9PE20	Signal recognition particle 9 kDa protein
13399	dirMS_041712_NAR_120mM_minus.8280.8280.3	3	8.57	1	1.11E+05		(K)QLELRQ	(K)Q/L E/L R Q/E E E/R(R)		99.6	443.8975	1329.676	0.0022	1.7	4.49	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
13400	dirMS_041712_NAR_120mM_minus.8703.8809.2	2	8.57	1	1.51E+06	M174m	(R)VKYETEL	(R)V/K|Y E|T E L A m R(Q)	m:Oxidized methionine	101.97	628.3209	1239.64	15.9943	-0.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13401	dirMS_041712_NAR_20mM_minus.12770.12770.2	2	8.57	0	2.43E+05	M179m M	(K)mFVLDE	(K)m F\V|L|D/E/A D\E m L S R(G)	m:Oxidized methionine	176.93	794.3534	1555.713	31.9864	-2.1	3.91	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
13402	dirMS_041712_NAR_20mM_minus.14378.14378.2	2	8.57	0	2.36E+05		(K)DAGVIAG	(K)D A\G\V|I/A|G L N V L R(I)		198.13	599.3503	1197.695	-0.0017	-1.4	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like

13403	dirMS_041712_NAR_30mM_minus2.15282.15282.2	2	8.57	0	6.32E+05		(R)YPVNSV	(R)Y/P/V|N S V N I/L K(A)		136.78	573.8282	1146.652	-0.0026	-2.3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
13404	dirMS_041712_NAR_30mM_minus2.7334.7334.2	2	8.57	0	1.61E+05		(R)AQAAGS	(R)A Q|A|A/G\S S V L R(E)		94.8	480.2603	959.527	-0.0135	-14.1	9.79	38843.2	6.48	HUMAN	Q96EK9	Protein KTI12 homolog
13405	dirMS_041712_NAR_40mM_minus2.13726.13726.3	3	8.57	0	1.22E+05		(R)VAAGLP	(R)V A|A G\L|P P I/L V H T D A A Q A L G K(Q)		164.87	648.0401	1942.112	-0.0063	-3.2	6.71	17974.2	4.97	HUMAN	C9JNL5	Selenocysteine lyase (Fragment)
13406	dirMS_041712_NAR_50mM_minus2.12714.12714.3	3	8.57	0	1.03E+06	M114m M:	(R)AGKPVIC	(R)A G K\P V I|C\A T\Q/m/L\E S m/I K(K)	C:Carbamidomethylation m:Oxid	139.93	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
13407	dirMS_041712_NAR_50mM_minus2.13512.13512.3	3	8.57	1	1.88E+05		(R)LAIKLPD	(R)L A/I K\L/P D D Q I P K(T)		145.48	450.9376	1350.799	-0.0009	-0.7	5.96	26413	9.18	HUMAN	B1APP6	6-phosphofructokinase type C (Fragment)
13408	dirMS_041712_NAR_50mM_minus2.7878.7878.3	3	8.57	1	1.50E+05		(K)TAVCDIP	(K)T/A|V/C D I/P P R G L K(M)	C:Carbamidomethylation	111.93	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
13409	dirMS_041712_NAR_50mM_minus2.9339.9339.3	3	8.57	0	4.40E+04	M247m	(K)AQAGEG	(K)A Q|A|G/E G V R P S P m Q L E L R(M)	m:Oxidized methionine	121.08	618.9899	1838.954	16.001	3.3	6.19	30809	6.18	HUMAN	F2Z2Y4	Pyridoxal kinase
13410	dirMS_041712_NAR_60mM_minus.8668.8668.3	3	8.57	0	2.74E+05		(R)LAQGHT	(R)L A/Q G H/T/T V/D E L A R(R)		107.93	470.9153	1410.734	-0.0022	-1.6	5.32	533778	5.74	HUMAN	Q15149	Plectin
13411	dirMS_041712_NAR_120mM_plus.5971.5971.4	4	8.57	2	5.37E+05		(R)KTGQAP	(R)K T G Q\A/P/G Y/S/Y/T A A N K N K(G)		83.92	450.4826	1798.908	0.0003	0.2	9.83	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
13412	dirMS_041712_NAR_120mM_plus.7581.7581.2	2	8.57	1	1.19E+06		(R)AQYDEL	(R)A Q|Y D/E/L A R K(N)		93.32	547.2874	1093.564	0.0039	3.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13413	dirMS_041712_NAR_120mM_plus.8134.8134.3	3	8.57	0	7.47E+05		(K)LFNHAN	(K)L/F/N H/A N Q E/V Q R(H)		96.6	452.5653	1355.681	-0.0001	-0.1	6.75	87537	9.67	HUMAN	Q9Y446	Plakophilin-3
13414	dirMS_041712_NAR_30mM_plus2.22747.22747.2	2	8.57	0	1.80E+04		(R)IDLAVLL	(R)I/D\L A/V\L/L G K(T)		177.12	471.3029	941.603	-0.0045	-4.7	5.84	113668.7	6.2	HUMAN	F8W726	Ubiquitin-associated protein 2-like
13415	dirMS_041712_NAR_30mM_plus2.9690.9690.2	2	8.57	0	7.42E+05		(K)EAESSPF	(K)E A E/S/S/P/F V E/R(L)		105.1	575.7726	1150.537	0.0004	0.4	4.25	92752.5	4.76	HUMAN	P14625	Endoplasmin
13416	dirMS_041712_NAR_50mM_plus2.11311.11311.3	3	8.57	1	3.48E+05		(K)DLFPYEE	(K)D L/F/P Y/E E/S|K E/K(F)		127.05	462.2257	1384.663	-0.0005	-0.4	4.41	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
13417	dirMS_041712_NAR_50mM_plus2.13183.13183.3	3	8.57	1	1.00E+06		(K)ASLAETD	(K)A/S|L/A E/T D K/I T L E\V A K(L)		137.4	530.2925	1588.879	-0.0163	-10.2	4.68	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
13418	dirMS_041712_NAR_50mM_plus2.7204.7204.3	3	8.57	0	1.68E+05		(R)SGSSQEL	(R)S G/S S/Q/E/L D V/K/P S A S P Q E R(S)		103.85	634.6443	1901.92	-0.0016	-0.8	4.68	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
13419	dirMS_041712_NAR_50mM_plus2.9072.9072.3	3	8.57	1	3.16E+05		(K)VLLQSKD	(K)V L|L/Q S K D Q\I/T A G/N A A R(K)		114.58	562.315	1684.934	-0.0036	-2.1	8.72	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
13420	dirMS_041712_NAR_60mM_plus.20830.20830.3	3	8.57	1	1.40E+05		(K)TFVNITP	(K)T F/V N/I|T/P A E V G V L V G K D R(S)		170.55	639.0248	1915.065	-0.0049	-2.6	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
13421	dirMS_041712_NAR_60mM_plus.21607.21613.3	3	8.57	1	7.08E+05		(K)EIIDLVLD	(K)E I|I/D/L V L D/R/I R(K)		180.73	452.2733	1354.805	0.0001	0.1	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
13422	dirMS_041712_NAR_60mM_plus.9367.9367.2	2	8.57	0	1.98E+06		(R)IGAEVYH	(R)I/G/A/E V/Y H\N L K(N)		107.55	572.3143	1143.616	0.0056	4.9	6.75	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
13423	dirMS_041712_NAR_120mM_minus.11015.11166.3	3	8.56	0	5.83E+05		(R)GLHQSIE	(R)G L/H\Q S\I|E E/F/R(A)		114.27	405.8796	1215.612	0.0126	10.4	5.4	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
13424	dirMS_041712_NAR_120mM_minus.16877.16877.3	3	8.56	1	5.46E+05	S155s	(R)ISVEGsF	(R)I/S/V E G s F L/A/V K/R(L)	s:Phosphorylated S	146.88	462.5714	1305.753	79.9471	-13.9	8.75	40893.7	9.8	HUMAN	Q6ZSC3	RNA-binding protein 43
13425	dirMS_041712_NAR_20mM_minus.8526.8526.2	2	8.56	0	1.29E+04		(R)YEIEETET	(R)Y E|I/E E T E/T V T K(S)		134.38	671.3246	1341.642	-0.0001	-0.1	4.09	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
13426	dirMS_041712_NAR_30mM_minus2.14636.14636.2	2	8.56	0	1.89E+05		(K)WIWFEN	(K)W|I|W F E N S|K(N)		133.52	555.2675	1109.542	-0.0137	-12.4	6	224627.6	6.68	HUMAN	B5MCY1	Uncharacterized protein (Fragment)
13427	dirMS_041712_NAR_30mM_minus2.16075.16075.2	2	8.56	0	2.24E+04		(K)SEGGFIW	(K)S E|G/G F/I/W/A C K(N)	C:Carbamidomethylation	141.03	577.7702	1154.53	0.0032	2.8	5.72	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
13428	dirMS_041712_NAR_30mM_minus2.16723.16723.2	2	8.56	0	2.30E+05		(K)NAAGAL	(K)N A|A|G A L D L/L K(E)		144.35	493.2881	985.568	0.0013	1.3	5.84	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
13429	dirMS_041712_NAR_40mM_minus2.13089.13089.3	3	8.56	1	7.25E+04		(R)VTTVTEI	(R)V T/T V/T E I/G K/D V|I/G L R(I)		160.8	534.3113	1600.927	-0.0075	-4.7	6.04	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
13430	dirMS_041712_NAR_50mM_minus2.10341.10341.3	3	8.56	0	7.23E+04		(R)LTSPIVST	(R)L T|S P I/V S T/H L D|T R(N)		127.37	480.6	1439.785	0.0002	0.1	6.74	58760.2	5.26	HUMAN	Q6ZTN6	Ankyrin repeat domain-containing protein 13D
13431	dirMS_041712_NAR_50mM_minus2.17035.17035.3	3	8.56	0	2.33E+05		(K)TVSGVN	(K)T V|S/G V N G P/L V I L/D H V K(V)		164.72	549.9835	1647.943	-0.0069	-4.2	6.41	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
13432	dirMS_041712_NAR_50mM_minus2.17521.17521.3	3	8.56	0	4.20E+05		(K)VAHALA	(K)V A H A L A E\G\L G\V I/A C\I G/E K(L)	C:Carbamidomethylation	168.75	603.3247	1807.974	-0.0139	-7.7	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
13433	dirMS_041712_NAR_60mM_minus.15640.15640.3	3	8.56	1	5.80E+05	M81m	(K)EVNKFQ	(K)E V/N K F\Q m/A/Y/S N|L L R(A)	m:Oxidized methionine	146.75	576.9619	1712.879	15.9923	-1.5	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
13434	dirMS_041712_NAR_60mM_minus.15672.15672.3	3	8.56	1	3.64E+05		(K)KANLQID	(K)K A N L\Q I D Q\I|N/T D/L N L/E R(S)		147.98	666.6911	1998.061	-0.0027	-1.3	4.56	227783.5	5.5	HUMAN	P35579	Myosin-9
13435	dirMS_041712_NAR_60mM_minus.16081.16081.3	3	8.56	1	2.70E+05		(K)ELKIDIIP	(K)E L K I D I\I|P N/P/Q E R(T)		149.07	522.2935	1564.869	-0.0034	-2.2	4.68	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
13436	dirMS_041712_NAR_120mM_plus.11000.11000.3	3	8.56	0	1.35E+06		(R)GSAVHQ	(R)G S/A/V/H Q L/S E E/L R(C)		110.93	442.5657	1325.681	0.0017	1.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
13437	dirMS_041712_NAR_20mM_plus.10427.10427.2	2	8.56	0	1.08E+05		(K)VQISPDS	(K)V/Q\I/S/P D S/G G L P E/R(S)		144.47	677.8458	1354.696	-0.0118	-8.7	4.37	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
13438	dirMS_041712_NAR_20mM_plus.14669.14669.2	2	8.56	0	3.89E+04	M185m	(K)LAVNmV	(K)L/A\V/N m/V|P F P R(L)	m:Oxidized methionine	172.75	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
13439	dirMS_041712_NAR_20mM_plus.8873.8873.2	2	8.56	0	9.66E+05	M239m	(K)EITALAP	(K)E I/T A/L/A/P/S T m K(I)	m:Oxidized methionine	132.4	589.309	1161.618	15.9923	-2.2	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
13440	dirMS_041712_NAR_30mM_plus2.4214.4214.2	2	8.56	0	5.38E+05	M558m	(R)mGANN	(R)m/G|A/N N L\E/R(M)	m:Oxidized methionine	70.05	460.7158	904.431	15.9938	-1.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
13441	dirMS_041712_NAR_30mM_plus2.5935.5935.2	2	8.56	0	3.25E+04		(R)LEGGSG	(R)L E|G G/S/G\G D/S E V Q R(T)		85.37	645.797	1290.592	-0.0053	-4.1	4.14	44954.5	8.44	HUMAN	A8K3Z3	26S protease regulatory subunit 8
13442	dirMS_041712_NAR_40mM_plus2.10966.10966.3	3	8.56	1	9.41E+04	T1551t	(R)MARIILQ	(R)M A/R I/I L Q D E/D V/t T K(I)	t:N-acetylglucosamine (T)	130.8	612.652	1632.863	203.0789	-0.2	4.56	211740	6.46	HUMAN	F8VSZ4	Plexin-A1
13443	dirMS_041712_NAR_50mM_plus2.12269.12269.3	3	8.56	1	2.80E+05		(R)ESDVPLK	(R)E S/D V/P L K\T E/E/F/E V\T K(T)		132.68	584.2981	1750.874	0.0052	3	4.25	18909	6.21	HUMAN	Q969H8	UPF0556 protein C19orf10
13444	dirMS_041712_NAR_50mM_plus2.13231.13231.3	3	8.56	0	2.15E+06		(R)SCTVNIM	(R)S/C|T/V/N I/M\F G\T/P\Q E H/R(N)	C:Carbamidomethylation	138.4	592.9438	1776.816	0.0012	0.7	6.47	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
13445	dirMS_041712_NAR_50mM_plus2.15025.15025.3	3	8.56	1	3.88E+05		(K)LIVAYVD	(K)L I/V/A\Y V D D/L D R R(G)		147.17	483.2728	1447.79	0.0135	9.3	4.43	124127.1	8.81	HUMAN	O14776	Transcription elongation regulator 1
13446	dirMS_041712_NAR_50mM_plus2.6750.6750.3	3	8.56	1	5.64E+05		(K)IVADKDY	(K)I/V|A/D K D Y S V T A/N S/K(I)		101	504.2628	1510.775	-0.0009	-0.6	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
13447	dirMS_041712_NAR_50mM_plus2.7705.7705.3	3	8.56	0	5.89E+04	M144m	(K)GLSSDN	(K)G L|S S D/N K/P m V/N/L/D K(L)	m:Oxidized methionine	106.45	511.9224	1517.763	15.9898	-3.3	5.96	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
13448	dirMS_041712_NAR_60mM_plus.15668.15668.3	3	8.56	1	1.59E+05		(K)LDVSNEL	(K)L D/V S N E/L R R K(I)		138.48	410.5704	1229.696	0.0006	0.5	8.75	122214.1	7.46	HUMAN	P28749	Retinoblastoma-like protein 1
13449	dirMS_041712_NAR_120mM_minus.5194.5194.3	3	8.55	1	3.17E+05		(R)LRAETEQ	(R)L R A E T\E|Q/G/E/Q Q/R(Q)		81.13	482.2432	1444.714	0.0012	0.8	4.79	533778	5.74	HUMAN	Q15149	Plectin
13450	dirMS_041712_NAR_30mM_minus2.12050.12050.2	2	8.55	0	8.77E+05		(R)EYQELM	(R)E Y/Q/E/L/M/N V/K(L)		119	577.2825	1153.556	0.0019	1.7	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
13451	dirMS_041712_NAR_30mM_minus2.6332.6332.2	2	8.55	0	1.91E+04		(K)EVEEDEY	(K)E V|E/E D/E/Y/K(A)		89.48	520.7257	1040.442	0.0023	2.2	3.91	92752.5	4.76	HUMAN	P14625	Endoplasmin
13452	dirMS_041712_NAR_40mM_minus2.11951.11951.3	3	8.55	1	4.89E+04		(R)SLGEIPIV	(R)S L|G E I/P/I V E S E I K K(E)		153.57	514.6302	1541.879	-0.0025	-1.6	4.78	108281.4	5.72	HUMAN	P53618	Coatomer subunit beta
13453	dirMS_041712_NAR_50mM_minus2.12300.12300.3	3	8.55	0	1.00E+05		(K)IVLDNSV	(K)I V|L D N S V/F/S/E H R(N)		138.13	472.5813	1415.728	0.0016	1.1	5.32	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
13454	dirMS_041712_NAR_50mM_minus2.17041.17041.3	3	8.55	0	6.44E+04		(R)ILVTLLH	(R)I/L/V/T L/L/H T L E R(M)		165.27	436.6057	1307.805	-0.002	-1.5	6.75	45212.4	9.41	HUMAN	B7Z233	Acetyl-CoA acetyltransferase, cytosolic
13455	dirMS_041712_NAR_50mM_minus2.6191.6191.3	3	8.55	0	4.44E+05	M434m	(R)LESGmQ	(R)L/E|S G m Q N\M S I H T K(T)	m:Oxidized methionine	97.77	497.9018	1475.698	15.9927	-1.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
13456	dirMS_041712_NAR_120mM_plus.18631.18631.4	4	8.55	0	4.36E+04		(R)LGWDPK	(R)L/G\W D P K/P/G E/G H L/D A L L R(G)		150.98	469.253	1873.992	-0.0017	-0.9	5.38	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
13457	dirMS_041712_NAR_20mM_plus.13613.13613.2	2	8.55	0	5.50E+04		(K)IFVGGLS	(K)I F/V/G G/L S/P D T/P E E K(I)		165.28	744.8731	1488.758	-0.0191	-12.8	4.14	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
13458	dirMS_041712_NAR_20mM_plus.14663.14664.2	2	8.55	0	2.11E+05		(K)VSTLPAIT	(K)V/S|T/L/P A I T L K(L)		172.53	521.8283	1042.651	-0.0013	-1.3	8.72	20599.3	9.19	HUMAN	H7C1V0	Cathepsin D light chain (Fragment)
13459	dirMS_041712_NAR_20mM_plus.16248.16248.3	3	8.55	0	1.32E+05		(R)LLDAQLA	(R)L L D A Q\L A T G G\I/V D/P R(L)		183.53	513.6218	1538.854	-0.0028	-1.8	4.21	533778	5.74	HUMAN	Q15149	Plectin
13460	dirMS_041712_NAR_20mM_plus.17688.17688.3	3	8.55	0	1.12E+04		(R)IINEPTA	(R)I I/N E\P T A\A A\I|A/Y G L D/R(T)		193.42	563.3055	1687.901	0.0006	0.3	4.37	25598.3	6.45	HUMAN	E7EP11	Heat shock 70 kDa protein 1A/1B
13461	dirMS_041712_NAR_20mM_plus.8108.8108.2	2	8.55	0	2.09E+05		(R)FGQGGA	(R)F G/Q/G G A/G/P V|G G Q G P R(G)		125.22	671.3361	1341.666	-0.0009	-0.7	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
13462	dirMS_041712_NAR_30mM_plus2.14699.14699.2	2	8.55	0	6.45E+05		(R)TFEDFVR	(R)T F|E|D/F V R(I)		130.13	457.225	913.441	0.0013	1.4	4.37	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
13463	dirMS_041712_NAR_30mM_plus2.21760.21923.2	2	8.55	0	1.28E+05		(K)YLFTLIR	(K)Y/L|F/T/L I/R(A)		170.02	463.2766	925.551	-0.0046	-5	8.75	103914.7	5.19	HUMAN	B4DZ67	Nuclear pore complex protein Nup107
13464	dirMS_041712_NAR_40mM_plus2.11358.11358.3	3	8.55	1	4.34E+04		(R)SASELTA	(R)S A/S E L/T/A G A E A/E A E E V K T G K(C)		132.83	659.9938	1977.961	0.0057	2.9	4.32	49419.7	5.36	HUMAN	Q9H0U9	Testis-specific Y-encoded-like protein 1
13465	dirMS_041712_NAR_50mM_plus2.18674.18674.3	3	8.55	0	3.49E+05		(R)LLLDGAP	(R)L L/L/D G A/P L I A I H K(A)		165.83	458.622	1373.852	-0.0001	0	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
13466	dirMS_041712_NAR_50mM_plus2.20692.20692.3	3	8.55	1	1.36E+05		(R)GGPNIIT	(R)G/G P/N|I/I T L/A D I V K D/P V S/R(T)		176.98	622.3526	1865.049	-0.0058	-3.1	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
13467	dirMS_041712_NAR_50mM_plus2.22298.22298.3	3	8.55	0	1.52E+06		(R)DALSDLA	(R)D A/L/S\D/L/A L H/F L N K(M)		191.78	486.2644	1456.78	-0.0008	-0.6	5.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
13468	dirMS_041712_NAR_50mM_plus2.7212.7212.3	3	8.55	1	3.91E+04		(R)IVEQDTM	(R)I/V/E Q D T M/P P K/G V/R(H)		103.58	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
13469	dirMS_041712_NAR_50mM_plus2.9360.9360.3	3	8.55	0	2.91E+05		(K)GLSSDN	(K)G L/S/S/D N K/P M V\N L D K(L)		116.17	506.5928	1517.763	0.001	0.7	5.96	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
13470	dirMS_041712_NAR_60mM_plus.11558.11558.3	3	8.55	1	4.83E+05		(R)GMDLQ	(R)G M/D L Q/P/G N A L K/R(F)		118	433.8981	1299.684	-0.004	-3.1	8.75	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
13471	dirMS_041712_NAR_60mM_plus.17198.17198.3	3	8.55	0	2.04E+05		(K)THLPGFV	(K)T H\L\P G\F|V|E Q A E/A L K(A)		147.35	513.9442	1539.817	0.0015	1	5.37	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
13472	dirMS_041712_NAR_60mM_plus.8680.8680.3	3	8.55	1	1.65E+05		(R)SSGGSYR	(R)S S|G G S/Y R D S Y D S Y A/T H N/E(-)		103.02	665.9403	1995.795	0.0112	5.6	4.81	18647.7	9.51	HUMAN	Q14011	Cold-inducible RNA-binding protein
13473	dirMS_041712_NAR_30mM_minus2.16204.16204.2	2	8.54	0	8.44E+03		(K)EQFLDG	(K)E Q/F/L/D/G D G W/T/S R(W)		142.25	705.8174	1410.628	-0.0009	-0.6	4.03	28545.1	4.5	HUMAN	K7EJB9	Calreticulin (Fragment)
13474	dirMS_041712_NAR_30mM_minus2.6233.6233.2	2	8.54	0	9.08E+04		(R)EAEEVYR	(R)E A/E/E/V/Y/R(N)		88.12	448.2136	895.416	0.0043	4.8	4.25	54793.4	10.51	HUMAN	B7Z4Q3	Putative RNA-binding protein Luc7-like 2
13475	dirMS_041712_NAR_30mM_minus2.8558.8689.2	2	8.54	0	5.08E+05		(K)ALELDSN	(K)A L|E|L|D/S N N\E K(G)		101.4	566.7699	1132.548	-0.0155	-13.7	4.14	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
13476	dirMS_041712_NAR_40mM_minus2.8913.8913.3	3	8.54	1	5.45E+04		(R)IVAPGKG	(R)I/V|A|P G K G I L A A/D E/S T G S I A K(R)		135.25	633.355	1898.059	-0.0089	-4.7	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
13477	dirMS_041712_NAR_50mM_minus2.14678.14678.3	3	8.54	0	8.03E+04	M1280m	(R)QARPTY	(R)Q A R P T\Y A|T/A/m|L Q/S L L K(-)	m:Oxidized methionine	151.87	603.3247	1791.979	15.981	-7.7	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
13478	dirMS_041712_NAR_50mM_minus2.16479.16479.3	3	8.54	1	1.87E+04		(R)EVQLEEL	(R)E V/Q|L/E E L E A A R D L V/S K(E)		161.82	610.3273	1828.965	0.0023	1.2	4.25	45984.6	6.24	HUMAN	B4E1G6	Galactokinase
13479	dirMS_041712_NAR_50mM_minus2.17889.17889.3	3	8.54	0	2.88E+05		(K)HNQLPL	(K)H N Q L\P L\V|I\E\F/T E/Q/T/A/P K(I)		170.08	655.6843	1965.044	-0.0057	-2.9	5.4	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
13480	dirMS_041712_NAR_60mM_minus.11892.11892.3	3	8.54	1	3.74E+05		(K)NQVAM	(K)N Q|V|A/M/N P T N T V/F D A K R(L)		126.55	602.6357	1805.896	-0.0037	-2.1	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
13481	dirMS_041712_NAR_60mM_minus.8360.8360.3	3	8.54	1	2.30E+04		(R)VASSTLL	(R)V/A/S S/T\L L D/D R R(N)		106.95	411.5582	1232.659	0.0007	0.6	5.93	108806.2	4.84	HUMAN	O60763	General vesicular transport factor p115
13482	dirMS_041712_NAR_60mM_minus.9798.9798.2	2	8.54	1	4.41E+05		(R)LQAEIEG	(R)L Q|A E|I/E/G L/K G Q R(A)		114.13	671.3768	1341.748	-0.0022	-1.6	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
13483	dirMS_041712_NAR_20mM_plus.13891.13891.2	2	8.54	0	1.26E+05	M62m	(R)DASLmV	(R)D A/S L m/V/T N D/G A T I L/K(N)	m:Oxidized methionine	167.72	782.8922	1548.794	15.9833	-7.4	4.21	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
13484	dirMS_041712_NAR_20mM_plus.15585.15585.2	2	8.54	0	8.27E+04		(-)SDVLELT	(-)S D\V L/E/L|T/D D N F E S R(I)		179.25	820.3754	1639.745	-0.0011	-0.6	3.77	13747.3	6.8	HUMAN	H7BZJ3	Thioredoxin (Fragment)
13485	dirMS_041712_NAR_20mM_plus.18917.18917.2	2	8.54	0	1.05E+05		(K)DTSYLFIT	(K)D T S Y/L|F\I/T/G P D V V/K(S)		201.92	777.9049	1554.805	-0.0025	-1.6	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
13486	dirMS_041712_NAR_20mM_plus.7931.7931.2	2	8.54	0	3.83E+05	M239m	(K)EVDEQm	(K)E V|D/E Q m\L N V/Q/N K(N)	m:Oxidized methionine	125	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13487	dirMS_041712_NAR_30mM_plus2.10532.10532.3	3	8.54	0	1.53E+05		(R)QQEELLA	(R)Q Q E E\L\L/A/E/E/N Q R(L)		108.58	496.2449	1486.713	0.0069	4.7	4.09	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
13488	dirMS_041712_NAR_30mM_plus2.12843.12843.2	2	8.54	0	3.36E+05		(K)YEELQSL	(K)Y/E|E|L Q/S L/A G/K(H)		120.4	569.2905	1137.579	-0.0049	-4.3	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
13489	dirMS_041712_NAR_30mM_plus2.14261.14261.2	2	8.54	0	9.48E+05	M320m	(K)YmACCL	(K)Y m|A C C L/L/Y R(G)	C:Carbamidomethylation m:Oxid	127.2	633.2777	1249.553	15.9955	0.5	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
13490	dirMS_041712_NAR_30mM_plus2.8514.8514.2	2	8.54	0	2.28E+05		(K)DVDEAY	(K)D V|D\E/A\Y M/N K(V)		98.55	542.7341	1084.462	-0.0006	-0.6	4.03	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
13491	dirMS_041712_NAR_40mM_plus2.18069.18069.3	3	8.54	0	9.77E+04	M159m	(R)SVAAIHP	(R)S V|A A I H/P S L E I P m L I/P K(E)	m:Oxidized methionine	172.8	611.3472	1816.04	15.9869	-4.4	6.47	31606.3	6.72	HUMAN	B4E329	Phosphoribosyl pyrophosphate synthase-associated protein 2
13492	dirMS_041712_NAR_50mM_plus2.20251.20251.3	3	8.54	1	1.34E+05		(R)TTPTFFP	(R)T T|P/T/F F P K D I L T L R(L)		174.85	550.6455	1649.926	-0.0042	-2.5	8.41	23437.3	8.14	HUMAN	I3L0S5	76 kDa lysosomal alpha-glucosidase (Fragment)
13493	dirMS_041712_NAR_50mM_plus2.20670.20670.3	3	8.54	1	1.70E+05		(R)VNSKFDT	(R)V/N|S K F D T\I|Y/Q I/L/L K(K)		177.62	561.3209	1681.952	-0.0042	-2.5	8.47	72626.7	9.13	HUMAN	Q14258	E3 ubiquitin/ISG15 ligase TRIM25
13494	dirMS_041712_NAR_50mM_plus2.21790.21790.3	3	8.54	1	2.08E+05		(R)KVPELM	(R)K V P E L\M E\M|F L/P A T K(N)		185.52	545.2925	1633.869	-0.0063	-3.8	6.14	95051	6.63	HUMAN	B3KXW5	AP-1 complex subunit gamma-1
13495	dirMS_041712_NAR_60mM_plus.12213.12213.3	3	8.54	1	1.07E+06		(K)AVPREEL	(K)A V|P R E E L F V/T/S/K(L)		120.7	459.257	1375.758	-0.0015	-1.1	6.19	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
13496	dirMS_041712_NAR_60mM_plus.14415.14416.3	3	8.54	1	1.69E+05		(R)VSLEEIYS	(R)V/S/L E E I/Y/S G C T\K/K(M)	C:Carbamidomethylation	131.98	505.2598	1513.757	0.0082	5.4	6.11	27186.8	9.34	HUMAN	B4DX52	DnaJ homolog subfamily B member 1
13497	dirMS_041712_NAR_60mM_plus.15147.15272.3	3	8.54	1	2.39E+05		(R)DGRGAL	(R)D G R G A L Q N\I\I|P A S T G A A K(A)		136.5	580.6497	1739.94	-0.0053	-3.1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
13498	dirMS_041712_NAR_60mM_plus.18463.18500.3	3	8.54	1	1.61E+05		(R)CRVDLP	(R)C R V D L|P|L|A V/L S K(M)	C:Carbamidomethylation	154.13	457.599	1370.782	0	0	8.75	7765.6	8.23	HUMAN	H3BSA6	dCTP pyrophosphatase 1
13499	dirMS_041712_NAR_60mM_plus.5323.5323.2	2	8.54	0	2.28E+04		(R)YIDTEHG	(R)Y I/D/T E/H\G/G S Q A R(F)		85.4	667.3076	1333.613	-0.0052	-3.9	5.32	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
13500	dirMS_041712_NAR_120mM_minus.13769.13769.3	3	8.53	1	3.29E+05		(R)EMDRET	(R)E\M D/R E T\L/I/D/V\A R(T)		129.65	483.2462	1447.721	0.0031	2.1	4.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
13501	dirMS_041712_NAR_120mM_minus.4719.4719.3	3	8.53	1	3.47E+05		(K)AGADEE	(K)A/G/A D/E E R A E T A/R(L)		76.67	425.8687	1275.592	-0.0008	-0.7	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
13502	dirMS_041712_NAR_120mM_minus.6816.6816.2	2	8.53	0	4.89E+05		(K)HQPTAII	(K)H Q|P T A I|I A/K(T)		91.83	489.7898	978.573	-0.0008	-0.8	8.76	63448.4	7.29	HUMAN	B4E022	Transketolase
13503	dirMS_041712_NAR_120mM_minus.8727.8727.3	3	8.53	0	7.90E+05		(R)QYDISDP	(R)Q/Y/D/I/S/D/P Q/R P R(L)		101.62	458.8971	1374.676	0.0007	0.5	5.96	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
13504	dirMS_041712_NAR_20mM_minus.13853.13853.2	2	8.53	0	3.08E+05		(K)LGGSAV	(K)L G G\S A V|I/S L E G K|P L(-)		188.9	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
13505	dirMS_041712_NAR_20mM_minus.7007.7007.2	2	8.53	0	4.38E+05	M281m	(R)AEAESm	(R)A E|A E S/m Y Q/I/K(Y)	m:Oxidized methionine	117.82	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
13506	dirMS_041712_NAR_30mM_minus2.19145.19145.2	2	8.53	0	7.98E+04		(R)ALFLIPR	(R)A/L|F L I/P R(N)		158.92	415.2685	829.529	0.0003	0.3	9.79	40728.4	6.05	HUMAN	C9J338	TRAF2 and NCK-interacting protein kinase (Fragment)
13507	dirMS_041712_NAR_50mM_minus2.17801.17801.3	3	8.53	1	3.97E+05		(R)LKLPSIPL	(R)L K L P S I\P L\V|P V S A Q K(R)		169.73	530.669	1589.999	-0.0064	-4.1	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
13508	dirMS_041712_NAR_50mM_minus2.18402.18402.3	3	8.53	0	1.54E+04		(K)ALESPER	(K)A L|E/S/P E R P F L A\I L G/G A K(V)		176.02	590.3356	1768.996	-0.0033	-1.9	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
13509	dirMS_041712_NAR_50mM_minus2.7673.7673.3	3	8.53	1	3.75E+04		(K)NSDEAD	(K)N S/D E A/D L V/P A K E A N V K(C)		110.73	567.289	1699.85	0.0027	1.6	4.32	19439.5	4.97	HUMAN	B5MD17	Chromobox protein homolog 1 (Fragment)
13510	dirMS_041712_NAR_50mM_minus2.9127.9127.3	3	8.53	1	4.63E+04	M621m	(R)mVDVVE	(R)m V/D/V V E/K/E D V N E/A I R(L)	m:Oxidized methionine	120.13	587.962	1745.874	15.9976	1.5	4.18	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
13511	dirMS_041712_NAR_60mM_minus.14405.14405.3	3	8.53	0	3.95E+05		(K)LPNLTHL	(K)L/P N L T H/L/N L S G N K(L)		140.27	474.2636	1420.791	-0.0144	-10.2	8.76	18070.1	3.52	HUMAN	Q5T6W8	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member B (Fragment)

13512	dirMS_041712_NAR_60mM_minus.8083.8083.3	3	8.53	1	1.18E+05		(K)FAAKGE	(K)F/A/A K G E G Q|L/G P A E/R(A)		105.53	477.5852	1430.739	0.0024	1.7	6.14	96306.4	6.41	HUMAN	P13639	Elongation factor 2
13513	dirMS_041712_NAR_120mM_plus.15286.15286.4	4	8.53	1	1.47E+06		(R)VKPAPD	(R)V/K P\A P D E T/S F/S E A L/L K R(N)		133.4	472.7599	1888.017	0.0003	0.2	6.15	43289.6	5.19	HUMAN	Q12905	Interleukin enhancer-binding factor 2
13514	dirMS_041712_NAR_20mM_plus.11268.11268.2	2	8.53	0	1.29E+05		(K)VGLQVV	(K)V/G/L/Q V|V/A V K(A)		150.52	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
13515	dirMS_041712_NAR_20mM_plus.15357.15357.2	2	8.53	0	1.68E+04	M73m	(R)AILVDLE	(R)A I L|V\D L|E|P G T\m D S V R(S)	m:Oxidized methionine	177.98	816.4181	1615.836	15.9929	-1.2	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
13516	dirMS_041712_NAR_20mM_plus.16487.16487.3	3	8.53	0	6.48E+04	M137m M:	(R)IIGATDS	(R)I/I|G A T D S S/G E L/m F L m K(W)	m:Oxidized methionine	185.8	582.2872	1712.86	31.9873	-1.5	4.37	19439.5	4.97	HUMAN	B5MD17	Chromobox protein homolog 1 (Fragment)
13517	dirMS_041712_NAR_20mM_plus.18801.18801.2	2	8.53	0	3.80E+04		(K)EIIDLVLI	(K)E I I/D/L/V/L D R(I)		201.17	543.313	1085.62	-0.0014	-1.3	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
13518	dirMS_041712_NAR_20mM_plus.8603.8603.2	2	8.53	0	1.99E+05		(R)VPPPPPI	(R)V/P|P/P/P P I A R(A)		130.4	472.2851	943.572	-0.0094	-10	9.72	32085.2	8.93	HUMAN	B4DY08	Heterogeneous nuclear ribonucleoproteins C1/C2
13519	dirMS_041712_NAR_30mM_plus2.15113.15298.2	2	8.53	0	4.22E+05		(R)ELFVMA	(R)E L|F/V/M/A/R(E)		132.52	433.2345	865.46	0.0017	2	6.1	44954.5	8.44	HUMAN	A8K3Z3	26S protease regulatory subunit 8
13520	dirMS_041712_NAR_30mM_plus2.15340.15340.2	2	8.53	0	2.76E+05		(R)LLCNFM	(R)L/L/C/N|F M R(Q)	C:Carbamidomethylation	132.95	477.2409	953.47	0.005	5.2	9.75	18685.5	9.45	HUMAN	B4DEV8	Proteasome subunit alpha type
13521	dirMS_041712_NAR_30mM_plus2.16828.16828.2	2	8.53	0	2.83E+05		(R)SIQADG	(R)S I|Q|A D G/L/V W G S S K(L)		140.9	674.3475	1347.69	-0.0026	-1.9	5.55	24934.4	4.5	HUMAN	P24534	Elongation factor 1-beta
13522	dirMS_041712_NAR_50mM_plus2.13738.13738.3	3	8.53	1	1.88E+06		(R)QATKDA	(R)Q A\T K D A G T\I/A/G/L/N/V L R(I)		140	543.3085	1627.913	-0.0016	-1	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
13523	dirMS_041712_NAR_50mM_plus2.14068.14068.3	3	8.53	1	7.15E+05		(R)ALPAVQ	(R)A L/P A/V Q Q N N L D/E D L I R/K(L)		142.6	646.3522	1937.045	-0.003	-1.6	4.56	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
13524	dirMS_041712_NAR_50mM_plus2.18422.18422.3	3	8.53	1	5.37E+05		(K)VIAATNI	(K)V I|A/A T/N R V D I L D/P A L L R(S)		164.52	617.3645	1850.086	-0.0069	-3.7	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
13525	dirMS_041712_NAR_60mM_plus.10504.10504.3	3	8.53	1	8.18E+05		(K)TAVCDIF	(K)T A/V C D\I/P P R G L K(M)	C:Carbamidomethylation	111.95	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
13526	dirMS_041712_NAR_60mM_plus.10659.10659.3	3	8.53	1	3.21E+04		(R)LRQLAEI	(R)L R Q L A E\E D|L/A/Q Q/R(A)		112.7	523.9486	1569.834	-0.0031	-2	4.68	533778	5.74	HUMAN	Q15149	Plectin
13527	dirMS_041712_NAR_60mM_plus.21767.21767.3	3	8.53	0	3.64E+05		(K)LPLGLLL	(K)L/P|L/G L L/L/H P F R(D)		183.05	425.9357	1275.794	-0.001	-0.8	9.75	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
13528	dirMS_041712_NAR_120mM_minus.7473.7473.3	3	8.52	0	1.37E+05		(R)EVRPDT	(R)E V R P D T Q/Y/T G/R(K)		94.9	441.2234	1321.65	0.0061	4.6	6.17	34187.3	9.64	HUMAN	C9K060	Uncharacterized methyltransferase WBSCR22
13529	dirMS_041712_NAR_30mM_minus2.18497.18497.2	2	8.52	0	9.87E+03		(K)LNLGTV	(K)L N|L/G/T V G F Y R(T)		154.28	570.3115	1139.621	-0.005	-4.4	8.75	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
13530	dirMS_041712_NAR_30mM_minus2.8380.8380.2	2	8.52	0	2.70E+04	M496m	(R)YmDLAE	(R)Y m|D|L/A/E N A R(F)	m:Oxidized methionine	100.4	549.7514	1082.494	16.002	6.5	4.37	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
13531	dirMS_041712_NAR_50mM_minus2.11483.11483.3	3	8.52	1	1.22E+05		(K)MLVSGA	(K)M L|V/S G A/G D I/K\L T K(D)		132.95	444.9227	1332.756	-0.002	-1.5	8.35	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
13532	dirMS_041712_NAR_50mM_minus2.14805.14805.3	3	8.52	1	4.43E+04		(R)SLSELES	(R)S L|S/E L E/S L K L P A E S N E K(I)		152.55	625.3311	1873.975	0.0034	1.8	4.49	90274.8	6.92	HUMAN	P22059	Oxysterol-binding protein 1
13533	dirMS_041712_NAR_50mM_minus2.8683.8683.3	3	8.52	1	4.19E+04	M88m	(K)DVDEAY	(K)D V/D E A/Y/m N K V/E L\E/S R(L)	m:Oxidized methionine	117.5	605.2817	1797.832	15.9982	1.8	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
13534	dirMS_041712_NAR_60mM_minus.7537.7537.3	3	8.52	1	5.70E+04		(K)TEADAE	(K)T E|A D|A E/K/T/F E E K(Q)		101.08	466.5515	1397.643	-0.0031	-2.2	4.25	32503.1	5.29	HUMAN	H7BY16	Nucleolin (Fragment)
13535	dirMS_041712_NAR_60mM_minus.8077.8077.3	3	8.52	0	1.29E+05		(K)EAYPDH	(K)E A/Y/P D H T Q F E K(N)		105.03	455.5427	1364.612	0.0018	1.3	4.65	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1
13536	dirMS_041712_NAR_60mM_minus.9700.9700.3	3	8.52	0	3.05E+05		(R)KPLLESG	(R)K\P L L\E|S/G T L G T K(G)		114.13	415.25	1243.726	0.0098	7.9	8.59	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
13537	dirMS_041712_NAR_120mM_plus.12346.12346.4	4	8.52	1	2.14E+06		(K)TLTTVQ	(K)T L T T V Q G I/A D D/Y D K K/K(L)		117.6	449.7412	1795.944	-0.0006	-0.4	5.71	13778.5	7.96	HUMAN	K7EM18	Eukaryotic translation initiation factor 1
13538	dirMS_041712_NAR_20mM_plus.11471.11471.2	2	8.52	0	2.15E+05		(K)VGLQVV	(K)V|G\L Q/V V/A V/K(A)		151.5	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
13539	dirMS_041712_NAR_20mM_plus.15117.15117.2	2	8.52	0	5.88E+04		(R)EQLAIAE	(R)E Q L/A|I/A/E F/A R(S)		176.1	574.312	1147.611	0.0061	5.3	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
13540	dirMS_041712_NAR_20mM_plus.17549.17549.3	3	8.52	0	8.98E+04	M215m	(K)TLNDELI	(K)T L\N D/E L/E I|I E/G m/K(F)	m:Oxidized methionine	193.08	507.5886	1504.756	15.9949	0	4	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
13541	dirMS_041712_NAR_30mM_plus2.20991.20991.2	2	8.52	0	3.86E+05		(K)AIDLFTD	(K)A I|D|L F T D/A/I K(L)		164.47	553.8012	1106.609	-0.0141	-12.7	4.21	18141.9	4.7	HUMAN	F6VDH7	Hsc70-interacting protein (Fragment)
13542	dirMS_041712_NAR_30mM_plus2.21412.21412.2	2	8.52	0	1.58E+05		(R)VFIGNLI	(R)V/F|I G/N/L N T L/V V K(K)		167.38	658.8983	1316.794	-0.0043	-3.3	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
13543	dirMS_041712_NAR_30mM_plus2.8409.8409.2	2	8.52	1	5.70E+05		(K)LSERNLK	(K)L/S|E R/N L K(C)		98.27	430.2487	859.5	-0.0095	-11	8.75	35968	9.26	HUMAN	Q8N5C1	Protein FAM26E
13544	dirMS_041712_NAR_40mM_plus2.15976.15976.3	3	8.52	1	1.24E+05		(K)LFTAESL	(K)L F/T A/E S L/I/G L K|N P E K(S)		160.25	553.9799	1659.932	-0.0065	-3.9	6.14	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
13545	dirMS_041712_NAR_50mM_plus2.16348.16348.3	3	8.52	1	8.73E+04		(K)ESQAKD	(K)E S Q/A K D V I/E/E/Y F/K(C)		152.72	529.2635	1585.774	0.0015	1	4.41	14914.1	6.84	HUMAN	P25398	40S ribosomal protein S12
13546	dirMS_041712_NAR_50mM_plus2.18357.18357.3	3	8.52	1	3.49E+05		(R)GDSVIV	(R)G D|S V/I/V V L R N/P L I A G K(-)		165.37	550.9999	1650.99	-0.005	-3	8.75	6144.3	10.23	HUMAN	K7EJB5	Small nuclear ribonucleoprotein Sm D2
13547	dirMS_041712_NAR_50mM_plus2.21888.21888.3	3	8.52	1	1.23E+04		(R)NNILLEL	(R)N/N/I L L E L/I Q Y D N R E K(R)		186.87	625.6716	1874.997	0.0032	1.7	4.68	62866	5.73	HUMAN	C9IZH7	Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 11 protein
13548	dirMS_041712_NAR_50mM_plus2.7394.7394.3	3	8.52	1	1.96E+05	M32m	(K)GGImLP	(K)G G/I/m L/P E K S Q G K(V)	m:Oxidized methionine	104.6	420.8922	1244.667	15.9953	0.3	8.59	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
13549	dirMS_041712_NAR_60mM_plus.13952.13952.3	3	8.52	0	1.56E+06		(K)LAQANG	(K)L A/Q/A|N/G W G/V/M\V/S H R(S)		129.07	509.2606	1525.769	-0.002	-1.3	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
13550	dirMS_041712_NAR_60mM_plus.14790.14790.3	3	8.52	1	9.63E+04		(R)KFLDGIY	(R)K F\L D G\I\Y/V/S/E/K(G)		133.93	433.5671	1298.699	-0.0123	-9.5	6.07	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
13551	dirMS_041712_NAR_60mM_plus.6812.6812.3	3	8.52	1	6.59E+05		(R)EKVPGG	(R)E K/V\P G G\L|Q/G S Q D/R(G)		94.18	457.576	1370.702	0.0112	8.2	6.17	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
13552	dirMS_041712_NAR_120mM_minus.13896.13896.4	4	8.51	2	5.43E+05		(R)KLVIIEGI	(R)K\L V I\I|E/G D L/E R T E/E/R(A)		129.85	450.7512	1799.986	-0.0032	-1.8	4.58	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
13553	dirMS_041712_NAR_120mM_minus.16890.16890.4	4	8.51	0	8.94E+05		(K)HLEINPL	(K)H L E I N/P D H S\I/I|E/T L R(Q)		146.6	447.4904	1786.945	-0.0049	-2.7	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
13554	dirMS_041712_NAR_30mM_minus2.11782.11782.2	2	8.51	0	5.59E+05	M64m	(K)VmYGFC	(K)V m|Y/G F/C S V K(D)	C:Carbamidomethylation m:Oxid	117.33	553.7611	1090.506	16.0089	12.7	8.56	76925.9	4.46	HUMAN	A8MV58	Drebrin
13555	dirMS_041712_NAR_40mM_minus2.9626.9626.2	2	8.51	0	1.24E+06		(R)VAPEEH	(R)V A/P E E H|P V L L/T E/A\P L N/P K(A)		139.8	977.5343	1954.064	-0.0031	-1.6	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
13556	dirMS_041712_NAR_60mM_minus.10809.10809.3	3	8.51	1	5.44E+05	M239m	(R)MSMKE	(R)M/S/M K E V\D E\Q/m|L/N V\Q|N K(N)	m:Oxidized methionine	119.9	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13557	dirMS_041712_NAR_60mM_minus.16708.16708.3	3	8.51	1	1.72E+05		(K)VSEQGL	(K)V/S|E/Q/G L I E I L K K(V)		152.9	452.9408	1356.81	-0.0018	-1.4	6.11	12899.6	6.59	HUMAN	K7EL31	Programmed cell death protein 5
13558	dirMS_041712_NAR_60mM_minus.18217.18217.3	3	8.51	1	9.62E+04		(K)NIPIPTLI	(K)N I/P I/P T L K D/F A/K(A)		162.68	452.9408	1356.789	0.0193	14.2	8.59	20960.6	7.05	HUMAN	H0YKU1	Tropomodulin-3 (Fragment)
13559	dirMS_041712_NAR_60mM_minus.20125.20125.3	3	8.51	0	4.05E+05		(K)GHYTEG	(K)G H Y T E G A E/L\V|D S V/L/D V/V/R(K)		184.27	653.6647	1958.982	-0.0022	-1.1	4.31	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
13560	dirMS_041712_NAR_60mM_minus.8928.8928.3	3	8.51	0	4.32E+03		(R)TLHSDD	(R)T L H S\D D E G T|V/L/D D S R(A)		109.43	553.919	1659.746	-0.0032	-1.9	4.03	23307.1	5.11	HUMAN	E9PMH2	Peptidyl-prolyl cis-trans isomerase (Fragment)
13561	dirMS_041712_NAR_120mM_plus.8084.8084.2	2	8.51	0	1.42E+06		(R)HQGVM	(R)H Q|G V|M/V/G\M G Q K(D)		96.13	586.2888	1171.571	-0.0007	-0.6	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
13562	dirMS_041712_NAR_120mM_plus.9776.9776.4	4	8.51	2	1.93E+05		(R)LSNKVE	(R)L/S N\K V E A I D/V E E/A K/R(L)		104.45	425.9848	1700.918	-0.0004	-0.2	4.87	11656.4	9.79	HUMAN	E5RHP5	DNA replication licensing factor MCM4 (Fragment)
13563	dirMS_041712_NAR_120mM_plus.9863.9883.3	3	8.51	0	3.61E+05	M140m	(K)HYGPGV	(K)H Y\G/P G\W\V|S m A N A G K(D)	m:Oxidized methionine	104.77	497.5659	1474.69	15.9936	-0.9	8.6	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
13564	dirMS_041712_NAR_20mM_plus.14148.14148.2	2	8.51	0	1.57E+06	M313m	(R)TVQSLEI	(R)T V/Q|S\L/E|I D/L/D/S m R(N)	m:Oxidized methionine	170.15	761.8738	1506.747	15.9935	-0.9	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13565	dirMS_041712_NAR_30mM_plus2.10325.10325.2	2	8.51	0	5.36E+04		(K)TAVCDIF	(K)T A|V|C/D/I/P/P/R(G)	C:Carbamidomethylation	108.98	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
13566	dirMS_041712_NAR_30mM_plus2.6989.6991.2	2	8.51	0	5.05E+05		(K)ISDSEGF	(K)I/S|D/S E/G F K(A)		91.13	441.7168	882.42	0.006	6.8	4.37	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
13567	dirMS_041712_NAR_40mM_plus2.8298.8298.2	2	8.51	1	8.53E+04		(R)KQNDVF	(R)K Q N/D/V/F\G E\A\E|Q(-)		109.63	632.7929	1264.58	-0.0019	-1.5	4.14	51209.4	5	HUMAN	P31150	Rab GDP dissociation inhibitor alpha
13568	dirMS_041712_NAR_50mM_plus2.18187.18187.3	3	8.51	1	5.21E+05		(K)VIAATNI	(K)V I/A|A T N R V D I L/D/P A L L R(S)		164.43	617.3645	1850.086	-0.0069	-3.7	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
13569	dirMS_041712_NAR_50mM_plus2.19908.19908.3	3	8.51	0	2.50E+05		(K)LFLFHTS	(K)L F L F/H T S L|P\I/A E/A/P G K(L)		172.83	580.9943	1740.968	0	0	6.75	108105.4	6.57	HUMAN	E7EP00	Protein transport protein Sec24C
13570	dirMS_041712_NAR_50mM_plus2.21365.21365.3	3	8.51	0	8.95E+04		(K)GAEILEV	(K)G A/E I L/E/V/L/H/S L P A V R(Q)		183.4	535.3092	1603.917	-0.0036	-2.2	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
13571	dirMS_041712_NAR_50mM_plus2.5729.5729.3	3	8.51	1	1.05E+06		(K)TAGPIAS	(K)T A/G|P I/A S\A Q K Q P A G K(V)		91.92	475.5987	1424.786	-0.0041	-2.8	10	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
13572	dirMS_041712_NAR_50mM_plus2.9578.9578.3	3	8.51	0	7.71E+05		(R)DNIQGI	(R)D N|I/Q G I/T K/P A I R(R)		117.22	442.5902	1325.754	0.0025	1.9	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
13573	dirMS_041712_NAR_60mM_plus.10795.10795.2	2	8.51	1	1.07E+06		(R)VKYETEL	(R)V/K|Y/E/T E L A M R(Q)		113.57	620.326	1239.64	0.0045	3.7	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13574	dirMS_041712_NAR_60mM_plus.11153.11153.3	3	8.51	0	8.16E+05		(K)NFYQEH	(K)N F/Y Q E H/P D L A R(R)		116	463.8897	1389.655	0	0	5.32	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
13575	dirMS_041712_NAR_60mM_plus.15571.15571.3	3	8.51	1	2.97E+05	M320m	(K)YmACCL	(K)Y m/A C C L L Y R G D/V V|P K(E)	C:Carbamidomethylation m:Oxid	138.05	620.9638	1844.886	15.9913	-2	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
13576	dirMS_041712_NAR_60mM_plus.6680.6680.3	3	8.51	1	6.89E+05		(R)NKQTYS	(R)N K Q/T Y/S/T\E/P N/N L K(A)		92.93	512.9257	1536.765	-0.0027	-1.8	8.5	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
13577	dirMS_041712_NAR_20mM_minus.14417.14417.2	2	8.5	0	2.52E+05		(R)APGSGL	(R)A/P/G S G L/A/L L/P L K(I)		198.32	568.8551	1136.704	-0.0008	-0.7	8.8	266161	5.68	HUMAN	E9PPU0	Epiplakin
13578	dirMS_041712_NAR_30mM_minus2.12363.12423.2	2	8.5	0	6.40E+04		(K)LVPVLSA	(K)L V|P/V/L S/A K(A)		119.63	413.7746	826.54	0.0023	2.7	8.75	37710.6	6.36	HUMAN	P37837	Transaldolase
13579	dirMS_041712_NAR_30mM_minus2.17694.17694.2	2	8.5	0	3.80E+04		(R)ALCYLVL	(R)A L/C|Y L V L/K(Q)	C:Carbamidomethylation	150.68	490.2854	979.564	-0.001	-1	8.63	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
13580	dirMS_041712_NAR_30mM_minus2.7926.8012.2	2	8.5	0	3.27E+05		(K)VYPSSLS	(K)V Y|P S S/L/S/K(I)		98	440.7384	880.477	-0.0079	-9	8.56	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
13581	dirMS_041712_NAR_30mM_minus2.9128.9274.2	2	8.5	0	6.65E+05		(K)MPSGEF	(K)M/P/S/G E F/A/R(I)		104.28	447.7121	894.414	0.0031	3.5	5.75	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
13582	dirMS_041712_NAR_50mM_minus2.10594.10594.3	3	8.5	1	7.44E+03		(K)VAVVAG	(K)V/A|V|V A/G Y G D V G K/G C A Q A L R(G)	C:Carbamidomethylation	129.78	630.9952	1890.985	-0.0144	-7.6	8.56	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
13583	dirMS_041712_NAR_50mM_minus2.14749.14749.3	3	8.5	1	4.18E+05		(K)GCLELIK	(K)G C/L E L I K E T G\V|P I/A\G R(H)	C:Carbamidomethylation	151.82	571.6494	1712.936	-0.0027	-1.6	6.14	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
13584	dirMS_041712_NAR_60mM_minus.11432.11432.3	3	8.5	1	3.65E+05		(R)FPGQLN	(R)F/P/G Q/L N A D L/R K(L)		122.82	420.2346	1258.69	-0.001	-0.8	8.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
13585	dirMS_041712_NAR_60mM_minus.15691.15691.3	3	8.5	1	3.64E+05		(K)KANLQII	(K)K A N L Q I D Q|I/N|T/D|L N L E R(S)		147.98	666.6911	1998.061	-0.0027	-1.3	4.56	227783.5	5.5	HUMAN	P35579	Myosin-9
13586	dirMS_041712_NAR_120mM_plus.11389.11389.3	3	8.5	1	1.45E+06		(K)KAEAGA	(K)K A E A G A G S\A/T E/F/Q F/R(G)		112.88	523.9272	1569.766	0.0015	0.9	6.14	18897.4	10.15	HUMAN	P46783	40S ribosomal protein S10
13587	dirMS_041712_NAR_20mM_plus.10380.10418.3	3	8.5	0	1.35E+05	M592m M:	(R)mGPAm	(R)m G/P A m\G\P A\L/G\A G I E/R(M)	m:Oxidized methionine	144.65	487.2418	1427.713	31.9975	5.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
13588	dirMS_041712_NAR_20mM_plus.10611.10611.2	2	8.5	0	4.02E+04		(R)TPTAPA	(R)T/P\T/A|P/A V N/L A G A R(T)		145.83	619.8456	1238.685	-0.0012	-1	9.41	300351.7	12.1	HUMAN	Q9UQ35	Serine/arginine repetitive matrix protein 2
13589	dirMS_041712_NAR_40mM_plus2.9498.9498.3	3	8.5	0	2.64E+04		(K)ASQEPSI	(K)A S Q|E/P S/P K/P G T E V I|P A A P R(K)		119.18	644.6779	1932.018	0.0006	0.3	6.19	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
13590	dirMS_041712_NAR_50mM_plus2.12246.12246.3	3	8.5	1	2.80E+05		(R)ESDVPLI	(R)E S D V/P/L/K|T E E F E V T K(T)		132.68	584.2981	1750.874	0.0052	3	4.25	18909	6.21	HUMAN	Q969H8	UPF0556 protein C19orf10
13591	dirMS_041712_NAR_50mM_plus2.12771.12771.3	3	8.5	0	5.66E+05		(R)FDAERP	(R)F/D|A E R P V D/C S\V/I V V N K(Q)	C:Carbamidomethylation	135.77	616.6476	1847.932	-0.0038	-2	4.56	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
13592	dirMS_041712_NAR_50mM_plus2.18945.18945.3	3	8.5	1	2.23E+05		(K)IGEEFLT	(K)I/G E/E F/L/T D L S Q L K K(L)		167.02	540.965	1620.884	-0.0039	-2.4	4.68	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
13593	dirMS_041712_NAR_60mM_plus.12549.12549.3	3	8.5	1	7.18E+05		(K)VFDGIPI	(K)V F D G I/P/P/P Y/D K K(K)		122.43	459.2464	1375.726	-0.001	-0.7	5.93	23633.9	11.02	HUMAN	P40429	60S ribosomal protein L13a
13594	dirMS_041712_NAR_60mM_plus.13093.13093.3	3	8.5	0	5.53E+05		(R)SGGMEI	(R)S/G/G|M/E R P F V L A R(A)		124.78	440.5673	1319.689	-0.0015	-1.2	9.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
13595	dirMS_041712_NAR_60mM_plus.14269.14269.3	3	8.5	1	6.64E+05		(K)WKDSDI	(K)W K D S D E/A|D|L/V/L A K(E)		131	497.2559	1489.753	-0.0002	-0.1	4.23	20982.2	5.23	HUMAN	Q13185	Chromobox protein homolog 3
13596	dirMS_041712_NAR_60mM_plus.18809.18809.3	3	8.5	1	1.11E+05		(K)LSKNEVI	(K)L S\K N E V/L M V|N I/G S L/S T G G R(V)		155.83	659.0238	1975.064	-0.0072	-3.7	8.75	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
13597	dirMS_041712_NAR_30mM_minus2.10772.10815.2	2	8.49	0	3.05E+05		(R)FVTLSAT	(R)F V|T|L/S A T N A K(T)		112.58	526.2919	1051.578	-0.0017	-1.6	8.75	72873.4	5.73	HUMAN	Q96S55	ATPase WRNIP1
13598	dirMS_041712_NAR_30mM_minus2.13262.13302.2	2	8.49	0	3.32E+04		(R)TSGSVYI	(R)T/S|G/S/V/Y I/T L K(K)		125.93	534.7976	1068.594	-0.0056	-5.3	8.26	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
13599	dirMS_041712_NAR_30mM_minus2.16105.16105.2	2	8.49	0	6.11E+04		(R)NELESYA	(R)N E|L|E/S Y A Y/S L/K(N)		141.13	658.8239	1316.637	0.0037	2.8	4.53	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
13600	dirMS_041712_NAR_30mM_minus2.7602.7602.2	2	8.49	0	6.58E+05		(R)EQALAV	(R)E Q|A L A/V/S/R(N)		96.32	437.2408	873.479	-0.0045	-5.2	6.1	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
13601	dirMS_041712_NAR_50mM_minus2.11599.11599.3	3	8.49	0	1.78E+05		(K)GIHPTIIS	(K)G I H\P T\I|I|S E/S F Q/K(A)		134.48	486.2632	1456.78	-0.0044	-3	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
13602	dirMS_041712_NAR_50mM_minus2.14086.14086.3	3	8.49	0	1.50E+05		(K)SIEIPRP	(K)S I|E|I/P R P V D G V E V/P/G C G K(I)	C:Carbamidomethylation	148.28	636.9917	1908.985	-0.0242	-12.7	4.68	34243.5	4.88	HUMAN	K7ENG2	Splicing factor U2AF 65 kDa subunit
13603	dirMS_041712_NAR_60mM_minus.16436.16436.3	3	8.49	1	1.30E+05		(K)WVAIQS	(K)W/V|A|I Q S V S A W/P E K R(G)		151.77	552.9674	1656.886	0.002	1.2	8.75	6412.4	9.52	HUMAN	J3KSS4	Cytosolic non-specific dipeptidase (Fragment)
13604	dirMS_041712_NAR_120mM_plus.13074.13074.3	3	8.49	1	4.67E+05		(R)KQITME	(R)K Q I T\M/E/E/L/V/R(S)		122.05	416.2263	1246.682	-0.018	-14.5	6.14	533778	5.74	HUMAN	Q15149	Plectin
13605	dirMS_041712_NAR_50mM_plus2.10756.10756.3	3	8.49	0	2.02E+05		(R)ILDEIEEI	(R)I L/D/E/I/E E H N I K(I)		123.78	451.5743	1352.706	0.0027	2	4.4	37167.8	5.8	HUMAN	B5MCX3	Septin-2
13606	dirMS_041712_NAR_50mM_plus2.18163.18163.3	3	8.49	0	2.29E+05		(R)DIKPDNI	(R)D I K\P D N\F\L/M/G I G/R(H)		163.4	492.5943	1475.767	0.0008	0.6	5.96	27968.7	9.69	HUMAN	D6REM4	Casein kinase I isoform alpha
13607	dirMS_041712_NAR_60mM_plus.10501.10708.2	2	8.49	1	1.68E+06		(R)VKYETEL	(R)V/K|Y/E/T E L A M/R(Q)		113.15	620.326	1239.64	0.0045	3.7	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13608	dirMS_041712_NAR_60mM_plus.8895.8895.3	3	8.49	1	5.08E+05		(K)MQASIE	(K)M/Q/A S I E K/G G S L P K(V)		103.85	449.2449	1345.714	0.0057	4.3	8.35	32745.6	4.64	HUMAN	P06748	Nucleophosmin
13609	dirMS_041712_NAR_120mM_minus.13997.13997.4	4	8.48	1	1.58E+06		(K)ASIHEA	(K)A/S\I/H/E A W T D G K E A M L/K(H)		130	447.476	1786.879	0.0029	1.6	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
13610	dirMS_041712_NAR_120mM_minus.5585.5585.3	3	8.48	1	1.23E+05		(K)CDSSPD	(K)C/D/S\S/P/D/S A/E D V R/K(V)	C:Carbamidomethylation	83.98	489.2132	1465.622	0.0027	1.8	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
13611	dirMS_041712_NAR_20mM_minus.11608.11608.2	2	8.48	0	2.23E+05		(R)GDLGIEI	(R)G D L/G/I/E|I/P A E K(V)		163.93	571.3078	1141.61	-0.0016	-1.4	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
13612	dirMS_041712_NAR_20mM_minus.13619.13619.2	2	8.48	0	2.06E+05		(K)LGGSAV	(K)L G/G/S A\V I/S L E/G/K|P L(-)		187.78	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
13613	dirMS_041712_NAR_30mM_minus2.19691.19691.2	2	8.48	0	3.52E+05		(R)ASLSLW	(R)A S\L/S/L W Q/A M/E/K(G)		163.07	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
13614	dirMS_041712_NAR_30mM_minus2.7137.7278.2	2	8.48	0	1.16E+05		(K)MQAVQ	(K)M Q|A|V/Q/E A/T R(L)		94	517.257	1033.509	-0.0028	-2.7	5.75	533778	5.74	HUMAN	Q15149	Plectin
13615	dirMS_041712_NAR_30mM_minus2.7482.7482.2	2	8.48	0	2.90E+05		(K)AEYLCR(	(K)A E|Y/L/C/R(I)	C:Carbamidomethylation	95.65	406.1957	811.377	0.0074	9.1	6.04	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
13616	dirMS_041712_NAR_30mM_minus2.9579.9579.2	2	8.48	0	1.74E+05		(K)QTTCWI	(K)Q T\T|C/W/D|G V/R(N)	C:Carbamidomethylation	106.35	561.7582	1122.5	0.0095	8.4	5.84	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1
13617	dirMS_041712_NAR_20mM_plus.14624.14624.2	2	8.48	0	3.89E+04	M185m	(K)LAVNm	(K)L A/V/N m V/P F\P R(L)	m:Oxidized methionine	172.75	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
13618	dirMS_041712_NAR_20mM_plus.8484.8484.2	2	8.48	0	4.73E+04		(K)EAESSPF	(K)E A E S|S/P/F/V E/R(L)		128.55	575.7771	1150.537	0.0094	8.2	4.25	92752.5	4.76	HUMAN	P14625	Endoplasmin
13619	dirMS_041712_NAR_20mM_plus.9597.9597.2	2	8.48	0	8.24E+04	M2819m	(K)GLPSPYI	(K)G L|P S/P Y N m S S A P G S R(S)	m:Oxidized methionine	137.4	768.8596	1520.716	15.9957	0.5	8.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
13620	dirMS_041712_NAR_30mM_plus2.18584.18584.3	3	8.48	0	4.97E+05		(R)SSFYVN	(R)S S F Y V N G L/T/L/G G Q K(C)		150.95	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)

13621	dirMS_041712_NAR_30mM_plus2.4743.4743.2	2	8.48	0	8.70E+05	M571m	(R)mGANSI	(R)m/G\A|N/S L/E/R(M)	m:Oxidized methionine	75.93	447.2119	877.42	15.9969	2.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
13622	dirMS_041712_NAR_40mM_plus2.11802.11802.2	2	8.48	0	1.96E+05		(R)FPGQLN	(R)F/P/G Q\L N A\D|L R(K)		135.88	565.7995	1130.595	-0.0036	-3.1	5.84	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
13623	dirMS_041712_NAR_40mM_plus2.18504.18524.3	3	8.48	1	6.91E+04		(R)KAIIIFVP	(R)K\A\I I I\F\V|P V P Q L K(S)		175.18	489.3186	1465.95	-0.0092	-6.3	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
13624	dirMS_041712_NAR_50mM_plus2.16290.16441.3	3	8.48	1	1.18E+06		(K)FLVYVAI	(K)F L|V/Y V A N F D E K D/P/R(T)		154.53	571.6265	1712.864	0.0007	0.4	4.56	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
13625	dirMS_041712_NAR_50mM_plus2.18967.18967.3	3	8.48	1	2.87E+05		(R)DSIVAEL	(R)D S/I|V/A E L/D/R E M S R(S)		167.4	507.5872	1520.737	0.0097	6.4	4.32	34709.6	4.98	HUMAN	O14579	Coatomer subunit epsilon
13626	dirMS_041712_NAR_60mM_plus.20923.20923.3	3	8.48	1	1.31E+05		(K)TFVNITP	(K)T F/V\N/I/T/P A/E V G V L V G K D R(S)		170.62	639.0248	1915.065	-0.0049	-2.6	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
13627	dirMS_041712_NAR_120mM_minus.11000.11000.3	3	8.47	1	6.07E+05		(R)FYKNEG	(R)F Y|K/N\E G G T W/S V E/K(V)		113.78	515.5834	1544.738	-0.0023	-1.5	6.14	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
13628	dirMS_041712_NAR_120mM_minus.14792.14792.2	2	8.47	0	7.65E+05		(R)DWSHYI	(R)D/W|S H/Y F/K(I)		135	491.725	982.442	0.001	1	6.74	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13629	dirMS_041712_NAR_120mM_minus.17452.17452.4	4	8.47	2	2.94E+05		(R)NLKASLI	(R)N L K A S\L/E/N/S L R E V/E A/R(Y)		150.27	458.0011	1828.988	-0.005	-2.7	6.23	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13630	dirMS_041712_NAR_120mM_minus.6962.6962.2	2	8.47	0	4.18E+05		(K)HNAAFC	(K)H|N|A A/F C Y/K(L)	C:Carbamidomethylation	92.42	505.7282	1010.451	-0.0021	-2.1	8.6	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
13631	dirMS_041712_NAR_20mM_minus.13344.13344.2	2	8.47	0	6.93E+04		(K)SILFVPTS	(K)S/I L/F\V|P/T S A P R(G)		183.6	594.3411	1187.678	-0.0034	-2.8	9.47	92752.5	4.76	HUMAN	P14625	Endoplasmin
13632	dirMS_041712_NAR_30mM_minus2.12997.12997.2	2	8.47	0	2.66E+05		(K)AFCGFEI	(K)A F|C|G F E D/P R(T)	C:Carbamidomethylation	124.05	549.7307	1098.467	-0.0132	-12	4.37	533778	5.74	HUMAN	Q15149	Plectin
13633	dirMS_041712_NAR_30mM_minus2.13496.13496.2	2	8.47	0	8.11E+04		(K)FAFQAE	(K)F A|F/Q/A/E V/N R(M)		127.52	541.2823	1081.543	0.0148	13.7	6	92752.5	4.76	HUMAN	P14625	Endoplasmin
13634	dirMS_041712_NAR_30mM_minus2.16228.16228.2	2	8.47	0	2.52E+04		(R)VFSGLVS	(R)V F|S/G L/V S T/G L K(V)		141.38	554.3215	1107.641	-0.0051	-4.6	8.72	96306.4	6.41	HUMAN	P13639	Elongation factor 2
13635	dirMS_041712_NAR_40mM_minus2.13766.13766.3	3	8.47	1	4.48E+04		(K)FGEVVD	(K)F/G\E/V/V D C T/L K L D\P I T G R(S)	C:Carbamidomethylation	165.3	640.6656	1919.989	-0.0073	-3.8	4.56	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
13636	dirMS_041712_NAR_40mM_minus2.6923.6923.2	2	8.47	0	5.73E+05		(R)GYSFTTT	(R)G Y|S|F/T/T T A E/R(E)		111.93	566.7661	1132.527	-0.002	-1.8	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
13637	dirMS_041712_NAR_40mM_minus2.8285.8285.3	3	8.47	0	3.89E+03		(R)LLELGPK	(R)L L\E\L/G/P K/P E V A Q Q T R(K)		129.42	560.3204	1678.949	-0.002	-1.2	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
13638	dirMS_041712_NAR_40mM_minus2.9183.9183.2	2	8.47	0	6.88E+04		(K)WSLLQC	(K)W/S/L/L/Q Q Q K(T)		136.33	515.7871	1030.568	-0.0011	-1.1	8.75	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
13639	dirMS_041712_NAR_50mM_minus2.11409.11409.3	3	8.47	1	2.41E+04		(R)ESDVPLI	(R)E S/D V/P L K|T E E F E V T K(T)		133.62	584.3049	1750.874	0.0256	14.6	4.25	18909	6.21	HUMAN	Q969H8	UPF0556 protein C19orf10
13640	dirMS_041712_NAR_50mM_minus2.8596.8596.3	3	8.47	1	8.68E+04		(R)YESLTDF	(R)Y/E/S L T D/P S K L/D S/G K(E)		116.32	513.9233	1539.754	0.0017	1.1	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
13641	dirMS_041712_NAR_60mM_minus.11080.11080.3	3	8.47	1	3.17E+06		(R)DGKLVS	(R)D G K L V\S E|S/S/D/V/L|P K(-)		122.2	491.927	1473.78	-0.0131	-8.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
13642	dirMS_041712_NAR_60mM_minus.11527.11527.3	3	8.47	1	3.06E+05		(R)LSFDKD	(R)L/S/F D|K D A/M V A/R(A)		123.5	418.2174	1252.635	0.0022	1.8	5.96	35556.4	9.3	HUMAN	F2Z393	Transaldolase
13643	dirMS_041712_NAR_60mM_minus.14265.14265.3	3	8.47	1	2.99E+05	M108m	(R)DSIVAEL	(R)D S/I/V/A/E/L D R E m S R(S)	m:Oxidized methionine	138.78	512.9153	1520.737	15.994	-0.6	4.32	34709.6	4.98	HUMAN	O14579	Coatomer subunit epsilon
13644	dirMS_041712_NAR_60mM_minus.4711.4711.3	3	8.47	0	6.11E+05	M46m M4	(R)HQGVm	(R)H Q G V\m|V/G/m G Q K(D)	m:Oxidized methionine	77.87	401.8579	1171.571	31.9881	-1.4	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
13645	dirMS_041712_NAR_60mM_minus.9831.9831.3	3	8.47	0	4.34E+05		(K)LQVEEVI	(K)L Q|V E E V/H/Q L S\R(-)		114.55	446.5761	1337.717	-0.0034	-2.6	5.4	14571.2	5.15	HUMAN	F5GX50	Diablo homolog, mitochondrial (Fragment)
13646	dirMS_041712_NAR_120mM_plus.19394.19394.3	3	8.47	1	6.90E+05		(K)YNQLLRI	(K)Y/N|Q/L/L/R I E E E L G S K(A)		155.23	564.6353	1691.896	-0.0049	-2.9	4.79	47510.4	7.04	HUMAN	P06733	Alpha-enolase
13647	dirMS_041712_NAR_120mM_plus.9968.9968.3	3	8.47	1	1.87E+05		(R)RQQEQ	(R)R/Q Q E Q\Q/V|P I/L E/K(F)		105.5	499.2719	1495.823	-0.0216	-14.4	6.14	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
13648	dirMS_041712_NAR_20mM_plus.12211.12211.2	2	8.47	0	1.66E+05		(K)DLAGSII	(K)D L|A/G S I/I G/K(G)		157.83	437.2558	873.504	0.0003	0.4	5.84	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
13649	dirMS_041712_NAR_20mM_plus.14959.14959.2	2	8.47	0	1.45E+05		(K)VLEQLT	(K)V L\E/Q/L/T G Q/T|P V/F S K(A)		174.65	773.9244	1546.848	-0.006	-3.9	5.97	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
13650	dirMS_041712_NAR_20mM_plus.18687.18687.2	2	8.47	0	2.09E+05		(R)IITLAGP	(R)I I/T\L/A/G P T N A/I F K(A)		200.88	679.9039	1358.804	-0.0037	-2.7	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
13651	dirMS_041712_NAR_20mM_plus.19341.19341.2	2	8.47	0	1.20E+04		(K)SLNILTA	(K)S/L|N/I/L T/A F/Q K(K)		205.02	567.8286	1134.652	-0.0018	-1.6	8.47	18172.6	7.77	HUMAN	F8VY02	Endoplasmic reticulum resident protein 29
13652	dirMS_041712_NAR_20mM_plus.7634.7634.2	2	8.47	0	2.01E+05	M328m	(K)ALmDEV	(K)A L/m/D E/V V/K(A)	m:Oxidized methionine	122.5	460.741	904.481	15.9939	-1.1	4.37	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
13653	dirMS_041712_NAR_30mM_plus2.16810.16810.2	2	8.47	0	7.00E+05		(R)FGLNVS	(R)F G\L/N/V/S S I S R(K)		140.15	540.3016	1079.584	0.0115	10.7	9.75	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
13654	dirMS_041712_NAR_30mM_plus2.6055.6055.2	2	8.47	0	1.21E+05		(R)AQLGGI	(R)A/Q|L|G|G P E A A K(S)		85.97	471.2542	941.505	-0.0039	-4.2	6.05	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
13655	dirMS_041712_NAR_40mM_plus2.18987.18987.3	3	8.47	1	2.99E+05		(R)GGPNIIT	(R)G G P\N I|I/T L A|D I V K D P V S R(T)		178.88	622.3522	1865.049	-0.007	-3.8	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
13656	dirMS_041712_NAR_40mM_plus2.7486.7486.2	2	8.47	0	3.20E+05		(K)ASLENSI	(K)A S\L|E/N/S L R(E)		104.95	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13657	dirMS_041712_NAR_50mM_plus2.12639.12639.3	3	8.47	1	5.35E+05		(K)FSIEDLK	(K)F/S/I/E/D L K A Q/P K(Q)		134.4	425.8966	1275.694	-0.0191	-15	6.07	13579.2	9.99	HUMAN	E9PPQ6	Thymocyte nuclear protein 1 (Fragment)
13658	dirMS_041712_NAR_50mM_plus2.19134.19134.3	3	8.47	0	4.79E+05		(R)CRPDQL	(R)C R P D Q L\T G|L/S|L L/P L S E K(A)	C:Carbamidomethylation	168.18	643.0148	1927.032	-0.0019	-1	6.07	533778	5.74	HUMAN	Q15149	Plectin
13659	dirMS_041712_NAR_60mM_plus.12755.12755.3	3	8.47	1	9.60E+05	M232m	(R)MSmKE	(R)M S m K E V D E Q|M/L N/V|Q N K(N)	m:Oxidized methionine	123.5	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13660	dirMS_041712_NAR_60mM_plus.16871.16872.3	3	8.47	1	9.34E+05		(R)STNKGT.	(R)S T N K G T\A Y T\F/F/T/P G N L K(Q)		144.9	616.3117	1846.933	-0.0128	-7	9.7	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
13661	dirMS_041712_NAR_60mM_plus.5758.5758.3	3	8.47	1	8.96E+04		(R)NTAELQ	(R)N T|A E/L Q/P E S G K R(K)		88.4	443.8995	1329.676	0.0082	6.2	6.14	59955.3	4.28	HUMAN	O15355	Protein phosphatase 1G
13662	dirMS_041712_NAR_60mM_plus.6331.6346.3	3	8.47	1	2.83E+05	M357m	(K)AELDDTI	(K)A E|L/D D/T P m R G R(Q)	m:Oxidized methionine	91.9	426.203	1260.6	15.9943	-0.5	4.56	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
13663	dirMS_041712_NAR_60mM_plus.7853.7853.3	3	8.47	1	5.18E+05		(K)FAAKGE	(K)F/A A K G E G Q|L/G/P A E R(A)		99.2	477.5865	1430.739	0.0063	4.4	6.14	96306.4	6.41	HUMAN	P13639	Elongation factor 2
13664	dirMS_041712_NAR_120mM_minus.17654.17654.4	4	8.46	1	5.13E+05		(R)GFGHIG	(R)G F\G H I G I\A/V/P/D V/Y/S A C K R(F)	C:Carbamidomethylation	150.47	487.502	1946.991	-0.0044	-2.2	8.6	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
13665	dirMS_041712_NAR_20mM_minus.10818.10818.3	3	8.46	0	1.20E+05		(K)IISNASC	(K)I I\S N\A/S C T/T/N/C L\A/P L A/K(V)	C:Carbamidomethylation	156.2	611.9784	1833.92	0.0009	0.5	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
13666	dirMS_041712_NAR_30mM_minus2.11868.11868.2	2	8.46	0	3.34E+05		(R)FGISSVP	(R)F G/I/S/S V/P T K(G)		118.18	468.2614	935.52	-0.0041	-4.4	8.75	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
13667	dirMS_041712_NAR_30mM_minus2.18177.18201.2	2	8.46	1	1.09E+05		(R)LVLDSVI	(R)L V|L/D/S V K L E\A(-)		152.97	543.8223	1086.641	-0.0032	-2.9	4.37	10137.3	4.59	HUMAN	E5RIW3	Tubulin-specific chaperone A
13668	dirMS_041712_NAR_30mM_minus2.9424.9425.2	2	8.46	0	1.30E+05	M15m	(K)mLVSGA	(K)m/L|V|S G A G/D/I K(L)	m:Oxidized methionine	105.52	503.7677	990.529	15.9993	4.3	5.59	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
13669	dirMS_041712_NAR_50mM_minus2.12715.12715.3	3	8.46	0	1.03E+06	M114m M	(R)AGKPVI	(R)A G K|P V I/C\A T Q/m|L E S m I K(K)	C:Carbamidomethylation m:Oxid	139.93	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
13670	dirMS_041712_NAR_50mM_minus2.12802.12802.3	3	8.46	0	9.74E+04		(R)LLVGND	(R)L/L|V/G N D D V H I/I/A R(S)		141.02	478.9368	1434.806	-0.0105	-7.3	5.21	376926.5	4.99	HUMAN	H0Y5W0	E3 ubiquitin-protein ligase HUWE1 (Fragment)
13671	dirMS_041712_NAR_50mM_minus2.14820.14820.3	3	8.46	0	2.83E+05		(R)SLESLHS	(R)S L|E/S L H\S F V A A A T/K(E)		153	487.596	1460.774	-0.0009	-0.6	6.47	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
13672	dirMS_041712_NAR_60mM_minus.16120.16120.3	3	8.46	0	2.43E+05		(R)HDPTSEI	(R)H D P T S E|N\I/L Q L V K(A)		150.12	498.6051	1493.796	0.0049	3.3	5.32	13564.4	5.9	HUMAN	F8VZ98	Serine/threonine-protein kinase D1 (Fragment)
13673	dirMS_041712_NAR_60mM_minus.17931.17931.3	3	8.46	1	2.57E+05		(K)LEALKDI	(K)L E A L K D|L|A/S\L S R(D)		161.6	439.2618	1315.758	0.0129	9.8	6.07	18679.9	4.7	HUMAN	C9IZR8	Engulfment and cell motility protein 1 (Fragment)
13674	dirMS_041712_NAR_60mM_minus.17947.17947.3	3	8.46	0	3.59E+03		(R)GGYVLH	(R)G G|Y\V|L H I\G T I Y/G D L K(V)		161.65	535.9574	1605.863	-0.0059	-3.7	6.74	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
13675	dirMS_041712_NAR_60mM_minus.9114.9114.3	3	8.46	1	1.62E+05	M232m M	(R)MSmKE	(R)M/S/m K E V D E Q m/L N\V|Q N/K(N)	m:Oxidized methionine	110.57	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13676	dirMS_041712_NAR_20mM_plus.12310.12310.3	3	8.46	0	1.73E+05		(K)IISNASC	(K)I I S N\A\S/C T T N/C L/A/P L A K(V)	C:Carbamidomethylation	158.35	611.9768	1833.92	-0.0039	-2.1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
13677	dirMS_041712_NAR_30mM_plus2.15859.15859.2	2	8.46	0	3.16E+05		(R)YSVDIPL	(R)Y/S|V/D I P L D/K(T)		136.12	525.2819	1049.551	0.0052	4.9	4.21	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
13678	dirMS_041712_NAR_30mM_plus2.17879.17879.2	2	8.46	0	5.11E+04		(R)MQFGVI	(R)M Q|F/G\V|P L\A/R(N)		146.85	509.7774	1018.55	-0.0027	-2.7	9.5	43069.5	9.24	HUMAN	B4DK85	Glutaryl-CoA dehydrogenase, mitochondrial
13679	dirMS_041712_NAR_30mM_plus2.8431.8431.2	2	8.46	0	1.08E+05		(K)LYEQLSC	(K)L/Y|E Q/L S/G/K(-)		97.47	469.2488	937.499	-0.0086	-9.2	6	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
13680	dirMS_041712_NAR_40mM_plus2.18274.18274.3	3	8.46	0	6.68E+04		(K)ISSIQSIV	(K)I S|S I Q/S I|V/P A L E/I A/N A H R(K)		173.63	640.3668	1919.071	0.015	7.8	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
13681	dirMS_041712_NAR_50mM_plus2.11040.11040.3	3	8.46	1	2.37E+05		(K)AAAFEE	(K)A A|A|F E E Q E N E T V V V K E K(M)		125.5	640.9957	1920.955	0.0176	9.2	4.32	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
13682	dirMS_041712_NAR_50mM_plus2.14212.14212.3	3	8.46	0	5.08E+05		(K)VTHAVV	(K)V T H A V V T V/P/A/Y/F/N D A Q R(Q)		142.7	629.9955	1887.971	0.0008	0.4	6.71	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
13683	dirMS_041712_NAR_50mM_plus2.17793.17829.3	3	8.46	1	2.23E+05		(K)MGVGKI	(K)M/G/V/G K L E/M/Y/V L/N P V K(S)		161.72	559.9739	1677.907	0.0005	0.3	8.26	75482.2	6.34	HUMAN	D6RA32	Microtubule-associated protein 1B (Fragment)
13684	dirMS_041712_NAR_50mM_plus2.21899.21899.3	3	8.46	0	2.98E+04		(K)GLAPDLI	(K)G L|A/P D L P E D L Y H/L I K(K)		186.45	565.3101	1693.916	-0.0002	-0.1	4.54	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
13685	dirMS_041712_NAR_50mM_plus2.6229.6229.3	3	8.46	1	1.09E+05		(R)VVSSIEC	(R)V/V/S S I E/Q K/T E G A E K(K)		96.73	502.2651	1504.785	-0.0046	-3	4.79	8491.4	6.28	HUMAN	E5RIR4	14-3-3 protein zeta/delta (Fragment)
13686	dirMS_041712_NAR_50mM_plus2.7520.7520.3	3	8.46	0	3.69E+05		(R)VGQAVI	(R)V/G Q A V/D\V/V/G Q A/G K P K(T)		105.72	484.9438	1452.817	-0.0001	0	8.56	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
13687	dirMS_041712_NAR_60mM_plus.13092.13092.3	3	8.46	0	5.53E+05		(R)SGGMEI	(R)S/G|G M/E R P F V L A R(A)		124.78	440.5673	1319.689	-0.0015	-1.2	9.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
13688	dirMS_041712_NAR_60mM_plus.16940.16940.3	3	8.46	1	6.46E+06		(K)LKVPEW	(K)L/K/V P E|W|V/D T/V K(L)		145.73	438.5872	1313.746	0.0007	0.5	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
13689	dirMS_041712_NAR_60mM_plus.6507.6529.3	3	8.46	1	1.72E+06		(R)TKTEISEI	(R)T\K T E\I|S/E/M/N R(N)		92.8	403.5374	1208.594	0.0037	3	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
13690	dirMS_041712_NAR_120mM_minus.9138.9138.3	3	8.45	0	7.27E+05		(K)HTGPNS	(K)H T G P N/S P D T|A/N/D/G F V R(L)		103.4	562.2599	1684.767	-0.0022	-1.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
13691	dirMS_041712_NAR_30mM_minus2.11296.11296.2	2	8.45	0	2.17E+05		(R)GGGGNI	(R)G G G G N/F|G/P G/P/G S N\F/R(G)		114.83	689.3185	1377.629	0.0003	0.2	9.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
13692	dirMS_041712_NAR_30mM_minus2.16453.16453.2	2	8.45	0	2.53E+05		(R)ASLEAAI	(R)A S L E A\A|I/A|D A|E/Q R(G)		143.58	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
13693	dirMS_041712_NAR_60mM_minus.10427.10427.3	3	8.45	0	1.96E+05		(R)LSNLALV	(R)L/S\N L/A L V K/P E/K(T)		118.55	404.5829	1211.736	-0.0017	-1.4	8.59	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
13694	dirMS_041712_NAR_60mM_minus.11718.11718.3	3	8.45	1	4.61E+05	M232m	(R)MSmKE	(R)M S m K E V D E\Q\M|L|N V Q N/K(N)	m:Oxidized methionine	125.58	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13695	dirMS_041712_NAR_60mM_minus.14217.14217.3	3	8.45	1	3.30E+05		(R)QATKDA	(R)Q A T K D A G T/I A/G/L/N V/L R(I)		138.87	543.3073	1627.913	-0.0052	-3.2	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
13696	dirMS_041712_NAR_60mM_minus.17356.17356.3	3	8.45	1	4.19E+06		(R)VSFELFA	(R)V S/F/E/L F A D K\V/P K(T)		157.6	460.5911	1379.757	0.0018	1.3	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
13697	dirMS_041712_NAR_120mM_plus.12279.12279.2	2	8.45	1	2.95E+05		(R)KGDIFLV	(R)K|G D/I/F\L V/R(G)		117.28	474.2836	947.567	-0.0074	-7.8	8.75	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
13698	dirMS_041712_NAR_120mM_plus.4209.4210.2	2	8.45	1	1.38E+06	M310m	(R)TKTEISEI	(R)T K|T/E/I/S E m N/R(N)	m:Oxidized methionine	69.87	612.7976	1208.594	15.994	-0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
13699	dirMS_041712_NAR_120mM_plus.5233.5398.3	3	8.45	1	7.24E+05	M117m	(K)EmQLRC	(K)E m/Q/L/R/Q E/E/E R(R)	m:Oxidized methionine	80.92	455.2145	1347.632	15.9968	1.4	4.49	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
13700	dirMS_041712_NAR_120mM_plus.6488.6488.3	3	8.45	1	8.96E+05		(R)TKTEISEI	(R)T K T E I|S/E/M N R(N)		87.45	403.5365	1208.594	0.001	0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
13701	dirMS_041712_NAR_30mM_plus2.5922.5922.2	2	8.45	0	2.12E+05		(R)STSYGYS	(R)S T/S/Y/G/Y/S R(S)		85.37	460.7158	920.411	0.0135	14.7	8.31	25655.9	8.94	HUMAN	Q13242	Serine/arginine-rich splicing factor 9
13702	dirMS_041712_NAR_40mM_plus2.12540.12540.3	3	8.45	0	1.29E+05	M114m M	(R)AGKPVI	(R)A G K\P V I C A/T/Q\m/L\E S m I K(K)	C:Carbamidomethylation m:Oxid	139.77	637.0002	1876.969	32.0167	14.1	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
13703	dirMS_041712_NAR_40mM_plus2.14009.14009.3	3	8.45	0	2.05E+05		(K)VALLLLD	(K)V A\L\L/L L D\Q G A S P H/A/A A K(N)		148.23	558.9886	1674.954	-0.0025	-1.5	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
13704	dirMS_041712_NAR_40mM_plus2.19000.19000.3	3	8.45	1	1.11E+05		(K)NLGIPIIT	(K)N L/G\I/P I I T V/L/G D S K N N V R(A)		178.17	641.701	1923.102	-0.0137	-7.1	8.75	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
13705	dirMS_041712_NAR_40mM_plus2.6105.6105.2	2	8.45	0	1.78E+04		(R)NGYDYC	(R)N G Y|D/Y|G Q|C/R(L)	C:Carbamidomethylation	94.57	566.7355	1132.448	0.0161	14.2	5.83	25655.9	8.94	HUMAN	Q13242	Serine/arginine-rich splicing factor 9
13706	dirMS_041712_NAR_40mM_plus2.7369.7369.2	2	8.45	0	2.20E+05		(R)AQYDEL	(R)A Q|Y/D/E/L A R(K)		102.77	483.2372	965.469	-0.0016	-1.6	4.37	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13707	dirMS_041712_NAR_50mM_plus2.11329.11329.3	3	8.45	1	1.17E+06		(K)VGDKVL	(K)V G D K V L|L|P/E/Y G G T K(V)		126.95	492.6069	1475.81	-0.0043	-2.9	6.04	5189.9	4.56	HUMAN	B8ZZ54	10 kDa heat shock protein, mitochondrial
13708	dirMS_041712_NAR_50mM_plus2.13067.13067.3	3	8.45	1	2.49E+05		(K)NSVTPD	(K)N S/V/T/P D M M/E/E M Y K K(A)		137.03	568.2557	1702.748	0.0041	2.4	4.68	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
13709	dirMS_041712_NAR_50mM_plus2.15192.15192.3	3	8.45	1	5.18E+05		(K)LIVAYVD	(K)L I/V/A Y V D/D L D R/R(G)		148.08	483.2728	1447.79	0.0135	9.3	4.43	124127.1	8.81	HUMAN	O14776	Transcription elongation regulator 1
13710	dirMS_041712_NAR_50mM_plus2.17665.17719.3	3	8.45	1	4.60E+05		(R)ALQALEI	(R)A L/Q|A/L/E/E L R L Q\A E E A E R(R)		161.13	657.011	1969.035	-0.0164	-8.4	4.33	533778	5.74	HUMAN	Q15149	Plectin
13711	dirMS_041712_NAR_60mM_plus.10356.10372.3	3	8.45	1	1.30E+06		(R)IITEGFE	(R)I I/T/E/G F E/A A K E K(A)		112.13	445.9046	1335.716	-0.0162	-12.1	4.79	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
13712	dirMS_041712_NAR_60mM_plus.9034.9034.3	3	8.45	0	1.59E+06		(K)EFHLNES	(K)E F H L N\E/S/G D/P/S/S K(S)		105.52	482.8882	1446.65	0.0005	0.3	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
13713	dirMS_041712_NAR_120mM_minus.15550.15550.4	4	8.44	2	1.39E+05		(R)EDLRLPI	(R)E D L R L/P/E/G D L/G K E I E Q K(Y)		139.4	493.0108	1969.024	-0.0023	-1.2	4.36	16346.3	4.85	HUMAN	I3L397	Eukaryotic translation initiation factor 5A-1 (Fragment)
13714	dirMS_041712_NAR_120mM_minus.7031.7031.3	3	8.44	1	3.75E+05	M71m	(R)VNEARE	(R)V/N/E/A R/E E L m/R(M)	m:Oxidized methionine	92.97	421.542	1246.621	15.9906	-3.4	4.79	16201.6	6.74	HUMAN	B7ZB63	ADP-ribosylation factor 3
13715	dirMS_041712_NAR_120mM_minus.8855.8855.3	3	8.44	0	8.92E+05		(K)HTGPNS	(K)H T\G\P N\S\P D T A/N D/G F V R(L)		103.08	562.2599	1684.767	-0.0022	-1.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
13716	dirMS_041712_NAR_30mM_minus2.10210.10210.2	2	8.44	0	5.82E+05		(K)TGTVSLI	(K)T G T/V|S/L E/V R(L)		109.57	481.2669	961.531	-0.0048	-5	5.66	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
13717	dirMS_041712_NAR_30mM_minus2.13205.13327.2	2	8.44	0	5.72E+05		(K)IYFMAG	(K)I/Y|F|M/A/G S S R(K)		126.68	516.2552	1031.498	0.0052	5.1	8.75	92752.5	4.76	HUMAN	P14625	Endoplasmin
13718	dirMS_041712_NAR_30mM_minus2.18288.18288.2	2	8.44	0	8.63E+04		(R)LIEDFLA	(R)L/I|E D/F/L/A R(S)		153.52	488.7803	976.546	0.0071	7.3	4.37	15119.1	4.81	HUMAN	A6NDN0	Trafficking protein particle complex 3, isoform CRA_a
13719	dirMS_041712_NAR_30mM_minus2.19234.19234.2	2	8.44	0	8.70E+05		(K)MSIYQA	(K)M/S\I/Y Q/A M/W K(G)		159.02	579.2789	1157.548	0.0023	2	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
13720	dirMS_041712_NAR_50mM_minus2.12911.12911.3	3	8.44	0	1.28E+05		(K)ITHLSTL	(K)I T H L S T L\Q|V/G S/L N/V K(C)		141.65	537.3126	1609.927	-0.0039	-2.4	8.76	26760.1	8.93	HUMAN	H3BPK3	Hydroxyacylglutathione hydrolase, mitochondrial (Fragment)
13721	dirMS_041712_NAR_50mM_minus2.15365.15365.3	3	8.44	1	2.25E+04		(K)CEFQDA	(K)C E\F Q/D A|Y/V\L L/S E/K K(I)	C:Carbamidomethylation	156.05	577.2917	1729.847	0.014	8.1	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
13722	dirMS_041712_NAR_50mM_minus2.6104.6104.3	3	8.44	0	4.44E+05	M437m	(R)LESGMC	(R)L/E/S G M Q N m S I/H/T K(T)	m:Oxidized methionine	97.77	497.9018	1475.698	15.9927	-1.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
13723	dirMS_041712_NAR_60mM_minus.14848.14848.3	3	8.44	1	2.72E+05		(R)KLQEEEI	(R)K L Q E E E\L|L|A/T/Q/V D\M R(A)		142.8	601.6438	1802.932	-0.0148	-8.2	4.41	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
13724	dirMS_041712_NAR_60mM_minus.15508.15508.3	3	8.44	1	1.59E+05		(R)SEIDLFN	(R)S E|I/D/L/F/N I R K(E)		146.45	412.2311	1234.679	-0.0003	-0.2	5.79	24754.5	4.77	HUMAN	D6RBE9	Annexin
13725	dirMS_041712_NAR_60mM_minus.18178.18178.3	3	8.44	1	4.80E+05		(K)TQLNLLI	(K)T Q/L N L/L/L D/K L R(S)		163.37	442.9403	1326.81	-0.004	-3	8.41	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
13726	dirMS_041712_NAR_60mM_minus.18461.18461.3	3	8.44	0	2.38E+05		(K)SQLDIIIH	(K)S Q/L/D I/I I/H/S L K(K)		164.08	422.9181	1266.742	-0.0019	-1.5	6.46	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
13727	dirMS_041712_NAR_120mM_plus.10384.10384.3	3	8.44	1	2.55E+05		(R)LRQLAEI	(R)L R Q L A\E E\D|L|A/Q Q/R(A)		107.03	523.949	1569.834	-0.0019	-1.2	4.68	533778	5.74	HUMAN	Q15149	Plectin
13728	dirMS_041712_NAR_20mM_plus.15699.15699.3	3	8.44	0	2.07E+05		(K)TITLEVEI	(K)T/I T L E V\E/P/S D\T I E N V K(A)		179.07	596.6463	1787.927	-0.003	-1.7	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
13729	dirMS_041712_NAR_20mM_plus.17012.17313.2	2	8.44	0	2.79E+05		(K)LFLVQLC	(K)L F|L|V/Q/L Q E K(A)		189.8	559.3342	1117.662	-0.0004	-0.4	6	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)

13730	dirMS_041712_NAR_30mM_plus2.15365.15855.2	2	8.44	0	1.14E+06		(R)LSFVTP	(R)L/S|F V/T|P/R(H)		134.08	410.2436	819.472	0.0076	9.3	9.75	509686.6	4.85	HUMAN	Q14517	Protocadherin Fat 1
13731	dirMS_041712_NAR_30mM_plus2.20586.20586.2	2	8.44	0	3.61E+05		(K)GGIVG	(K)G G I\V/G/M/T/L/P I\A R(D)		161.75	592.8453	1184.682	0.0013	1.1	9.75	27150.8	7.95	HUMAN	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2
13732	dirMS_041712_NAR_30mM_plus2.6594.6594.2	2	8.44	0	4.74E+05		(R)SPDNP	(R)S P/D|N/P M/N/Q R(A)		88.88	529.7357	1058.468	-0.0042	-4	5.55	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
13733	dirMS_041712_NAR_40mM_plus2.10401.10401.2	2	8.44	0	7.90E+03		(K)WQMN	(K)W Q|M|N\P Y D R(G)		125.77	555.2453	1109.483	0	0	5.83	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
13734	dirMS_041712_NAR_50mM_plus2.8759.8759.3	3	8.44	0	7.58E+05		(R)AALAHS	(R)A A L\A H S E E\V\T/A|S Q V A A T K(T)		113.45	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
13735	dirMS_041712_NAR_60mM_plus.11116.11116.2	2	8.44	0	2.12E+06		(K)GIVEFAS	(K)G I/V/E/F/A S\K/P A A R(K)		116.18	623.3504	1245.695	-0.0015	-1.2	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
13736	dirMS_041712_NAR_60mM_plus.5208.5208.3	3	8.44	0	2.64E+04		(R)TATEKP	(R)T A/T/E K/P/G P A\E A A R(Q)		84.77	433.5671	1298.67	0.0168	13	5.81	49823.3	9.39	HUMAN	B4DQQ4	NADPH:adrenodoxin oxidoreductase, mitochondrial
13737	dirMS_041712_NAR_120mM_minus.12899.12899.4	4	8.43	0	4.68E+05		(K)LSQPPLE	(K)L S/Q P P L E Q T/Q L/Q V K(T)		125.08	402.9764	1608.896	-0.0118	-7.3	6	131573.4	9.73	HUMAN	B7ZKT8	C11orf30 protein
13738	dirMS_041712_NAR_120mM_minus.7318.7339.3	3	8.43	1	1.49E+06		(R)CREMD	(R)C R E\M|D|E\Q/I/R(L)	C:Carbamidomethylation	93.97	412.8591	1236.546	0.0168	13.6	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
13739	dirMS_041712_NAR_30mM_minus2.12788.12788.2	2	8.43	0	3.27E+05		(R)GGAEQ	(R)G G A\E/Q/F/M/E E T/E R(S)		122.7	692.2961	1383.584	0.0004	0.3	4.09	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
13740	dirMS_041712_NAR_30mM_minus2.15159.15159.2	2	8.43	0	5.54E+05	M316m	(R)ISEQFTA	(R)I/S\E/Q F/T/A/m F/R(R)	m:Oxidized methionine	135.18	623.3014	1229.598	15.9972	1.8	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
13741	dirMS_041712_NAR_30mM_minus2.16834.16834.2	2	8.43	0	2.88E+05		(K)NSLESY	(K)N\S\L/E/S/Y/A\F/N M K(A)		146.23	652.3031	1303.599	0.0002	0.2	6	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
13742	dirMS_041712_NAR_50mM_minus2.11596.11596.3	3	8.43	0	2.80E+05	M291m	(K)TGEEIFG	(K)T/G\E/E|I/F G T I G m R P N A K(N)	m:Oxidized methionine	134.18	579.6239	1720.869	15.9885	-3.7	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
13743	dirMS_041712_NAR_50mM_minus2.7730.7730.3	3	8.43	1	4.75E+04		(K)TTSPPE	(K)T T/S/P P E V S G Y S Y E/K T E/R(S)		110.92	644.3067	1930.903	0.0027	1.4	4.78	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
13744	dirMS_041712_NAR_50mM_minus2.8663.8663.3	3	8.43	1	9.59E+04		(K)ALDLDS	(K)A L/D L/D/S S/C K/E A|A D G Y Q R(C)	C:Carbamidomethylation	117.47	633.6221	1898.855	-0.0031	-1.7	4.23	60404.6	6.4	HUMAN	F5H0T1	Stress-induced-phosphoprotein 1
13745	dirMS_041712_NAR_60mM_minus.13479.13479.3	3	8.43	1	5.27E+05		(R)KLVIIES	(R)K L V I\I/E/S/D/L/E R(A)		135.37	438.9202	1314.763	-0.0167	-12.7	4.68	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
13746	dirMS_041712_NAR_60mM_minus.14840.14840.3	3	8.43	1	5.91E+05		(K)TDKTLV	(K)T/D K T L\V|L|L/M/G K(E)		142.57	406.9088	1218.713	-0.0008	-0.6	8.26	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
13747	dirMS_041712_NAR_120mM_plus.6925.6925.2	2	8.43	0	5.95E+04		(R)HLTGEF	(R)H/L|T G E\F\E/K(K)		90.07	480.743	960.479	0.0002	0.2	5.4	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
13748	dirMS_041712_NAR_20mM_plus.17519.17519.2	2	8.43	0	3.36E+04		(R)YLTVAA	(R)Y L|T/V/A A V F R(G)		192.65	520.3009	1039.593	0.001	1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13749	dirMS_041712_NAR_30mM_plus2.12917.12990.2	2	8.43	0	4.85E+05		(R)GQVVSL	(R)G Q|V|V/S L/I R(M)		120.77	436.2709	871.536	-0.0015	-1.7	9.75	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
13750	dirMS_041712_NAR_30mM_plus2.16054.16054.2	2	8.43	0	2.80E+05		(R)YSVDIPL	(R)Y/S\V/D I P L D K(T)		136.33	525.2819	1049.551	0.0052	4.9	4.21	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
13751	dirMS_041712_NAR_30mM_plus2.20292.20292.2	2	8.43	0	2.12E+05		(K)LYNLFLK	(K)L/Y/N\L\F L K(I)		159.43	455.7738	910.54	0.0007	0.7	8.59	41666	7.73	HUMAN	E9PDQ8	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial
13752	dirMS_041712_NAR_30mM_plus2.9665.9665.2	2	8.43	0	1.36E+06		(R)QLSSGV	(R)Q L|S/S/G V/S E I R(H)		104.9	538.2855	1075.574	-0.0105	-9.8	6	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
13753	dirMS_041712_NAR_60mM_plus.15985.15985.3	3	8.43	0	5.19E+05		(R)VWYVS	(R)V W|Y V S N I D G T H I A K(T)		139.98	534.9464	1602.828	-0.0028	-1.8	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
13754	dirMS_041712_NAR_120mM_minus.12145.12145.3	3	8.42	1	3.21E+05		(K)TLTTVQ	(K)T L|T/T V Q G I A D/D Y D K K K(L)		120.02	599.3185	1795.944	-0.0027	-1.5	5.71	13778.5	7.96	HUMAN	K7EM18	Eukaryotic translation initiation factor 1
13755	dirMS_041712_NAR_120mM_minus.13255.13255.3	3	8.42	2	2.61E+05		(R)AQKDEE	(R)A Q/K D E E K M/E I Q E/I/Q L K(E)		126.68	654.0058	1960.006	-0.0027	-1.4	4.58	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
13756	dirMS_041712_NAR_20mM_minus.7492.7492.2	2	8.42	0	5.95E+05	M239m	(K)EVDEQ	(K)E V D E|Q/m L/N|V/Q N K(N)	m:Oxidized methionine	123.4	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13757	dirMS_041712_NAR_30mM_minus2.15322.15322.2	2	8.42	0	6.18E+05		(R)YPVNSV	(R)Y/P|V/N S V N I L K(A)		136.87	573.8282	1146.652	-0.0026	-2.3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
13758	dirMS_041712_NAR_30mM_minus2.9091.9318.2	2	8.42	0	9.75E+05		(K)TLEEAIR	(K)T L|E/E/A I/R(S)		105.13	416.2371	831.457	0.0099	11.9	4.53	51583.6	7.73	HUMAN	B4DVE7	Annexin
13759	dirMS_041712_NAR_50mM_minus2.9607.9607.3	3	8.42	0	1.30E+05		(K)MIVDPV	(K)M I/V D/P V E/P H G E/M/K(F)		122.47	494.5757	1481.713	-0.0002	-0.1	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
13760	dirMS_041712_NAR_60mM_minus.16121.16121.3	3	8.42	0	2.43E+05		(R)HDPTSE	(R)H D/P T S E\N\I/L Q L/V/K(A)		150.12	498.6051	1493.796	0.0049	3.3	5.32	13564.4	5.9	HUMAN	F8VZ98	Serine/threonine-protein kinase D1 (Fragment)
13761	dirMS_041712_NAR_20mM_plus.12806.12806.2	2	8.42	0	2.85E+04	M92m	(R)ImNTFS	(R)I m|N T/F/S V/V\P S P K(V)	m:Oxidized methionine	160.95	668.3516	1319.703	15.9931	-1.3	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
13762	dirMS_041712_NAR_20mM_plus.14969.14969.2	2	8.42	0	1.45E+05		(K)VLEQLT	(K)V L/E\Q\L/T/G/Q T/P V F S K(A)		174.65	773.9244	1546.848	-0.006	-3.9	5.97	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
13763	dirMS_041712_NAR_20mM_plus.7992.7992.2	2	8.42	0	4.21E+05	M239m	(K)EVDEQ	(K)E V|D E/Q/m L/N V/Q N K(N)	m:Oxidized methionine	125.1	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13764	dirMS_041712_NAR_20mM_plus.8057.8057.2	2	8.42	0	5.68E+03		(K)VEIIAND	(K)V E|I/I/A/N D Q G N R(T)		124.97	614.8177	1228.628	0.0001	0.1	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
13765	dirMS_041712_NAR_30mM_plus2.18003.18003.2	2	8.42	0	2.34E+05		(R)QITLND	(R)Q I/T/L/N D/L/P V G R(S)		147.82	613.3465	1225.69	-0.0042	-3.4	5.84	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
13766	dirMS_041712_NAR_30mM_plus2.19299.19299.2	2	8.42	0	1.16E+05		(K)YPQLLP	(K)Y/P Q/L L/P/G I\R(G)		153.48	528.814	1056.62	0.0007	0.6	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
13767	dirMS_041712_NAR_40mM_plus2.13959.13959.3	3	8.42	0	1.01E+04		(R)EMQDV	(R)E M/Q/D/V/D L A E/V K P L V/E K(G)		148.42	614.9934	1842.952	0.0139	7.5	4.18	18328.6	4.58	HUMAN	E5RGM5	Protein NDRG1 (Fragment)
13768	dirMS_041712_NAR_40mM_plus2.14644.14644.3	3	8.42	1	1.63E+05		(R)DLIDFD	(R)D L|I/D F D D R Q Q I Y A A/E K(A)		152.68	647.3228	1939.94	0.0142	7.3	4.03	334221.3	6.44	HUMAN	P15924	Desmoplakin
13769	dirMS_041712_NAR_40mM_plus2.6808.6808.2	2	8.42	0	4.44E+04		(K)SFQQSS	(K)S F|Q/Q/S/S L S R(D)		100.17	520.2619	1039.517	-0.0002	-0.2	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
13770	dirMS_041712_NAR_50mM_plus2.10869.10869.3	3	8.42	1	2.43E+06		(R)MQKEIT	(R)M Q K E I T|A|L|A/P S/T M K(I)		124.03	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
13771	dirMS_041712_NAR_50mM_plus2.11444.11444.3	3	8.42	1	2.61E+05		(K)CATITP	(K)C A/T/I/T/P D/E/A R V E E F K(L)	C:Carbamidomethylation	127.75	589.2842	1765.843	-0.0045	-2.5	4.41	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
13772	dirMS_041712_NAR_50mM_plus2.15328.15328.3	3	8.42	1	8.32E+05		(R)GFPTIYF	(R)G F/P T/I/Y F S/P A N/K K(L)		148.8	490.5973	1469.779	-0.0014	-0.9	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
13773	dirMS_041712_NAR_60mM_plus.12860.12860.3	3	8.42	1	8.89E+05	M232m	(R)MSmKE	(R)M S m K E V D E|Q\M|L/N V|Q N K(N)	m:Oxidized methionine	123.58	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
13774	dirMS_041712_NAR_20mM_minus.12224.12224.2	2	8.41	0	1.42E+05		(K)LVSIGAE	(K)L V/S|I/G A E E I/V D G\N A K(M)		171.32	757.9044	1514.806	-0.0045	-3	4.14	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
13775	dirMS_041712_NAR_20mM_minus.12288.12288.2	2	8.41	0	9.27E+05	M313m	(R)TVQSLE	(R)T V/Q/S\L|E|I\D L/D S m R(N)	m:Oxidized methionine	171.15	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13776	dirMS_041712_NAR_30mM_minus2.12219.12219.2	2	8.41	0	4.11E+04		(K)QALSGF	(K)Q/A/L/S/G F/G Y R(L)		119.07	499.7499	998.505	-0.0129	-12.9	8.75	21925.1	5.16	HUMAN	O75340	Programmed cell death protein 6
13777	dirMS_041712_NAR_30mM_minus2.16681.17190.2	2	8.41	0	7.70E+05		(K)MIFVGI	(K)M/I|F/V/G I/K(K)		145.97	404.2383	807.48	-0.0104	-12.9	8.5	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
13778	dirMS_041712_NAR_30mM_minus2.8024.8024.2	2	8.41	0	1.04E+05	M35m	(K)SmIEISR	(K)S m|I/E/I/S R(T)	m:Oxidized methionine	98.78	426.2191	835.434	15.9967	2.1	5.72	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
13779	dirMS_041712_NAR_40mM_minus2.7062.7062.3	3	8.41	0	2.47E+05	M115m	(R)VmLGET	(R)V m|L/G E T/N P A D S/K/P G T I R(G)	m:Oxidized methionine	113.97	601.3082	1785.916	15.9937	-0.7	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
13780	dirMS_041712_NAR_60mM_minus.9320.9320.3	3	8.41	0	9.34E+04		(K)GHENVE	(K)G H E N V E\A|A/Q/A/E Y/I E K(F)		111.78	563.2673	1687.792	-0.0049	-2.9	4.48	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
13781	dirMS_041712_NAR_120mM_plus.10627.10627.2	2	8.41	1	1.54E+06		(R)VKYETEL	(R)V/K|Y|E/T E\L A M/R(Q)		107.93	620.3237	1239.64	-0.0001	0	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13782	dirMS_041712_NAR_120mM_plus.7867.7867.2	2	8.41	0	4.94E+05		(K)STTTGH	(K)S T|T/T/G H L I Y/K(C)		95.3	560.8014	1120.6	-0.0042	-3.7	8.34	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
13783	dirMS_041712_NAR_120mM_plus.8148.8148.3	3	8.41	2	4.62E+05		(K)TPKGPS	(K)T P K|G P S/S V|E/D/I\K A K(M)		96.4	486.2728	1456.801	0.0033	2.2	8.17	32745.6	4.64	HUMAN	P06748	Nucleophosmin
13784	dirMS_041712_NAR_120mM_plus.8732.8732.3	3	8.41	1	2.74E+04		(R)TNYNDR	(R)T/N/Y/N D R Y D E/I|R(R)		99.25	486.8905	1458.661	-0.0038	-2.6	4.55	30166.2	10.79	HUMAN	P62424	60S ribosomal protein L7a
13785	dirMS_041712_NAR_20mM_plus.13989.13989.2	2	8.41	0	9.86E+04	M313m	(R)TVQSLE	(R)T V|Q\S\L/E|I D L/D S m R(N)	m:Oxidized methionine	168.37	761.8738	1506.747	15.9935	-0.9	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13786	dirMS_041712_NAR_20mM_plus.14625.14625.2	2	8.41	0	3.89E+04	M185m	(K)LAVNm	(K)L A\V/N m/V/P F/P R(L)	m:Oxidized methionine	172.75	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
13787	dirMS_041712_NAR_20mM_plus.17046.17046.3	3	8.41	0	2.18E+05		(K)VQIAVA	(K)V Q\I\A V\A|N\A|Q E/L L Q R(M)		188.22	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
13788	dirMS_041712_NAR_20mM_plus.18154.18154.2	2	8.41	0	1.31E+05	M153m	(K)VVTYG	(K)V V T|Y|G m A N L L T G P K(R)	m:Oxidized methionine	196.32	740.3997	1463.793	15.9995	3.1	8.56	28454.5	6.24	HUMAN	B0AZP7	Synaptic vesicle membrane protein VAT-1 homolog
13789	dirMS_041712_NAR_30mM_plus2.14457.14469.2	2	8.41	0	6.21E+05		(R)GIFTSEI	(R)G I|F|T/S E I G T/K(Q)		128.88	526.7806	1052.562	-0.0083	-7.9	6	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
13790	dirMS_041712_NAR_40mM_plus2.7231.7603.2	2	8.41	0	2.20E+05		(R)SGYFDEI	(R)S/G|Y|F D/E R(Y)		104.03	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
13791	dirMS_041712_NAR_50mM_plus2.13362.13362.3	3	8.41	0	1.99E+05		(K)LVRPPV	(K)L V R P P V\Q|V|Y/G I E/G R(Y)		138.6	528.3069	1582.906	-0.0002	-0.2	8.75	8249.6	10.2	HUMAN	H7C086	ATP synthase subunit O, mitochondrial (Fragment)
13792	dirMS_041712_NAR_50mM_plus2.13632.13632.3	3	8.41	1	7.89E+05		(R)LAIYRAE	(R)L/A/I/Y R A E T E E G P/D\V L R(W)		139.13	611.3256	1831.955	0.0074	4	4.41	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
13793	dirMS_041712_NAR_50mM_plus2.6555.6555.3	3	8.41	1	9.00E+04	M251m	(K)mQASIE	(K)m/Q/A S I E/K/G G S L/P K(V)	m:Oxidized methionine	99.67	454.5791	1345.714	16.0083	9.9	8.35	32745.6	4.64	HUMAN	P06748	Nucleophosmin
13794	dirMS_041712_NAR_60mM_plus.17531.17531.3	3	8.41	1	8.46E+05		(R)DKLNNL	(R)D K L N\N\L|V/L/F D K(A)		148.4	440.2499	1318.737	-0.0014	-1	5.96	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
13795	dirMS_041712_NAR_60mM_plus.20742.20742.3	3	8.41	0	6.87E+05		(R)LGFHLP	(R)L G F H/L\P L\E/V/A/Y/Q R(G)		168.68	514.9568	1542.843	0.0131	8.5	6.75	533778	5.74	HUMAN	Q15149	Plectin
13796	dirMS_041712_NAR_60mM_plus.6984.6986.3	3	8.41	1	2.25E+06		(K)IQDKEG	(K)I Q|D K E G I|P/P D Q Q R(L)		94.45	508.5982	1523.781	-0.0012	-0.8	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
13797	dirMS_041712_NAR_60mM_plus.7490.7490.3	3	8.41	1	1.14E+04		(R)KEAESS	(R)K E A E S S|P/F V/E R(L)		96.68	426.883	1278.632	0.002	1.6	4.79	92752.5	4.76	HUMAN	P14625	Endoplasmin
13798	dirMS_041712_NAR_120mM_minus.10795.10795.3	3	8.4	0	2.83E+05		(R)ILRPWQ	(R)I/L/R P W/Q|S S E T R(S)		112.95	458.2485	1372.733	-0.0022	-1.6	9.6	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
13799	dirMS_041712_NAR_120mM_minus.12234.12234.2	2	8.4	0	9.16E+04		(K)HLSVND	(K)H/L|S/V/N D|L P V G R(S)		120.85	603.8309	1206.659	-0.0044	-3.7	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
13800	dirMS_041712_NAR_30mM_minus2.5426.5426.2	2	8.4	0	1.66E+05		(K)YIDENQ	(K)Y I|D/E/N Q/D R(Y)		83.68	526.7389	1052.464	0.0062	5.9	4.03	6412.4	9.52	HUMAN	J3KSS4	Cytosolic non-specific dipeptidase (Fragment)
13801	dirMS_041712_NAR_30mM_minus2.8399.8399.2	2	8.4	0	1.09E+05		(K)CAMTAL	(K)C A/M/T A/L/S S/K(L)	C:Carbamidomethylation	100.45	484.7299	968.454	-0.0014	-1.5	8.75	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
13802	dirMS_041712_NAR_50mM_minus2.15173.15173.3	3	8.4	0	1.70E+05		(R)NSSHAG	(R)N S/S H A G A F\V I V/T/E/E A I A K(G)		154.33	615.3184	1843.955	-0.0142	-7.7	5.4	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
13803	dirMS_041712_NAR_120mM_plus.17949.17949.3	3	8.4	1	2.44E+05		(K)YRGFTIP	(K)Y R/G\F T\I|P/E/A F R(G)		147.67	452.9069	1356.706	0.0003	0.2	8.75	27264.5	5.09	HUMAN	O00299	Chloride intracellular channel protein 1
13804	dirMS_041712_NAR_20mM_plus.14349.14349.2	2	8.4	0	6.82E+04		(R)ELAQQV	(R)E L A Q/Q V Q/Q V/A D/D/Y/G K(C)		170.75	846.4161	1691.824	0.0014	0.8	4.03	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
13805	dirMS_041712_NAR_20mM_plus.8701.8701.2	2	8.4	0	2.34E+05		(R)VPPPPP	(R)V/P|P/P P P I A R(A)		130.57	472.2851	943.572	-0.0094	-10	9.72	32085.2	8.93	HUMAN	B4DY08	Heterogeneous nuclear ribonucleoproteins C1/C2
13806	dirMS_041712_NAR_30mM_plus2.20315.20315.2	2	8.4	0	8.64E+03		(R)ILLLGLD	(R)I L|L|L/G|L D N A G K(T)		161.75	563.8448	1126.683	-0.0007	-0.6	5.84	20626.3	6.76	HUMAN	P36405	ADP-ribosylation factor-like protein 3
13807	dirMS_041712_NAR_30mM_plus2.20976.20976.2	2	8.4	0	3.79E+05		(K)AIDLFTD	(K)A I|D L|F T D A I K(L)		164.42	553.8012	1106.609	-0.0141	-12.7	4.21	18141.9	4.7	HUMAN	F6VDH7	Hsc70-interacting protein (Fragment)
13808	dirMS_041712_NAR_30mM_plus2.22459.22459.2	2	8.4	0	1.02E+05		(R)SLDMDS	(R)S L/D/M/D S I/I A E/V K(A)		173.67	660.8437	1320.671	0.0086	6.5	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
13809	dirMS_041712_NAR_30mM_plus2.6857.6880.2	2	8.4	0	6.17E+04		(R)VYSTSV	(R)V/Y|S|T/S V/T G S R(E)		90.47	528.7673	1056.532	-0.0047	-4.4	8.72	9437.4	9.69	HUMAN	Q5T123	SH3 domain binding glutamic acid-rich protein like 3
13810	dirMS_041712_NAR_30mM_plus2.7994.7994.2	2	8.4	0	8.04E+05		(K)QGGGG	(K)Q G\G/G/G G/G G S V|P G I/E/R(M)		96.93	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
13811	dirMS_041712_NAR_50mM_plus2.11440.11440.3	3	8.4	1	4.13E+05		(K)GFALVG	(K)G F|A L/V/G V/G S E A S S K K(L)		127.98	479.5962	1436.774	-0.0003	-0.2	8.59	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
13812	dirMS_041712_NAR_50mM_plus2.22524.22524.3	3	8.4	1	1.26E+06		(R)GVMLA	(R)G V/M/L/A/V/D/A V I A E L K K(Q)		195.7	519.6393	1556.908	-0.0047	-3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
13813	dirMS_041712_NAR_60mM_plus.10120.10120.2	2	8.4	0	2.03E+06		(K)GIVEFS	(K)G I|V|E/F/S G K/P A A R(K)		111.3	616.3425	1231.679	-0.0016	-1.3	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
13814	dirMS_041712_NAR_20mM_minus.11000.11288.2	2	8.39	0	1.30E+05	M148m	(R)DLTDYL	(R)D L|T|D/Y/L/m K(I)	m:Oxidized methionine	160.17	507.7443	998.486	15.995	0.1	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
13815	dirMS_041712_NAR_50mM_minus2.12886.12886.3	3	8.39	1	1.80E+05		(K)GGELVY	(K)G G\E|L/V/Y T D\S E A R D V F E K(A)		141.5	638.9739	1914.908	-0.0008	-0.4	4.18	533778	5.74	HUMAN	Q15149	Plectin
13816	dirMS_041712_NAR_50mM_minus2.16973.16973.3	3	8.39	0	1.02E+05		(K)LILPHVD	(K)L I|L/P H V D/I Q L K(Y)		164.9	430.2702	1288.799	-0.0027	-2.1	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
13817	dirMS_041712_NAR_60mM_minus.14979.14979.3	3	8.39	1	1.08E+05		(K)KVEEVV	(K)K V E\E V\V|Y D L S I R(G)		143.75	483.9327	1449.795	-0.0112	-7.7	4.68	25685.9	6.4	HUMAN	E9PGT1	Translin
13818	dirMS_041712_NAR_120mM_plus.15134.15134.4	4	8.39	1	6.14E+05		(K)LRLFAVL	(K)L R L F A V/L/E Q L S P V/R(A)		132.4	411.0032	1640.985	0.0063	3.9	9.6	52671.6	6.38	HUMAN	Q9P2S5	WD repeat-containing protein WRAP73
13819	dirMS_041712_NAR_20mM_plus.13875.13875.2	2	8.39	0	1.34E+05		(R)GGIVDE	(R)G G I|V/D|E G/A L L R(A)		167.83	550.3066	1099.611	-0.0047	-4.3	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
13820	dirMS_041712_NAR_20mM_plus.16642.16642.3	3	8.39	0	2.14E+05		(K)VQIAVA	(K)V Q\I A V A\N\A/Q|E/L L Q R(M)		186.3	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
13821	dirMS_041712_NAR_20mM_plus.17764.17764.2	2	8.39	0	8.14E+04		(R)TTLLPGL	(R)T T/L/L/P G/L L K(T)		193.85	478.3131	955.619	0.0003	0.3	8.41	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
13822	dirMS_041712_NAR_30mM_plus2.15296.15439.2	2	8.39	0	7.58E+05		(R)QPTPPF	(R)Q P/T/P/P F/F G/R(D)		133.13	523.7794	1046.542	0.0097	9.3	9.75	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
13823	dirMS_041712_NAR_30mM_plus2.16493.16493.2	2	8.39	0	1.38E+05		(R)STLNEIY	(R)S T|L/N E/I\Y F/G K(T)		139.07	586.3039	1171.599	0.0012	1	5.72	29580	6.46	HUMAN	B1AK87	Capping protein (Actin filament) muscle Z-line, beta
13824	dirMS_041712_NAR_30mM_plus2.6635.6635.2	2	8.39	0	3.84E+05		(R)SPDNP	(R)S/P/D\N|P/M N Q\R(A)		88.78	529.7357	1058.468	-0.0042	-4	5.55	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
13825	dirMS_041712_NAR_30mM_plus2.6823.6823.2	2	8.39	0	9.23E+04		(R)GAEQLA	(R)G A|E|Q/L\A/E/G G\R(M)		90.18	494.2448	987.485	-0.0031	-3.1	4.53	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b
13826	dirMS_041712_NAR_40mM_plus2.9162.9162.2	2	8.39	0	9.58E+04		(R)LSIYEAR	(R)L S/I/Y/E/A R(C)		116.18	426.2316	851.462	-0.0062	-7.3	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
13827	dirMS_041712_NAR_50mM_plus2.10105.10105.3	3	8.39	1	5.94E+04		(K)ITIKNDP	(K)I T/I/K N D|P S/L P\E P/K(C)		120.53	484.6079	1451.81	-0.0013	-0.9	6.07	20203.8	9.79	HUMAN	B4DG16	Asparagine--tRNA ligase, cytoplasmic
13828	dirMS_041712_NAR_50mM_plus2.16094.16094.3	3	8.39	1	3.24E+04		(R)LKLPAV	(R)L K L P A V\V/T/A D/L R(L)		152.68	432.6039	1295.805	-0.0074	-5.7	8.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
13829	dirMS_041712_NAR_50mM_plus2.20144.20144.3	3	8.39	1	1.14E+05		(R)FLIPVLN	(R)F L/I|P V L N G L E/K/K(E)		174.58	457.6182	1370.841	-0.0006	-0.4	8.59	142001.7	5.82	HUMAN	Q92797	Symplekin
13830	dirMS_041712_NAR_50mM_plus2.21480.21480.3	3	8.39	1	8.47E+04		(K)ITPENLP	(K)I T/P E N L/P Q I L L/Q L K R(R)		183.3	592.694	1776.074	-0.0067	-3.8	8.75	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
13831	dirMS_041712_NAR_50mM_plus2.7699.7699.3	3	8.39	1	5.37E+04		(K)AEAAVV	(K)A E A A V/V A/V/A E K R(E)		106.47	405.2314	1213.69	-0.0103	-8.5	6.19	13360.2	9.87	HUMAN	Q8IZQ5	Selenoprotein H
13832	dirMS_041712_NAR_60mM_plus.10562.10562.2	2	8.39	1	1.66E+06		(R)VKYETEL	(R)V/K|Y/E|T E L A M\R(Q)		113.13	620.326	1239.64	0.0045	3.7	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13833	dirMS_041712_NAR_60mM_plus.5480.5480.3	3	8.39	1	1.34E+05		(K)CDSSPD	(K)C/D/S S P D S A/E/D/V R K(V)	C:Carbamidomethylation	86.15	489.2128	1465.622	0.0015	1	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
13834	dirMS_041712_NAR_60mM_plus.8350.8350.3	3	8.39	1	1.32E+05	M185m	(K)ALIEmE	(K)A L|I/E|m E K Q Q/Q D Q V D R(N)	m:Oxidized methionine	101.85	616.3117	1830.901	16.0191	13.1	4.32	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)
13835	dirMS_041712_NAR_20mM_minus.11299.11299.2	2	8.38	0	2.36E+05		(K)LSELEAA	(K)L/S/E/L/E A/A/L Q R(A)		159.67	565.3134	1129.621	-0.0016	-1.5	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
13836	dirMS_041712_NAR_20mM_minus.13590.13590.2	2	8.38	0	1.48E+05		(R)QAQEYE	(R)Q\A/Q/E/Y/E A L\L N/I K(V)		186.9	710.3754	1419.748	-0.0043	-3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13837	dirMS_041712_NAR_20mM_minus.14452.14452.2	2	8.38	0	2.09E+05		(K)DAGVIA	(K)D A\G\V|I/A G L/N/V L R(I)		198.25	599.3503	1197.695	-0.0017	-1.4	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
13838	dirMS_041712_NAR_30mM_minus2.11785.11785.2	2	8.38	0	2.89E+05		(R)AFPGPL	(R)A F|P/G/P L A/K(D)		117.83	400.7352	800.467	-0.0034	-4.2	8.8	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A

13839	dirMS_041712_NAR_30mM_minus2.7854.7913.2	2	8.38	0	4.61E+05		(K)IYSSEAIK	(K)I/Y|S S E A/I/K(S)		97.85	455.7458	910.488	-0.0037	-4.1	6	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
13840	dirMS_041712_NAR_40mM_minus2.10987.10987.3	3	8.38	0	7.92E+05		(R)QVSASE	(R)Q V/S A S/E L H/T S G I L/G/P E T L R(D)		148.75	665.6822	1995.051	-0.0185	-9.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
13841	dirMS_041712_NAR_40mM_minus2.14949.14949.3	3	8.38	1	7.94E+04		(R)VLEALLP	(R)V L|E A/L L\P L K G L E E R(V)		173.35	527.317	1579.942	-0.0053	-3.4	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
13842	dirMS_041712_NAR_50mM_minus2.15168.15168.3	3	8.38	0	3.97E+05		(R)DGLAFN	(R)D G L/A\F N A/L/I H R(H)		155.22	409.5594	1226.664	-0.0004	-0.3	6.74	146974	5.55	HUMAN	C9JRP8	Spectrin beta chain, non-erythrocytic 4
13843	dirMS_041712_NAR_50mM_minus2.16430.16481.3	3	8.38	0	1.75E+05	M1m	(-)mKPLVVI	(-)m K P L\V V/F\V|L/G/G P G\A\G K(G)	m:Oxidized methionine	161.27	529.3077	1569.919	15.99	-3.1	10	22450.2	5.44	HUMAN	P30085	UMP-CMP kinase
13844	dirMS_041712_NAR_50mM_minus2.5330.5330.3	3	8.38	0	8.24E+05		(K)TATPQQ	(K)T A/T/P Q\Q A Q E V H E K(L)		88.02	489.5768	1466.723	-0.0075	-5.1	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
13845	dirMS_041712_NAR_60mM_minus.18571.18571.3	3	8.38	1	1.24E+04		(K)GYPPED	(K)G Y/P/P E D/I F N L V/G K/K(V)		165.4	526.2842	1576.837	0.0011	0.7	6.07	40763.2	6.29	HUMAN	Q9NR45	Sialic acid synthase
13846	dirMS_041712_NAR_120mM_plus.9439.9439.3	3	8.38	1	1.26E+05		(R)SRAEAES	(R)S R A E A\E/S\M/Y Q/I/K(Y)		104.18	471.5662	1412.684	0.0002	0.1	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
13847	dirMS_041712_NAR_20mM_plus.12489.12489.2	2	8.38	0	1.78E+05		(R)GVEICIA	(R)G V\E/I/C/I|A/T P G R(L)	C:Carbamidomethylation	158.8	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
13848	dirMS_041712_NAR_20mM_plus.17631.17631.2	2	8.38	0	5.44E+04	M215m	(K)TLNDELE	(K)T L|N D E L/E/I/I/E G m K(F)	m:Oxidized methionine	193.07	760.8799	1504.756	15.9962	0.8	4	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
13849	dirMS_041712_NAR_50mM_plus2.10732.10732.3	3	8.38	1	5.02E+05		(R)VAVEEV	(R)V/A|V/E/E/V D E E G K F V R(L)		124.33	535.9422	1605.812	0.0002	0.1	4.25	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
13850	dirMS_041712_NAR_50mM_plus2.21404.21404.3	3	8.38	1	1.71E+05		(K)TGLSSEC	(K)T G L|S/S E Q T V N V L A Q I L K R(L)		183	653.0385	1957.108	-0.0067	-3.4	8.41	48481.7	6.95	HUMAN	E7EUG6	General transcription factor IIF subunit 1
13851	dirMS_041712_NAR_50mM_plus2.21460.21460.3	3	8.38	1	8.47E+04		(K)ITPENLP	(K)I T/P|E N L P Q I L L Q L K R(R)		183.3	592.694	1776.074	-0.0067	-3.8	8.75	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
13852	dirMS_041712_NAR_50mM_plus2.9303.9303.3	3	8.38	1	2.75E+05		(R)TNAENE	(R)T N|A E N E F V/T I/K K(D)		115.83	465.2518	1393.732	0.0087	6.2	5.81	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
13853	dirMS_041712_NAR_60mM_plus.12324.12324.3	3	8.38	1	9.36E+05		(R)LSFDKDA	(R)L/S/F D K D/A M/V/A/R(A)		121.18	418.2158	1252.635	-0.0026	-2.1	5.96	35556.4	9.3	HUMAN	F2Z393	Transaldolase
13854	dirMS_041712_NAR_60mM_plus.17251.17251.3	3	8.38	0	1.75E+04		(R)IYSHSLLI	(R)I Y S H/S|L\L/P V L/R(S)		147.6	433.2569	1297.763	-0.0065	-5	8.75	60871.9	6.3	HUMAN	B4DJ93	Phosphoribosylformylglycinamidine cyclo-ligase
13855	dirMS_041712_NAR_60mM_plus.5227.5227.3	3	8.38	1	4.08E+05		(K)VSSAEGA	(K)V/S/S/A E G A\A K E E/P K(R)		85.05	434.8867	1302.654	-0.008	-6.2	4.79	4801.6	11.17	HUMAN	F2Z2W6	Non-histone chromosomal protein HMG-14
13856	dirMS_041712_NAR_60mM_plus.8368.8368.3	3	8.38	0	6.61E+05	M148m	(R)AHSSmV	(R)A H S S\m\V/G/V/N L/P Q K(A)	m:Oxidized methionine	102.07	461.9069	1367.71	15.9962	0.9	8.8	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
13857	dirMS_041712_NAR_120mM_minus.14311.14311.4	4	8.37	2	6.16E+05		(K)MEIATKI	(K)M E\I/A T K/D/P L N P I K Q D|V K(K)		131.68	485.7686	1940.052	0.0004	0.2	5.88	33115.9	5.54	HUMAN	Q15181	Inorganic pyrophosphatase
13858	dirMS_041712_NAR_120mM_minus.15842.15842.4	4	8.37	1	3.85E+05		(R)ALEHFTI	(R)A L E H F T D L/Y/D/I/K R(A)		140.32	405.9646	1620.838	-0.0015	-0.9	5.38	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
13859	dirMS_041712_NAR_30mM_minus2.16096.16096.2	2	8.37	0	2.24E+04		(K)SEGGFIV	(K)S E|G G/F/I/W/A/C/K(N)	C:Carbamidomethylation	141.03	577.7702	1154.53	0.0032	2.8	5.72	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
13860	dirMS_041712_NAR_30mM_minus2.16251.16251.2	2	8.37	0	8.74E+03		(R)SETDLLD	(R)S E|T D L|L/D/I R(S)		141.68	531.2806	1061.547	0.0066	6.2	4.03	51583.6	7.73	HUMAN	B4DVE7	Annexin
13861	dirMS_041712_NAR_50mM_minus2.14968.14968.3	3	8.37	1	1.14E+04		(R)VRLGDV	(R)V R L G D V\I S I|Q/P C P D V K(Y)	C:Carbamidomethylation	153.7	599.3283	1795.974	-0.0031	-1.7	5.93	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
13862	dirMS_041712_NAR_50mM_minus2.7700.7700.3	3	8.37	0	1.57E+04		(K)VVQVSA	(K)V V/Q|V/S A G D S H T A A L/T D D G R(V)		111.02	633.641	1898.92	-0.0118	-6.2	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
13863	dirMS_041712_NAR_60mM_minus.15001.15001.3	3	8.37	0	2.01E+05		(R)IYIPLPEP	(R)I Y|I/P L/P E P H A/R(A)		143.9	435.9153	1305.731	0	0	6.75	49472.3	6.75	HUMAN	O75351	Vacuolar protein sorting-associated protein 4B
13864	dirMS_041712_NAR_120mM_plus.15087.15087.4	4	8.37	2	7.32E+05		(K)AMGDA	(K)A/M/G/D A E/I K D G E R L P L A V K(D)		132.55	479.0094	1913.016	-0.0003	-0.2	4.78	99900.1	5.04	HUMAN	B4DZI8	Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b
13865	dirMS_041712_NAR_40mM_plus2.12988.13131.3	3	8.37	0	3.41E+05		(K)NLPPSGA	(K)N L|P P S\G A V P V/T G I/P P H V V/K(V)		143.43	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
13866	dirMS_041712_NAR_40mM_plus2.17657.17657.3	3	8.37	0	3.79E+04		(R)AGLGSG	(R)A G L/G/S/G L S L/S G L V/H P E\L S R(S)		170.98	617.3431	1850.013	0.0017	0.9	6.79	73325.2	9.19	HUMAN	F5H2A9	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial
13867	dirMS_041712_NAR_40mM_plus2.6181.6181.3	3	8.37	1	3.14E+04		(R)AQLGGP	(R)A Q|L/G G P E/A A K S D E T A\A K(-)		95.22	548.6136	1643.824	0.0027	1.7	4.68	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
13868	dirMS_041712_NAR_50mM_plus2.19325.19325.3	3	8.37	0	5.40E+05		(K)HLLQAP	(K)H L\L Q A\P\L D D A|Q/E I|L/Q A\R(F)		169.5	644.3484	1931.035	-0.0039	-2	4.54	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
13869	dirMS_041712_NAR_50mM_plus2.7668.7668.3	3	8.37	1	1.64E+05		(K)VDDSSEI	(K)V/D|D/S S E D/K T E F T V K(N)		106.45	533.9169	1599.738	-0.0023	-1.4	4.11	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
13870	dirMS_041712_NAR_50mM_plus2.8842.8842.3	3	8.37	0	7.69E+05		(R)AALAHS	(R)A A L A H S\E E V/T|A/S Q V A\A T K(T)		113.47	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
13871	dirMS_041712_NAR_60mM_plus.19823.19823.3	3	8.37	0	3.29E+04		(K)SFLIWVN	(K)S F|L I/W V N E E D|H T R(V)		163.53	549.2699	1645.797	-0.0017	-1.1	4.65	29478.9	6.26	HUMAN	E9PCP8	Creatine kinase U-type, mitochondrial
13872	dirMS_041712_NAR_120mM_minus.11635.11635.4	4	8.36	2	9.96E+05		(R)SGKYDLI	(R)S G K Y D\L/D\F K/S/P D/D/P S R(Y)		117.92	457.4692	1826.855	-0.0006	-0.3	4.58	47510.4	7.04	HUMAN	P06733	Alpha-enolase
13873	dirMS_041712_NAR_120mM_minus.20392.20392.4	4	8.36	0	2.45E+05		(K)ALEHAFQ	(K)A L E H A F Q L E/H/I/M D/L T R(L)		167.78	481.7478	1923.975	-0.0052	-2.7	5.27	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
13874	dirMS_041712_NAR_20mM_minus.6406.6406.2	2	8.36	0	1.57E+05		(R)VLADPSI	(R)V L|A/D/P S D D T K(G)		107.4	530.7615	1060.516	0	0	3.93	266161	5.68	HUMAN	E9PPU0	Epiplakin
13875	dirMS_041712_NAR_20mM_minus.8699.8724.2	2	8.36	0	1.86E+05		(K)LVLVGDG	(K)L V|L|V/G D/G G T G K(T)		136.13	508.2919	1015.578	-0.0017	-1.7	5.84	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
13876	dirMS_041712_NAR_30mM_minus2.9701.9701.2	2	8.36	1	3.71E+05		(K)DVEAKT	(K)D/V/E A K T M/R(L)		107.03	475.2457	949.477	0.007	7.4	6.07	100477.3	8.42	HUMAN	E7EQC8	Rap guanine nucleotide exchange factor 3
13877	dirMS_041712_NAR_50mM_minus2.13076.13076.3	3	8.36	2	2.99E+04	S215s	(K)SRVsKLE	(K)S R/V s K/L E/E E/L A A E R(K)	s:N-acetylglucosamine (S)	141.2	607.3158	1616.86	203.0726	-3.7	4.94	31947.9	5.88	HUMAN	B1AMN7	CTTNBP2 N-terminal like (Fragment)
13878	dirMS_041712_NAR_60mM_minus.11613.11613.3	3	8.36	0	1.53E+05		(K)DLQHPN	(K)D L Q/H/P/N E F I R(G)		124.7	423.5497	1268.638	-0.0037	-2.9	5.32	15826.6	6.3	HUMAN	E9PKQ1	Coatomer subunit beta (Fragment)
13879	dirMS_041712_NAR_60mM_minus.6106.6106.3	3	8.36	1	1.45E+06		(K)DSYVGD	(K)D S|Y/V/G D E A Q S K R(G)		90.98	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
13880	dirMS_041712_NAR_120mM_plus.4288.4288.2	2	8.36	1	1.14E+06	M310m	(R)TKTEISEI	(R)T K|T/E/I S E m N R(N)	m:Oxidized methionine	70.07	612.7976	1208.594	15.994	-0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
13881	dirMS_041712_NAR_20mM_plus.12309.12309.3	3	8.36	0	1.73E+05		(K)IISNASC	(K)I I S N|A\S C T T/N C L/A|P L A K(V)	C:Carbamidomethylation	158.35	611.9768	1833.92	-0.0039	-2.1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
13882	dirMS_041712_NAR_20mM_plus.16194.16194.2	2	8.36	0	5.91E+04	M511m	(K)LmDVGL	(K)L/m/D/V G L I/A/I R(-)	m:Oxidized methionine	182.93	558.8267	1100.65	15.9965	1.4	5.84	60404.6	6.4	HUMAN	F5H0T1	Stress-induced-phosphoprotein 1
13883	dirMS_041712_NAR_20mM_plus.17315.17315.3	3	8.36	0	1.57E+05		(R)TTVPQLI	(R)T T V P Q L|L/A/S V Q R(W)		191.12	438.2581	1312.758	0.0014	1.1	9.41	266161	5.68	HUMAN	E9PPU0	Epiplakin
13884	dirMS_041712_NAR_20mM_plus.18899.18899.2	2	8.36	0	1.05E+05		(K)DTSYLFI	(K)D T S Y/L F/I/T/G P/D V V K(S)		201.92	777.9049	1554.805	-0.0025	-1.6	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
13885	dirMS_041712_NAR_20mM_plus.7164.7164.2	2	8.36	0	8.61E+04		(K)VAPAPA	(K)V A/P A/P A V/V/K(K)		116.67	426.2703	851.535	-0.0016	-1.9	8.72	30166.2	10.79	HUMAN	P62424	60S ribosomal protein L7a
13886	dirMS_041712_NAR_30mM_plus2.18973.18973.2	2	8.36	0	2.57E+05		(K)LAFNSLL	(K)L/A|F/N/S L L E K(A)		152.85	517.7928	1034.588	-0.0097	-9.4	6	109088.4	7.19	HUMAN	O75400	Pre-mRNA-processing factor 40 homolog A
13887	dirMS_041712_NAR_30mM_plus2.20062.20062.2	2	8.36	0	1.78E+05		(R)MLDMG	(R)M L|D M/G/F/E/P Q I R(K)		159.08	668.8241	1336.639	0.0021	1.6	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
13888	dirMS_041712_NAR_30mM_plus2.20105.20105.2	2	8.36	0	1.04E+04	M378m	(K)mFLNLLS	(K)m F|L/N L L S P/R(T)	m:Oxidized methionine	158.6	553.8012	1090.608	15.9874	-6.8	9.5	73080.2	9.04	HUMAN	O00178	GTP-binding protein 1
13889	dirMS_041712_NAR_30mM_plus2.20897.20897.2	2	8.36	0	4.92E+05		(K)QEFLINL	(K)Q E/F/L/I/N|L V K(Q)		163	552.331	1103.646	0.0088	8	6	72331.1	5.39	HUMAN	J3KMX3	Alpha-fetoprotein
13890	dirMS_041712_NAR_30mM_plus2.21493.21493.2	2	8.36	0	2.87E+05		(R)EADDIVI	(R)E A|D D/I/V/N W/L/K(K)		167.55	601.81	1202.605	0.0075	6.3	4.03	26363.4	4.91	HUMAN	I3L312	Protein disulfide-isomerase (Fragment)
13891	dirMS_041712_NAR_50mM_plus2.10096.10096.3	3	8.36	0	7.46E+05		(R)GISEETT	(R)G I/S/E/E T T T/G V H N L Y K(M)		120.05	550.2759	1648.818	-0.0045	-2.8	5.4	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
13892	dirMS_041712_NAR_50mM_plus2.10244.10244.3	3	8.36	0	3.78E+05		(R)MVQVH	(R)M/V/Q V H E L/S C E\G I S K(S)	C:Carbamidomethylation	121.6	539.5992	1616.777	0.006	3.7	5.38	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
13893	dirMS_041712_NAR_50mM_plus2.10788.10788.3	3	8.36	1	5.53E+05		(R)VAVEEV	(R)V/A/V/E E V/D E E G K F V R(L)		124.45	535.9422	1605.812	0.0002	0.1	4.25	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
13894	dirMS_041712_NAR_50mM_plus2.17517.17517.3	3	8.36	1	2.56E+05		(K)GSFLDKI	(K)G S/F/L/D K/I/S/P S V L R(N)		160.13	473.6038	1418.8	-0.0033	-2.4	8.75	64248.4	9.08	HUMAN	Q9BW04	Specifically androgen-regulated gene protein
13895	dirMS_041712_NAR_50mM_plus2.7509.7509.3	3	8.36	1	5.04E+04		(K)ALAAAG	(K)A L/A|A A/G Y/D V E\K/N N S R(I)		105.45	526.9339	1578.787	0.0001	0.1	6.11	21864.9	11.03	HUMAN	P10412	Histone H1.4
13896	dirMS_041712_NAR_50mM_plus2.8638.8638.3	3	8.36	0	9.82E+04		(K)TPHPVLT	(K)T P H P V L\T|P\V/A/A N\Q A K(Q)		112.42	515.284	1543.859	-0.0217	-14	8.44	94320	8.88	HUMAN	H0Y837	Nuclear pore complex protein Nup214 (Fragment)
13897	dirMS_041712_NAR_60mM_plus.11762.11762.2	2	8.36	0	1.31E+06		(R)FAQHGT	(R)F/A|Q|H|G/T F E Y E Y S Q R(W)		118.65	881.8928	1762.782	-0.0037	-2.1	5.4	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
13898	dirMS_041712_NAR_60mM_plus.20981.20981.3	3	8.36	0	4.25E+05		(R)SLHDALC	(R)S L H D A\L C|V L/A Q T/V K(D)	C:Carbamidomethylation	172.07	518.9516	1554.831	0.0094	6.1	6.46	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
13899	dirMS_041712_NAR_120mM_minus.13399.13399.3	3	8.35	2	2.61E+05		(R)AQKDEE	(R)A Q|K/D E E/K\M/E I Q|E/I\Q L K(E)		126.68	654.0058	1960.006	-0.0027	-1.4	4.58	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
13900	dirMS_041712_NAR_120mM_minus.8776.8776.3	3	8.35	0	1.36E+05		(K)THEDIEA	(K)T H|E D\I|E/A/Q/I R(E)		101.17	404.5343	1211.602	-0.0131	-10.8	4.65	17408.8	4.66	HUMAN	B4DGZ4	Splicing factor 3B subunit 1
13901	dirMS_041712_NAR_30mM_minus2.13978.13978.2	2	8.35	0	2.84E+05		(R)NLVDNIT	(R)N L|V/D/N/I T G Q R(L)		130	565.3015	1129.596	-0.0003	-0.3	5.84	533778	5.74	HUMAN	Q15149	Plectin
13902	dirMS_041712_NAR_30mM_minus2.9069.9069.2	2	8.35	0	4.00E+05		(K)DVDEAY	(K)D V|D|E|A Y M/N K(V)		103.58	542.736	1084.462	0.0032	2.9	4.03	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
13903	dirMS_041712_NAR_40mM_minus2.11190.11190.3	3	8.35	0	3.60E+05		(R)DAGEGL	(R)D A/G|E/G L/L A V Q I T D Q E G/K|P K(R)		148.37	657.0157	1969.024	0.0089	4.5	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
13904	dirMS_041712_NAR_40mM_minus2.12778.12778.3	3	8.35	0	3.09E+05		(R)DVQIGD	(R)D V|Q/I/G D I/V T/V G E C R P L S K(T)	C:Carbamidomethylation	159.6	662.684	1986.033	0.005	2.5	4.56	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
13905	dirMS_041712_NAR_40mM_minus2.6134.6134.2	2	8.35	0	1.51E+05		(K)AQYEDIA	(K)A Q|Y E/D I A N R(S)		101.52	540.2599	1079.512	0.0009	0.8	4.37	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
13906	dirMS_041712_NAR_50mM_minus2.11618.11618.3	3	8.35	0	2.76E+05	M291m	(K)TGEEIFG	(K)T/G\E|E/I/F G/T I G m R P N A K(N)	m:Oxidized methionine	134.2	579.6239	1720.869	15.9885	-3.7	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
13907	dirMS_041712_NAR_50mM_minus2.16879.16879.3	3	8.35	1	2.91E+05		(R)SELELTL	(R)S E|L/E/L/T L G K L E Q/V R(S)		163.75	538.9725	1614.906	-0.0032	-2	4.78	533778	5.74	HUMAN	Q15149	Plectin
13908	dirMS_041712_NAR_50mM_minus2.17922.17922.3	3	8.35	0	4.36E+05		(K)LVLIGSN	(K)L V|L I/G S N/H S L P F L/K(F)		171.27	513.3077	1537.91	-0.0015	-1	8.76	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
13909	dirMS_041712_NAR_60mM_minus.5708.5708.2	2	8.35	1	4.42E+06		(K)DSYVGD	(K)D S/Y|V|G D E A Q/S K/R(G)		87.58	677.8144	1354.623	-0.0018	-1.3	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
13910	dirMS_041712_NAR_60mM_minus.6443.6443.3	3	8.35	0	4.44E+04		(K)IVVQPET	(K)I V V Q/P E/T\Q H R(A)		94.27	402.8887	1206.659	-0.0074	-6.1	6.75	168774.8	5.17	HUMAN	E9PHR7	Nuclear factor of-activated T-cells 5
13911	dirMS_041712_NAR_60mM_minus.7615.7615.3	3	8.35	1	4.43E+04		(R)LVDSVKI	(R)L/V\D S V/K/E N A G/T/V R(I)		101.53	463.2554	1387.754	-0.0023	-1.7	6.07	43814.8	5.94	HUMAN	Q9BRX2	Protein pelota homolog
13912	dirMS_041712_NAR_120mM_plus.11575.11575.3	3	8.35	2	6.08E+05		(R)SGKYDLI	(R)S G K/Y\D L D/F K/S/P\D D/P S R(Y)		113.63	609.6232	1826.855	-0.0005	-0.3	4.58	47510.4	7.04	HUMAN	P06733	Alpha-enolase
13913	dirMS_041712_NAR_120mM_plus.15928.15928.4	4	8.35	1	3.73E+05	M202m	(K)ILGSGISS	(K)I L G S G I S/S/S S V L/H G/m V F K/K(E)	m:Oxidized methionine	136.77	491.5215	1947.073	15.991	-2	10	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
13914	dirMS_041712_NAR_120mM_plus.4752.4752.3	3	8.35	1	6.67E+03		(R)LRAETEC	(R)L R A E T E/Q/G/E/Q Q R(Q)		75.72	482.2449	1444.714	0.0063	4.3	4.79	533778	5.74	HUMAN	Q15149	Plectin
13915	dirMS_041712_NAR_20mM_plus.10618.10618.2	2	8.35	0	4.78E+04		(K)GILAADE	(K)G I|L|A/A|D/E S T/G S I A K(R)		145.93	666.8531	1332.7	-0.0016	-1.2	4.37	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
13916	dirMS_041712_NAR_20mM_plus.11636.11636.2	2	8.35	0	1.37E+05		(R)ANTFVA	(R)A N/T/F|V/A/E L/K(G)		152.98	496.7735	992.541	-0.0014	-1.4	6.05	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
13917	dirMS_041712_NAR_30mM_plus2.22312.22312.2	2	8.35	0	2.00E+05		(K)NSSYFVE	(K)N S S Y F/V/E/W/I/P N N V K(V)		171.95	848.9189	1696.833	-0.0024	-1.4	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
13918	dirMS_041712_NAR_40mM_plus2.7715.7715.2	2	8.35	0	5.58E+04		(R)VIGSGCI	(R)V I|G S/G C/N L D/S/A R(F)	C:Carbamidomethylation	105.37	624.8021	1248.6	-0.0032	-2.6	5.81	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
13919	dirMS_041712_NAR_50mM_plus2.15210.15210.3	3	8.35	1	5.49E+05		(R)AALDKA	(R)A A|L D K A\T V L|L S M S K(G)		148.22	483.2728	1447.819	-0.015	-10.4	8.64	50974.6	5.31	HUMAN	B5ME91	Programmed cell death protein 4
13920	dirMS_041712_NAR_50mM_plus2.21308.21308.3	3	8.35	1	1.82E+05		(K)ALFEEVF	(K)A L\F E/E/V/P E L/L/T E A E K K(E)		182.42	615.9987	1845.984	-0.0029	-1.6	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
13921	dirMS_041712_NAR_50mM_plus2.8656.8656.3	3	8.35	1	1.17E+05		(K)TENSGEA	(K)T E|N/S/G E|A L A K\V E D S N P\Q/K(T)		112.38	639.6441	1916.92	-0.0018	-1	4.41	13579.2	9.99	HUMAN	E9PPQ6	Thymocyte nuclear protein 1 (Fragment)
13922	dirMS_041712_NAR_50mM_plus2.9430.9430.3	3	8.35	0	7.71E+05		(R)DNIQGIT	(R)D N|I/Q/G I T K/P A I R(R)		117.22	442.5902	1325.754	0.0025	1.9	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
13923	dirMS_041712_NAR_60mM_plus.11266.11266.3	3	8.35	0	3.95E+05		(R)LNSKPPI	(R)L N/S K/P P N/I/G F K(K)		116.27	405.5675	1214.689	-0.0012	-1	10	40826.7	9.22	HUMAN	Q9Y295	Developmentally-regulated GTP-binding protein 1
13924	dirMS_041712_NAR_60mM_plus.17173.17173.3	3	8.35	1	4.65E+05		(R)GPIKFNV	(R)G P I K F N|V W/D/T A G Q E K(F)		146.62	563.9572	1689.86	-0.0024	-1.4	6.07	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
13925	dirMS_041712_NAR_120mM_minus.17915.17915.4	4	8.34	1	1.74E+05		(K)SKNILFV	(K)S K N I L F/V/I T K P D V/Y K(S)		151.63	442.0108	1765.026	-0.0045	-2.5	9.53	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
13926	dirMS_041712_NAR_120mM_minus.9687.9687.3	3	8.34	1	3.36E+05		(R)ALSTGEK	(R)A L|S T/G E K G F G Y/K(G)		107	419.8868	1257.647	-0.0015	-1.2	8.54	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
13927	dirMS_041712_NAR_20mM_minus.10923.10923.2	2	8.34	0	1.71E+05	M148m	(R)DLTDYLm	(R)D L/T/D/Y/L m K(I)	m:Oxidized methionine	157.15	507.7443	998.486	15.995	0.1	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
13928	dirMS_041712_NAR_20mM_minus.14540.14540.2	2	8.34	0	6.60E+04	M332m	(R)IVSQLLT	(R)I V/S Q L L T L m/D G L/K(Q)	m:Oxidized methionine	200.2	723.9145	1430.829	15.993	-1.3	5.84	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
13929	dirMS_041712_NAR_20mM_minus.6409.6409.2	2	8.34	0	1.57E+05		(R)VLADPSI	(R)V/L|A\D|P S D D T K(G)		107.4	530.7615	1060.516	0	0	3.93	266161	5.68	HUMAN	E9PPU0	Epiplakin
13930	dirMS_041712_NAR_20mM_minus.9206.9206.2	2	8.34	0	1.90E+05	M239m	(K)EITALAP	(K)E I/T\A|L/A/P S T m K(I)	m:Oxidized methionine	141.92	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
13931	dirMS_041712_NAR_30mM_minus2.9051.9051.2	2	8.34	0	6.53E+04		(R)GTPQQI	(R)G T/P/Q/Q/I D Y A R(Q)		103.72	574.7879	1148.57	-0.0009	-0.8	5.83	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
13932	dirMS_041712_NAR_50mM_minus2.11094.11094.3	3	8.34	0	1.29E+05		(R)IELGDVT	(R)I E|L G D/V T/P H/N I K(Q)		131.2	445.912	1335.727	-0.0052	-3.9	5.32	14942.8	8.71	HUMAN	C9J5D1	N-alpha-acetyltransferase 50
13933	dirMS_041712_NAR_50mM_minus2.12566.12566.3	3	8.34	0	3.06E+05		(K)AASDIAM	(K)A A S/D I A M/T E\L/P P T H P I R(L)		139.55	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
13934	dirMS_041712_NAR_50mM_minus2.14185.14185.3	3	8.34	1	1.56E+05		(K)KGVNLP	(K)K G V N L P G A\A\V/D\L/P A V S E K(D)		148.73	588.9987	1764.985	-0.0039	-2.2	6.07	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
13935	dirMS_041712_NAR_60mM_minus.15865.15865.3	3	8.34	1	3.56E+04		(K)AKEIGAD	(K)A K E\I/G A D\L V/L/Q I/S K(E)		147.3	495.6258	1484.868	-0.0054	-3.7	6.11	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
13936	dirMS_041712_NAR_60mM_minus.17240.17240.3	3	8.34	1	3.68E+05		(R)KAPSDLY	(R)K\A P S D\L|Y/Q/I I/L/K(A)		156.28	463.6095	1388.815	-0.0008	-0.6	8.5	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
13937	dirMS_041712_NAR_60mM_minus.8274.8274.2	2	8.34	1	5.97E+04	M174m	(R)VKYETEL	(R)V/K|Y/E/T E/L A m R(Q)	m:Oxidized methionine	106.05	628.3198	1239.64	15.9921	-2.2	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13938	dirMS_041712_NAR_120mM_plus.11739.11739.3	3	8.34	0	5.02E+05		(R)HSSLAG	(R)H S S L A G/C\Q/I/I/N Y R(T)	C:Carbamidomethylation	114.17	506.9192	1518.748	-0.0051	-3.4	8.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
13939	dirMS_041712_NAR_120mM_plus.17986.17986.3	3	8.34	1	3.36E+05		(K)YRGFTIP	(K)Y R G\F\T\I/P E/A F R(G)		148	452.9069	1356.706	0.0003	0.2	8.75	27264.5	5.09	HUMAN	O00299	Chloride intracellular channel protein 1
13940	dirMS_041712_NAR_120mM_plus.6859.6859.3	3	8.34	1	9.66E+04		(K)SNKDGG	(K)S N\K D G/G N Q|E|V/E I/A R(C)		89.93	506.2499	1516.735	0.0001	0.1	4.68	10305.6	6.94	HUMAN	H7C330	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
13941	dirMS_041712_NAR_20mM_plus.11524.11524.2	2	8.34	0	1.10E+05		(R)ANTFVA	(R)A N/T/F V|A E L K(G)		152.75	496.7735	992.541	-0.0014	-1.4	6.05	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
13942	dirMS_041712_NAR_20mM_plus.19209.19209.2	2	8.34	0	1.33E+05		(R)EGDVLT	(R)E G D\V/L/T\L/L/E S E R(E)		203.58	680.8536	1360.696	0.0045	3.3	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
13943	dirMS_041712_NAR_20mM_plus.9784.9784.2	2	8.34	0	1.99E+05		(K)VASGCLI	(K)V A/S G C/L/D/I/N S S V\K(G)	C:Carbamidomethylation	139.38	675.3376	1349.673	-0.005	-3.7	5.81	56837	7.19	HUMAN	E7ETT1	Propionyl-CoA carboxylase beta chain, mitochondrial
13944	dirMS_041712_NAR_30mM_plus2.11389.11389.2	2	8.34	0	6.42E+04		(R)QINDIQI	(R)Q I/N/D/I/Q/L S/R(D)		112.97	543.7971	1086.59	-0.0033	-3	5.84	36900.6	5.38	HUMAN	Q13347	Eukaryotic translation initiation factor 3 subunit I
13945	dirMS_041712_NAR_30mM_plus2.20528.20528.2	2	8.34	0	1.65E+05		(K)GSFSEQ	(K)G S F S|E/Q|G I\N E F L/R(E)		161.08	742.362	1483.718	-0.0009	-0.6	4.53	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
13946	dirMS_041712_NAR_30mM_plus2.22780.22780.3	3	8.34	0	4.63E+05		(R)ELSDFIS	(R)E L S D F\I/S/Y/L Q R(E)		177.23	457.5693	1370.695	-0.0017	-1.2	4.37	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
13947	dirMS_041712_NAR_40mM_plus2.9918.9918.3	3	8.34	0	1.48E+04		(R)AQIFAN	(R)A Q\I F A N\T/V/D N/A R(I)		122.43	440.561	1319.67	-0.0018	-1.4	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18

13948	dirMS_041712_NAR_50mM_plus2.15347.15347.3	3	8.34	1	8.13E+05		(R)GFPTIYF	(R)G F|P T/I Y F/S/P A N K K(L)		148.83	490.5973	1469.779	-0.0014	-0.9	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
13949	dirMS_041712_NAR_50mM_plus2.15463.15463.3	3	8.34	1	9.88E+05		(R)KVPGVT	(R)K V P G V T A I\E|L|D E D T/G T/F/R(I)		149.83	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
13950	dirMS_041712_NAR_50mM_plus2.15822.15822.3	3	8.34	1	1.94E+05		(K)LKLSILYF	(K)L K L S I L/Y/P/A T T G R(N)		151.17	478.2888	1432.852	-0.0004	-0.3	9.99	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
13951	dirMS_041712_NAR_50mM_plus2.17448.17448.3	3	8.34	1	4.78E+05		(R)ELELKVP	(R)E|L/E/L K V/P L/V/V R(L)		159.83	432.2745	1294.809	-0.0004	-0.3	6.24	20422.4	5.35	HUMAN	H0Y852	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial (Fragment)
13952	dirMS_041712_NAR_50mM_plus2.20103.20103.3	3	8.34	0	2.68E+05		(R)LQSLPF	(R)L Q\S/L/P F/A L/T H/L N L K(A)		173.9	532.3178	1594.931	0.0073	4.6	8.76	175851.7	5.01	HUMAN	Q14160	Protein scribble homolog
13953	dirMS_041712_NAR_60mM_plus.18205.18205.3	3	8.34	1	3.37E+05		(R)IRIDSLS	(R)I R I D\S L\S\A/Q|L/S/Q L Q K(Q)		153.28	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
13954	dirMS_041712_NAR_60mM_plus.5182.5182.3	3	8.34	1	4.08E+05		(K)VSSAEG	(K)V/S/S/A E G A\A K E E/P K(R)		85.05	434.8867	1302.654	-0.008	-6.2	4.79	4801.6	11.17	HUMAN	F2Z2W6	Non-histone chromosomal protein HMG-14
13955	dirMS_041712_NAR_120mM_minus.5605.5605.3	3	8.33	1	1.10E+05		(K)VSQGVE	(K)V/S Q/G V E/D/G/P D T/K R(A)		84.03	463.2365	1387.681	0.0137	9.9	4.56	33726	7.84	HUMAN	B3KNJ4	SUMO-1 activating enzyme subunit 1, isoform CRA_a
13956	dirMS_041712_NAR_30mM_minus2.17696.17696.3	3	8.33	0	1.27E+05		(R)SLAALSC	(R)S L\A A\L|S Q I/A Y/Q R(N)		150.78	440.9139	1320.727	0.0001	0.1	8.46	64225	6.66	HUMAN	E7EX44	Caldesmon
13957	dirMS_041712_NAR_40mM_minus2.14318.14318.3	3	8.33	1	1.61E+05		(K)TGISDVF	(K)T G I/S D\V\F A K N D\L/A/V/V D/V R(I)		168.48	640.3454	1919.023	-0.0016	-0.8	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
13958	dirMS_041712_NAR_40mM_minus2.8162.8162.3	3	8.33	0	1.18E+04	M33m	(R)VLTEDE	(R)V L/T E/D E m G H/P E I G D A I A/R(L)	m:Oxidized methionine	127.97	656.9824	1952.938	15.9944	-0.2	4.17	40874	5.06	HUMAN	E9PCI9	Farnesyl pyrophosphate synthase
13959	dirMS_041712_NAR_50mM_minus2.6662.6662.3	3	8.33	1	5.62E+04		(R)AVASQP	(R)A V|A\S Q/P D S V D A A E R A E K(F)		104.9	581.9591	1743.851	0.012	6.9	4.32	81955.5	5.78	HUMAN	E9PHT6	Pantothenate kinase 4
13960	dirMS_041712_NAR_60mM_minus.14900.14900.3	3	8.33	1	1.58E+05		(R)SEIDLLN	(R)S E|I D/L/L\N I/R R(E)		142.73	410.2411	1228.701	0.0079	6.5	5.79	75617.5	5.46	HUMAN	A6NN80	Annexin
13961	dirMS_041712_NAR_60mM_minus.17890.17890.3	3	8.33	1	4.78E+05		(R)KVESLQ	(R)K V E S\L Q/E E|I/A/F L K(K)		160.22	511.9529	1533.852	-0.0081	-5.3	4.79	49709.6	5.19	HUMAN	B0YJC4	Vimentin
13962	dirMS_041712_NAR_120mM_plus.10560.10560.2	2	8.33	1	1.77E+06		(R)VKYETEL	(R)V/K|Y E/T E L/A M R(Q)		107.83	620.3237	1239.64	-0.0001	0	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
13963	dirMS_041712_NAR_120mM_plus.16351.16351.4	4	8.33	1	8.96E+05		(R)ALEHFT	(R)A L/E/H F T D L/Y/D/I K/R(A)		138.43	405.9647	1620.838	-0.0011	-0.7	5.38	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
13964	dirMS_041712_NAR_20mM_plus.10633.10633.2	2	8.33	0	4.60E+04		(R)SGYLLPD	(R)S G Y|L L/P D/T K(A)		145.88	497.2665	993.525	0.0006	0.6	5.55	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
13965	dirMS_041712_NAR_20mM_plus.14163.14163.2	2	8.33	0	1.01E+05		(R)ELAVQIY	(R)E L A|V/Q/I Y E E/A/R(K)		169.88	660.839	1320.679	-0.0087	-6.6	4.25	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
13966	dirMS_041712_NAR_20mM_plus.15737.15737.2	2	8.33	0	3.22E+05		(K)VGINYQ	(K)V G I N Y\Q|P P T\V/V|P G G D L A K(V)		179.12	912.9952	1824.985	-0.0023	-1.3	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
13967	dirMS_041712_NAR_20mM_plus.16691.16691.2	2	8.33	0	2.39E+05		(K)VQIAVA	(K)V Q|I A/V|A N A/Q E L/L Q R(M)		186.53	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
13968	dirMS_041712_NAR_30mM_plus2.17755.17755.2	2	8.33	0	2.19E+05		(R)YCAQD	(R)Y C|A|Q/D|A/F F Q V K(E)	C:Carbamidomethylation	146.07	688.8174	1376.63	-0.0028	-2.1	5.83	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
13969	dirMS_041712_NAR_40mM_plus2.10034.10034.2	2	8.33	0	1.20E+05		(R)YSGSYN	(R)Y/S\G/S Y/N D/Y L R(A)		123.83	619.2788	1237.548	0.0019	1.6	5.83	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
13970	dirMS_041712_NAR_40mM_plus2.9030.9030.3	3	8.33	0	4.93E+04		(K)VVQVSA	(K)V V\Q|V/S A/G D S H T A A\L T D D G R(V)		115.07	633.6448	1898.92	-0.0004	-0.2	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
13971	dirMS_041712_NAR_50mM_plus2.10223.10223.3	3	8.33	0	3.78E+05		(R)MVQVH	(R)M V|Q\V/H E L/S C/E G I/S K(S)	C:Carbamidomethylation	121.6	539.5992	1616.777	0.006	3.7	5.38	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
13972	dirMS_041712_NAR_50mM_plus2.16117.16117.3	3	8.33	1	5.13E+04		(R)DVDFEL	(R)D V/D/F E|L I K V E G K(V)		152.78	464.5859	1391.742	0.0015	1.1	4.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
13973	dirMS_041712_NAR_50mM_plus2.19323.19347.3	3	8.33	1	8.77E+05		(R)ASLEAA	(R)A S|L E/A/A/I A/D/A E Q R G E L A I K(D)		170.55	652.6835	1956.04	-0.0037	-1.9	4.41	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
13974	dirMS_041712_NAR_50mM_plus2.19833.19833.3	3	8.33	0	5.26E+04		(K)GLCLLE	(K)G L C|L/L/E Q I D S/F K P P Q R(S)	C:Carbamidomethylation	172.9	634.3344	1900.995	-0.0063	-3.3	6.07	45536.8	9.03	HUMAN	B7Z1K2	HBS1-like protein
13975	dirMS_041712_NAR_50mM_plus2.20994.20994.3	3	8.33	0	3.79E+05	S1387s	(R)LIHLSTA	(R)L/I H L S T A P|E A/s L P A R(S)	s:N-acetylglucosamine (S)	179.62	593.6536	1575.885	203.0609	-10.4	6.75	176978	9.15	HUMAN	O14514	Brain-specific angiogenesis inhibitor 1
13976	dirMS_041712_NAR_60mM_plus.15525.15558.3	3	8.33	1	7.28E+05		(K)KLLDLV	(K)K\L L D L\V|Q|Q/S/C/N Y K(Q)	C:Carbamidomethylation	137.97	536.9512	1608.841	-0.0024	-1.5	8.5	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
13977	dirMS_041712_NAR_60mM_plus.17368.17368.3	3	8.33	1	3.74E+05		(R)KVPGVT	(R)K V P G V T A\I|E\L|D E/D/T G T F R(I)		148.18	650.0017	1948.002	-0.0117	-6	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
13978	dirMS_041712_NAR_120mM_minus.13012.13012.3	3	8.32	1	1.39E+05		(R)VGDLYS	(R)V/G/D/L/Y S D/L\R D G R(N)		125.03	455.898	1365.676	0.0037	2.7	4.43	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
13979	dirMS_041712_NAR_20mM_minus.9748.9748.2	2	8.32	0	2.50E+05	M33m	(K)VAGmD	(K)V A\G m/D|V|E L/T/V E/E R(N)	m:Oxidized methionine	147.53	732.355	1447.71	15.993	-1.3	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
13980	dirMS_041712_NAR_40mM_minus2.14476.14476.3	3	8.32	0	1.74E+04		(K)SLCIPFK	(K)S L/C|I/P/F K P L C E L Q P G A K(C)	C:Carbamidomethylation	170.4	653.3446	1958.024	-0.0046	-2.3	8.31	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
13981	dirMS_041712_NAR_40mM_minus2.15428.15428.3	3	8.32	1	3.04E+05		(R)GGPNIIT	(R)G G/P/N I|I/T L/A/D\I V K D/P V S R(T)		178.43	622.3523	1865.049	-0.0067	-3.6	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
13982	dirMS_041712_NAR_50mM_minus2.10429.10429.3	3	8.32	1	1.08E+05	M72m	(R)TEmENE	(R)T/E/m E N E|F V L/I/K K(D)	m:Oxidized methionine	127.55	499.5937	1480.772	15.995	0	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
13983	dirMS_041712_NAR_50mM_minus2.17680.17680.3	3	8.32	0	1.96E+05		(R)DVCTEL	(R)D V|C/T E L/L/P L/I K P Q G R(V)	C:Carbamidomethylation	168.92	580.3212	1738.952	-0.003	-1.7	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
13984	dirMS_041712_NAR_50mM_minus2.8535.8535.3	3	8.32	1	1.85E+04	M244m	(K)ILIANTG	(K)I L|I A N/T G m/D/T D K I K(I)	m:Oxidized methionine	116.43	516.9426	1532.835	15.978	-10.9	5.96	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
13985	dirMS_041712_NAR_60mM_minus.17252.17252.3	3	8.32	0	9.52E+04		(R)GFGHIG	(R)G F G H I G I A\V|P D V/Y S A/C K(R)	C:Carbamidomethylation	156.02	597.6347	1790.889	0.0001	0.1	6.74	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
13986	dirMS_041712_NAR_120mM_plus.10219.10750.3	3	8.32	1	6.04E+06	S65s	(R)FIGDYE	(R)F I G D Y E P|N T G/K L Y s R(L)	s:N-acetylglucosamine (S)	108.65	654.972	1759.865	203.0365	-21.9	6.07	27176.8	9.3	HUMAN	Q6T310	Ras-like protein family member 11A
13987	dirMS_041712_NAR_120mM_plus.24000.24000.4	4	8.32	2	2.52E+05		(R)RGVML	(R)R G V M L|A/V/D A/V/I/A E L K K(Q)		179.92	429.0075	1713.009	-0.001	-0.6	8.59	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
13988	dirMS_041712_NAR_120mM_plus.9565.9565.3	3	8.32	0	1.07E+05		(K)STAGDT	(K)S T/A/G D T H L/G G E D F D/N R(M)		103.08	564.579	1691.726	-0.0031	-1.9	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
13989	dirMS_041712_NAR_20mM_plus.12725.12725.2	2	8.32	0	1.18E+05	M137m	(K)IEVIEIm	(K)I E|V|I E|I/m T D R(G)	m:Oxidized methionine	160.8	617.8225	1218.64	15.9979	2.4	4.14	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
13990	dirMS_041712_NAR_20mM_plus.12874.12874.2	2	8.32	0	1.44E+05		(R)LVVPAS	(R)L V|V/P\A\S Q C\G S\L/I/G K(G)	C:Carbamidomethylation	161.58	714.8991	1428.788	0.003	2.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
13991	dirMS_041712_NAR_20mM_plus.14695.14695.2	2	8.32	0	1.98E+05	M179m M	(K)mFVLDE	(K)m F/V|L/D E|A D E m/L S R(G)	m:Oxidized methionine	173.6	794.3555	1555.713	31.9906	0.5	3.91	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
13992	dirMS_041712_NAR_20mM_plus.16339.16339.2	2	8.32	0	8.43E+04		(R)AYILNLV	(R)A Y|I/L/N L V K(Q)		183.77	467.2905	933.577	-0.0031	-3.3	8.63	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
13993	dirMS_041712_NAR_20mM_plus.17007.17007.2	2	8.32	0	1.41E+05		(K)FATEAAI	(K)F A/T E/A/A I/T I L\R(I)		188.72	603.3442	1205.689	-0.0077	-6.4	6	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
13994	dirMS_041712_NAR_20mM_plus.18312.18312.2	2	8.32	0	1.70E+05		(R)LTGQLF	(R)L/T G Q/L|F/L/G\G S I V K(G)		197.02	666.8962	1332.789	-0.0034	-2.6	8.75	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
13995	dirMS_041712_NAR_20mM_plus.8207.8207.2	2	8.32	0	1.06E+05		(K)VTEDTS	(K)V/T/E/D/T/S/S V L R(S)		126.02	553.7889	1106.569	0.0017	1.6	4.37	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
13996	dirMS_041712_NAR_30mM_plus2.17906.17906.2	2	8.32	0	6.24E+04		(K)TFEVCD	(K)T\F|E/V/C D L/P V R(A)	C:Carbamidomethylation	147.03	618.3057	1235.609	-0.0048	-3.9	4.37	99900.1	5.04	HUMAN	B4DZI8	Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b
13997	dirMS_041712_NAR_30mM_plus2.18409.18409.2	2	8.32	0	2.24E+05		(K)TTFEDL	(K)T T|F/E/D L I Q/R(C)		149.45	561.7934	1122.579	0.0006	0.5	4.37	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
13998	dirMS_041712_NAR_30mM_plus2.21580.21580.2	2	8.32	0	1.45E+05		(R)IITLAGP	(R)I I\T/L/A/G P T N A I/F K(A)		168.18	679.9016	1358.804	-0.0083	-6.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
13999	dirMS_041712_NAR_40mM_plus2.8313.8313.2	2	8.32	1	8.53E+04		(R)KQNDV	(R)K Q N D V/F|G E\A\E|Q(-)		109.63	632.7929	1264.58	-0.0019	-1.5	4.14	51209.4	5	HUMAN	P31150	Rab GDP dissociation inhibitor alpha
14000	dirMS_041712_NAR_50mM_plus2.7542.7542.3	3	8.32	0	3.69E+05		(R)VGQAV	(R)V/G Q/A V D V/V/G Q\A G K/P/K(T)		105.72	484.9438	1452.817	-0.0001	0	8.56	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
14001	dirMS_041712_NAR_60mM_plus.12738.12738.3	3	8.32	0	3.02E+05		(R)ILHLLG	(R)I L H L|L G Q/E/G P K(T)		123.6	402.2397	1204.705	-0.0003	-0.2	6.75	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
14002	dirMS_041712_NAR_60mM_plus.9470.9470.2	2	8.32	0	4.97E+05		(K)SYCAEIA	(K)S Y/C\A/E|I/A H N V/S S K(N)	C:Carbamidomethylation	107.47	733.3425	1465.674	0.0037	2.5	6.47	15730.4	11.67	HUMAN	D3YTB1	60S ribosomal protein L32 (Fragment)
14003	dirMS_041712_NAR_30mM_minus2.10345.10362.2	2	8.31	0	4.22E+05		(K)NQLAVL	(K)N\Q|L|A/V/L/R(V)		110.38	407.2465	813.494	-0.0084	-10.3	9.75	25129.7	5.1	HUMAN	Q9Y3E7	Charged multivesicular body protein 3
14004	dirMS_041712_NAR_30mM_minus2.11563.11563.2	2	8.31	0	3.67E+05		(K)EIAEAYL	(K)E I/A/E/A Y/L/G K(T)		115.85	497.265	993.525	-0.0024	-2.4	4.53	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
14005	dirMS_041712_NAR_30mM_minus2.19249.19249.2	2	8.31	0	2.12E+05		(K)SYELPD	(K)S Y E|L/P D G Q V I/T I/G N E R(F)		159.07	895.9492	1790.892	-0.0008	-0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
14006	dirMS_041712_NAR_30mM_minus2.6634.6634.2	2	8.31	0	3.96E+04		(R)LQDTSS	(R)L/Q/D/T/S S Y A K(I)		91.87	506.7468	1012.495	-0.0082	-8.1	5.83	334221.3	6.44	HUMAN	P15924	Desmoplakin
14007	dirMS_041712_NAR_50mM_minus2.17448.17448.3	3	8.31	1	3.48E+05		(K)GYPPED	(K)G Y/P/P E D I F N L V/G K/K(V)		167.23	526.2832	1576.837	-0.0019	-1.2	6.07	40763.2	6.29	HUMAN	Q9NR45	Sialic acid synthase
14008	dirMS_041712_NAR_50mM_minus2.7139.7139.3	3	8.31	1	3.00E+04		(R)GIEPTG	(R)G I\E/P/T G N M V/K Q/P A K(F)		107.48	490.5972	1469.778	-0.001	-0.7	8.59	258215.9	5.48	HUMAN	E7EN95	Filamin-B
14009	dirMS_041712_NAR_120mM_plus.5379.5379.2	2	8.31	0	1.88E+05		(K)YLPHSA	(K)Y L|P/H/S A G R(Y)		81.35	450.7388	900.469	0.0017	1.9	8.75	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
14010	dirMS_041712_NAR_120mM_plus.6512.6512.2	2	8.31	1	2.84E+05		(R)SIAKEGF	(R)S I|A/K/E G/F E K(I)		87.12	504.7715	1008.536	-0.0003	-0.3	5.86	17213.7	10.05	HUMAN	B7Z712	60 kDa heat shock protein, mitochondrial
14011	dirMS_041712_NAR_30mM_plus2.12757.12757.2	2	8.31	0	5.53E+05		(R)CNNVLY	(R)C/N\N/V|L/Y/I/R(G)	C:Carbamidomethylation	120.78	526.2726	1051.535	0.0026	2.5	8.75	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F
14012	dirMS_041712_NAR_30mM_plus2.6426.6426.2	2	8.31	0	1.26E+05		(R)AVVISG	(R)A V|V I/S G A G K(M)		88.03	401.2461	801.483	0.002	2.6	8.8	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
14013	dirMS_041712_NAR_40mM_plus2.17815.17815.3	3	8.31	0	1.42E+05		(R)DIKPQN	(R)D I\K P Q N\L\L|L D/P D T A V/L K(L)		170.92	631.6874	1893.069	-0.0215	-11.4	4.43	47257	9.38	HUMAN	P49841	Glycogen synthase kinase-3 beta
14014	dirMS_041712_NAR_50mM_plus2.18901.19011.3	3	8.31	1	3.01E+05		(R)DSIVAEL	(R)D S/I/V/A/E/L D/R E M S R(S)		167.35	507.5872	1520.737	0.0097	6.4	4.32	34709.6	4.98	HUMAN	O14579	Coatomer subunit epsilon
14015	dirMS_041712_NAR_60mM_plus.12698.12698.3	3	8.31	0	5.74E+05		(K)GSYSLS	(K)G S|Y/S/L S H V Y T/P N D V R(M)		123.12	565.6098	1694.813	0.0016	0.9	6.74	63566.6	6.3	HUMAN	P07686	Beta-hexosaminidase subunit beta
14016	dirMS_041712_NAR_60mM_plus.9637.9637.3	3	8.31	0	9.53E+05		(K)GHENVE	(K)G H E N\V\E\A\A|Q/A E Y I E K(F)		107.98	563.2692	1687.792	0.0008	0.5	4.48	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
14017	dirMS_041712_NAR_120mM_minus.13831.13831.3	3	8.3	1	3.29E+05		(R)EMDRE	(R)E M/D R E T\L/I/D/V A R(T)		129.65	483.2462	1447.721	0.0031	2.1	4.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
14018	dirMS_041712_NAR_120mM_minus.19706.19706.3	3	8.3	1	1.51E+05		(K)GTKHLS	(K)G T K H L|S/P Y A T L T\V G D S S H K(T)		163.07	667.0203	1999.024	0.022	11	8.51	123367.7	5.57	HUMAN	Q9BSJ8	Extended synaptotagmin-1
14019	dirMS_041712_NAR_30mM_minus2.14564.14564.2	2	8.3	0	2.19E+05		(K)QVSVFQ	(K)Q V/S/V/F/Q/A M/K(K)		132.58	519.2752	1037.545	-0.0017	-1.6	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
14020	dirMS_041712_NAR_30mM_minus2.16953.16953.2	2	8.3	0	3.39E+05		(K)FANPFP	(K)F/A/N|P/F/P A A V R(G)		146.38	545.2937	1089.584	-0.0039	-3.5	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
14021	dirMS_041712_NAR_50mM_minus2.12906.12906.3	3	8.3	1	1.79E+05		(K)GGELVY	(K)G G E|L|V|Y/T D S E A R D V F E K(A)		141.53	638.9739	1914.908	-0.0008	-0.4	4.18	533778	5.74	HUMAN	Q15149	Plectin
14022	dirMS_041712_NAR_60mM_minus.14230.14241.3	3	8.3	1	1.50E+05		(R)KGVEGL	(R)K G V E\G\L\I/D\I|E/N/P N R(V)		139.28	518.6141	1553.828	-0.0004	-0.3	4.68	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
14023	dirMS_041712_NAR_60mM_minus.18560.18560.3	3	8.3	1	1.72E+05		(K)VVLDDK	(K)V/V/L D/D/K D Y/F L F R(D)		165.12	510.6099	1529.8	0.0153	10	4.43	5189.9	4.56	HUMAN	B8ZZ54	10 kDa heat shock protein, mitochondrial
14024	dirMS_041712_NAR_120mM_plus.21448.21448.3	3	8.3	1	2.33E+05		(R)GLFIIDD	(R)G L|F/I/I D/D/K/G\I L R(Q)		165.98	453.9377	1359.8	-0.0009	-0.7	5.96	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
14025	dirMS_041712_NAR_20mM_plus.16518.16518.2	2	8.3	0	2.36E+05		(R)ADLIAYL	(R)A/D L|I/A Y\L\K(K)		184.45	453.7678	906.529	-0.0012	-1.3	5.88	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
14026	dirMS_041712_NAR_20mM_plus.18648.18648.2	2	8.3	0	1.58E+05		(R)IITLTGP	(R)I I/T|L/T/G P T N A I F K(A)		200.32	694.9091	1388.815	-0.0039	-2.8	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
14027	dirMS_041712_NAR_20mM_plus.7995.7995.2	2	8.3	0	8.91E+04		(K)VEIIAND	(K)V E|I/I/A N\D Q G N R(T)		124.3	614.8177	1228.628	0.0001	0.1	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
14028	dirMS_041712_NAR_30mM_plus2.11239.11239.3	3	8.3	0	2.98E+05	M304m	(R)MGQM	(R)M G Q M A M/G G/A m/G I/N N/R(G)	m:Oxidized methionine	112.7	518.8921	1538.67	15.9923	-1.7	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
14029	dirMS_041712_NAR_30mM_plus2.17920.17920.3	3	8.3	0	1.70E+05		(R)MADAL	(R)M A\D\A L\D/N/Y/V/I/R(G)		146.95	427.5478	1280.63	-0.0015	-1.2	4.21	15838.9	7.03	HUMAN	H0Y5U0	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
14030	dirMS_041712_NAR_30mM_plus2.8361.8361.2	2	8.3	0	5.91E+05		(R)FAQIVQ	(R)F/A|Q/I V Q/K(G)		97.57	417.2466	833.488	-0.002	-2.4	8.75	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
14031	dirMS_041712_NAR_40mM_plus2.13030.13030.3	3	8.3	0	2.84E+05		(K)NLPPSG	(K)N L/P P S\G A V P V T G I/P P H V V K(V)		143.33	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
14032	dirMS_041712_NAR_50mM_plus2.10122.10122.3	3	8.3	1	3.09E+05		(R)LGLPGD	(R)L G|L|P/G D E/V D N K V K(G)		120.28	461.9229	1383.748	0.0063	4.6	4.56	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
14033	dirMS_041712_NAR_50mM_plus2.10134.10134.3	3	8.3	0	4.13E+05		(R)MVQVH	(R)M/V|Q/V H E\L G C E G I/S K(S)	C:Carbamidomethylation	120.23	529.5984	1586.767	0.0141	8.9	5.38	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
14034	dirMS_041712_NAR_60mM_plus.12333.12333.3	3	8.3	1	2.56E+04		(R)VFDKEG	(R)V F/D/K E G\N G T/V/M G A E/I R(H)		120.43	574.9548	1722.848	0.0019	1.1	4.68	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
14035	dirMS_041712_NAR_60mM_plus.16415.16415.3	3	8.3	0	7.53E+06		(R)EHALLA	(R)E H A\L L\A|Y/T\L/G V K(Q)		143.45	438.9179	1314.742	-0.0025	-1.9	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
14036	dirMS_041712_NAR_60mM_plus.9061.9061.3	3	8.3	1	3.28E+05		(K)SEETLDE	(K)S E|E|T L D/E G P/P K Y T K(S)		105.1	531.9256	1593.764	-0.002	-1.3	4.41	25233.4	9.34	HUMAN	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3
14037	dirMS_041712_NAR_60mM_plus.9427.9427.3	3	8.3	1	1.94E+06		(K)VVWVE	(K)V V|W V/E E S D/K/R(S)		107.43	416.221	1246.643	0.0058	4.7	4.68	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
14038	dirMS_041712_NAR_120mM_minus.13998.13998.4	4	8.29	1	1.58E+06		(K)ASIHEA	(K)A/S\I H E A W T D|G K/E A M/L/K(H)		130	447.476	1786.879	0.0029	1.6	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
14039	dirMS_041712_NAR_20mM_minus.12089.12089.2	2	8.29	0	8.92E+05	M313m	(R)TVQSLE	(R)T V/Q|S/L|E I D L D S m R(N)	m:Oxidized methionine	170.45	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
14040	dirMS_041712_NAR_50mM_minus2.14884.14884.3	3	8.29	1	2.56E+05	S1088s	(K)LYSAFC	(K)L/Y/S A F C A s/H T K/V P K(V)	C:Carbamidomethylation s:N-ace	152.8	604.6516	1608.82	203.12	22.4	9.7	171889.5	6.32	HUMAN	F5GZ53	T-lymphoma invasion and metastasis-inducing protein 1
14041	dirMS_041712_NAR_60mM_minus.17447.17447.3	3	8.29	0	2.98E+05		(K)GSDHSA	(K)G S D H\S A S L/E|P G/E L/A E L V R(S)		156.93	622.9764	1866.919	-0.0045	-2.4	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
14042	dirMS_041712_NAR_120mM_plus.7275.7275.2	2	8.29	1	4.77E+05		(K)SLDEME	(K)S/L|D/E/M/E/K Q/Q R(E)		91.18	632.3059	1263.6	0.0047	3.8	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
14043	dirMS_041712_NAR_20mM_plus.17858.17858.2	2	8.29	0	1.61E+05		(R)TVQSLE	(R)T V|Q|S|L/E I D L D S M R(N)		194.87	753.8776	1506.747	0.0011	0.7	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
14044	dirMS_041712_NAR_20mM_plus.18044.18044.2	2	8.29	0	3.08E+05		(R)ILVATN	(R)I L|V/A/T N L F G R(G)		195.02	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
14045	dirMS_041712_NAR_30mM_plus2.16599.16599.2	2	8.29	0	1.85E+05		(K)SIELFYK	(K)S/I|E/L F Y/K(F)		140.02	450.2484	899.487	0.0022	2.5	5.72	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
14046	dirMS_041712_NAR_30mM_plus2.8915.8915.2	2	8.29	0	1.11E+05		(R)LQLEAT	(R)L Q|L/E\A/T E R(Q)		99.87	480.2606	959.516	-0.0017	-1.8	4.53	533778	5.74	HUMAN	Q15149	Plectin
14047	dirMS_041712_NAR_40mM_plus2.11548.11548.2	2	8.29	0	1.31E+05		(R)FPGQLN	(R)F/P/G/Q L/N A\D|L R(K)		134.3	565.7995	1130.595	-0.0036	-3.1	5.84	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
14048	dirMS_041712_NAR_50mM_plus2.12312.12312.3	3	8.29	1	7.86E+05		(K)IEVEKPF	(K)I/E/V E K P F A I/A K/E(-)		133.12	458.5944	1373.767	0.0012	0.8	5.01	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
14049	dirMS_041712_NAR_50mM_plus2.16369.16369.3	3	8.29	0	3.28E+04		(R)EVIDLLK	(R)E V|I|D/L L/K P D Q V E G I Q K(S)		154.37	608.6724	1824.011	-0.0087	-4.7	4.32	156557.7	5.52	HUMAN	Q86UP2	Kinectin
14050	dirMS_041712_NAR_60mM_plus.15829.15829.3	3	8.29	1	1.05E+06		(R)MSMKE	(R)M S M K E V D\E\Q/M/L/N|V/Q N K(N)		140.15	641.9696	1923.897	-0.003	-1.6	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
14051	dirMS_041712_NAR_60mM_plus.16064.16064.3	3	8.29	1	5.44E+05		(R)VTNRDI	(R)V T\N R D\I\I|C/Q I/A/Y A R(I)	C:Carbamidomethylation	140.87	564.9631	1692.885	-0.0103	-6.1	8.71	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
14052	dirMS_041712_NAR_60mM_plus.16509.16509.2	2	8.29	0	7.16E+05		(R)EHALLA	(R)E H|A\L|L|A Y T/L G V K(Q)		143.67	657.8735	1314.742	-0.0019	-1.4	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
14053	dirMS_041712_NAR_120mM_minus.4509.4509.3	3	8.28	1	5.14E+05	M310m	(R)TKTEISE	(R)T K T E\I/S E/m/N R(N)	m:Oxidized methionine	73.92	408.8693	1208.594	15.9994	3.7	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
14054	dirMS_041712_NAR_20mM_minus.10183.10183.2	2	8.28	0	1.24E+05		(R)YALYDA	(R)Y A/L/Y/D A T Y E/T K(E)		150.82	669.3156	1337.626	-0.0021	-1.5	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
14055	dirMS_041712_NAR_60mM_minus.15123.15123.3	3	8.28	0	2.01E+05		(R)IYIPLPE	(R)I Y I P L/P\E/P H A R(A)		143.9	435.9153	1305.731	0	0	6.75	49472.3	6.75	HUMAN	O75351	Vacuolar protein sorting-associated protein 4B
14056	dirMS_041712_NAR_60mM_minus.8772.8772.3	3	8.28	1	1.14E+05		(K)YAGKDG	(K)Y/A G K/D G\Y N Y/T/L\S/K(T)		109.12	493.9126	1479.711	0.0118	8	8.38	11854.4	6.57	HUMAN	P31949	Protein S100-A11

14057	dirMS_041712_NAR_120mM_plus.5962.5962.2	2	8.28	1	2.29E+06		(K)IREEYPD	(K)I R/E/E|Y\P/D|R(I)		84.93	539.2694	1077.532	-0.0008	-0.8	4.68	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
14058	dirMS_041712_NAR_120mM_plus.9698.9698.4	4	8.28	2	3.92E+06		(R)VLTVINC	(R)V L/T V/I N Q/T Q K E N L R K(F)		104.23	446.7653	1784.039	0.0005	0.3	9.99	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
14059	dirMS_041712_NAR_120mM_plus.9771.9771.3	3	8.28	2	3.06E+05		(R)TGLIKGS	(R)T G L|I K G S G T\A/E/V E/L K/K(G)		104.5	544.3167	1630.937	-0.0019	-1.1	8.17	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
14060	dirMS_041712_NAR_20mM_plus.13631.13631.2	2	8.28	0	8.21E+04		(R)ATLYVTA	(R)A T L Y|V|T A I\E D R(Q)		166.28	626.3269	1251.658	-0.0114	-9.1	4.37	24376.8	6.08	HUMAN	E9PIX6	Protein arginine N-methyltransferase 1 (Fragment)
14061	dirMS_041712_NAR_20mM_plus.18138.18138.2	2	8.28	0	9.83E+04		(R)APGSGL	(R)A/P\G S G L/A L/L|P L/K(I)		196.67	568.8548	1136.704	-0.0014	-1.3	8.8	266161	5.68	HUMAN	E9PPU0	Epiplakin
14062	dirMS_041712_NAR_20mM_plus.18529.18529.3	3	8.28	0	2.20E+05		(R)LSVEEA\	(R)L S\V E E A V\A A\G\V|V/G/G E I Q E K(L)		198.53	629.0001	1884.991	-0.0056	-2.9	4.09	266161	5.68	HUMAN	E9PPU0	Epiplakin
14063	dirMS_041712_NAR_20mM_plus.18806.18806.2	2	8.28	0	2.87E+05		(K)LAVEALS	(K)L A\V E A/L|S/S L/D G D|L A G R(Y)		200.48	793.9214	1586.838	-0.0029	-1.8	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
14064	dirMS_041712_NAR_30mM_plus2.13467.13693.2	2	8.28	0	1.15E+06		(R)TILMMG	(R)T I|L|M/M\G/R(Y)		124.67	411.226	821.437	0.0075	9.2	9.41	96306.4	6.41	HUMAN	P13639	Elongation factor 2
14065	dirMS_041712_NAR_30mM_plus2.18700.18700.2	2	8.28	0	6.67E+05		(R)SYNDEL(	(R)S Y/N/D E/L/Q F L E K(I)		152.13	693.335	1385.658	0.0044	3.2	4.14	19338.9	5.33	HUMAN	E7EQS9	tRNA-splicing ligase RtcB homolog
14066	dirMS_041712_NAR_40mM_plus2.10459.10459.2	2	8.28	0	9.40E+04		(K)IGGIGTV	(K)I/G/G I/G/T/V/P/V G R(V)		125.75	513.3081	1025.61	-0.0013	-1.2	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
14067	dirMS_041712_NAR_40mM_plus2.16166.16166.3	3	8.28	0	4.11E+04		(K)VLISSLQ	(K)V/L|I/S/S L Q D C L H G I/E/S K(S)	C:Carbamidomethylation	161.47	600.3172	1798.937	0.0003	0.2	5.32	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
14068	dirMS_041712_NAR_50mM_plus2.10011.10011.3	3	8.28	0	2.40E+04	M457m M4	(R)mGPLGL	(R)m G|P\L/G L D/H m A\S S I E/R(M)	m:Oxidized methionine	119.67	549.2613	1613.777	31.9919	1.3	5.3	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
14069	dirMS_041712_NAR_50mM_plus2.11024.11024.3	3	8.28	1	3.72E+05		(K)LAEQAE	(K)L/A|E Q/A E R Y D D/M A/A C M K(S)	C:Carbamidomethylation	125.2	634.6126	1901.819	0.0042	2.2	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
14070	dirMS_041712_NAR_50mM_plus2.20811.20811.3	3	8.28	0	2.27E+05		(K)HSQFIG\	(K)H S\Q F I G\Y/P I/T L F V E K(E)		178.9	593.6536	1778.948	-0.0013	-0.8	6.75	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
14071	dirMS_041712_NAR_50mM_plus2.22051.22051.3	3	8.28	1	5.77E+05		(K)AGFLDLI	(K)A/G/F/L/D L/K D F L P K(E)		188.87	455.2587	1363.762	-0.0005	-0.3	6	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
14072	dirMS_041712_NAR_50mM_plus2.8124.8124.3	3	8.28	0	1.26E+05		(K)QLAVAE	(K)Q L A V/A E G K/P/P E\A P K(G)		109.72	478.9337	1434.795	-0.0086	-6	6.14	24364.9	9.64	HUMAN	H0YIP0	Methionine--tRNA ligase, cytoplasmic (Fragment)
14073	dirMS_041712_NAR_60mM_plus.14643.14643.3	3	8.28	1	5.27E+05		(K)NKDQGT	(K)N K D Q G T Y E|D/Y/V/E/G L R(V)		133.25	596.2816	1786.824	0.006	3.4	4.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
14074	dirMS_041712_NAR_120mM_minus.14652.14652.4	4	8.27	1	1.24E+05	M251m	(K)FSHEEIA	(K)F S H E\E I|A|m/A T/V T A/L R R(T)	m:Oxidized methionine	133.6	462.7415	1831.948	15.9958	0.5	6.76	39795.8	9.08	HUMAN	H3BQN4	Fructose-bisphosphate aldolase
14075	dirMS_041712_NAR_120mM_minus.5601.5601.3	3	8.27	1	1.23E+05		(K)CDSSPD:	(K)C D\S/S|P D S/A/E D V R K(V)	C:Carbamidomethylation	83.98	489.2132	1465.622	0.0027	1.8	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
14076	dirMS_041712_NAR_30mM_minus2.18187.18187.2	2	8.27	0	7.01E+04		(R)SYNDEL(	(R)S Y/N\D E|L Q F/L|E/K(I)		153.58	693.3327	1385.658	-0.0002	-0.2	4.14	19338.9	5.33	HUMAN	E7EQS9	tRNA-splicing ligase RtcB homolog
14077	dirMS_041712_NAR_30mM_minus2.18828.18828.2	2	8.27	0	4.54E+05		(R)ISEQFTA	(R)I/S/E/Q/F/T A M/F/R(R)		157.42	615.3038	1229.598	0.002	1.6	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
14078	dirMS_041712_NAR_30mM_minus2.9491.9491.2	2	8.27	0	4.94E+05		(K)ELSEALT	(K)E L/S E A/L/T/R(H)		106.03	459.7452	918.489	-0.006	-6.5	4.53	83905.8	6.62	HUMAN	P41250	Glycine--tRNA ligase
14079	dirMS_041712_NAR_50mM_minus2.10869.10869.3	3	8.27	1	6.27E+03		(K)ELALQPI	(K)E L\A L/Q/P K/D D I/V D R(A)		129.33	504.6068	1511.806	-0.0006	-0.4	4.23	83905.8	6.62	HUMAN	P41250	Glycine--tRNA ligase
14080	dirMS_041712_NAR_50mM_minus2.12854.12854.3	3	8.27	0	4.13E+06	M84m	(K)YPIEHGI	(K)Y/P/I E/H G I I|T N/W D D\m E K(I)	m:Oxidized methionine	141.63	659.6398	1960.911	15.9939	-0.5	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
14081	dirMS_041712_NAR_50mM_minus2.17600.17600.3	3	8.27	0	2.60E+05		(R)LLLDGAI	(R)L/L/L/D G A/P L I A I H K(A)		168.5	458.6218	1373.852	-0.0007	-0.5	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
14082	dirMS_041712_NAR_50mM_minus2.17802.17802.3	3	8.27	0	3.07E+05		(K)HNQLPL	(K)H N Q L P L\V\I|E|F/T E/Q T/A P K(I)		170.02	655.6843	1965.044	-0.0057	-2.9	5.4	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
14083	dirMS_041712_NAR_50mM_minus2.6158.6158.2	2	8.27	0	3.56E+04		(K)AGFAGD	(K)A G|F/A/G D|D A P R(A)		97.78	488.7293	976.448	0.003	3.1	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
14084	dirMS_041712_NAR_50mM_minus2.9005.9005.3	3	8.27	1	1.13E+04		(K)TLQEVTI	(K)T L/Q/E/V/T E M D S V K R(Y)		119.4	512.5962	1535.773	0.0007	0.4	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
14085	dirMS_041712_NAR_50mM_minus2.9743.9743.3	3	8.27	0	2.51E+05		(K)TSEVDL/	(K)T S/E V/D L/A K/P L V K(F)		123.18	433.9205	1299.752	-0.0049	-3.8	5.73	17178.3	5.63	HUMAN	C9IZF9	Programmed cell death 6-interacting protein (Fragment)
14086	dirMS_041712_NAR_60mM_minus.12789.12789.3	3	8.27	1	2.28E+05		(K)TTVKDLS	(K)T\T\V K D L S E|L/G/S V/R(T)		130.95	468.9273	1404.769	-0.0019	-1.4	5.74	533778	5.74	HUMAN	Q15149	Plectin
14087	dirMS_041712_NAR_60mM_minus.13693.13693.3	3	8.27	0	4.50E+05		(R)ANPQVC	(R)A N|P Q V/G V A F P H/I K(H)		135.95	459.9265	1377.764	0.0012	0.9	8.8	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
14088	dirMS_041712_NAR_60mM_minus.6989.6989.3	3	8.27	1	3.61E+05		(K)LDEREA(	(K)L/D/E R E A G I/T E K(V)		98.2	420.8852	1260.643	-0.002	-1.6	4.41	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
14089	dirMS_041712_NAR_120mM_plus.8500.8500.3	3	8.27	0	3.43E+05		(R)NHYNEE	(R)N H\Y N E/E|M/S N L R(N)		97.83	469.5419	1406.612	-0.0006	-0.4	5.4	334221.3	6.44	HUMAN	P15924	Desmoplakin
14090	dirMS_041712_NAR_120mM_plus.8926.8926.2	2	8.27	0	6.37E+05		(K)HFVALST	(K)H|F|V A/L/S/T N T T K(V)		99.38	609.8311	1218.648	0.0072	5.9	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
14091	dirMS_041712_NAR_20mM_plus.17567.17567.2	2	8.27	0	1.28E+05		(K)LATQSN	(K)L A T Q/S N E I/T I|P V/T F E S R(A)		193.23	953.4986	1905.992	-0.0017	-0.9	4.53	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
14092	dirMS_041712_NAR_20mM_plus.6538.6538.2	2	8.27	0	1.42E+05		(R)GAGSIA(	(R)G A/G/S I|A/G A/S A S/P K(E)		108.47	537.277	1073.559	-0.0118	-11	8.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
14093	dirMS_041712_NAR_30mM_plus2.21182.21182.2	2	8.27	0	2.85E+05		(R)FDAMPF	(R)F/D|A\M/P F T L R(A)		166.32	549.276	1097.545	-0.0001	-0.1	5.84	42088	5.39	HUMAN	F8VTY8	Proliferation-associated protein 2G4
14094	dirMS_041712_NAR_40mM_plus2.15105.15105.3	3	8.27	0	2.87E+05		(K)GVTIIGP	(K)G V T I/I/G/P A T V/G G I K P G C F K(I)	C:Carbamidomethylation	156.07	624.683	1872.041	-0.0067	-3.6	10	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
14095	dirMS_041712_NAR_50mM_plus2.10967.10967.3	3	8.27	0	6.36E+04		(K)MVMIQI	(K)M/V|M|I/Q/D/G/P Q N T G A\D K P L R(I)		125.3	657.663	1970.979	-0.0042	-2.1	5.71	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
14096	dirMS_041712_NAR_50mM_plus2.7031.7031.3	3	8.27	1	6.00E+05		(K)IVADKD\	(K)I V|A D K D Y S V/T A N/S K(I)		101.95	504.2628	1510.775	-0.0009	-0.6	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
14097	dirMS_041712_NAR_60mM_plus.11578.11578.3	3	8.27	1	1.25E+06		(K)FGQYNK	(K)F/G Q/Y N K E D|P T S F R(L)		117.23	530.2507	1588.739	-0.0015	-0.9	6.07	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
14098	dirMS_041712_NAR_60mM_plus.14578.14578.3	3	8.27	1	7.09E+05		(R)ELISNSSI	(R)E L|I/S/N/S/S D A\L D K I R(Y)		132.23	520.952	1560.823	0.0187	12	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
14099	dirMS_041712_NAR_60mM_plus.18060.18060.3	3	8.27	1	4.97E+04		(R)ARFEELN	(R)A R F\E E\L\N\A|D L F/R(G)		151.58	494.2554	1480.754	-0.0027	-1.8	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
14100	dirMS_041712_NAR_60mM_plus.19916.19916.3	3	8.27	1	1.46E+05		(R)SELELTL(	(R)S E|L/E/L/T L/G K\L E Q V R(S)		163.83	538.9738	1614.906	0.0007	0.5	4.78	533778	5.74	HUMAN	Q15149	Plectin
14101	dirMS_041712_NAR_60mM_plus.20152.20152.3	3	8.27	1	6.74E+04		(K)KSVEEV/	(K)K S V E E V A S/E|I\Q/P/F L R(G)		165.4	577.9775	1731.928	-0.0096	-5.6	4.79	334221.3	6.44	HUMAN	P15924	Desmoplakin
14102	dirMS_041712_NAR_120mM_minus.14359.14359.4	4	8.26	1	1.15E+05		(R)ETNLDSI	(R)E T N L D S\L/P L/V D/T/H S K R(T)		132.23	456.992	1824.945	0.0012	0.6	5.38	53707.8	5.06	HUMAN	P08670	Vimentin
14103	dirMS_041712_NAR_120mM_minus.5647.5647.3	3	8.26	1	1.23E+05		(K)CDSSPD:	(K)C D/S/S/P D S A/E/D V R K(V)	C:Carbamidomethylation	83.98	489.2132	1465.622	0.0027	1.8	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
14104	dirMS_041712_NAR_20mM_minus.12016.12016.2	2	8.26	0	5.08E+05	M313m	(R)TVQSLEI	(R)T V\Q/S L/E/I D/L|D\S m R(N)	m:Oxidized methionine	169.92	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
14105	dirMS_041712_NAR_30mM_minus2.14359.14359.2	2	8.26	0	2.26E+05		(R)GIFTSEI(	(R)G I|F/T S/E\I G T K(Q)		131.88	526.7803	1052.562	-0.0089	-8.5	6	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
14106	dirMS_041712_NAR_30mM_minus2.18245.18245.2	2	8.26	0	8.12E+04		(K)SCDFLSS	(K)S C|D|F|L/S/S F R(D)	C:Carbamidomethylation	153.88	559.7501	1118.494	-0.0006	-0.5	5.55	42963.5	5.19	HUMAN	P35237	Serpin B6
14107	dirMS_041712_NAR_40mM_minus2.11234.11301.3	3	8.26	1	1.21E+05		(K)VIDPATA	(K)V I|D|P A/T A T S V D L R D/I K(I)		149.38	571.9828	1713.938	-0.0043	-2.5	4.43	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
14108	dirMS_041712_NAR_50mM_minus2.11417.11417.3	3	8.26	1	5.31E+04		(K)ILDSVGII	(K)I L/D\S/V G I E/A D D D R L N K(V)		133.65	591.6389	1772.902	-0.0003	-0.2	4.04	11664.7	4.42	HUMAN	P05387	60S acidic ribosomal protein P2
14109	dirMS_041712_NAR_50mM_minus2.17095.17095.3	3	8.26	1	8.56E+04		(K)YVLINW	(K)Y/V/L I\N W V/G E D V P/D A R K(C)		165.32	625.3311	1873.981	-0.0019	-1	4.56	76925.9	4.46	HUMAN	A8MV58	Drebrin
14110	dirMS_041712_NAR_60mM_minus.14950.14950.3	3	8.26	1	3.66E+05		(R)IKIGDPL	(R)I K I G D P/L|L E/D/T R(M)		142.88	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
14111	dirMS_041712_NAR_60mM_minus.15792.15792.3	3	8.26	1	2.86E+05		(R)GFPTIYF	(R)G F/P T/I/Y/F S/P A N K K(L)		147.27	490.5972	1469.779	-0.0017	-1.1	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
14112	dirMS_041712_NAR_60mM_minus.18444.18444.3	3	8.26	0	1.13E+04		(R)HLEPAL/	(R)H L\E P A L\A|F Q/L E/L N/R(M)		163.17	550.9705	1650.896	0.0007	0.4	5.4	97883.4	6.02	HUMAN	F6QQI9	Acetyl-CoA carboxylase 2
14113	dirMS_041712_NAR_60mM_minus.8020.8032.3	3	8.26	1	3.68E+05		(K)IQDKEGI	(K)I Q/D K E G I|P/P D Q Q R(L)		104.43	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
14114	dirMS_041712_NAR_120mM_plus.19921.19921.3	3	8.26	0	1.23E+04		(K)SFLIWVI	(K)S F\L/I/W V/N E E/D/H T R(V)		157.53	549.2711	1645.797	0.0019	1.1	4.65	29478.9	6.26	HUMAN	E9PCP8	Creatine kinase U-type, mitochondrial
14115	dirMS_041712_NAR_120mM_plus.6072.6072.3	3	8.26	1	3.76E+04		(R)YDSNSG	(R)Y/D|S/N S G G E R E I Q R(T)		85.05	504.2287	1510.688	-0.0165	-10.9	4.68	41280.4	4.9	HUMAN	B4DR63	26S protease regulatory subunit 4
14116	dirMS_041712_NAR_20mM_plus.12097.12097.2	2	8.26	0	3.48E+04		(K)IGPLGLS	(K)I G|P/L/G L S/P K(K)		156.22	441.2754	881.545	-0.002	-2.2	8.75	17989.4	9.77	HUMAN	P30050	60S ribosomal protein L12
14117	dirMS_041712_NAR_20mM_plus.16104.16104.2	2	8.26	0	4.27E+05		(K)DAGTIA(	(K)D A/G\T\I/A G L/N V L R(I)		183.53	600.3422	1199.674	0.0029	2.4	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
14118	dirMS_041712_NAR_20mM_plus.17609.17609.2	2	8.26	0	9.20E+04	M148m	(K)TFAPEEI	(K)T F/A|P E E/I/S A m V L T K(M)	m:Oxidized methionine	193.48	776.8996	1536.798	15.9941	-0.5	4.53	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
14119	dirMS_041712_NAR_20mM_plus.6659.6659.3	3	8.26	0	4.40E+04	M266m	(R)TQPmTA	(R)T Q|P m T A\Q/A/A/S Y R(A)	m:Oxidized methionine	110.62	447.5458	1324.631	15.9914	-2.6	8.41	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
14120	dirMS_041712_NAR_30mM_plus2.13622.13642.2	2	8.26	0	3.98E+05		(K)IIGDTFV	(K)I I|G D/T F V/K(I)		124.35	446.7576	892.514	-0.0059	-6.6	5.84	66612.6	7.28	HUMAN	F8W720	GMP synthase [glutamine-hydrolyzing]
14121	dirMS_041712_NAR_40mM_plus2.9051.9051.2	2	8.26	0	4.64E+05		(R)DPYGFG	(R)D P Y/G/F/G D/S/R(D)		116.32	507.2256	1013.432	0.0116	11.5	4.21	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
14122	dirMS_041712_NAR_50mM_plus2.10700.10700.3	3	8.26	1	2.46E+06		(R)MQKEIT	(R)M Q\K E I T/A\L/A/P/S T M K(I)		124.03	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
14123	dirMS_041712_NAR_60mM_plus.12820.12820.3	3	8.26	1	5.25E+05		(K)ESNGPV	(K)E S N/G/P V/K V W/G/S I/K(G)		124.25	467.5853	1400.753	-0.0119	-8.5	8.69	16163.7	5.7	HUMAN	P00441	Superoxide dismutase [Cu-Zn]
14124	dirMS_041712_NAR_60mM_plus.17137.17137.3	3	8.26	1	4.62E+05		(R)GPIKFN\	(R)G P\I K\F N\V|W/D/T\A G Q E K(F)		146.55	563.9572	1689.86	-0.0024	-1.4	6.07	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
14125	dirMS_041712_NAR_60mM_plus.18760.18760.3	3	8.26	1	3.96E+06		(R)VSFELFA	(R)V/S/F E/L F A D K V/P K(T)		155.83	460.5914	1379.757	0.0027	2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
14126	dirMS_041712_NAR_60mM_plus.7866.7866.3	3	8.26	1	2.95E+05		(K)NGRVEII	(K)N G R V E I\I|A|N\D Q G N R(I)		99.02	519.2682	1555.794	-0.0035	-2.2	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
14127	dirMS_041712_NAR_60mM_plus.7973.7973.3	3	8.26	1	4.32E+05		(R)QLQLEA	(R)Q\L\Q/L\E/A E/E/Q R K(Q)		99.77	457.9111	1371.723	-0.0039	-2.9	4.79	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
14128	dirMS_041712_NAR_30mM_minus2.13248.13248.2	2	8.25	0	3.32E+04		(R)TSGSVYI	(R)T/S|G S/V/Y I/T/L/K(K)		125.93	534.7976	1068.594	-0.0056	-5.3	8.26	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
14129	dirMS_041712_NAR_30mM_minus2.14498.14498.2	2	8.25	0	2.19E+05		(K)QVSVFQ	(K)Q V|S V/F/Q/A M/K(K)		132.58	519.2752	1037.545	-0.0017	-1.6	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
14130	dirMS_041712_NAR_50mM_minus2.15506.15506.3	3	8.25	0	2.83E+05	M118m	(R)AGKPVI(	(R)A G K\P V I\C A\T Q/M/L/E/S m I/K(K)	C:Carbamidomethylation m:Oxid	155.87	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
14131	dirMS_041712_NAR_60mM_minus.11799.11799.3	3	8.25	0	2.59E+05	M42m	(K)GVGISVI	(K)G V/G I/S V/L/E m S H R(S)	m:Oxidized methionine	126	434.2267	1284.673	15.9927	-1.7	6.75	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
14132	dirMS_041712_NAR_120mM_plus.10401.10401.3	3	8.25	0	9.69E+05		(R)GFCLPPI	(R)G F C/L/P/P/H/C S R(G)	C:Carbamidomethylation	107.53	410.8593	1230.551	0.0127	10.3	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
14133	dirMS_041712_NAR_120mM_plus.6692.6692.2	2	8.25	0	3.02E+05	M88m	(R)NGVmP:	(R)N G\V|m|P/S H/F S/R(G)	m:Oxidized methionine	88.17	574.2686	1131.536	15.9935	-1.2	9.75	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
14134	dirMS_041712_NAR_30mM_plus2.11282.11282.2	2	8.25	0	4.41E+05		(K)TTDGYLI	(K)T/T|D/G|Y/L L R(L)		112.48	469.75	938.494	-0.0014	-1.5	5.5	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
14135	dirMS_041712_NAR_30mM_plus2.20422.20422.3	3	8.25	0	3.84E+05		(K)SYELPD(	(K)S Y\E|L/P D G Q V/I/T I/G/N E R(F)		160.12	597.6334	1790.892	-0.0063	-3.5	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
14136	dirMS_041712_NAR_40mM_plus2.12694.13177.3	3	8.25	0	4.27E+05		(K)NLPPSG/	(K)N L|P\P S G A V/P V/T/G I/P P H V V K(V)		143.32	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
14137	dirMS_041712_NAR_40mM_plus2.8219.8219.2	2	8.25	0	2.86E+05		(R)FGSGMI	(R)F/G|S/G/M N M G R(I)		109.45	478.706	956.408	-0.003	-3.1	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
14138	dirMS_041712_NAR_50mM_plus2.10159.10159.3	3	8.25	1	1.66E+05		(R)LAEVEA/	(R)L/A|E V/E/A A/L E K Q R(Q)		120.27	452.9215	1356.748	0.0018	1.3	4.79	533778	5.74	HUMAN	Q15149	Plectin
14139	dirMS_041712_NAR_50mM_plus2.21392.21392.3	3	8.25	1	1.92E+05		(R)LIALLEVI	(R)L\I/A|L/L E V L S Q K R(M)		183.22	461.6293	1382.873	0.0004	0.3	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
14140	dirMS_041712_NAR_50mM_plus2.7566.7566.3	3	8.25	1	2.08E+05		(K)EAIEGTY	(K)E A I/E/G T/Y/I D/K K(C)		105.35	422.8907	1266.658	-0.0001	0	4.68	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
14141	dirMS_041712_NAR_50mM_plus2.9029.9029.3	3	8.25	1	3.16E+05		(K)VLLQSKI	(K)V L/L/Q/S/K D Q\I/T A G N A A R(K)		114.58	562.315	1684.934	-0.0036	-2.1	8.72	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
14142	dirMS_041712_NAR_50mM_plus2.9740.9740.3	3	8.25	1	8.03E+04		(K)LKGEAT\	(K)L K G E A\T\V/S\F D/D/P P S A K(A)		117.67	554.6155	1661.838	-0.0061	-3.7	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
14143	dirMS_041712_NAR_60mM_plus.15067.15067.3	3	8.25	1	1.67E+05		(R)GYISPYF	(R)G Y/I S/P Y/F I N/T S K G Q K(C)		134.73	568.2935	1702.88	-0.014	-8.2	9.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
14144	dirMS_041712_NAR_60mM_plus.8813.8813.3	3	8.25	1	8.04E+05		(R)QLQLAC	(R)Q L\Q|L\A Q/E/A/A/Q K/R(L)		104.95	461.9268	1383.77	-0.0044	-3.2	8.75	533778	5.74	HUMAN	Q15149	Plectin
14145	dirMS_041712_NAR_60mM_plus.9764.9764.3	3	8.25	1	2.15E+05		(R)GPGLVK	(R)G P/G L/V K Q E/D/F R(D)		109.68	415.8936	1245.659	0.0076	6.1	6.07	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
14146	dirMS_041712_NAR_60mM_plus.9777.9777.3	3	8.25	1	3.91E+05		(K)VADWT(	(K)V/A|D/W/T G A T Y Q D K R(Y)		109.03	504.2484	1510.728	0.0022	1.4	5.93	31956.7	9.73	HUMAN	B0QYA5	Eukaryotic translation initiation factor 3 subunit D (Fragment)
14147	dirMS_041712_NAR_120mM_minus.10592.10592.3	3	8.24	0	3.90E+05		(R)GFCLPPI	(R)G F\C L/P/P/H C S R(G)	C:Carbamidomethylation	113.15	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
14148	dirMS_041712_NAR_20mM_minus.13126.13126.3	3	8.24	0	4.00E+05		(K)TITLEVEI	(K)T I T L E\V E/P S/D T/I E N V/K(A)		183.03	596.6453	1787.927	-0.006	-3.3	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
14149	dirMS_041712_NAR_30mM_minus2.13301.13301.2	2	8.24	0	3.32E+04		(R)TSGSVYI	(R)T/S/G S/V/Y/I/T L K(K)		125.93	534.7976	1068.594	-0.0056	-5.3	8.26	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
14150	dirMS_041712_NAR_50mM_minus2.10402.10402.3	3	8.24	1	9.57E+03		(K)AELEIQK	(K)A E/L/E|I/Q K/D\A L E/P G Q R(V)		126.97	566.2988	1696.886	-0.0046	-2.7	4.41	14613.6	6.73	HUMAN	G5E9J2	Adenine phosphoribosyltransferase
14151	dirMS_041712_NAR_50mM_minus2.6823.6823.3	3	8.24	1	3.85E+04		(K)DISTNYY	(K)D I/S T/N Y Y/A S/Q K K(T)		105.43	473.238	1417.696	0.0037	2.6	8.43	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
14152	dirMS_041712_NAR_50mM_minus2.8664.8664.3	3	8.24	1	9.59E+04		(K)ALDLDS:	(K)A L/D L/D/S S C K E A/A D/G Y/Q R(C)	C:Carbamidomethylation	117.47	633.6221	1898.855	-0.0031	-1.7	4.23	60404.6	6.4	HUMAN	F5H0T1	Stress-induced-phosphoprotein 1
14153	dirMS_041712_NAR_60mM_minus.15895.15895.3	3	8.24	1	3.21E+05		(R)IDTRNEL	(R)I/D T R N E\L\E|S Y/A Y S L K(N)		148.33	601.3049	1801.897	0.0035	1.9	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
14154	dirMS_041712_NAR_60mM_minus.16160.16160.3	3	8.24	0	2.11E+05		(R)FDASFF(	(R)F D A S/F\F/G V H/P K(Q)		149.6	417.8768	1251.616	0.0002	0.1	6.74	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
14155	dirMS_041712_NAR_60mM_minus.7928.7928.3	3	8.24	1	4.17E+05		(K)KGTVEG	(K)K\G T V E\G\F\E|P A D N K(C)		103.35	464.5665	1391.68	0.0048	3.5	4.68	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
14156	dirMS_041712_NAR_20mM_plus.10739.10739.2	2	8.24	0	3.71E+04		(K)STLTDSL	(K)S T/L T/D/S L/V C K(A)	C:Carbamidomethylation	146.22	562.2896	1123.566	0.0056	5	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
14157	dirMS_041712_NAR_20mM_plus.18551.18551.2	2	8.24	0	1.86E+05		(R)VFIGNLI	(R)V/F|I/G N\L/N T L V\V|K(K)		200.07	658.8999	1316.794	-0.0011	-0.9	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
14158	dirMS_041712_NAR_30mM_plus2.16577.16577.3	3	8.24	0	3.99E+05		(K)LLDLVQ(	(K)L L D\L V Q/Q/S C/N Y K(Q)	C:Carbamidomethylation	139.18	494.2566	1480.746	0.0088	5.9	5.83	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
14159	dirMS_041712_NAR_30mM_plus2.17149.17149.2	2	8.24	0	1.48E+05		(K)WPLYM:	(K)W/P/L/Y M S T|K(N)		143.55	513.2647	1025.513	0.0097	9.4	8.59	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
14160	dirMS_041712_NAR_40mM_plus2.13457.13457.3	3	8.24	0	9.16E+03		(K)MVMIQI	(K)M V/M/I Q/D G P L/P T G A D K/P L R(I)		145.45	647.0084	1939.014	-0.0033	-1.7	5.71	61981.6	8.97	HUMAN	Q96I24	Far upstream element-binding protein 3
14161	dirMS_041712_NAR_50mM_plus2.13546.13546.3	3	8.24	0	1.13E+06		(K)AASDIAI	(K)A A|S\D I/A M T E L/P P T H/P I R(L)		139.28	607.3177	1819.937	0.0015	0.8	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
14162	dirMS_041712_NAR_50mM_plus2.14998.15161.3	3	8.24	0	7.61E+05		(R)QIFHPE(	(R)Q/I/F H/P E Q L I T G K(E)		147.45	470.9293	1410.774	-0.0006	-0.4	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
14163	dirMS_041712_NAR_50mM_plus2.20347.20347.3	3	8.24	0	1.29E+05		(R)AFIDPLG	(R)A F|I/D/P L G L P D R P F Y R(H)		175.4	592.986	1776.943	0.0003	0.2	6	84557.3	6.5	HUMAN	Q04609	Glutamate carboxypeptidase 2
14164	dirMS_041712_NAR_50mM_plus2.20848.20848.3	3	8.24	1	7.61E+04		(K)TSAQVV	(K)T S/A/Q V V/L D/G L V D K I G D|V K(C)		178.37	619.6814	1857.033	-0.0031	-1.7	4.43	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
14165	dirMS_041712_NAR_50mM_plus2.22236.22236.3	3	8.24	0	1.00E+06		(R)GGHPPA	(R)G G H P P A I Q|S\L\I/N/L/L/A D\N R(Y)		191.08	629.3448	1886.024	-0.0044	-2.3	6.74	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5

14166	dirMS_041712_NAR_50mM_plus2.9165.9165.3	3	8.24	1	6.64E+05		(K)TAVCDIF	(K)T/A|V/C/D I/P P R G L K(M)	C:Carbamidomethylation	115.62	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
14167	dirMS_041712_NAR_60mM_plus.18823.18823.3	3	8.24	1	2.18E+05		(R)TKEEALE	(R)T K E E A L\E L|I/N G Y I/Q K(I)		155.85	583.6498	1748.943	-0.008	-4.6	4.78	16245.7	9.47	HUMAN	K7EMU7	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1
14168	dirMS_041712_NAR_120mM_minus.13871.13871.4	4	8.23	1	1.62E+06		(K)ASIHEAV	(K)A/S|I/H E A W T D/G K E A M L/K(H)		129.97	447.476	1786.879	0.0029	1.6	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
14169	dirMS_041712_NAR_120mM_minus.17333.17376.4	4	8.23	2	5.34E+05		(K)KDEKTD	(K)K\D E K T D T L\E D\L/F P/T/T K(I)		149.03	470.992	1880.949	-0.0026	-1.4	4.44	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
14170	dirMS_041712_NAR_120mM_minus.17444.17444.4	4	8.23	1	5.36E+05		(R)GFGHIG	(R)G F G H I G I/A\V/P D/V Y S/A C K R(F)	C:Carbamidomethylation	150.38	487.502	1946.991	-0.0044	-2.2	8.6	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
14171	dirMS_041712_NAR_30mM_minus2.14888.14888.2	2	8.23	0	2.26E+05		(K)NMVLFT	(K)N/M|V|L F T/R(Q)		134.87	440.7384	880.471	-0.0014	-1.6	9.75	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1
14172	dirMS_041712_NAR_30mM_minus2.17438.17438.2	2	8.23	0	1.74E+05		(K)LLCGLLA	(K)L L|C/G/L L/A E R(L)	C:Carbamidomethylation	149.58	522.7963	1044.587	-0.0017	-1.6	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
14173	dirMS_041712_NAR_30mM_minus2.8260.8260.2	2	8.23	0	4.30E+05		(K)SFQQSSI	(K)S F|Q/Q/S S/L S/R(D)		99.93	520.2591	1039.517	-0.0058	-5.6	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
14174	dirMS_041712_NAR_30mM_minus2.8549.8549.2	2	8.23	0	8.75E+04		(K)VQAINV	(K)V/Q|A|I/N/V/S S R(F)		101.12	487.2765	973.543	0.0032	3.3	9.72	26810.9	5.15	HUMAN	Q96C19	EF-hand domain-containing protein D2
14175	dirMS_041712_NAR_50mM_minus2.15235.15235.3	3	8.23	0	3.58E+05	M118m	(R)AGKPVI	(R)A G K\P V I C A T Q|M|L/E S m I K(K)	C:Carbamidomethylation m:Oxid	155	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
14176	dirMS_041712_NAR_50mM_minus2.16844.16844.3	3	8.23	0	4.60E+05		(K)NILFVITK	(K)N I/L/F V/I/T K P D V Y/K(S)		164.12	517.2991	1549.899	-0.0161	-10.4	8.5	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
14177	dirMS_041712_NAR_50mM_minus2.16862.16862.3	3	8.23	1	2.96E+05		(R)SELELTL	(R)S E/L/E/L/T L/G K L E Q V R(S)		163.73	538.9725	1614.906	-0.0032	-2	4.78	533778	5.74	HUMAN	Q15149	Plectin
14178	dirMS_041712_NAR_50mM_minus2.17919.17919.3	3	8.23	0	4.27E+05	M203m	(R)DTGIFLD	(R)D T/G I/F/L/D L m H L K(K)	m:Oxidized methionine	170.33	473.5826	1402.74	15.9933	-1.1	5.21	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
14179	dirMS_041712_NAR_50mM_minus2.7642.7642.3	3	8.23	0	1.15E+03	M44m M4	(K)SGTGIA	(K)S G\T/G/I/A/A/m S V m/R P E Q\I m K(S)	m:Oxidized methionine	111.57	652.3177	1906.955	47.9838	-0.5	8.46	8797.3	9.3	HUMAN	H3BR50	V-type proton ATPase 16 kDa proteolipid subunit
14180	dirMS_041712_NAR_60mM_minus.16729.16729.3	3	8.23	0	1.78E+05		(R)LLIHQSL	(R)L L|I H Q\S\L/A|G G|I/I/G V K(G)		153.38	506.9823	1518.937	-0.0043	-2.8	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
14181	dirMS_041712_NAR_120mM_plus.22900.23083.3	3	8.23	1	4.87E+05		(K)GLAPDLI	(K)G L|A|P D L/P E/D L Y H L I K K(A)		174.02	608.0076	1822.011	-0.0027	-1.5	5.38	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
14182	dirMS_041712_NAR_120mM_plus.9115.9115.3	3	8.23	1	4.91E+05		(R)SGRGGN	(R)S G R/G G N|F\G|F G D/S R(G)		101.07	438.538	1313.598	0.0013	1	9.32	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
14183	dirMS_041712_NAR_20mM_plus.11984.11984.2	2	8.23	0	3.87E+05	T660t S666	(R)APLPtSP	(R)A/P L/P t S/P Q P P/s P/R(Q)	t:Phosphorylated T s:Phosph	155.77	752.8363	1344.727	159.9383	3.7	9.79	73666	6.97	HUMAN	E7EWG4	Ubiquitin-associated protein 2
14184	dirMS_041712_NAR_20mM_plus.14617.14617.2	2	8.23	0	1.56E+05		(K)LVILANN	(K)L V/I L/A/N N C/P A L/R(K)	C:Carbamidomethylation	172.43	677.3851	1353.767	-0.0042	-3.1	9.75	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
14185	dirMS_041712_NAR_20mM_plus.9382.9382.2	2	8.23	0	8.44E+04		(R)ALEESNY	(R)A L|E/E/S N/Y\E L E/G K(I)		136.35	691.3246	1381.648	-0.0062	-4.5	4.09	59054.3	5.14	HUMAN	P13645	Keratin, type I cytoskeletal 10
14186	dirMS_041712_NAR_30mM_plus2.10565.10604.2	2	8.23	0	5.97E+05		(R)VPVDVA	(R)V/P|V|D/V A Y/R(R)		109.12	459.757	918.504	0.0024	2.6	5.8	266161	5.68	HUMAN	E9PPU0	Epiplakin
14187	dirMS_041712_NAR_30mM_plus2.16148.16341.2	2	8.23	0	6.81E+05		(K)LVFDGLF	(K)L V|F/D/G L/R(K)		137.62	410.2436	819.472	0.0076	9.3	5.84	334221.3	6.44	HUMAN	P15924	Desmoplakin
14188	dirMS_041712_NAR_30mM_plus2.18319.18319.2	2	8.23	0	5.23E+05		(R)EQLAIAE	(R)E/Q L/A I|A/E F A R(S)		148.52	574.3083	1147.611	-0.0013	-1.1	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
14189	dirMS_041712_NAR_30mM_plus2.4490.4490.2	2	8.23	0	3.37E+05		(R)SMPEQT	(R)S M|P/E/Q T G E/K(-)		73.05	503.7289	1006.451	-0.0005	-0.5	4.53	12955	9.87	HUMAN	P62888	60S ribosomal protein L30
14190	dirMS_041712_NAR_40mM_plus2.19396.19396.3	3	8.23	1	1.40E+05		(R)TEGLSVL	(R)T E|G\L/S V L S Q A M A V I K E K(I)		181.73	602.0005	1803.988	-0.0015	-0.8	5.81	31604.9	6.88	HUMAN	G3V4T5	Eukaryotic translation initiation factor 2 subunit 1 (Fragment)
14191	dirMS_041712_NAR_40mM_plus2.6279.6279.2	2	8.23	1	2.84E+05		(R)YSGGNY	(R)Y/S|G G N Y R D N|Y|D|N(-)		95.58	719.2857	1437.567	-0.0024	-1.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
14192	dirMS_041712_NAR_50mM_plus2.20773.20773.3	3	8.23	1	1.63E+05		(R)LLLQQLE	(R)L L/L/Q/Q L/E A T L/E T G K R(F)		178.48	571.6722	1712.991	0.0115	6.7	6.14	113203.2	6.21	HUMAN	Q14CX7	N-alpha-acetyltransferase 25, NatB auxiliary subunit
14193	dirMS_041712_NAR_60mM_plus.13530.13530.3	3	8.23	1	4.74E+05		(R)ISVYYNE	(R)I/S|V/Y Y N/E A T/G G K Y V P R(A)		126.6	606.3113	1816.923	-0.0035	-1.9	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
14194	dirMS_041712_NAR_60mM_plus.13683.13683.3	3	8.23	1	4.08E+05		(K)SGYLAGI	(K)S/G Y/L/A/G D K L/L/P Q R(V)		128.58	473.2654	1417.78	0.0019	1.3	8.31	67933	6.08	HUMAN	P26038	Moesin
14195	dirMS_041712_NAR_120mM_minus.18930.18930.4	4	8.22	1	4.10E+05		(R)HATALEI	(R)H A T A L E|E|L/S E Q L E Q A K R(F)		158.33	489.0065	1953.004	0.0006	0.3	4.91	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
14196	dirMS_041712_NAR_30mM_minus2.17554.17554.2	2	8.22	0	1.62E+05		(K)GFLIDGY	(K)G F\L|I/D/G Y P R(E)		150.2	519.2752	1037.542	0.0017	1.6	5.83	15567.5	8.13	HUMAN	H0Y4J6	Adenylate kinase isoenzyme 1 (Fragment)
14197	dirMS_041712_NAR_40mM_minus2.10951.10951.3	3	8.22	0	7.73E+04		(K)SPAPPLL	(K)S P\A/P/P L L|H V A A L G Q K(Q)		148.05	500.2927	1498.874	-0.0105	-7	8.49	17549.1	10.39	HUMAN	E5RFJ3	DBIRD complex subunit KIAA1967 (Fragment)
14198	dirMS_041712_NAR_40mM_minus2.13794.13794.3	3	8.22	1	4.48E+04		(K)FGEVVD	(K)F/G\E|V|V/D C T L K L D P I T G\R(S)	C:Carbamidomethylation	165.3	640.6656	1919.989	-0.0073	-3.8	4.56	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
14199	dirMS_041712_NAR_60mM_minus.13209.13209.3	3	8.22	0	4.87E+05		(K)GIHPTIIS	(K)G I\H\P\T\I|I/S/E S F Q K(A)		133.43	486.2642	1456.78	-0.0014	-1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
14200	dirMS_041712_NAR_60mM_minus.6581.6581.3	3	8.22	0	5.72E+04		(K)ELVSDAI	(K)E L/V/S D A N Q/H V K(S)		95.22	413.8839	1239.633	0.0044	3.5	5.32	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
14201	dirMS_041712_NAR_120mM_plus.12503.12503.2	2	8.22	0	7.45E+05		(K)HLSVND	(K)H L|S|V N D/L\P V G R(S)		119.2	603.8321	1206.659	-0.002	-1.7	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
14202	dirMS_041712_NAR_120mM_plus.12880.12880.3	3	8.22	1	5.10E+05		(R)IFSVTNG	(R)I/F/S V T N G G Q E R/K(F)		120.55	445.9007	1335.701	-0.014	-10.5	8.75	60194.1	8.26	HUMAN	P21397	Amine oxidase [flavin-containing] A
14203	dirMS_041712_NAR_120mM_plus.15271.15271.4	4	8.22	1	6.04E+05		(K)KKELEEI	(K)K\K E L E E I V/Q|P I/I/S K(L)		133.32	414.2493	1653.978	-0.0032	-1.9	6.23	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
14204	dirMS_041712_NAR_120mM_plus.4639.4639.3	3	8.22	0	6.19E+05		(R)THSQGG	(R)T H\S Q G G\Y/G/S Q G Y/K(Y)		74.07	457.2092	1369.613	-0.0001	-0.1	8.2	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
14205	dirMS_041712_NAR_20mM_plus.13082.13082.2	2	8.22	0	6.67E+04		(R)LAPDYD	(R)L/A/P D/Y/D|A L D V A N K(I)		162.68	702.8524	1404.7	-0.003	-2.1	3.93	22029.9	10.62	HUMAN	A8MUS3	60S ribosomal protein L23a
14206	dirMS_041712_NAR_20mM_plus.13823.13823.2	2	8.22	0	4.19E+04		(K)IVLTNPV	(K)I V/L|T/N/P V/C T E V G E K(I)	C:Carbamidomethylation	167.07	779.9082	1558.815	-0.0054	-3.5	4.53	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
14207	dirMS_041712_NAR_20mM_plus.14975.14975.2	2	8.22	0	2.17E+05		(K)GLAITFV	(K)G L A I/T/F/V/S D E N D A\K(I)		175.3	740.3693	1479.733	-0.0012	-0.8	4.03	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
14208	dirMS_041712_NAR_20mM_plus.15875.15875.3	3	8.22	0	8.77E+03		(R)SSFYVN	(R)S S\F Y V N G L/T/L/G G Q/K(C)		179.37	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
14209	dirMS_041712_NAR_20mM_plus.16505.16505.2	2	8.22	0	1.39E+05		(R)ELLIIGG	(R)E L|L|I|I/G G/V A A|R(D)		185.7	556.3437	1111.683	-0.0032	-2.9	6.1	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
14210	dirMS_041712_NAR_20mM_plus.18843.18843.3	3	8.22	0	1.25E+05		(K)IYVDDGI	(K)I Y V D D G L|I/S L/Q V K(Q)		200.67	488.2764	1462.815	-0.0005	-0.4	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
14211	dirMS_041712_NAR_30mM_plus2.13196.13196.2	2	8.22	0	1.13E+06		(K)NDLAVV	(K)N D|L|A/V/V D V R(I)		121.8	500.7769	1000.542	0.0043	4.3	4.21	76670.1	4.6	HUMAN	P19338	Nucleolin
14212	dirMS_041712_NAR_30mM_plus2.18967.18967.2	2	8.22	0	5.69E+05		(R)LSNIFVI	(R)L/S/N I|F/V/I/G K(G)		152.22	495.8019	990.598	-0.0017	-1.7	8.75	29825.4	10.37	HUMAN	P62701	40S ribosomal protein S4, X isoform
14213	dirMS_041712_NAR_50mM_plus2.10116.10116.3	3	8.22	0	7.46E+05		(R)GISEETT	(R)G I/S/E/E/T/T T G V H N\L Y K(M)		120.05	550.2759	1648.818	-0.0045	-2.8	5.4	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
14214	dirMS_041712_NAR_50mM_plus2.10136.10136.3	3	8.22	0	2.23E+05		(R)TITVALA	(R)T I|T/V|A/L A/D G G R P D N T G R(G)		120.23	571.9661	1713.888	-0.0041	-2.4	5.63	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
14215	dirMS_041712_NAR_50mM_plus2.7979.7979.3	3	8.22	1	3.43E+04	M250m	(K)TTDmAF	(K)T T|D/m A/P S/K E T E M A L A K(D)	m:Oxidized methionine	108.27	580.6104	1723.824	15.9925	-1.4	4.68	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
14216	dirMS_041712_NAR_60mM_plus.6936.6936.3	3	8.22	0	2.68E+05		(K)AGYSTD	(K)A G/Y/S|T D E/S\S/S S S L H/A T R(T)		94.6	585.9305	1755.778	-0.0011	-0.6	5.32	74564.3	5.95	HUMAN	P51116	Fragile X mental retardation syndrome-related protein 2
14217	dirMS_041712_NAR_60mM_plus.7088.7088.3	3	8.22	1	5.84E+05	M251m	(K)mQASIE	(K)m Q|A/S I E K G G S L/P K(V)	m:Oxidized methionine	95.58	454.578	1345.714	16.005	7.4	8.35	32745.6	4.64	HUMAN	P06748	Nucleophosmin
14218	dirMS_041712_NAR_60mM_plus.7501.7501.3	3	8.22	0	8.00E+05		(R)AAHSEG	(R)A A H S E G N T/T/A/G L D/M R(E)		96.85	510.9035	1530.697	-0.0006	-0.4	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
14219	dirMS_041712_NAR_30mM_minus2.7237.7237.2	2	8.21	0	1.08E+05		(K)ISEEVSR	(K)I S/E/E/V S R(N)		93.72	410.2139	819.421	-0.0001	-0.2	4.53	130968.8	5.09	HUMAN	D6RBW0	Centromere-associated protein E (Fragment)
14220	dirMS_041712_NAR_30mM_minus2.9235.9235.2	2	8.21	0	3.53E+05		(K)CAADLG	(K)C A|A\D/L/G L/N/K(G)	C:Carbamidomethylation	104.88	481.2466	961.477	0.0088	9.1	5.84	13915.8	6.43	HUMAN	P49773	Histidine triad nucleotide-binding protein 1
14221	dirMS_041712_NAR_40mM_minus2.14497.14497.3	3	8.21	1	2.00E+05		(R)GLLPGLL	(R)G L/L/P|G/L L P\A/P A D K L T P K(G)		169.47	567.6813	1701.031	-0.0016	-0.9	8.59	153084.9	5.55	HUMAN	Q6P2E9	Enhancer of mRNA-decapping protein 4
14222	dirMS_041712_NAR_40mM_minus2.8112.8112.3	3	8.21	0	1.18E+04	M33m	(R)VLTEDE	(R)V L|T E/D E m G H P E I G D A I A R(L)	m:Oxidized methionine	127.97	656.9824	1952.938	15.9944	-0.2	4.17	40874	5.06	HUMAN	E9PCI9	Farnesyl pyrophosphate synthase
14223	dirMS_041712_NAR_50mM_minus2.13810.13810.3	3	8.21	1	2.93E+05		(K)LTEDKAI	(K)L T/E D K A D/V Q/S\I I/G/L Q R(F)		146.48	595.9939	1785.97	-0.0034	-1.9	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
14224	dirMS_041712_NAR_50mM_minus2.14568.14568.3	3	8.21	1	2.00E+05		(R)IIDSLFN	(R)I/I/D S/L F/N T V T D K K(I)		150.83	498.612	1493.821	0.0005	0.3	5.96	44813.4	7.79	HUMAN	B4DN25	UDP-glucose 6-dehydrogenase
14225	dirMS_041712_NAR_50mM_minus2.15446.15446.3	3	8.21	1	8.63E+04		(R)YRVPDV	(R)Y R V P D\V\L\V\A/D/P P I A R(L)		155.97	560.9824	1680.943	-0.0105	-6.3	5.96	96499.9	5.43	HUMAN	F5H6X6	Neutral alpha-glucosidase AB
14226	dirMS_041712_NAR_60mM_minus.18160.18160.3	3	8.21	1	1.76E+04		(R)VTFSGLF	(R)V T|F S G L R D T V/T/P G E L L K(A)		162.32	611.6719	1833.012	-0.0105	-5.7	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
14227	dirMS_041712_NAR_20mM_plus.13390.13390.3	3	8.21	0	1.24E+04		(R)LFSCEVD	(R)L/F S C E V D G K P/Q P/S V/K(C)	C:Carbamidomethylation	165.15	564.2873	1690.847	0.0005	0.3	6.07	98826.2	5.71	HUMAN	Q9UMF0	Intercellular adhesion molecule 5
14228	dirMS_041712_NAR_20mM_plus.15090.15090.2	2	8.21	0	2.08E+04		(R)IAAAILN	(R)I/A/A|A/I/L/N/T P D L R(K)		175.3	634.3708	1267.737	-0.0025	-2	5.84	43371.1	9.64	HUMAN	E7ERW2	Aspartate aminotransferase
14229	dirMS_041712_NAR_20mM_plus.16259.16289.2	2	8.21	0	1.11E+05		(K)TIIPLISQ	(K)T I\I|P L/I/S Q C T P K(V)	C:Carbamidomethylation	184.03	685.8877	1370.771	-0.0031	-2.2	8.41	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
14230	dirMS_041712_NAR_20mM_plus.19305.19305.3	3	8.21	0	2.67E+05		(R)LAGTQP	(R)L A G T Q P L/E/V|L/E A V Q R(S)		204.35	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
14231	dirMS_041712_NAR_40mM_plus2.13497.13497.3	3	8.21	1	2.44E+04		(R)IIEFVPTK	(R)I I\E F V P/T K T P Y D/P R(W)		146.22	559.3044	1675.905	-0.0067	-4	6.07	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
14232	dirMS_041712_NAR_40mM_plus2.16299.16299.3	3	8.21	1	1.48E+05		(R)VYAEDP	(R)V Y|A E/D/P Y K S F/G\L/P S I G R(L)		161.83	633.6593	1898.965	-0.0013	-0.7	6.04	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
14233	dirMS_041712_NAR_50mM_plus2.16007.16177.3	3	8.21	1	5.97E+05		(R)YRVPDV	(R)Y R V P D\V\L\V|A/D/P P I A R(L)		152.38	560.9825	1680.943	-0.0102	-6.1	5.96	96499.9	5.43	HUMAN	F5H6X6	Neutral alpha-glucosidase AB
14234	dirMS_041712_NAR_50mM_plus2.7376.7376.3	3	8.21	0	7.23E+04		(R)QSSGPG	(R)Q S S/G/P/G/A/S S G T/S G D H G E L V V R(I)		104.67	662.3136	1984.932	-0.0056	-2.8	5.32	20818.7	4.89	HUMAN	E9PL71	Elongation factor 1-delta (Fragment)
14235	dirMS_041712_NAR_60mM_plus.8227.8227.3	3	8.21	1	2.68E+06	M174m	(R)VKYETEL	(R)V/K Y E T E|L/A m/R(Q)	m:Oxidized methionine	101.47	419.2169	1239.64	15.996	0.8	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
14236	dirMS_041712_NAR_20mM_minus.7569.7569.2	2	8.2	0	8.22E+05	M239m	(K)EVDEQm	(K)E V/D E Q/m L/N|V|Q/N K(N)	m:Oxidized methionine	124.22	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
14237	dirMS_041712_NAR_30mM_minus2.12111.12111.2	2	8.2	0	2.15E+05		(K)IGVTVLS	(K)I/G/V/T/V/L S R(I)		119.17	422.7649	844.525	-0.0026	-3	9.75	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
14238	dirMS_041712_NAR_40mM_minus2.7501.7501.3	3	8.2	1	1.82E+05	M88m	(K)DVDEAY	(K)D V|D\E/A/Y/m N K V E L E S R(L)	m:Oxidized methionine	120.62	605.2801	1797.832	15.9934	-0.8	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
14239	dirMS_041712_NAR_60mM_minus.8267.8267.3	3	8.2	2	1.02E+05		(K)NLKVPS	(K)N L K V\P S G Q N|A/D|V Q K T D\N(-)		105.95	609.9772	1827.92	-0.0025	-1.4	5.96	11018.4	8.89	HUMAN	B0AZT5	N-alpha-acetyltransferase 50
14240	dirMS_041712_NAR_120mM_plus.14811.14811.4	4	8.2	2	1.64E+06		(R)YLYTLVI	(R)Y L\Y T/L/V/I/T D K E/K A E K(L)		131.12	454.2533	1813.995	-0.0032	-1.8	6.18	7621.9	10.1	HUMAN	J3KT73	60S ribosomal protein L38
14241	dirMS_041712_NAR_120mM_plus.6493.6493.2	2	8.2	0	4.57E+05		(K)HQPTAII	(K)H Q|P T A I|I A K(T)		87.75	489.7897	978.573	-0.001	-1	8.76	63448.4	7.29	HUMAN	B4E022	Transketolase
14242	dirMS_041712_NAR_120mM_plus.9170.9170.4	4	8.2	2	2.31E+05		(K)NSLTSKD	(K)N S/L T S K D/P D/I K A Q Y/Q/Q R(W)		101.47	498.7603	1992.015	0.0049	2.4	8.5	16598.6	5.48	HUMAN	J3QR48	Importin subunit beta-1 (Fragment)
14243	dirMS_041712_NAR_20mM_plus.11263.11263.3	3	8.2	0	1.04E+05		(R)GCITIIG	(R)G C\I/T I\I G/G/G/D T/A/T C C A K(W)	C:Carbamidomethylation	150.12	585.5999	1754.787	-0.0019	-1.1	5.84	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
14244	dirMS_041712_NAR_20mM_plus.13097.13097.2	2	8.2	0	9.34E+04		(K)TAVVVG	(K)T A V|V/V/G/T I|T D D V R(V)		162.3	673.3693	1345.732	-0.0008	-0.6	4.21	14643	11.93	HUMAN	F8VUA6	60S ribosomal protein L18 (Fragment)
14245	dirMS_041712_NAR_20mM_plus.14732.14732.2	2	8.2	0	1.98E+05	M179m M	(K)mFVLDE	(K)m F|V|L\D/E A D E m/L S R(G)	m:Oxidized methionine	173.6	794.3555	1555.713	31.9906	0.5	3.91	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
14246	dirMS_041712_NAR_20mM_plus.16690.16690.2	2	8.2	0	2.39E+05		(K)VQIAVA	(K)V Q|I A\V|A N/A/Q/E\L\L Q/R(M)		186.53	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
14247	dirMS_041712_NAR_20mM_plus.19059.19059.2	2	8.2	0	1.91E+05		(R)STGEAF	(R)S T G E A/F|V/Q/F A/S Q/E I/A E K(A)		202.2	921.4477	1841.892	-0.0035	-1.9	4.25	24249.1	6.99	HUMAN	D6RBM0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
14248	dirMS_041712_NAR_30mM_plus2.14643.14733.2	2	8.2	0	7.63E+05		(R)GVEICIA	(R)G V\E|I|C/I/A|T/P G R(L)	C:Carbamidomethylation	130.1	586.8051	1172.609	-0.0063	-5.4	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
14249	dirMS_041712_NAR_30mM_plus2.16603.16603.2	2	8.2	0	2.74E+05		(K)VQQTVC	(K)V Q|Q\T/V/Q D/L F G/R(A)		139.48	645.842	1290.68	-0.0034	-2.6	5.81	73964.5	5.87	HUMAN	P38646	Stress-70 protein, mitochondrial
14250	dirMS_041712_NAR_30mM_plus2.16614.16614.3	3	8.2	0	3.70E+05		(K)LLDLVQ	(K)L L D L V|Q|Q/S/C N Y K(Q)	C:Carbamidomethylation	139.25	494.2566	1480.746	0.0088	5.9	5.83	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
14251	dirMS_041712_NAR_30mM_plus2.21677.21677.2	2	8.2	0	3.25E+05		(R)FSWNV	(R)F S/W N|V W|P S S R(L)		169.15	633.3085	1265.606	0.0035	2.8	9.75	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
14252	dirMS_041712_NAR_30mM_plus2.22075.22075.2	2	8.2	0	1.83E+05		(K)NSSYFVE	(K)N S\S Y/F V/E/W/I/P N N V K(V)		171.72	848.9189	1696.833	-0.0024	-1.4	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
14253	dirMS_041712_NAR_40mM_plus2.10629.10629.3	3	8.2	0	1.85E+05		(K)VGSLDN	(K)V/G S L D N V/G H L/P A/G G A V K(I)		128.15	530.9567	1590.86	-0.0043	-2.7	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
14254	dirMS_041712_NAR_40mM_plus2.14954.14954.3	3	8.2	1	1.93E+05		(K)ALLQDK	(K)A L L Q D K D V\I|A\I/N Q/D/P L G K(Q)		154.6	651.0303	1951.086	-0.0095	-4.9	4.43	49507.6	5.35	HUMAN	P06280	Alpha-galactosidase A
14255	dirMS_041712_NAR_40mM_plus2.17046.17046.3	3	8.2	0	4.41E+05		(R)IHFPLAT	(R)I H F\P L\A T\Y\A|P V I/S A E K(A)		167.57	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
14256	dirMS_041712_NAR_50mM_plus2.14300.14300.3	3	8.2	1	8.83E+05		(K)ATLPSPD	(K)A/T/L/P S P D K/L P/G F/K(M)		143.57	457.5906	1370.768	-0.0106	-7.7	8.64	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
14257	dirMS_041712_NAR_50mM_plus2.16295.16295.3	3	8.2	1	1.28E+05		(K)ILLAELE	(K)I L|L A/E L/E Q L K G Q/G K(S)		153.83	513.9741	1539.911	-0.0027	-1.8	6.14	49709.6	5.19	HUMAN	B0YJC4	Vimentin
14258	dirMS_041712_NAR_50mM_plus2.6148.6148.3	3	8.2	0	1.25E+05		(R)SGSMDF	(R)S/G\S/M D|P S G/A/H P S V/R(Q)		96.5	462.214	1384.627	0.0001	0	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
14259	dirMS_041712_NAR_50mM_plus2.8150.8150.3	3	8.2	1	9.41E+04		(R)QAVTNF	(R)Q/A V/T N/P N N T/F/Y A T K/R(L)		109.92	575.628	1724.872	-0.002	-1.2	9.99	6809.6	9.69	HUMAN	D6RA73	Stress-70 protein, mitochondrial (Fragment)
14260	dirMS_041712_NAR_60mM_plus.12832.12832.3	3	8.2	1	9.21E+05	M232m	(R)MSmKE	(R)M S m K E V D E Q|M|L/N V/Q/N K(N)	m:Oxidized methionine	123.55	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
14261	dirMS_041712_NAR_60mM_plus.17318.17318.3	3	8.2	0	9.72E+05		(R)QIFHPE	(R)Q I/F H/P E/Q/L I/T G K(E)		147.23	470.9225	1410.774	-0.021	-14.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
14262	dirMS_041712_NAR_60mM_plus.18933.18933.3	3	8.2	0	1.66E+05		(R)NHPGLL	(R)N H/P G L L\L|M/D/T T/F R(D)		156.68	505.6001	1514.778	0.0073	4.8	6.74	130372.9	6.37	HUMAN	P11498	Pyruvate carboxylase, mitochondrial
14263	dirMS_041712_NAR_60mM_plus.9185.9185.3	3	8.2	0	3.00E+05		(K)QEYDES	(K)Q E Y/D E S/G/P/S I/V H R(K)		106.35	506.2392	1516.703	0.0004	0.3	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
14264	dirMS_041712_NAR_120mM_minus.11071.11071.3	3	8.19	1	2.36E+05		(R)TNEKVE	(R)T/N E K V E/L Q/E L/N D/R(F)		114.1	529.9368	1587.797	-0.0014	-0.9	4.41	49709.6	5.19	HUMAN	B0YJC4	Vimentin
14265	dirMS_041712_NAR_120mM_minus.11250.11250.3	3	8.19	0	1.74E+05		(R)GFCLPPH	(R)G F\C L/P/P/H C S R(G)	C:Carbamidomethylation	114.25	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
14266	dirMS_041712_NAR_120mM_minus.5626.5626.3	3	8.19	1	1.47E+04		(R)LRSQDSI	(R)L R S/Q D S|M/S/S/D T/A/R(T)		84.15	485.2229	1453.67	-0.0158	-10.9	5.96	86292.1	5.81	HUMAN	J3KQ69	DNA replication licensing factor MCM3
14267	dirMS_041712_NAR_30mM_minus2.16290.16290.2	2	8.19	0	1.09E+05		(K)FGVIFAG	(K)F/G|V|I/F/A G A Q K(N)		141.95	519.2901	1037.578	-0.0049	-4.7	8.75	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
14268	dirMS_041712_NAR_40mM_minus2.15836.15836.3	3	8.19	0	3.27E+05		(R)DLLDTVI	(R)D L|L D/T|V L/P/H L Y N E T K(V)		185.3	590.9795	1770.927	-0.0033	-1.9	4.54	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
14269	dirMS_041712_NAR_40mM_minus2.8093.8093.3	3	8.19	0	1.18E+04	M33m	(R)VLTEDE	(R)V/L/T/E/D E m G H/P E I G D/A I A R(L)	m:Oxidized methionine	127.97	656.9824	1952.938	15.9944	-0.2	4.17	40874	5.06	HUMAN	E9PCI9	Farnesyl pyrophosphate synthase
14270	dirMS_041712_NAR_50mM_minus2.13079.13079.3	3	8.19	1	1.07E+04		(K)LLQSIGC	(K)L L/Q\S I/G Q A/P E/S I S E K E L K(L)		142.28	657.3639	1970.08	-0.0033	-1.7	4.79	60972	5.25	HUMAN	A6NCK0	NEDD8-activating enzyme E1 regulatory subunit
14271	dirMS_041712_NAR_50mM_minus2.14255.14255.3	3	8.19	1	4.19E+05		(R)LYSILGT	(R)L Y/S I/L G T T/L K D E G K(L)		148.5	513.2863	1537.847	-0.0029	-1.9	6.07	66876.9	6.17	HUMAN	O75083	WD repeat-containing protein 1
14272	dirMS_041712_NAR_60mM_minus.18199.18199.3	3	8.19	0	9.48E+04		(R)NSVSNF	(R)N S/V|S N F/L/H S/L E R(G)		162.5	468.2409	1402.707	0.0008	0.6	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
14273	dirMS_041712_NAR_60mM_minus.8562.8562.3	3	8.19	0	3.02E+05		(K)EFHLNES	(K)E F H\L N E/S/G D/P S S/K(S)		108.08	482.8882	1446.65	0.0005	0.3	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
14274	dirMS_041712_NAR_60mM_minus.8644.8667.3	3	8.19	1	2.84E+05		(R)LGTPELS	(R)L G\T/P E/L/S T/A E R K(E)		108.45	434.572	1301.706	-0.0045	-3.5	6.14	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1

14275	dirMS_041712_NAR_60mM_minus.8742.8742.3	3	8.19	1	8.60E+04		(R)FVKQDC	(R)F V K Q D|Q|V/C I A/R(L)	C:Carbamidomethylation	108.42	455.2427	1363.715	-0.0015	-1.1	8.75	53458.1	5.47	HUMAN	H3BR35	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A (Fragment)
14276	dirMS_041712_NAR_120mM_plus.9703.9703.3	3	8.19	1	9.78E+05		(R)STGKGI	(R)S T/G K/G I V E/F A S K/P/A A/R(K)		104.22	540.2974	1618.891	-0.0135	-8.3	9.99	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
14277	dirMS_041712_NAR_20mM_plus.10278.10278.2	2	8.19	0	9.56E+04		(K)LEAEIAT	(K)L E|A E/I A/T Y R(R)		143.43	533.2797	1065.557	-0.0054	-5	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
14278	dirMS_041712_NAR_20mM_plus.10785.10785.2	2	8.19	0	2.19E+05	M33m	(K)VAGmD	(K)V A/G/m|D V/E/L/T/V E E R(N)	m:Oxidized methionine	147.28	732.3555	1447.71	15.994	-0.6	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
14279	dirMS_041712_NAR_20mM_plus.17813.17813.2	2	8.19	0	8.16E+04		(K)VNIIPIIA	(K)V/N/I|I/P I I/A K(A)		194.62	490.8283	980.65	-0.001	-1	8.72	51212	5.84	HUMAN	A6NFQ9	Septin-8
14280	dirMS_041712_NAR_40mM_plus2.17699.17699.3	3	8.19	1	2.12E+05		(K)TGISDVF	(K)T G\I/S D V F A/K N D L/A V/V D V/R(I)		169.72	640.3451	1919.023	-0.0025	-1.3	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
14281	dirMS_041712_NAR_50mM_plus2.10233.10233.3	3	8.19	1	5.63E+05	S34s	(R)ASQIRYs	(R)A S\Q|I R Y/s V P E E T E K(G)	s:N-acetylglucosamine (S)	120.2	613.9672	1636.818	203.0694	-5.4	4.79	102255.6	4.91	HUMAN	Q9Y5G4	Protocadherin gamma-A9
14282	dirMS_041712_NAR_50mM_plus2.14043.14043.3	3	8.19	1	5.36E+05		(K)GGELVY	(K)G G E|L|V/Y T D S E A R D V F/E K(A)		141.68	638.9735	1914.908	-0.002	-1.1	4.18	533778	5.74	HUMAN	Q15149	Plectin
14283	dirMS_041712_NAR_50mM_plus2.18088.18088.3	3	8.19	2	3.44E+05	S717s	(R)YPsQPR	(R)Y/P/s Q/P/R G D T V D L A K K(I)	s:N-acetylglucosamine (S)	163.12	626.6508	1674.881	203.0569	-12	8.5	82720.6	6.2	HUMAN	P54802	Alpha-N-acetylglucosaminidase
14284	dirMS_041712_NAR_50mM_plus2.8351.8351.3	3	8.19	1	3.49E+05		(R)VAVEAK	(R)V/A/V E/A K N P A D L/P K(L)		110.53	451.2563	1351.758	-0.0036	-2.7	6.04	96306.4	6.41	HUMAN	P13639	Elongation factor 2
14285	dirMS_041712_NAR_60mM_plus.15146.15146.3	3	8.19	0	4.82E+04		(K)HIGLVYS	(K)H I G L\V Y S/G\M/G/P D/Y R(V)		135.85	522.2648	1564.758	0.0222	14.2	6.74	26012.2	6.92	HUMAN	P25787	Proteasome subunit alpha type-2
14286	dirMS_041712_NAR_60mM_plus.19472.19472.3	3	8.19	0	1.33E+05		(R)NSVSNF	(R)N S|V/S N F L H/S L E/R(G)		161.23	468.2401	1402.707	-0.0016	-1.1	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
14287	dirMS_041712_NAR_60mM_plus.5674.5674.3	3	8.19	1	1.91E+05		(R)SSGGGY	(R)S S/G/G G Y/S/G D R S G G G Y G G D\R(S)		88.07	583.5777	1748.722	-0.0033	-1.9	5.68	21563.9	10.01	HUMAN	K7EKB2	TATA-binding protein-associated factor 2N (Fragment)
14288	dirMS_041712_NAR_120mM_minus.19983.19983.3	3	8.18	1	2.47E+05		(R)AKFEELN	(R)A K F E E L N/M/D/L/F/R(S)		164.85	504.9216	1512.752	-0.0013	-0.8	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
14289	dirMS_041712_NAR_120mM_minus.6563.6583.3	3	8.18	1	3.19E+05		(R)LNGTLRI	(R)L/N|G T/L R E D D/N/R(I)		90.27	434.8858	1302.64	0.0032	2.4	4.56	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
14290	dirMS_041712_NAR_20mM_minus.13281.13281.2	2	8.18	0	7.86E+04		(K)SILFVPT	(K)S I\L|F|V|P T S A P R(G)		183.45	594.3411	1187.678	-0.0034	-2.8	9.47	92752.5	4.76	HUMAN	P14625	Endoplasmin
14291	dirMS_041712_NAR_20mM_minus.7987.7987.2	2	8.18	0	4.16E+04		(K)VVTDTD	(K)V/V|T/D/T D E/T E L A R(Q)		129.38	674.8314	1348.659	-0.0035	-2.6	3.91	36396.8	5.02	HUMAN	P05198	Eukaryotic translation initiation factor 2 subunit 1
14292	dirMS_041712_NAR_50mM_minus2.16534.16534.3	3	8.18	0	1.77E+05		(R)GGYVLH	(R)G G/Y/V/L/H/I G T I Y G D L/K(V)		161.78	535.9583	1605.863	-0.0032	-2	6.74	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
14293	dirMS_041712_NAR_50mM_minus2.16580.16580.3	3	8.18	1	9.23E+04		(R)DSEQVA	(R)D S/E/Q/V/A E/L K Q/E L A T L K(S)		163.05	601.3217	1801.954	-0.0036	-2	4.41	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
14294	dirMS_041712_NAR_50mM_minus2.18885.18885.3	3	8.18	1	2.06E+06		(R)LIALLEVI	(R)L I/A L L/E/V/L S Q K R(M)		183.82	461.6289	1382.873	-0.0008	-0.6	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
14295	dirMS_041712_NAR_60mM_minus.14722.14722.3	3	8.18	1	2.09E+05		(R)IKIGDPL	(R)I K I G D P\L/L/E D/T R(M)		142.92	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
14296	dirMS_041712_NAR_60mM_minus.16373.16373.3	3	8.18	1	1.44E+05		(K)KLSTIAL	(K)K L S T I A/L\A|L/G V E|R(T)		151.45	457.6153	1370.837	-0.0052	-3.8	8.75	52669.1	4.73	HUMAN	A8MY67	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform
14297	dirMS_041712_NAR_60mM_minus.17166.17166.3	3	8.18	1	3.63E+05		(R)KAPSDL	(R)K\A P S D\L\Y|Q/I\I L/K(A)		156.17	463.6095	1388.815	-0.0008	-0.6	8.5	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
14298	dirMS_041712_NAR_60mM_minus.7333.7333.3	3	8.18	1	6.21E+05	M136m M:	(K)VKEGmN	(K)V K E G m N\I/V/E/A m E R(F)	m:Oxidized methionine	100.3	513.25	1505.745	31.9904	0.4	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
14299	dirMS_041712_NAR_20mM_plus.13601.13601.2	2	8.18	0	3.22E+05	M148m	(R)DLTDYL	(R)D L|T/D Y/L m K(I)	m:Oxidized methionine	165.17	507.7439	998.486	15.9942	-0.7	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
14300	dirMS_041712_NAR_20mM_plus.18409.18409.2	2	8.18	0	1.22E+05		(R)GVVQEL	(R)G V V/Q|E/L Q/Q/A I\S K(L)		198.05	650.3656	1299.727	-0.0028	-2.1	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
14301	dirMS_041712_NAR_30mM_plus2.4476.4476.2	2	8.18	0	2.94E+05		(K)EDAAN	(K)E/D|A\A/N/N/Y A R(G)		72.85	512.2281	1023.449	-0.0001	-0.1	4.37	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
14302	dirMS_041712_NAR_30mM_plus2.9357.9357.2	2	8.18	0	2.53E+05		(R)ALELEQ	(R)A L/E/L/E/Q/E/R(K)		101.5	494.2566	987.511	-0.0046	-4.7	4.25	67933	6.08	HUMAN	P26038	Moesin
14303	dirMS_041712_NAR_40mM_plus2.17487.17487.3	3	8.18	0	2.47E+04		(R)GTEDITS	(R)G/T/E/D I T|S P H G I/P L D L L D R(V)		169.42	650.3372	1948.997	-0.0004	-0.2	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
14304	dirMS_041712_NAR_50mM_plus2.10992.10992.3	3	8.18	1	2.59E+06		(R)VCEEIAI	(R)V/C E E\I/A\I|I P S K/K(L)	C:Carbamidomethylation	125.03	462.9247	1386.766	-0.0066	-4.7	6.11	21927.8	9.55	HUMAN	H0YK46	40S ribosomal protein S17 (Fragment)
14305	dirMS_041712_NAR_50mM_plus2.11118.11118.3	3	8.18	0	1.68E+05		(K)ADDGRF	(K)A/D/D G R P F/P Q V I/K(S)		125.2	448.2419	1342.711	-0.0002	-0.2	6	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
14306	dirMS_041712_NAR_50mM_plus2.14430.14430.3	3	8.18	0	1.56E+06		(K)SLTNDW	(K)S L/T N D|W E D H L/A V K(H)		143.63	509.9193	1527.744	-0.0005	-0.3	4.53	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
14307	dirMS_041712_NAR_50mM_plus2.15313.15313.3	3	8.18	1	5.61E+05		(R)LAAELNI	(R)L A|A/E/L N K/F M L E/K(V)		149.15	469.5948	1406.771	-0.0014	-1	6.14	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
14308	dirMS_041712_NAR_50mM_plus2.16390.16390.3	3	8.18	0	3.28E+04		(R)EVIDLLK	(R)E V\I/D|L|L/K\P D Q V E G I Q K(S)		154.37	608.6724	1824.011	-0.0087	-4.7	4.32	156557.7	5.52	HUMAN	Q86UP2	Kinectin
14309	dirMS_041712_NAR_50mM_plus2.7190.7190.3	3	8.18	1	3.91E+04		(R)IVEQDT	(R)I/V|E Q/D T M/P/P K G V R(H)		103.58	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
14310	dirMS_041712_NAR_60mM_plus.13294.13294.3	3	8.18	1	5.17E+05		(R)LDDRVY	(R)L/D/D R V/Y/A/M/C Q I K(S)	C:Carbamidomethylation	125.82	504.5817	1511.735	-0.0039	-2.6	5.96	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
14311	dirMS_041712_NAR_60mM_plus.18257.18257.3	3	8.18	1	2.20E+05		(R)ARFEEL	(R)A R F E/E\L|C/S/D/L F R(S)	C:Carbamidomethylation	152.5	514.9194	1542.737	0.0067	4.3	4.68	25598.3	6.45	HUMAN	E7EP11	Heat shock 70 kDa protein 1A/1B
14312	dirMS_041712_NAR_60mM_plus.20308.20308.3	3	8.18	1	4.21E+05		(K)NAAGAL	(K)N\A/A/G A L D L L K E L K(N)		166.93	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
14313	dirMS_041712_NAR_60mM_plus.6780.6780.2	2	8.18	1	1.07E+06		(R)KTGQAP	(R)K\T/G/Q/A|P G Y S Y T A A\N K(N)		94.03	778.8881	1556.77	-0.0014	-0.9	9.53	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
14314	dirMS_041712_NAR_120mM_minus.12255.12294.3	3	8.17	0	2.03E+04		(K)HLSVND	(K)H L\S V N D|L/P V\G/R(S)		120.75	402.8907	1206.659	-0.0014	-1.2	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
14315	dirMS_041712_NAR_120mM_minus.8517.8517.3	3	8.17	1	4.92E+05		(R)LKVTEG	(R)L K V T E G G E/P/Y R(L)		100.45	416.885	1248.658	-0.0178	-14.3	6.14	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
14316	dirMS_041712_NAR_20mM_minus.11797.11797.2	2	8.17	0	1.15E+05	M98m	(R)TLTIVDT	(R)T L\T\I/V/D|T G/I G m T K(A)	m:Oxidized methionine	166.93	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
14317	dirMS_041712_NAR_20mM_minus.7139.7139.2	2	8.17	0	3.67E+05	M281m	(R)AEAESm	(R)A E|A|E S m Y Q/I/K(Y)	m:Oxidized methionine	118.07	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
14318	dirMS_041712_NAR_30mM_minus2.14350.14649.2	2	8.17	0	3.72E+05		(R)VDFNVP	(R)V/D|F/N V/P M/K(N)		132.25	475.2457	949.481	0.003	3.1	5.81	30303.6	9.08	HUMAN	E7ERH5	Phosphoglycerate kinase
14319	dirMS_041712_NAR_30mM_minus2.15593.15593.2	2	8.17	0	1.72E+05		(K)EILFYDR	(K)E I|L/F/Y D/R(I)		137.77	478.2479	955.488	0.0002	0.2	4.37	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b
14320	dirMS_041712_NAR_30mM_minus2.17513.17632.2	2	8.17	0	1.72E+05		(K)GFLIDGY	(K)G F|L|I/D/G Y/P R(E)		150.27	519.2752	1037.542	0.0017	1.6	5.83	15567.5	8.13	HUMAN	H0Y4J6	Adenylate kinase isoenzyme 1 (Fragment)
14321	dirMS_041712_NAR_40mM_minus2.14054.14054.3	3	8.17	0	5.38E+05		(R)IHFPLAT	(R)I H F\P L A\T\Y\A|P V/I S A E K(A)		167.63	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
14322	dirMS_041712_NAR_40mM_minus2.14126.14126.3	3	8.17	0	1.64E+04		(R)LLEVLSG	(R)L L E V L\S/G E/I L/P K P T K(G)		167.47	546.333	1636.988	-0.0039	-2.4	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
14323	dirMS_041712_NAR_50mM_minus2.10211.10211.3	3	8.17	0	1.37E+05		(K)VGSLDN	(K)V/G|S L D N V/G H/L P A G G A V K(I)		126.83	530.9592	1590.86	0.0032	2	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
14324	dirMS_041712_NAR_60mM_minus.17187.17187.3	3	8.17	0	7.22E+04	M55m	(R)DIKPDNI	(R)D I K P D N F|L/m/G I G R(H)	m:Oxidized methionine	155.68	497.9256	1475.767	15.9947	-0.1	5.96	27968.7	9.69	HUMAN	D6REM4	Casein kinase I isoform alpha
14325	dirMS_041712_NAR_60mM_minus.18412.18412.3	3	8.17	0	6.14E+04		(K)YAPLHL	(K)Y A|P L H L V/P L I E R(L)		163.8	474.2805	1420.831	-0.0041	-2.9	6.75	147553.6	6.73	HUMAN	E7EVF4	Cytoplasmic FMR1-interacting protein 2
14326	dirMS_041712_NAR_60mM_minus.19327.19327.3	3	8.17	0	4.54E+05		(R)THNGES	(R)T H N G E S V S\Y/L F S H\V/P L(-)		171.93	596.2923	1786.876	-0.0135	-7.6	5.92	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
14327	dirMS_041712_NAR_60mM_minus.9002.9002.3	3	8.17	1	3.60E+05	M232m M:	(R)MSmKE	(R)M/S m/K E V D E\Q m|L/N\V Q/N\K(N)	m:Oxidized methionine	110.3	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
14328	dirMS_041712_NAR_120mM_plus.22402.22402.4	4	8.17	2	3.40E+05		(R)TKIDPSA	(R)T K I D P S A/L|V Q K/L E L/D/V R(S)		171.28	482.0309	1925.107	-0.0048	-2.5	5.79	22331.4	11.18	HUMAN	C9JJU7	Protein FAM207A (Fragment)
14329	dirMS_041712_NAR_20mM_plus.14419.14419.3	3	8.17	0	1.19E+05		(R)LQEAGIL	(R)L Q\E A G\I/L/S/A\E E/L Q R(L)		171.5	519.6131	1556.828	-0.0031	-2	4.25	533778	5.74	HUMAN	Q15149	Plectin
14330	dirMS_041712_NAR_20mM_plus.17084.17084.2	2	8.17	0	9.18E+04		(R)AVLVDLI	(R)A V L\V/D\L|E/P G T|M D\S V R(S)		189.4	801.414	1601.82	0.0004	0.2	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
14331	dirMS_041712_NAR_20mM_plus.8233.8233.2	2	8.17	0	9.61E+04		(K)TAVCDIF	(K)T A|V/C D|I/P\P R(G)	C:Carbamidomethylation	127.58	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
14332	dirMS_041712_NAR_30mM_plus2.10359.10359.2	2	8.17	0	8.32E+05		(R)FAQMLE	(R)F/A|Q/M L/E/K(V)		108.32	433.7317	866.444	0.0121	13.9	6	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
14333	dirMS_041712_NAR_30mM_plus2.5560.5560.2	2	8.17	0	6.33E+04		(R)IAGQVA	(R)I/A|G Q V A|A/A\N K(K)		83.32	471.772	942.537	0	0	8.75	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
14334	dirMS_041712_NAR_40mM_plus2.10871.10871.3	3	8.17	1	3.16E+05		(R)DGKLVS	(R)D G K/L V\S E/S/S D/V\L/P K(-)		128.88	491.9315	1473.78	0.0004	0.3	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
14335	dirMS_041712_NAR_40mM_plus2.12084.12084.2	2	8.17	0	1.63E+05		(K)VYFDLR	(K)V/Y/F D/L R(I)		137.07	406.7184	812.43	-0.0006	-0.7	5.8	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
14336	dirMS_041712_NAR_40mM_plus2.6420.6420.2	2	8.17	0	1.22E+04		(R)IYVSANS	(R)I Y|V/S A N S G/A/R(I)		96.83	519.2719	1037.537	-0.0009	-0.9	8.75	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
14337	dirMS_041712_NAR_50mM_plus2.18606.18606.3	3	8.17	0	4.06E+05		(R)AVSILPL	(R)A V/S/I/L P/L L G/H/G\V P R(L)		165.87	476.9615	1428.869	0.0014	1	9.8	66841.7	7.74	HUMAN	F5H721	WW domain-binding protein 11
14338	dirMS_041712_NAR_60mM_plus.12397.12397.3	3	8.17	0	9.17E+05		(K)TKPYIQ	(K)T K|P Y I Q V/D/I/G G G Q T K(T)		121.42	535.6249	1604.864	-0.0041	-2.6	8.17	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
14339	dirMS_041712_NAR_20mM_minus.14498.14498.3	3	8.16	0	1.37E+05		(R)LSVEEA	(R)L S V E E A V A A G\V/V/G/G E I Q/E K(L)		199.57	629.0005	1884.991	-0.0044	-2.3	4.09	266161	5.68	HUMAN	E9PPU0	Epiplakin
14340	dirMS_041712_NAR_20mM_minus.14704.14704.2	2	8.16	0	1.77E+05		(K)TAVETA	(K)T A\V|E/T/A/V/L\L\L R(I)		201.35	593.3613	1185.72	-0.0048	-4.1	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
14341	dirMS_041712_NAR_20mM_minus.7642.7642.2	2	8.16	0	7.24E+05	M239m	(K)EVDEQn	(K)E V/D E/Q m L\N|V/Q N K(N)	m:Oxidized methionine	125	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
14342	dirMS_041712_NAR_30mM_minus2.12163.12163.2	2	8.16	0	2.12E+05		(K)IGVTVLS	(K)I/G/V/T/V L S R(I)		119.42	422.7649	844.525	-0.0026	-3	9.75	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
14343	dirMS_041712_NAR_30mM_minus2.12504.12504.2	2	8.16	0	7.31E+05		(R)GVVGPE	(R)G V|V/G/P E/L Y G R(L)		122.47	523.7834	1046.563	-0.0034	-3.2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
14344	dirMS_041712_NAR_30mM_minus2.18988.18988.3	3	8.16	0	1.49E+05		(K)SYELPD	(K)S Y\E L P\D G Q V/I/T\I G N E R(F)		158.68	597.6343	1790.892	-0.0036	-2	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
14345	dirMS_041712_NAR_30mM_minus2.20477.20477.2	2	8.16	0	4.58E+05		(R)FLTWIL	(R)F L|T/W I/L/N R(Y)		175.92	531.8089	1062.61	0.001	1	9.75	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
14346	dirMS_041712_NAR_30mM_minus2.5506.5526.2	2	8.16	0	1.70E+05		(K)YIDENQI	(K)Y/I|D/E N Q D/R(Y)		83.98	526.7389	1052.464	0.0062	5.9	4.03	6412.4	9.52	HUMAN	J3KSS4	Cytosolic non-specific dipeptidase (Fragment)
14347	dirMS_041712_NAR_30mM_minus2.7238.7238.2	2	8.16	0	1.16E+05		(K)MQAVQ	(K)M/Q|A|V Q E/A/T R(L)		94	517.257	1033.509	-0.0028	-2.7	5.75	533778	5.74	HUMAN	Q15149	Plectin
14348	dirMS_041712_NAR_60mM_minus.5105.5105.3	3	8.16	1	4.16E+04		(K)VSQGVE	(K)V/S\Q/G V E D G P D T K R(A)		83.18	463.2294	1387.681	-0.0076	-5.4	4.56	33726	7.84	HUMAN	B3KNJ4	SUMO-1 activating enzyme subunit 1, isoform CRA_a
14349	dirMS_041712_NAR_60mM_minus.8910.8910.3	3	8.16	1	4.58E+04		(K)YIDENQI	(K)Y/I/D\E/N Q/D R\Y I K(K)		109.38	486.2395	1456.707	-0.0027	-1.9	4.56	6412.4	9.52	HUMAN	J3KSS4	Cytosolic non-specific dipeptidase (Fragment)
14350	dirMS_041712_NAR_120mM_plus.7884.7884.2	2	8.16	0	1.36E+05		(R)VNGGYS	(R)V N|G G Y/S\G L R(D)		95.12	461.7364	922.474	-0.0086	-9.3	8.72	73195.4	6.04	HUMAN	P33908	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA
14351	dirMS_041712_NAR_120mM_plus.9893.9893.3	3	8.16	1	1.73E+06		(K)SKFDNL	(K)S K\F D N L|Y/G/C/R(E)	C:Carbamidomethylation	104.62	420.5351	1259.584	0.007	5.6	8.31	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
14352	dirMS_041712_NAR_20mM_plus.12367.12367.2	2	8.16	0	1.73E+05		(R)GVEICIA	(R)G V\E\I|C/I/A\T/P G R(L)	C:Carbamidomethylation	158.5	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
14353	dirMS_041712_NAR_20mM_plus.15200.15200.3	3	8.16	0	7.27E+04		(K)GVEGLI	(K)G V\E G L|I/D I/E N/P N/R(V)		176.42	475.9154	1425.733	-0.0016	-1.1	4.14	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
14354	dirMS_041712_NAR_20mM_plus.16211.16211.2	2	8.16	0	4.99E+04		(R)LIDFLES	(R)L I/D/F/L E/S G K(T)		183.38	511.28	1021.556	-0.0037	-3.6	4.37	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
14355	dirMS_041712_NAR_20mM_plus.16707.16707.2	2	8.16	0	2.48E+05		(K)VQIAVA	(K)V Q/I|A V|A N A|Q E L L/Q R(M)		186.6	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
14356	dirMS_041712_NAR_20mM_plus.17523.17523.3	3	8.16	0	6.85E+04		(K)LAAVDA	(K)L A A\V D A T\V|N\Q V/L/A S R(Y)		192.37	509.9542	1527.849	-0.0009	-0.6	5.84	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
14357	dirMS_041712_NAR_20mM_plus.18363.18363.2	2	8.16	0	6.91E+04	M78m	(K)LVSDEm	(K)L V|S|D\E/m/V\V E L I E K(N)	m:Oxidized methionine	197.37	760.3973	1503.797	15.9899	-3.3	4	17727.3	6.31	HUMAN	F8VZG5	Adenylate kinase 2, mitochondrial
14358	dirMS_041712_NAR_20mM_plus.7450.7450.3	3	8.16	0	2.14E+05		(K)TGQAPG	(K)T G\Q A|P G Y S/Y/T/A A/N K(N)		119.53	476.8963	1428.675	-0.001	-0.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
14359	dirMS_041712_NAR_20mM_plus.9500.9500.2	2	8.16	0	9.59E+04		(R)ALEESN	(R)A L\E/E/S N Y E/L E G K(I)		136.52	691.3246	1381.648	-0.0062	-4.5	4.09	59054.3	5.14	HUMAN	P13645	Keratin, type I cytoskeletal 10
14360	dirMS_041712_NAR_30mM_plus2.21768.21768.2	2	8.16	0	2.27E+05		(R)TTNFAG	(R)T T\N F A/G I L|S/Q\G L/R(I)		169.38	689.3749	1377.748	-0.006	-4.3	9.41	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
14361	dirMS_041712_NAR_30mM_plus2.9120.9260.2	2	8.16	0	5.38E+05		(R)MQSFGI	(R)M/Q|S/F G/M/K(T)		102.07	414.6908	828.374	0.0001	0.1	8.5	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
14362	dirMS_041712_NAR_40mM_plus2.17544.17544.3	3	8.16	0	2.09E+04		(R)IHFPLAT	(R)I H F P L A T Y\A/P V I S/A E K(A)		169.42	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
14363	dirMS_041712_NAR_50mM_plus2.13613.13640.3	3	8.16	1	1.73E+06		(K)VLSSRVI	(K)V L/S|S R V H T V E E K(S)		140.02	461.9229	1383.759	-0.0049	-3.5	6.73	50449.1	4.98	HUMAN	Q7Z3Y8	Keratin, type I cytoskeletal 27
14364	dirMS_041712_NAR_50mM_plus2.16761.16761.3	3	8.16	0	2.32E+05		(K)GFDILGI	(K)G F/D I/L/G I K/P V Q R(M)		156.23	448.2656	1342.784	-0.0019	-1.4	8.75	52817.9	6.2	HUMAN	F5H3T8	Arginine--tRNA ligase, cytoplasmic
14365	dirMS_041712_NAR_50mM_plus2.9361.9361.3	3	8.16	0	2.91E+05		(K)GLSSDN	(K)G L|S/S D/N K/P/M V N\L D K(L)		116.17	506.5928	1517.763	0.001	0.7	5.96	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
14366	dirMS_041712_NAR_60mM_plus.14810.14810.3	3	8.16	1	9.63E+04		(R)KFLDGIY	(R)K F L D G I/Y/V/S E/K(G)		133.93	433.5671	1298.699	-0.0123	-9.5	6.07	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
14367	dirMS_041712_NAR_60mM_plus.18719.18719.3	3	8.16	1	3.96E+06		(R)VSFELFA	(R)V/S/F E/L F A D K V/P/K(T)		155.83	460.5914	1379.757	0.0027	2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
14368	dirMS_041712_NAR_60mM_plus.20415.20415.3	3	8.16	1	4.21E+05		(K)NAAGAL	(K)N A/A/G A/L D L L K E L K(N)		166.93	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
14369	dirMS_041712_NAR_60mM_plus.20843.20843.3	3	8.16	0	8.00E+03		(-)MKPLVV	(-)M/K P L V V/F|V/L/G/G/P G A G K(G)		170.57	523.9774	1569.919	-0.0009	-0.6	10	22450.2	5.44	HUMAN	P30085	UMP-CMP kinase
14370	dirMS_041712_NAR_120mM_minus.17450.17450.4	4	8.15	2	4.72E+05		(K)KDEKTD	(K)K D E K T D T L E D L|F/P T/T/K(I)		149.15	470.992	1880.949	-0.0026	-1.4	4.44	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
14371	dirMS_041712_NAR_20mM_minus.11536.11536.2	2	8.15	0	2.36E+05		(R)GALQNI	(R)G A/L\Q/N I|I\P A S T G A A K(A)		164.25	706.3976	1411.79	-0.0024	-1.7	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
14372	dirMS_041712_NAR_30mM_minus2.11863.11863.2	2	8.15	0	9.21E+05		(K)EVDEQN	(K)E V D E/Q M L N/V|Q/N K(N)		117.53	723.8476	1446.689	-0.0014	-1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
14373	dirMS_041712_NAR_30mM_minus2.16456.16456.2	2	8.15	0	1.48E+05		(K)SQLLSYII	(K)S/Q|L|L/S/Y I D R(L)		143.07	547.7949	1094.584	-0.0015	-1.4	5.55	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
14374	dirMS_041712_NAR_40mM_minus2.14301.14301.3	3	8.15	1	1.83E+05		(K)ITSDEPL	(K)I/T/S D E/P L T K D/D I\P V F L R(H)		168.45	653.6833	1959.043	-0.008	-4.1	4.23	22313.1	4.9	HUMAN	B1AHE4	Ataxin 10 (Fragment)
14375	dirMS_041712_NAR_40mM_minus2.9628.9628.3	3	8.15	0	3.04E+04		(K)VVEIAPA	(K)V/V/E I A/P/A A H L/D/P Q L R(T)		139.12	543.6435	1628.912	0.0041	2.5	5.32	58266.4	9.46	HUMAN	B4DN00	Pyruvate carboxylase, mitochondrial
14376	dirMS_041712_NAR_50mM_minus2.11482.11482.3	3	8.15	1	1.22E+05		(K)MLVSGA	(K)M/L/V/S/G A G\D/I K L T K(D)		132.95	444.9227	1332.756	-0.002	-1.5	8.35	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
14377	dirMS_041712_NAR_50mM_minus2.12323.12323.3	3	8.15	0	2.81E+05		(K)QLTEED	(K)Q L/T/E/E D/G V H S V I E E N I K(C)		138.65	647.3249	1939.961	-0.0006	-0.3	4.25	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
14378	dirMS_041712_NAR_50mM_minus2.14794.14794.3	3	8.15	1	1.76E+05		(K)EILDKFT	(K)E\I/L/D K F/T E/E V V K(Q)		152.17	483.932	1449.784	-0.0021	-1.4	4.41	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
14379	dirMS_041712_NAR_60mM_minus.12281.12281.3	3	8.15	1	7.93E+05		(K)AVIFCLS	(K)A V/I/F/C L S A D/K K(C)	C:Carbamidomethylation	127.92	417.9007	1251.677	0.011	8.8	8.64	15739.2	9.3	HUMAN	F6RFD5	Destrin
14380	dirMS_041712_NAR_60mM_minus.14530.14530.3	3	8.15	0	1.41E+05		(K)NFDLRP	(K)N/F|D/L R P G V I V/R(-)		141.02	429.2503	1285.738	-0.0012	-0.9	9.6	33192.3	6.77	HUMAN	B4DN45	S-adenosylmethionine synthase
14381	dirMS_041712_NAR_60mM_minus.16649.16649.3	3	8.15	0	1.71E+05		(R)LLIHQSL	(R)L L I/H Q S\L/A/G G I I G V K(G)		153.33	506.9823	1518.937	-0.0043	-2.8	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
14382	dirMS_041712_NAR_120mM_plus.5725.5725.2	2	8.15	0	1.16E+05		(R)QLLEGEI	(R)Q/L|L/E/G E/E S/R(M)		83.28	530.7704	1060.527	0.0066	6.2	4.25	37677.8	5.16	HUMAN	F5GY66	Keratin, type II cytoskeletal 1b
14383	dirMS_041712_NAR_20mM_plus.16177.16177.2	2	8.15	0	6.61E+04		(R)LLDAQL	(R)L L D A/Q/L|A\T G G\I V D|P R(L)		183.85	769.9362	1538.854	0.0114	7.4	4.21	533778	5.74	HUMAN	Q15149	Plectin

14384	dirMS_041712_NAR_20mM_plus.16882.16882.2	2	8.15	0	2.11E+05		(K)VLTPELY	(K)V L|T/P E/L Y A/E L R(A)		188.68	652.3664	1303.726	-0.0001	-0.1	4.53	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
14385	dirMS_041712_NAR_30mM_plus2.19831.19831.3	3	8.15	0	1.31E+05		(K)GFAFVQ	(K)G F|A F V|Q/Y V N/E R(N)		157.48	443.8907	1329.659	-0.0011	-0.8	6	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
14386	dirMS_041712_NAR_30mM_plus2.7329.7329.2	2	8.15	0	3.05E+05		(K)GSAITG	(K)G S A|I|T/G P V A K(E)		92.77	450.7605	900.515	-0.0012	-1.3	8.75	8956.4	10.28	HUMAN	J3KTJ3	60S ribosomal protein L23
14387	dirMS_041712_NAR_40mM_plus2.15787.15787.3	3	8.15	0	1.40E+05		(K)VAIVKP	(K)V/A|I/V K/P G V/P M/E I V L N K(E)		160.32	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
14388	dirMS_041712_NAR_40mM_plus2.17813.17813.3	3	8.15	1	2.48E+06		(R)LFVGNL	(R)L/F|V|G N L/P A D I T E D E F K R(L)		170.28	655.3421	1964.012	-0.0006	-0.3	4.32	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
14389	dirMS_041712_NAR_50mM_plus2.18250.18250.2	2	8.15	0	5.68E+05		(R)IHFPLAT	(R)I H|F|P L A/T Y/A P V I S A E K(A)		164.68	878.9842	1756.963	-0.0021	-1.2	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
14390	dirMS_041712_NAR_50mM_plus2.19825.19825.3	3	8.15	1	2.79E+05		(K)DRDVTF	(K)D R D V\T F\S|P/A T/I/E N E L I/K(F)		172.62	650.0048	1948.002	-0.0024	-1.2	4.32	8027.1	8.38	HUMAN	H7C2D6	Mesencephalic astrocyte-derived neurotrophic factor (Fragment)
14391	dirMS_041712_NAR_50mM_plus2.8748.8748.3	3	8.15	1	2.21E+05		(K)TTSPPE	(K)T|T/S/P/P E V S G Y S Y E K T E/R(S)		113.33	644.3093	1930.903	0.0105	5.4	4.78	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
14392	dirMS_041712_NAR_60mM_plus.5808.5808.3	3	8.15	1	8.67E+04		(R)CLSSAT	(R)C L/S S A T/D/P Q T K R(K)	C:Carbamidomethylation	88.38	455.226	1363.663	0	0	8.75	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
14393	dirMS_041712_NAR_60mM_plus.9820.9820.3	3	8.15	2	3.92E+05	M309m M	(K)TFPTmK	(K)T F P T m K/m F E|Y/V/R N D R(D)	m:Oxidized methionine	109.6	656.3024	1934.925	31.9675	-11.4	8.25	45384.5	7.88	HUMAN	O77932	Protein Dom3Z
14394	dirMS_041712_NAR_20mM_minus.10003.10003.3	3	8.14	0	4.94E+04	S723s S72	(R)ELsNFYF	(R)E L s N\F Y/F s/I/I/K(D)	s:Phosphorylated S	151.17	507.558	1360.715	159.9447	7.9	6.1	106950.6	6.06	HUMAN	F6SBX2	Isoleucine--tRNA ligase, mitochondrial
14395	dirMS_041712_NAR_20mM_minus.7160.7160.2	2	8.14	0	1.42E+05		(R)AAQVA	(R)A A Q|V|A|Q D E E I A R(L)		119.02	650.8255	1300.649	-0.0054	-4.2	4.14	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
14396	dirMS_041712_NAR_30mM_minus2.11394.11623.2	2	8.14	0	1.22E+06		(K)ACTILLR	(K)A/C|T/I L/L/R(G)	C:Carbamidomethylation	116.3	423.7463	846.487	-0.0013	-1.5	9.79	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
14397	dirMS_041712_NAR_50mM_minus2.12582.12582.3	3	8.14	0	1.06E+06	M114m M	(R)AGKPVI	(R)A G K|P V\I\C\A\T Q\m/L E S m/I K(K)	C:Carbamidomethylation m:Oxid	139.83	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
14398	dirMS_041712_NAR_50mM_minus2.9240.9240.3	3	8.14	0	1.99E+05		(K)VGQEIE	(K)V/G/Q/E I E/V/R/P G I V S K(D)		120.43	504.2902	1510.859	-0.0027	-1.8	6.11	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
14399	dirMS_041712_NAR_60mM_minus.13489.13489.3	3	8.14	1	1.16E+05	M160m	(K)FRQDL	(K)F R Q D L\m\N|I|A/G T T L S S K(L)	m:Oxidized methionine	135.43	599.9744	1781.921	15.9872	-4.3	8.75	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
14400	dirMS_041712_NAR_60mM_minus.16889.16889.3	3	8.14	1	3.95E+05		(R)ARFEEL	(R)A R F E\E L N/A/D/L/F R(G)		153.98	494.2594	1480.754	0.0093	6.3	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
14401	dirMS_041712_NAR_20mM_plus.12479.12479.3	3	8.14	0	5.11E+04		(K)VNQIGS	(K)V N\Q I G S V/T E/S/I Q A/C/K(L)	C:Carbamidomethylation	159.02	545.2781	1633.821	-0.0016	-1	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
14402	dirMS_041712_NAR_20mM_plus.13041.13041.2	2	8.14	0	4.13E+03	M107m	(K)LYmVLIT	(K)L/Y/m/V L I T T/K(N)	m:Oxidized methionine	162.38	549.3156	1081.633	15.9913	-3.3	8.59	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
14403	dirMS_041712_NAR_20mM_plus.16178.16178.2	2	8.14	0	6.61E+04		(R)LLDAQL	(R)L L/D\A/Q\L|A T G G I V\D/P R(L)		183.85	769.9362	1538.854	0.0114	7.4	4.21	533778	5.74	HUMAN	Q15149	Plectin
14404	dirMS_041712_NAR_30mM_plus2.14690.14690.2	2	8.14	0	5.85E+05		(K)IGLDFCK	(K)I/G/L/D F/C K(Y)	C:Carbamidomethylation	129.58	426.7164	852.428	-0.0029	-3.4	5.84	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
14405	dirMS_041712_NAR_30mM_plus2.18384.18384.2	2	8.14	0	6.04E+04		(K)NLGTAL	(K)N L|G/T/A L/A E L R(T)		150	529.3028	1057.6	-0.0017	-1.6	6	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
14406	dirMS_041712_NAR_30mM_plus2.18549.18549.2	2	8.14	0	7.16E+05		(K)AAIDWF	(K)A A/I/D\W F D/G/K(E)		150.85	511.7539	1022.494	0.0064	6.2	4.21	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
14407	dirMS_041712_NAR_40mM_plus2.10165.10165.3	3	8.14	0	1.35E+05	M1087m	(R)mPLPAP	(R)m P/L|P A/P S L S H\Q/P/P P A P R(V)	m:Oxidized methionine	124.5	603.6536	1792.953	15.9936	-0.7	9.52	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
14408	dirMS_041712_NAR_40mM_plus2.11951.11951.2	2	8.14	0	1.59E+05		(K)VYFDLR	(K)V/Y|F D/L R(I)		137.05	406.7184	812.43	-0.0006	-0.7	5.8	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
14409	dirMS_041712_NAR_40mM_plus2.16241.16241.3	3	8.14	0	5.88E+05		(R)FGVPVI	(R)F G\V/P V/I/A D G G I Q N/V G H I A K(A)		162.43	631.3436	1892.039	-0.0226	-12	6.74	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
14410	dirMS_041712_NAR_50mM_plus2.19142.19256.3	3	8.14	1	3.50E+05		(K)GVPTGF	(K)G V|P/T/G F I L P I R D/I R(A)		169.55	518.6453	1553.916	0.0051	3.3	9.6	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
14411	dirMS_041712_NAR_50mM_plus2.20160.20160.3	3	8.14	1	1.14E+05		(R)FLIPVLN	(R)F L|I/P/V L/N G L E K K(E)		174.58	457.6182	1370.841	-0.0006	-0.4	8.59	142001.7	5.82	HUMAN	Q92797	Symplekin
14412	dirMS_041712_NAR_50mM_plus2.22201.22201.3	3	8.14	1	1.35E+06		(K)EGGLGP	(K)E G/G L/G/P/L/N I P L L A D V T R R(L)		191	631.029	1891.076	-0.0035	-1.9	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
14413	dirMS_041712_NAR_50mM_plus2.8387.8387.3	3	8.14	0	5.68E+04		(K)AAGARP	(K)A A|G A/R P L T S|P/E/S/L S R(D)		110.75	504.9436	1512.813	0.0034	2.2	9.64	119157.2	5.4	HUMAN	B0UX83	HLA-B associated transcript 3
14414	dirMS_041712_NAR_120mM_minus.14739.14739.4	4	8.13	2	3.07E+05		(K)AMGDA	(K)A/M|G/D A E I/K D G E R L P L A/V K(D)		134.3	479.0049	1913.016	-0.0183	-9.6	4.78	99900.1	5.04	HUMAN	B4DZI8	Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b
14415	dirMS_041712_NAR_120mM_minus.4863.4863.3	3	8.13	1	5.64E+05		(K)AGADEE	(K)A/G/A D/E/E R/A E T A R(L)		77.52	425.8687	1275.592	-0.0008	-0.7	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
14416	dirMS_041712_NAR_20mM_minus.7261.7261.2	2	8.13	0	2.46E+04		(K)IAVAAQ	(K)I A|V/A A/Q/N C/Y K(V)	C:Carbamidomethylation	120.58	569.2917	1137.572	0.004	3.5	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
14417	dirMS_041712_NAR_30mM_minus2.7605.7639.2	2	8.13	0	5.92E+05		(R)TGLEDP	(R)T/G|L/E|D|P E/R(Y)		95.83	458.7238	916.437	0.0033	3.6	4.14	21781.4	5.48	HUMAN	E7ERA5	Myosin-10 (Fragment)
14418	dirMS_041712_NAR_50mM_minus2.16450.16450.3	3	8.13	0	1.77E+05		(R)GGYVLH	(R)G G Y/V/L/H/I G T I/Y G D\L K(V)		161.78	535.9583	1605.863	-0.0032	-2	6.74	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
14419	dirMS_041712_NAR_50mM_minus2.9641.9641.3	3	8.13	1	1.78E+05	M183m	(R)VEVERD	(R)V/E|V E/R D N L A E/D I m R(L)	m:Oxidized methionine	122.23	568.9459	1688.827	15.9959	0.6	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
14420	dirMS_041712_NAR_60mM_minus.11737.11737.3	3	8.13	1	4.61E+05	M232m	(R)MSmKE	(R)M S m K E V\D\E\Q|M|L|N V Q N K(N)	m:Oxidized methionine	125.58	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
14421	dirMS_041712_NAR_60mM_minus.12592.12592.3	3	8.13	0	1.73E+05		(K)LAQAN	(K)L/A Q A/N/G W/G V/M\V S H R(S)		129.93	509.2631	1525.769	0.0055	3.6	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
14422	dirMS_041712_NAR_60mM_minus.16908.16908.3	3	8.13	1	3.13E+05		(R)LKLPAV	(R)L K L P A V\V/T A D/L R(L)		154.02	432.6056	1295.805	-0.0023	-1.8	8.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
14423	dirMS_041712_NAR_60mM_minus.6569.6569.3	3	8.13	1	5.36E+04	M279m	(K)LGREEP	(K)L G R E E P A|M/S\m/D A/N G\K(I)	m:Oxidized methionine	95.3	541.2478	1605.736	15.9929	-1.2	4.68	99900.1	5.04	HUMAN	B4DZI8	Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b
14424	dirMS_041712_NAR_120mM_plus.13073.13181.3	3	8.13	1	5.40E+05		(R)KQITME	(R)K Q I\T\M|E/E/L/V/R(S)		122.28	416.2263	1246.682	-0.018	-14.5	6.14	533778	5.74	HUMAN	Q15149	Plectin
14425	dirMS_041712_NAR_20mM_plus.14808.14808.2	2	8.13	0	1.98E+05	M179m M	(K)mFVLDE	(K)m F\V|L|D E\A\D E m/L S R(G)	m:Oxidized methionine	173.6	794.3555	1555.713	31.9906	0.5	3.91	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
14426	dirMS_041712_NAR_20mM_plus.17074.17074.2	2	8.13	0	9.70E+04		(R)AIVAIEN	(R)A I\V A\I|E\N|P/A D V\S V I S S R(N)		188.97	870.9764	1740.949	-0.0035	-2	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
14427	dirMS_041712_NAR_20mM_plus.18052.18052.2	2	8.13	0	1.37E+05	T87t	(R)TVQStV	(R)T V|Q/S/t V P E D/A E K(R)	t:N-acetylglucosamine (T)	195.22	753.8776	1303.638	203.1103	20.5	4.14	240718.5	8.34	HUMAN	A6NIW2	Dedicator of cytokinesis protein 11
14428	dirMS_041712_NAR_20mM_plus.19072.19072.3	3	8.13	0	2.07E+05		(K)TLETQS	(K)T L E T Q S A\L/G\P A L Q A/A F K(L)		202.57	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
14429	dirMS_041712_NAR_30mM_plus2.12645.12645.2	2	8.13	0	1.62E+05		(K)NAGVE	(K)N A|G\V|E/G S L I/V E K(I)		120.17	608.3313	1215.658	-0.0026	-2.2	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
14430	dirMS_041712_NAR_30mM_plus2.16414.16414.3	3	8.13	0	4.34E+05		(K)LLDLVQ	(K)L L D\L V/Q|Q/S/C N Y K(Q)	C:Carbamidomethylation	139.02	494.2566	1480.746	0.0088	5.9	5.83	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
14431	dirMS_041712_NAR_40mM_plus2.10086.10086.2	2	8.13	0	1.20E+05		(R)YSGSYN	(R)Y/S|G S/Y/N/D/Y L R(A)		123.83	619.2788	1237.548	0.0019	1.6	5.83	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
14432	dirMS_041712_NAR_40mM_plus2.17490.17490.3	3	8.13	1	2.00E+05		(R)GDSVIV	(R)G D/S V|I V V/L R N P L I A G K(-)		168.75	551.0007	1650.99	-0.0026	-1.6	8.75	6144.3	10.23	HUMAN	K7EJB5	Small nuclear ribonucleoprotein Sm D2
14433	dirMS_041712_NAR_50mM_plus2.13569.13569.3	3	8.13	0	1.13E+06		(K)AASDIA	(K)A A|S D|I\A M|T E\L/P P T H P I R(L)		139.33	607.3177	1819.937	0.0015	0.8	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
14434	dirMS_041712_NAR_50mM_plus2.14669.14669.3	3	8.13	0	1.17E+06		(R)EHALLA	(R)E H A\L\L A|Y/T/L/G/V K(Q)		145.75	438.9176	1314.742	-0.0034	-2.6	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
14435	dirMS_041712_NAR_50mM_plus2.17462.17573.3	3	8.13	1	5.87E+05		(R)LNRLPA	(R)L N R L P A\A G\V|G/D\M|V/M A T V K(K)		160.33	614.9984	1842.993	-0.0122	-6.6	8.75	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
14436	dirMS_041712_NAR_60mM_plus.15817.15817.3	3	8.13	0	1.93E+05		(K)NFDLRP	(K)N/F/D/L R/P G V I V R(-)		140.05	429.248	1285.738	-0.0081	-6.3	9.6	33192.3	6.77	HUMAN	B4DN45	S-adenosylmethionine synthase
14437	dirMS_041712_NAR_60mM_plus.6856.6856.2	2	8.13	0	2.45E+05		(R)MEELH	(R)M/E/E|L|H|N/Q E/M/Q K(R)		94.28	708.8155	1416.625	-0.0009	-0.6	4.75	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
14438	dirMS_041712_NAR_20mM_minus.11054.11054.2	2	8.12	0	1.47E+06	M92m	(R)ImNTFS	(R)I/m|N T F/S\V/V/P S P K(V)	m:Oxidized methionine	157.23	668.3513	1319.703	15.9925	-1.8	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
14439	dirMS_041712_NAR_20mM_minus.13651.13651.2	2	8.12	0	1.36E+05		(K)DIYALIS	(K)D I/Y/A\L/I\S D Q K(H)		186.98	583.3076	1165.61	-0.002	-1.7	4.21	266161	5.68	HUMAN	E9PPU0	Epiplakin
14440	dirMS_041712_NAR_20mM_minus.8088.8088.2	2	8.12	0	1.02E+05		(R)ATTGYP	(R)A T T/G|Y|P\D/P/Y G G E K(L)		130.38	678.3078	1355.611	-0.0031	-2.3	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
14441	dirMS_041712_NAR_30mM_minus2.13029.13269.2	2	8.12	0	8.01E+05		(K)ELSDIAL	(K)E L|S/D/I/A/L/R(I)		124.92	458.753	916.51	-0.0111	-12.1	4.37	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
14442	dirMS_041712_NAR_30mM_minus2.16315.16315.3	3	8.12	0	3.83E+04		(R)FPQLDS	(R)F P Q L D\S T/S/F/A N S/R(D)		142.2	490.5716	1469.702	-0.0017	-1.1	5.84	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
14443	dirMS_041712_NAR_40mM_minus2.12833.12833.3	3	8.12	0	3.62E+05	M460m	(R)ISIEmN	(R)I/S/I/E m N G/T L E D/Q L S H L K(Q)	m:Oxidized methionine	158.97	648.6649	1927.979	16.0008	3	4.65	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
14444	dirMS_041712_NAR_40mM_minus2.14422.14422.3	3	8.12	1	2.00E+05		(R)GLLPGL	(R)G L L/P\G L\L/P\A P A/D/K L/T P K(G)		169.47	567.6813	1701.031	-0.0016	-0.9	8.59	153084.9	5.55	HUMAN	Q6P2E9	Enhancer of mRNA-decapping protein 4
14445	dirMS_041712_NAR_50mM_minus2.11435.11435.3	3	8.12	0	6.07E+04		(R)GPVPAK	(R)G P\V/P A K/P T V L F/E K(M)		133.5	461.6052	1382.804	-0.0032	-2.3	8.59	110755.6	7.92	HUMAN	B4DH53	MAP1S light chain
14446	dirMS_041712_NAR_50mM_minus2.17138.17138.3	3	8.12	0	1.66E+05	M195m	(R)LHFFmP	(R)L H F F m P G/F\A/P L T S R(G)	m:Oxidized methionine	165.48	546.2872	1620.835	16.0115	10.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
14447	dirMS_041712_NAR_50mM_minus2.5216.5216.3	3	8.12	0	8.95E+04		(R)AEAEAG	(R)A E\A|E A/G\S P R P D|P R(E)		87.28	451.5573	1352.655	0.002	1.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
14448	dirMS_041712_NAR_50mM_minus2.9973.9973.3	3	8.12	1	1.23E+05		(R)VGEPVA	(R)V G/E P V/A L S E/E E R L K(L)		124.88	519.2824	1555.833	0	0	4.49	8516.9	5.1	HUMAN	E9PIL8	Splicing factor 3B subunit 2 (Fragment)
14449	dirMS_041712_NAR_60mM_minus.17143.17143.3	3	8.12	0	7.22E+04	M55m	(R)DIKPDN	(R)D I K P D N\F\L/m/G I G R(H)	m:Oxidized methionine	155.68	497.9256	1475.767	15.9947	-0.1	5.96	27968.7	9.69	HUMAN	D6REM4	Casein kinase I isoform alpha
14450	dirMS_041712_NAR_120mM_plus.16473.16473.3	3	8.12	1	5.02E+05		(K)NTKIEVL	(K)N T K I E V L/E/E/E L/R(L)		139.35	491.6024	1472.795	-0.0029	-1.9	4.49	334221.3	6.44	HUMAN	P15924	Desmoplakin
14451	dirMS_041712_NAR_20mM_plus.17876.17876.2	2	8.12	0	1.89E+05		(K)VANVSL	(K)V A/N/V/S L L A/L Y K(G)		195.2	595.8558	1190.714	-0.01	-8.4	8.56	15978.4	10.84	HUMAN	P62266	40S ribosomal protein S23
14452	dirMS_041712_NAR_20mM_plus.7461.7461.3	3	8.12	0	2.12E+05		(K)TGQAP	(K)T G\Q A|P G\Y S Y T/A/A N K(N)		119.53	476.8963	1428.675	-0.001	-0.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
14453	dirMS_041712_NAR_20mM_plus.8133.8133.2	2	8.12	0	1.33E+04		(K)TAVCDI	(K)T/A|V/C/D I\P P R(G)	C:Carbamidomethylation	127.25	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
14454	dirMS_041712_NAR_30mM_plus2.16874.16874.2	2	8.12	0	5.10E+05		(K)FFVGGN	(K)F F/V/G G N W/K(M)		142.28	477.7447	954.483	-0.0011	-1.1	8.75	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
14455	dirMS_041712_NAR_30mM_plus2.18767.18767.2	2	8.12	0	5.13E+04		(R)LINLVG	(R)L I|N|L|V/G E/S L R(L)		152.52	557.33	1113.663	-0.0099	-8.9	6	119157.2	5.4	HUMAN	B0UX83	HLA-B associated transcript 3
14456	dirMS_041712_NAR_30mM_plus2.6279.6279.2	2	8.12	0	3.31E+05	M369m	(R)FGSGM	(R)F/G|S/G/M/N m G R(I)	m:Oxidized methionine	87.53	486.7048	956.408	15.9946	-0.3	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
14457	dirMS_041712_NAR_40mM_plus2.15855.15855.3	3	8.12	1	7.42E+04		(K)VLDSGA	(K)V L/D S G A/P I\K I|P V G P E T L G R(I)		160.05	640.3668	1919.096	-0.0102	-5.3	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
14458	dirMS_041712_NAR_50mM_plus2.12873.12873.3	3	8.12	0	4.15E+05		(K)YYVTIID	(K)Y Y\V T I/I/D/A/P G H/R(D)		135.5	468.9142	1404.727	0.001	0.7	6.74	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
14459	dirMS_041712_NAR_50mM_plus2.20056.20056.3	3	8.12	0	2.83E+05		(R)LQSLPF	(R)L Q/S\L/P F/A L T/H/L N L K(A)		173.82	532.3178	1594.931	0.0073	4.6	8.76	175851.7	5.01	HUMAN	Q14160	Protein scribble homolog
14460	dirMS_041712_NAR_50mM_plus2.20669.20669.3	3	8.12	1	1.70E+05		(R)VNSKFD	(R)V/N S K F D T\I/Y/Q I L L K(K)		177.62	561.3209	1681.952	-0.0042	-2.5	8.47	72626.7	9.13	HUMAN	Q14258	E3 ubiquitin/ISG15 ligase TRIM25
14461	dirMS_041712_NAR_50mM_plus2.7700.7700.3	3	8.12	1	5.17E+04		(K)AAAAAS	(K)A A|A/A|A S/A A G\P G G L V A G K E E K(K)		106.4	575.9777	1725.913	0.0056	3.2	6.18	28364.3	5.45	HUMAN	A6NIH7	Protein unc-119 homolog B
14462	dirMS_041712_NAR_60mM_plus.11765.11765.3	3	8.12	1	2.93E+06		(K)KAEAGA	(K)K A E A G A G S A|T/E/F/Q\F R(G)		118.23	523.9277	1569.766	0.003	1.9	6.14	18897.4	10.15	HUMAN	P46783	40S ribosomal protein S10
14463	dirMS_041712_NAR_60mM_plus.21148.21148.3	3	8.12	1	3.16E+04		(K)LKEAELL	(K)L K E A E L|L\E/P L/M/P A I/R(A)		173.85	574.9975	1722.982	-0.0043	-2.5	4.79	56164.6	6.01	HUMAN	E9PP73	Coatomer subunit beta (Fragment)
14464	dirMS_041712_NAR_60mM_plus.6153.6153.3	3	8.12	1	4.67E+04		(R)ALCDYK	(R)A L|C D/Y K Q D Q K(I)	C:Carbamidomethylation	90.68	423.5361	1268.594	-0.0002	-0.2	6.01	334221.3	6.44	HUMAN	P15924	Desmoplakin
14465	dirMS_041712_NAR_120mM_minus.13980.13980.4	4	8.11	1	1.60E+06		(K)ASIHEA	(K)A S/I/H E A W T D|G K/E A M L/K(H)		129.98	447.476	1786.879	0.0029	1.6	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
14466	dirMS_041712_NAR_30mM_minus2.12176.12176.2	2	8.11	0	4.11E+04		(K)QALSGF	(K)Q/A/L|S/G F/G/Y/R(L)		119.07	499.7499	998.505	-0.0129	-12.9	8.75	21925.1	5.16	HUMAN	O75340	Programmed cell death protein 6
14467	dirMS_041712_NAR_30mM_minus2.19367.19367.2	2	8.11	0	5.23E+05		(R)LFDQAF	(R)L F/D Q|A/F G/L/P\R(L)		161.92	582.315	1163.621	0.002	1.7	5.84	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
14468	dirMS_041712_NAR_40mM_minus2.6170.6170.2	2	8.11	0	9.42E+05		(R)STFSTN	(R)S T|F/S/T N Y R(S)		101.98	488.2302	975.453	0.0001	0.1	8.46	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
14469	dirMS_041712_NAR_50mM_minus2.12145.12145.3	3	8.11	1	7.12E+04		(R)LADLEA	(R)L/A|D L E/A L K/V A D/S K(T)		137.23	458.2586	1372.768	-0.007	-5.1	4.56	33736.6	5.14	HUMAN	O75792	Ribonuclease H2 subunit A
14470	dirMS_041712_NAR_60mM_minus.11820.11820.3	3	8.11	1	4.61E+05	M230m	(R)mSMKE	(R)m/S M K E\V D E Q|M/L|N V Q N K(N)	m:Oxidized methionine	125.58	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
14471	dirMS_041712_NAR_60mM_minus.16728.16728.3	3	8.11	1	3.82E+05		(R)ARFEEL	(R)A R F E E\L|N|A/D/L/F/R(G)		153.95	494.2594	1480.754	0.0093	6.3	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
14472	dirMS_041712_NAR_120mM_plus.11109.11365.2	2	8.11	1	8.18E+05		(R)ALAAFL	(R)A L|A/A F/L/K K(S)		112.15	431.2797	861.556	-0.0035	-4.1	10	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
14473	dirMS_041712_NAR_20mM_plus.15914.15914.2	2	8.11	0	4.98E+03		(R)SSFYVN	(R)S S F|Y/V/N/G L|T L/G G Q K(C)		180.83	735.8818	1470.759	-0.0024	-1.6	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
14474	dirMS_041712_NAR_20mM_plus.16001.16001.2	2	8.11	0	1.13E+05		(R)GTPLISP	(R)G T/P/L/I S P L I K(W)		181.32	519.8306	1038.656	-0.0018	-1.8	8.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
14475	dirMS_041712_NAR_20mM_plus.9223.9223.2	2	8.11	0	4.54E+04		(R)IIYGGSV	(R)I I|Y/G G S\V T/G A T C K(E)	C:Carbamidomethylation	135.4	663.8412	1326.672	0.0029	2.2	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
14476	dirMS_041712_NAR_30mM_plus2.19918.19918.2	2	8.11	0	2.34E+05		(K)LALFQA	(K)L/A|L/F Q A\I G/K(E)		158.4	480.795	960.588	-0.005	-5.2	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
14477	dirMS_041712_NAR_30mM_plus2.4191.4191.2	2	8.11	0	1.20E+06	M299m M	(K)NmmAA	(K)N m|m A/A C/D|P/R(H)	C:Carbamidomethylation m:Oxid	69.6	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
14478	dirMS_041712_NAR_40mM_plus2.10405.10405.3	3	8.11	0	9.18E+03		(R)AIGSAS	(R)A I/G S A S E G\A Q S/S L/Q E V/Y/H K(S)		125.7	654.654	1961.956	-0.0089	-4.5	5.4	20148.5	4.65	HUMAN	B4E2V4	Proteasome (Prosome, macropain) subunit, alpha type, 5, isoform CRA_c
14479	dirMS_041712_NAR_40mM_plus2.13977.13977.3	3	8.11	1	1.79E+05		(R)GDVVPK	(R)G D V\V/P K D V N\A A I A T I K(T)		147.77	537.6381	1610.911	-0.0115	-7.1	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
14480	dirMS_041712_NAR_50mM_plus2.14066.14066.3	3	8.11	1	5.17E+05		(K)GGELVY	(K)G G\E L/V/Y T D S E A R D V F E K(A)		141.72	638.9735	1914.908	-0.002	-1.1	4.18	533778	5.74	HUMAN	Q15149	Plectin
14481	dirMS_041712_NAR_50mM_plus2.17303.17303.3	3	8.11	0	2.43E+04		(K)TAMLLA	(K)T A|M/L|L/A L Q R P E L V\E R(L)		159	580.6633	1739.984	-0.0083	-4.8	5.81	34746.4	9.67	HUMAN	Q8NFV4	Alpha/beta hydrolase domain-containing protein 11
14482	dirMS_041712_NAR_50mM_plus2.19221.19221.3	3	8.11	1	3.89E+05		(K)ILDVASL	(K)I/L/D/V A S L E V L N E V N R R(S)		169.95	614.0109	1840.029	-0.0105	-5.7	4.68	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
14483	dirMS_041712_NAR_50mM_plus2.8644.8644.3	3	8.11	1	6.42E+04	M40m	(R)LVGGP	(R)L/V|G G P m D/A/S V E E E G V R/R(A)	m:Oxidized methionine	112.35	606.2972	1800.891	15.9862	-4.8	4.41	16027.2	9.57	HUMAN	P01034	Cystatin-C
14484	dirMS_041712_NAR_60mM_plus.18309.18309.3	3	8.11	1	2.99E+05		(K)LLQDFF	(K)L L|Q/D F F N G R D L N K(S)		152.7	527.2793	1579.823	0.0006	0.4	5.96	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
14485	dirMS_041712_NAR_60mM_plus.5550.5550.3	3	8.11	0	1.11E+06		(K)TATPQQ	(K)T A|T|P/Q Q\A Q/E V H E K(L)		87.6	489.5727	1466.723	-0.0198	-13.5	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
14486	dirMS_041712_NAR_60mM_plus.6196.6196.3	3	8.11	1	4.67E+04		(R)ALCDYK	(R)A/L/C/D/Y K Q D Q K(I)	C:Carbamidomethylation	90.68	423.5361	1268.594	-0.0002	-0.2	6.01	334221.3	6.44	HUMAN	P15924	Desmoplakin
14487	dirMS_041712_NAR_120mM_minus.11001.11001.3	3	8.1	1	6.07E+05		(R)FYKNEG	(R)F/Y/K N E G G T/W/S V E K(V)		113.78	515.5834	1544.738	-0.0023	-1.5	6.14	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
14488	dirMS_041712_NAR_20mM_minus.8929.8929.2	2	8.1	0	2.76E+05		(R)ALGQNF	(R)A L|G Q/N|P T N A E V/L K(V)		138.8	677.871	1354.733	0.0022	1.6	6.05	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
14489	dirMS_041712_NAR_20mM_minus.9054.9054.2	2	8.1	0	6.54E+04	M68m M7	(R)NLAmG	(R)N L A/m\G/V|N L\T S m S K(I)	m:Oxidized methionine	139.73	699.34	1365.687	31.9862	-2.6	8.75	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
14490	dirMS_041712_NAR_30mM_minus2.10288.10288.2	2	8.1	0	7.87E+05		(K)IGALEG	(K)I/G/A L/E G Y R(G)		109.57	439.737	878.473	-0.0063	-7.2	6	20203.8	9.79	HUMAN	B4DG16	Asparagine--tRNA ligase, cytoplasmic
14491	dirMS_041712_NAR_30mM_minus2.14480.14480.2	2	8.1	0	2.18E+04	M294m	(R)YmTEVD	(R)Y/m|T E V D Y S N K(Q)	m:Oxidized methionine	133.43	633.2775	1249.541	16.0072	9.7	4.37	79520	6.37	HUMAN	F5H142	Caprin-2 (Fragment)
14492	dirMS_041712_NAR_30mM_minus2.18335.18335.2	2	8.1	0	7.87E+04		(K)QVVHQI	(K)Q V\V/H Q/L\E E E K(K)		153.68	619.8134	1238.638	-0.018	-14.5	4.75	70872.2	7.84	HUMAN	H3BPF8	Uncharacterized protein

14493	dirMS_041712_NAR_30mM_minus2.8334.8334.2	2	8.1	0	4.59E+05		(K)SFQQSSI	(K)S F|Q/Q/S S/L/S R(D)		100.27	520.2591	1039.517	-0.0058	-5.6	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
14494	dirMS_041712_NAR_30mM_minus2.9931.9931.2	2	8.1	0	1.11E+05		(K)SQLNSQ	(K)S Q|L/N/S Q S V E/I T K(L)		108.32	667.348	1333.696	-0.0071	-5.3	5.72	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
14495	dirMS_041712_NAR_40mM_minus2.15641.15641.3	3	8.1	0	1.90E+05		(K)GAEILEV	(K)G A|E|I/L E V L/H S L P A V R(Q)		182.13	535.3104	1603.917	0	0	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
14496	dirMS_041712_NAR_40mM_minus2.16111.16111.3	3	8.1	1	6.57E+05		(R)ELAILLG	(R)E L|A I|L|L G M L D/P A E K D E K(G)		189.62	629.0034	1884.999	-0.003	-1.6	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
14497	dirMS_041712_NAR_60mM_minus.11925.11925.3	3	8.1	0	1.92E+05		(R)ILHLLGQ	(R)I/L/H\L L/G Q E G P/K(T)		126.37	402.2384	1204.705	-0.0042	-3.5	6.75	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
14498	dirMS_041712_NAR_60mM_minus.11956.11956.3	3	8.1	1	5.69E+04		(R)IKQLQNI	(R)I K Q L Q N\I|S L/A/A/A S G G A K(E)		126.58	557.3237	1669.959	-0.003	-1.8	10	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
14499	dirMS_041712_NAR_60mM_minus.13036.13036.3	3	8.1	1	5.71E+04	S547s	(R)RAIQILN	(R)R A|I/Q I L N\E G A S/s E K(G)	s:N-acetylglucosamine (S)	133.1	573.6304	1515.813	203.0641	-8.9	6.14	100294.3	6.29	HUMAN	Q9NXC5	WD repeat-containing protein mio
14500	dirMS_041712_NAR_60mM_minus.19780.19829.3	3	8.1	1	1.78E+06		(K)EIIDLVLI	(K)E I|I/D/L V/L D R I R(K)		179.85	452.2739	1354.805	0.0019	1.4	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
14501	dirMS_041712_NAR_60mM_minus.5322.5322.3	3	8.1	1	5.73E+04		(K)IECDDKC	(K)I E/C/D D K/G D G S/C D/V R(Y)	C:Carbamidomethylation	85.25	542.5547	1625.653	-0.0035	-2.1	4.04	283472.4	5.71	HUMAN	P21333	Filamin-A
14502	dirMS_041712_NAR_60mM_minus.6459.6459.3	3	8.1	0	3.61E+05		(K)AVTEQG	(K)A V|T/E Q G H E L/S N E E R(N)		94.27	533.585	1598.741	-0.0001	0	4.48	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
14503	dirMS_041712_NAR_60mM_minus.9819.9819.3	3	8.1	0	7.93E+05		(K)LVQGAE	(K)L V Q/G A E S G C H S E/K(E)	C:Carbamidomethylation	114.85	467.8879	1401.643	0.0064	4.6	5.4	21682.3	9.62	HUMAN	E9PIM7	Protein HID1
14504	dirMS_041712_NAR_60mM_minus.9830.9830.3	3	8.1	0	4.34E+05		(K)LQVEEVI	(K)L Q|V E E V/H Q L S R(-)		114.55	446.5761	1337.717	-0.0034	-2.6	5.4	14571.2	5.15	HUMAN	F5GX50	Diablo homolog, mitochondrial (Fragment)
14505	dirMS_041712_NAR_20mM_plus.15819.15819.2	2	8.1	0	1.12E+05		(R)GTPLISP	(R)G T/P L/I S/P L I K(W)		180.8	519.8306	1038.656	-0.0018	-1.8	8.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
14506	dirMS_041712_NAR_20mM_plus.17560.17560.3	3	8.1	0	3.61E+04	M74m	(R)mIAGQV	(R)m I A G Q\V\L/D\I/N L/A/A E P K(V)	m:Oxidized methionine	193.18	566.9751	1682.915	15.9962	0.7	4.37	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
14507	dirMS_041712_NAR_20mM_plus.18719.18719.2	2	8.1	0	8.32E+04	M80m	(R)APLPDLY	(R)A P|L|P D L Y|P F G T m R(G)	m:Oxidized methionine	200.37	747.3751	1477.751	15.9921	-1.9	5.88	81122.9	9.03	HUMAN	H3BLZ8	Probable ATP-dependent RNA helicase DDX17
14508	dirMS_041712_NAR_30mM_plus2.6343.6343.2	2	8.1	0	8.62E+04		(K)EVYPEAI	(K)E V/Y/P/E A R(K)		87.3	432.2218	863.426	0.0106	12.2	4.53	17921.1	9.84	HUMAN	H7BZW6	Histone deacetylase complex subunit SAP18 (Fragment)
14509	dirMS_041712_NAR_50mM_plus2.15359.15359.3	3	8.1	0	2.43E+04		(K)VALLLLD	(K)V A\L L L/L D/Q G/A S/P H\A A A K(N)		147.53	558.9877	1674.954	-0.0052	-3.1	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
14510	dirMS_041712_NAR_50mM_plus2.20386.20386.3	3	8.1	1	1.87E+04		(K)SSVLENF	(K)S S/V/L/E/N F V G R D F L P\R(G)		176.38	579.3128	1735.913	0.0113	6.5	5.79	73288.1	8.96	HUMAN	E5RHK8	Dynamin-3
14511	dirMS_041712_NAR_50mM_plus2.8213.8213.3	3	8.1	0	1.26E+05		(K)QLAVAE	(K)Q L|A V|A\E/G K/P P E A P K(G)		109.72	478.9337	1434.795	-0.0086	-6	6.14	24364.9	9.64	HUMAN	H0YIP0	Methionine--tRNA ligase, cytoplasmic (Fragment)
14512	dirMS_041712_NAR_60mM_plus.12165.12165.3	3	8.1	1	1.01E+06	M230m	(R)mSMKE\	(R)m S M K E V\D\E\Q|M|L/N V\Q N K(N)	m:Oxidized methionine	120.57	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
14513	dirMS_041712_NAR_120mM_minus.7708.7708.3	3	8.09	1	2.87E+04		(K)AYAGDK	(K)A Y/A G D K/A E/E I G/R(H)		95.85	427.2156	1279.628	0.0045	3.5	4.68	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
14514	dirMS_041712_NAR_120mM_minus.9866.9866.3	3	8.09	1	3.00E+05		(K)AYPLAD	(K)A Y/P L/A D/A H L T K K(L)		108.42	443.2499	1327.737	-0.0017	-1.3	8.55	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
14515	dirMS_041712_NAR_20mM_minus.14438.14438.2	2	8.09	0	2.19E+05		(K)DAGVIA	(K)D A G\V|I/A/G L/N V L/R(I)		198.2	599.3503	1197.695	-0.0017	-1.4	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
14516	dirMS_041712_NAR_20mM_minus.14677.14677.2	2	8.09	0	9.62E+04		(K)IYVDDGI	(K)I Y|V/D D G\L/I|S L Q V K(Q)		201.6	731.9104	1462.815	-0.0016	-1.1	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
14517	dirMS_041712_NAR_30mM_minus2.6168.6168.2	2	8.09	0	2.75E+05		(K)TSEVNC	(K)T/S|E|V/N C Y R(C)	C:Carbamidomethylation	87.85	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
14518	dirMS_041712_NAR_50mM_minus2.10131.10131.3	3	8.09	1	1.02E+05		(R)ALRETLF	(R)A L R E T L|P/A/E/Q D L T T K(N)		125.55	562.6354	1685.907	-0.0152	-9	4.68	26790	6.25	HUMAN	F5GX11	Proteasome subunit alpha type-1
14519	dirMS_041712_NAR_50mM_minus2.8610.8610.3	3	8.09	0	1.13E+05		(R)LGYAVYI	(R)L/G Y A/V/Y E/T/P T A H N G A K(N)		117.02	564.6215	1691.839	0.0112	6.6	6.75	25016.4	5.65	HUMAN	B3KR28	Toll-interacting protein
14520	dirMS_041712_NAR_60mM_minus.10405.10405.3	3	8.09	1	1.09E+05		(K)TCVFEKE	(K)T C|V|F/E|K E N D/P S V M R(S)	C:Carbamidomethylation	117.63	571.2615	1711.778	-0.0079	-4.6	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
14521	dirMS_041712_NAR_60mM_minus.11311.11311.3	3	8.09	1	3.02E+06		(R)MQKEIT	(R)M Q K\E I T A/L|A/P S/T M K(I)		123.32	516.9421	1548.812	-0.0007	-0.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
14522	dirMS_041712_NAR_60mM_minus.12756.12756.3	3	8.09	0	4.76E+05		(K)GIHPTIIS	(K)G I H\P T I\I/S/E/S F Q/K(A)		131.07	486.2642	1456.78	-0.0014	-1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
14523	dirMS_041712_NAR_60mM_minus.12889.12889.3	3	8.09	0	2.55E+05		(K)AQIHDL\	(K)A Q I H D\L\V|L|V G/G S T R(I)		131.63	489.2745	1465.812	-0.0032	-2.2	6.79	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
14524	dirMS_041712_NAR_60mM_minus.14931.14931.3	3	8.09	1	3.72E+05		(R)IKIGDPL	(R)I K I G\D/P L|L/E|D/T R(M)		142.87	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
14525	dirMS_041712_NAR_60mM_minus.18226.18226.3	3	8.09	1	1.92E+04		(R)ELRVEQI	(R)E L R V E Q E/S L|L/T A F R(C)		162.8	564.3094	1690.912	0.0014	0.8	4.79	54229.5	5.12	HUMAN	Q9UBB4	Ataxin-10
14526	dirMS_041712_NAR_60mM_minus.6970.6970.3	3	8.09	1	1.30E+05		(R)LCAGAS	(R)L/C/A/G A S/E D I R E K(L)	C:Carbamidomethylation	97.1	450.2225	1348.652	0.0004	0.3	4.68	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
14527	dirMS_041712_NAR_60mM_minus.9789.9789.3	3	8.09	0	9.17E+04		(K)YAVTTG	(K)Y/A|V/T/T/G D H G I I R(T)		114.47	434.9021	1302.68	0.0117	9	6.74	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
14528	dirMS_041712_NAR_120mM_plus.5818.5818.4	4	8.09	2	5.67E+05		(R)KTGQAP	(R)K\T G Q A|P/G/Y S/Y/T A A N K N K(G)		83.7	450.4826	1798.908	0.0003	0.2	9.83	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
14529	dirMS_041712_NAR_30mM_plus2.17877.17877.2	2	8.09	0	2.26E+05		(R)ILNVPQE	(R)I L|N\V/P Q/E L/Y E K(G)		146.68	673.3645	1345.736	-0.0145	-10.8	4.53	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
14530	dirMS_041712_NAR_40mM_plus2.7988.7988.2	2	8.09	0	1.57E+04		(K)IGNCPFS	(K)I/G/N/C/P F S Q R(L)	C:Carbamidomethylation	107.5	539.7602	1078.51	0.0033	3	9.75	27264.5	5.09	HUMAN	O00299	Chloride intracellular channel protein 1
14531	dirMS_041712_NAR_50mM_plus2.10074.10074.3	3	8.09	1	5.94E+04		(K)ITIKNDP	(K)I T|I K N D\P S L P/E/P K(C)		120.53	484.6079	1451.81	-0.0013	-0.9	6.07	20203.8	9.79	HUMAN	B4DG16	Asparagine--tRNA ligase, cytoplasmic
14532	dirMS_041712_NAR_50mM_plus2.12155.12155.3	3	8.09	1	1.20E+06		(K)ASLENSL	(K)A/S/L/E/N S L R E V/E/A R(Y)		132.27	491.9313	1473.766	0.0138	9.3	4.79	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
14533	dirMS_041712_NAR_50mM_plus2.21664.21664.3	3	8.09	0	1.01E+05		(K)THLPLAL	(K)T H L\P L A\L L/P Q T L L D/Q K(V)		183.97	601.0191	1801.058	-0.0154	-8.6	6.41	22243.5	7.91	HUMAN	E9PKR8	Sulfotransferase 1A2 (Fragment)
14534	dirMS_041712_NAR_50mM_plus2.22276.22276.3	3	8.09	0	8.92E+05		(R)GGHPPA	(R)G G H P P A\I Q\S L/I/N L/L\A/D/N R(Y)		191.37	629.3448	1886.024	-0.0044	-2.3	6.74	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
14535	dirMS_041712_NAR_50mM_plus2.9517.9517.3	3	8.09	0	2.45E+05		(R)LVKPGN	(R)L/V/K/P G N Q N/T/Q V/T E A W/N\K(V)		117.08	643.0046	1927.003	-0.004	-2.1	8.59	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
14536	dirMS_041712_NAR_120mM_minus.6081.6081.3	3	8.08	1	5.64E+05		(K)TCEESSF	(K)T/C\E E S/S/F/C K/R(Q)	C:Carbamidomethylation	86.8	435.1849	1303.541	-0.0004	-0.3	5.81	10576.1	11.44	HUMAN	E9PRF8	Neutral alpha-glucosidase AB
14537	dirMS_041712_NAR_120mM_minus.9801.9801.4	4	8.08	2	8.39E+04		(K)LTDCVVI	(K)L T\D C V\V/M R D/P/A/S K/R(S)	C:Carbamidomethylation	107.88	412.714	1647.831	0.0036	2.2	8.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
14538	dirMS_041712_NAR_20mM_minus.12469.12469.2	2	8.08	0	5.98E+04		(K)LLGELLQ	(K)L L|G E\L/L/Q D N A K(L)		173.23	607.3406	1213.679	-0.0048	-3.9	4.37	35556.4	9.3	HUMAN	F2Z393	Transaldolase
14539	dirMS_041712_NAR_20mM_minus.13252.13252.2	2	8.08	0	8.22E+04		(K)SILFVPTS	(K)S I L/F\V|P/T S A P R(G)		183.38	594.3411	1187.678	-0.0034	-2.8	9.47	92752.5	4.76	HUMAN	P14625	Endoplasmin
14540	dirMS_041712_NAR_20mM_minus.14669.14669.2	2	8.08	0	9.62E+04		(K)IYVDDGI	(K)I Y|V/D D/G L I\S L/Q V K(Q)		201.6	731.9104	1462.815	-0.0016	-1.1	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
14541	dirMS_041712_NAR_20mM_minus.14717.14717.2	2	8.08	0	8.83E+04		(R)IITLTGPT	(R)I I|T/L/T|G P T N A I F K(A)		201.33	694.9107	1388.815	-0.0007	-0.5	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
14542	dirMS_041712_NAR_30mM_minus2.10061.10063.2	2	8.08	0	9.47E+04		(R)NVISSSS	(R)N/V|I|S S S S F K(L)		108.82	484.7528	968.505	-0.0064	-6.6	8.75	53941.6	6.3	HUMAN	C9JFE4	COP9 signalosome complex subunit 1
14543	dirMS_041712_NAR_30mM_minus2.18090.18111.2	2	8.08	0	1.96E+05		(K)VADIGL/	(K)V A\D|I|G L A\A W G R(K)		152.82	564.8076	1128.616	-0.0081	-7.2	5.81	48285.8	5.93	HUMAN	P23526	Adenosylhomocysteinase
14544	dirMS_041712_NAR_50mM_minus2.16344.16344.3	3	8.08	0	1.75E+05	M1m	(-)mKPLVVI	(-)m K P L V V\F\V/L/G G/P G\A G K(G)	m:Oxidized methionine	161.27	529.3077	1569.919	15.99	-3.1	10	22450.2	5.44	HUMAN	P30085	UMP-CMP kinase
14545	dirMS_041712_NAR_60mM_minus.5330.5330.3	3	8.08	1	5.73E+04		(K)IECDDKC	(K)I/E|C D D K G/D/G S C D/V R(Y)	C:Carbamidomethylation	85.25	542.5547	1625.653	-0.0035	-2.1	4.04	283472.4	5.71	HUMAN	P21333	Filamin-A
14546	dirMS_041712_NAR_60mM_minus.6091.6091.3	3	8.08	1	1.65E+06		(K)DSYVGD	(K)D S/Y\V/G D E A Q/S K/R(G)		90.88	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
14547	dirMS_041712_NAR_60mM_minus.9518.9518.3	3	8.08	0	6.34E+04		(K)EAQLYA	(K)E A Q/L/Y A/A Q A H/L/K(L)		113.07	448.2371	1342.711	-0.0146	-10.9	6.85	28309.6	4.17	HUMAN	E9PI86	Nuclear autoantigenic sperm protein (Fragment)
14548	dirMS_041712_NAR_20mM_plus.14100.14100.3	3	8.08	0	4.03E+05	M313m	(R)TVQSLEI	(R)T V\Q S L E I/D/L/D S/m R(N)	m:Oxidized methionine	168.7	508.2519	1506.747	15.9943	-0.4	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
14549	dirMS_041712_NAR_20mM_plus.17215.17215.3	3	8.08	0	1.85E+05		(R)AIVAIEN	(R)A I/V A I E/N/P/A/D/V S V I S S R(N)		189.12	580.9864	1740.949	-0.0044	-2.5	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
14550	dirMS_041712_NAR_20mM_plus.18278.18278.2	2	8.08	0	3.78E+04		(R)GSYGDL	(R)G S Y G D|L|G G/P I I/T T Q V T I/P K(D)		197.32	959.0189	1917.033	-0.0022	-1.2	5.83	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
14551	dirMS_041712_NAR_20mM_plus.8078.8078.2	2	8.08	0	8.95E+04		(R)AAPGAE	(R)A A/P/G/A E F A P N K(R)		125.58	536.7749	1072.542	0.0003	0.3	6.05	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
14552	dirMS_041712_NAR_20mM_plus.9290.9290.2	2	8.08	0	9.62E+03		(K)AEPVEV	(K)A E/P V E V\V/A/P/R(G)		135.58	533.798	1066.589	-0.0004	-0.4	4.53	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
14553	dirMS_041712_NAR_30mM_plus2.5512.5512.2	2	8.08	0	2.75E+05		(R)TGPPMC	(R)T/G/P/P/M/G S/R(F)		82.27	401.6975	802.388	0.0001	0.2	9.41	27441.6	6.68	HUMAN	Q15056	Eukaryotic translation initiation factor 4H
14554	dirMS_041712_NAR_50mM_plus2.14130.14130.3	3	8.08	1	6.91E+04		(K)VVSSSIV	(K)V V|S S S/I V D K Y I G E S A\R(L)		142.2	570.6392	1709.907	-0.0038	-2.2	6.04	29938.9	6.07	HUMAN	H0YJC0	26S protease regulatory subunit 10B (Fragment)
14555	dirMS_041712_NAR_50mM_plus2.19691.19691.3	3	8.08	1	1.99E+05		(R)KAIIIFVP	(R)K A I I I F\V|P V P Q L K(S)		172.13	489.3212	1465.95	-0.0014	-1	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
14556	dirMS_041712_NAR_50mM_plus2.5308.5308.3	3	8.08	0	3.81E+05	M116m	(R)ATAPQT	(R)A/T/A/P Q/T Q H V/S P m R(Q)	m:Oxidized methionine	87.6	480.5727	1423.711	15.9925	-1.7	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
14557	dirMS_041712_NAR_60mM_plus.18458.18458.3	3	8.08	0	2.08E+05		(K)DHGLEV	(K)D H\G L E\V|L/G\L V/R(V)		153.68	403.2318	1207.679	0.0015	1.2	5.32	17732.8	5.85	HUMAN	F5GYJ1	U8 snoRNA-decapping enzyme
14558	dirMS_041712_NAR_120mM_minus.6003.6003.3	3	8.07	1	5.64E+05		(K)TCEESSF	(K)T|C|E/E/S/S F C K/R(Q)	C:Carbamidomethylation	86.8	435.1849	1303.541	-0.0004	-0.3	5.81	10576.1	11.44	HUMAN	E9PRF8	Neutral alpha-glucosidase AB
14559	dirMS_041712_NAR_20mM_minus.7049.7049.2	2	8.07	0	4.77E+05	M281m	(R)AEAESm	(R)A E|A/E|S m Y/Q I/K(Y)	m:Oxidized methionine	117.9	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
14560	dirMS_041712_NAR_30mM_minus2.11866.11866.2	2	8.07	0	7.78E+04		(R)SGYLLPD	(R)S G|Y/L/L/P D/T K(A)		116.72	497.265	993.525	-0.0024	-2.4	5.55	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
14561	dirMS_041712_NAR_30mM_minus2.8122.8122.2	2	8.07	0	8.16E+04		(K)SLAAEEE	(K)S L/A|A E/E/E A A R(Q)		98.37	523.7597	1046.511	0.0008	0.8	4.25	533778	5.74	HUMAN	Q15149	Plectin
14562	dirMS_041712_NAR_50mM_minus2.12049.12061.3	3	8.07	1	1.78E+05		(K)SAPSIPK	(K)S A|P S/I/P K E N F/S C L T R(L)	C:Carbamidomethylation	137.22	569.6251	1706.853	0.0077	4.5	8.46	23209	6.92	HUMAN	B9A041	Malate dehydrogenase, cytoplasmic
14563	dirMS_041712_NAR_50mM_minus2.12898.12898.3	3	8.07	0	4.17E+06	M84m	(K)YPIEHGI	(K)Y/P/I E H G I I\T N/W/D\D m E K(I)	m:Oxidized methionine	141.65	659.6398	1960.911	15.9939	-0.5	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
14564	dirMS_041712_NAR_50mM_minus2.17870.17870.3	3	8.07	0	4.27E+05	M203m	(R)DTGIFLD	(R)D T|G I/F/L/D L m H L K(K)	m:Oxidized methionine	170.33	473.5826	1402.74	15.9933	-1.1	5.21	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
14565	dirMS_041712_NAR_50mM_minus2.6133.6133.3	3	8.07	1	5.69E+04	M322m	(K)AAGSGE	(K)A A|G/S G E L/G V T m K G P K(G)	m:Oxidized methionine	97.78	473.5826	1402.736	15.9974	1.7	8.64	258215.9	5.48	HUMAN	E7EN95	Filamin-B
14566	dirMS_041712_NAR_60mM_minus.16917.16917.3	3	8.07	1	2.55E+05		(K)YAVLYQ	(K)Y A|V\L/Y Q/P L F D K/R(F)		154.55	504.9409	1512.821	-0.0128	-8.4	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
14567	dirMS_041712_NAR_60mM_minus.9346.9346.3	3	8.07	0	1.02E+06		(K)QEYDES	(K)Q E/Y D E/S/G/P/S I/V H/R(K)		111.27	506.2391	1516.703	0.0001	0.1	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
14568	dirMS_041712_NAR_120mM_plus.18007.18007.3	3	8.07	1	3.63E+05		(K)YRGFTIP	(K)Y R G F T I|P/E/A F R(G)		148.07	452.9069	1356.706	0.0003	0.2	8.75	27264.5	5.09	HUMAN	O00299	Chloride intracellular channel protein 1
14569	dirMS_041712_NAR_20mM_plus.12958.12958.2	2	8.07	0	2.33E+04		(K)AVDSLVI	(K)A V\D S L/V/P/I G R(G)		162.43	513.8007	1026.594	-0.0001	-0.1	5.88	48851.3	9.2	HUMAN	K7EK63	ATP synthase subunit alpha, mitochondrial
14570	dirMS_041712_NAR_20mM_plus.15232.15232.2	2	8.07	0	5.88E+04		(R)EQLAIAE	(R)E Q/L/A/I/A/E F A R(S)		176.1	574.312	1147.611	0.0061	5.3	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
14571	dirMS_041712_NAR_20mM_plus.17194.17194.3	3	8.07	0	1.94E+05		(R)AIVAIEN	(R)A I\V\A\I E N/P\A/D V/S V/I S S R(N)		189.08	580.9864	1740.949	-0.0044	-2.5	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
14572	dirMS_041712_NAR_30mM_plus2.17146.17146.2	2	8.07	0	2.63E+05		(K)YYTLFGF	(K)Y/Y/T/L F G/R(S)		142.65	460.2391	919.467	0.0037	4	8.59	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
14573	dirMS_041712_NAR_30mM_plus2.7437.7437.2	2	8.07	0	6.39E+05		(R)AMNGES	(R)A M|N|G E S L/D G/R(Q)		93.25	525.238	1049.468	0.0007	0.7	4.37	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
14574	dirMS_041712_NAR_40mM_plus2.14935.14935.3	3	8.07	0	1.82E+05		(K)GLPQTA	(K)G L/P Q T A V C N L N I/T L/P A H K(K)	C:Carbamidomethylation	154.48	649.6838	1947.048	-0.0112	-5.7	8.76	112066.5	5.59	HUMAN	B1AQT2	Ankyrin 3, node of Ranvier (Ankyrin G)
14575	dirMS_041712_NAR_40mM_plus2.5555.5555.2	2	8.07	0	2.45E+05	M299m	(K)NmMAA	(K)N m|M\A\A C\D|P R(H)	C:Carbamidomethylation m:Oxid	89.2	541.2145	1065.427	15.9943	-0.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
14576	dirMS_041712_NAR_50mM_plus2.10392.10392.3	3	8.07	0	5.07E+04		(K)TGVAVN	(K)T G V|A/V/N K P A E F T V D A K(H)		122.18	549.6293	1646.875	-0.0015	-0.9	5.73	283472.4	5.71	HUMAN	P21333	Filamin-A
14577	dirMS_041712_NAR_50mM_plus2.10434.10434.3	3	8.07	0	1.42E+05		(R)ILSKPIEV	(R)I L|S K P I E V Q/V/G G R(S)		122.35	465.9487	1395.832	-0.0003	-0.2	8.75	117873.5	9.45	HUMAN	Q7L014	Probable ATP-dependent RNA helicase DDX46
14578	dirMS_041712_NAR_50mM_plus2.10770.10770.3	3	8.07	1	5.44E+05		(R)VAVEEV	(R)V A|V/E/E/V D E E G K/F V R(L)		124.43	535.9422	1605.812	0.0002	0.1	4.25	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
14579	dirMS_041712_NAR_50mM_plus2.8247.8247.3	3	8.07	0	1.26E+05		(K)QLAVAE	(K)Q/L/A\V A E G K/P/P E A/P K(G)		109.72	478.9337	1434.795	-0.0086	-6	6.14	24364.9	9.64	HUMAN	H0YIP0	Methionine--tRNA ligase, cytoplasmic (Fragment)
14580	dirMS_041712_NAR_50mM_plus2.8973.8973.3	3	8.07	0	1.80E+05		(K)TPVEPE\	(K)T P V E\P E V/A/I/H R(I)		113.98	416.5627	1247.674	-0.0007	-0.6	5.37	5429.1	9.6	HUMAN	E5RIP1	40S ribosomal protein S20
14581	dirMS_041712_NAR_50mM_plus2.9053.9053.3	3	8.07	1	4.14E+05		(K)TAVCDIF	(K)T A|V C D I/P/P R G L K(M)	C:Carbamidomethylation	115.08	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
14582	dirMS_041712_NAR_60mM_plus.17493.17493.3	3	8.07	1	3.74E+05		(R)KVPGVT	(R)K\V P G V T A\I|E|L D/E/D|T/G T F R(I)		148.18	650.0017	1948.002	-0.0117	-6	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
14583	dirMS_041712_NAR_20mM_minus.13761.13837.2	2	8.06	0	2.58E+05		(R)IVLLDSS	(R)I V|L|L/D/S S L\E Y K(K)		189.27	640.3594	1279.714	-0.0029	-2.2	4.37	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
14584	dirMS_041712_NAR_30mM_minus2.16932.16932.2	2	8.06	0	2.83E+05		(R)FFMGNC	(R)F F|M/G N Q V L K(V)		145.95	542.2866	1083.566	0.0004	0.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
14585	dirMS_041712_NAR_30mM_minus2.17736.17736.2	2	8.06	0	3.94E+05		(K)GNFNYII	(K)G N|F|N/Y/I/E/F/T R(I)		151.3	630.8052	1260.601	0.0024	1.9	6	20513.6	4.62	HUMAN	J3QRS3	Myosin regulatory light chain 12A
14586	dirMS_041712_NAR_60mM_minus.6360.6360.3	3	8.06	0	5.08E+04		(R)CPPGVV	(R)C P|P G V V/P A C H N S K(D)	C:Carbamidomethylation	94.08	474.8938	1422.662	0.0052	3.6	8.76	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
14587	dirMS_041712_NAR_60mM_minus.7368.7368.3	3	8.06	0	1.52E+05		(K)TIEAEAA	(K)T I/E/A/E/A A H/G T V T R(H)		100.22	452.5678	1355.691	-0.0025	-1.9	5.37	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
14588	dirMS_041712_NAR_120mM_plus.12397.12397.4	4	8.06	2	8.44E+05		(K)KGTVEG	(K)K\G T V E\G F\E/P/A D N K C/L L/R(A)	C:Carbamidomethylation	118.8	484.2468	1933.98	-0.0147	-7.6	6.18	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
14589	dirMS_041712_NAR_120mM_plus.13910.13910.4	4	8.06	1	9.40E+05		(K)AGKFPSI	(K)A G K\F\P S/L/L T/H N E N M V A K(V)		126.23	464.9972	1856.969	-0.0018	-0.9	8.64	25002	10.06	HUMAN	P62906	60S ribosomal protein L10a
14590	dirMS_041712_NAR_20mM_plus.10008.10008.2	2	8.06	0	1.66E+05		(K)GEATVSI	(K)G E A/T/V/S F/D D/P P S A K(A)		140.58	710.8324	1420.659	-0.0015	-1.1	4.03	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
14591	dirMS_041712_NAR_20mM_plus.12461.12461.3	3	8.06	0	5.11E+04		(K)VNQIGS'	(K)V N|Q I\G S\V/T E/S I Q A C K(L)	C:Carbamidomethylation	159.02	545.2781	1633.821	-0.0016	-1	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
14592	dirMS_041712_NAR_20mM_plus.12786.12786.2	2	8.06	0	2.85E+05	M316m	(R)ISEQFTA	(R)I/S E/Q|F/T A m\F R(R)	m:Oxidized methionine	161.28	623.3012	1229.598	15.9968	1.5	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
14593	dirMS_041712_NAR_20mM_plus.12902.12902.2	2	8.06	0	3.28E+05	M316m	(R)ISEQFTA	(R)I/S E/Q/F/T/A m F R(R)	m:Oxidized methionine	161.45	623.3012	1229.598	15.9968	1.5	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
14594	dirMS_041712_NAR_20mM_plus.17054.17054.2	2	8.06	0	1.09E+05		(R)ALLFIPR	(R)A L|L|F/I/P R(R)		189	415.2675	829.529	-0.0017	-2.1	9.79	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
14595	dirMS_041712_NAR_30mM_plus2.17752.17858.2	2	8.06	0	2.76E+05		(K)YNLGLD	(K)Y/N|L/G/L D/L/R(T)		146.15	482.2695	963.526	0.0059	6.1	5.83	43177.5	7.2	HUMAN	B3KV55	Glutamate dehydrogenase
14596	dirMS_041712_NAR_40mM_plus2.10571.10571.3	3	8.06	0	1.05E+05	M147m	(K)LQmEAF	(K)L Q/m/E A/P H\I I/V/G T P G R(V)	m:Oxidized methionine	127.2	545.6274	1618.873	15.9943	-0.4	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
14597	dirMS_041712_NAR_40mM_plus2.14963.14963.3	3	8.06	1	2.18E+05		(R)VVVDAL	(R)V V/V/D A L S/G L K/G D/L A G/R(Y)		154.27	523.9701	1569.896	-0.0001	-0.1	5.93	26949.2	7.99	HUMAN	C9JSQ1	Creatine kinase U-type, mitochondrial (Fragment)
14598	dirMS_041712_NAR_50mM_plus2.10305.10305.3	3	8.06	0	1.09E+05		(K)MSIAQC	(K)M/S/I|A Q C T S S/H/P I I/R(Q)	C:Carbamidomethylation	121.63	534.2701	1600.793	0.0023	1.5	9.52	18283.4	9.29	HUMAN	Q8N8C4	Coiled-coil-helix-coiled-coil-helix domain-containing protein 5
14599	dirMS_041712_NAR_50mM_plus2.12574.12574.3	3	8.06	1	2.58E+04		(R)SGKAPIL	(R)S G K A\P I L\I/A/T|D V/A S R(G)		134.2	500.2911	1498.859	0	0	8.46	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
14600	dirMS_041712_NAR_50mM_plus2.20903.20903.3	3	8.06	1	4.35E+04		(R)ITSEAED	(R)I/T|S E A E D L V A/N F/F/P K K(L)		178	603.6541	1808.943	0.0049	2.7	4.68	14931.6	5.53	HUMAN	B7Z8D3	Proteasome activator complex subunit 3
14601	dirMS_041712_NAR_50mM_plus2.6105.6266.3	3	8.06	0	5.83E+05	M70m	(K)EAPPmE	(K)E A/P/P/m E K|P E/V V K(T)	m:Oxidized methionine	96.68	457.2387	1353.708	15.9933	-1.2	4.79	14798.1	10.35	HUMAN	K7EJ78	40S ribosomal protein S15 (Fragment)

14602	dirMS_041712_NAR_60mM_plus.20489.20574.3	3	8.06	1	7.14E+05		(R)LDLAGR	(R)L/D/L/A/G R D L T D Y L M K(I)		168.28	541.9516	1623.841	-0.0008	-0.5	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
14603	dirMS_041712_NAR_120mM_minus.8893.8893.2	2	8.05	0	5.46E+05		(K)HFVALS	(K)H/F|V/A L S/T N T/T K(V)		103.23	609.8267	1218.648	-0.0016	-1.3	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
14604	dirMS_041712_NAR_30mM_minus2.18329.18329.2	2	8.05	0	2.18E+05		(K)YPQLLP	(K)Y/P\Q L L/P G I R(G)		154.88	528.816	1056.62	0.0047	4.4	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
14605	dirMS_041712_NAR_30mM_minus2.6399.6399.2	2	8.05	0	1.44E+05	M796m	(R)mNEAF	(R)m N\E|A|F/G D|T K(F)	m:Oxidized methionine	88.32	514.726	1012.44	16.0043	9.1	4.37	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
14606	dirMS_041712_NAR_30mM_minus2.8843.8843.2	2	8.05	0	4.96E+05		(K)SDPVVS	(K)S D|P/V/V S/Y R(E)		102.6	461.7315	922.463	-0.0071	-7.7	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
14607	dirMS_041712_NAR_40mM_minus2.12720.12720.3	3	8.05	0	1.36E+05		(K)IEVIKPG	(K)I/E/V I/K/P G D L G V D L T S K(L)		159	561.989	1683.953	-0.0003	-0.2	4.56	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
14608	dirMS_041712_NAR_40mM_minus2.8163.8163.3	3	8.05	0	2.24E+05	M35m	(K)AASDIA	(K)A A S|D I/A/m T/E/L/P P T H P I R(L)	m:Oxidized methionine	128.48	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
14609	dirMS_041712_NAR_50mM_minus2.10806.10806.3	3	8.05	1	2.11E+04		(K)LAEQAE	(K)L/A/E Q/A E R Y D D M/A A A M/K(A)		128.58	604.9489	1812.825	0.0067	3.7	4.32	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
14610	dirMS_041712_NAR_50mM_minus2.17982.17982.3	3	8.05	1	2.28E+05	M116m	(R)ELAILLG	(R)E L\A/I/L/L/G m L/D P A E K D E K(G)	m:Oxidized methionine	170.82	634.3353	1884.999	15.9927	-1.2	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
14611	dirMS_041712_NAR_60mM_minus.20131.20131.3	3	8.05	0	4.05E+05		(K)GHYTEG	(K)G H Y T E G A E\L|V/D S/V/L/D/V V R(K)		184.27	653.6647	1958.982	-0.0022	-1.1	4.31	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
14612	dirMS_041712_NAR_60mM_minus.7035.7035.3	3	8.05	0	1.08E+05		(K)TQAYQD	(K)T Q|A Y Q D\Q K/P G/T S G/L R(K)		97.53	550.6109	1649.824	-0.006	-3.7	8.25	61733.3	6.3	HUMAN	P36871	Phosphoglucomutase-1
14613	dirMS_041712_NAR_120mM_plus.12588.12588.4	4	8.05	2	9.28E+05		(K)KGTVEG	(K)K G T V E/G F\E/P A D/N K C L L R(A)	C:Carbamidomethylation	118.9	484.2468	1933.98	-0.0147	-7.6	6.18	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
14614	dirMS_041712_NAR_120mM_plus.18825.18825.4	4	8.05	0	3.53E+05		(K)APIRPDI	(K)A/P I/R P D I V\N F V/H T N L R(K)		151.62	466.2639	1862.04	-0.0058	-3.1	9.65	18988.7	11.2	HUMAN	H3BTP7	60S ribosomal protein L4 (Fragment)
14615	dirMS_041712_NAR_20mM_plus.11001.11001.2	2	8.05	0	1.17E+05		(K)EITALAP	(K)E I/T A/L/A P S/T M K(I)		148.15	581.3129	1161.618	0.0001	0.1	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
14616	dirMS_041712_NAR_20mM_plus.18955.18955.2	2	8.05	0	2.10E+05		(R)IITLAGP	(R)I I/T L A/G/P T\N A\I F K(A)		201.07	679.9039	1358.804	-0.0037	-2.7	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
14617	dirMS_041712_NAR_40mM_plus2.6643.6643.2	2	8.05	0	5.65E+04		(K)AGFAGD	(K)A/G/F/A|G D|D A P R(A)		98.63	488.728	976.448	0.0004	0.4	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
14618	dirMS_041712_NAR_40mM_plus2.7907.7907.2	2	8.05	0	1.43E+05		(K)ASLENSL	(K)A/S/L|E N|S L/R(E)		106.82	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
14619	dirMS_041712_NAR_50mM_plus2.13853.13853.3	3	8.05	1	1.05E+07		(R)TEMENE	(R)T/E|M E N E\F V L/I K K(D)		141.17	494.262	1480.772	-0.0001	-0.1	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
14620	dirMS_041712_NAR_50mM_plus2.17036.17036.3	3	8.05	1	7.43E+05		(K)DNNGVI	(K)D/N/N G/V/I/G L L E/P M K K(S)		158.23	509.9448	1527.82	-0.0001	-0.1	6.07	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
14621	dirMS_041712_NAR_50mM_plus2.21338.21338.3	3	8.05	0	8.95E+04		(K)GAEILEV	(K)G A E I|L E V/L H/S L/P A V/R(Q)		183.4	535.3092	1603.917	-0.0036	-2.2	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
14622	dirMS_041712_NAR_50mM_plus2.6115.6115.3	3	8.05	1	2.74E+04		(R)AQLGGP	(R)A Q|L/G/G P E A A K S D E T A A K(-)		96.15	548.6114	1643.824	-0.0039	-2.3	4.68	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
14623	dirMS_041712_NAR_50mM_plus2.8822.8822.3	3	8.05	1	2.37E+04		(R)GGSDDS	(R)G G S D D/S S K D|P/I/D V N Y E K(L)		114.08	609.2765	1825.809	0.0063	3.5	4.03	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
14624	dirMS_041712_NAR_60mM_plus.18601.18601.3	3	8.05	1	3.72E+06		(R)VSFELFA	(R)V S/F E L/F A/D K V P K(T)		155.8	460.5914	1379.757	0.0027	2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
14625	dirMS_041712_NAR_120mM_minus.12524.12524.3	3	8.04	1	3.39E+05	M316m	(R)ISEQFTA	(R)I/S/E Q/F T A m F R/R(K)	m:Oxidized methionine	122.32	467.9028	1385.699	15.9944	-0.4	9.6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
14626	dirMS_041712_NAR_120mM_minus.7722.7722.3	3	8.04	1	1.88E+05	M42m	(R)SRNTDE	(R)S R N T\D\E\m|V/E/L/R(I)	m:Oxidized methionine	95.92	455.8866	1349.648	15.9975	1.9	4.68	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
14627	dirMS_041712_NAR_20mM_minus.13154.13154.3	3	8.04	0	4.00E+05		(K)TITLEVEI	(K)T I T\L E\V E/P/S D/T I E/N V K(A)		183.03	596.6453	1787.927	-0.006	-3.3	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
14628	dirMS_041712_NAR_20mM_minus.7563.7563.2	2	8.04	0	8.03E+05	M239m	(K)EVDEQm	(K)E V|D E/Q m\L/N|V/Q/N K(N)	m:Oxidized methionine	124.12	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
14629	dirMS_041712_NAR_20mM_minus.9918.9943.2	2	8.04	0	1.42E+05		(K)GNIQTFT	(K)G N/I Q T F T/V F F S R(E)		149.92	708.8627	1416.727	-0.0089	-6.3	9.75	99668.9	5.79	HUMAN	E7EQM8	Netrin receptor DCC
14630	dirMS_041712_NAR_30mM_minus2.18349.18349.2	2	8.04	0	2.28E+05		(K)YPQLLP	(K)Y/P/Q/L/L/P G I R(G)		154.92	528.816	1056.62	0.0047	4.4	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
14631	dirMS_041712_NAR_50mM_minus2.14434.14434.3	3	8.04	0	4.26E+05		(R)QIFHPE	(R)Q I F/H/P E Q L I T/G K(E)		149.72	470.9286	1410.774	-0.0027	-1.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
14632	dirMS_041712_NAR_50mM_minus2.6780.6780.3	3	8.04	1	2.52E+05		(R)ASVDTK	(R)A S/V/D T K E A E G A|P Q V E A G K(R)		104.8	596.2904	1786.882	-0.0251	-14	4.41	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
14633	dirMS_041712_NAR_60mM_minus.9827.9827.3	3	8.04	1	2.35E+05	M145m	(K)IDKTDY	(K)I D K T D Y/m/V/G S/Y/G P R(A)	m:Oxidized methionine	115.05	539.9245	1601.763	15.9961	0.8	5.96	21671	5.37	HUMAN	J3KTF8	Rho GDP-dissociation inhibitor 1 (Fragment)
14634	dirMS_041712_NAR_120mM_plus.14475.14475.4	4	8.04	1	8.86E+05		(K)GLDPAR	(K)G L|D|P A R V N V P|V I/G G H A G K(T)		129.65	439.9998	1756.982	-0.0043	-2.5	8.76	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
14635	dirMS_041712_NAR_20mM_plus.12496.12496.3	3	8.04	0	3.48E+05		(K)IISNASC	(K)I I\S N\A/S C T T N/C L A/P L/A K(V)	C:Carbamidomethylation	159.53	611.9768	1833.92	-0.0039	-2.1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
14636	dirMS_041712_NAR_20mM_plus.14279.14279.2	2	8.04	0	6.63E+05	M73m	(R)AVLVDLI	(R)A V L/V/D L\E|P G T/m D S V R(S)	m:Oxidized methionine	171.02	809.4082	1601.82	15.9888	-3.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
14637	dirMS_041712_NAR_20mM_plus.14573.14573.2	2	8.04	0	4.50E+04	M256m	(R)SLDmDS	(R)S L/D m/D S I/I A E/V K(A)	m:Oxidized methionine	171.72	668.8371	1320.671	15.9954	0.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
14638	dirMS_041712_NAR_20mM_plus.14618.14618.3	3	8.04	0	1.37E+05		(R)LQEAGIL	(R)L Q E\A G I\L/S A/E/E L/Q R(L)		172.1	519.6131	1556.828	-0.0031	-2	4.25	533778	5.74	HUMAN	Q15149	Plectin
14639	dirMS_041712_NAR_20mM_plus.15889.15889.2	2	8.04	0	4.78E+05	M73m	(R)AILVDLE	(R)A I/L V/D L/E|P G/T m D S V R(S)	m:Oxidized methionine	179.88	816.4181	1615.836	15.9929	-1.2	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
14640	dirMS_041712_NAR_20mM_plus.16283.16283.2	2	8.04	0	2.55E+04		(R)LLFNDV	(R)L L/F/N/D V/Q T L K(D)		184.1	595.8432	1190.678	0.0012	1	5.84	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
14641	dirMS_041712_NAR_20mM_plus.18000.18000.3	3	8.04	0	1.69E+05		(R)LSVLGAI	(R)L S\V L G A|I/T S/V/Q Q R(L)		196.12	457.9354	1371.795	-0.0038	-2.8	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
14642	dirMS_041712_NAR_20mM_plus.18895.18895.2	2	8.04	0	9.72E+04		(K)LTVYTTL	(K)L/T/V/Y|T T/L I D V T K(G)		200.92	683.8948	1366.783	-0.0005	-0.4	5.83	42194.9	8.75	HUMAN	E7EMM4	Acid ceramidase
14643	dirMS_041712_NAR_20mM_plus.9895.9895.2	2	8.04	0	2.18E+05		(K)LVSESSD	(K)L V/S E/S/S D V L|P K(-)		140.12	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
14644	dirMS_041712_NAR_30mM_plus2.10847.10847.2	2	8.04	0	5.76E+05		(-)MIEVVC	(-)M I|E/V|V C N D/R(L)	C:Carbamidomethylation	109.78	568.2669	1135.523	0.0031	2.7	4.37	4334.2	11.58	HUMAN	K7EQ43	Ubiquitin-like protein 5
14645	dirMS_041712_NAR_30mM_plus2.20787.20787.2	2	8.04	0	2.90E+05		(K)LVLPSLIS	(K)L V|L/P/S L I/S S R(I)		163.93	542.8382	1084.672	-0.0033	-3.1	9.75	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
14646	dirMS_041712_NAR_30mM_plus2.22301.22301.2	2	8.04	0	2.00E+05		(K)NSSYFVE	(K)N S/S/Y F V/E/W I/P N N V/K(V)		171.95	848.9189	1696.833	-0.0024	-1.4	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
14647	dirMS_041712_NAR_30mM_plus2.7181.7181.2	2	8.04	0	1.13E+05		(K)TEISEM	(K)T E|I/S E|M/N R(N)		92.12	490.2294	979.451	0.0002	0.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
14648	dirMS_041712_NAR_30mM_plus2.9421.9421.2	2	8.04	0	5.75E+04		(K)TAVCDIF	(K)T A|V/C/D\I/P\P R(G)	C:Carbamidomethylation	104.02	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
14649	dirMS_041712_NAR_50mM_plus2.16065.16065.3	3	8.04	1	7.23E+05		(R)EGLTSIE	(R)E G L/T/S/I|E/E V T K N L Q K(F)		152.15	563.6357	1688.907	-0.014	-8.3	4.79	533778	5.74	HUMAN	Q15149	Plectin
14650	dirMS_041712_NAR_50mM_plus2.18595.18595.3	3	8.04	1	9.64E+05		(R)LKLPSIP	(R)L K L P S\I/P L V/P V S A Q K(R)		166.78	530.6702	1589.999	-0.0028	-1.8	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
14651	dirMS_041712_NAR_50mM_plus2.21710.21710.3	3	8.04	1	1.83E+05		(K)LKVNFLF	(K)L K V N F L/P E/I/I T L S K(E)		184.42	539.0011	1614.983	0.0058	3.6	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
14652	dirMS_041712_NAR_50mM_plus2.22259.22259.3	3	8.04	1	1.35E+06		(K)EGGLGP	(K)E G G/L/G/P L/N I P L L A D V T R R(L)		191	631.029	1891.076	-0.0035	-1.9	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
14653	dirMS_041712_NAR_50mM_plus2.7079.7079.3	3	8.04	1	3.75E+04		(R)ASVDTK	(R)A S/V/D T K E A E G\A/P Q V E A G K(R)		103.02	596.2908	1786.882	-0.0239	-13.4	4.41	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
14654	dirMS_041712_NAR_60mM_plus.12614.12614.3	3	8.04	1	1.14E+06		(R)MLFKDD	(R)M/L/F/K D D Y/P S S/P P K(C)		123.57	508.9175	1524.74	-0.0023	-1.5	5.71	20685.4	9.18	HUMAN	B0QYN7	SUMO-conjugating enzyme UBC9
14655	dirMS_041712_NAR_60mM_plus.14641.14641.3	3	8.04	1	5.27E+05		(K)NKDQGT	(K)N K D Q G T/Y\E|D\Y/V/E G L/R(V)		133.25	596.2816	1786.824	0.006	3.4	4.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
14656	dirMS_041712_NAR_120mM_minus.10211.10211.3	3	8.03	0	1.28E+05		(R)QSVEND	(R)Q|S/V/E N D I/H G L R(K)		109.87	423.2169	1267.639	-0.0028	-2.2	5.32	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
14657	dirMS_041712_NAR_120mM_minus.13878.13878.4	4	8.03	2	5.43E+05		(R)KLVIIEGI	(R)K\L V I\I|E/G D/L/E R T E E R(A)		129.85	450.7512	1799.986	-0.0032	-1.8	4.58	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
14658	dirMS_041712_NAR_120mM_minus.18042.18042.3	3	8.03	1	2.86E+05		(R)ARFEELN	(R)A R\F E E\L|N/A/D|L F/R(G)		153.08	494.2561	1480.754	-0.0006	-0.4	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
14659	dirMS_041712_NAR_120mM_minus.4286.4286.3	3	8.03	1	5.59E+05		(R)EPGPAG	(R)E P/G P/A G/R G D G D/S G R(S)		70.7	443.2041	1327.599	-0.0008	-0.6	4.56	558007.1	5.44	HUMAN	P58107	Epiplakin
14660	dirMS_041712_NAR_120mM_minus.8166.8166.3	3	8.03	1	3.68E+05		(R)FSEGTSA	(R)F/S/E/G T S A D|R E I Q R(T)		98.6	499.2436	1495.714	0.0027	1.8	4.68	7809.8	5.24	HUMAN	H0YJX2	26S protease regulatory subunit 10B (Fragment)
14661	dirMS_041712_NAR_20mM_minus.14467.14467.2	2	8.03	0	5.86E+04		(K)LAAELSA	(K)L A A E L S/A T/L/E Q A/A/A T/A R(V)		198.88	843.955	1686.902	0.0006	0.4	4.53	558007.1	5.44	HUMAN	P58107	Epiplakin
14662	dirMS_041712_NAR_30mM_minus2.10410.10410.2	2	8.03	0	1.29E+06		(K)TFEINPR	(K)T F|E/I/N P/R(H)		111.37	438.7375	876.457	0.0103	11.8	5.66	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
14663	dirMS_041712_NAR_30mM_minus2.13225.13225.2	2	8.03	0	4.80E+05		(K)IYFMAG	(K)I Y|F/M/A G S S R(K)		126.58	516.2552	1031.498	0.0052	5.1	8.75	92752.5	4.76	HUMAN	P14625	Endoplasmin
14664	dirMS_041712_NAR_40mM_minus2.7690.7690.3	3	8.03	0	6.54E+04		(K)EVVKPV	(K)E V V/K/P V P I/T/S P A V S K(V)		123.68	517.6416	1550.915	-0.005	-3.2	8.69	65142.1	9.24	HUMAN	Q96HC4	PDZ and LIM domain protein 5
14665	dirMS_041712_NAR_40mM_minus2.8001.8001.3	3	8.03	0	6.14E+04		(R)EALLSSA	(R)E A|L/L/S/S/A\V D H G S D E V K(F)		126.95	552.9398	1656.807	-0.0027	-1.6	4.31	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
14666	dirMS_041712_NAR_50mM_minus2.18218.18218.3	3	8.03	0	2.30E+05		(K)ILFIFIDSI	(K)I L/F I/F\I D S D H T D N Q R(I)		172.8	611.9745	1833.913	-0.004	-2.2	4.41	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
14667	dirMS_041712_NAR_50mM_minus2.8827.8827.3	3	8.03	1	2.18E+05		(K)VCGDSD	(K)V/C|G D/S D K/G F V V I/N Q/K(G)	C:Carbamidomethylation	118.03	555.9474	1665.826	0.0012	0.7	5.93	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
14668	dirMS_041712_NAR_50mM_minus2.9169.9169.3	3	8.03	1	9.32E+04		(K)GDVAVV	(K)G D V A V V R I N S/P N/S/K(V)		119.97	485.9282	1455.791	-0.0214	-14.7	8.75	83739.9	9.43	HUMAN	P40939	Trifunctional enzyme subunit alpha, mitochondrial
14669	dirMS_041712_NAR_20mM_plus.10218.10218.3	3	8.03	0	1.24E+05	M281m M	(R)NmPQA	(R)N m/P Q A D A\m|V/L/V A R(N)	m:Oxidized methionine	143.35	483.2393	1415.713	31.99	0.1	5.84	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
14670	dirMS_041712_NAR_20mM_plus.13165.13165.2	2	8.03	0	4.22E+03		(R)VLQALE	(R)V/L|Q/A L E G\L K(M)		162.88	485.8004	970.593	0.0004	0.4	5.97	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
14671	dirMS_041712_NAR_20mM_plus.9805.9805.2	2	8.03	0	7.68E+04		(R)TDYNAS	(R)T D/Y N A|S/V/S V/P D/S S/G P E R(I)		138.97	890.9015	1780.798	-0.0027	-1.5	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
14672	dirMS_041712_NAR_30mM_plus2.11012.11031.2	2	8.03	0	5.63E+05		(R)LMDVM	(R)L/M/D/V M/A/K(E)		110.92	404.2125	807.41	0.0074	9.2	5.84	52796.2	5.19	HUMAN	E7EUT8	Splicing factor 3A subunit 3
14673	dirMS_041712_NAR_30mM_plus2.15525.15525.2	2	8.03	0	4.01E+05		(R)MAGAIA	(R)M A|G A/I/A Q/G L I R(A)		133.67	550.816	1100.624	0.0002	0.2	9.5	4449.1	11.42	HUMAN	F8WEI0	Pyrroline-5-carboxylate reductase 3
14674	dirMS_041712_NAR_30mM_plus2.17730.17730.2	2	8.03	0	3.17E+05		(K)SLEDQV	(K)S L|E/D Q/V|E M L R(T)		145.83	610.3003	1219.599	-0.0054	-4.4	4.14	61161.1	4.34	HUMAN	K7ELL7	Glucosidase 2 subunit beta
14675	dirMS_041712_NAR_50mM_plus2.15262.15262.3	3	8.03	0	2.34E+05		(R)LASTLVH	(R)L/A/S T/L V/H L G E Y Q/A A V D/G A R(K)		148.03	657.6802	1971.029	-0.0034	-1.7	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
14676	dirMS_041712_NAR_50mM_plus2.16726.16726.3	3	8.03	0	4.75E+05		(K)SPVTTLL	(K)S P V|T/T L L E C M|H K(L)	C:Carbamidomethylation	155.32	472.5735	1415.702	0.0038	2.7	6.47	142137.5	9.17	HUMAN	E7ENU4	Double-stranded RNA-specific adenosine deaminase
14677	dirMS_041712_NAR_50mM_plus2.9158.9158.3	3	8.03	1	7.57E+05	M239m	(R)MQKEIT	(R)M Q K E I T A\L/A|P S T m K(I)	m:Oxidized methionine	115.63	522.2726	1548.812	15.9908	-2.6	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
14678	dirMS_041712_NAR_60mM_plus.10375.10375.2	2	8.03	0	9.30E+05		(R)SSGPYG	(R)S S/G/P Y G/G G/G Q Y F/A K/P\R(N)		112.17	814.8941	1628.782	-0.0007	-0.4	9.7	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
14679	dirMS_041712_NAR_60mM_plus.16109.16109.3	3	8.03	1	5.27E+05		(R)VTNRDII	(R)V/T N R D I\I\C|Q/I/A Y A R(I)	C:Carbamidomethylation	141	564.9631	1692.885	-0.0103	-6.1	8.71	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
14680	dirMS_041712_NAR_60mM_plus.19009.19009.3	3	8.03	1	2.62E+05		(K)YGKLEVA	(K)Y G K L\E V A\N/L/L/L Q K(S)		156.68	496.9628	1488.878	-0.0046	-3.1	8.5	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
14681	dirMS_041712_NAR_60mM_plus.19080.19080.3	3	8.03	0	4.67E+05		(K)LDLCTTV	(K)L D\L C T/T V/L P Q I E K(L)	C:Carbamidomethylation	157.97	510.6056	1529.824	-0.0221	-14.5	4.37	30578.7	6.26	HUMAN	H3BTU7	Katanin p80 WD40 repeat-containing subunit B1 (Fragment)
14682	dirMS_041712_NAR_60mM_plus.20127.20127.3	3	8.03	1	1.54E+05		(R)ELIKVLEI	(R)E L I K V\L\E E A N/Q/A I N/P K(L)		165.17	603.6768	1809.012	0.0042	2.3	4.79	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
14683	dirMS_041712_NAR_60mM_plus.9373.9373.3	3	8.03	0	3.55E+05		(K)KPPLLN	(K)K\P P L L N\N\A/D/S/V Q/A K(V)		107.23	498.9471	1494.828	-0.0007	-0.5	8.59	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
14684	dirMS_041712_NAR_20mM_minus.11092.11092.2	2	8.02	0	8.55E+04		(K)VIDPATA	(K)V/I|D/P A T A/T\S V D L R(D)		158.42	679.3706	1357.732	0.0018	1.3	4.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
14685	dirMS_041712_NAR_20mM_minus.8830.8830.2	2	8.02	0	1.75E+05		(K)IVVVTAC	(K)I V|V|V/T A G/V R(Q)		137.98	457.2947	913.583	-0.0008	-0.9	9.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
14686	dirMS_041712_NAR_50mM_minus2.12989.12989.3	3	8.02	1	1.60E+05		(K)GGELVY	(K)G G E/L/V|Y T D S E A R D V F E K(A)		141.68	638.9739	1914.908	-0.0008	-0.4	4.18	533778	5.74	HUMAN	Q15149	Plectin
14687	dirMS_041712_NAR_60mM_minus.15017.15017.3	3	8.02	1	1.43E+05		(R)LAIKLPD	(R)L/A I K\L/P D D Q I/P K(T)		143.45	450.939	1350.799	0.0033	2.5	5.96	26413	9.18	HUMAN	B1APP6	6-phosphofructokinase type C (Fragment)
14688	dirMS_041712_NAR_60mM_minus.17894.17894.3	3	8.02	1	3.70E+05		(K)NLRDIDE	(K)N L R D I\D|E\V/S\S/L L R(T)		160.93	510.6099	1529.828	-0.013	-8.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
14689	dirMS_041712_NAR_120mM_plus.11656.11656.2	2	8.02	0	3.00E+05		(K)HMLPTV	(K)H/M|L/P T V L/R(M)		113.93	483.7811	966.555	-0.0004	-0.4	9.75	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
14690	dirMS_041712_NAR_30mM_plus2.10808.10808.2	2	8.02	0	4.56E+05		(K)CIAMCM	(K)C I|A|M C M D/R(Y)	C:Carbamidomethylation	109.65	528.7093	1056.409	0.002	1.9	5.84	9122.2	9.22	HUMAN	K7EIT2	Mitochondrial import inner membrane translocase subunit Tim13
14691	dirMS_041712_NAR_30mM_plus2.13719.13739.2	2	8.02	0	6.07E+05		(K)LVPVGY	(K)L V|P/V/G Y G I K(K)		125.42	473.2901	945.577	-0.0039	-4.1	8.59	24934.4	4.5	HUMAN	P24534	Elongation factor 1-beta
14692	dirMS_041712_NAR_30mM_plus2.4681.4681.2	2	8.02	0	2.78E+05		(R)MDDYCI	(R)M/D/D/Y C/R(R)	C:Carbamidomethylation	75.27	430.1579	859.307	0.0012	1.4	4.21	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
14693	dirMS_041712_NAR_30mM_plus2.6014.6039.2	2	8.02	0	1.06E+05		(K)MGGDIA	(K)M/G/G\D/I/A N/R(V)		85.85	417.2016	833.393	0.0025	3	5.59	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
14694	dirMS_041712_NAR_40mM_plus2.11840.11840.3	3	8.02	0	4.24E+04		(K)AASAGV	(K)A A|S A/G V P Y/H G E/V P V S L A/R(A)		136.07	594.314	1780.934	-0.0066	-3.7	6.79	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
14695	dirMS_041712_NAR_40mM_plus2.12014.12014.3	3	8.02	0	1.14E+04		(R)TVVSGS	(R)T V|V/S/G/S C A A H\S L L I T T E G K(L)	C:Carbamidomethylation	137.22	644.3327	1930.99	-0.0067	-3.5	6.41	56825.2	9.49	HUMAN	Q9P258	Protein RCC2
14696	dirMS_041712_NAR_50mM_plus2.11005.11005.3	3	8.02	0	4.34E+05		(R)EALLSSA	(R)E A/L/L/S/S/A\V D H/G S D E V K(F)		124.85	552.9403	1656.807	-0.0012	-0.7	4.31	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
14697	dirMS_041712_NAR_60mM_plus.15734.15734.3	3	8.02	0	3.40E+05		(R)VWYVSN	(R)V W|Y/V S N I/D/G T H I A K(T)		139.45	534.9464	1602.828	-0.0028	-1.8	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
14698	dirMS_041712_NAR_60mM_plus.16281.16281.3	3	8.02	1	2.26E+05		(K)GIDRYNI	(K)G I D R Y N|P|E|N L A/T L E R(Y)		141.93	587.635	1760.893	-0.0021	-1.2	4.68	24768.8	4.76	HUMAN	B7ZAM9	Eukaryotic translation initiation factor 3 subunit K
14699	dirMS_041712_NAR_60mM_plus.9398.9398.2	2	8.02	0	1.27E+06		(K)STAGDT	(K)S T/A/G D T H/L|G G E D|F D|N R(M)		107.4	846.3654	1691.726	-0.0021	-1.2	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
14700	dirMS_041712_NAR_120mM_minus.15543.15543.4	4	8.01	2	1.22E+06		(R)ALKDEEI	(R)A L K D E E/K M E\L Q/E I Q L/K(E)		139.23	487.0126	1945.031	-0.0025	-1.3	4.58	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
14701	dirMS_041712_NAR_20mM_minus.14503.14503.3	3	8.01	0	1.37E+05		(R)LSVEEAV	(R)L S\V E E A V A A G\V/V/G/G E I Q E K(L)		199.57	629.0005	1884.991	-0.0044	-2.3	4.09	266161	5.68	HUMAN	E9PPU0	Epiplakin
14702	dirMS_041712_NAR_30mM_minus2.10397.10397.2	2	8.01	0	2.81E+05		(R)ETAEAD	(R)E T/A\E|A/D/V/A/S L/N R(R)		110.08	638.3134	1275.618	0.002	1.6	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
14703	dirMS_041712_NAR_30mM_minus2.13050.13050.2	2	8.01	1	1.89E+05		(K)KITIADC	(K)K\I\T/I\A D C G Q|L|E(-)	C:Carbamidomethylation	124.85	624.3176	1247.63	-0.0021	-1.7	4.75	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
14704	dirMS_041712_NAR_60mM_minus.8622.8622.3	3	8.01	0	3.02E+05		(K)EFHLNES	(K)E/F H L N E/S/G/D/P S S K(S)		108.08	482.8882	1446.65	0.0005	0.3	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
14705	dirMS_041712_NAR_20mM_plus.15718.15718.3	3	8.01	0	1.66E+05		(R)GNPTVE	(R)G N P T V E/V/D\L F/T/S/K(G)		179.97	469.577	1406.716	0.0003	0.2	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
14706	dirMS_041712_NAR_20mM_plus.9322.9322.3	3	8.01	0	3.09E+04		(R)SVSLTGA	(R)S V\S L\T G A/P E/S V Q K(A)		135.52	434.9007	1302.69	-0.0024	-1.9	5.72	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
14707	dirMS_041712_NAR_30mM_plus2.15841.15841.2	2	8.01	0	3.11E+05		(R)YSVDIPL	(R)Y/S/V/D/I/P L D K(T)		136.1	525.2819	1049.551	0.0052	4.9	4.21	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
14708	dirMS_041712_NAR_30mM_plus2.20163.20163.2	2	8.01	0	2.09E+05		(R)FLSGLEL	(R)F L/S\G L E/L/V\K(Q)		159.07	503.3003	1005.598	-0.0046	-4.6	6	13715.7	11.37	HUMAN	Q5JZ02	TP53 regulating kinase
14709	dirMS_041712_NAR_30mM_plus2.20442.20442.2	2	8.01	0	1.80E+05		(K)GSFSEQ	(K)G S/F/S E Q/G I/N E/F L\R(E)		161	742.362	1483.718	-0.0009	-0.6	4.53	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
14710	dirMS_041712_NAR_30mM_plus2.21561.21561.2	2	8.01	0	3.33E+05		(R)NSYLEVI	(R)N/S|Y|L/E V L/L K(L)		167.98	539.8092	1078.614	-0.0032	-2.9	6	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6

14711	dirMS_041712_NAR_40mM_plus2.16239.16239.2	2	8.01	0	1.50E+05		(R)YLTVAA	(R)Y L|T V/A/A V F R(G)		162.03	520.2997	1039.593	-0.0014	-1.3	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
14712	dirMS_041712_NAR_40mM_plus2.18703.18703.3	3	8.01	0	6.98E+04		(R)QGTPLI	(R)Q G T P L I/A F/S L L/P H E Q K(R)		175.37	593.6623	1778.98	-0.0076	-4.3	6.75	6068.8	5.09	HUMAN	I3L4E8	Pre-rRNA-processing protein TSR1 homolog (Fragment)
14713	dirMS_041712_NAR_40mM_plus2.6298.6298.2	2	8.01	0	7.65E+04		(R)VTDALN	(R)V/T/D/A/L N A T R(A)		96.63	480.7594	960.511	0.0006	0.7	5.81	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
14714	dirMS_041712_NAR_40mM_plus2.6961.6961.2	2	8.01	0	7.26E+04		(R)LTEGCS	(R)L/T/E/G C S/F R(R)	C:Carbamidomethylation	101	485.2217	969.446	-0.0097	-10	6	5988.9	10.55	HUMAN	C9J1C5	40S ribosomal protein S27
14715	dirMS_041712_NAR_40mM_plus2.7161.7162.2	2	8.01	1	1.67E+05		(R)KNPNYD	(R)K\N P N\Y|D|L(-)		102.13	432.2161	863.426	-0.0008	-1	5.83	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
14716	dirMS_041712_NAR_50mM_plus2.12430.12430.3	3	8.01	1	2.69E+05		(K)KVPQVS	(K)K\V\P Q V S T/P T|L/V/E V S R(N)		133.32	547.3169	1639.938	-0.0016	-1	8.75	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
14717	dirMS_041712_NAR_50mM_plus2.13404.13404.3	3	8.01	0	1.74E+05		(K)LGDVYV	(K)L/G D\V/Y V N D/A F\G T A/H R(A)		138.82	545.6029	1634.792	0.002	1.2	5.21	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
14718	dirMS_041712_NAR_50mM_plus2.13678.13678.3	3	8.01	0	8.72E+05		(K)AASDIA	(K)A A S D/I/A/M T E/L/P P T H P I R(L)		140	607.3177	1819.937	0.0015	0.8	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
14719	dirMS_041712_NAR_50mM_plus2.20225.20225.3	3	8.01	0	1.11E+05		(K)ALESPE	(K)A L|E/S P\E R P F L A I L G G/A K(V)		174.73	590.3344	1768.996	-0.0069	-3.9	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
14720	dirMS_041712_NAR_60mM_plus.16174.16174.3	3	8.01	0	5.79E+05		(R)ETHSAL	(R)E T H S A L/G|P A\L|Q/A A/F K(L)		141.82	514.2744	1540.812	-0.0032	-2.1	6.85	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
14721	dirMS_041712_NAR_120mM_minus.11606.11606.3	3	8	1	1.18E+05		(K)TLQEVT	(K)T L/Q/E\V/T/E M/D S V K R(Y)		117.33	512.5957	1535.773	-0.0008	-0.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
14722	dirMS_041712_NAR_30mM_minus2.10732.10752.2	2	8	0	1.22E+05		(R)LDDSFV	(R)L/D|D/S F V/R(G)		112.53	426.2191	851.426	0.0052	6.1	4.21	30468.2	9.09	HUMAN	K7EIH8	DnaJ homolog subfamily C member 7 (Fragment)
14723	dirMS_041712_NAR_50mM_minus2.13685.13685.3	3	8	0	2.19E+04		(R)DLSHIG	(R)D L S H I G D A V|V/I/S C A K(D)	C:Carbamidomethylation	145.88	528.9397	1584.805	-0.0005	-0.3	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
14724	dirMS_041712_NAR_120mM_plus.18034.18034.3	3	8	1	3.86E+05		(K)YRGFTIP	(K)Y R G F T\I/P E/A F R(G)		148.13	452.9069	1356.706	0.0003	0.2	8.75	27264.5	5.09	HUMAN	O00299	Chloride intracellular channel protein 1
14725	dirMS_041712_NAR_20mM_plus.11258.11258.2	2	8	0	1.33E+05		(R)YALYDA	(R)Y/A|L|Y/D/A T Y/E T K(E)		150.25	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
14726	dirMS_041712_NAR_20mM_plus.11274.11274.2	2	8	0	7.33E+04		(R)IASLEVE	(R)I A S\L/E/V/E/N\Q S L R(G)		150.3	679.8662	1358.727	-0.0023	-1.7	4.53	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
14727	dirMS_041712_NAR_20mM_plus.12949.12949.2	2	8	0	3.25E+05	M316m	(R)ISEQFTA	(R)I/S E/Q/F/T A m F R(R)	m:Oxidized methionine	161.5	623.3012	1229.598	15.9968	1.5	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
14728	dirMS_041712_NAR_20mM_plus.8067.8067.2	2	8	0	4.21E+05	M239m	(K)EVDEQ	(K)E V/D\E/Q m L\N|V Q/N K(N)	m:Oxidized methionine	125.1	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
14729	dirMS_041712_NAR_30mM_plus2.6154.6154.2	2	8	0	1.22E+04		(R)FSSSSGY	(R)F/S|S S S/G/Y G G G S S R(V)		86.68	618.2674	1235.529	-0.0012	-1	8.75	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
14730	dirMS_041712_NAR_30mM_plus2.9768.9784.2	2	8	0	1.36E+06		(R)QLSSGV	(R)Q L|S/S/G/V/S E/I R(H)		104.9	538.2855	1075.574	-0.0105	-9.8	6	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
14731	dirMS_041712_NAR_60mM_plus.15059.15059.3	3	8	1	2.99E+04		(R)ELAFQIS	(R)E L/A/F/Q I/S K/E/Y E R(F)		135.27	504.9258	1512.769	-0.0064	-4.3	4.79	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
14732	dirMS_041712_NAR_60mM_plus.9793.9920.3	3	8	1	2.15E+05		(R)GPGLVK	(R)G P|G L/V K/Q E D/F/R(D)		109.68	415.8936	1245.659	0.0076	6.1	6.07	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
14733	dirMS_041712_NAR_30mM_minus2.16454.16454.2	2	7.99	0	1.33E+05		(K)STFVNIL	(K)S T|F/V\N I L/K(Q)		142.97	461.2712	921.54	-0.0053	-5.7	8.47	23232.7	5.07	HUMAN	D6RCP9	Deoxycytidine kinase
14734	dirMS_041712_NAR_30mM_minus2.17574.17574.2	2	7.99	0	1.66E+05		(K)GFLIDGY	(K)G F|L|I/D/G Y P R(E)		150.23	519.2752	1037.542	0.0017	1.6	5.83	15567.5	8.13	HUMAN	H0Y4J6	Adenylate kinase isoenzyme 1 (Fragment)
14735	dirMS_041712_NAR_30mM_minus2.19493.19493.2	2	7.99	0	3.54E+05		(R)ASLSLW	(R)A S L/S\L/W/Q A M/E/K(G)		162.45	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
14736	dirMS_041712_NAR_40mM_minus2.6974.6974.2	2	7.99	0	5.85E+05		(R)GYSFTT	(R)G/Y|S\F/T/T T\A E R(E)		111.95	566.7661	1132.527	-0.002	-1.8	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
14737	dirMS_041712_NAR_50mM_minus2.15485.15485.3	3	7.99	0	4.75E+05		(R)DGLAFN	(R)D G/L/A/F N A/L/I H R(H)		155.62	409.5594	1226.664	-0.0004	-0.3	6.74	146974	5.55	HUMAN	C9JRP8	Spectrin beta chain, non-erythrocytic 4
14738	dirMS_041712_NAR_50mM_minus2.9715.9715.3	3	7.99	0	7.08E+04		(R)ELTLEKP	(R)E L T L/E/K/P/E L K(A)		123.67	400.5678	1199.688	0.0007	0.6	4.79	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
14739	dirMS_041712_NAR_60mM_minus.13340.13340.3	3	7.99	0	1.01E+05		(R)DLNYCF	(R)D L N/Y C F/S G M/S D/H R(Y)	C:Carbamidomethylation	135.35	534.5588	1601.647	0.0147	9.2	5.21	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
14740	dirMS_041712_NAR_60mM_minus.8062.8062.3	3	7.99	1	2.69E+05		(K)LNVTEQ	(K)L N/V/T E Q E/K I\D K(L)		105.47	439.57	1316.706	-0.0102	-7.7	4.68	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
14741	dirMS_041712_NAR_120mM_plus.9892.9892.3	3	7.99	1	1.73E+06		(K)SKFDNL	(K)S K\F D N L/Y/G/C/R(E)	C:Carbamidomethylation	104.62	420.5351	1259.584	0.007	5.6	8.31	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
14742	dirMS_041712_NAR_20mM_plus.10879.10935.2	2	7.99	0	2.31E+04		(K)EVPAVP	(K)E V/P A/V/P E T L K(K)		147.52	541.8074	1082.609	-0.0017	-1.6	4.53	29282.3	10.71	HUMAN	P18124	60S ribosomal protein L7
14743	dirMS_041712_NAR_30mM_plus2.11668.11668.2	2	7.99	0	5.15E+05		(R)SGEGEV	(R)S G E|G/E/V S/G L/M R(K)		114.07	561.2662	1121.526	-0.0004	-0.4	4.53	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
14744	dirMS_041712_NAR_30mM_plus2.13216.13236.2	2	7.99	0	5.70E+05		(K)CPFTGN	(K)C/P/F|T/G N V S I R(G)	C:Carbamidomethylation	122.88	575.7876	1150.567	0.0006	0.5	9.75	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
14745	dirMS_041712_NAR_30mM_plus2.16056.16056.2	2	7.99	0	2.08E+05		(R)IGSGFD	(R)I/G\S/G F/D N|I/D I K(S)		136.95	589.8053	1178.605	-0.0019	-1.6	4.21	20631.5	6.98	HUMAN	D6RAX2	C-terminal-binding protein 1 (Fragment)
14746	dirMS_041712_NAR_30mM_plus2.16268.16268.2	2	7.99	0	1.77E+05		(R)VEVTEF	(R)V E|V|T E/F E\D I K(S)		137.82	604.8021	1208.604	-0.0076	-6.3	4	30992.3	4.14	HUMAN	B2REB8	Protein SET
14747	dirMS_041712_NAR_50mM_plus2.17195.17195.3	3	7.99	1	1.07E+06		(K)DNNGVI	(K)D N|N/G V I/G L/L/E P M K K(S)		158.58	509.9448	1527.82	-0.0001	-0.1	6.07	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
14748	dirMS_041712_NAR_50mM_plus2.21501.21501.3	3	7.99	1	8.47E+04		(K)ITPENLP	(K)I T|P E N L/P Q I L/L Q L K R(R)		183.3	592.694	1776.074	-0.0067	-3.8	8.75	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
14749	dirMS_041712_NAR_60mM_plus.5644.5644.3	3	7.99	1	3.86E+04		(R)TLEEKE	(R)T L E E/K/E/Q E/E A R(L)		87.77	454.555	1361.654	-0.0039	-2.8	4.32	95923.1	9.67	HUMAN	Q9BUQ8	Probable ATP-dependent RNA helicase DDX23
14750	dirMS_041712_NAR_20mM_minus.10989.10989.2	2	7.98	0	9.96E+04		(K)GTIQVIT	(K)G T/I Q/V|I T Q G T/S L K(N)		157.17	673.3789	1345.769	-0.018	-13.4	8.75	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
14751	dirMS_041712_NAR_20mM_minus.14659.14659.2	2	7.98	0	8.83E+04		(R)IITLTGP	(R)I I/T L|T\G/P T N A I F K(A)		201.33	694.9107	1388.815	-0.0007	-0.5	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
14752	dirMS_041712_NAR_30mM_minus2.11883.11905.2	2	7.98	0	7.98E+05		(K)GIPYTLN	(K)G I|P/Y/T|L N G K(K)		117.87	481.7625	962.531	-0.0128	-13.3	8.59	13353.1	8.96	HUMAN	F5H3E3	Acetoacetyl-CoA synthetase (Fragment)
14753	dirMS_041712_NAR_30mM_minus2.15468.15468.2	2	7.98	0	1.82E+05		(K)EILFYDR	(K)E/I/L/F/Y D R(I)		137.48	478.2479	955.488	0.0002	0.2	4.37	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b
14754	dirMS_041712_NAR_50mM_minus2.12603.12603.3	3	7.98	0	1.09E+06	M114m M:	(R)AGKPVI	(R)A G K\P V I/C A\T Q/m\L E/S m|I K(K)	C:Carbamidomethylation m:Oxid	139.87	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
14755	dirMS_041712_NAR_50mM_minus2.13458.13458.3	3	7.98	1	1.37E+05		(K)IDSRLE	(K)I/D/S R L E\Q Y/T/S A/I E G T K(S)		144.62	604.3145	1810.918	0.0108	6	4.68	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
14756	dirMS_041712_NAR_50mM_minus2.15769.15769.3	3	7.98	0	9.69E+04		(K)INLEAA	(K)I N|L\E/A A E L G E I S D|I H T K(L)		158.72	618.326	1852.965	-0.0016	-0.9	4.4	84268.2	6.32	HUMAN	Q9UHD2	Serine/threonine-protein kinase TBK1
14757	dirMS_041712_NAR_50mM_minus2.7094.7094.3	3	7.98	1	6.97E+04	M1489m	(R)ALEEAm	(R)A L\E/E/A m E/Q K A/E L E R(L)	m:Oxidized methionine	107.35	554.9379	1646.805	15.9937	-0.7	4.33	227783.5	5.5	HUMAN	P35579	Myosin-9
14758	dirMS_041712_NAR_50mM_minus2.8835.8835.3	3	7.98	1	7.72E+04		(R)SATKVT	(R)S A/T K V T A D\V\I/N A A E/K(L)		118.25	506.6094	1517.817	-0.0033	-2.2	5.79	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
14759	dirMS_041712_NAR_60mM_minus.13719.13719.3	3	7.98	1	2.40E+04	N1100n	(K)IKVNWT	(K)I K V N W/T/P E/I n K(E)	n:N-acetylglucosamine (N)	135.68	515.6165	1341.753	203.0824	2	8.59	228081	6.98	HUMAN	A6NHR9	Structural maintenance of chromosomes flexible hinge domain-containing protein 1
14760	dirMS_041712_NAR_60mM_minus.6587.6587.3	3	7.98	1	1.06E+05	M199m	(R)mLQAD	(R)m L|Q\A/D/P N K\V S A R(A)	m:Oxidized methionine	95.15	449.2329	1329.694	15.9898	-3.8	8.5	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
14761	dirMS_041712_NAR_60mM_minus.9976.9976.3	3	7.98	1	1.25E+05		(R)AGTGVD	(R)A G/T/G V/D/N V D L E A A T R\K(G)		115.55	539.6117	1616.824	-0.0033	-2	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
14762	dirMS_041712_NAR_120mM_plus.13105.13105.3	3	7.98	1	2.97E+06		(K)VKLEAEI	(K)V K L E A E\I|A/T Y R(R)		121.7	431.5774	1292.721	-0.0032	-2.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
14763	dirMS_041712_NAR_120mM_plus.24546.24546.3	3	7.98	0	1.62E+05		(K)GHYTEG	(K)G H Y T E G A E\L\V|D/S/V L/D V V R(K)		184.27	653.6605	1958.982	-0.0148	-7.6	4.31	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
14764	dirMS_041712_NAR_20mM_plus.19029.19029.2	2	7.98	0	8.73E+04		(R)EGDVLT	(R)E G D V/L/T/L/L E\S E R(E)		203	680.8536	1360.696	0.0045	3.3	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
14765	dirMS_041712_NAR_30mM_plus2.16110.16110.2	2	7.98	0	3.24E+05		(R)MGPNIY	(R)M/G|P N I/Y E/L R(T)		136.63	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
14766	dirMS_041712_NAR_30mM_plus2.19322.19322.2	2	7.98	0	2.98E+05		(K)TVDNFV	(K)T V/D\N F|V/A L/A T G E K(G)		155	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
14767	dirMS_041712_NAR_30mM_plus2.20329.20329.3	3	7.98	0	4.80E+05		(K)SYELPD	(K)S Y E\L/P D G Q\V I/T/I G N E R(F)		159.93	597.6334	1790.892	-0.0063	-3.5	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
14768	dirMS_041712_NAR_30mM_plus2.7162.7162.2	2	7.98	0	1.13E+05		(K)TEISEM	(K)T E|I/S\E/M N R(N)		92.12	490.2294	979.451	0.0002	0.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
14769	dirMS_041712_NAR_30mM_plus2.8570.8570.2	2	7.98	0	8.11E+05		(R)FSELTAE	(R)F/S/E L/T/A E K(L)		99.37	462.7408	924.467	0.007	7.6	4.53	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
14770	dirMS_041712_NAR_30mM_plus2.9810.9968.2	2	7.98	0	7.57E+05		(R)LQTQVF	(R)L Q|T Q/V/F/K(L)		105.23	432.2494	863.499	-0.007	-8.1	8.75	16684.5	11.19	HUMAN	B5MCT8	40S ribosomal protein S9
14771	dirMS_041712_NAR_40mM_plus2.19635.19635.3	3	7.98	1	1.67E+05		(K)LGFAGL	(K)L/G/F/A/G L V Q E I S F G T T K D K(M)		183.78	637.673	1911.022	-0.0178	-9.3	6.07	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
14772	dirMS_041712_NAR_50mM_plus2.10680.10680.3	3	7.98	1	5.66E+05		(R)ELLTLDE	(R)E L L/T/L D E K D/P R(R)		123.8	443.5761	1328.706	0.0081	6.1	4.32	9591.1	10.94	HUMAN	A8MXK4	40S ribosomal protein S9
14773	dirMS_041712_NAR_50mM_plus2.17395.17395.3	3	7.98	0	1.70E+05		(K)SLLKPFC	(K)S L\L K/P F/C A A L L K(H)	C:Carbamidomethylation	159.82	454.2717	1360.802	-0.0016	-1.1	10	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
14774	dirMS_041712_NAR_60mM_plus.13400.13400.3	3	7.98	0	6.14E+05	M1m	(-)mVNHFI	(-)m V N H F I/A E/F/K(R)	m:Oxidized methionine	126.2	417.8778	1235.624	15.9947	-0.2	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
14775	dirMS_041712_NAR_60mM_plus.15458.15458.3	3	7.98	0	3.36E+05		(R)VQIEHIS	(R)V Q/I E/H I S S L/I/K(L)		137.37	422.9171	1266.742	-0.0049	-3.8	6.72	47748.2	6.08	HUMAN	O00231	26S proteasome non-ATPase regulatory subunit 11
14776	dirMS_041712_NAR_120mM_minus.4237.4237.3	3	7.97	1	6.83E+05		(R)EPGPAG	(R)E P/G/P/A G/R G D G D S G R(S)		70.47	443.2041	1327.599	-0.0008	-0.6	4.56	558007.1	5.44	HUMAN	P58107	Epiplakin
14777	dirMS_041712_NAR_20mM_minus.13106.13106.2	2	7.97	0	3.30E+05	M35m	(K)NDIAINE	(K)N D I\A|I|N E L m K(R)	m:Oxidized methionine	181.88	588.7948	1160.598	15.9843	-9	4.37	28354	7.11	HUMAN	B4DXI8	26S proteasome non-ATPase regulatory subunit 7
14778	dirMS_041712_NAR_20mM_minus.13166.13166.2	2	7.97	0	1.10E+05	M329m	(K)ALELNm	(K)A L/E L/N m L S L K(G)	m:Oxidized methionine	182.6	574.3232	1131.644	15.9949	0	6.05	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
14779	dirMS_041712_NAR_20mM_minus.13242.13242.2	2	7.97	0	8.84E+03		(-)SDVLELT	(-)S D V\L E/L/T/D D N/F E S R(I)		183.1	820.373	1639.745	-0.0059	-3.6	3.77	13747.3	6.8	HUMAN	H7BZJ3	Thioredoxin (Fragment)
14780	dirMS_041712_NAR_20mM_minus.8714.8714.2	2	7.97	0	8.10E+04		(R)SPSDSST	(R)S P S D S S T A/S/T/P V A/E/Q I E/R(A)		136.52	931.4377	1861.877	-0.0093	-5	4.14	76925.9	4.46	HUMAN	A8MV58	Drebrin
14781	dirMS_041712_NAR_30mM_minus2.10518.10560.2	2	7.97	0	1.09E+06		(K)TIAPALV	(K)T I|A/P A L/V S K(K)		111.75	450.2803	899.556	-0.0027	-3	8.41	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
14782	dirMS_041712_NAR_30mM_minus2.17152.17152.2	2	7.97	0	1.16E+05		(R)TLINELV	(R)T/L|I/N E\L V K(G)		146.6	465.2877	929.567	0.0015	1.6	5.66	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
14783	dirMS_041712_NAR_30mM_minus2.9270.9270.2	2	7.97	0	3.53E+05		(K)CAADLG	(K)C/A|A D|L/G L/N K(G)	C:Carbamidomethylation	104.88	481.2466	961.477	0.0088	9.1	5.84	13915.8	6.43	HUMAN	P49773	Histidine triad nucleotide-binding protein 1
14784	dirMS_041712_NAR_40mM_minus2.14461.14461.3	3	7.97	0	1.74E+04		(K)SLCIPFKI	(K)S L C|I/P F/K P L C E L\Q/P G A K(C)	C:Carbamidomethylation	170.4	653.3446	1958.024	-0.0046	-2.3	8.31	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
14785	dirMS_041712_NAR_60mM_minus.15117.15117.3	3	7.97	1	1.80E+05		(K)IKDLSTV	(K)I K D L S T|V/E/A L/Q N L/K(N)		144.25	524.6378	1571.9	-0.0015	-0.9	6.07	13242.4	4.17	HUMAN	E9PPH5	Acidic leucine-rich nuclear phosphoprotein 32 family member E (Fragment)
14786	dirMS_041712_NAR_60mM_minus.5190.5190.3	3	7.97	0	2.36E+04		(K)AAGPSL	(K)A A|G P/S L/S H T S/G G T Q S K(V)		83.72	495.9133	1485.729	-0.0039	-2.6	8.8	68764.6	6.96	HUMAN	P27694	Replication protein A 70 kDa DNA-binding subunit
14787	dirMS_041712_NAR_120mM_plus.5815.5815.3	3	7.97	1	3.87E+05		(R)LNGTLRI	(R)L/N/G T L R/E D/D/N R(I)		83.52	434.8849	1302.64	0.0005	0.4	4.56	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
14788	dirMS_041712_NAR_20mM_plus.16520.16520.2	2	7.97	0	1.71E+05		(R)LLEAQIA	(R)L L/E\A\Q|I/A T G G I I D/P K(E)		185.37	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
14789	dirMS_041712_NAR_20mM_plus.18855.18855.2	2	7.97	0	2.42E+05		(K)IYVDDGI	(K)I Y|V/D D/G L\I S L/Q V K(Q)		200.75	731.9068	1462.815	-0.0088	-6	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
14790	dirMS_041712_NAR_30mM_plus2.12866.12866.2	2	7.97	0	2.93E+05		(K)LDADYP	(K)L D|A/D|Y/P L R(V)		120.88	481.7538	962.494	0.0062	6.4	4.21	18169.4	9.62	HUMAN	F8VVL1	Density-regulated protein
14791	dirMS_041712_NAR_30mM_plus2.19141.19141.2	2	7.97	0	2.13E+05		(K)TVDNFV	(K)T V|D N/F V A L A T G E K(G)		154.18	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
14792	dirMS_041712_NAR_40mM_plus2.6809.6809.2	2	7.97	0	1.97E+04		(K)TPGPGA	(K)T/P|G/P/G A Q S A L R(A)		100.07	527.7842	1054.564	-0.0029	-2.7	9.41	14466.4	9.92	HUMAN	E5RH77	40S ribosomal protein S14
14793	dirMS_041712_NAR_50mM_plus2.10903.11211.3	3	7.97	1	4.55E+05		(R)AIPNNQ	(R)A I|P/N N Q/V/L G K I E R(A)		125.48	484.6151	1451.833	-0.0021	-1.5	8.79	16368.4	9.95	HUMAN	O60869	Endothelial differentiation-related factor 1
14794	dirMS_041712_NAR_50mM_plus2.17563.17563.3	3	7.97	0	3.57E+05		(R)LLLDIPL	(R)L L\L/D|I/P\L Q T P H K(L)		160.8	463.2819	1387.831	0.0004	0.3	6.74	198852.6	5.95	HUMAN	A6NKT7	RanBP2-like and GRIP domain-containing protein 3
14795	dirMS_041712_NAR_50mM_plus2.7076.7118.3	3	7.97	0	3.21E+05	T374t	(R)TAAtLAT	(R)T/A|A t L/A/T H E L R(A)	t:N-acetylglucosamine (T)	103.07	462.9074	1183.643	203.0647	-10.6	6.41	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
14796	dirMS_041712_NAR_50mM_plus2.7225.7225.3	3	7.97	0	1.68E+05		(R)SGSSQE	(R)S G/S S Q/E\L D V K/P S A/S/P Q E R(S)		103.85	634.6443	1901.92	-0.0016	-0.8	4.68	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
14797	dirMS_041712_NAR_60mM_plus.14586.14586.3	3	7.97	1	4.71E+05		(K)ISNYGW	(K)I/S|N Y G W/D Q S D K/F V K(I)		132.32	562.9416	1686.812	-0.002	-1.2	5.96	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
14798	dirMS_041712_NAR_60mM_plus.6564.6564.2	2	7.97	0	1.25E+05		(K)EMQPTH	(K)E M/Q|P T H/P I R(L)		92.78	554.782	1108.557	-0.0001	-0.1	6.85	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
14799	dirMS_041712_NAR_120mM_minus.13978.13978.4	4	7.96	1	1.60E+06		(K)ASIHEA	(K)A/S\I/H E/A W/T D/G K E A M L K(H)		129.98	447.476	1786.879	0.0029	1.6	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
14800	dirMS_041712_NAR_20mM_minus.13541.13541.3	3	7.96	0	1.87E+05		(R)ETTDTD	(R)E T T D T D T A D Q/V I/A/S/F K(V)		186.33	581.2735	1741.813	-0.0067	-3.9	3.84	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
14801	dirMS_041712_NAR_20mM_minus.14499.14499.3	3	7.96	0	1.37E+05		(R)LSVEEA	(R)L S V E E A V A A G\V/V/G/G E/I Q E K(L)		199.57	629.0005	1884.991	-0.0044	-2.3	4.09	266161	5.68	HUMAN	E9PPU0	Epiplakin
14802	dirMS_041712_NAR_30mM_minus2.16475.16475.2	2	7.96	0	2.61E+05		(R)ASLEAAI	(R)A S L/E/A/A/I/A/D A\E Q R(G)		143.62	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
14803	dirMS_041712_NAR_30mM_minus2.7403.7403.2	2	7.96	0	5.70E+05		(R)DATME	(R)D A/T/M/E\V Q R(G)		94.93	475.2269	949.441	0.0058	6.1	4.37	558007.1	5.44	HUMAN	P58107	Epiplakin
14804	dirMS_041712_NAR_40mM_minus2.12048.12048.3	3	7.96	1	9.22E+04		(K)IIVDELK	(K)I I|V/D E L/K Q E V/I S T S S K(A)		154.43	597.0023	1788.995	-0.003	-1.7	4.68	30149.5	5.96	HUMAN	D6RAC2	Guanine nucleotide-binding protein subunit beta-2-like 1
14805	dirMS_041712_NAR_40mM_minus2.12387.12387.3	3	7.96	0	6.96E+04		(R)VYALPE	(R)V Y/A L/P/E D L/V E V K/P K(M)		156.27	533.9726	1599.899	0.004	2.5	4.68	69862.6	5.58	HUMAN	B4DGB4	Plastin-3
14806	dirMS_041712_NAR_50mM_minus2.11930.11930.3	3	7.96	1	3.61E+05		(K)AVLFCLS	(K)A V|L F/C L/S E D K K(N)	C:Carbamidomethylation	136.03	437.2326	1309.682	0.0012	0.9	6.11	22956	8.8	HUMAN	E9PK25	Cofilin-1
14807	dirMS_041712_NAR_60mM_minus.16566.16566.3	3	7.96	1	1.92E+05		(K)VSEQGL	(K)V/S E Q/G L I E I L K K(V)		152.75	452.9408	1356.81	-0.0018	-1.4	6.11	12899.6	6.59	HUMAN	K7EL31	Programmed cell death protein 5
14808	dirMS_041712_NAR_60mM_minus.18674.18674.3	3	7.96	0	2.97E+05		(K)LHDNLII	(K)L H D N L\I|I/S/D/L E/N T V K(K)		165.95	575.3117	1723.922	-0.0019	-1.1	4.54	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
14809	dirMS_041712_NAR_60mM_minus.18972.18972.3	3	7.96	0	2.97E+05		(K)HNQLPL	(K)H N Q\L P\L/V\I\E/F T E Q T A/P K(I)		168.03	655.6847	1965.044	-0.0045	-2.3	5.4	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
14810	dirMS_041712_NAR_120mM_plus.4663.4663.3	3	7.96	0	8.70E+05		(R)YINTEH	(R)Y/I/N\T E/H G G S Q A R(F)		74.22	444.8857	1332.629	0.0134	10.1	6.75	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
14811	dirMS_041712_NAR_120mM_plus.8704.8704.3	3	7.96	1	4.30E+04		(R)RQQEEL	(R)R\Q Q E E\L|L/A/E E N Q/R(L)		99.1	548.2767	1642.814	0.0012	0.7	4.49	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
14812	dirMS_041712_NAR_20mM_plus.11970.11970.3	3	7.96	0	6.79E+04	M108m	(K)LATQLT	(K)L A\T Q L\T/G/P/V/m/P V R(N)	m:Oxidized methionine	155.43	466.9291	1382.782	15.9903	-3.3	9.75	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
14813	dirMS_041712_NAR_20mM_plus.16273.16273.3	3	7.96	0	4.63E+04	M223m	(K)VLNNmE	(K)V L N N m E I\G T S/L/F D/E E G A K(I)	m:Oxidized methionine	183.37	661.6522	1966.943	15.9994	2.3	4	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
14814	dirMS_041712_NAR_20mM_plus.7984.7984.3	3	7.96	0	4.52E+05	M239m	(K)EVDEQ	(K)E V/D E Q\m/L N V/Q/N K(N)	m:Oxidized methionine	125.12	488.2328	1446.689	15.9945	-0.3	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
14815	dirMS_041712_NAR_20mM_plus.8085.8105.3	3	7.96	0	4.51E+05	M239m	(K)EVDEQ	(K)E V\D E/Q m/L/N V Q/N K(N)	m:Oxidized methionine	125.13	488.2328	1446.689	15.9945	-0.3	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
14816	dirMS_041712_NAR_30mM_plus2.12455.12455.2	2	7.96	0	4.64E+05		(R)QGVDA	(R)Q/G\V/D A/D I/N/G L R(Q)		118.1	579.2997	1157.591	0.0012	1	4.21	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
14817	dirMS_041712_NAR_30mM_plus2.20656.20656.2	2	7.96	1	3.42E+05		(R)LGRGLEI	(R)L G R/G L E/L A E V K(S)		162.05	592.8453	1184.7	-0.0164	-13.9	6.14	197734.4	8.99	HUMAN	Q9BY89	Uncharacterized protein KIAA1671
14818	dirMS_041712_NAR_30mM_plus2.20797.20797.2	2	7.96	0	1.27E+05		(K)SVVTSIF	(K)S V|V/T S I F G V K(N)		162.85	518.799	1036.604	-0.013	-12.5	8.47	132902.3	5.82	HUMAN	J3KR24	Isoleucine--tRNA ligase, cytoplasmic
14819	dirMS_041712_NAR_50mM_plus2.12267.12267.3	3	7.96	1	1.70E+05		(K)DVDEAY	(K)D V/D/E A Y M N K V/E L E/S R(L)		132.47	599.9499	1797.832	0.0028	1.6	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)

14820	dirMS_041712_NAR_50mM_plus2.6823.6823.3	3	7.96	1	1.30E+05		(K)EETQPP	(K)E E\T Q/P/P V/A L K/K(E)		100.88	413.9019	1239.694	-0.0032	-2.6	6.24	45021.6	8.74	HUMAN	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein
14821	dirMS_041712_NAR_50mM_plus2.9312.9312.3	3	7.96	1	1.90E+05		(R)EVLEKQ	(R)E V|L E K Q\P V|L/S Q/T E A R(D)		116.27	576.3137	1726.933	-0.0068	-4	4.79	29260.8	5.72	HUMAN	P28070	Proteasome subunit beta type-4
14822	dirMS_041712_NAR_60mM_plus.12299.12299.3	3	7.96	1	9.36E+05		(R)LSFDKD	(R)L/S/F D/K/D/A M V/A R(A)		121.18	418.2158	1252.635	-0.0026	-2.1	5.96	35556.4	9.3	HUMAN	F2Z393	Transaldolase
14823	dirMS_041712_NAR_60mM_plus.15976.15976.3	3	7.96	1	2.52E+05		(R)TSFLDD	(R)T S/F/L/D D A F R K(N)		139.92	400.5399	1199.605	-0.0004	-0.3	5.62	21195.7	6.97	HUMAN	H0YJ21	Cytoplasmic dynein 1 heavy chain 1 (Fragment)
14824	dirMS_041712_NAR_60mM_plus.17135.17135.3	3	7.96	0	9.90E+05		(R)QIFHPE	(R)Q I F H P E/Q/L/I/T G K(E)		146.82	470.9225	1410.774	-0.021	-14.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
14825	dirMS_041712_NAR_60mM_plus.19504.19504.3	3	7.96	0	1.33E+05		(R)NSVSNF	(R)N S|V/S/N F/L/H S L E R(G)		161.23	468.2401	1402.707	-0.0016	-1.1	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
14826	dirMS_041712_NAR_60mM_plus.5554.5554.3	3	7.96	0	3.12E+05	S6s	(-)MEFNPs	(-)M/E/F N P\s/D H P/R(A)	s:N-acetylglucosamine (S)	87.4	478.2118	1229.537	203.0841	3.3	5.3	33586.7	7.86	HUMAN	Q8ND76-3	Isoform 3 of Cyclin-Y
14827	dirMS_041712_NAR_60mM_plus.7441.7441.3	3	7.96	0	5.01E+05		(R)SSGHSS	(R)S S G H S\S S E\L|S|P D A V E K(A)		96.95	539.584	1616.74	-0.0024	-1.5	4.65	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
14828	dirMS_041712_NAR_120mM_minus.6232.6232.3	3	7.95	1	1.08E+05		(K)ISQRDE	(K)I/S/Q R/D E N/G/E L R(L)		88.63	439.5579	1316.655	0.0038	2.9	4.68	59955.3	4.28	HUMAN	O15355	Protein phosphatase 1G
14829	dirMS_041712_NAR_40mM_minus2.12028.12028.3	3	7.95	0	1.48E+05		(K)AAPEAS	(K)A A/P E A S S/P P A S P L Q H L L/P G K(A)		154.52	656.6876	1968.055	-0.0067	-3.4	6.79	84649.8	5.82	HUMAN	Q96TA1	Niban-like protein 1
14830	dirMS_041712_NAR_50mM_minus2.12890.12890.3	3	7.95	1	2.33E+05		(R)QATKDA	(R)Q A T K D A G T\I A/G L/N/V L R(I)		140.57	543.3085	1627.913	-0.0016	-1	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
14831	dirMS_041712_NAR_50mM_minus2.8399.8399.3	3	7.95	1	1.94E+05		(K)GILAAD	(K)G I/L/A/A/D E S/T G S I A K R(L)		115.23	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
14832	dirMS_041712_NAR_60mM_minus.14038.14038.3	3	7.95	0	2.45E+05		(R)VLVVHD	(R)V/L|V/V/H D G F E G L A K(G)		138.57	461.9241	1383.763	-0.0053	-3.9	5.32	18719.9	6.91	HUMAN	F8VP00	6-phosphofructokinase, muscle type (Fragment)
14833	dirMS_041712_NAR_60mM_minus.15401.15401.3	3	7.95	1	3.11E+04		(R)VEKIPG	(R)V E K I/P G G I|I/E/D/S C V\L R(G)	C:Carbamidomethylation	144.78	595.6552	1784.958	-0.0064	-3.6	4.68	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
14834	dirMS_041712_NAR_60mM_minus.18132.18132.3	3	7.95	1	5.46E+05		(K)IKTLFPL	(K)I K T L F|P/L/I E/A K(K)		162.7	424.9345	1272.793	-0.0036	-2.9	8.59	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
14835	dirMS_041712_NAR_60mM_minus.4650.4650.3	3	7.95	1	6.72E+04		(R)AAEEED	(R)A A/E\E/E/D E A D/P/K R(Q)		77.55	453.872	1359.602	-0.0008	-0.6	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
14836	dirMS_041712_NAR_120mM_plus.10450.10450.3	3	7.95	1	2.43E+05		(R)LRQLAE	(R)L R Q L A\E E\D/L/A/Q/Q R(A)		107.07	523.949	1569.834	-0.0019	-1.2	4.68	533778	5.74	HUMAN	Q15149	Plectin
14837	dirMS_041712_NAR_120mM_plus.10755.10755.3	3	7.95	1	1.21E+06		(R)EKLEME	(R)E K L E M E/M E/A/A/R(H)		109.52	446.2171	1336.623	0.0132	9.9	4.49	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)
14838	dirMS_041712_NAR_120mM_plus.20288.20288.4	4	7.95	1	3.55E+07		(K)AAIDWF	(K)A A|I/D/W/F D G K E F H G N I I K(V)		159.08	491.0027	1960.992	-0.0026	-1.3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
14839	dirMS_041712_NAR_120mM_plus.8027.8027.2	2	7.95	0	4.64E+05		(K)STTTGH	(K)S T/T/T/G/H L/I/Y K(C)		95.25	560.8014	1120.6	-0.0042	-3.7	8.34	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
14840	dirMS_041712_NAR_20mM_plus.10876.10876.2	2	7.95	0	6.91E+04		(K)LSELEPG	(K)L S E\L/E|P G T/G D/L R(F)		147.3	643.8371	1286.659	0.0083	6.4	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
14841	dirMS_041712_NAR_20mM_plus.12688.12688.2	2	7.95	0	2.75E+04		(K)YDGIILP	(K)Y D|G I/I/L|P G/K(-)		160.08	488.2764	975.551	-0.0054	-5.6	5.83	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
14842	dirMS_041712_NAR_20mM_plus.12997.12997.2	2	7.95	0	4.94E+05	M1m N6n	(-)mPLFPnL	(-)m P|L F|P n L/P R(L)	m:Oxidized methionine n:N-	162.05	652.3439	1084.597	219.0833	6.9	9.5	39133.5	4.5	HUMAN	Q8TD91-2	Isoform 2 of Melanoma-associated antigen C3
14843	dirMS_041712_NAR_20mM_plus.14362.14362.3	3	7.95	0	3.00E+04	M61m	(R)IIPGFm	(R)I I|P/G F m C Q/G G D/F T R(H)	C:Carbamidomethylation m:Oxid	170.67	538.9176	1598.745	15.9929	-1.3	5.84	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
14844	dirMS_041712_NAR_20mM_plus.16607.16607.2	2	7.95	0	1.46E+05		(K)TVDNFV	(K)T V|D\N F/V/A L A T G E K(G)		185.95	682.8565	1364.706	0.0001	0.1	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
14845	dirMS_041712_NAR_30mM_plus2.12948.12966.2	2	7.95	0	1.46E+05		(K)YALSVG	(K)Y/A|L/S/V/G Y R(H)		121	464.7467	928.489	-0.0026	-2.8	8.59	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
14846	dirMS_041712_NAR_30mM_plus2.13194.13194.2	2	7.95	0	1.13E+06		(K)NDLAVV	(K)N D|L/A|V V/D/V R(I)		121.8	500.7769	1000.542	0.0043	4.3	4.21	76670.1	4.6	HUMAN	P19338	Nucleolin
14847	dirMS_041712_NAR_30mM_plus2.15836.15836.2	2	7.95	0	3.25E+05		(R)FDVSGY	(R)F D|V/S/G/Y/P T I K(I)		136.32	563.7923	1126.578	-0.0006	-0.5	5.83	73273.4	4.96	HUMAN	P13667	Protein disulfide-isomerase A4
14848	dirMS_041712_NAR_30mM_plus2.16677.16677.2	2	7.95	0	1.33E+06		(R)AALQELI	(R)A A/L/Q|E/L/L/S K(G)		139.22	486.7894	972.572	-0.0009	-0.9	6.05	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
14849	dirMS_041712_NAR_30mM_plus2.20122.20122.2	2	7.95	0	1.22E+04		(R)ALDTM	(R)A L|D|T M|N/F D V\I K(G)		159.3	633.8315	1266.64	0.0159	12.5	4.21	68197.9	9.58	HUMAN	B1ANR0	Poly(A) binding protein, cytoplasmic 4 (Inducible form)
14850	dirMS_041712_NAR_30mM_plus2.6015.6015.2	2	7.95	0	1.06E+05		(K)MGGDI	(K)M/G/G/D/I/A N R(V)		85.85	417.2016	833.393	0.0025	3	5.59	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
14851	dirMS_041712_NAR_50mM_plus2.12290.12290.3	3	7.95	1	2.80E+05		(R)ESDVPL	(R)E S/D V/P L K|T E E F\E V T K(T)		132.68	584.2981	1750.874	0.0052	3	4.25	18909	6.21	HUMAN	Q969H8	UPF0556 protein C19orf10
14852	dirMS_041712_NAR_60mM_plus.18051.18051.3	3	7.95	0	2.19E+04		(K)ACQSIY	(K)A C/Q|S I Y P L H D V F V/R(K)	C:Carbamidomethylation	152.08	568.9563	1704.853	0.0017	1	6.79	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
14853	dirMS_041712_NAR_60mM_plus.18251.18251.3	3	7.95	1	7.30E+05		(K)QLDDLK	(K)Q|L/D D L/K V/E\L/S Q L R(V)		153.58	519.6254	1556.864	-0.0026	-1.7	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
14854	dirMS_041712_NAR_30mM_minus2.13852.13852.2	2	7.94	0	4.88E+04		(K)EYTLDV	(K)E Y/T/L/D/V/Y R(L)		128.87	529.7691	1058.515	0.0156	14.8	4.37	59484.7	6.61	HUMAN	P54577	Tyrosine--tRNA ligase, cytoplasmic
14855	dirMS_041712_NAR_40mM_minus2.15827.15827.3	3	7.94	0	6.75E+05		(K)GLAPDLI	(K)G L|A/P D/L P E D L Y H\L I K(K)		184.57	565.3111	1693.916	0.0028	1.7	4.54	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
14856	dirMS_041712_NAR_50mM_minus2.8828.8828.3	3	7.94	1	1.04E+05	M477m	(R)TLKIPA	(R)T L/K I/P A\m/T/I A/K(N)	m:Oxidized methionine	118.22	401.5779	1186.723	15.9964	1.2	10	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
14857	dirMS_041712_NAR_120mM_plus.10777.10777.3	3	7.94	1	4.83E+06	S306s	(R)DHHMS	(R)D H/H M S G W s|Y/K R V E K(S)	s:N-acetylglucosamine (S)	108.9	654.972	1759.833	203.0681	-5.7	8.51	51648.4	5.55	HUMAN	B7XGB9	Protein phosphatase 1M
14858	dirMS_041712_NAR_20mM_plus.12606.12606.3	3	7.94	0	3.48E+05		(K)IISNASC	(K)I I\S N|A S C T T/N C L A|P L/A K(V)	C:Carbamidomethylation	159.53	611.9768	1833.92	-0.0039	-2.1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
14859	dirMS_041712_NAR_20mM_plus.12829.12829.2	2	7.94	0	3.64E+05		(K)LSELEA	(K)L S/E|L/E A/A L Q R(A)		161.65	565.3132	1129.621	-0.002	-1.8	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
14860	dirMS_041712_NAR_20mM_plus.18538.18538.3	3	7.94	0	2.15E+05		(R)LSVEEA	(R)L S V E E A V A A G\V/V/G G E I/Q E K(L)		198.57	629.0001	1884.991	-0.0056	-2.9	4.09	266161	5.68	HUMAN	E9PPU0	Epiplakin
14861	dirMS_041712_NAR_20mM_plus.8996.8996.2	2	7.94	0	2.34E+05		(R)VLTVIN	(R)V/L|T V/I/N Q T Q K(E)		132.9	572.3399	1143.673	-0.0007	-0.6	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
14862	dirMS_041712_NAR_30mM_plus2.20503.20503.2	2	7.94	0	1.73E+05		(K)LGLENAI	(K)L/G L/E/N/A E|A L/I R(L)		161.18	599.8397	1198.679	-0.0069	-5.7	4.53	61411.3	8.74	HUMAN	P10155	60 kDa SS-A/Ro ribonucleoprotein
14863	dirMS_041712_NAR_30mM_plus2.5993.5993.2	2	7.94	0	2.86E+04		(R)TTDGSL	(R)T T\D\G S|L/Q/N|T S S E G S R(L)		85.65	770.3467	1539.688	-0.002	-1.3	4.37	66105.7	7.3	HUMAN	A8MQB8	Fragile X mental retardation protein 1
14864	dirMS_041712_NAR_30mM_plus2.7883.7900.2	2	7.94	0	8.24E+05		(R)DYDDM	(R)D/Y|D|D\M/S P R(R)		95.95	499.6972	998.388	-0.0013	-1.3	3.93	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
14865	dirMS_041712_NAR_40mM_plus2.19093.19093.3	3	7.94	1	3.19E+05		(R)GGPNIIT	(R)G G/P N I/I/T L A D I V K/D P V S R(T)		178.95	622.3522	1865.049	-0.007	-3.8	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
14866	dirMS_041712_NAR_50mM_plus2.15395.15492.3	3	7.94	0	4.51E+06		(R)MGPLGL	(R)M/G/P|L/G L D H M/A S S I E R(M)		150.22	538.6007	1613.777	0.0101	6.3	5.3	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
14867	dirMS_041712_NAR_50mM_plus2.9225.9225.3	3	7.94	1	8.76E+05		(K)TAVCDI	(K)T/A|V C D/I/P P R G L K(M)	C:Carbamidomethylation	116.07	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
14868	dirMS_041712_NAR_30mM_minus2.15639.15639.2	2	7.93	0	1.54E+05		(K)AMTGV	(K)A M/T/G V/E Q|W/P Y/R(A)		138.4	669.3172	1337.631	-0.0036	-2.7	6.04	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
14869	dirMS_041712_NAR_30mM_minus2.17244.17244.2	2	7.93	0	2.65E+05		(K)FEDENFI	(K)F/E/D|E N F I\L/K(H)		147.73	577.7894	1154.573	-0.0013	-1.1	4.14	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
14870	dirMS_041712_NAR_30mM_minus2.6958.6958.2	2	7.93	0	8.10E+04		(R)ESLSEEE	(R)E S/L/S/E/E E A Q/K(M)		92.15	575.2682	1149.527	0.0021	1.9	4.09	57188.9	5.97	HUMAN	H7C3A1	Serrate RNA effector molecule homolog (Fragment)
14871	dirMS_041712_NAR_30mM_minus2.7279.7279.2	2	7.93	0	3.81E+05		(K)QQTLEA	(K)Q\Q/T/L/E|A E E/A/K(R)		93.42	573.7846	1146.564	-0.0018	-1.6	4.25	76925.9	4.46	HUMAN	A8MV58	Drebrin
14872	dirMS_041712_NAR_40mM_minus2.9029.9029.3	3	7.93	0	2.56E+04		(K)AASAGV	(K)A A/S/A/G\V P Y H G E V/P V S L A R(A)		135.53	594.3141	1780.934	-0.0063	-3.5	6.79	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
14873	dirMS_041712_NAR_50mM_minus2.11312.11312.3	3	7.93	1	2.12E+05		(K)MLVSG	(K)M L/V/S/G A G D/I K L T K(D)		132.33	444.9227	1332.756	-0.002	-1.5	8.35	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
14874	dirMS_041712_NAR_50mM_minus2.16181.16181.3	3	7.93	1	4.05E+05		(K)LFTAESL	(K)L F/T/A E S L/I G L K N/P E K(S)		160.43	553.9759	1659.932	-0.0185	-11.1	6.14	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
14875	dirMS_041712_NAR_50mM_minus2.16558.16558.3	3	7.93	0	8.79E+04		(K)VSHLLGI	(K)V/S H L L\G I N V/T/D/F T R(G)		162.08	524.6237	1571.854	0.0025	1.6	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
14876	dirMS_041712_NAR_60mM_minus.14199.14199.3	3	7.93	1	3.30E+05		(R)QATKD	(R)Q A T K D A G T I/A/G L/N V/L/R(I)		138.87	543.3073	1627.913	-0.0052	-3.2	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
14877	dirMS_041712_NAR_120mM_plus.14185.14185.4	4	7.93	1	5.84E+05		(R)LEAPELP	(R)L E|A/P E/L P V K/V/N P T K P R(R)		127.5	447.7616	1788.038	-0.0132	-7.4	8.59	10558	9.4	HUMAN	H0YE28	Protein C11orf31 (Fragment)
14878	dirMS_041712_NAR_120mM_plus.6490.6490.2	2	7.93	0	5.24E+05	M46m	(R)HQGVm	(R)H/Q/G V m\V G M G Q/K(D)	m:Oxidized methionine	87.48	594.2868	1171.571	15.9953	0.3	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
14879	dirMS_041712_NAR_120mM_plus.7540.7540.2	2	7.93	1	1.19E+06		(R)AQYDEL	(R)A Q|Y/D/E L A R K(N)		93.32	547.2874	1093.564	0.0039	3.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
14880	dirMS_041712_NAR_120mM_plus.8317.8317.4	4	7.93	2	3.75E+06		(K)GAVAED	(K)G A V\A/E/D G D E L R T E/P E A K K(S)		97.05	479.4909	1914.94	0.0014	0.8	4.36	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
14881	dirMS_041712_NAR_30mM_plus2.14167.14167.2	2	7.93	0	1.46E+06		(K)TIDPELL	(K)T I|D/P E L/L/G K(M)		127.55	493.2867	985.556	0.0097	9.8	4.37	60786.2	8.94	HUMAN	B4DYH8	N-acetylglucosamine-6-sulfatase
14882	dirMS_041712_NAR_40mM_plus2.12782.12782.3	3	7.93	1	3.04E+05		(R)VLELVSI	(R)V L|E L/V/S I T A N/K N T C P G\D R(S)	C:Carbamidomethylation	142.37	663.0201	1987.028	0.018	9.1	6.04	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
14883	dirMS_041712_NAR_40mM_plus2.15157.15157.3	3	7.93	0	1.21E+05		(R)QVVQGI	(R)Q V\V|Q|G L\L/S E/T Y/L E A H R(I)		155.78	614.9934	1842.971	-0.0052	-2.8	5.4	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
14884	dirMS_041712_NAR_40mM_plus2.17906.17906.3	3	7.93	0	1.24E+05		(R)GFGFITF	(R)G F/G F/I/T\F/T N/P E H A S V A M R(A)		172.02	661.3289	1981.959	0.0133	6.7	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
14885	dirMS_041712_NAR_50mM_plus2.18574.18574.3	3	7.93	0	1.81E+05		(K)ASVITQ	(K)A S/V/I/T Q V/F H V/P L E E R(K)		166.42	575.6533	1724.933	0.0124	7.2	5.4	24511.6	6.62	HUMAN	C9J5E5	Vigilin (Fragment)
14886	dirMS_041712_NAR_50mM_plus2.9739.9739.3	3	7.93	0	5.62E+05		(R)DNIQGI	(R)D N/I/Q/G\I T K/P A/I R(R)		117.37	442.5902	1325.754	0.0025	1.9	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
14887	dirMS_041712_NAR_60mM_plus.13753.13754.3	3	7.93	1	1.40E+06		(R)EMDRET	(R)E M/D R E T/L|I/D/V A R(T)		128.93	483.2457	1447.721	0.0016	1.1	4.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
14888	dirMS_041712_NAR_60mM_plus.20812.20812.3	3	7.93	1	2.71E+05		(K)CKIPALD	(K)C K I/P A/L|D L/L I K(L)	C:Carbamidomethylation	169.63	428.5975	1283.776	0.0024	1.9	8.59	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
14889	dirMS_041712_NAR_120mM_minus.20227.20227.3	3	7.92	0	2.29E+05		(K)KPGGFD	(K)K P|G G\F D\I/S/L/F Y/R(D)		166.37	467.2504	1399.737	-0.0002	-0.2	8.59	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
14890	dirMS_041712_NAR_120mM_minus.7317.7317.3	3	7.92	1	1.49E+06		(R)CREMD	(R)C R E\M/D|E/Q/I/R(L)	C:Carbamidomethylation	93.97	412.8591	1236.546	0.0168	13.6	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
14891	dirMS_041712_NAR_120mM_minus.8397.8397.4	4	7.92	1	1.31E+05		(R)LLSDAT	(R)L L S/D/A T V E K D/E S H A G/K(V)		100.08	425.7181	1699.85	0.0009	0.5	4.75	40240.9	6.39	HUMAN	Q14320	Protein FAM50A
14892	dirMS_041712_NAR_30mM_minus2.11885.11885.2	2	7.92	0	9.21E+05		(K)EVDEQ	(K)E V|D E/Q M L|N V Q/N K(N)		117.53	723.8476	1446.689	-0.0014	-1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
14893	dirMS_041712_NAR_30mM_minus2.17591.17591.2	2	7.92	1	2.08E+05	M799m	(K)DLLmND	(K)D L|L m/N D R L P G K(K)	m:Oxidized methionine	149.75	644.3426	1271.678	16.0003	4.2	5.96	165919.5	8.96	HUMAN	Q9NTI5	Sister chromatid cohesion protein PDS5 homolog B
14894	dirMS_041712_NAR_40mM_minus2.13513.13513.3	3	7.92	1	3.72E+04		(K)VTLVVG	(K)V T|L/V/V G A/S Q D I I/P Q L K K(K)		163.58	603.696	1809.084	-0.011	-6.1	8.56	25180.2	5.34	HUMAN	E7EMS6	Catechol O-methyltransferase (Fragment)
14895	dirMS_041712_NAR_40mM_minus2.8148.8148.3	3	7.92	0	2.15E+05	M35m	(K)AASDIA	(K)A A/S D I/A m T/E/L/P/P T H P I R(L)	m:Oxidized methionine	128.43	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
14896	dirMS_041712_NAR_40mM_minus2.9534.9534.3	3	7.92	0	2.91E+04	M5m	(R)EmQDVI	(R)E m/Q/D/V D L A E V K/P L V E K(G)	m:Oxidized methionine	138.73	620.3199	1842.952	15.9934	-0.8	4.18	18328.6	4.58	HUMAN	E5RGM5	Protein NDRG1 (Fragment)
14897	dirMS_041712_NAR_50mM_minus2.7437.7437.3	3	7.92	1	3.43E+04		(K)ATQPET	(K)A T Q|P/E/T/T E E V T D L K R(Q)		109.37	573.2875	1717.86	-0.0123	-7.2	4.41	72152.1	5.27	HUMAN	A0MZ66	Shootin-1
14898	dirMS_041712_NAR_50mM_minus2.8718.8718.3	3	7.92	1	1.53E+05		(K)SPFEVS	(K)S/P/F/E V S V D K/A\Q G D A S K(V)		117.75	555.6099	1664.813	0.0025	1.5	4.56	258215.9	5.48	HUMAN	E7EN95	Filamin-B
14899	dirMS_041712_NAR_60mM_minus.14224.14224.3	3	7.92	1	2.27E+05		(R)TFNTST	(R)T F/N/T\S T/G G L/L L/P S D T K R(S)		138.82	603.3262	1807.955	0.0092	5.1	8.41	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
14900	dirMS_041712_NAR_60mM_minus.15010.15011.3	3	7.92	0	1.11E+06		(R)AMGIET	(R)A M G/I E T S D I|A D V/P S D T S K(N)		142.85	612.9513	1836.853	-0.0138	-7.5	3.84	136983.7	6.37	HUMAN	E2QRH8	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-4
14901	dirMS_041712_NAR_60mM_minus.15121.15121.3	3	7.92	1	2.35E+04		(K)IREIADG	(K)I R E I A D G\L/C/L E V/E/G K(M)	C:Carbamidomethylation	143.95	567.965	1701.884	-0.0035	-2.1	4.41	18253.3	4.7	HUMAN	E9PJF7	Translationally-controlled tumor protein (Fragment)
14902	dirMS_041712_NAR_60mM_minus.17910.17910.3	3	7.92	1	4.58E+05		(R)KVESLQI	(R)K V E|S L/Q|E\E/I A F L K(K)		160.27	511.9529	1533.852	-0.0081	-5.3	4.79	49709.6	5.19	HUMAN	B0YJC4	Vimentin
14903	dirMS_041712_NAR_60mM_minus.6604.6604.3	3	7.92	0	5.20E+04		(R)ATAPQT	(R)A T A/P Q\T Q/H V/S P M/R(Q)		95.48	475.2404	1423.711	-0.0044	-3.1	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
14904	dirMS_041712_NAR_120mM_plus.13443.13443.4	4	7.92	1	1.27E+06		(K)DKFNEC	(K)D K F\N\E\C/G H V\L Y A D/I K(M)	C:Carbamidomethylation	123.87	452.9713	1808.864	-0.0002	-0.1	5.38	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
14905	dirMS_041712_NAR_120mM_plus.4124.4124.3	3	7.92	1	1.49E+07	M310m	(R)TKTEISE	(R)T K/T E\I|S/E m N R(N)	m:Oxidized methionine	69.7	408.8687	1208.594	15.9976	2.2	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
14906	dirMS_041712_NAR_120mM_plus.8779.8907.2	2	7.92	0	8.36E+05		(K)HFVALS	(K)H/F|V/A L/S T N T\T\K(V)		99.1	609.8311	1218.648	0.0072	5.9	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
14907	dirMS_041712_NAR_20mM_plus.11402.11402.2	2	7.92	0	3.45E+05		(K)LITPAVV	(K)L I|T|P A/V V S E/R(L)		151	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
14908	dirMS_041712_NAR_20mM_plus.15127.15127.2	2	7.92	0	9.49E+04		(K)AILFVPR	(K)A I|L|F V P R(R)		176.08	408.2606	815.514	0.0001	0.2	9.79	57660.2	6.38	HUMAN	Q9NQH7	Probable Xaa-Pro aminopeptidase 3
14909	dirMS_041712_NAR_20mM_plus.16677.16677.2	2	7.92	0	1.68E+05		(K)TVDNFV	(K)T V|D N/F/V/A L A T G E K(G)		186.03	682.8565	1364.706	0.0001	0.1	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
14910	dirMS_041712_NAR_20mM_plus.9997.9997.2	2	7.92	0	1.56E+05		(K)YQAVTA	(K)Y Q|A|V/T A T L E E K(R)		139.92	626.8223	1252.642	-0.0046	-3.7	4.53	23633.9	11.02	HUMAN	P40429	60S ribosomal protein L13a
14911	dirMS_041712_NAR_30mM_plus2.18330.18543.2	2	7.92	0	5.63E+05		(K)TLVLLM	(K)T L|V|L/L/M/G K(E)		150.3	437.774	874.543	-0.0023	-2.6	8.41	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
14912	dirMS_041712_NAR_30mM_plus2.5735.5735.2	2	7.92	0	1.69E+05	M57m	(K)EmGTPD	(K)E m|G T/P/D/V R(I)	m:Oxidized methionine	84.38	460.7158	904.419	16.005	11	4.37	15175.4	10.46	HUMAN	B7Z4C8	60S ribosomal protein L31
14913	dirMS_041712_NAR_40mM_plus2.10041.10041.2	2	7.92	0	2.43E+05		(K)EQFAW	(K)E Q/F/A/W/R(H)		122.9	418.706	836.405	-0.0002	-0.3	6.1	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
14914	dirMS_041712_NAR_40mM_plus2.10943.10943.3	3	7.92	1	1.72E+05		(R)DGKLVS	(R)D G/K L V S E/S/S/D/V L/P K(-)		129.73	491.9315	1473.78	0.0004	0.3	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
14915	dirMS_041712_NAR_40mM_plus2.12956.12956.2	2	7.92	0	3.87E+04		(R)AALQELI	(R)A/A/L|Q E L L/S K(G)		142.18	486.7911	972.572	0.0025	2.6	6.05	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
14916	dirMS_041712_NAR_40mM_plus2.15954.15954.3	3	7.92	0	2.95E+05		(K)VAIVKP	(K)V A/I V K P G\V|P M E/I V L/N K(E)		160.92	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
14917	dirMS_041712_NAR_40mM_plus2.17714.17714.3	3	7.92	1	1.96E+05		(R)LKLPSIP	(R)L K L P\S I/P L\V/P V S A Q K(R)		170.73	530.671	1589.999	-0.0004	-0.3	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
14918	dirMS_041712_NAR_50mM_plus2.11391.11391.3	3	7.92	1	2.80E+06	M72m	(R)TEmENE	(R)T\E|m/E N E F/V L I/K K(D)	m:Oxidized methionine	127.98	499.5943	1480.772	15.9968	1.2	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
14919	dirMS_041712_NAR_50mM_plus2.21455.21455.3	3	7.92	1	3.90E+05	M145m	(R)GVmLA	(R)G V/m/L A/V D A V I A E/L\K K(Q)	m:Oxidized methionine	182.6	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
14920	dirMS_041712_NAR_60mM_plus.11761.11761.2	2	7.92	0	1.31E+06		(R)FAQHGT	(R)F A Q/H/G\T\F E/Y|E Y S Q R(W)		118.65	881.8928	1762.782	-0.0037	-2.1	5.4	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
14921	dirMS_041712_NAR_120mM_minus.13814.13814.3	3	7.91	1	5.35E+05		(K)ASIHEA	(K)A S I/H\E A\W\T D/G K E A M/L K(H)		130.1	596.2973	1786.879	-0.0019	-1.1	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
14922	dirMS_041712_NAR_120mM_minus.20420.20420.4	4	7.91	0	2.45E+05		(K)ALEHAF	(K)A L E H/A F Q L E H/I/M D/L T/R(L)		167.78	481.7478	1923.975	-0.0052	-2.7	5.27	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
14923	dirMS_041712_NAR_120mM_minus.6187.6187.3	3	7.91	0	1.54E+05		(K)IAGHPL	(K)I/A G H/P L A/Q N E R(C)		87.88	402.5466	1205.639	-0.0133	-11	6.75	18455.6	6.76	HUMAN	F8W8K5	Sorting nexin-12
14924	dirMS_041712_NAR_120mM_minus.6872.6872.2	2	7.91	0	1.12E+05		(R)ITEFCHR	(R)I/T E F C H/R(F)	C:Carbamidomethylation	91.57	481.7295	962.451	0.0005	0.5	6.75	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
14925	dirMS_041712_NAR_20mM_minus.10305.10305.2	2	7.91	0	9.31E+03		(R)VILEIDN	(R)V I|L/E I/D/N/A R(L)		152.68	521.7964	1042.589	-0.0036	-3.5	4.37	19213.2	4.66	HUMAN	K7EMD9	Keratin, type I cytoskeletal 13 (Fragment)
14926	dirMS_041712_NAR_30mM_minus2.10898.10898.2	2	7.91	0	3.92E+05		(R)NGDFLP	(R)N/G|D/F/L/P T|R(L)		112.67	460.2363	919.463	0.0021	2.3	5.84	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
14927	dirMS_041712_NAR_50mM_minus2.12680.12697.3	3	7.91	0	2.16E+05		(R)LVVVLC	(R)L/V|V V|L/C N L K P Q K(M)	C:Carbamidomethylation	140.23	470.9508	1410.85	-0.0123	-8.7	10	59484.7	6.61	HUMAN	P54577	Tyrosine--tRNA ligase, cytoplasmic
14928	dirMS_041712_NAR_60mM_minus.17339.17339.3	3	7.91	0	3.22E+05		(K)GSDHSA	(K)G S D H S A\S L\E/P/G E\L A E L V R(S)		156.83	622.9764	1866.919	-0.0045	-2.4	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)

14929	dirMS_041712_NAR_120mM_plus.6474.6474.2	2	7.91	0	4.57E+05		(K)HQPTAII	(K)H/Q|P T A/I\I A/K(T)		87.75	489.7897	978.573	-0.001	-1	8.76	63448.4	7.29	HUMAN	B4E022	Transketolase
14930	dirMS_041712_NAR_30mM_plus2.14519.14519.2	2	7.91	0	5.73E+05		(K)CCSGAII	(K)C C|S G A I I/V/L/T/K(S)	C:Carbamidomethylation	128.2	611.3189	1221.633	-0.0025	-2	8.75	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
14931	dirMS_041712_NAR_30mM_plus2.16643.16643.2	2	7.91	0	3.08E+05		(R)SIQADG	(R)S I/Q/A/D/G L V W G S S\K(L)		140.3	674.3475	1347.69	-0.0026	-1.9	5.55	24934.4	4.5	HUMAN	P24534	Elongation factor 1-beta
14932	dirMS_041712_NAR_30mM_plus2.8150.8150.2	2	7.91	0	5.70E+05		(K)LAQLEE	(K)L/A|Q/L E/E A K(Q)		97.12	451.2545	901.499	0.0028	3.1	4.53	28965.2	9.43	HUMAN	P24539	ATP synthase subunit b, mitochondrial
14933	dirMS_041712_NAR_40mM_plus2.19027.19027.3	3	7.91	1	6.36E+03		(R)VISGVL	(R)V I|S G V/L Q L/G N I V F K K(E)		178.52	539.0014	1614.994	-0.0045	-2.8	10	227783.5	5.5	HUMAN	P35579	Myosin-9
14934	dirMS_041712_NAR_40mM_plus2.7499.7499.2	2	7.91	0	1.91E+05		(R)SGYFDE	(R)S/G\Y/F D/E R(Y)		104.13	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
14935	dirMS_041712_NAR_50mM_plus2.15306.15306.3	3	7.91	1	8.89E+05		(R)GDVVPK	(R)G D\V|V|P K D V N A\A I/A T I K(T)		148.05	537.6393	1610.911	-0.0079	-4.9	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
14936	dirMS_041712_NAR_60mM_plus.5461.5461.3	3	7.91	1	1.34E+05		(K)CDSSPD	(K)C D/S S/P D S/A/E D/V R K(V)	C:Carbamidomethylation	86.15	489.2128	1465.622	0.0015	1	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
14937	dirMS_041712_NAR_20mM_minus.10327.10327.2	2	7.9	0	9.30E+04		(R)NTGIICT	(R)N T|G\I/I/C T I/G/P A\S/R(S)	C:Carbamidomethylation	152.63	680.3561	1359.705	0	0	9.75	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
14938	dirMS_041712_NAR_20mM_minus.12210.12210.3	3	7.9	0	5.02E+05	M256m	(R)SLDmDS	(R)S L D m D\S\I/I A E/V K(A)	m:Oxidized methionine	171.03	446.227	1320.671	15.9949	0	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
14939	dirMS_041712_NAR_20mM_minus.7089.7089.2	2	7.9	0	4.77E+05	M281m	(R)AEAESm	(R)A E|A|E/S m Y Q I/K(Y)	m:Oxidized methionine	117.9	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
14940	dirMS_041712_NAR_30mM_minus2.11506.11506.2	2	7.9	0	2.45E+04		(K)FSASGEL	(K)F S|A/S G E L/G/N\G N I K(L)		116.38	647.3253	1293.643	0	0	6	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
14941	dirMS_041712_NAR_30mM_minus2.11613.11613.2	2	7.9	0	8.32E+05		(K)LVSESSD	(K)L V|S E S/S D\V L/P K(-)		115.87	587.3211	1173.636	-0.0012	-1	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
14942	dirMS_041712_NAR_30mM_minus2.14523.14548.2	2	7.9	0	2.50E+05		(R)YYFEGIK	(R)Y/Y|F/E/G I/K(Q)		132.45	460.2363	919.456	0.0093	10.1	6	23092.1	6.93	HUMAN	G3V438	Activator of 90 kDa heat shock protein ATPase homolog 1 (Fragment)
14943	dirMS_041712_NAR_30mM_minus2.15285.15285.2	2	7.9	0	4.79E+04		(K)LCDFGF	(K)L/C|D F/G F A R(A)	C:Carbamidomethylation	135.8	493.2343	985.456	0.0053	5.4	5.84	143554.7	5.57	HUMAN	A8MU99	Serine/threonine-protein kinase 36
14944	dirMS_041712_NAR_30mM_minus2.5416.5416.2	2	7.9	0	9.57E+04		(K)DSYVGD	(K)D S Y/V/G D E A Q S K(R)		83.82	599.7632	1198.522	-0.0031	-2.6	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
14945	dirMS_041712_NAR_30mM_minus2.6180.6180.2	2	7.9	0	4.42E+04		(K)SSSPLSS	(K)S S/S|P L/S S T\R(S)		87.13	461.2392	921.464	0.0075	8.2	9.47	55757.3	5.55	HUMAN	O94919	Endonuclease domain-containing 1 protein
14946	dirMS_041712_NAR_30mM_minus2.9760.9760.2	2	7.9	0	1.91E+05	M129m	(K)ILYSQCG	(K)I L|Y|S Q/C G D V m R(A)	C:Carbamidomethylation m:Oxid	107.67	679.3145	1341.629	15.9928	-1.6	5.83	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
14947	dirMS_041712_NAR_40mM_minus2.15583.15583.3	3	7.9	1	6.69E+05		(K)LLPLVSD	(K)L L/P L V/S D E V F I R D V A K(V)		180.35	605.3511	1814.042	-0.0035	-1.9	4.56	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
14948	dirMS_041712_NAR_50mM_minus2.8981.8981.3	3	7.9	1	1.31E+05	M227m	(R)mQKEIT	(R)m Q K E I T|A|L|A/P S/T M K(I)	m:Oxidized methionine	119.48	522.2727	1548.812	15.9911	-2.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
14949	dirMS_041712_NAR_120mM_plus.5568.5568.4	4	7.9	1	4.14E+05		(K)VGGTSD	(K)V G G T/S D\V/E/V N/E K K D/R(V)		82.25	408.9601	1632.819	-0.0002	-0.1	4.78	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
14950	dirMS_041712_NAR_120mM_plus.8193.8193.3	3	7.9	1	2.71E+06		(R)AAPGAE	(R)A A/P G A/E F/A/P N/K R(R)		96.73	410.2196	1228.643	0.001	0.8	8.79	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
14951	dirMS_041712_NAR_20mM_plus.14309.14309.2	2	7.9	0	1.12E+05	S414s	(R)NVLsAG	(R)N V L/s A G G S G/E/V/K(A)	s:N-acetylglucosamine (S)	170.03	660.839	1117.585	203.0859	5	6	141906.6	5.55	HUMAN	G5E9Z3	NIMA (Never in mitosis gene a)-related kinase 1, isoform CRA_e
14952	dirMS_041712_NAR_20mM_plus.8601.8601.2	2	7.9	0	1.50E+05		(K)TAVCDI	(K)T A|V/C|D/I/P\P R(G)	C:Carbamidomethylation	129.58	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
14953	dirMS_041712_NAR_30mM_plus2.10422.10422.2	2	7.9	0	5.36E+04		(K)TAVCDI	(K)T A|V|C D I|P|P R(G)	C:Carbamidomethylation	108.98	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
14954	dirMS_041712_NAR_30mM_plus2.10593.10593.2	2	7.9	0	3.64E+05		(K)TGTVSL	(K)T G/T/V/S/L E/V/R(L)		109.23	481.2676	961.531	-0.0034	-3.5	5.66	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
14955	dirMS_041712_NAR_30mM_plus2.13576.13576.2	2	7.9	0	7.98E+05		(K)DLSELG	(K)D L/S/E/L/G S/V/R(T)		125.25	488.2554	975.511	-0.007	-7.2	4.37	533778	5.74	HUMAN	Q15149	Plectin
14956	dirMS_041712_NAR_30mM_plus2.14497.14497.2	2	7.9	0	2.43E+05		(K)IVVLLQ	(K)I V|V|L L/Q R(L)		128.43	420.7864	840.567	-0.001	-1.2	9.75	28772.3	6.28	HUMAN	A6NJG9	Proteasome activator complex subunit 1
14957	dirMS_041712_NAR_30mM_plus2.21574.21574.2	2	7.9	0	3.33E+05		(R)NSYLEV	(R)N S|Y/L/E/V L L K(L)		168.02	539.8092	1078.614	-0.0032	-2.9	6	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
14958	dirMS_041712_NAR_50mM_plus2.17958.17958.3	3	7.9	0	1.06E+06		(K)ALSAIA	(K)A L|S A I/A D/L\L/T N E H E R(V)		163.55	551.6254	1652.86	0.0014	0.9	4.65	105417.2	6.41	HUMAN	C9JZR2	Catenin delta-1
14959	dirMS_041712_NAR_50mM_plus2.8122.8122.3	3	7.9	1	2.64E+05	M227m M	(R)mQKEIT	(R)m Q K E I T\A\L|A/P S T m K(I)	m:Oxidized methionine	108.98	527.6045	1548.812	31.9865	-2.1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
14960	dirMS_041712_NAR_60mM_plus.9684.9684.3	3	7.9	0	9.53E+05		(K)GHENVE	(K)G H E N V/E A\A|Q/A/E Y/I/E K(F)		107.98	563.2692	1687.792	0.0008	0.5	4.48	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
14961	dirMS_041712_NAR_120mM_minus.17194.17194.4	4	7.89	1	5.17E+05		(K)YYVTIID	(K)Y Y\V T I/I/D/A/P G H R D F I K(N)		147.97	477.7556	1908.001	-0.0008	-0.4	6.75	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
14962	dirMS_041712_NAR_120mM_minus.6690.6690.4	4	7.89	1	2.10E+05		(K)LNLLGR	(K)L/N L L G\R\C N Y S Q/S E R(N)	C:Carbamidomethylation	90.75	428.221	1709.839	0.0234	13.7	8.75	115909.2	9.41	HUMAN	C9J6P4	Zinc finger CCCH-type antiviral protein 1
14963	dirMS_041712_NAR_20mM_minus.10790.10790.3	3	7.89	0	1.40E+05		(K)VNQIGS	(K)V N Q I\G S V/T|E/S I/Q A/C K(L)	C:Carbamidomethylation	155.38	545.2807	1633.821	0.0062	3.8	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
14964	dirMS_041712_NAR_30mM_minus2.18940.18940.2	2	7.89	0	2.35E+05		(K)MAILQI	(K)M/A|I/L/Q I M K(E)		158.08	474.2745	947.542	0.0001	0.1	8.5	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
14965	dirMS_041712_NAR_30mM_minus2.7196.7196.2	2	7.89	0	3.86E+05		(K)QQTLEA	(K)Q Q/T L/E/A/E E/A K(R)		93.4	573.7846	1146.564	-0.0018	-1.6	4.25	76925.9	4.46	HUMAN	A8MV58	Drebrin
14966	dirMS_041712_NAR_50mM_minus2.10670.10670.3	3	7.89	1	7.44E+03		(K)VAVVAG	(K)V/A\V/V/A G Y G D/V G K/G C A Q A L R(G)	C:Carbamidomethylation	129.78	630.9952	1890.985	-0.0144	-7.6	8.56	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
14967	dirMS_041712_NAR_50mM_minus2.11075.11075.3	3	7.89	0	1.29E+05		(R)IELGDV	(R)I E|L G D V T/P H/N I/K(Q)		131.2	445.912	1335.727	-0.0052	-3.9	5.32	14942.8	8.71	HUMAN	C9J5D1	N-alpha-acetyltransferase 50
14968	dirMS_041712_NAR_50mM_minus2.12656.12656.3	3	7.89	1	2.33E+05		(R)QATKD	(R)Q/A T K D A G T I|A/G L/N V\L R(I)		140.57	543.3085	1627.913	-0.0016	-1	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
14969	dirMS_041712_NAR_50mM_minus2.18065.18065.3	3	7.89	0	2.87E+05		(R)SLHDAL	(R)S L H D A L\C|V/L/A Q/T V K(D)	C:Carbamidomethylation	171.73	518.9488	1554.831	0.001	0.6	6.46	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
14970	dirMS_041712_NAR_60mM_minus.17362.17362.3	3	7.89	1	3.41E+05		(R)KAPSDL	(R)K/A P S D\L|Y/Q/I I L K(A)		156.37	463.6095	1388.815	-0.0008	-0.6	8.5	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
14971	dirMS_041712_NAR_60mM_minus.7846.7846.3	3	7.89	0	1.10E+05		(K)LFQECC	(K)L F|Q/E C/C P/H\S T D/R(V)	C:Carbamidomethylation	103.25	517.2229	1549.652	0.0019	1.2	5.32	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
14972	dirMS_041712_NAR_120mM_plus.15345.15345.4	4	7.89	2	7.47E+05		(R)AGEVER	(R)A/G|E V E R D L D K A D/S/M I R(L)		133.27	451.9773	1804.886	0.0016	0.9	4.44	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
14973	dirMS_041712_NAR_120mM_plus.18762.18762.4	4	7.89	0	4.90E+05		(R)LGWDP	(R)L/G W D P K/P G E G H L/D A L L R(G)		150.83	469.253	1873.992	-0.0017	-0.9	5.38	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
14974	dirMS_041712_NAR_120mM_plus.19196.19196.3	3	7.89	1	6.13E+05		(R)HGVQEL	(R)H/G/V Q E\L\E|I/E\L Q\S Q L S K K(A)		153.85	656.0237	1966.06	-0.0038	-2	5.5	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
14975	dirMS_041712_NAR_120mM_plus.9957.9957.3	3	7.89	1	1.05E+06		(K)IFRDGE	(K)I F R D G E E/A/G A/Y/D/G P R(T)		104.97	551.5927	1652.766	-0.0028	-1.7	4.32	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
14976	dirMS_041712_NAR_20mM_plus.14003.14003.2	2	7.89	0	1.34E+05		(R)GGIVDE	(R)G G I|V|D\E G A/L L R(A)		167.83	550.3066	1099.611	-0.0047	-4.3	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
14977	dirMS_041712_NAR_20mM_plus.15422.15422.3	3	7.89	0	5.72E+05		(K)VGINYQ	(K)V G I N Y Q/P P T V V/P G/G D L A K(V)		178.95	608.9991	1824.985	-0.0027	-1.5	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
14978	dirMS_041712_NAR_20mM_plus.16597.16597.2	2	7.89	0	6.78E+04	M50m	(R)DSLLQD	(R)D S L|L|Q/D G E|F\S\m D|L R(T)	m:Oxidized methionine	185.63	821.3739	1625.748	15.993	-1.2	3.84	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
14979	dirMS_041712_NAR_30mM_plus2.11016.11016.2	2	7.89	0	3.33E+05		(K)SLEDVV	(K)S L|E/D/V/V R(A)		110.9	409.2268	817.441	0.0049	6	4.37	163032.4	6.38	HUMAN	F5H335	Eukaryotic translation initiation factor 3 subunit A
14980	dirMS_041712_NAR_30mM_plus2.18535.18535.2	2	7.89	0	1.63E+05		(R)VLVFVM	(R)V/L|V/F/V/M G K(E)		150.42	446.7659	892.533	-0.0079	-8.9	8.72	9912.2	9.69	HUMAN	C9J712	Profilin-2
14981	dirMS_041712_NAR_30mM_plus2.21070.21070.2	2	7.89	0	5.16E+05		(K)IPDWFL	(K)I/P|D/W/F L N R(Q)		165.55	530.785	1060.557	0.0053	5	5.84	9767.1	11.41	HUMAN	J3JS69	40S ribosomal protein S18
14982	dirMS_041712_NAR_30mM_plus2.22197.22197.3	3	7.89	0	4.55E+05		(R)VGNLGL	(R)V G N L G L A|T S/F/F/N/E R(N)		172.7	508.9306	1524.781	-0.0033	-2.1	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
14983	dirMS_041712_NAR_50mM_plus2.10997.10997.3	3	7.89	0	2.31E+05		(K)TKPYIQ	(K)T K\P Y I\Q V/D|I/G G G Q T/K(T)		125.32	535.6231	1604.864	-0.0095	-5.9	8.17	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
14984	dirMS_041712_NAR_50mM_plus2.11408.11408.3	3	7.89	1	5.72E+04		(K)LVEVIKT	(K)L/V|E V I K T/P/M T S Q K(T)		127.9	491.9468	1473.834	-0.0087	-5.9	8.59	35407.1	6.73	HUMAN	E9PF18	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial
14985	dirMS_041712_NAR_50mM_plus2.18461.18461.3	3	7.89	1	3.94E+05		(K)VCSTND	(K)V/C|S T N D L K E\L L I/F N K(Q)	C:Carbamidomethylation	166.02	598.6527	1793.947	-0.0031	-1.7	6.04	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
14986	dirMS_041712_NAR_50mM_plus2.19285.19285.3	3	7.89	0	9.44E+04		(K)TIADLEL	(K)T I|A/D L E/L/H Y Q E F I R(N)		169.88	583.3027	1747.901	-0.0078	-4.5	4.65	334221.3	6.44	HUMAN	P15924	Desmoplakin
14987	dirMS_041712_NAR_50mM_plus2.9014.9014.3	3	7.89	1	2.23E+05		(R)LAEQAE	(R)L/A|E Q A E R Y D D M/A/S A M K(A)		114.55	610.2777	1828.82	-0.0019	-1	4.32	7741.6	5.25	HUMAN	A2IDB1	14-3-3 protein eta
14988	dirMS_041712_NAR_120mM_minus.17505.17505.4	4	7.88	1	5.43E+05		(R)GFGHIG	(R)G F/G H I G I A\V/P D V Y/S/A C K R(F)	C:Carbamidomethylation	150.4	487.502	1946.991	-0.0044	-2.2	8.6	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
14989	dirMS_041712_NAR_120mM_minus.8050.8050.2	2	7.88	0	1.24E+05	M49m	(R)HQGVM	(R)H Q|G V\M V G/m G Q/K(D)	m:Oxidized methionine	97.98	594.2863	1171.571	15.9943	-0.5	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
14990	dirMS_041712_NAR_20mM_minus.12358.12358.2	2	7.88	0	5.54E+05	M73m	(R)AVLVDL	(R)A V L\V\D|L/E|P G T\m D S\V/R(S)	m:Oxidized methionine	172.43	809.4088	1601.82	15.99	-3	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
14991	dirMS_041712_NAR_20mM_minus.13484.13484.3	3	7.88	0	7.87E+05	M221m	(R)ALTVPEL	(R)A L\T V/P E L T Q Q m F D A/K(N)	m:Oxidized methionine	186.22	569.9577	1691.867	15.9913	-2.1	4.37	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
14992	dirMS_041712_NAR_30mM_minus2.10103.10103.2	2	7.88	0	6.04E+04		(R)MYAAL	(R)M Y|A/A/L/G D/P K(A)		109.15	483.2423	965.476	0.0012	1.3	5.59	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
14993	dirMS_041712_NAR_30mM_minus2.7125.7125.2	2	7.88	0	3.54E+04		(K)ETEGDV	(K)E T|E/G D V/T S V K(D)		92.93	532.7579	1064.511	-0.0021	-2	4.14	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
14994	dirMS_041712_NAR_50mM_minus2.12065.12065.3	3	7.88	1	2.47E+04		(K)SSPVDL	(K)S S/P/V/D L V T A T D Q K V E K(M)		136.9	572.9736	1716.901	0.0048	2.8	4.56	17343.9	8.78	HUMAN	E5RG13	Inositol monophosphatase 1 (Fragment)
14995	dirMS_041712_NAR_50mM_minus2.12712.12712.3	3	7.88	0	1.03E+06	M114m M	(R)AGKPVI	(R)A G K\P V I\C A\T|Q/m L E S m I/K(K)	C:Carbamidomethylation m:Oxid	139.93	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
14996	dirMS_041712_NAR_50mM_minus2.13322.13322.3	3	7.88	0	3.47E+05		(R)AVAIDL	(R)A V A I/D L/P G L G H/S K(E)		144.55	426.5785	1277.721	-0.0003	-0.2	6.79	19983.6	8.14	HUMAN	B4DQI4	Alpha/beta hydrolase domain-containing protein 14B
14997	dirMS_041712_NAR_50mM_minus2.14847.14847.3	3	7.88	0	3.91E+04		(K)IAILTCP	(K)I A|I/L T C/P F E/P P K P K(T)	C:Carbamidomethylation	152.75	537.6375	1610.898	0.0005	0.3	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
14998	dirMS_041712_NAR_50mM_minus2.15382.15382.3	3	7.88	0	3.99E+05	M118m	(R)AGKPVI	(R)A G K\P V I C A T|Q/M/L/E S m I K(K)	C:Carbamidomethylation m:Oxid	155.45	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
14999	dirMS_041712_NAR_50mM_minus2.17699.17699.3	3	7.88	0	3.56E+05		(K)VAHALA	(K)V A H A L A E G\L|G\V|I/A C I G/E K(L)	C:Carbamidomethylation	168.93	603.3247	1807.974	-0.0139	-7.7	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
15000	dirMS_041712_NAR_120mM_plus.12223.12223.4	4	7.88	1	2.72E+06		(K)TLTTVQ	(K)T L T T V Q/G/I/A D D Y D K/K K(L)		117.32	449.7412	1795.944	-0.0006	-0.4	5.71	13778.5	7.96	HUMAN	K7EM18	Eukaryotic translation initiation factor 1
15001	dirMS_041712_NAR_120mM_plus.9903.9903.3	3	7.88	1	6.69E+05		(R)QRGGA	(R)Q R G G\A E G E|L/Q/A L/R(A)		105.02	462.2473	1384.729	-0.0018	-1.3	6.14	533778	5.74	HUMAN	Q15149	Plectin
15002	dirMS_041712_NAR_120mM_plus.9946.9946.4	4	7.88	0	2.44E+05		(R)GHAAFT	(R)G H A A F T/S D/P K/P T\I/E/V S G/K(K)		105.2	461.2368	1841.939	-0.0138	-7.5	6.75	15844.7	6.65	HUMAN	E5RI06	Glutathione reductase, mitochondrial (Fragment)
15003	dirMS_041712_NAR_20mM_plus.19322.19322.2	2	7.88	0	6.38E+04		(R)AFITNIP	(R)A F|I|T\N|I/P F D V K(W)		205.15	632.8492	1264.694	-0.0025	-2	5.88	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
15004	dirMS_041712_NAR_30mM_plus2.18227.18227.2	2	7.88	0	2.51E+05		(K)TTFEDL	(K)T T|F/E D L|I/Q R(C)		148.87	561.7934	1122.579	0.0006	0.5	4.37	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
15005	dirMS_041712_NAR_30mM_plus2.6755.6803.2	2	7.88	0	9.41E+04		(R)TAYGPN	(R)T A|Y/G/P N G M N K(M)		90.1	526.7446	1052.483	-0.001	-1	8.26	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
15006	dirMS_041712_NAR_40mM_plus2.12985.12985.3	3	7.88	1	2.05E+05		(K)VVIKSEA	(K)V/V|I/K S E A/A S P A\L P V I T K(V)		143.5	575.0089	1723.036	-0.0243	-14.1	8.56	54060.7	8.97	HUMAN	Q99958	Forkhead box protein C2
15007	dirMS_041712_NAR_50mM_plus2.11488.11488.3	3	7.88	1	2.02E+05		(R)MVDVV	(R)M/V/D V/V/E K E D V N E A I R(L)		128.03	582.6309	1745.874	0.0043	2.5	4.18	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
15008	dirMS_041712_NAR_50mM_plus2.15465.15465.3	3	7.88	1	3.87E+05		(R)LAAELN	(R)L/A|A E L N K F M L/E K(V)		149.1	469.5948	1406.771	-0.0014	-1	6.14	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
15009	dirMS_041712_NAR_50mM_plus2.19156.19156.3	3	7.88	0	4.98E+05		(R)GFGFITF	(R)G F\G\F|I/T/F T N/P E H A S V A M R(A)		168.98	661.3258	1981.959	0.004	2	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
15010	dirMS_041712_NAR_50mM_plus2.7099.7099.3	3	7.88	1	3.75E+04		(R)ASVDTK	(R)A S/V D T K E A E G/A|P/Q\V E A\G K(R)		103.02	596.2908	1786.882	-0.0239	-13.4	4.41	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
15011	dirMS_041712_NAR_50mM_plus2.8892.8892.3	3	7.88	0	2.04E+05		(K)VVQVSA	(K)V V|Q/V/S/A G D S H T A/A L T D D/G R(V)		113.45	633.6509	1898.92	0.0179	9.4	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
15012	dirMS_041712_NAR_60mM_plus.11270.11270.3	3	7.88	1	3.12E+05		(R)AGTGVD	(R)A G T/G V/D N V D L/E A A\T R K(G)		116.3	539.6102	1616.824	-0.0078	-4.8	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
15013	dirMS_041712_NAR_60mM_plus.13922.13922.3	3	7.88	1	9.47E+05		(K)TTVKDL	(K)T\T/V K D L/S E|L/G S V/R(T)		129.53	468.9268	1404.769	-0.0034	-2.4	5.74	533778	5.74	HUMAN	Q15149	Plectin
15014	dirMS_041712_NAR_60mM_plus.6872.6872.3	3	7.88	0	1.86E+05		(R)YVLHCQ	(R)Y/V/L/H/C Q\G T E E/E K(I)	C:Carbamidomethylation	94.37	498.2304	1492.674	0.003	2	4.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
15015	dirMS_041712_NAR_60mM_plus.8108.8108.3	3	7.88	1	6.02E+05		(R)KQSTDE	(R)K Q S T D E\E/V/T S/L/A/K(S)		100.85	479.2461	1435.728	-0.0037	-2.6	4.68	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
15016	dirMS_041712_NAR_60mM_plus.9779.9779.3	3	7.88	0	2.64E+05		(R)ASHPED	(R)A S H|P E D|P A/S V V E/A R(K)		108.63	488.9052	1464.708	-0.0067	-4.6	4.65	54796.9	5.9	HUMAN	Q9UHL4	Dipeptidyl peptidase 2
15017	dirMS_041712_NAR_120mM_minus.16606.16606.3	3	7.87	0	6.43E+05		(R)EHALLA	(R)E H A L\L\A\Y/T/L G V K(Q)		145.15	438.9186	1314.742	-0.0004	-0.3	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
15018	dirMS_041712_NAR_20mM_minus.11545.11545.2	2	7.87	0	2.12E+05		(R)GDLGIEI	(R)G D L/G|I|E/I/P A E K(V)		163.87	571.3078	1141.61	-0.0016	-1.4	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
15019	dirMS_041712_NAR_20mM_minus.11763.11763.2	2	7.87	0	2.75E+05		(R)GALQNI	(R)G A L|Q/N/I|I P A S\T G A A/K(A)		165.47	706.3976	1411.79	-0.0024	-1.7	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
15020	dirMS_041712_NAR_20mM_minus.7010.7010.2	2	7.87	0	4.44E+05	M281m	(R)AEAESm	(R)A E|A/E/S m Y Q I K(Y)	m:Oxidized methionine	117.82	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
15021	dirMS_041712_NAR_30mM_minus2.11006.11006.2	2	7.87	0	5.09E+05		(R)FASGGC	(R)F A|S/G/G C D N L\I/K(L)	C:Carbamidomethylation	113.48	591.2858	1181.562	0.0024	2	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
15022	dirMS_041712_NAR_30mM_minus2.9210.9210.2	2	7.87	0	4.11E+04		(R)TYQASS	(R)T Y|Q/A/S S\A\A F R(Y)		104.48	551.2778	1101.532	0.016	14.5	8.41	26240.9	9.1	HUMAN	Q92567	Protein FAM168A
15023	dirMS_041712_NAR_40mM_minus2.12003.12003.3	3	7.87	1	1.80E+05		(K)AGTQIE	(K)A/G T|Q/I/E N I D E D/F R D G L K(L)		153.87	640.9843	1920.93	0.0086	4.5	4.11	59872.5	4.85	HUMAN	F5GXS2	Alpha-actinin-4
15024	dirMS_041712_NAR_40mM_minus2.13154.13154.2	2	7.87	0	9.01E+04		(K)SYELPD	(K)S Y E\L|P D G Q V/I|T/I/G N E R(F)		161.43	895.9483	1790.892	-0.0026	-1.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
15025	dirMS_041712_NAR_50mM_minus2.8060.8060.3	3	7.87	1	1.06E+05		(K)GILAAD	(K)G I/L/A/A/D E S/T G S I A K R(L)		113.4	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
15026	dirMS_041712_NAR_60mM_minus.11250.11250.3	3	7.87	1	7.95E+05		(K)MKEIAE	(K)M/K E I A E/A/Y/L/G K(T)		122.48	418.226	1252.661	0.0029	2.3	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
15027	dirMS_041712_NAR_60mM_minus.16872.16872.3	3	7.87	1	3.95E+05		(R)ARFEEL	(R)A R\F E E\L\N|A/D|L/F R(G)		153.98	494.2594	1480.754	0.0093	6.3	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
15028	dirMS_041712_NAR_60mM_minus.17196.17196.3	3	7.87	0	2.69E+05		(K)GSDHSA	(K)G S D H\S A S L\E|P G/E L A/E L V R(S)		156.67	622.9764	1866.919	-0.0045	-2.4	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
15029	dirMS_041712_NAR_60mM_minus.18923.18936.3	3	7.87	1	2.36E+05		(R)DSIVAEL	(R)D S/I|V|A/E L D R E M S R(S)		167.97	507.5858	1520.737	0.0055	3.6	4.32	34709.6	4.98	HUMAN	O14579	Coatomer subunit epsilon
15030	dirMS_041712_NAR_120mM_plus.10897.10897.4	4	7.87	1	1.33E+06		(K)VVQHLG	(K)V/V Q/H|L G P A T D F Y/K K(L)		110.45	401.4712	1602.864	-0.0009	-0.6	8.48	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
15031	dirMS_041712_NAR_20mM_plus.12120.12120.2	2	7.87	0	3.75E+04		(R)LCYYIGA	(R)L C Y/Y I|G A T D D A A T/K(I)	C:Carbamidomethylation	156.62	781.3622	1561.72	-0.0032	-2	4.21	21156.2	9.41	HUMAN	P55145	Mesencephalic astrocyte-derived neurotrophic factor
15032	dirMS_041712_NAR_20mM_plus.7586.7586.2	2	7.87	0	3.86E+04		(K)IAVAAQ	(K)I A|V|A/A|Q/N C Y K(V)	C:Carbamidomethylation	121.72	569.2902	1137.572	0.001	0.9	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
15033	dirMS_041712_NAR_30mM_plus2.11690.11690.2	2	7.87	0	5.15E+05		(R)SGEGEV	(R)S G\E|G E|V S/G L M|R(K)		114.07	561.2662	1121.526	-0.0004	-0.4	4.53	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
15034	dirMS_041712_NAR_30mM_plus2.12101.12101.2	2	7.87	0	6.83E+05		(K)CGDLVF	(K)C G/D L/V/F|A/K(M)	C:Carbamidomethylation	116.12	455.2298	909.45	0.0025	2.7	5.84	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
15035	dirMS_041712_NAR_30mM_plus2.16736.16736.2	2	7.87	0	5.99E+04		(R)AALQEL	(R)A/A|L/Q E L L/S K(G)		140.78	486.7894	972.572	-0.0009	-0.9	6.05	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
15036	dirMS_041712_NAR_30mM_plus2.19920.19920.2	2	7.87	0	1.49E+05		(K)SNSVEM	(K)S N\S V/E|M/D/W V L K(H)		157.9	654.3191	1307.63	0.0009	0.7	4.37	49548	5.89	HUMAN	P55795	Heterogeneous nuclear ribonucleoprotein H2
15037	dirMS_041712_NAR_30mM_plus2.9569.9569.2	2	7.87	0	4.23E+05		(K)QTTCW	(K)Q T/T|C/W|D|G V R(N)	C:Carbamidomethylation	104.3	561.7585	1122.5	0.0101	9	5.84	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1

15038	dirMS_041712_NAR_40mM_plus2.13332.13332.3	3	7.87	0	3.20E+05		(K)LQMEA	(K)L Q|M E A P H I/I/V/G T P G R(V)		144.1	540.2954	1618.873	-0.0017	-1.1	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
15039	dirMS_041712_NAR_50mM_plus2.10205.10205.3	3	7.87	0	6.39E+04		(R)TIVITSH	(R)T I|V I T/S/H/P G Q I V K(H)		120.92	464.946	1392.821	0.0025	1.8	8.44	27999.4	5.61	HUMAN	B7Z5C0	DnaJ homolog subfamily A member 1
15040	dirMS_041712_NAR_50mM_plus2.11178.11178.3	3	7.87	1	8.51E+04		(R)SAAETV	(R)S/A|A\E T\V T/K G G I M L P E K(S)		126.63	544.624	1631.867	-0.0098	-6	5.86	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
15041	dirMS_041712_NAR_60mM_plus.11510.11510.3	3	7.87	0	3.70E+05		(R)SLGTAD	(R)S L/G T A D/V/H F E/R(K)		116.88	411.2075	1231.607	0.0014	1.1	5.3	27557.2	11.05	HUMAN	E9PB61	THO complex subunit 4
15042	dirMS_041712_NAR_60mM_plus.14282.14282.3	3	7.87	1	1.22E+06		(K)AVLFCLS	(K)A V/L/F C/L/S E D K/K(N)	C:Carbamidomethylation	131.62	437.2332	1309.682	0.003	2.3	6.11	22956	8.8	HUMAN	E9PK25	Cofilin-1
15043	dirMS_041712_NAR_60mM_plus.18349.18349.3	3	7.87	1	5.69E+05		(R)IRIDSLS	(R)I R I D S L\S/A|Q|L|S Q L Q K(Q)		153.68	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
15044	dirMS_041712_NAR_20mM_minus.12094.12094.2	2	7.86	0	9.21E+05	M313m	(R)TVQSLEI	(R)T V/Q|S L E|I D\L\D S m/R(N)	m:Oxidized methionine	170.48	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
15045	dirMS_041712_NAR_30mM_minus2.15704.15704.2	2	7.86	0	9.77E+04		(R)GSTDNL	(R)G S\T D N/L/M/D/D I E/R(A)		138.77	683.3009	1365.595	-0.0006	-0.4	3.84	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
15046	dirMS_041712_NAR_50mM_minus2.10203.10203.3	3	7.86	0	1.60E+05	M392m	(K)EmNPAL	(K)E m N/P A L|G/I|D C L H K(G)	C:Carbamidomethylation m:Oxid	125.95	505.2416	1497.719	15.9914	-2.3	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
15047	dirMS_041712_NAR_50mM_minus2.11553.11553.3	3	7.86	0	2.88E+05	M291m	(K)TGEEIFG	(K)T G/E|E|I F/G/T I G m R P N A K(N)	m:Oxidized methionine	134.13	579.6239	1720.869	15.9885	-3.7	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
15048	dirMS_041712_NAR_50mM_minus2.13157.13157.3	3	7.86	1	1.01E+05		(R)TEMENE	(R)T E|M/E N E F V/L I K K(D)		142.92	494.2621	1480.772	0.0002	0.1	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
15049	dirMS_041712_NAR_50mM_minus2.15188.15188.3	3	7.86	1	1.33E+05		(K)VSEQGL	(K)V/S/E Q/G L I E I L K K(V)		154.37	452.9385	1356.81	-0.0087	-6.4	6.11	12899.6	6.59	HUMAN	K7EL31	Programmed cell death protein 5
15050	dirMS_041712_NAR_50mM_minus2.8128.8128.3	3	7.86	1	1.73E+05		(K)GILAADE	(K)G I/L\A A/D E S T G/S I A/K R(L)		114.03	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
15051	dirMS_041712_NAR_50mM_minus2.8390.8390.3	3	7.86	1	1.99E+05		(K)GILAADE	(K)G I/L/A A/D E S/T G S I A K R(L)		115.2	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
15052	dirMS_041712_NAR_60mM_minus.14736.14736.3	3	7.86	0	4.34E+05		(K)AVGHPF	(K)A V G\H P F V|I/Q/L G R(I)		141.95	431.9182	1293.743	-0.0026	-2	9.8	124524.8	5.71	HUMAN	O14980	Exportin-1
15053	dirMS_041712_NAR_120mM_plus.8802.8802.2	2	7.86	0	5.19E+05		(R)NGVMP	(R)N G\V|M/P S H F S R(G)		99.72	566.274	1131.536	0.0043	3.8	9.75	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
15054	dirMS_041712_NAR_20mM_plus.11220.11220.2	2	7.86	0	2.10E+05		(K)LITPAVV	(K)L I/T/P A V\V S E R(L)		150.02	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
15055	dirMS_041712_NAR_20mM_plus.13566.13566.2	2	7.86	0	1.45E+05	M273m	(K)mISDAIP	(K)m\I|S D/A/I/P E/L K(A)	m:Oxidized methionine	165.55	566.7967	1116.597	15.9892	-5	4.37	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
15056	dirMS_041712_NAR_20mM_plus.19187.19187.2	2	7.86	0	9.61E+04		(K)SLNILTA	(K)S L/N\I/L/T/A/F Q K(K)		203.9	567.8286	1134.652	-0.0018	-1.6	8.47	18172.6	7.77	HUMAN	F8VY02	Endoplasmic reticulum resident protein 29
15057	dirMS_041712_NAR_20mM_plus.19295.19295.3	3	7.86	0	2.73E+05		(R)LAGTQP	(R)L A G T Q P L/E|V/L/E A V Q R(S)		204.33	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
15058	dirMS_041712_NAR_30mM_plus2.11824.11824.2	2	7.86	0	1.26E+06		(R)GGGGNI	(R)G G\G G/N/F/G/P G P G S N F R(G)		114.42	689.3175	1377.629	-0.0017	-1.2	9.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
15059	dirMS_041712_NAR_30mM_plus2.7042.7042.2	2	7.86	0	1.83E+04		(R)SGGGGG	(R)S G G G/G/G/G G L/G S G G S I R(S)		92.03	616.8023	1232.598	-0.0005	-0.4	9.47	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
15060	dirMS_041712_NAR_40mM_plus2.13902.13902.3	3	7.86	1	3.97E+05		(R)QVFGEA	(R)Q V/F G E A T K|Q P G I T F I A A/K(F)		147.58	636.0176	1906.043	-0.005	-2.6	8.59	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
15061	dirMS_041712_NAR_40mM_plus2.8419.8419.2	2	7.86	0	6.97E+04		(R)QLSSGV	(R)Q L/S S/G V/S E I/R(H)		110.07	538.2862	1075.574	-0.0091	-8.5	6	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
15062	dirMS_041712_NAR_50mM_plus2.20931.20931.3	3	7.86	1	2.06E+05		(R)GGGNQ	(R)G G G N Q|V S L L/N V V/M D/L K K(C)		179.03	591.3291	1771.974	-0.0007	-0.4	8.59	218583	5.58	HUMAN	F5GWX5	Chromodomain-helicase-DNA-binding protein 4
15063	dirMS_041712_NAR_50mM_plus2.6444.6444.3	3	7.86	1	1.31E+05	M365m	(R)IVEQDT	(R)I V|E/Q D\T m/P P/K G V R(H)	m:Oxidized methionine	98.88	495.9283	1469.778	15.9923	-1.8	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
15064	dirMS_041712_NAR_60mM_plus.10141.10141.3	3	7.86	1	1.48E+06		(K)IFRDGEE	(K)I F R D G E E|A G A|Y/D G P R(T)		111.47	551.593	1652.766	-0.0019	-1.1	4.32	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
15065	dirMS_041712_NAR_60mM_plus.11537.11537.3	3	7.86	0	1.67E+06		(K)AQVARP	(K)A Q|V/A R P G G D T I F/G K(I)		116.72	472.9241	1416.759	-0.0016	-1.2	8.79	7323.5	9.4	HUMAN	D6RC06	Histidine triad nucleotide-binding protein 1
15066	dirMS_041712_NAR_60mM_plus.14732.14732.3	3	7.86	1	1.87E+05		(R)MLATLF	(R)M L\A/T|L F K D/E R(C)		132.97	408.5544	1223.645	0.0034	2.8	5.82	40481.5	6.48	HUMAN	B3KST5	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis), isoform CRA_a
15067	dirMS_041712_NAR_120mM_minus.17218.17218.3	3	7.85	1	7.58E+04		(R)LVGALRI	(R)L V G A L R/E T|V V A/A R(A)		148.32	452.2751	1354.816	-0.0058	-4.3	9.6	75310.9	6.11	HUMAN	C9JIL1	von Willebrand factor A domain-containing protein 7
15068	dirMS_041712_NAR_120mM_minus.20782.20782.4	4	7.85	1	5.83E+05		(R)SLHDAL	(R)S L H D A L\C/V/L/A Q T V K D S R(T)	C:Carbamidomethylation	173.1	479.0049	1912.991	0.0068	3.6	6.47	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
15069	dirMS_041712_NAR_120mM_minus.7969.8034.2	2	7.85	0	4.26E+05		(K)FHSQLM	(K)F/H|S|Q/L M R(L)		97.85	459.7343	918.461	-0.0001	-0.1	9.75	10225.7	7.97	HUMAN	P49458	Signal recognition particle 9 kDa protein
15070	dirMS_041712_NAR_20mM_minus.11144.11144.2	2	7.85	0	1.99E+04		(R)LLAEPVF	(R)L/L|A|E/P V P G I K(A)		158.82	518.822	1036.64	-0.0034	-3.3	6	12039.9	9.34	HUMAN	F8VSD4	Ubiquitin-conjugating enzyme E2 N
15071	dirMS_041712_NAR_20mM_minus.13155.13155.2	2	7.85	0	2.98E+05	M35m	(K)NDIAINE	(K)N D I\A|I|N E L m/K(R)	m:Oxidized methionine	181.98	588.7948	1160.598	15.9843	-9	4.37	28354	7.11	HUMAN	B4DXI8	26S proteasome non-ATPase regulatory subunit 7
15072	dirMS_041712_NAR_20mM_minus.14445.14445.2	2	7.85	0	2.15E+05		(K)DAGVIA	(K)D A G/V|I/A/G L N V L R(I)		198.23	599.3503	1197.695	-0.0017	-1.4	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
15073	dirMS_041712_NAR_30mM_minus2.16141.16141.2	2	7.85	0	1.41E+05		(K)GCSFLPD	(K)G C\S/F/L|P D/P Y Q\K(Q)	C:Carbamidomethylation	141.02	656.3051	1311.604	-0.0009	-0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
15074	dirMS_041712_NAR_30mM_minus2.6752.6752.2	2	7.85	0	3.89E+05		(K)VLEEEEC	(K)V/L/E/E\E E Q R(R)		90.38	516.2552	1031.5	0.0027	2.7	4.09	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
15075	dirMS_041712_NAR_40mM_minus2.12665.12665.3	3	7.85	1	2.01E+05		(K)DVLFLKD	(K)D V|L|F/L K/D C V/G\P E V E K(A)	C:Carbamidomethylation	158.43	583.3021	1747.893	-0.0018	-1	4.32	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
15076	dirMS_041712_NAR_40mM_minus2.14218.14218.3	3	7.85	0	1.23E+05		(R)GTEDITS	(R)G T/E D/I/T/S P H G/I/P L D\L\L/D R(V)		168.55	650.3366	1948.997	-0.0022	-1.1	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
15077	dirMS_041712_NAR_50mM_minus2.10776.10776.3	3	7.85	1	2.88E+05		(K)NQVAM	(K)N Q|V|A M N\P T/N T V/F D A K R(L)		129.02	602.6379	1805.896	0.0029	1.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
15078	dirMS_041712_NAR_60mM_minus.11078.11078.3	3	7.85	1	2.36E+05		(K)VTVAGL	(K)V/T V/A/G/L/A G/K D/P V Q C S R(D)	C:Carbamidomethylation	121.13	553.2923	1657.869	-0.0067	-4	8.72	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
15079	dirMS_041712_NAR_60mM_minus.6356.6356.3	3	7.85	1	7.12E+04		(R)ATEGM	(R)A/T/E/G M V V/A D K N C S K(I)	C:Carbamidomethylation	94.05	503.9042	1509.704	-0.0055	-3.7	6.11	15607.8	9.99	HUMAN	B4E0P1	Proteasome (Prosome, macropain) subunit, beta type, 7, isoform CRA_b
15080	dirMS_041712_NAR_60mM_minus.6867.6867.3	3	7.85	1	5.61E+05	M286m M	(R)VVDLm	(R)V/V/D/L m A H m A S K E(-)	m:Oxidized methionine	96.77	454.8843	1330.649	31.989	-0.6	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
15081	dirMS_041712_NAR_120mM_plus.17813.17813.3	3	7.85	1	1.36E+06	M25m	(R)KAHQm	(R)K A/H Q m S|L\E G F T R(Y)	m:Oxidized methionine	146.13	474.2314	1404.705	15.9744	-14.4	8.76	9196.3	5.85	HUMAN	F5GZK3	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase zeta-1 (Fragment)
15082	dirMS_041712_NAR_120mM_plus.7084.7084.3	3	7.85	0	3.43E+05		(K)SQFSDKI	(K)S Q/F/S D K/P V Q D/R(G)		90.42	436.2209	1306.639	0.0095	7.3	5.68	13194	9.99	HUMAN	E9PI70	Chitinase domain-containing protein 1 (Fragment)
15083	dirMS_041712_NAR_20mM_plus.11943.11943.2	2	7.85	0	1.12E+05		(R)IYVVDV	(R)I Y|V/V|D\V G S E\P R(A)		156.08	617.3237	1233.647	-0.0073	-5.9	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
15084	dirMS_041712_NAR_20mM_plus.14319.14319.2	2	7.85	0	3.41E+04		(R)IALTDN	(R)I A|L|T|D\N/A L I\A R(S)		170.65	585.8432	1170.684	-0.005	-4.2	5.84	24489.6	10.74	HUMAN	A8MUD9	60S ribosomal protein L7
15085	dirMS_041712_NAR_20mM_plus.16471.16471.3	3	7.85	0	6.48E+04	M137m M	(R)IIGATDS	(R)I I G A T D S\S/G/E/L m/F L/m/K(W)	m:Oxidized methionine	185.8	582.2872	1712.86	31.9873	-1.5	4.37	19439.5	4.97	HUMAN	B5MD17	Chromobox protein homolog 1 (Fragment)
15086	dirMS_041712_NAR_30mM_plus2.7573.7573.2	2	7.85	0	2.11E+05		(R)IAVVGE	(R)I/A|V|V/G E G R(E)		93.87	400.7369	800.462	0.004	5.1	6	27082.1	9.06	HUMAN	D6RD66	WD repeat-containing protein 1 (Fragment)
15087	dirMS_041712_NAR_40mM_plus2.13723.13747.3	3	7.85	1	1.07E+05	T1512t	(R)NLPSKIP	(R)N/L P S K I P L|P/T A M t S G/S K(S)	t:N-acetylglucosamine (T)	147.17	649.0215	1741.952	203.0983	9.7	10	205932.9	8.96	HUMAN	Q92545	Transmembrane protein 131
15088	dirMS_041712_NAR_50mM_plus2.10734.10734.3	3	7.85	0	4.29E+05		(K)MIVDPV	(K)M/I/V D/P V E/P H G\E M K(F)		123.43	494.5783	1481.713	0.0076	5.2	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
15089	dirMS_041712_NAR_50mM_plus2.14895.14895.3	3	7.85	2	3.55E+05	M99m N10	(K)KIRmLV	(K)K\I/R/m L V A E n\G/K(K)	m:Oxidized methionine n:N-	146.43	493.2734	1258.73	219.0756	0.9	9.99	22643.3	4.51	HUMAN	B4DHB5	Cyclin-D1-binding protein 1
15090	dirMS_041712_NAR_50mM_plus2.17004.17004.3	3	7.85	1	1.94E+06		(R)VTTVTEI	(R)V/T/T V/T E I G K D V/I G L R(I)		156.75	534.308	1600.927	-0.0174	-10.9	6.04	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
15091	dirMS_041712_NAR_60mM_plus.9794.9794.3	3	7.85	1	2.15E+05		(R)GPGLVK	(R)G/P/G L V K/Q/E D/F R(D)		109.68	415.8936	1245.659	0.0076	6.1	6.07	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
15092	dirMS_041712_NAR_120mM_minus.4904.4904.3	3	7.84	1	4.18E+05		(R)AAEEED	(R)A A E E E D/E/A/D P K/R(Q)		78.88	453.8716	1359.602	-0.002	-1.5	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
15093	dirMS_041712_NAR_120mM_minus.8650.8650.3	3	7.84	0	6.84E+05		(R)SNTENL	(R)S N/T E/N L/S Q/H/F R(K)		101.77	444.8813	1332.629	0.0002	0.2	6.47	43303.4	8.7	HUMAN	F8VRN8	LIM domain and actin-binding protein 1
15094	dirMS_041712_NAR_20mM_minus.13100.13100.2	2	7.84	0	2.21E+05		(R)GVVDSE	(R)G V V D S E/D|I|P L N L/S R(E)		182.98	757.3944	1513.786	-0.0041	-2.7	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
15095	dirMS_041712_NAR_20mM_minus.13552.13552.2	2	7.84	0	1.32E+05		(K)DIYALIS	(K)D I/Y/A/L I/S D Q K(H)		186.45	583.3076	1165.61	-0.002	-1.7	4.21	266161	5.68	HUMAN	E9PPU0	Epiplakin
15096	dirMS_041712_NAR_30mM_minus2.5704.5704.2	2	7.84	0	4.13E+04		(R)AAEDDE	(R)A/A|E/D D E/D/D D V/D T K(K)		85.35	719.2778	1437.55	-0.0016	-1.1	3.5	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
15097	dirMS_041712_NAR_30mM_minus2.7048.7048.2	2	7.84	0	3.29E+05		(R)TYDETY	(R)T/Y|D/E T Y Q R(Y)		92.88	538.2398	1075.469	0.0032	3	4.37	40616.6	9.46	HUMAN	H0YHI8	Protein phosphatase 1 regulatory subunit 12A (Fragment)
15098	dirMS_041712_NAR_40mM_minus2.15613.15613.3	3	7.84	1	4.96E+05		(K)ALFEEV	(K)A L|F/E E/V/P E/L L T E A E K K(E)		181.8	615.9988	1845.984	-0.0026	-1.4	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
15099	dirMS_041712_NAR_60mM_minus.10769.10769.3	3	7.84	1	8.74E+04		(K)TLQEVT	(K)T L|Q E/V/T/E M D S V K R(Y)		119.92	512.5957	1535.773	-0.0008	-0.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
15100	dirMS_041712_NAR_120mM_plus.6097.6097.3	3	7.84	0	6.54E+05		(K)QRPQAT	(K)Q\R P Q A\T/A/E/Q I/R(L)		85.85	433.2367	1297.697	-0.0016	-1.2	9.6	113668.7	6.2	HUMAN	F8W726	Ubiquitin-associated protein 2-like
15101	dirMS_041712_NAR_20mM_plus.10548.10548.2	2	7.84	0	5.43E+03		(K)IDATSAS	(K)I D/A/T/S A/S/V/L A S R(F)		145.42	595.8217	1190.638	-0.0014	-1.2	5.84	73273.4	4.96	HUMAN	P13667	Protein disulfide-isomerase A4
15102	dirMS_041712_NAR_20mM_plus.10632.10632.2	2	7.84	0	4.02E+04		(R)TPTAPA	(R)T P T/A/P A/V N L A G A R(T)		145.83	619.8456	1238.685	-0.0012	-1	9.41	300351.7	12.1	HUMAN	Q9UQ35	Serine/arginine repetitive matrix protein 2
15103	dirMS_041712_NAR_20mM_plus.15071.15071.2	2	7.84	0	2.08E+04		(R)IAAAILN	(R)I A A\A|I|L/N T P D L R(K)		175.3	634.3708	1267.737	-0.0025	-2	5.84	43371.1	9.64	HUMAN	E7ERW2	Aspartate aminotransferase
15104	dirMS_041712_NAR_20mM_plus.16097.16097.2	2	7.84	0	4.77E+04		(K)DAGTIA	(K)D A/G T/I|A/G L N V L R(I)		182.22	600.3422	1199.674	0.0029	2.4	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
15105	dirMS_041712_NAR_20mM_plus.9925.9925.2	2	7.84	0	1.64E+05		(K)YQAVTA	(K)Y Q|A|V/T A T L E E K(R)		139.63	626.8223	1252.642	-0.0046	-3.7	4.53	23633.9	11.02	HUMAN	P40429	60S ribosomal protein L13a
15106	dirMS_041712_NAR_30mM_plus2.13029.13029.2	2	7.84	0	6.18E+05		(K)STLTDSL	(K)S T|L/T|D\S L V/C K(A)	C:Carbamidomethylation	121.23	562.2876	1123.566	0.0016	1.4	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
15107	dirMS_041712_NAR_30mM_plus2.20286.20286.2	2	7.84	0	2.80E+05		(R)FEELNA	(R)F E|E/L/N\A/D L F R(G)		160.95	627.3106	1253.616	-0.0022	-1.7	4.14	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
15108	dirMS_041712_NAR_40mM_plus2.10148.10148.3	3	7.84	0	1.35E+05	M1087m	(R)mPLPAP	(R)m P L/P A/P S L/S H/Q/P P P A P R(V)	m:Oxidized methionine	124.5	603.6536	1792.953	15.9936	-0.7	9.52	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
15109	dirMS_041712_NAR_40mM_plus2.12131.12131.2	2	7.84	0	1.61E+05		(K)VYFDLR	(K)V/Y/F D|L/R(I)		137.08	406.7184	812.43	-0.0006	-0.7	5.8	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
15110	dirMS_041712_NAR_40mM_plus2.19010.19010.3	3	7.84	1	3.06E+05		(R)GGPNIIT	(R)G G/P N/I|I|T L A D I V K D/P V S R(T)		178.9	622.3522	1865.049	-0.007	-3.8	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
15111	dirMS_041712_NAR_40mM_plus2.5427.5427.2	2	7.84	0	2.74E+04		(K)TYGQST	(K)T Y|G/Q/S T Y S R(Q)		88.83	531.7462	1062.485	0.0001	0.1	8.25	14693.3	4.69	HUMAN	C9JLS9	26S protease regulatory subunit 7 (Fragment)
15112	dirMS_041712_NAR_40mM_plus2.9627.9627.3	3	7.84	1	6.15E+04		(R)VEPADA	(R)V E|P/A D A S G T E K A/F E/P A T G R(V)		119.55	644.9798	1932.93	-0.0049	-2.5	4.41	54713.8	5.69	HUMAN	P49189	4-trimethylaminobutyraldehyde dehydrogenase
15113	dirMS_041712_NAR_50mM_plus2.20051.20051.3	3	7.84	0	4.85E+05		(K)ALIEVLQ	(K)A L/I/E V L Q/P L I A E H Q A R(R)		174.2	601.0191	1801.033	0.0097	5.4	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
15114	dirMS_041712_NAR_50mM_plus2.20245.20245.3	3	7.84	0	2.29E+05		(K)GHVDIL	(K)G H V D I L A|P T V/Q E|L A/A L E K(E)		174.67	635.3536	1904.049	-0.0025	-1.3	4.65	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
15115	dirMS_041712_NAR_50mM_plus2.6858.6858.3	3	7.84	1	7.87E+05		(K)IVADKD	(K)I/V/A D K D Y S/V/T A N S K(I)		101.32	504.2628	1510.775	-0.0009	-0.6	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
15116	dirMS_041712_NAR_60mM_plus.13105.13105.3	3	7.84	0	1.08E+05		(R)LHLSPV	(R)L H L S P V|Q I F D D G R(K)		125.67	499.594	1496.786	-0.0182	-12.1	5.21	64646.1	6.72	HUMAN	E9PEJ1	T-cell surface protein tactile
15117	dirMS_041712_NAR_60mM_plus.14541.14868.3	3	7.84	1	6.85E+05		(R)ELAVQI	(R)E L/A/V/Q/I/Y E E A R K(F)		133.23	483.5949	1448.774	-0.0042	-2.9	4.79	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
15118	dirMS_041712_NAR_60mM_plus.17164.17164.3	3	7.84	1	2.91E+05		(R)ASLISAV	(R)A S/L I/S A/V/S D K L R(W)		146.83	420.5832	1259.732	0.0033	2.6	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
15119	dirMS_041712_NAR_60mM_plus.18396.18396.3	3	7.84	1	1.49E+05		(R)ARFEEL	(R)A R F E E\L|C S D/L F R(S)	C:Carbamidomethylation	153.23	514.9194	1542.737	0.0067	4.3	4.68	25598.3	6.45	HUMAN	E7EP11	Heat shock 70 kDa protein 1A/1B
15120	dirMS_041712_NAR_120mM_minus.8008.8008.3	3	7.83	0	9.40E+04		(R)SCYDLS	(R)S/C/Y/D/L S C H/A/R(A)	C:Carbamidomethylation	97.97	423.5114	1268.515	0.005	3.9	6.46	83905.8	6.62	HUMAN	P41250	Glycine--tRNA ligase
15121	dirMS_041712_NAR_20mM_minus.9577.9577.3	3	7.83	0	1.30E+04	M175m	(R)LEQGQ	(R)L E Q G Q A\I/D/D L/m/P A Q/K(-)	m:Oxidized methionine	146.08	558.2794	1656.826	15.9975	1.5	4.03	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
15122	dirMS_041712_NAR_30mM_minus2.11419.11419.2	2	7.83	0	3.28E+05		(R)VQELPL	(R)V Q|E L P/L A R(I)		115.63	463.2738	925.547	-0.0062	-6.7	5.97	16202.4	6.61	HUMAN	E9PI99	Nuclear transcription factor Y subunit gamma (Fragment)
15123	dirMS_041712_NAR_40mM_minus2.14474.14474.3	3	7.83	1	1.27E+05		(R)LKLPSIP	(R)L K L P\S I\P\L|V|P V S A Q K(R)		169.47	530.6703	1589.999	-0.0025	-1.6	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
15124	dirMS_041712_NAR_50mM_minus2.15444.15444.3	3	7.83	1	1.02E+05		(K)YAVLYQ	(K)Y/A V/L/Y Q/P L F D K R(F)		155.68	504.9453	1512.821	0.0004	0.3	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
15125	dirMS_041712_NAR_60mM_minus.16297.16297.3	3	7.83	1	4.39E+05		(K)NIYVLQE	(K)N I/Y|V/L Q E/L D/N P G A K/R(I)		150.83	577.3128	1729.923	0.0007	0.4	6.07	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
15126	dirMS_041712_NAR_120mM_plus.18894.18894.4	4	7.83	0	3.26E+05		(K)APIRPDI	(K)A/P/I R P D I|V/N/F V/H T N L R(K)		151.9	466.2639	1862.04	-0.0058	-3.1	9.65	18988.7	11.2	HUMAN	H3BTP7	60S ribosomal protein L4 (Fragment)
15127	dirMS_041712_NAR_20mM_plus.18032.18032.2	2	7.83	0	1.49E+05		(R)TVQSLEI	(R)T V/Q/S/L|E\I\D L D S M R(N)		195.15	753.8776	1506.747	0.0011	0.7	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
15128	dirMS_041712_NAR_20mM_plus.8395.8395.2	2	7.83	0	1.04E+05	M607m M	(R)mGLAm	(R)m G L|A/m/G G/G G/G A S F/D R(A)	m:Oxidized methionine	128.17	708.3061	1383.614	31.9905	0.5	5.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
15129	dirMS_041712_NAR_30mM_plus2.16683.16825.2	2	7.83	0	4.15E+05		(R)LWDLTT	(R)L W|D|L/T/T/G T T T R(R)		140.42	632.8304	1264.653	0.0003	0.3	5.84	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
15130	dirMS_041712_NAR_30mM_plus2.22310.22328.2	2	7.83	0	3.01E+05		(K)CMPTFC	(K)C M|P T F Q F|F K(K)	C:Carbamidomethylation	172.77	603.2777	1205.548	-0.0001	-0.1	8.75	9680	5.77	HUMAN	B1ALW1	Thioredoxin
15131	dirMS_041712_NAR_40mM_plus2.16250.16250.3	3	7.83	0	4.11E+04		(K)VLISSLQ	(K)V/L/I|S/S L Q D C L H G\I E S K(S)	C:Carbamidomethylation	161.47	600.3172	1798.937	0.0003	0.2	5.32	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
15132	dirMS_041712_NAR_40mM_plus2.7234.7297.2	2	7.83	0	1.75E+04		(K)EEYGPG	(K)E E|Y/G P G V/Q G K(E)		102.88	532.252	1063.506	-0.0087	-8.2	4.53	60692.5	7.44	HUMAN	D6RDG4	Centrosomal protein POC5
15133	dirMS_041712_NAR_50mM_plus2.14129.14129.3	3	7.83	1	6.91E+04		(K)VVSSSIV	(K)V V|S/S S I/V D K Y I/G E S A R(L)		142.2	570.6392	1709.907	-0.0038	-2.2	6.04	29938.9	6.07	HUMAN	H0YJC0	26S protease regulatory subunit 10B (Fragment)
15134	dirMS_041712_NAR_50mM_plus2.15604.15604.3	3	7.83	1	1.01E+06		(R)KVPGVT	(R)K\V P G V/T A/I|E L/D/E\D/T/G T F R(I)		149.87	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
15135	dirMS_041712_NAR_50mM_plus2.17399.17399.3	3	7.83	1	2.24E+05		(K)GSFLDKI	(K)G S/F/L D\K I/S/P S V L R(N)		159.93	473.6038	1418.8	-0.0033	-2.4	8.75	64248.4	9.08	HUMAN	Q9BW04	Specifically androgen-regulated gene protein
15136	dirMS_041712_NAR_50mM_plus2.5917.5925.3	3	7.83	0	3.28E+05		(K)TVEAEA	(K)T\V|E/A E A A/H/G T V T R(H)		94.9	447.8962	1341.676	-0.0017	-1.2	5.37	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
15137	dirMS_041712_NAR_60mM_plus.10876.10876.3	3	7.83	1	2.07E+05		(R)VKYETEL	(R)V K Y E T E/L|A/M/R(Q)		114.87	413.8859	1239.64	0.003	2.4	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
15138	dirMS_041712_NAR_60mM_plus.14296.14296.3	3	7.83	1	6.49E+05		(K)WKDSDE	(K)W K D S D E/A/D\L/V/L A/K(E)		131.03	497.2559	1489.753	-0.0002	-0.1	4.23	20982.2	5.23	HUMAN	Q13185	Chromobox protein homolog 3
15139	dirMS_041712_NAR_120mM_minus.14589.14589.4	4	7.82	2	3.97E+05		(K)IANILKD	(K)I A N\I\L K/D K D P/P I/P V A K(I)		133.75	433.764	1732.037	-0.0026	-1.5	8.5	73273.4	4.96	HUMAN	P13667	Protein disulfide-isomerase A4
15140	dirMS_041712_NAR_120mM_minus.17250.17250.4	4	7.82	2	5.35E+05		(R)YEEIVKE	(R)Y E/E I V K/E V/S/T Y/I K/K(I)		148.72	432.9911	1728.942	0.0007	0.4	6.23	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
15141	dirMS_041712_NAR_120mM_minus.20834.20834.4	4	7.82	1	5.83E+05		(R)SLHDAL	(R)S L H D A\L C/V/L A Q/T V K/D/S R(T)	C:Carbamidomethylation	173.1	479.0049	1912.991	0.0068	3.6	6.47	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
15142	dirMS_041712_NAR_120mM_minus.8605.8605.3	3	7.82	1	6.61E+05	M2372m	(R)RGYFDE	(R)R G Y\F D|E E/m/N/R(V)	m:Oxidized methionine	101.67	444.8632	1316.569	16.0062	8.5	4.68	266161	5.68	HUMAN	E9PPU0	Epiplakin
15143	dirMS_041712_NAR_20mM_minus.10454.10454.2	2	7.82	0	1.44E+05		(R)IYVVDV	(R)I Y|V|V/D/V G S/E P R(A)		152.93	617.3216	1233.647	-0.0115	-9.3	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
15144	dirMS_041712_NAR_30mM_minus2.12315.12315.2	2	7.82	0	1.33E+05		(K)SIYYITG	(K)S I|Y Y/I/T/G E S K(E)		121.08	580.7949	1160.583	-0.0009	-0.7	5.72	16789.1	8.77	HUMAN	H0Y5S7	Heat shock protein HSP 90-beta (Fragment)
15145	dirMS_041712_NAR_40mM_minus2.9457.9457.3	3	7.82	0	9.99E+04		(K)AASDIA	(K)A A\S D|I\A|M T E L/P/P T H P I R(L)		138.25	607.3174	1819.937	0.0006	0.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
15146	dirMS_041712_NAR_50mM_minus2.10460.10460.3	3	7.82	1	2.39E+05		(K)NQVAM	(K)N Q|V\A M/N P T/N T/V F D A K R(L)		128.35	602.6379	1805.896	0.0029	1.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)

15147	dirMS_041712_NAR_50mM_minus2.14091.14091.3	3	7.82	1	2.89E+05	M93m	(K)SELVAm	(K)S E|L|V/A m L E/E E E L R/K(A)	m:Oxidized methionine	148.75	564.6215	1675.857	15.9928	-1.2	4.32	18679.2	5.61	HUMAN	B4DWW1	ADP-ribosylation factor-like protein 1
15148	dirMS_041712_NAR_50mM_minus2.7735.7735.3	3	7.82	1	1.66E+04	M26m	(K)LAEQAE	(K)L/A/E Q/A E R Y D D M A A C m K(S)	C:Carbamidomethylation m:Oxid	111.05	639.9511	1901.819	16.0197	12.9	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
15149	dirMS_041712_NAR_60mM_minus.8335.8335.3	3	7.82	0	7.55E+04		(K)HTGPNS	(K)H T G P N\S\P D T|A/N/D/G\F V R(L)		106.42	562.2608	1684.767	0.0005	0.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
15150	dirMS_041712_NAR_120mM_plus.17087.17087.4	4	7.82	2	6.27E+05	N555n	(R)ITDnPEG	(R)I T D/n P E G K W L G/R T A R(G)	n:N-acetylglucosamine (N)	142.4	479.9954	1713.903	203.0567	-11.8	8.75	91877.7	6.48	HUMAN	B4DLN2	FYN-binding protein
15151	dirMS_041712_NAR_20mM_plus.11413.11413.2	2	7.82	0	2.16E+05		(R)YALYDA	(R)Y A|L|Y/D/A T/Y E T K(E)		151.1	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
15152	dirMS_041712_NAR_20mM_plus.19107.19107.2	2	7.82	0	2.70E+04		(R)STGEAF	(R)S T G E\A F|V/Q/F A|S Q E I/A/E K(A)		203.23	921.4477	1841.892	-0.0035	-1.9	4.25	24249.1	6.99	HUMAN	D6RBM0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
15153	dirMS_041712_NAR_30mM_plus2.17044.17044.2	2	7.82	0	2.27E+05		(K)ACGNFG	(K)A C|G\N F/G/I\P/C\E L R(V)	C:Carbamidomethylation	142.65	697.3237	1393.635	0.005	3.6	6.05	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
15154	dirMS_041712_NAR_30mM_plus2.23521.23521.2	2	7.82	0	1.80E+05		(R)IAIYELLF	(R)I A|I|Y E L/L F K(E)		190.25	555.3331	1109.661	-0.0016	-1.4	6	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
15155	dirMS_041712_NAR_30mM_plus2.7022.7023.2	2	7.82	0	1.55E+05		(R)SLGYTG	(R)S L|G/Y T/G A R(N)		90.92	412.7157	824.426	-0.002	-2.4	8.46	12587.1	5.85	HUMAN	Q8NFU3	Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 1
15156	dirMS_041712_NAR_40mM_plus2.10352.10352.2	2	7.82	0	2.87E+04		(K)YNNCWI	(K)Y N|N|C W L/A/R(T)	C:Carbamidomethylation	125.6	548.7522	1096.499	-0.0022	-2	8.75	55416	8.63	HUMAN	H0YM31	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
15157	dirMS_041712_NAR_40mM_plus2.10806.10806.3	3	7.82	1	4.32E+05		(R)DGKLVS	(R)D G K L\V\S|E/S S/D|V L P K(-)		128.65	491.9315	1473.78	0.0004	0.3	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
15158	dirMS_041712_NAR_40mM_plus2.12296.12296.3	3	7.82	0	2.67E+05		(K)AASDIAI	(K)A A\S D/I/A M/T/E L/P P T H P I R(L)		139.33	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
15159	dirMS_041712_NAR_40mM_plus2.13320.13320.3	3	7.82	1	1.17E+05		(R)ETFEKTP	(R)E T/F E K/T/P V E/V/P V G G F K(G)		144.53	588.6444	1763.921	-0.0028	-1.6	4.79	533778	5.74	HUMAN	Q15149	Plectin
15160	dirMS_041712_NAR_50mM_plus2.11016.11016.3	3	7.82	0	1.94E+05		(K)ADDGRF	(K)A/D/D G/R/P F/P Q\V I K(S)		125.1	448.2419	1342.711	-0.0002	-0.2	6	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
15161	dirMS_041712_NAR_50mM_plus2.6989.6989.3	3	7.82	1	6.65E+05		(K)IVADKD	(K)I V/A D/K D/Y S V/T A N S K(I)		101.85	504.2628	1510.775	-0.0009	-0.6	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
15162	dirMS_041712_NAR_60mM_plus.19425.19425.3	3	7.82	1	1.69E+04		(K)RSIQFVD	(K)R S I Q\F|V/D W/C/P T G/F K(V)	C:Carbamidomethylation	159.92	580.9558	1740.853	0.0002	0.1	8.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
15163	dirMS_041712_NAR_60mM_plus.20659.20659.3	3	7.82	1	4.94E+05		(R)DSIVAEL	(R)D S\I/V/A\E L/D R E M S R(S)		168.35	507.5883	1520.737	0.013	8.6	4.32	34709.6	4.98	HUMAN	O14579	Coatomer subunit epsilon
15164	dirMS_041712_NAR_60mM_plus.6746.6747.3	3	7.82	1	4.05E+05		(R)GPPPPP	(R)G P|P|P/P P/T A S E P T R/R(S)		93.85	487.2585	1459.765	-0.0043	-2.9	9.6	124127.1	8.81	HUMAN	O14776	Transcription elongation regulator 1
15165	dirMS_041712_NAR_120mM_minus.11703.11703.4	4	7.81	1	4.65E+05		(K)AAQASD	(K)A A|Q/A S D/L E K I H L D/E K(S)		117.83	417.7202	1667.86	-0.0009	-0.6	4.75	37710.6	6.36	HUMAN	P37837	Transaldolase
15166	dirMS_041712_NAR_120mM_minus.14902.14902.4	4	7.81	1	3.27E+05		(K)LDKAQII	(K)L D\K A Q I\H\D\L V\L\V/G/G/S T R(I)		135.53	456.2581	1822.018	-0.0076	-4.1	6.75	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
15167	dirMS_041712_NAR_120mM_minus.20030.20030.3	3	7.81	1	2.47E+05		(R)AKFEELN	(R)A K F E E\L\N|M/D/L/F R(S)		164.85	504.9216	1512.752	-0.0013	-0.8	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
15168	dirMS_041712_NAR_120mM_minus.6023.6023.3	3	7.81	1	5.64E+05		(K)TCEESSF	(K)T/C/E E/S/S F C/K R(Q)	C:Carbamidomethylation	86.8	435.1849	1303.541	-0.0004	-0.3	5.81	10576.1	11.44	HUMAN	E9PRF8	Neutral alpha-glucosidase AB
15169	dirMS_041712_NAR_120mM_minus.7980.7980.3	3	7.81	1	1.05E+05		(R)GIPAPEE	(R)G I|P/A/P E E/E R T R(Q)		97.63	418.8859	1254.644	-0.0005	-0.4	4.79	23092.1	6.93	HUMAN	G3V438	Activator of 90 kDa heat shock protein ATPase homolog 1 (Fragment)
15170	dirMS_041712_NAR_30mM_minus2.16551.16551.2	2	7.81	1	4.00E+05	M427m	(K)TFmGKA	(K)T/F|m G K A Q N Q/K(Y)	m:Oxidized methionine	143.83	584.7961	1152.583	16.0019	6	10	70579.2	10.03	HUMAN	Q96MC4	Protein LOC100653515
15171	dirMS_041712_NAR_30mM_minus2.5754.5754.2	2	7.81	0	5.20E+04		(K)AAQEEY	(K)A A|Q/E|E/Y V/K(R)		85.57	469.2383	937.462	0.0068	7.2	4.53	39795.8	9.08	HUMAN	H3BQN4	Fructose-bisphosphate aldolase
15172	dirMS_041712_NAR_50mM_minus2.17558.17558.3	3	7.81	0	2.60E+05		(R)LLLDGAI	(R)L/L|L D G A/P L I A I H K(A)		168.5	458.6218	1373.852	-0.0007	-0.5	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
15173	dirMS_041712_NAR_50mM_minus2.8989.8989.3	3	7.81	1	1.31E+05	M227m	(R)mQKEIT	(R)m Q K E\I T/A\L\A/P S T M K(I)	m:Oxidized methionine	119.48	522.2727	1548.812	15.9911	-2.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
15174	dirMS_041712_NAR_50mM_minus2.9465.9465.3	3	7.81	0	1.62E+05	M329m	(K)SNmGHI	(K)S N/m G H P E/P A/S G L/A A L A/K(V)	m:Oxidized methionine	122.68	556.279	1650.827	15.9956	0.4	6.47	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
15175	dirMS_041712_NAR_60mM_minus.11466.11466.3	3	7.81	1	1.64E+05		(K)NVDILKD	(K)N/V|D I/L K/D P E T\V K(Q)		124.33	457.5867	1370.753	-0.007	-5.1	4.56	124524.8	5.71	HUMAN	O14980	Exportin-1
15176	dirMS_041712_NAR_60mM_minus.15740.15740.3	3	7.81	1	3.52E+05		(R)IFDSEEIL	(R)I F/D S E/E I/L A/G Y K/R(E)		148.53	514.2713	1540.801	-0.0012	-0.8	4.68	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
15177	dirMS_041712_NAR_60mM_minus.18009.18009.3	3	7.81	1	8.27E+04		(R)GIGFGD	(R)G I/G\F/G D/I F K E/G S V\K(L)		161.53	485.2617	1453.769	0.002	1.4	6.07	71678	6.07	HUMAN	Q9Y5K6	CD2-associated protein
15178	dirMS_041712_NAR_120mM_plus.4674.4674.3	3	7.81	1	2.69E+05		(R)LKQSAEI	(R)L K Q S A E/E/Q/A/Q/A R(A)		74.47	453.5701	1358.702	-0.0065	-4.8	6.14	533778	5.74	HUMAN	Q15149	Plectin
15179	dirMS_041712_NAR_120mM_plus.8058.8058.3	3	7.81	2	2.08E+05	M53m	(K)LTDCVV	(K)L/T/D/C V V m R D/P A S K/R(S)	C:Carbamidomethylation m:Oxid	95.88	555.2807	1647.831	15.997	1.3	8.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
15180	dirMS_041712_NAR_20mM_plus.13316.13316.2	2	7.81	0	4.16E+05	M148m	(R)DLTDYLr	(R)D L|T|D/Y L m K(I)	m:Oxidized methionine	164.53	507.7439	998.486	15.9942	-0.7	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
15181	dirMS_041712_NAR_30mM_plus2.10885.10885.2	2	7.81	0	5.81E+05		(K)EAAENS	(K)E A|A/E/N S L V/A/Y K(A)		110.2	597.8036	1194.6	-0.0002	-0.1	4.53	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
15182	dirMS_041712_NAR_30mM_plus2.11301.11301.2	2	7.81	0	4.39E+05		(K)TTDGYLI	(K)T/T|D/G Y L L/R(L)		112.55	469.75	938.494	-0.0014	-1.5	5.5	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
15183	dirMS_041712_NAR_30mM_plus2.12835.12835.2	2	7.81	0	3.14E+05		(K)QQIQSIC	(K)Q Q/I/Q/S I/Q Q S I E R(L)		120.75	729.3893	1457.771	0.0006	0.4	6	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
15184	dirMS_041712_NAR_30mM_plus2.16805.16805.2	2	7.81	0	3.48E+05		(K)QLQEMI	(K)Q L/Q/E M L G/L/S K(V)		140.83	573.8112	1146.619	-0.0036	-3.1	6	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
15185	dirMS_041712_NAR_30mM_plus2.16882.16882.2	2	7.81	0	3.72E+05		(K)SNQQLV	(K)S N/Q Q/L/V/D I I E K(V)		141.28	643.8504	1286.695	-0.0015	-1.2	4.37	22568.6	6.35	HUMAN	B3KQ25	Proteasome activator complex subunit 3
15186	dirMS_041712_NAR_30mM_plus2.18236.18444.2	2	7.81	0	1.64E+04		(K)VVNSILA	(K)V V|N/S\I L A/F/R(E)		149.52	509.8031	1018.604	-0.0055	-5.4	9.72	56564.1	6.56	HUMAN	B4DNW0	Aminoacylase-1
15187	dirMS_041712_NAR_30mM_plus2.20825.20825.2	2	7.81	0	1.89E+05		(K)GGIVGM	(K)G G I|V|G|M/T/L P I A R(D)		162.95	592.8453	1184.682	0.0013	1.1	9.75	27150.8	7.95	HUMAN	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2
15188	dirMS_041712_NAR_40mM_plus2.12870.12870.3	3	7.81	0	7.57E+04		(R)GVVGG	(R)G V\V/G G/V T G I I/T K/P V/E G A K(K)		142.2	561.3291	1681.985	-0.012	-7.1	8.59	424721.6	6.38	HUMAN	Q709C8	Vacuolar protein sorting-associated protein 13C
15189	dirMS_041712_NAR_40mM_plus2.7709.7709.2	2	7.81	0	1.42E+05		(R)SGYFDEI	(R)S/G|Y/F D/E/R(Y)		104.62	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
15190	dirMS_041712_NAR_50mM_plus2.11363.11363.3	3	7.81	1	1.25E+06		(K)NQVAM	(K)N Q|V|A M/N/P T N T V/F D A K/R(L)		127.8	602.6354	1805.896	-0.0046	-2.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
15191	dirMS_041712_NAR_50mM_plus2.15009.15009.3	3	7.81	0	8.53E+05		(K)LHIIEVG	(K)L H I\I E V G T|P/P T G N Q/P F P K(K)		147.05	649.0216	1945.054	-0.0039	-2	6.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
15192	dirMS_041712_NAR_50mM_plus2.16467.16467.3	3	7.81	0	7.49E+05		(K)ANIVHLI	(K)A N\I V H L\M\L|S|S/P E Q I Q K(Q)		154.68	603.3265	1807.974	-0.0085	-4.7	6.79	104619	5.75	HUMAN	F8W904	Exportin-2
15193	dirMS_041712_NAR_20mM_minus.12307.12307.3	3	7.8	0	4.95E+05	M256m	(R)SLDmDS	(R)S L\D m\D S I/I A E V K(A)	m:Oxidized methionine	171.55	446.227	1320.671	15.9949	0	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
15194	dirMS_041712_NAR_30mM_minus2.19223.19223.2	2	7.8	0	8.88E+05		(K)MSIYQA	(K)M/S/I\Y/Q/A M W/K(G)		159	579.2789	1157.548	0.0023	2	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
15195	dirMS_041712_NAR_30mM_minus2.5125.5125.2	2	7.8	0	1.17E+05		(R)SNAEDT	(R)S N\A/E/D/T/L R(S)		81.43	453.2209	905.432	0.0022	2.5	4.37	533778	5.74	HUMAN	Q15149	Plectin
15196	dirMS_041712_NAR_40mM_minus2.14948.14948.3	3	7.8	0	9.28E+05		(K)ISSIQSIV	(K)I/S\S I/Q|S/I V/P A L E I A N/A H R(K)		172.32	640.3618	1919.071	0	0	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
15197	dirMS_041712_NAR_50mM_minus2.17242.17242.3	3	7.8	0	1.05E+06	M195m	(R)LHFFmP	(R)L H F F m\P G|F/A/P L T S R(G)	m:Oxidized methionine	167.33	546.2872	1620.835	16.0115	10.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
15198	dirMS_041712_NAR_50mM_minus2.9596.9596.3	3	7.8	1	5.72E+05		(R)DGKLVS	(R)D G K\L V\S E|S/S D V L/P K(-)		122.92	491.9322	1473.78	0.0025	1.7	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
15199	dirMS_041712_NAR_120mM_plus.10648.10669.3	3	7.8	0	1.23E+06		(R)GLHQSIE	(R)G L/H Q S\I/E/E/F/R(A)		109.27	405.8796	1215.612	0.0126	10.4	5.4	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
15200	dirMS_041712_NAR_120mM_plus.12361.12361.3	3	7.8	1	7.57E+05		(R)EIAQDFI	(R)E I/A/Q D F/K/T D/L R(F)		118.22	445.9007	1335.69	-0.0028	-2.1	4.56	14166.5	11.62	HUMAN	B4DEB1	Histone H3
15201	dirMS_041712_NAR_120mM_plus.19355.19355.3	3	7.8	1	6.90E+05		(K)YNQLLRI	(K)Y/N|Q/L|L R I E E E L G S K(A)		155.23	564.6353	1691.896	-0.0049	-2.9	4.79	47510.4	7.04	HUMAN	P06733	Alpha-enolase
15202	dirMS_041712_NAR_120mM_plus.4693.4693.3	3	7.8	1	2.52E+05		(R)LKQSAEI	(R)L/K Q S A E E|Q/A/Q A R(A)		74.55	453.5701	1358.702	-0.0065	-4.8	6.14	533778	5.74	HUMAN	Q15149	Plectin
15203	dirMS_041712_NAR_120mM_plus.6826.6826.3	3	7.8	0	4.08E+05		(K)SQFSDKI	(K)S Q|F S/D/K/P V Q D R(G)		89.32	436.2209	1306.639	0.0095	7.3	5.68	13194	9.99	HUMAN	E9PI70	Chitinase domain-containing protein 1 (Fragment)
15204	dirMS_041712_NAR_20mM_plus.10591.10591.2	2	7.8	0	4.60E+04		(R)SGYLLPD	(R)S G Y|L/L|P/D T K(A)		145.88	497.2665	993.525	0.0006	0.6	5.55	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
15205	dirMS_041712_NAR_20mM_plus.10743.10743.2	2	7.8	0	1.38E+04	M33m	(K)VAGmD	(K)V A G m D V|E/L\T/V/E E R(N)	m:Oxidized methionine	146.43	732.3555	1447.71	15.994	-0.6	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
15206	dirMS_041712_NAR_20mM_plus.13164.13164.2	2	7.8	0	3.05E+05		(K)LSELEAA	(K)L/S|E\L|E A A/L/Q R(A)		162.3	565.3132	1129.621	-0.002	-1.8	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
15207	dirMS_041712_NAR_20mM_plus.14632.14632.2	2	7.8	0	1.51E+05		(K)LVILANN	(K)L V|I|L|A/N N C/P A L R(K)	C:Carbamidomethylation	172.47	677.3851	1353.767	-0.0042	-3.1	9.75	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
15208	dirMS_041712_NAR_30mM_plus2.12087.12207.2	2	7.8	0	7.46E+05		(K)EQFAWI	(K)E Q/F/A/W/R(H)		116.93	418.7093	836.405	0.0064	7.6	6.1	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
15209	dirMS_041712_NAR_30mM_plus2.17399.17399.2	2	7.8	0	6.98E+04		(K)WPLYMS	(K)W/P/L/Y M S T K(N)		144.88	513.2647	1025.513	0.0097	9.4	8.59	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
15210	dirMS_041712_NAR_30mM_plus2.6097.6140.2	2	7.8	0	4.34E+05	M29m	(K)ELGTVm	(K)E L/G T/V/m/R(M)	m:Oxidized methionine	86.22	411.2138	805.424	15.9967	2.1	6.1	16439	4.08	HUMAN	C9J7T9	Troponin C type 2 (Fast), isoform CRA_a
15211	dirMS_041712_NAR_30mM_plus2.6270.6270.2	2	7.8	0	8.62E+04		(K)EVYPEAI	(K)E V|Y/P E/A R(K)		87.3	432.2218	863.426	0.0106	12.2	4.53	17921.1	9.84	HUMAN	H7BZW6	Histone deacetylase complex subunit SAP18 (Fragment)
15212	dirMS_041712_NAR_30mM_plus2.7342.7342.2	2	7.8	0	1.04E+05		(R)QYEMGI	(R)Q/Y/E/M/G E/C T R(G)	C:Carbamidomethylation	92.9	587.2365	1173.466	-0.0006	-0.5	4.53	28385.1	9.78	HUMAN	Q01081	Splicing factor U2AF 35 kDa subunit
15213	dirMS_041712_NAR_40mM_plus2.14877.14877.3	3	7.8	0	5.15E+05		(K)IAILTCPI	(K)I/A|I/L T C/P F E/P P K P K(T)	C:Carbamidomethylation	153.6	537.6381	1610.898	0.0023	1.4	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
15214	dirMS_041712_NAR_40mM_plus2.8993.8993.2	2	7.8	0	3.51E+04		(K)QGYVIYI	(K)Q G/Y/V I/Y/R(I)		115.2	449.7407	898.478	-0.004	-4.5	8.59	20608.6	11.48	HUMAN	E7ENU7	Ribosomal protein L15 (Fragment)
15215	dirMS_041712_NAR_50mM_plus2.11169.11169.3	3	7.8	1	3.14E+05		(R)DLDRIAC	(R)D L/D R I\A G Q/V/A/A A/N K(K)		126.77	481.2661	1441.776	0.008	5.5	5.96	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
15216	dirMS_041712_NAR_50mM_plus2.21478.21478.3	3	7.8	1	3.74E+05	M145m	(R)GVmLA	(R)G V/m/L/A V/D/A V/I A E L K K(Q)	m:Oxidized methionine	182.63	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
15217	dirMS_041712_NAR_50mM_plus2.8228.8228.3	3	7.8	0	1.26E+05		(K)QLAVAE	(K)Q L|A V|A\E/G K/P P E A/P K(G)		109.72	478.9337	1434.795	-0.0086	-6	6.14	24364.9	9.64	HUMAN	H0YIP0	Methionine--tRNA ligase, cytoplasmic (Fragment)
15218	dirMS_041712_NAR_50mM_plus2.9056.9056.3	3	7.8	1	2.37E+05		(K)LLDGPST	(K)L/L\D G P S T E K/D L D/E K(K)		115.12	520.5958	1559.78	-0.0071	-4.5	4.11	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
15219	dirMS_041712_NAR_60mM_plus.7469.7469.3	3	7.8	1	7.00E+05		(R)LVDSVKI	(R)L V/D S V K/E N A G T V R(I)		97.73	463.2618	1387.754	0.0169	12.2	6.07	43814.8	5.94	HUMAN	Q9BRX2	Protein pelota homolog
15220	dirMS_041712_NAR_120mM_minus.11344.11344.3	3	7.79	0	2.31E+05		(R)GFCLPPI	(R)G F\C L/P/P H/C S R(G)	C:Carbamidomethylation	116.42	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
15221	dirMS_041712_NAR_20mM_minus.10736.10736.2	2	7.79	0	6.61E+04		(K)VNQIGS	(K)V N Q\I/G/S V/T\E S I/Q A C K(L)	C:Carbamidomethylation	155.45	817.4099	1633.821	-0.0089	-5.4	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
15222	dirMS_041712_NAR_20mM_minus.13807.13807.2	2	7.79	0	4.04E+05		(K)LGGSAV	(K)L G G S A\V|I/S L E/G K/P L(-)		188.7	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
15223	dirMS_041712_NAR_20mM_minus.14432.14432.2	2	7.79	0	9.57E+04		(R)LTGQLFI	(R)L T|G Q/L/F L/G G S I V\K(G)		198.62	666.8967	1332.789	-0.0024	-1.8	8.75	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
15224	dirMS_041712_NAR_50mM_minus2.11248.11248.3	3	7.79	2	1.37E+05		(K)IEELNKT	(K)I/E E L/N/K T\R E E Q I/Q K(K)		132	586.6522	1757.939	0.0028	1.6	4.95	265319.7	6.09	HUMAN	E7EUV3	Ankyrin repeat domain-containing protein 17
15225	dirMS_041712_NAR_60mM_minus.11903.11903.3	3	7.79	0	1.92E+05		(R)ILHLLGQ	(R)I/L H\L L/G Q/E/G P K(T)		126.37	402.2384	1204.705	-0.0042	-3.5	6.75	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
15226	dirMS_041712_NAR_60mM_minus.16056.16056.3	3	7.79	1	3.04E+04		(K)LPFPIIDI	(K)L P/F/P I I D D R N/R(E)		149.15	452.5849	1355.743	-0.0029	-2.1	5.96	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
15227	dirMS_041712_NAR_120mM_plus.14640.14640.3	3	7.79	1	1.72E+06		(R)QLREYQ	(R)Q L R E Y Q/E/L/M N/V/K(L)		129.28	517.6042	1550.8	-0.0015	-1	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
15228	dirMS_041712_NAR_120mM_plus.5453.5463.2	2	7.79	1	9.47E+04		(K)FKDPNA	(K)F/K|D|P N A/P K(R)		81.82	458.7454	916.489	-0.0052	-5.6	8.59	24408.7	5.92	HUMAN	B2RPK0	Putative high mobility group protein B1-like 1
15229	dirMS_041712_NAR_120mM_plus.8655.8655.2	2	7.79	0	7.93E+05		(K)HFVALS	(K)H/F|V/A L S\T N T\T K(V)		99.05	609.8311	1218.648	0.0072	5.9	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
15230	dirMS_041712_NAR_30mM_plus2.17264.17264.2	2	7.79	0	2.65E+05		(K)VSTLPAI	(K)V/S/T/L/P A I T L K(L)		143.65	521.8272	1042.651	-0.0035	-3.4	8.72	20599.3	9.19	HUMAN	H7C1V0	Cathepsin D light chain (Fragment)
15231	dirMS_041712_NAR_30mM_plus2.18336.18336.2	2	7.79	0	5.10E+04		(K)LIQLQFE	(K)L I|Q/L Q F|E V(-)		149.37	495.2847	989.567	-0.0045	-4.5	4	5560.2	5.09	HUMAN	F8VV91	POC1 centriolar protein homolog B
15232	dirMS_041712_NAR_30mM_plus2.5039.5039.2	2	7.79	0	4.39E+05		(K)QASEGP	(K)Q/A/S E G/P L K(G)		78.18	415.225	829.441	0.0013	1.6	6	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
15233	dirMS_041712_NAR_30mM_plus2.8201.8201.2	2	7.79	0	5.69E+05		(R)STFSTNY	(R)S T/F/S/T N Y R(S)		96.3	488.2306	975.453	0.0009	0.9	8.46	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
15234	dirMS_041712_NAR_40mM_plus2.11360.11360.3	3	7.79	0	1.53E+04		(R)MGQMA	(R)M G Q M A\M/G G A\M/G I/N/N/R(G)		133	513.5589	1538.67	-0.0073	-4.8	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
15235	dirMS_041712_NAR_40mM_plus2.11936.11936.3	3	7.79	1	2.13E+05		(R)VVDALG	(R)V V|D A/L/G N A I/D G K G P I G S K(T)		137.02	570.9838	1710.939	-0.0016	-1	5.93	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
15236	dirMS_041712_NAR_40mM_plus2.13302.13302.3	3	7.79	1	1.17E+05		(R)ETFEKTP	(R)E T/F E K T/P V E/V/P V G G F K(G)		144.53	588.6444	1763.921	-0.0028	-1.6	4.79	533778	5.74	HUMAN	Q15149	Plectin
15237	dirMS_041712_NAR_50mM_plus2.15146.15146.3	3	7.79	1	3.83E+05		(R)MGLAIS	(R)M/G L\A/I/S L V/A T E K E K(V)		147.57	497.2822	1489.829	0.0026	1.7	5.9	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
15238	dirMS_041712_NAR_50mM_plus2.18277.18352.3	3	7.79	0	3.57E+05		(K)MLNIHP	(K)M/L/N I/H/P S L L/P S F K(G)		164.5	499.6132	1496.829	-0.0043	-2.9	8.52	60871.9	6.3	HUMAN	B4DJ93	Phosphoribosylformylglycinamidine cyclo-ligase
15239	dirMS_041712_NAR_50mM_plus2.8904.8904.3	3	7.79	0	1.80E+05		(K)TPVEPE	(K)T P V E/P E V/A|I H R(I)		113.98	416.5627	1247.674	-0.0007	-0.6	5.37	5429.1	9.6	HUMAN	E5RIP1	40S ribosomal protein S20
15240	dirMS_041712_NAR_60mM_plus.10521.10521.2	2	7.79	1	2.08E+05		(R)LQAEIEG	(R)L Q/A\E|I/E G/L K/G Q R(A)		113.08	671.3774	1341.748	-0.001	-0.7	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
15241	dirMS_041712_NAR_60mM_plus.10818.10818.2	2	7.79	1	9.74E+05		(R)VKYETEL	(R)V/K|Y|E/T E L A M R(Q)		113.65	620.326	1239.64	0.0045	3.7	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
15242	dirMS_041712_NAR_60mM_plus.7083.7099.2	2	7.79	0	4.34E+05		(K)SVPADL	(K)S V|P|A/D/L S R P K(S)		95.35	535.3025	1069.6	-0.0023	-2.2	8.46	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
15243	dirMS_041712_NAR_120mM_minus.17110.17110.4	4	7.78	1	2.93E+05		(R)ELDTVTI	(R)E L D T\V/T L/E D I/K E H V/K(Q)		148.33	442.9877	1768.933	-0.0038	-2.1	4.5	61090.6	8.58	HUMAN	O43242	26S proteasome non-ATPase regulatory subunit 3
15244	dirMS_041712_NAR_20mM_minus.14663.14663.2	2	7.78	0	9.62E+04		(K)IYVDDGI	(K)I/Y|V D/D\G L I\S L Q V|K(Q)		201.6	731.9104	1462.815	-0.0016	-1.1	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
15245	dirMS_041712_NAR_30mM_minus2.15029.15029.2	2	7.78	1	6.03E+06		(K)INWSKQ	(K)I N\W S/K/Q\Q K(R)		134.48	516.281	1031.563	-0.0085	-8.3	10	526822	6.64	HUMAN	Q9NZJ4	Sacsin
15246	dirMS_041712_NAR_30mM_minus2.5251.5251.2	2	7.78	0	6.29E+05		(R)TDTGEP	(R)T/D|T G E\P M G R(G)		82.28	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
15247	dirMS_041712_NAR_30mM_minus2.5441.5441.2	2	7.78	0	4.03E+05		(R)TDTGEP	(R)T\D|T/G E P M G R(G)		82.9	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
15248	dirMS_041712_NAR_40mM_minus2.13432.13432.3	3	7.78	0	1.46E+05		(K)VAIVKPC	(K)V/A/I V/K P G V|P M/E/I V L N K(E)		163.22	569.6777	1707.024	-0.0052	-3	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
15249	dirMS_041712_NAR_50mM_minus2.10883.10883.3	3	7.78	1	5.21E+05		(K)QQEAAL	(K)Q\Q E A/A/L E/L/E E L/K/K(K)		131.05	510.2775	1528.822	-0.0038	-2.5	4.49	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
15250	dirMS_041712_NAR_50mM_minus2.11291.11291.3	3	7.78	0	1.66E+04		(R)VVVLMC	(R)V V\V L/M/G S T/S D L/G H C E K(I)	C:Carbamidomethylation	132.28	577.9535	1731.84	0.0055	3.2	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
15251	dirMS_041712_NAR_50mM_minus2.16899.16899.3	3	7.78	1	1.27E+05		(K)NIPIPTLI	(K)N I\P/I/P T L K D/F A/K(A)		163.62	452.9385	1356.789	0.0124	9.1	8.59	20960.6	7.05	HUMAN	H0YKU1	Tropomodulin-3 (Fragment)
15252	dirMS_041712_NAR_50mM_minus2.9587.9587.3	3	7.78	1	6.36E+04		(R)LVGGPM	(R)L/V|G G/P M D A S V E E E G V R R(A)		122.72	600.976	1800.891	0.0226	12.5	4.41	16027.2	9.57	HUMAN	P01034	Cystatin-C
15253	dirMS_041712_NAR_60mM_minus.18641.18641.3	3	7.78	0	1.54E+05		(K)KPGGFD	(K)K P G G F D/I/S L/F/Y R(D)		165.25	467.2495	1399.737	-0.0029	-2.1	8.59	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
15254	dirMS_041712_NAR_120mM_plus.4125.4125.2	2	7.78	1	1.28E+06	M310m	(R)TKTEISE	(R)T/K|T E/I/S/E m N R(N)	m:Oxidized methionine	69.7	612.7976	1208.594	15.994	-0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
15255	dirMS_041712_NAR_120mM_plus.6772.6772.2	2	7.78	0	8.91E+04		(K)SYSEDDI	(K)S Y|S|E D D I/H R(S)		88.72	561.2464	1121.486	-0.0003	-0.2	4.53	55504.9	9.2	HUMAN	F8W840	YTH domain family protein 1

15256	dirMS_041712_NAR_20mM_plus.14756.14756.3	3	7.78	0	5.44E+04	M174m	(K)AmGAA	(K)A m G A A Q V\V|V/T D/L/S A T R(L)	m:Oxidized methionine	173.1	535.9457	1589.832	15.991	-2.5	5.88	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
15257	dirMS_041712_NAR_20mM_plus.17920.17920.2	2	7.78	0	9.08E+04		(K)SLESLDT	(K)S L|E/S|L/D\T S\L F A K(N)		195.17	655.8428	1310.684	-0.0055	-4.2	4.37	52796.2	5.19	HUMAN	E7EUT8	Splicing factor 3A subunit 3
15258	dirMS_041712_NAR_30mM_plus2.5815.5815.2	2	7.78	0	1.64E+05		(K)TSEVNC	(K)T\S|E/V/N C Y R(C)	C:Carbamidomethylation	84.77	514.7261	1028.447	-0.0016	-1.6	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
15259	dirMS_041712_NAR_30mM_plus2.8950.8950.2	2	7.78	0	3.22E+05		(R)FGQGG	(R)F G Q/G G/A|G/P V/G G\Q G P R(G)		100.47	671.3359	1341.666	-0.0013	-1	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
15260	dirMS_041712_NAR_40mM_plus2.18956.18956.3	3	7.78	0	3.84E+05		(R)DYLHLP	(R)D Y\L H L\P P E\I\V/P A T\L R(R)		177.72	578.6565	1733.959	-0.0035	-2	5.32	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
15261	dirMS_041712_NAR_50mM_plus2.8255.8255.3	3	7.78	0	9.46E+04		(K)ATAGDT	(K)A T/A/G/D/T H L G G E D F D N R(L)		110.23	559.2487	1675.731	0.0009	0.5	4.22	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
15262	dirMS_041712_NAR_50mM_plus2.8734.8734.3	3	7.78	0	7.40E+05		(R)AALAHS	(R)A A L A H S E E\V|T|A|S Q V A A T K(T)		113.43	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
15263	dirMS_041712_NAR_60mM_plus.13627.13627.3	3	7.78	0	8.95E+05		(K)NVDDIL	(K)N V/D|D I L/K/P|P G R(E)		127.77	408.563	1223.674	0.0002	0.2	5.96	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
15264	dirMS_041712_NAR_60mM_plus.19748.19748.3	3	7.78	1	4.05E+04		(K)SLLGKD	(K)S L/L/G K D\V L F/L K(D)		162.9	411.5915	1232.761	-0.0013	-1.1	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
15265	dirMS_041712_NAR_60mM_plus.20420.20420.3	3	7.78	0	1.25E+06		(R)IHFPLAT	(R)I H/F P L A T Y A/P V/I S A E K(A)		166.1	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
15266	dirMS_041712_NAR_60mM_plus.7162.7162.2	2	7.78	0	3.11E+05		(K)TIEAEA	(K)T I|E|A/E/A/A H|G T V T R(H)		95.57	678.3494	1355.691	0.0002	0.1	5.37	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
15267	dirMS_041712_NAR_120mM_minus.16061.16061.4	4	7.77	1	6.84E+04		(K)QLEAID	(K)Q L E A I/D Q L H/L E Y A/K R(A)		141.72	457.499	1826.976	-0.0018	-1	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
15268	dirMS_041712_NAR_120mM_minus.18460.18460.3	3	7.77	1	1.91E+05		(R)ARFEEL	(R)A R F E E\L|N A/D/L/F/R(G)		155.52	494.2561	1480.754	-0.0006	-0.4	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
15269	dirMS_041712_NAR_120mM_minus.7932.7932.3	3	7.77	1	3.44E+05		(R)LCAGAS	(R)L/C|A G A/S E D/I R E K(L)	C:Carbamidomethylation	97.58	450.224	1348.652	0.0049	3.6	4.68	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
15270	dirMS_041712_NAR_20mM_minus.14699.14699.3	3	7.77	0	3.68E+05		(K)LAVEAL	(K)L/A V E\A L S S/L/D G D L A/G R(Y)		201.3	529.6163	1586.838	-0.0041	-2.6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
15271	dirMS_041712_NAR_20mM_minus.8806.8806.2	2	7.77	0	1.72E+05		(K)IVVVTA	(K)I V|V|V/T A G V/R(Q)		137.97	457.2947	913.583	-0.0008	-0.9	9.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
15272	dirMS_041712_NAR_30mM_minus2.8441.8441.2	2	7.77	0	1.09E+05		(K)CAMTAL	(K)C A|M/T/A L S S K(L)	C:Carbamidomethylation	100.45	484.7299	968.454	-0.0014	-1.5	8.75	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
15273	dirMS_041712_NAR_40mM_minus2.8074.8074.3	3	7.77	0	1.70E+05	M35m	(K)AASDIA	(K)A A|S D I|A m T E/L/P P T H P I R(L)	m:Oxidized methionine	128.2	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
15274	dirMS_041712_NAR_50mM_minus2.10538.10538.3	3	7.77	1	2.76E+05		(K)NQVAM	(K)N Q|V|A/M/N/P T N T V/F D A K R(L)		128.5	602.6379	1805.896	0.0029	1.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
15275	dirMS_041712_NAR_50mM_minus2.13528.13528.3	3	7.77	0	2.87E+05		(K)VIQYLAY	(K)V I|Q\Y L/A Y V/A/S S H K(S)		144.65	493.6043	1478.8	-0.0018	-1.2	8.48	227783.5	5.5	HUMAN	P35579	Myosin-9
15276	dirMS_041712_NAR_50mM_minus2.14064.14064.3	3	7.77	0	5.03E+04		(K)MLDAE	(K)M/L/D A/E D\I/V/N T A\R P D E K(A)		148.05	606.2965	1816.875	0.0004	0.2	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
15277	dirMS_041712_NAR_50mM_minus2.8550.8550.3	3	7.77	1	2.43E+05		(R)AGTGV	(R)A G/T/G V/D N V D/L E/A A T R\K(G)		116.55	539.6119	1616.824	-0.0027	-1.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
15278	dirMS_041712_NAR_50mM_minus2.9727.9727.3	3	7.77	0	7.38E+04		(R)ELTLEKP	(R)E L/T/L/E K/P E L K(A)		123.72	400.5678	1199.688	0.0007	0.6	4.79	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
15279	dirMS_041712_NAR_60mM_minus.4741.4741.3	3	7.77	1	1.35E+06		(R)AAEEED	(R)A A|E|E E D E A/D P K R(Q)		78.07	453.872	1359.602	-0.0008	-0.6	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
15280	dirMS_041712_NAR_60mM_minus.6464.6464.3	3	7.77	1	8.87E+04		(K)SESPKEP	(K)S E/S/P K E|P E/Q L R(K)		94.9	433.8887	1299.654	-0.0024	-1.8	4.78	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
15281	dirMS_041712_NAR_120mM_plus.10142.10142.4	4	7.77	2	2.11E+06		(K)MQASIE	(K)M Q/A S I E K G G S L/P K V E/A/K(F)		105.87	443.9944	1772.958	-0.0017	-1	8.25	32745.6	4.64	HUMAN	P06748	Nucleophosmin
15282	dirMS_041712_NAR_20mM_plus.6724.6724.3	3	7.77	0	1.25E+05	M136m	(R)LVAGE	(R)L V\A G E m G Q N E|P D Q/G G Q R(G)	m:Oxidized methionine	111.45	601.2753	1785.818	15.9929	-1.1	4.14	17508.7	8.03	HUMAN	Q5H928	3-hydroxyacyl-CoA dehydrogenase type-2
15283	dirMS_041712_NAR_20mM_plus.9357.9357.3	3	7.77	0	1.27E+05		(K)SVTNED	(K)S V\T N E/D\V/T Q/E E L G G A K(T)		136	559.6039	1676.797	-0.0002	-0.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
15284	dirMS_041712_NAR_30mM_plus2.14691.14691.2	2	7.77	0	3.22E+05		(R)YQETFN	(R)Y Q|E|T/F N/V/I E R(C)		129.92	649.8225	1298.638	0.0002	0.1	4.53	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
15285	dirMS_041712_NAR_40mM_plus2.11738.11738.2	2	7.77	0	3.85E+04		(K)IAWALS	(K)I/A|W/A/L S R(K)		135.12	408.7393	816.473	-0.0013	-1.6	9.75	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
15286	dirMS_041712_NAR_40mM_plus2.12914.12914.2	2	7.77	0	4.67E+04		(K)ALWFQ	(K)A L/W/F/Q G R(C)		142.58	439.2366	877.468	-0.002	-2.3	9.79	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
15287	dirMS_041712_NAR_40mM_plus2.8314.8314.2	2	7.77	0	7.91E+04		(K)FGGAFC	(K)F/G|G A/F/C/R(Y)	C:Carbamidomethylation	109.7	407.6883	814.366	0.0029	3.5	9.75	33411.4	5.35	HUMAN	Q96QR8	Transcriptional activator protein Pur-beta
15288	dirMS_041712_NAR_40mM_plus2.8984.8984.3	3	7.77	0	9.66E+04	S148s	(R)VSAIVE	(R)V/S/A I V\E/Q s W/R(D)	s:N-acetylglucosamine (S)	115.02	459.8999	1174.622	203.0636	-11.4	5.97	17429.2	5.06	HUMAN	P49459	Ubiquitin-conjugating enzyme E2 A
15289	dirMS_041712_NAR_50mM_plus2.10029.10029.3	3	7.77	1	2.08E+05		(K)GVAIN	(K)G V/A/I/N M V/T E E D/K R(T)		119.98	487.9171	1461.737	0.0001	0.1	4.68	46381.4	5.32	HUMAN	P60842	Eukaryotic initiation factor 4A-I
15290	dirMS_041712_NAR_50mM_plus2.11313.11313.3	3	7.77	1	2.98E+05		(R)ETGVDL	(R)E T/G V/D L T K D N M/A L Q/R(V)		127.18	564.2856	1690.843	-0.0006	-0.4	4.56	73964.5	5.87	HUMAN	P38646	Stress-70 protein, mitochondrial
15291	dirMS_041712_NAR_50mM_plus2.13940.13940.3	3	7.77	0	1.30E+06		(K)DLAGCI	(K)D L/A/G C I/H/G L S N V K(L)	C:Carbamidomethylation	140.57	461.9061	1383.705	-0.0012	-0.8	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
15292	dirMS_041712_NAR_50mM_plus2.5206.5211.3	3	7.77	0	5.02E+05	M434m M	(R)LESGmC	(R)L/E|S/G m Q N m S I/H/T K(T)	m:Oxidized methionine	86.25	503.2336	1475.698	31.9881	-1.1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
15293	dirMS_041712_NAR_50mM_plus2.9620.9620.3	3	7.77	0	3.09E+05		(R)EIVHIQA	(R)E/I\V H I Q A G Q/C/G N Q I G A K(F)	C:Carbamidomethylation	117.67	608.3107	1822.923	-0.0053	-2.9	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
15294	dirMS_041712_NAR_60mM_plus.11304.11304.2	2	7.77	0	7.25E+05		(R)GSAVHC	(R)G S A\V/H|Q/L/S E E/L R(C)		116.43	663.3438	1325.681	-0.0005	-0.4	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
15295	dirMS_041712_NAR_60mM_plus.18919.18919.3	3	7.77	1	1.52E+05		(R)LGLSTL	(R)L/G\L/S/T/L G E L/K Q N L S R(S)		155.95	543.6465	1628.933	-0.008	-4.9	8.75	22294.4	5.26	HUMAN	O43399	Tumor protein D54
15296	dirMS_041712_NAR_120mM_minus.9343.9343.2	2	7.76	0	1.66E+04		(K)HVVFIA	(K)H|V|V/F I A/Q/R(R)		105.2	485.2837	969.563	-0.0027	-2.8	9.75	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
15297	dirMS_041712_NAR_120mM_minus.9356.9356.3	3	7.76	0	3.59E+05		(R)GAGGQ	(R)G A G G Q S M S E A/P T G/D H A|P A P T R(M)		105.28	665.6353	1994.899	-0.0071	-3.6	5.32	199069.4	5.12	HUMAN	G3V3X5	Latent-transforming growth factor beta-binding protein 2
15298	dirMS_041712_NAR_20mM_minus.11535.11535.2	2	7.76	0	2.05E+05		(R)GDLGIEI	(R)G D/L/G/I|E I/P A E K(V)		163.83	571.3078	1141.61	-0.0016	-1.4	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
15299	dirMS_041712_NAR_20mM_minus.13450.13450.3	3	7.76	0	8.37E+04		(R)LLDAQL	(R)L L D A Q L A|T G G\I/V D/P R(L)		184.95	513.6197	1538.854	-0.0091	-5.9	4.21	533778	5.74	HUMAN	Q15149	Plectin
15300	dirMS_041712_NAR_30mM_minus2.14130.14130.2	2	7.76	0	1.69E+05		(R)VPELFA	(R)V/P/E/L/F A N R(G)		129.95	473.2631	945.515	0.0037	3.9	5.97	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
15301	dirMS_041712_NAR_30mM_minus2.14903.14903.2	2	7.76	0	1.40E+05		(R)WALSQ	(R)W/A/L|S Q/S N P S A L R(E)		134.55	665.3481	1329.691	-0.0021	-1.5	9.75	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
15302	dirMS_041712_NAR_30mM_minus2.18287.18325.2	2	7.76	0	1.27E+05		(K)GLGILSL	(K)G L|G/I L/S/L K(Q)		154.3	400.7655	800.524	-0.0003	-0.4	8.75	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
15303	dirMS_041712_NAR_40mM_minus2.9556.9556.3	3	7.76	0	2.91E+04	M5m	(R)EmQDVI	(R)E m/Q|D/V D L/A/E V/K P L V E K(G)	m:Oxidized methionine	138.73	620.3199	1842.952	15.9934	-0.8	4.18	18328.6	4.58	HUMAN	E5RGM5	Protein NDRG1 (Fragment)
15304	dirMS_041712_NAR_60mM_minus.13774.13774.3	3	7.76	1	2.11E+05		(R)MTGSEF	(R)M/T/G/S E F D F E E M K/R(K)		136.43	536.2333	1606.688	-0.0023	-1.4	4.41	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
15305	dirMS_041712_NAR_60mM_minus.16858.16858.3	3	7.76	1	2.55E+05		(R)YRVPDV	(R)Y R V P D V\L V/A/D/P P I\A R(L)		154.5	560.9843	1680.943	-0.0048	-2.9	5.96	96499.9	5.43	HUMAN	F5H6X6	Neutral alpha-glucosidase AB
15306	dirMS_041712_NAR_60mM_minus.19021.19021.3	3	7.76	0	5.31E+05		(R)LGFHLPI	(R)L G F H L P L/E|V/A Y/Q R(G)		168.52	514.9512	1542.843	-0.0037	-2.4	6.75	533778	5.74	HUMAN	Q15149	Plectin
15307	dirMS_041712_NAR_120mM_plus.8085.8085.2	2	7.76	0	1.42E+06		(R)HQGVM	(R)H Q|G V M V/G|M/G Q K(D)		96.13	586.2888	1171.571	-0.0007	-0.6	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
15308	dirMS_041712_NAR_20mM_plus.10965.10965.3	3	7.76	0	1.01E+05		(K)ALIAAQ	(K)A L\I A A Q Y|S/G A Q V R(V)		147.88	449.9174	1347.738	-0.0003	-0.2	8.79	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
15309	dirMS_041712_NAR_20mM_plus.15882.15882.2	2	7.76	0	5.34E+04		(K)IGIVGLP	(K)I/G|I/V/G/L/P N V G K(S)		180.67	533.8346	1066.662	0	0	8.75	12416	9.45	HUMAN	C9JTK6	Obg-like ATPase 1 (Fragment)
15310	dirMS_041712_NAR_20mM_plus.9210.9210.2	2	7.76	0	1.50E+05	S1426s	(K)SLAEML	(K)S L|A/E/M L I s/K(N)	s:N-acetylglucosamine (S)	134.97	597.8227	991.549	203.0889	8	5.72	202703.7	9.01	HUMAN	G3V1B5	Down syndrome cell adhesion molecule like 1, isoform CRA_a
15311	dirMS_041712_NAR_30mM_plus2.18830.18830.2	2	7.76	0	1.24E+05		(K)SGYQAL	(K)S G Y|Q/A|L/P W V R(Y)		151.98	588.8123	1176.616	0.0013	1.1	8.46	40310.4	6.69	HUMAN	B4DDG7	AP-1 complex subunit mu-1
15312	dirMS_041712_NAR_30mM_plus2.19558.19558.2	2	7.76	0	1.85E+04		(K)MNEFLE	(K)M/N|E|F/L/E N F/E K(N)		155.87	650.7974	1300.588	-0.0003	-0.2	4.25	28580.2	9.35	HUMAN	Q9UFN0	Protein NipSnap homolog 3A
15313	dirMS_041712_NAR_30mM_plus2.20317.20317.2	2	7.76	0	2.51E+04		(R)YISPDQL	(R)Y I|S|P D Q L A D L Y/K(S)		160.07	713.3669	1425.726	0.0005	0.4	4.21	47510.4	7.04	HUMAN	P06733	Alpha-enolase
15314	dirMS_041712_NAR_30mM_plus2.4274.4274.2	2	7.76	0	4.63E+05	M558m	(R)mGANN	(R)m/G|A|N/N L/E/R(M)	m:Oxidized methionine	70.25	460.7158	904.431	15.9938	-1.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
15315	dirMS_041712_NAR_30mM_plus2.4910.4910.2	2	7.76	0	7.35E+05		(R)MGQTM	(R)M/G/Q/T M/E/R(I)		77.3	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
15316	dirMS_041712_NAR_30mM_plus2.6345.6345.2	2	7.76	0	1.09E+05		(K)FNYSGS	(K)F N|Y/S/G S G G R(S)		87.1	472.7087	944.422	-0.0119	-12.6	8.75	96205.6	9.06	HUMAN	G5E9M5	Interleukin enhancer binding factor 3, 90kDa, isoform CRA_b
15317	dirMS_041712_NAR_50mM_plus2.11594.11594.3	3	7.76	1	1.45E+05		(K)QQEAAL	(K)Q Q/E/A/A/L/E/L E E L K/K(K)		128.47	510.2769	1528.822	-0.0056	-3.6	4.49	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
15318	dirMS_041712_NAR_50mM_plus2.12989.12989.3	3	7.76	0	1.99E+05		(K)ASEAGE	(K)A S|E|A/G E/V/P F N H E I\L R(E)		136.12	556.9507	1668.834	0.0035	2.1	4.75	36406	5.47	HUMAN	E7EM64	COP9 signalosome complex subunit 6
15319	dirMS_041712_NAR_50mM_plus2.16389.16389.3	3	7.76	0	3.28E+04		(R)EVIDLLK	(R)E V/I/D L/L/K/P D Q V/E G I Q/K(S)		154.37	608.6724	1824.011	-0.0087	-4.7	4.32	156557.7	5.52	HUMAN	Q86UP2	Kinectin
15320	dirMS_041712_NAR_50mM_plus2.20689.20689.3	3	7.76	1	1.70E+05		(R)VNSKFD	(R)V/N S K F D T\I/Y Q\I/L L K(K)		177.62	561.3209	1681.952	-0.0042	-2.5	8.47	72626.7	9.13	HUMAN	Q14258	E3 ubiquitin/ISG15 ligase TRIM25
15321	dirMS_041712_NAR_60mM_plus.15174.15174.3	3	7.76	1	5.45E+05		(K)IFYPETTI	(K)I/F/Y/P E T T/D I Y D R K(N)		135.85	554.2751	1660.822	-0.011	-6.6	4.56	189876.1	6.08	HUMAN	P46940	Ras GTPase-activating-like protein IQGAP1
15322	dirMS_041712_NAR_120mM_minus.12421.12421.3	3	7.75	1	3.40E+05	M316m	(R)ISEQFTA	(R)I/S/E/Q/F T A m F\R/R(K)	m:Oxidized methionine	121.92	467.9028	1385.699	15.9944	-0.4	9.6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
15323	dirMS_041712_NAR_120mM_minus.17553.17553.3	3	7.75	2	1.94E+05		(R)GYSFTTT	(R)G Y/S F/T/T T A E R E I V R D\I K(E)		150.6	662.6807	1986.029	-0.0015	-0.8	6.18	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
15324	dirMS_041712_NAR_120mM_minus.18822.18822.4	4	7.75	1	1.40E+05		(R)SLRDLTF	(R)S L R D L\T|P E/H L/P L L/R(N)		158.47	415.7434	1659.954	-0.0023	-1.4	6.47	38779.2	5.93	HUMAN	Q96C86	m7GpppX diphosphatase
15325	dirMS_041712_NAR_20mM_minus.13568.13568.2	2	7.75	0	3.86E+03		(K)DAGTIA	(K)D A G T/I/A/G L/N V L/R(I)		186.57	600.3403	1199.674	-0.0009	-0.8	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
15326	dirMS_041712_NAR_40mM_minus2.6240.6240.2	2	7.75	0	9.42E+05		(R)STFSTN	(R)S T|F|S T/N Y R(S)		101.98	488.2302	975.453	0.0001	0.1	8.46	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
15327	dirMS_041712_NAR_50mM_minus2.12088.12088.3	3	7.75	1	6.63E+04		(R)IAAAILN	(R)I/A/A\A I L N/T/P D L R K(Q)		137.15	465.9459	1395.832	-0.0087	-6.2	8.75	43371.1	9.64	HUMAN	E7ERW2	Aspartate aminotransferase
15328	dirMS_041712_NAR_60mM_minus.11991.11991.3	3	7.75	0	1.77E+05	M271m	(R)DLSYCLS	(R)D L|S/Y/C L/S G m Y D H R(Y)	C:Carbamidomethylation m:Oxid	126.72	544.8984	1616.683	15.9975	1.6	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
15329	dirMS_041712_NAR_60mM_minus.12165.12165.2	2	7.75	1	8.94E+04		(R)SVETLKE	(R)S/V|E/T L K E\M\I/K(S)		127.63	589.327	1177.65	-0.003	-2.5	5.86	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
15330	dirMS_041712_NAR_60mM_minus.14166.14166.3	3	7.75	0	1.96E+05		(K)IVNFLLQ	(K)I V|N/F L/L Q/H\S A K(V)		138.25	423.9167	1269.731	0.0042	3.3	8.76	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
15331	dirMS_041712_NAR_20mM_plus.16503.16503.3	3	7.75	0	9.63E+04		(K)LGGSAV	(K)L G G S A\V\I\S L/E/G K/P L(-)		185.5	447.5974	1340.778	-0.0007	-0.6	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
15332	dirMS_041712_NAR_20mM_plus.16633.16633.2	2	7.75	0	7.92E+04	M137m M	(R)IIGATDS	(R)I I/G A|T D/S S G E L m F L m K(W)	m:Oxidized methionine	185.65	872.926	1712.86	31.985	-2.8	4.37	19439.5	4.97	HUMAN	B5MD17	Chromobox protein homolog 1 (Fragment)
15333	dirMS_041712_NAR_20mM_plus.8147.8147.2	2	7.75	0	1.91E+05		(R)FGQGG	(R)F G\Q\G/G A/G/P V/G G Q G/P R(G)		125.3	671.3361	1341.666	-0.0009	-0.7	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
15334	dirMS_041712_NAR_30mM_plus2.10556.10556.2	2	7.75	0	2.76E+05		(K)NFGDQF	(K)N F|G D/Q/P D/I R(C)		109.17	531.2555	1061.501	0.0027	2.5	4.21	136658.9	5.13	HUMAN	Q15393	Splicing factor 3B subunit 3
15335	dirMS_041712_NAR_30mM_plus2.18949.19034.2	2	7.75	0	1.32E+05		(K)LAFNSLL	(K)L/A|F/N S/L\L E K(A)		152.68	517.7928	1034.588	-0.0097	-9.4	6	109088.4	7.19	HUMAN	O75400	Pre-mRNA-processing factor 40 homolog A
15336	dirMS_041712_NAR_30mM_plus2.4194.4194.2	2	7.75	0	1.20E+06	M299m M	(K)NmmAA	(K)N m|m/A A C D|P R(H)	C:Carbamidomethylation m:Oxid	69.6	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
15337	dirMS_041712_NAR_50mM_plus2.14626.14626.3	3	7.75	0	1.26E+05		(R)NAASHG	(R)N A|A S/H G A A F\V E F D V H L S/K(D)		144.78	633.9873	1899.935	0.0126	6.6	5.99	30730.7	8.65	HUMAN	H0Y565	Glycerophosphocholine phosphodiesterase GPCPD1 (Fragment)
15338	dirMS_041712_NAR_50mM_plus2.18000.18000.3	3	7.75	1	2.83E+05		(K)AKIGLIQ	(K)A K\I G\L I/Q/F/C L S/A/P K(T)	C:Carbamidomethylation	162.33	515.9649	1545.882	-0.002	-1.3	10	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
15339	dirMS_041712_NAR_50mM_plus2.19916.19916.3	3	7.75	0	1.44E+05		(R)QADFVC	(R)Q A D F V/Q/T|P/I T G/I F G G/H I R(S)		172.82	653.0218	1957.029	0.0218	11.2	6.74	16981.3	4.55	HUMAN	H3BNA1	Ubiquitin carboxyl-terminal hydrolase 10 (Fragment)
15340	dirMS_041712_NAR_60mM_plus.18223.18223.3	3	7.75	1	3.28E+05		(K)LLQDFF	(K)L/L/Q/D/F/F N/G R D L N K(S)		152.55	527.2793	1579.823	0.0006	0.4	5.96	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
15341	dirMS_041712_NAR_60mM_plus.6644.6644.3	3	7.75	1	6.89E+05		(R)NKQTYS	(R)N K Q T|Y S\T E/P N N L K(A)		92.93	512.9257	1536.765	-0.0027	-1.8	8.5	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
15342	dirMS_041712_NAR_60mM_plus.8488.8488.3	3	7.75	1	4.16E+05		(K)QGIETPE	(K)Q G I/E/T/P E D Q N D/L R K(M)		102.63	548.2719	1642.803	-0.002	-1.2	4.32	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
15343	dirMS_041712_NAR_20mM_minus.10455.10455.2	2	7.74	0	1.44E+05		(R)IYVVDV	(R)I Y|V|V/D V G S/E P R(A)		152.93	617.3216	1233.647	-0.0115	-9.3	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
15344	dirMS_041712_NAR_40mM_minus2.10971.10971.3	3	7.74	1	1.92E+04		(R)ETFEKTF	(R)E T/F E/K T P V E V/P\V/G\G F K(G)		149.23	588.6423	1763.921	-0.0091	-5.1	4.79	533778	5.74	HUMAN	Q15149	Plectin
15345	dirMS_041712_NAR_60mM_minus.13175.13175.3	3	7.74	1	1.84E+05		(K)KVPQVS	(K)K V P\Q\V S T|P T/L/V E V S/R(N)		133.67	547.317	1639.938	-0.0013	-0.8	8.75	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
15346	dirMS_041712_NAR_60mM_minus.13576.13576.3	3	7.74	0	1.01E+05		(R)LSSTDD	(R)L S/S/T D D G Y I D L Q/F K(K)		135.35	534.591	1601.769	-0.0109	-6.8	3.93	7992.4	9.92	HUMAN	Q5JWB9	Chromosome 20 open reading frame 30 (Fragment)
15347	dirMS_041712_NAR_60mM_minus.17641.17641.3	3	7.74	1	3.97E+06		(R)VSFELFA	(R)V/S|F E L/F A D K V P K(T)		157.8	460.5911	1379.757	0.0018	1.3	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
15348	dirMS_041712_NAR_60mM_minus.5282.5282.3	3	7.74	0	6.24E+05		(R)AEAEAG	(R)A E|A\E/A/G S P R P D/P R(E)		84.27	451.5562	1352.655	-0.0013	-0.9	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
15349	dirMS_041712_NAR_60mM_minus.7206.7206.3	3	7.74	1	3.73E+05	M136m M	(K)VKEGm	(K)V/K E G m N\I V/E A/m/E R(F)	m:Oxidized methionine	99.93	513.25	1505.745	31.9904	0.4	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
15350	dirMS_041712_NAR_120mM_plus.12398.12398.4	4	7.74	2	8.44E+05		(K)KGTVEG	(K)K G T V\E/G\F\E|P/A D N K C L L R(A)	C:Carbamidomethylation	118.8	484.2468	1933.98	-0.0147	-7.6	6.18	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
15351	dirMS_041712_NAR_120mM_plus.18738.18738.4	4	7.74	0	1.39E+05		(R)LGWDP	(R)L G W D\P K/P G E G/H/L D/A L L R(G)		151.57	469.253	1873.992	-0.0017	-0.9	5.38	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
15352	dirMS_041712_NAR_120mM_plus.7171.7171.3	3	7.74	1	3.79E+05		(K)IYEDGD	(K)I/Y/E D/G D D D M K R(T)		90.88	452.8635	1356.574	0.0023	1.7	4.03	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
15353	dirMS_041712_NAR_20mM_plus.11467.11467.2	2	7.74	0	2.15E+05		(K)VGLQV	(K)V/G/L/Q V V\A V|K(A)		151.5	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
15354	dirMS_041712_NAR_20mM_plus.14020.14020.2	2	7.74	0	1.64E+05	M98m	(R)TLTIVDT	(R)T L|T/I|V\D T G/I G m T K(A)	m:Oxidized methionine	167.8	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
15355	dirMS_041712_NAR_20mM_plus.18042.18042.2	2	7.74	0	1.84E+05		(K)VANVSL	(K)V/A/N\V|S L L\A L Y K(G)		195.4	595.8558	1190.714	-0.01	-8.4	8.56	15978.4	10.84	HUMAN	P62266	40S ribosomal protein S23
15356	dirMS_041712_NAR_20mM_plus.18585.18585.3	3	7.74	0	4.71E+05		(K)LAVEAL	(K)L A V E\A\L S S/L D/G D/L A G R(Y)		200.38	529.6164	1586.838	-0.0038	-2.4	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
15357	dirMS_041712_NAR_20mM_plus.19205.19205.2	2	7.74	0	1.31E+05		(R)ALIAGG	(R)A L I|A\G/G G\A|P E I/E\L A L R(L)		204.53	775.9467	1550.89	-0.0039	-2.5	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
15358	dirMS_041712_NAR_30mM_plus2.12755.12755.2	2	7.74	0	3.24E+05		(K)IGVTVLS	(K)I/G/V/T/V L S/R(I)		120.08	422.7657	844.525	-0.001	-1.1	9.75	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
15359	dirMS_041712_NAR_30mM_plus2.13090.13090.2	2	7.74	0	6.07E+05		(K)GDYPLE	(K)G D/Y|P/L E A V R(M)		121.83	510.2633	1019.516	0.0037	3.6	4.37	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
15360	dirMS_041712_NAR_30mM_plus2.8998.9016.2	2	7.74	0	3.10E+05		(K)SETDTSL	(K)S E|T/D/T S/L/I R(G)		100.88	511.2577	1021.516	-0.0079	-7.7	4.37	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
15361	dirMS_041712_NAR_50mM_plus2.10878.10878.3	3	7.74	1	2.69E+05		(K)NVDILK	(K)N/V/D I L\K D/P E T V/K(Q)		124.72	457.5906	1370.753	0.0047	3.4	4.56	124524.8	5.71	HUMAN	O14980	Exportin-1
15362	dirMS_041712_NAR_50mM_plus2.19245.19245.3	3	7.74	1	1.15E+05		(K)GLKVNL	(K)G L/K V N L\F|P|G L S P S A L/K(A)		169.47	547.6608	1640.973	-0.0056	-3.4	10	182819.3	4.77	HUMAN	Q9C0C2	182 kDa tankyrase-1-binding protein
15363	dirMS_041712_NAR_50mM_plus2.7479.7479.3	3	7.74	0	3.13E+05		(K)VSYGIG	(K)V S/Y/G I/G D E E H D Q E/G R(V)		105.08	564.2484	1690.73	0.0003	0.2	4.17	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
15364	dirMS_041712_NAR_60mM_plus.10514.11020.3	3	7.74	1	3.77E+07	S306s	(R)DHHMS	(R)D H H M S G\W\s|Y/K R V E K(S)	s:N-acetylglucosamine (S)	114.98	654.9726	1759.833	203.0699	-4.8	8.51	51648.4	5.55	HUMAN	B7XGB9	Protein phosphatase 1M

15365	dirMS_041712_NAR_60mM_plus.12128.12128.3	3	7.74	0	2.92E+05		(R)QADFEA	(R)Q A D/F E/A/H/N I L R(E)		120.55	438.558	1313.66	-0.0002	-0.2	5.32	66612.6	7.28	HUMAN	F8W720	GMP synthase [glutamine-hydrolyzing]
15366	dirMS_041712_NAR_60mM_plus.18898.18898.3	3	7.74	1	1.07E+04		(K)LLVYEAL	(K)L/L|V/Y/E A L/E/Y A K R(A)		156.65	489.9411	1467.821	-0.0118	-8.1	6.14	32535.6	9.19	HUMAN	B4DZW6	Regulator of microtubule dynamics protein 1
15367	dirMS_041712_NAR_20mM_minus.14495.14495.3	3	7.73	0	1.37E+05		(R)LSVEEA\	(R)L S V E E A V\A A G/V|V/G G E I Q E K(L)		199.57	629.0005	1884.991	-0.0044	-2.3	4.09	266161	5.68	HUMAN	E9PPU0	Epiplakin
15368	dirMS_041712_NAR_20mM_minus.14715.14715.2	2	7.73	0	1.69E+05		(K)TAVETA\	(K)T A/V/E|T A/V L|L L R(I)		201.4	593.3613	1185.72	-0.0048	-4.1	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
15369	dirMS_041712_NAR_20mM_minus.7509.7509.2	2	7.73	0	1.47E+05	M21m	(K)ATAVmF	(K)A T/A/V/m|P D/G Q F K(D)	m:Oxidized methionine	122.73	590.7864	1164.572	15.9938	-1	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
15370	dirMS_041712_NAR_20mM_minus.9581.9581.3	3	7.73	0	9.16E+03	M175m	(R)LEQGQA	(R)L E Q G Q A\I D D\L/m/P A Q K(-)	m:Oxidized methionine	146.8	558.2794	1656.826	15.9975	1.5	4.03	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
15371	dirMS_041712_NAR_30mM_minus2.15763.15763.2	2	7.73	0	4.68E+04		(R)INEILSN/	(R)I N|E|I/L S/N A L/K(R)		139.15	557.8242	1114.647	-0.0055	-5	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
15372	dirMS_041712_NAR_30mM_minus2.5528.5528.2	2	7.73	0	1.77E+05		(R)LYQAGE	(R)L|Y/Q/A/G E|G R(L)		84.58	447.2217	893.448	-0.0114	-12.8	6	38089.6	6.79	HUMAN	B4DT77	Annexin
15373	dirMS_041712_NAR_30mM_minus2.7148.7148.2	2	7.73	1	6.94E+04		(R)YANARD	(R)Y A/N\A R/D/R(N)		93.02	433.2178	865.428	0.0008	1	8.75	26150.7	7.9	HUMAN	D6RIE5	RING finger protein 150 (Fragment)
15374	dirMS_041712_NAR_30mM_minus2.8353.8353.2	2	7.73	0	4.65E+05		(K)SFQQSSI	(K)S/F/Q/Q/S/S L S/R(D)		100.35	520.2591	1039.517	-0.0058	-5.6	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
15375	dirMS_041712_NAR_30mM_minus2.9211.9211.2	2	7.73	0	4.87E+05		(R)NQPQFC	(R)N Q|P/Q F/Q Q M R(Q)		105.05	588.7841	1176.558	0.0031	2.6	9.75	35061.2	4.66	HUMAN	G5E9P0	RAD23 homolog B (S. cerevisiae), isoform CRA_a
15376	dirMS_041712_NAR_40mM_minus2.11404.11404.3	3	7.73	0	7.18E+05		(R)TIQVENS	(R)T I/Q|V E N\S H L I/L/T G A/G A L N K(V)		150.88	660.3663	1979.092	-0.0077	-3.9	6.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
15377	dirMS_041712_NAR_40mM_minus2.13476.13476.3	3	7.73	0	1.27E+04		(R)DLKPSNI	(R)D L K P S N L L/I/N T/T C/D L K(I)	C:Carbamidomethylation	163.35	615.6649	1844.979	0.0015	0.8	5.96	30925	5.63	HUMAN	B3KR49	Mitogen-activated protein kinase 3
15378	dirMS_041712_NAR_50mM_minus2.15423.15423.3	3	7.73	0	2.31E+04		(R)ALYYLQI	(R)A L/Y Y/L/Q I H|P Q E L R(Q)		155.47	548.6303	1643.89	-0.0141	-8.6	6.79	122967	5.33	HUMAN	F5GY55	DNA damage-binding protein 1
15379	dirMS_041712_NAR_60mM_minus.10485.10485.3	3	7.73	1	1.97E+05	M477m	(R)TLKIPAm	(R)T L/K I/P A m/T I|A K(N)	m:Oxidized methionine	118.38	401.5767	1186.723	15.9928	-1.8	10	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
15380	dirMS_041712_NAR_60mM_minus.15035.15035.3	3	7.73	0	2.96E+05		(K)WIGLDL!	(K)W/I/G L D L/S/N/G K/P R(D)		143.43	452.5849	1355.743	-0.0029	-2.1	8.75	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
15381	dirMS_041712_NAR_60mM_minus.18850.18850.3	3	7.73	1	2.67E+05		(K)NAAGAL	(K)N A/A/G A\L D L L K E L K(N)		166.87	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
15382	dirMS_041712_NAR_30mM_plus2.17292.17292.2	2	7.73	0	6.98E+04		(K)WPLYM!	(K)W/P L/Y/M/S T K(N)		144.88	513.2647	1025.513	0.0097	9.4	8.59	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
15383	dirMS_041712_NAR_30mM_plus2.19634.19725.2	2	7.73	0	4.04E+05		(R)AITGASL	(R)A I|T/G/A/S L/A D I M A K(R)		156.62	631.3424	1261.682	-0.0045	-3.6	5.88	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
15384	dirMS_041712_NAR_30mM_plus2.20364.20364.2	2	7.73	0	3.12E+05		(R)FEELNAI	(R)F/E|E L|N A/D L F/R(G)		161.05	627.3106	1253.616	-0.0022	-1.7	4.14	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
15385	dirMS_041712_NAR_30mM_plus2.20999.20999.2	2	7.73	0	1.61E+05		(R)GVVQEL	(R)G V|V Q/E L/Q/Q A I/S K(L)		164.98	650.3632	1299.727	-0.0076	-5.8	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
15386	dirMS_041712_NAR_50mM_plus2.15881.15881.3	3	7.73	1	3.70E+06		(K)ISDSEGF	(K)I/S D/S/E/G F K A N\L S L L R(R)		151.2	550.6331	1649.886	-0.001	-0.6	6.07	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
15387	dirMS_041712_NAR_50mM_plus2.21731.21747.3	3	7.73	0	1.12E+05		(R)GLAPVQ	(R)G L|A|P V/Q A Y L H I P D I I K(V)		184.93	583.336	1748.011	-0.0171	-9.8	6.74	58266.4	9.46	HUMAN	B4DN00	Pyruvate carboxylase, mitochondrial
15388	dirMS_041712_NAR_60mM_plus.17609.17609.3	3	7.73	1	3.49E+05		(R)GFSGGN	(R)G F|S/G G M/K D M/Y D Q V/L|K(F)		149.75	559.2674	1675.782	0.0058	3.5	5.96	269989.9	5.92	HUMAN	F8W8T8	Acetyl-CoA carboxylase 2
15389	dirMS_041712_NAR_60mM_plus.20102.20102.3	3	7.73	0	1.50E+04		(R)DFLLKPE	(R)D/F/L L K/P E L L R(A)		165.03	415.2483	1243.741	-0.0105	-8.5	6.07	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
15390	dirMS_041712_NAR_120mM_minus.10052.10052.3	3	7.72	0	5.96E+05		(R)HGESAV	(R)H G E\S A\W|N|L/E N/R(F)		109.4	438.2098	1312.603	0.012	9.1	5.4	28917.5	6.68	HUMAN	P18669	Phosphoglycerate mutase 1
15391	dirMS_041712_NAR_120mM_minus.14137.14137.3	3	7.72	0	4.33E+05		(K)NRPTSIS	(K)N R P T\S\I S|W/D/G L D/S G K(L)		130.63	544.9369	1632.798	-0.0015	-0.9	5.96	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
15392	dirMS_041712_NAR_120mM_minus.6204.6204.3	3	7.72	1	1.20E+05		(K)AQQELE	(K)A Q|Q/E/L E E Q T R R(A)		87.68	463.2365	1387.692	0.0025	1.8	4.79	67933	6.08	HUMAN	P26038	Moesin
15393	dirMS_041712_NAR_20mM_minus.13798.13798.2	2	7.72	0	4.04E+05		(K)LGGSAV	(K)L G G/S A V\I/S/L E/G\K|P L(-)		188.7	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
15394	dirMS_041712_NAR_20mM_minus.14475.14475.3	3	7.72	0	2.19E+05		(K)LAAELSA	(K)L A A E L S A\T L/E/Q\A/A/A T\A R(V)		198.9	562.9713	1686.902	-0.0027	-1.6	4.53	558007.1	5.44	HUMAN	P58107	Epiplakin
15395	dirMS_041712_NAR_20mM_minus.7092.7092.2	2	7.72	0	4.77E+05	M281m	(R)AEAESm	(R)A E|A/E|S m Y Q I K(Y)	m:Oxidized methionine	117.9	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
15396	dirMS_041712_NAR_30mM_minus2.16765.16765.2	2	7.72	0	2.44E+05		(R)FFMGN(	(R)F F/M/G N Q V L K(V)		145.28	542.2866	1083.566	0.0004	0.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
15397	dirMS_041712_NAR_40mM_minus2.13827.13827.3	3	7.72	1	3.98E+05		(R)VTFSGLF	(R)V/T/F/S\G L/R D T V\T P G E L L K(A)		164.73	611.6742	1833.012	-0.0036	-2	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
15398	dirMS_041712_NAR_50mM_minus2.13498.13498.3	3	7.72	1	1.31E+05		(K)IDSRLEQ	(K)I/D/S R L E Q\Y|T/S A/I/E G T K(S)		144.68	604.3145	1810.918	0.0108	6	4.68	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
15399	dirMS_041712_NAR_20mM_plus.11275.11275.2	2	7.72	0	1.61E+04		(R)GCITIIG(	(R)G C I/T I|I|G/G G D T A T C C A K(W)	C:Carbamidomethylation	150	877.8947	1754.787	-0.0049	-2.8	5.84	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
15400	dirMS_041712_NAR_20mM_plus.11519.11519.2	2	7.72	0	9.84E+04		(R)IASLEVE	(R)I A/S L/E/V|E/N Q S L R(G)		151.82	679.8662	1358.727	-0.0023	-1.7	4.53	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
15401	dirMS_041712_NAR_20mM_plus.12792.12792.2	2	7.72	0	3.16E+05		(K)LSELEAA	(K)L S/E/L|E A/A L Q R(A)		161.53	565.3132	1129.621	-0.002	-1.8	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
15402	dirMS_041712_NAR_20mM_plus.13842.13842.2	2	7.72	0	4.62E+04		(R)VVVDAL	(R)V V|V|D/A/L S G L K(G)		167.37	500.8034	1000.604	-0.0042	-4.2	5.81	26949.2	7.99	HUMAN	C9JSQ1	Creatine kinase U-type, mitochondrial (Fragment)
15403	dirMS_041712_NAR_20mM_plus.18128.18128.3	3	7.72	0	2.29E+03		(R)DSLTEIN	(R)D S L T E I N L/S A/S/L/L G R(V)		196.5	530.2925	1588.854	0.0089	5.6	4.37	151198.9	9.46	HUMAN	Q8NHM5-2	Isoform 2 of Lysine-specific demethylase 2B
15404	dirMS_041712_NAR_20mM_plus.8390.8390.2	2	7.72	0	1.06E+05		(K)TAVCDIF	(K)T A|V|C/D I/P|P/R(G)	C:Carbamidomethylation	127.63	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
15405	dirMS_041712_NAR_30mM_plus2.10446.10446.2	2	7.72	0	5.36E+04		(K)TAVCDIF	(K)T A|V/C/D/I/P\P R(G)	C:Carbamidomethylation	108.98	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
15406	dirMS_041712_NAR_30mM_plus2.12971.12971.2	2	7.72	0	3.86E+05		(K)QSLPPG	(K)Q/S L/P/P G L A V K(E)		121.55	505.3008	1009.604	-0.0097	-9.6	8.75	8274.8	10.19	HUMAN	P63173	60S ribosomal protein L38
15407	dirMS_041712_NAR_30mM_plus2.22297.22421.2	2	7.72	0	3.01E+05		(K)CMPTFC	(K)C M|P/T/F Q F/F K(K)	C:Carbamidomethylation	172.77	603.2777	1205.548	-0.0001	-0.1	8.75	9680	5.77	HUMAN	B1ALW1	Thioredoxin
15408	dirMS_041712_NAR_30mM_plus2.5801.5801.2	2	7.72	0	2.82E+04		(K)STSTPTS	(K)S T/S/T/P/T S/P G P R(T)		84.53	544.2682	1087.538	-0.0087	-8	9.47	41818.8	8.76	HUMAN	H3BRB0	Ataxin-2-like protein (Fragment)
15409	dirMS_041712_NAR_40mM_plus2.6039.6039.2	2	7.72	0	2.48E+05		(R)MGANN	(R)M/G|A N N L/E R(M)		94.25	452.7221	904.431	0.0064	7.1	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
15410	dirMS_041712_NAR_40mM_plus2.6196.6196.2	2	7.72	1	2.84E+05		(R)YSGGNY	(R)Y S|G G N Y/R D N\Y|D\N(-)		95.58	719.2857	1437.567	-0.0024	-1.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
15411	dirMS_041712_NAR_50mM_plus2.13656.13755.3	3	7.72	1	2.00E+06	M320m	(K)YmACCL	(K)Y/m|A C C L L Y R G D V\V/P/K(E)	C:Carbamidomethylation m:Oxid	140.55	620.9622	1844.886	15.9865	-4.5	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
15412	dirMS_041712_NAR_50mM_plus2.6209.6209.3	3	7.72	0	4.48E+04	M437m	(R)LESGMC	(R)L E|S G M Q/N m S I H/T K(T)	m:Oxidized methionine	97.02	497.9026	1475.698	15.9951	0.1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
15413	dirMS_041712_NAR_50mM_plus2.7229.7229.3	3	7.72	1	7.50E+04		(K)DISTNYY	(K)D I S/T N/Y/Y A\S Q K K(T)		103.52	473.2382	1417.696	0.0043	3	8.43	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
15414	dirMS_041712_NAR_60mM_plus.10645.11148.3	3	7.72	1	3.77E+07	S306s	(R)DHHMS(	(R)D H H M S G\W\s|Y/K R V E K(S)	s:N-acetylglucosamine (S)	114.98	654.9726	1759.833	203.0699	-4.8	8.51	51648.4	5.55	HUMAN	B7XGB9	Protein phosphatase 1M
15415	dirMS_041712_NAR_60mM_plus.14767.14767.3	3	7.72	1	3.86E+03		(R)KIEFPMI	(R)K\I E F\P M|P|N E E/A R(A)		135.33	487.578	1460.72	-0.0008	-0.5	4.79	44608.2	4.94	HUMAN	E9PM69	26S protease regulatory subunit 6A
15416	dirMS_041712_NAR_60mM_plus.17722.17722.3	3	7.72	0	4.55E+05		(R)FDASFF(	(R)F/D/A S F/F/G V H P K(Q)		149.22	417.8778	1251.616	0.0032	2.5	6.74	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
15417	dirMS_041712_NAR_60mM_plus.20289.20289.3	3	7.72	1	4.21E+05		(K)NAAGAL	(K)N A|A/G A/L D L/L K E L/K(N)		166.93	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
15418	dirMS_041712_NAR_20mM_minus.13047.13047.2	2	7.71	0	9.05E+05	M73m	(R)AILVDLE	(R)A I/L\V|D L/E/P G/T m D S V R(S)	m:Oxidized methionine	182.55	816.4184	1615.836	15.9935	-0.8	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
15419	dirMS_041712_NAR_20mM_minus.9641.9641.2	2	7.71	0	3.33E+05		(K)IGGIGTV	(K)I/G/G I|G T V|P V G R(V)		147.47	513.3075	1025.61	-0.0025	-2.4	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
15420	dirMS_041712_NAR_50mM_minus2.10518.10518.3	3	7.71	0	2.90E+05	M35m	(K)AASDIAr	(K)A A/S D\I/A m T/E/L/P P T H/P I R(L)	m:Oxidized methionine	127.9	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
15421	dirMS_041712_NAR_50mM_minus2.10924.10924.3	3	7.71	0	1.77E+05	M35m	(K)AASDIAr	(K)A A/S D I/A m T E L|P P T H/P I R(L)	m:Oxidized methionine	130.35	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
15422	dirMS_041712_NAR_50mM_minus2.12127.12127.3	3	7.71	1	7.12E+04		(R)LADLEAI	(R)L/A|D L/E A L K V A D S K(T)		137.23	458.2586	1372.768	-0.007	-5.1	4.56	33736.6	5.14	HUMAN	O75792	Ribonuclease H2 subunit A
15423	dirMS_041712_NAR_50mM_minus2.7687.7687.3	3	7.71	1	3.49E+04	M198m	(R)VFDKEG	(R)V/F/D K E G N G T|V/m|G A E I R(H)	m:Oxidized methionine	110.87	580.2847	1722.848	15.9916	-1.9	4.68	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
15424	dirMS_041712_NAR_60mM_minus.15105.15105.3	3	7.71	1	7.95E+04		(R)ALSNLES	(R)A L/S/N/L E/S I P G G Y N A L R/R(M)		144.1	610.9981	1830.982	-0.0023	-1.3	8.79	16443.8	5	HUMAN	H0YDS0	Ubiquilin-1 (Fragment)
15425	dirMS_041712_NAR_60mM_minus.8085.8085.3	3	7.71	1	2.63E+04		(R)YLAEVA(	(R)Y L/A\E V/A/C G D D R K(Q)	C:Carbamidomethylation	104.8	466.2187	1396.652	-0.011	-7.9	4.56	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
15426	dirMS_041712_NAR_60mM_minus.8151.8151.3	3	7.71	1	2.80E+05		(K)IQDKEGI	(K)I Q/D K E G/I|P P D Q Q R(L)		105.05	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
15427	dirMS_041712_NAR_120mM_plus.12743.12743.3	3	7.71	0	4.55E+05	N2453n	(R)VIYNFCr	(R)V I Y/N F C/n S V R(V)	C:Carbamidomethylation n:N-ac	120.97	492.2383	1271.62	203.0802	0.6	8.72	289749.1	6.36	HUMAN	Q5S007	Leucine-rich repeat serine/threonine-protein kinase 2
15428	dirMS_041712_NAR_120mM_plus.9432.9432.4	4	7.71	2	1.18E+06		(K)LTDCVVI	(K)L T|D/C/V V/M R D P A S K R(S)	C:Carbamidomethylation	102.65	412.7134	1647.831	0.0012	0.8	8.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
15429	dirMS_041712_NAR_20mM_plus.14961.14961.2	2	7.71	0	1.26E+05		(R)LLDAQL!	(R)L L/D A Q|L\S/T/G/G I V D\P S\K(S)		174.67	807.4389	1613.874	-0.004	-2.5	4.21	533778	5.74	HUMAN	Q15149	Plectin
15430	dirMS_041712_NAR_20mM_plus.17199.17199.2	2	7.71	0	9.17E+04		(R)AVLVDLI	(R)A V\L V D|L\E|P G T\M D S/V R(S)		189.58	801.414	1601.82	0.0004	0.2	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
15431	dirMS_041712_NAR_20mM_plus.9152.9152.2	2	7.71	0	5.96E+05	M239m	(K)EITALAP	(K)E I/T A L/A|P S T m K(I)	m:Oxidized methionine	133.15	589.309	1161.618	15.9923	-2.2	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
15432	dirMS_041712_NAR_30mM_plus2.17439.17439.2	2	7.71	0	2.29E+05		(K)VSTLPAI	(K)V/S/T|L/P A I T/L K(L)		144.12	521.8272	1042.651	-0.0035	-3.4	8.72	20599.3	9.19	HUMAN	H7C1V0	Cathepsin D light chain (Fragment)
15433	dirMS_041712_NAR_30mM_plus2.5633.5633.2	2	7.71	0	2.38E+05	M154m M:	(R)mGYmD	(R)m G\Y m D|P R(E)	m:Oxidized methionine	83.4	451.1814	869.364	31.9911	1.4	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
15434	dirMS_041712_NAR_40mM_plus2.10043.10043.2	2	7.71	0	1.20E+05		(R)YSGSYNI	(R)Y/S|G S/Y N D/Y L/R(A)		123.83	619.2788	1237.548	0.0019	1.6	5.83	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
15435	dirMS_041712_NAR_40mM_plus2.7665.7681.2	2	7.71	0	6.83E+05		(K)ASLENSI	(K)A S|L|E/N/S L R(E)		105.45	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
15436	dirMS_041712_NAR_50mM_plus2.15004.15004.3	3	7.71	1	3.81E+05		(K)LIVAYVD	(K)L/I|V/A/Y V D D L D R R(G)		147.12	483.2728	1447.79	0.0135	9.3	4.43	124127.1	8.81	HUMAN	O14776	Transcription elongation regulator 1
15437	dirMS_041712_NAR_60mM_plus.11641.11641.2	2	7.71	1	1.11E+06		(R)ALAAFLI	(R)A L|A|A F L K K(S)		117.4	431.2814	861.556	-0.0001	-0.1	10	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
15438	dirMS_041712_NAR_60mM_plus.16024.16024.3	3	7.71	1	5.56E+05		(R)VTNRDII	(R)V T\N R D\I\I|C/Q I/A Y/A R(I)	C:Carbamidomethylation	140.7	564.9631	1692.885	-0.0103	-6.1	8.71	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
15439	dirMS_041712_NAR_120mM_minus.10998.10998.3	3	7.7	0	6.08E+05		(R)ISNRPAF	(R)I/S/N\R P A\F|M|P S E G K(M)		113.93	478.5776	1433.721	-0.0023	-1.6	8.75	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
15440	dirMS_041712_NAR_120mM_minus.13253.13253.3	3	7.7	1	5.39E+05	M316m	(K)RISEQFT	(K)R I S E\Q\F|T/A m F|R(R)	m:Oxidized methionine	125.93	467.9028	1385.699	15.9944	-0.4	9.6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
15441	dirMS_041712_NAR_120mM_minus.20376.20376.4	4	7.7	0	2.45E+05		(K)ALEHAF(	(K)A/L E\H A F Q/L/E H I/M D L T R(L)		167.78	481.7478	1923.975	-0.0052	-2.7	5.27	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
15442	dirMS_041712_NAR_120mM_minus.20839.20839.4	4	7.7	1	5.83E+05		(R)SLHDAL(	(R)S L H D A L|C/V/L A/Q/T V K D/S R(T)	C:Carbamidomethylation	173.1	479.0049	1912.991	0.0068	3.6	6.47	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
15443	dirMS_041712_NAR_20mM_minus.14691.14691.2	2	7.7	0	1.35E+05		(R)IITLAGP	(R)I I/T\L/A G|P T N A I F K(A)		202.13	679.9047	1358.804	-0.0021	-1.5	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
15444	dirMS_041712_NAR_30mM_minus2.10666.10666.2	2	7.7	0	2.32E+05		(K)AGFAGD	(K)A G/F|A|G D Q I|P K(Y)		111.9	502.2645	1003.521	0.001	1	5.88	16745.9	5.33	HUMAN	G5E9Q5	ARP1 actin-related protein 1 homolog B, centractin beta (Yeast), isoform CRA_c
15445	dirMS_041712_NAR_120mM_plus.9047.9047.3	3	7.7	0	1.20E+06		(K)HTGPNS	(K)H T G\P N S P D T|A/N/D G F V/R(L)		100.17	562.26	1684.767	-0.0019	-1.2	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
15446	dirMS_041712_NAR_20mM_plus.7813.7813.2	2	7.7	0	2.08E+05		(R)ALANSL/	(R)A L|A/N/S/L A/C Q G K(Y)	C:Carbamidomethylation	123.85	566.7967	1132.578	0.0082	7.2	8.8	13951.6	9.48	HUMAN	H3BR68	Fructose-bisphosphate aldolase A (Fragment)
15447	dirMS_041712_NAR_30mM_plus2.15988.15988.2	2	7.7	0	5.47E+05		(R)YLCGLG/	(R)Y L/C/G L/G/A V G G V R(L)	C:Carbamidomethylation	137.12	611.3189	1221.641	-0.0103	-8.5	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
15448	dirMS_041712_NAR_30mM_plus2.16812.16812.2	2	7.7	0	7.00E+05		(R)FGLNVS!	(R)F G/L|N|V/S S/I S R(K)		140.15	540.3016	1079.584	0.0115	10.7	9.75	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
15449	dirMS_041712_NAR_40mM_plus2.10353.10353.3	3	7.7	0	9.18E+03		(R)AIGSASE	(R)A I|G S\A S/E G A Q S/S L Q E V Y\H K(S)		125.7	654.654	1961.956	-0.0089	-4.5	5.4	20148.5	4.65	HUMAN	B4E2V4	Proteasome (Prosome, macropain) subunit, alpha type, 5, isoform CRA_c
15450	dirMS_041712_NAR_40mM_plus2.13031.13031.3	3	7.7	0	2.84E+05		(K)NLPPSG/	(K)N L/P P S G A V/P V T G I/P P H V V K(V)		143.33	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
15451	dirMS_041712_NAR_50mM_plus2.6605.6605.3	3	7.7	1	4.18E+04		(R)TAEEPP(	(R)T A\E E/P P Q E K A/P E|P T D A R(K)		99.48	622.6353	1865.888	0.0038	2	4.25	86421.8	4.29	HUMAN	O43719	HIV Tat-specific factor 1
15452	dirMS_041712_NAR_50mM_plus2.8548.8548.3	3	7.7	1	2.38E+04	M22m	(K)LAEQAE	(K)L/A/E Q/A E R Y D/D m/A A C M/K(S)	C:Carbamidomethylation m:Oxid	113.12	639.9473	1901.819	16.0083	7	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
15453	dirMS_041712_NAR_50mM_plus2.9685.9685.3	3	7.7	1	3.32E+05		(R)AGTGVD	(R)A G|T/G/V/D N V D L E A A T R K(G)		117.42	539.6108	1616.824	-0.006	-3.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
15454	dirMS_041712_NAR_60mM_plus.17786.17786.3	3	7.7	1	1.13E+05		(K)WVAIQS	(K)W/V|A/I/Q S V/S A/W P E\K R(G)		150.05	552.9655	1656.886	-0.0037	-2.2	8.75	6412.4	9.52	HUMAN	J3KSS4	Cytosolic non-specific dipeptidase (Fragment)
15455	dirMS_041712_NAR_60mM_plus.18228.18228.3	3	7.7	1	3.80E+05		(R)IRIDSLS/	(R)I R I D S\L S\A/Q/L S\Q L/Q K(Q)		153.37	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
15456	dirMS_041712_NAR_120mM_minus.7524.7524.3	3	7.69	1	2.18E+05		(K)SKAEAE!	(K)S K A E A\E/S L/Y Q/S K(Y)		95.33	447.558	1340.669	-0.0098	-7.3	5.86	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
15457	dirMS_041712_NAR_30mM_minus2.11382.11382.2	2	7.69	0	2.37E+05		(R)QPSQGF	(R)Q P S/Q/G/P T/F G I/K(G)		115.4	580.3084	1159.611	-0.0011	-0.9	8.75	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
15458	dirMS_041712_NAR_30mM_minus2.15297.15297.2	2	7.69	0	6.42E+05		(R)YPVNSV	(R)Y/P/V|N S V N/I L K(A)		136.8	573.8282	1146.652	-0.0026	-2.3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
15459	dirMS_041712_NAR_30mM_minus2.15505.15505.2	2	7.69	0	1.08E+06	M746m	(R)DLHNQr	(R)D/L|H N Q|m I K(S)	m:Oxidized methionine	138.43	507.7594	998.509	16.0027	7.7	6.74	244993.9	9.17	HUMAN	Q13459	Unconventional myosin-IXb
15460	dirMS_041712_NAR_30mM_minus2.16342.16342.2	2	7.69	0	1.40E+05		(R)SLVSGLI	(R)S L|V/S/G|L I R(L)		142.12	422.7649	844.525	-0.0026	-3	9.47	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
15461	dirMS_041712_NAR_30mM_minus2.18266.18266.2	2	7.69	0	8.12E+04		(K)SCDFLSS	(K)S C|D|F/L/S/S F R(D)	C:Carbamidomethylation	153.88	559.7501	1118.494	-0.0006	-0.5	5.55	42963.5	5.19	HUMAN	P35237	Serpin B6
15462	dirMS_041712_NAR_30mM_minus2.7059.7059.2	2	7.69	0	2.58E+05		(R)ASYISSA	(R)A S|Y/I S/S A/R(L)		92.92	427.7216	854.437	-0.0007	-0.9	8.79	59288.4	7.16	HUMAN	Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)
15463	dirMS_041712_NAR_40mM_minus2.12205.12205.3	3	7.69	0	4.57E+05		(K)IAILTCPF	(K)I/A|I/L/T C/P F E/P P K P/K(T)	C:Carbamidomethylation	155.68	537.6382	1610.898	0.0026	1.6	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
15464	dirMS_041712_NAR_40mM_minus2.9526.9526.3	3	7.69	0	2.91E+04	M5m	(R)EmQDVI	(R)E m/Q/D/V D/L A E\V K/P L V E K(G)	m:Oxidized methionine	138.73	620.3199	1842.952	15.9934	-0.8	4.18	18328.6	4.58	HUMAN	E5RGM5	Protein NDRG1 (Fragment)
15465	dirMS_041712_NAR_50mM_minus2.11059.11059.3	3	7.69	1	8.29E+04		(K)LIPDSIGI	(K)L I/P D/S I G/K D I E K(A)		130.92	443.2546	1327.747	0.0025	1.9	4.56	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
15466	dirMS_041712_NAR_50mM_minus2.16386.16386.3	3	7.69	0	4.29E+05		(R)VLDPFTI	(R)V/L|D P/F T/I K/P L D R(K)		161.93	471.9411	1413.81	-0.0013	-0.9	5.93	63448.4	7.29	HUMAN	B4E022	Transketolase
15467	dirMS_041712_NAR_50mM_minus2.7728.7728.3	3	7.69	0	4.07E+04	M409m	(K)VLAmSG	(K)V L|A m/S G D/P N/Y/L H R(M)	m:Oxidized methionine	111.03	496.9173	1472.732	16.0059	7.4	6.71	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
15468	dirMS_041712_NAR_60mM_minus.15334.15334.2	2	7.69	0	3.99E+05		(R)EHALLA\	(R)E H A\L/L/A/Y T L/G\V\K(Q)		144.7	657.873	1314.742	-0.0029	-2.2	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
15469	dirMS_041712_NAR_60mM_minus.6573.6573.3	3	7.69	0	1.90E+04		(K)QPPTAA	(K)Q P/P/T A/A G/R/P V D A S P R(V)		95.1	507.2655	1519.798	-0.0156	-10.3	9.6	43421.2	6.21	HUMAN	E9PHI6	Cytoplasmic dynein 1 light intermediate chain 1
15470	dirMS_041712_NAR_60mM_minus.8999.8999.2	2	7.69	0	9.67E+05		(K)QEYDES(	(K)Q E|Y D E\S/G P S I/V H/R(K)		110.35	758.8539	1516.703	-0.0021	-1.4	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
15471	dirMS_041712_NAR_120mM_plus.20603.20603.4	4	7.69	1	2.15E+05		(K)AAIDWF	(K)A A I/D/W F D G K E F/H/G N I I/K(V)		161.23	491.0027	1960.992	-0.0026	-1.3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
15472	dirMS_041712_NAR_20mM_plus.10835.10835.2	2	7.69	0	7.09E+03	M142m	(R)VVNVSS	(R)V V|N V/S S I m/S V R(A)	m:Oxidized methionine	146.97	603.8291	1190.656	15.9948	-0.1	9.72	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
15473	dirMS_041712_NAR_20mM_plus.7285.7285.2	2	7.69	0	1.62E+05	M33m	(R)IDEmPE/	(R)I/D/E m|P E/A A V K(S)	m:Oxidized methionine	118.22	559.7742	1102.545	15.9962	1.2	4.14	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor

15474	dirMS_041712_NAR_30mM_plus2.20404.20404.2	2	7.69	0	6.53E+04		(K)SYELPD	(K)S Y|E|L/P D G Q V/I T I G N E R(F)		160.92	895.9487	1790.892	-0.0018	-1	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
15475	dirMS_041712_NAR_30mM_plus2.8498.8498.2	2	7.69	0	4.31E+05		(R)AVNYFS	(R)A/V/N Y F S K(V)		98.75	414.7159	828.425	-0.0005	-0.6	8.63	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
15476	dirMS_041712_NAR_40mM_plus2.11028.11028.2	2	7.69	0	7.20E+03		(R)GDFCIQ	(R)G D/F/C I/Q/V G R(-)	C:Carbamidomethylation	131.12	526.2539	1051.499	0.0016	1.5	5.84	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
15477	dirMS_041712_NAR_40mM_plus2.11570.11570.3	3	7.69	0	5.67E+04		(R)LDDTVH	(R)L D\D T/V H/V V/I A/T P G R(I)		134.08	498.2739	1492.812	-0.0047	-3.1	5.21	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
15478	dirMS_041712_NAR_40mM_plus2.19213.19213.3	3	7.69	1	1.93E+05		(K)TSAQVV	(K)T S/A/Q V/V/L D G L\V D K I G/D V K(C)		180.37	619.6811	1857.033	-0.004	-2.2	4.43	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
15479	dirMS_041712_NAR_40mM_plus2.7022.7022.2	2	7.69	0	4.94E+04		(R)YLSNAY	(R)Y/L/S/N A/Y A/R(E)		101.45	479.2437	957.479	0.0013	1.3	8.59	27264.5	5.09	HUMAN	O00299	Chloride intracellular channel protein 1
15480	dirMS_041712_NAR_50mM_plus2.10269.10269.3	3	7.69	0	1.09E+05		(K)MSIAQC	(K)M\S/I/A Q/C T/S S/H P I I R(Q)	C:Carbamidomethylation	121.63	534.2701	1600.793	0.0023	1.5	9.52	18283.4	9.29	HUMAN	Q8N8C4	Coiled-coil-helix-coiled-coil-helix domain-containing protein 5
15481	dirMS_041712_NAR_50mM_plus2.11143.11143.3	3	7.69	0	1.62E+05		(K)ADDGR	(K)A/D|D/G R P F|P Q V I/K(S)		125.23	448.2419	1342.711	-0.0002	-0.2	6	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
15482	dirMS_041712_NAR_50mM_plus2.20196.20196.3	3	7.69	0	5.30E+05		(R)QARPTY	(R)Q/A R P T Y\A\T A|M/L Q S L L K(-)		174.57	597.9962	1791.979	-0.0045	-2.5	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
15483	dirMS_041712_NAR_50mM_plus2.8121.8121.3	3	7.69	1	2.64E+05	M227m M	(R)mQKEIT	(R)m Q/K E I T A\L/A|P S T m K(I)	m:Oxidized methionine	108.98	527.6045	1548.812	31.9865	-2.1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
15484	dirMS_041712_NAR_60mM_plus.21145.21145.3	3	7.69	1	1.05E+05		(K)AKINEA	(K)A K I N E A V/E C/L/L/S L K(A)	C:Carbamidomethylation	173.75	529.9643	1587.878	0.0009	0.6	6.18	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
15485	dirMS_041712_NAR_60mM_plus.7118.7118.2	2	7.69	1	5.01E+05		(K)GKGGEI	(K)G K/G G E/I Q/P V/S V\K(V)		95.43	599.8427	1198.679	-0.0009	-0.7	8.59	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
15486	dirMS_041712_NAR_60mM_plus.8029.8029.3	3	7.69	1	4.21E+05		(R)QLQLEA	(R)Q L Q/L/E/A/E E Q R/K(Q)		99.95	457.9111	1371.723	-0.0039	-2.9	4.79	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
15487	dirMS_041712_NAR_120mM_minus.6089.6089.3	3	7.68	1	5.64E+05		(K)TCEESSF	(K)T/C|E/E/S S/F/C K R(Q)	C:Carbamidomethylation	86.8	435.1849	1303.541	-0.0004	-0.3	5.81	10576.1	11.44	HUMAN	E9PRF8	Neutral alpha-glucosidase AB
15488	dirMS_041712_NAR_20mM_minus.13392.13392.3	3	7.68	0	2.48E+05		(K)DAGTIA	(K)D A G T\I|A G L/N V/L R(I)		184.9	400.5632	1199.674	0.0008	0.7	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
15489	dirMS_041712_NAR_60mM_minus.18320.18320.3	3	7.68	0	1.21E+05		(R)LGIEGLS	(R)L G\I/E G L/S/L/H N V L/K(L)		163.43	464.9423	1392.821	-0.0086	-6.2	6.75	177928	5.42	HUMAN	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1
15490	dirMS_041712_NAR_120mM_plus.20906.20906.4	4	7.68	1	5.00E+05		(R)GIEKPPF	(R)G I E K/P P F E L/P D F I K R(T)		162.38	447.2518	1785.99	-0.0044	-2.5	6.18	98282.7	5.49	HUMAN	E9PPJ0	Splicing factor 3B subunit 2
15491	dirMS_041712_NAR_120mM_plus.5696.5696.4	4	7.68	2	4.56E+05		(R)KTGQAP	(R)K\T G Q\A|P/G Y S Y T/A/A N K N K(G)		83.45	450.4826	1798.908	0.0003	0.2	9.83	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
15492	dirMS_041712_NAR_120mM_plus.6906.6906.3	3	7.68	0	4.48E+05		(K)SQFSDKI	(K)S\Q|F/S D/K/P V Q D R(G)		89.6	436.2209	1306.639	0.0095	7.3	5.68	13194	9.99	HUMAN	E9PI70	Chitinase domain-containing protein 1 (Fragment)
15493	dirMS_041712_NAR_20mM_plus.14449.14449.2	2	7.68	0	1.44E+05		(K)VSTLPAI	(K)V/S/T|L/P A I T L K(L)		171.8	521.8283	1042.651	-0.0013	-1.3	8.72	20599.3	9.19	HUMAN	H7C1V0	Cathepsin D light chain (Fragment)
15494	dirMS_041712_NAR_20mM_plus.14998.14998.2	2	7.68	0	2.17E+05		(K)GLAITFV	(K)G L A\I|T/F|V/S D E/N D A K(I)		175.3	740.3693	1479.733	-0.0012	-0.8	4.03	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
15495	dirMS_041712_NAR_20mM_plus.15591.15591.3	3	7.68	0	1.25E+05		(R)GNPTVE	(R)G N/P T V E/V D/L F/T S K(G)		179.65	469.577	1406.716	0.0003	0.2	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
15496	dirMS_041712_NAR_30mM_plus2.15960.15960.2	2	7.68	0	1.14E+06		(R)MGAGM	(R)M G\A|G|M/G/F/G L E R(M)		137.22	563.2636	1125.518	0.002	1.7	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
15497	dirMS_041712_NAR_30mM_plus2.8889.8889.2	2	7.68	0	7.37E+05		(R)GMGPG	(R)G/M/G|P G T|P A G Y G R(G)		100.28	560.7657	1120.52	0.0037	3.3	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
15498	dirMS_041712_NAR_50mM_plus2.18491.18491.3	3	7.68	1	4.06E+05		(R)IAKEEIF	(R)I A K E E I/F G|P V Q/P L/F/K(F)		165.05	572.6586	1715.973	-0.0118	-6.9	6.14	57661.7	6.36	HUMAN	P30837	Aldehyde dehydrogenase X, mitochondrial
15499	dirMS_041712_NAR_60mM_plus.7431.7431.3	3	7.68	1	7.90E+05		(R)AVTGYK	(R)A/V/T G Y K/D/P Y/S G/K(L)		96.87	429.2193	1285.642	0.0011	0.8	8.47	533778	5.74	HUMAN	Q15149	Plectin
15500	dirMS_041712_NAR_60mM_plus.7957.7957.3	3	7.68	1	3.68E+05		(K)DISTNYY	(K)D I/S/T/N Y/Y/A S Q K K(T)		99.77	473.2367	1417.696	-0.0002	-0.2	8.43	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
15501	dirMS_041712_NAR_30mM_minus2.13784.13784.2	2	7.67	0	5.81E+05		(K)TCTFILR	(K)T\C|T/F/I/L R(G)	C:Carbamidomethylation	128.22	455.7458	910.481	0.0028	3.1	9.41	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
15502	dirMS_041712_NAR_30mM_minus2.16441.16441.2	2	7.67	0	2.53E+05		(R)ASLEAAI	(R)A S L E|A/A|I/A/D A E Q R(G)		143.58	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
15503	dirMS_041712_NAR_50mM_minus2.17363.17363.3	3	7.67	0	1.23E+05		(K)VHLVGI	(K)V H\L V G\I\D\I|F/T G K(K)		167.63	433.5856	1298.747	-0.0045	-3.4	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
15504	dirMS_041712_NAR_50mM_minus2.8431.8431.3	3	7.67	1	2.36E+05		(R)AGTGVD	(R)A G/T/G V D N V D/L E/A/A T R K(G)		116.53	539.6119	1616.824	-0.0027	-1.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
15505	dirMS_041712_NAR_60mM_minus.14548.14548.3	3	7.67	0	3.43E+05		(K)LPNLTH	(K)L/P/N L T/H/L N L S G N K(L)		140.83	474.2636	1420.791	-0.0144	-10.2	8.76	18070.1	3.52	HUMAN	Q5T6W8	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member B (Fragment)
15506	dirMS_041712_NAR_60mM_minus.17969.17969.3	3	7.67	1	5.33E+04		(K)VKLAAV	(K)V K L A A V D A T V N/Q/V|L A S R(Y)		161.3	585.6728	1755.012	-0.0085	-4.8	8.72	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
15507	dirMS_041712_NAR_60mM_minus.18284.18284.3	3	7.67	0	1.21E+05		(R)LGIEGLS	(R)L G I/E G L S L/H/N V/L/K(L)		163.43	464.9423	1392.821	-0.0086	-6.2	6.75	177928	5.42	HUMAN	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1
15508	dirMS_041712_NAR_60mM_minus.6173.6173.3	3	7.67	1	7.06E+05		(K)DSYVGD	(K)D S Y V/G/D E/A Q S K/R(G)		92.68	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
15509	dirMS_041712_NAR_120mM_plus.17631.17631.4	4	7.67	1	9.56E+04		(R)GFGHIG	(R)G F G H I G I A\V/P/D V Y/S A C K R(F)	C:Carbamidomethylation	146.87	487.5024	1946.991	-0.0028	-1.4	8.6	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
15510	dirMS_041712_NAR_20mM_plus.17155.17155.2	2	7.67	0	8.18E+04		(K)VNIIPIIA	(K)V/N|I I/P I I A K(A)		189.37	490.8283	980.65	-0.001	-1	8.72	51212	5.84	HUMAN	A6NFQ9	Septin-8
15511	dirMS_041712_NAR_30mM_plus2.19383.19383.2	2	7.67	0	5.76E+04		(R)QAQEYE	(R)Q A Q E/Y/E\A L L|N I K(V)		155.35	710.3766	1419.748	-0.0019	-1.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
15512	dirMS_041712_NAR_30mM_plus2.5862.5862.2	2	7.67	0	1.94E+05		(R)VISEYQK	(R)V/I/S E Y Q/K(L)		85.45	433.7317	866.462	-0.0057	-6.6	5.97	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
15513	dirMS_041712_NAR_40mM_plus2.18528.18528.3	3	7.67	1	3.08E+04		(K)LLLEGVE	(K)L L/L E/G V E N K L I/P/G/L K(I)		175.08	546.0066	1636.004	0.0009	0.5	6.14	59384	7.79	HUMAN	B7Z3Z9	Long-chain-fatty-acid--CoA ligase 1
15514	dirMS_041712_NAR_40mM_plus2.5912.5912.2	2	7.67	0	1.80E+04		(R)CAYVYK	(R)C|A\Y/V Y/K(A)	C:Carbamidomethylation	92.83	402.1918	803.376	0.0007	0.9	8.5	10702.2	10.89	HUMAN	C9K025	60S ribosomal protein L35a (Fragment)
15515	dirMS_041712_NAR_50mM_plus2.13277.13277.3	3	7.67	0	3.85E+05		(K)VQASLA	(K)V Q|A S L/A A N T F/T I T G H A E/T K(Q)		137.68	654.0087	1960.013	-0.0019	-1	6.72	11802.2	5.6	HUMAN	D6RDG3	Transcription factor BTF3 (Fragment)
15516	dirMS_041712_NAR_50mM_plus2.18696.18696.3	3	7.67	0	3.41E+05		(R)LLLDGA	(R)L L|L D/G\A P L/I A I H K(A)		165.85	458.622	1373.852	-0.0001	0	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
15517	dirMS_041712_NAR_50mM_plus2.7523.7523.3	3	7.67	0	1.09E+04		(K)VSYGIG	(K)V/S/Y/G/I/G D E E H\D Q E G R(V)		105.67	564.2484	1690.73	0.0003	0.2	4.17	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
15518	dirMS_041712_NAR_50mM_plus2.7857.7857.3	3	7.67	0	6.95E+04		(K)INVPELP	(K)I N V P/E L P/T P/D E D N K(L)		106.93	527.6045	1580.78	0.0187	11.8	3.91	77604	5.92	HUMAN	A1A528	Centromere/kinetochore protein zw10 homolog
15519	dirMS_041712_NAR_50mM_plus2.9139.9139.3	3	7.67	1	2.65E+05		(K)EVPAVP	(K)E V/P A V/P E/T L K K(K)		115.48	404.2395	1210.704	-0.0002	-0.2	6.24	29282.3	10.71	HUMAN	P18124	60S ribosomal protein L7
15520	dirMS_041712_NAR_60mM_plus.11265.11289.3	3	7.67	1	4.95E+05		(K)GAAPNV	(K)G A|A|P/N V V/Y/T Y T G K R(I)		116.45	499.594	1496.786	-0.0182	-12.1	9.7	11682.5	3.98	HUMAN	F8W084	Cleavage and polyadenylation-specificity factor subunit 6
15521	dirMS_041712_NAR_60mM_plus.18769.18769.3	3	7.67	0	4.81E+04		(R)HMSEFM	(R)H M S E F M E/C N L\N\E L\V K(H)	C:Carbamidomethylation	155.72	627.6148	1880.834	-0.0041	-2.2	4.75	26790	6.25	HUMAN	F5GX11	Proteasome subunit alpha type-1
15522	dirMS_041712_NAR_60mM_plus.20575.20671.3	3	7.67	1	4.98E+05		(R)DSIVAEL	(R)D S/I|V/A/E L D/R E M S R(S)		168.35	507.5883	1520.737	0.013	8.6	4.32	34709.6	4.98	HUMAN	O14579	Coatomer subunit epsilon
15523	dirMS_041712_NAR_60mM_plus.20738.20738.3	3	7.67	0	7.00E+05		(R)LGFHLPL	(R)L G F H L P L E/V|A/Y/Q R(G)		168.67	514.9568	1542.843	0.0131	8.5	6.75	533778	5.74	HUMAN	Q15149	Plectin
15524	dirMS_041712_NAR_20mM_minus.12422.12422.3	3	7.66	0	1.11E+06	M313m	(R)TVQSLEI	(R)T V Q S L E/I/D/L/D S m/R(N)	m:Oxidized methionine	171.68	508.2517	1506.747	15.9937	-0.8	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
15525	dirMS_041712_NAR_50mM_minus2.10581.10581.3	3	7.66	1	3.01E+05		(K)NQVAM	(K)N Q|V|A M|N/P T N T V F D A K R(L)		128.62	602.6379	1805.896	0.0029	1.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
15526	dirMS_041712_NAR_60mM_minus.10817.10817.3	3	7.66	1	3.89E+05		(K)TAVCDI	(K)T A|V/C D I/P P R G L K(M)	C:Carbamidomethylation	119.88	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
15527	dirMS_041712_NAR_60mM_minus.11260.11260.3	3	7.66	1	6.50E+04	M214m	(R)LAYKDLE	(R)L A Y K/D L/E I/Q m K(K)	m:Oxidized methionine	122.42	456.576	1351.729	15.9844	-7.7	6.07	49283	6.89	HUMAN	C9JZR4	ADP-ribosylation factor GTPase-activating protein 3
15528	dirMS_041712_NAR_60mM_minus.15023.15023.3	3	7.66	0	2.01E+05		(R)IYIPLPE	(R)I Y/I P L/P E P H/A R(A)		143.9	435.9153	1305.731	0	0	6.75	49472.3	6.75	HUMAN	O75351	Vacuolar protein sorting-associated protein 4B
15529	dirMS_041712_NAR_60mM_minus.7892.7892.3	3	7.66	1	4.95E+05		(R)YLAEVA	(R)Y/L/A/E/V/A T G E K R(A)		104.23	412.8902	1236.658	-0.0022	-1.8	6.14	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
15530	dirMS_041712_NAR_60mM_minus.8670.8670.3	3	7.66	1	5.21E+04	M227m M	(R)mQKEIT	(R)m/Q K E I T A\L/A|P/S T m K(I)	m:Oxidized methionine	108.17	527.6044	1548.812	31.9862	-2.3	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
15531	dirMS_041712_NAR_120mM_plus.10403.10403.3	3	7.66	1	7.18E+05		(K)IKGEHP	(K)I K|G E H|P/G L/S I/G D V A K(K)		107.97	507.6167	1520.843	-0.0076	-5	6.75	24408.7	5.92	HUMAN	B2RPK0	Putative high mobility group protein B1-like 1
15532	dirMS_041712_NAR_120mM_plus.5817.5817.2	2	7.66	1	1.28E+06		(K)IREEYPD	(K)I R/E/E|Y\P D|R(I)		84.52	539.2694	1077.532	-0.0008	-0.8	4.68	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
15533	dirMS_041712_NAR_20mM_plus.12324.12324.2	2	7.66	0	7.32E+04		(R)GSVLEP	(R)G S V/L/E|P E G T V E I K(F)		158.3	679.3577	1357.721	-0.0128	-9.4	4.25	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
15534	dirMS_041712_NAR_20mM_plus.16747.16747.3	3	7.66	0	2.85E+05		(K)VQIAVA	(K)V Q\I A V A\N A\Q/E L/L Q R(M)		186.82	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
15535	dirMS_041712_NAR_20mM_plus.19138.19138.2	2	7.66	0	2.21E+05		(K)ILTFDQL	(K)I L|T F/D Q L/A L D/S P K(G)		203.25	730.9063	1460.8	0.0058	4	4.21	14643	11.93	HUMAN	F8VUA6	60S ribosomal protein L18 (Fragment)
15536	dirMS_041712_NAR_30mM_plus2.19975.19975.2	2	7.66	0	1.29E+05		(R)YAFVMF	(R)Y/A|F/V M F K(T)		157.98	453.2369	905.459	0.0076	8.3	8.59	103045.5	7.1	HUMAN	B9ZVT1	RNA-binding protein 12B
15537	dirMS_041712_NAR_30mM_plus2.22358.22358.3	3	7.66	0	5.16E+05		(R)VGNLGL	(R)V G N L G L A\T/S/F/F/N E R(N)		172.82	508.9306	1524.781	-0.0033	-2.1	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
15538	dirMS_041712_NAR_30mM_plus2.5692.5692.2	2	7.66	0	6.92E+04		(R)AYGGSM	(R)A Y/G/G/S M C A K(C)	C:Carbamidomethylation	83.82	472.7087	944.396	0.0137	14.5	8.63	13520.9	11.92	HUMAN	P49207	60S ribosomal protein L34
15539	dirMS_041712_NAR_40mM_plus2.12090.12090.3	3	7.66	1	2.00E+04	M467m	(R)DmTLPP	(R)D m T L/P/P E T N V/I L T K\D K(A)	m:Oxidized methionine	137.58	610.9868	1814.957	15.989	-3.2	4.56	246695.2	5.91	HUMAN	E7EVA0	Microtubule-associated protein
15540	dirMS_041712_NAR_40mM_plus2.6458.6458.2	2	7.66	0	1.87E+05	M154m	(R)mGYMD	(R)m G Y\M D|P/R(E)	m:Oxidized methionine	97.03	443.1854	869.364	15.9991	4.7	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
15541	dirMS_041712_NAR_60mM_plus.6283.6283.3	3	7.66	1	3.09E+05		(R)GSCSTE	(R)G S/C/S T E V/E K E T Q E K(M)	C:Carbamidomethylation	91.08	537.9088	1611.717	-0.0048	-3	4.49	13871.4	9.22	HUMAN	O75348	V-type proton ATPase subunit G 1
15542	dirMS_041712_NAR_120mM_minus.12361.12361.3	3	7.65	1	3.31E+05		(K)LFNLSKE	(K)L/F N L S K/E D/D/V/R(Q)		121.4	445.9006	1335.69	-0.0031	-2.3	4.56	25082	11.29	HUMAN	A2A3R5	40S ribosomal protein S6
15543	dirMS_041712_NAR_30mM_minus2.8425.8425.2	2	7.65	0	1.09E+05		(K)CAMTAL	(K)C/A|M|T A/L/S S K(L)	C:Carbamidomethylation	100.45	484.7299	968.454	-0.0014	-1.5	8.75	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
15544	dirMS_041712_NAR_40mM_minus2.11764.11764.3	3	7.65	1	5.04E+05		(K)VALNVS	(K)V/A|L|N/V/S C A N L L D K D/I G S K(S)	C:Carbamidomethylation	153.28	639.6749	1917.011	-0.0008	-0.4	5.93	9239.5	7.98	HUMAN	E5RFT7	Copine-3 (Fragment)
15545	dirMS_041712_NAR_60mM_minus.14013.14013.3	3	7.65	1	2.51E+05		(R)VVISLQL	(R)V/V|I/S L Q/L/T A E K R(V)		138	452.9408	1356.821	-0.0131	-9.6	8.72	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
15546	dirMS_041712_NAR_60mM_minus.8879.8879.3	3	7.65	1	3.60E+05	M232m M	(R)MSmKE	(R)M/S/m K E V D\E\Q m/L|N V\Q N\K(N)	m:Oxidized methionine	110.3	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
15547	dirMS_041712_NAR_20mM_plus.16584.16584.2	2	7.65	0	1.41E+05		(K)TVDNFV	(K)T V|D N F/V/A L/A T G E/K(G)		185.9	682.8565	1364.706	0.0001	0.1	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
15548	dirMS_041712_NAR_30mM_plus2.17674.17779.2	2	7.65	0	2.17E+05		(K)LFDFPG	(K)L F|D/F/P G/R(G)		146.23	426.2291	851.441	0.0099	11.6	5.84	56825.2	9.49	HUMAN	Q9P258	Protein RCC2
15549	dirMS_041712_NAR_30mM_plus2.18460.18460.2	2	7.65	0	1.65E+05		(K)QFLSQF	(K)Q F|L/S|Q/F E M Q S R(K)		150.25	700.8358	1400.663	0.0016	1.2	6	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
15550	dirMS_041712_NAR_30mM_plus2.21758.21758.2	2	7.65	0	1.76E+04		(K)NGFLLD	(K)N G|F|L|L/D G F/P R(T)		169.18	568.3022	1135.59	0.0077	6.7	5.84	21283.1	6.45	HUMAN	F8VY04	Adenylate kinase 2, mitochondrial
15551	dirMS_041712_NAR_30mM_plus2.23525.23525.2	2	7.65	0	1.42E+06		(R)DLPLLLF	(R)D L/P/L/L/L F R(T)		189.65	493.8049	986.603	-0.0008	-0.8	5.84	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
15552	dirMS_041712_NAR_50mM_plus2.12134.12134.3	3	7.65	1	1.37E+06		(K)MLVSGA	(K)M/L/V/S/G A G D I K L T K(D)		131.3	444.9236	1332.756	0.0007	0.5	8.35	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
15553	dirMS_041712_NAR_60mM_plus.16381.16381.3	3	7.65	0	7.47E+05		(K)SPYQEF	(K)S P/Y|Q/E F T\D H L/V K(T)		142.52	488.5776	1463.717	0.0017	1.2	5.3	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
15554	dirMS_041712_NAR_60mM_plus.19544.19544.3	3	7.65	1	6.42E+05		(K)TVTAMD	(K)T V|T/A M/D V V/Y A L K R(Q)		160.8	489.6071	1466.804	0.0032	2.2	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
15555	dirMS_041712_NAR_20mM_minus.12223.12223.2	2	7.64	0	1.80E+05		(R)AAVIGP	(R)A A\V|I/G/P D/V F A K(L)		171.35	544.3103	1087.615	-0.0013	-1.2	5.88	266161	5.68	HUMAN	E9PPU0	Epiplakin
15556	dirMS_041712_NAR_30mM_minus2.11175.11175.2	2	7.64	0	3.93E+05		(R)GYSFTTT	(R)G Y|S|F/T T/T A E R(E)		114.55	566.7699	1132.527	0.0056	4.9	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
15557	dirMS_041712_NAR_30mM_minus2.13910.13910.2	2	7.64	0	3.02E+05	M313m	(K)NSLESYA	(K)N S\L/E/S Y/A F N m K(A)	m:Oxidized methionine	128.93	660.3011	1303.599	15.9962	1	6	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
15558	dirMS_041712_NAR_30mM_minus2.15319.15319.2	2	7.64	0	5.64E+05	M2249m	(K)MSIYQA	(K)M/S/I/Y/Q A/m W K(G)	m:Oxidized methionine	135.95	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
15559	dirMS_041712_NAR_40mM_minus2.15155.15155.3	3	7.64	0	1.36E+05		(R)NEVSFVI	(R)N E/V/S F/V/I H N L P V L A K(M)		175.1	560.6529	1679.948	-0.0038	-2.2	6.75	35663.7	5.91	HUMAN	B4DWK0	Selenide, water dikinase 1
15560	dirMS_041712_NAR_50mM_minus2.5991.5991.3	3	7.64	0	3.55E+04		(R)ATAPQT	(R)A T/A/P Q T Q/H V\S P\M R(Q)		96.35	475.244	1423.711	0.0064	4.5	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
15561	dirMS_041712_NAR_50mM_minus2.8619.8619.3	3	7.64	0	1.65E+05	M180m	(R)VVVLmG	(R)V V|V/L m G S/T S D L G H C E K(I)	C:Carbamidomethylation m:Oxid	117.55	583.2829	1731.84	15.9937	-0.7	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
15562	dirMS_041712_NAR_60mM_minus.7673.7673.3	3	7.64	1	5.65E+05		(R)YLAEVA	(R)Y L|A E|V/A/A G D D K K(G)		102.07	427.222	1279.653	-0.0014	-1.1	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
15563	dirMS_041712_NAR_60mM_minus.7916.7916.3	3	7.64	0	9.10E+04		(K)STGEPL	(K)S T|G E/P L G/H V P A/R(M)		103.75	407.5515	1220.638	0.0017	1.4	6.47	9840	8.09	HUMAN	C9J1K7	Lipoma-preferred partner (Fragment)
15564	dirMS_041712_NAR_60mM_minus.8775.8775.3	3	7.64	1	2.78E+05	M232m M	(R)MSmKE	(R)M/S m/K E V D\E Q m\L N/V\Q N/K(N)	m:Oxidized methionine	109.68	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
15565	dirMS_041712_NAR_120mM_plus.4366.4366.3	3	7.64	0	6.75E+05	M76m M7	(R)LTNSmM	(R)L/T/N/S m/M m/H/G/R(N)	m:Oxidized methionine	71.25	403.8446	1177.527	31.9918	1.6	9.75	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
15566	dirMS_041712_NAR_120mM_plus.4613.4619.3	3	7.64	0	6.19E+05		(R)THSQGG	(R)T H\S Q G G|Y|G S/Q G Y/K(Y)		74.07	457.2092	1369.613	-0.0001	-0.1	8.2	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
15567	dirMS_041712_NAR_20mM_plus.16951.16951.2	2	7.64	0	6.33E+04		(K)VLTPELY	(K)V L|T/P E L Y A E\L R(A)		188.15	652.3664	1303.726	-0.0001	-0.1	4.53	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
15568	dirMS_041712_NAR_30mM_plus2.11354.11354.2	2	7.64	0	4.49E+05		(R)NGDFLP	(R)N G\D|F/L/P T\R(L)		112.92	460.2391	919.463	0.0077	8.4	5.84	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
15569	dirMS_041712_NAR_30mM_plus2.15984.15984.2	2	7.64	0	3.03E+05		(R)YSVDIPL	(R)Y/S|V/D I/P L D K(T)		136.25	525.2819	1049.551	0.0052	4.9	4.21	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
15570	dirMS_041712_NAR_30mM_plus2.4178.4178.2	2	7.64	0	1.24E+06	M299m M	(K)NmmAA	(K)N m/m|A/A C D|P R(H)	C:Carbamidomethylation m:Oxid	69.55	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
15571	dirMS_041712_NAR_30mM_plus2.6872.6872.2	2	7.64	0	2.73E+05		(K)AEYLCR	(K)A E|Y/L C R(I)	C:Carbamidomethylation	90.82	406.1945	811.377	0.005	6.2	6.04	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
15572	dirMS_041712_NAR_40mM_plus2.17352.17352.3	3	7.64	0	8.70E+03		(R)VSAAVL	(R)V/S A/A|V/L/P L V H/P L P E G L R(A)		168.3	590.0215	1768.048	0.002	1.1	6.72	63124.2	9.53	HUMAN	E7EVU5	Nuclear receptor corepressor 1 (Fragment)
15573	dirMS_041712_NAR_40mM_plus2.18280.18280.3	3	7.64	0	1.04E+05		(K)VLSLPKP	(K)V/L/S\L/P K P T I\I/L/S/A Y Q R(K)		173.45	600.3613	1799.079	-0.0096	-5.3	9.99	80080.5	5.54	HUMAN	J3KMX1	Nuclear pore complex protein Nup88 (Fragment)
15574	dirMS_041712_NAR_40mM_plus2.5878.5878.2	2	7.64	0	6.04E+04		(K)SGYLSSE	(K)S G|Y|L/S/S E/R(L)		92.52	449.7162	898.427	-0.0014	-1.5	5.72	65692.2	5.7	HUMAN	E7EQR4	Ezrin
15575	dirMS_041712_NAR_40mM_plus2.8434.8434.2	2	7.64	0	8.22E+04		(K)DVNQQ	(K)D V|N/Q/Q E F V R(A)		110.82	567.78	1134.554	-0.0011	-1	4.37	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
15576	dirMS_041712_NAR_50mM_plus2.13585.13585.3	3	7.64	0	1.12E+06		(K)AASDIA	(K)A A/S D\I A M T/E L/P P T H P I R(L)		139.37	607.3177	1819.937	0.0015	0.8	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
15577	dirMS_041712_NAR_50mM_plus2.9349.9349.3	3	7.64	0	1.10E+05		(K)IATGHG	(K)I/A/T G H G Q Q|G V/T Q V/V L K(G)		116.23	545.9755	1635.918	-0.0057	-3.5	8.76	215469.1	7.09	HUMAN	A6NEM2	HCF N-terminal chain 5
15578	dirMS_041712_NAR_60mM_plus.16223.16223.3	3	7.64	0	2.86E+05		(R)DVRPYI	(R)D V R P Y\I\V|G A V V|R(G)		141.5	448.5963	1343.779	-0.005	-3.8	8.75	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
15579	dirMS_041712_NAR_60mM_plus.21082.21082.3	3	7.64	0	2.90E+05		(R)SLHDAL	(R)S L H D\A L\C|V/L/A Q T V K(D)	C:Carbamidomethylation	172.77	518.9516	1554.831	0.0094	6.1	6.46	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
15580	dirMS_041712_NAR_20mM_minus.14617.14617.3	3	7.63	0	3.68E+05		(K)LAVEALS	(K)L A V E A\L\S S/L/D/G D L/A G R(Y)		201.3	529.6163	1586.838	-0.0041	-2.6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
15581	dirMS_041712_NAR_30mM_minus2.13744.13744.2	2	7.63	0	4.92E+05		(R)AIENELL	(R)A I|E/N E/L L A R(N)		127.5	514.79	1028.574	-0.0008	-0.7	4.53	40519.5	5.04	HUMAN	B6F210	Glutathione synthetase
15582	dirMS_041712_NAR_30mM_minus2.17933.17933.2	2	7.63	0	5.28E+04		(R)ILFQEFR	(R)I/L/F/Q E/F/R(Q)		151.42	476.7657	952.525	-0.001	-1	6	232239.1	5.52	HUMAN	F2Z2U8	Myosin-14

15583	dirMS_041712_NAR_30mM_minus2.5392.5392.2	2	7.63	0	4.70E+05		(R)TDTGEP	(R)T D|T/G E P M G/R(G)		82.77	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
15584	dirMS_041712_NAR_40mM_minus2.15854.15854.3	3	7.63	0	5.44E+05		(K)GLAPDLI	(K)G L|A/P D L P E\D L Y H L/I K(K)		184.77	565.3111	1693.916	0.0028	1.7	4.54	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
15585	dirMS_041712_NAR_50mM_minus2.16329.16329.3	3	7.63	1	1.12E+05		(K)DNNGVI	(K)D N\N/G V I/G L/L E/P M K K(S)		160.8	509.9447	1527.82	-0.0004	-0.3	6.07	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
15586	dirMS_041712_NAR_60mM_minus.19241.19241.3	3	7.63	0	1.04E+06		(R)SLHDAL(	(R)S L H/D A L|C/V|L/A Q T V K(D)	C:Carbamidomethylation	171.22	518.9484	1554.831	-0.0002	-0.1	6.46	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
15587	dirMS_041712_NAR_120mM_plus.7968.7968.4	4	7.63	2	7.14E+05	M53m	(K)LTDCVV	(K)L T/D C V/V m R/D/P A/S K/R(S)	C:Carbamidomethylation m:Oxid	95.93	416.712	1647.831	15.9956	0.4	8.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
15588	dirMS_041712_NAR_20mM_plus.10766.10766.2	2	7.63	0	1.18E+05		(R)AGTGVD	(R)A/G/T G V|D N V/D L|E A A T R(K)		146.88	744.8731	1488.729	0.01	6.7	4.03	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
15589	dirMS_041712_NAR_20mM_plus.13500.13500.2	2	7.63	0	6.82E+04		(K)ADSLLA\	(K)A D/S L/L A V/V\K(R)		165.62	458.2789	915.551	-0.0004	-0.5	5.88	103309.5	5.34	HUMAN	A0AV56	SAFB protein
15590	dirMS_041712_NAR_20mM_plus.15136.15136.2	2	7.63	0	1.88E+05	M663m	(K)SAHGTN	(K)S A H G T N P|A S A H M/A G m K(I)	m:Oxidized methionine	176.33	792.3469	1567.71	15.9761	-11.9	8.51	114325.3	6.69	HUMAN	P23378	Glycine dehydrogenase [decarboxylating], mitochondrial
15591	dirMS_041712_NAR_20mM_plus.15515.15515.2	2	7.63	1	1.87E+05	N88n	(R)nFAEPC	(R)n F A|E|P/C E D S R R(S)	C:Carbamidomethylation n:N-ac	177.92	792.3469	1380.596	203.0904	7	4.68	12980.5	9.75	HUMAN	C9JXY5	Sentan
15592	dirMS_041712_NAR_20mM_plus.6740.6740.2	2	7.63	0	4.24E+04		(R)VISSIEQI	(R)V/I|S|S I/E/Q K(T)		111.22	452.2607	903.515	-0.0004	-0.5	5.97	18789.1	6.77	HUMAN	A2IDB2	14-3-3 protein eta (Fragment)
15593	dirMS_041712_NAR_20mM_plus.7389.7389.2	2	7.63	0	2.70E+05	M281m	(R)AEAESm	(R)A E|A|E S m Y Q I K(Y)	m:Oxidized methionine	118.85	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
15594	dirMS_041712_NAR_30mM_plus2.8948.8948.2	2	7.63	0	7.09E+05		(R)GMGPG	(R)G M/G/P G T|P A G Y G R(G)		100.33	560.7657	1120.52	0.0037	3.3	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
15595	dirMS_041712_NAR_50mM_plus2.10941.10941.3	3	7.63	0	6.36E+04		(K)MVMIQI	(K)M/V/M\I Q D/G P Q N T G A D K P L/R(I)		125.3	657.663	1970.979	-0.0042	-2.1	5.71	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
15596	dirMS_041712_NAR_50mM_plus2.16388.16388.3	3	7.63	1	1.22E+05		(R)EGIVTAT	(R)E G I/V/T/A T E Q E V K E D I A K(L)		154.88	620.658	1859.96	-0.0002	-0.1	4.25	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
15597	dirMS_041712_NAR_50mM_plus2.19005.19005.3	3	7.63	0	5.47E+05		(R)GFGFITF	(R)G F G F|I/T/F T N P/E H A S V A M R(A)		168.65	661.3258	1981.959	0.004	2	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
15598	dirMS_041712_NAR_50mM_plus2.20776.20776.3	3	7.63	1	4.35E+04		(R)ITSEAED	(R)I/T|S E A E D L V/A/N F F P K K(L)		178	603.6541	1808.943	0.0049	2.7	4.68	14931.6	5.53	HUMAN	B7Z8D3	Proteasome activator complex subunit 3
15599	dirMS_041712_NAR_60mM_plus.17629.17629.3	3	7.63	1	1.17E+05		(K)SIYGSRF	(K)S I/Y/G S R F P\D|E N F T L K(H)		148.95	591.9669	1773.881	0.0055	3.1	5.79	17888.9	8.97	HUMAN	H0Y548	Peptidyl-prolyl cis-trans isomerase (Fragment)
15600	dirMS_041712_NAR_60mM_plus.18932.18932.3	3	7.63	1	2.62E+05		(K)YGKLEV/	(K)Y G K L E V\A|N L/L/L Q K(S)		156.68	496.9628	1488.878	-0.0046	-3.1	8.5	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
15601	dirMS_041712_NAR_60mM_plus.6579.6579.3	3	7.63	0	7.03E+05		(K)LVDQSG	(K)L V/D Q/S G/P P H/E P K(F)		93.72	435.2257	1303.664	-0.0015	-1.2	5.32	142137.5	9.17	HUMAN	E7ENU4	Double-stranded RNA-specific adenosine deaminase
15602	dirMS_041712_NAR_120mM_minus.11980.12002.2	2	7.62	0	1.49E+05		(K)HMLPTV	(K)H/M|L|P T V L/R(M)		119.38	483.7804	966.555	-0.0018	-1.9	9.75	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
15603	dirMS_041712_NAR_30mM_minus2.5505.5505.2	2	7.62	0	8.98E+05	M139m	(R)LmDQNI	(R)L/m/D/Q N L/K(C)	m:Oxidized methionine	84.75	439.2266	861.45	15.9961	1.3	5.84	26611.3	4.47	HUMAN	A6NL28	Putative tropomyosin alpha-3 chain-like protein
15604	dirMS_041712_NAR_40mM_minus2.6274.6274.3	3	7.62	0	2.91E+04		(K)ASGGQD	(K)A S G G Q D G A/A S S A G/A A K(R)		102.57	435.8693	1305.603	-0.0096	-7.4	5.88	256666.6	6.03	HUMAN	O60287	Nucleolar pre-ribosomal-associated protein 1
15605	dirMS_041712_NAR_50mM_minus2.10745.10745.3	3	7.62	0	2.68E+05		(K)VFEGNR	(K)V/F|E/G N R P T N S I\V F T K(L)		129.25	570.3032	1708.902	-0.0066	-3.9	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
15606	dirMS_041712_NAR_50mM_minus2.16908.16908.3	3	7.62	1	2.31E+05		(K)SLLGKD\	(K)S L/L G K/D V\L F L/K(D)		164.22	411.5911	1232.761	-0.0025	-2.1	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
15607	dirMS_041712_NAR_50mM_minus2.8844.8844.3	3	7.62	1	1.04E+05	M477m	(R)TLKIPAm	(R)T L/K I/P/A m T I A K(N)	m:Oxidized methionine	118.22	401.5779	1186.723	15.9964	1.2	10	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
15608	dirMS_041712_NAR_60mM_minus.12076.12076.3	3	7.62	1	2.15E+05		(K)YADEEIP	(K)Y/A|D E E/I/P R S P F K(V)		127.3	484.5732	1451.717	-0.0115	-7.9	4.68	258215.9	5.48	HUMAN	E7EN95	Filamin-B
15609	dirMS_041712_NAR_60mM_minus.17586.17586.3	3	7.62	0	7.70E+04		(R)VSYFAVI	(R)V/S/Y/F A/V/F D G/H G G I R(A)		157.88	508.9291	1524.759	0.0134	8.8	6.71	23205.7	5.89	HUMAN	E9PC05	Integrin-linked kinase-associated serine/threonine phosphatase 2C (Fragment)
15610	dirMS_041712_NAR_120mM_plus.5572.5572.3	3	7.62	1	7.62E+04		(R)YGEDNR	(R)Y/G|E|D/N R G Y G G S Q/G G G R(G)		82.97	543.9055	1629.7	0.0019	1.2	6.07	26157.9	4.57	HUMAN	K7EL85	TATA-binding protein-associated factor 2N (Fragment)
15611	dirMS_041712_NAR_20mM_plus.12572.12572.2	2	7.62	0	9.34E+04	M91m	(R)AITGASL	(R)A I\T/G/A/S/L A/D I/m A K(R)	m:Oxidized methionine	159.93	639.3398	1261.682	15.9903	-3.6	5.88	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
15612	dirMS_041712_NAR_20mM_plus.14671.14671.2	2	7.62	0	8.06E+04		(K)NLYIISVI	(K)N L/Y/I I S V K(G)		173.1	475.2896	949.572	0.0002	0.2	8.59	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
15613	dirMS_041712_NAR_30mM_plus2.10844.10844.2	2	7.62	0	1.19E+06		(R)GLTSVIN	(R)G L/T/S/V/I/N/Q K(L)		110.87	480.2785	959.552	-0.0023	-2.4	8.75	36923.1	5.71	HUMAN	P07195	L-lactate dehydrogenase B chain
15614	dirMS_041712_NAR_30mM_plus2.21400.21400.2	2	7.62	0	2.72E+05		(R)EADDIVI	(R)E A D D I/V/N/W L/K(K)		167.42	601.81	1202.605	0.0075	6.3	4.03	26363.4	4.91	HUMAN	I3L312	Protein disulfide-isomerase (Fragment)
15615	dirMS_041712_NAR_30mM_plus2.22187.22187.2	2	7.62	0	2.57E+05		(K)CMPTFC	(K)C/M/P/T F Q F/F K(K)	C:Carbamidomethylation	172.67	603.2777	1205.548	-0.0001	-0.1	8.75	9680	5.77	HUMAN	B1ALW1	Thioredoxin
15616	dirMS_041712_NAR_30mM_plus2.4898.4898.2	2	7.62	0	5.37E+05	M571m	(R)mGANSI	(R)m/G|A/N S/L/E R(M)	m:Oxidized methionine	76.88	447.2119	877.42	15.9969	2.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
15617	dirMS_041712_NAR_30mM_plus2.8118.8118.2	2	7.62	0	2.03E+05		(R)GTQGAE	(R)G T/Q/G/A E E V L R(A)		96.55	530.2783	1059.543	0.0064	6	4.53	533778	5.74	HUMAN	Q15149	Plectin
15618	dirMS_041712_NAR_50mM_plus2.14778.14778.3	3	7.62	0	1.17E+06		(R)EHALLA\	(R)E H A\L L A|Y|T L G V/K(Q)		145.75	438.9176	1314.742	-0.0034	-2.6	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
15619	dirMS_041712_NAR_120mM_minus.13082.13082.4	4	7.61	0	4.86E+05		(K)SLGTRPI	(K)S L/G T R P P H V F A I/A D K(A)		125.17	402.9764	1608.886	-0.0019	-1.2	8.49	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
15620	dirMS_041712_NAR_120mM_minus.14886.14886.4	4	7.61	1	1.58E+05		(K)FLDAGH	(K)F L D A G H/K L N F/A|V/A/S R(K)		135.32	412.2282	1645.881	0.0101	6.1	8.76	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
15621	dirMS_041712_NAR_120mM_minus.8684.8684.3	3	7.61	1	2.90E+05		(R)IGNSYFK	(R)I/G N S Y/F/K E/E/K(Y)		101.85	405.54	1214.605	0.0003	0.2	6.14	60404.6	6.4	HUMAN	F5H0T1	Stress-induced-phosphoprotein 1
15622	dirMS_041712_NAR_120mM_minus.8830.8830.3	3	7.61	0	7.27E+05		(R)RPELEDS	(R)R P\E\L\E|D/S/T L/R(Y)		102.42	405.8796	1215.633	-0.0085	-7	4.68	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
15623	dirMS_041712_NAR_30mM_minus2.9572.9572.2	2	7.61	0	5.09E+05		(K)SVELED\	(K)S V/E/L E/D/V K(F)		106.12	459.7452	918.478	0.0053	5.7	4.14	40310.4	6.69	HUMAN	B4DDG7	AP-1 complex subunit mu-1
15624	dirMS_041712_NAR_50mM_minus2.12862.12862.3	3	7.61	1	2.33E+05		(R)QATKDA	(R)Q/A T K D A G T I/A/G|L/N\V L R(I)		140.57	543.3085	1627.913	-0.0016	-1	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
15625	dirMS_041712_NAR_60mM_minus.11506.11506.3	3	7.61	1	1.31E+05		(R)LSFDKD/	(R)L S/F D K D A M/V/A R(A)		124.22	418.2174	1252.635	0.0022	1.8	5.96	35556.4	9.3	HUMAN	F2Z393	Transaldolase
15626	dirMS_041712_NAR_60mM_minus.17220.17220.3	3	7.61	1	1.12E+05		(K)FLSPQD'	(K)F L/S/P/Q D T/F E A L K/R(N)		156.22	517.9425	1551.817	-0.0036	-2.3	6.07	97622	8.94	HUMAN	Q9NTZ6	RNA-binding protein 12
15627	dirMS_041712_NAR_60mM_minus.18813.18813.3	3	7.61	1	2.67E+05		(K)NAAGAL	(K)N A|A/G A L/D L/L K E L K(N)		166.87	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
15628	dirMS_041712_NAR_120mM_plus.6261.6261.2	2	7.61	1	3.49E+05		(K)DSYVGD	(K)D S/Y\V/G D/E A/Q S K/R(G)		86.28	677.815	1354.623	-0.0006	-0.5	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
15629	dirMS_041712_NAR_120mM_plus.7245.7350.3	3	7.61	1	2.23E+06		(K)EMQLR(	(K)E M/Q|L/R Q E E/E R(R)		91.67	449.8829	1347.632	0.002	1.5	4.49	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
15630	dirMS_041712_NAR_120mM_plus.9421.9488.3	3	7.61	1	6.52E+05		(R)GSNKLV	(R)G S N K L\V|I|E|E/A E R(S)		102.85	448.9084	1344.712	-0.0011	-0.8	4.79	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
15631	dirMS_041712_NAR_20mM_plus.12094.12094.2	2	7.61	0	1.20E+05		(R)IYVVDV(	(R)I/Y|V/V\D/V/G S/E P R(A)		156.17	617.3237	1233.647	-0.0073	-5.9	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
15632	dirMS_041712_NAR_20mM_plus.13092.13092.2	2	7.61	0	2.25E+05	M316m	(R)ISEQFTA	(R)I S|E/Q/F/T/A m F R(R)	m:Oxidized methionine	161.87	623.3012	1229.598	15.9968	1.5	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
15633	dirMS_041712_NAR_20mM_plus.16675.16675.3	3	7.61	0	2.39E+05		(K)VQIAVA	(K)V Q I A V A N\A\Q/E L/L/Q R(M)		186.48	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
15634	dirMS_041712_NAR_20mM_plus.17075.17075.2	2	7.61	0	9.70E+04		(R)AIVAIEN	(R)A I V/A/I/E|N P/A D\V S V I S S R(N)		188.97	870.9764	1740.949	-0.0035	-2	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
15635	dirMS_041712_NAR_20mM_plus.18291.18291.2	2	7.61	0	1.64E+05		(K)DAGVIA(	(K)D A\G\V|I/A|G L N V\L/R(I)		196.77	599.3505	1197.695	-0.0013	-1.1	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
15636	dirMS_041712_NAR_30mM_plus2.18248.18248.2	2	7.61	0	3.78E+04		(K)AILFVPR	(K)A I|L/F V/P R(R)		149.07	408.2604	815.514	-0.0003	-0.3	9.79	57660.2	6.38	HUMAN	Q9NQH7	Probable Xaa-Pro aminopeptidase 3
15637	dirMS_041712_NAR_30mM_plus2.21607.21607.2	2	7.61	0	3.30E+05		(R)NSYLEVI	(R)N S|Y|L E V/L L K(L)		168.07	539.8092	1078.614	-0.0032	-2.9	6	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
15638	dirMS_041712_NAR_50mM_plus2.9693.9693.3	3	7.61	1	3.32E+05		(R)AGTGVD	(R)A G T G V/D/N V/D L/E A A T R K(G)		117.42	539.6108	1616.824	-0.006	-3.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
15639	dirMS_041712_NAR_60mM_plus.5136.5136.3	3	7.61	1	2.84E+05	M23m	(K)LAQKNP	(K)L/A/Q/K N/P m/Y Q K(E)	m:Oxidized methionine	84.13	412.8904	1220.646	16.011	13	9.7	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
15640	dirMS_041712_NAR_120mM_minus.9337.9337.3	3	7.6	1	1.29E+05		(R)RADLNC	(R)R A\D L N Q G\I|G E|P Q/S P S R(R)		105.1	575.6264	1724.867	-0.0028	-1.6	6.07	26810.9	5.15	HUMAN	Q96C19	EF-hand domain-containing protein D2
15641	dirMS_041712_NAR_20mM_minus.8703.8703.2	2	7.6	0	8.10E+04		(R)SPSDSST	(R)S P S D S/S T A|S|T/P V A E Q I E R(A)		136.52	931.4377	1861.877	-0.0093	-5	4.14	76925.9	4.46	HUMAN	A8MV58	Drebrin
15642	dirMS_041712_NAR_30mM_minus2.12446.12446.2	2	7.6	0	2.44E+05		(K)STLTDSL	(K)S T/L/T/D/S L V C/K(A)	C:Carbamidomethylation	121.77	562.2838	1123.566	-0.006	-5.4	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
15643	dirMS_041712_NAR_30mM_minus2.12828.12828.2	2	7.6	0	3.17E+05		(R)GGAEQF	(R)G G A E Q/F/M/E/E/T E R(S)		122.73	692.2961	1383.584	0.0004	0.3	4.09	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
15644	dirMS_041712_NAR_30mM_minus2.15301.15301.2	2	7.6	0	7.59E+04		(R)QITVND	(R)Q I/T V/N/D L/P V G R(S)		136.35	606.3404	1211.674	-0.0007	-0.6	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
15645	dirMS_041712_NAR_30mM_minus2.8736.8736.2	2	7.6	0	1.17E+05		(R)TSVETAI	(R)T\S/V/E/T/A\L R(A)		101.98	438.7375	876.479	-0.0108	-12.3	5.66	19945.8	4.97	HUMAN	B4DG50	F-actin-capping protein subunit alpha-2
15646	dirMS_041712_NAR_40mM_minus2.8068.8068.3	3	7.6	0	1.24E+05	M147m	(K)LQmEAF	(K)L Q/m E A P H\I/I/V G T/P G R(V)	m:Oxidized methionine	127.3	545.627	1618.873	15.9931	-1.1	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
15647	dirMS_041712_NAR_50mM_minus2.11078.11078.3	3	7.6	1	5.96E+05		(R)IAEFTTN	(R)I/A|E F/T T N L/T E E E E K S K(S)		130.6	623.6418	1868.912	-0.0015	-0.8	4.32	227783.5	5.5	HUMAN	P35579	Myosin-9
15648	dirMS_041712_NAR_50mM_minus2.16429.16429.3	3	7.6	0	1.75E+05	M1m	(-)mKPLVVI	(-)m K P L V/V\F\V|L/G G P G\A G K(G)	m:Oxidized methionine	161.27	529.3077	1569.919	15.99	-3.1	10	22450.2	5.44	HUMAN	P30085	UMP-CMP kinase
15649	dirMS_041712_NAR_50mM_minus2.8722.8722.3	3	7.6	1	1.13E+05		(K)TAVCDIF	(K)T A|V/C/D I/P P R G L K(M)	C:Carbamidomethylation	117.28	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
15650	dirMS_041712_NAR_60mM_minus.5550.5550.3	3	7.6	1	2.64E+04		(K)QMNDE	(K)Q M N D|E K T/A A/D/Y K(I)		86.97	471.8812	1413.632	-0.0024	-1.7	4.56	9786.1	5.52	HUMAN	E9PS38	Protein NEDD8-MDP1
15651	dirMS_041712_NAR_60mM_minus.9814.9814.3	3	7.6	0	4.34E+05		(K)LQVEEVI	(K)L Q/V\E E V H/Q L/S/R(-)		114.55	446.5761	1337.717	-0.0034	-2.6	5.4	14571.2	5.15	HUMAN	F5GX50	Diablo homolog, mitochondrial (Fragment)
15652	dirMS_041712_NAR_120mM_plus.12118.12118.4	4	7.6	0	6.72E+05		(R)QATINIG	(R)Q A T I N I/G T/I/G H V A/H/G K(S)		117.05	404.9768	1616.887	-0.0013	-0.8	8.76	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
15653	dirMS_041712_NAR_120mM_plus.9747.9747.2	2	7.6	0	8.09E+05		(R)FATHAA	(R)F A|T/H/A/A A/L|S V R(N)		104.23	572.3112	1143.627	-0.0118	-10.3	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
15654	dirMS_041712_NAR_20mM_plus.17497.17497.3	3	7.6	0	6.85E+04		(K)LAAVDA	(K)L A/A V D A T V/N Q/V/L/A S R(Y)		192.37	509.9542	1527.849	-0.0009	-0.6	5.84	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
15655	dirMS_041712_NAR_20mM_plus.8027.8027.2	2	7.6	0	2.12E+05		(R)FGQGG/	(R)F G Q/G G/A|G/P V/G/G Q G/P R(G)		125.2	671.3361	1341.666	-0.0009	-0.7	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
15656	dirMS_041712_NAR_30mM_plus2.14394.14394.2	2	7.6	0	2.48E+05		(R)ELFEMA	(R)E L\F/E/M/A R(T)		128.73	448.2205	895.434	-0.0005	-0.5	4.53	33615.3	9.15	HUMAN	B7Z5E2	26S protease regulatory subunit 7
15657	dirMS_041712_NAR_30mM_plus2.16596.16596.2	2	7.6	0	1.38E+05		(R)STLNEIY	(R)S/T|L/N/E I Y F G K(T)		139.07	586.3039	1171.599	0.0012	1	5.72	29580	6.46	HUMAN	B1AK87	Capping protein (Actin filament) muscle Z-line, beta
15658	dirMS_041712_NAR_30mM_plus2.22429.22429.3	3	7.6	0	4.87E+05		(R)VGNLGL	(R)V G N\L G L A T/S/F/F/N E R(N)		172.88	508.9306	1524.781	-0.0033	-2.1	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
15659	dirMS_041712_NAR_30mM_plus2.6265.6265.2	2	7.6	0	2.49E+05		(R)MFNAEI	(R)M/F|N A E/N G/K(-)		86.58	455.7112	910.409	0.0064	7	5.75	37710.6	6.36	HUMAN	P37837	Transaldolase
15660	dirMS_041712_NAR_30mM_plus2.7943.7943.2	2	7.6	0	2.20E+05		(K)IAVAAQ	(K)I A|V/A|A Q N C Y/K(V)	C:Carbamidomethylation	96.05	569.2905	1137.572	0.0016	1.4	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
15661	dirMS_041712_NAR_40mM_plus2.12575.12575.3	3	7.6	0	3.76E+05		(K)AASDIAI	(K)A A\S D I A M/T E/L/P/P T H/P I R(L)		140.13	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
15662	dirMS_041712_NAR_60mM_plus.11367.11367.3	3	7.6	1	1.87E+06		(K)LKGEAT\	(K)L K G E A\T\V|S F/D D/P P S A K(A)		116.45	554.615	1661.838	-0.0076	-4.6	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
15663	dirMS_041712_NAR_60mM_plus.20644.20644.3	3	7.6	1	2.80E+05		(K)ITQDIFQ	(K)I/T/Q D I/F/Q Q/L L K R(G)		168.12	501.626	1502.869	-0.0055	-3.7	8.75	72796.9	6.75	HUMAN	A6NC17	Methionine--tRNA ligase, cytoplasmic
15664	dirMS_041712_NAR_60mM_plus.6625.6625.3	3	7.6	0	3.47E+05		(R)IAMGTV	(R)I A/M G T W/N V N G G K(Q)		93.58	416.5412	1247.62	-0.0111	-8.9	8.75	58091.3	9.17	HUMAN	B4DJU8	Synaptojanin-2
15665	dirMS_041712_NAR_120mM_minus.6710.6710.2	2	7.59	1	4.24E+06		(K)IREEYPD	(K)I R/E E/Y\P D|R(I)		90.72	539.2683	1077.532	-0.003	-2.8	4.68	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
15666	dirMS_041712_NAR_20mM_minus.13056.13056.2	2	7.59	0	1.87E+05		(K)LLCGLLA	(K)L L/C G/L L A E R(L)	C:Carbamidomethylation	181.23	522.7982	1044.587	0.0021	2	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
15667	dirMS_041712_NAR_20mM_minus.13544.13544.2	2	7.59	0	1.05E+05		(K)FIIPNVV	(K)F I/I/P N V V K(Y)		186.27	465.294	929.582	-0.0011	-1.2	8.75	17529.3	9.3	HUMAN	F5GXY2	L-lactate dehydrogenase A chain (Fragment)
15668	dirMS_041712_NAR_20mM_minus.9268.9268.2	2	7.59	0	2.52E+04		(K)IDATSAS	(K)I D\A/T/S/A/S/V/L/A S R(F)		142.23	595.8208	1190.638	-0.0032	-2.7	5.84	73273.4	4.96	HUMAN	P13667	Protein disulfide-isomerase A4
15669	dirMS_041712_NAR_30mM_minus2.19143.19143.3	3	7.59	0	1.74E+05		(K)SYELPD(	(K)S Y E\L/P D G Q\V/I/T/I/G/N E R(F)		158.92	597.6343	1790.892	-0.0036	-2	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
15670	dirMS_041712_NAR_40mM_minus2.14558.14558.3	3	7.59	1	1.12E+05		(R)LKLPSIPI	(R)L K\L P S I P L\V/P V/S A Q K(R)		169.62	530.6703	1589.999	-0.0025	-1.6	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
15671	dirMS_041712_NAR_40mM_minus2.7385.7385.3	3	7.59	0	1.00E+05		(K)ASQEPSI	(K)A S Q/E/P/S P K P G T E V I\P A A P R(K)		119.13	644.6737	1932.018	-0.012	-6.2	6.19	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
15672	dirMS_041712_NAR_50mM_minus2.12230.12230.3	3	7.59	1	1.52E+05	M331m	(R)YGSDIVF	(R)Y/G/S/D\I/V/P F S K V D E E Q m K(Y)	m:Oxidized methionine	137.82	663.3194	1971.937	16.0068	6	4.32	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
15673	dirMS_041712_NAR_50mM_minus2.18037.18037.3	3	7.59	1	6.74E+05		(R)VLEALLP	(R)V L|E A L L/P L K/G L E E R(V)		172.47	527.3171	1579.942	-0.005	-3.2	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
15674	dirMS_041712_NAR_50mM_minus2.18335.18335.3	3	7.59	1	7.44E+05		(R)KAIIIFVP	(R)K A I I I\F|V/P V P/Q L K(S)		174.03	489.3206	1465.95	-0.0032	-2.2	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
15675	dirMS_041712_NAR_20mM_plus.10691.10691.2	2	7.59	0	6.90E+04	M61m	(K)NQVAm	(K)N Q|V/A m N|P T/N T V/F D A K(R)	m:Oxidized methionine	146.22	833.3977	1649.795	15.9929	-1.2	5.84	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
15676	dirMS_041712_NAR_20mM_plus.12234.12281.2	2	7.59	0	9.16E+04	M78m	(K)TLVLLm(	(K)T L|V|L/L m/G K(E)	m:Oxidized methionine	157.5	445.7707	874.543	15.9911	-4.3	8.41	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
15677	dirMS_041712_NAR_30mM_plus2.15524.15524.2	2	7.59	0	5.99E+05		(R)QPTPPFI	(R)Q P/T/P/P F/F G R(D)		133.63	523.7794	1046.542	0.0097	9.3	9.75	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
15678	dirMS_041712_NAR_30mM_plus2.20055.20055.2	2	7.59	0	2.43E+05		(K)LYNLFLK	(K)L/Y|N/L F L K(I)		159.32	455.7738	910.54	0.0007	0.7	8.59	41666	7.73	HUMAN	E9PDQ8	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial
15679	dirMS_041712_NAR_40mM_plus2.5051.5051.2	2	7.59	0	1.96E+05	M154m M:	(R)mGYmD	(R)m/G Y\m D/P/R(E)	m:Oxidized methionine	84.68	451.1811	869.364	31.9905	0.7	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
15680	dirMS_041712_NAR_40mM_plus2.7694.7694.2	2	7.59	0	1.48E+05		(R)SGYFDEI	(R)S/G/Y/F D/E R(Y)		104.58	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
15681	dirMS_041712_NAR_50mM_plus2.20975.20975.3	3	7.59	0	5.51E+04		(R)LHFFMP	(R)L H F\F\M\P G\F|A|P\L T S R(G)		179.42	540.9498	1620.835	-0.0007	-0.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
15682	dirMS_041712_NAR_50mM_plus2.9339.9339.3	3	7.59	0	3.30E+05		(K)VEIMPPI	(K)V E|I\M|P\P/P P K/P K(D)		115.4	411.5726	1232.707	-0.0039	-3.2	8.56	53885.5	9	HUMAN	P11182	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial
15683	dirMS_041712_NAR_60mM_plus.16084.16084.3	3	7.59	1	5.34E+05		(R)VTNRDII	(R)V T/N R D I\I/C/Q I|A Y A R(I)	C:Carbamidomethylation	140.93	564.9631	1692.885	-0.0103	-6.1	8.71	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
15684	dirMS_041712_NAR_60mM_plus.7045.7045.2	2	7.59	1	4.51E+05		(K)IVSGKDY	(K)I V/S G K/D Y/N V/T A/N S/K(L)		95.18	748.3906	1495.775	-0.0012	-0.8	8.5	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
15685	dirMS_041712_NAR_20mM_minus.14516.14516.2	2	7.58	1	7.32E+04		(K)EILKIDG!	(K)E I\L K\I|D G S N/T/V D H K(N)		199.67	784.9262	1568.828	0.0173	11	5.38	131273.2	8.93	HUMAN	H7C5E4	5'-3' exoribonuclease 1 (Fragment)
15686	dirMS_041712_NAR_20mM_minus.14709.14709.3	3	7.58	0	3.68E+05		(K)LAVEALS	(K)L A\V E A\L S S L/D/G D/L A G R(Y)		201.3	529.6163	1586.838	-0.0041	-2.6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
15687	dirMS_041712_NAR_30mM_minus2.18599.18599.2	2	7.58	0	3.72E+05		(R)QAQEYE	(R)Q A|Q E/Y/E/A L L N I K(V)		154.87	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
15688	dirMS_041712_NAR_40mM_minus2.9456.9456.3	3	7.58	0	4.45E+04	M111m	(K)VADPTP	(K)V/A|D|P T/P F H I Q A E V T m K(T)	m:Oxidized methionine	138.23	600.6393	1783.905	15.9986	2.1	5.32	24897.7	9.84	HUMAN	A8MTM1	Carbonyl reductase [NADPH] 1
15689	dirMS_041712_NAR_50mM_minus2.15236.15236.3	3	7.58	1	3.58E+05	S435s	(K)AGDTLs(	(K)A G D T L s G/T/C L L I/A N K R(Q)	C:Carbamidomethylation s:N-ace	155	631.6612	1689.895	203.0738	-2.9	8.79	66423	6.25	HUMAN	Q86X55	Histone-arginine methyltransferase CARM1
15690	dirMS_041712_NAR_50mM_minus2.15472.15472.3	3	7.58	0	1.49E+05		(K)ICDQWD	(K)I/C|D Q W D/A L/G S L T H S R(R)	C:Carbamidomethylation	156.35	586.9489	1758.823	0.0094	5.3	5.21	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
15691	dirMS_041712_NAR_60mM_minus.16454.16454.3	3	7.58	1	1.39E+05		(K)KLSTIAL/	(K)K L S T I\A\L|A L/G V E/R(T)		151.68	457.6153	1370.837	-0.0052	-3.8	8.75	52669.1	4.73	HUMAN	A8MY67	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform

15692	dirMS_041712_NAR_60mM_minus.6043.6043.3	3	7.58	1	2.64E+06		(K)DSYVGD	(K)D S/Y/V/G D E A Q S K R(G)		90.58	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
15693	dirMS_041712_NAR_60mM_minus.6665.6665.3	3	7.58	1	2.14E+05		(K)IDDIRKP	(K)I/D/D/I R K P G E S E/E(-)		96.35	463.2294	1387.67	0.0037	2.7	4.37	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
15694	dirMS_041712_NAR_120mM_plus.8617.8617.2	2	7.58	0	7.31E+05		(K)HFVALS	(K)H|F|V|A L S T N T T K(V)		98.95	609.8311	1218.648	0.0072	5.9	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
15695	dirMS_041712_NAR_20mM_plus.12998.12998.2	2	7.58	0	2.94E+05	M316m	(R)ISEQFTA	(R)I/S|E/Q/F T A\m/F R(R)	m:Oxidized methionine	161.62	623.3012	1229.598	15.9968	1.5	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
15696	dirMS_041712_NAR_20mM_plus.18842.18842.3	3	7.58	0	1.25E+05		(K)IYVDDGI	(K)I Y V D D G\L/I/S L Q/V K(Q)		200.67	488.2764	1462.815	-0.0005	-0.4	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
15697	dirMS_041712_NAR_20mM_plus.9645.9645.2	2	7.58	0	6.10E+04		(K)ITLVSAA	(K)I T/L V/S A A/P G K(V)		137.97	478.793	956.577	0.0012	1.3	8.75	12480.3	9.05	HUMAN	F5H2L4	Acyl-coenzyme A thioesterase 13
15698	dirMS_041712_NAR_30mM_plus2.17987.17987.2	2	7.58	0	2.68E+05		(K)FEDENFI	(K)F/E|D E N\F\I L K(H)		147.02	577.7904	1154.573	0.0007	0.6	4.14	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
15699	dirMS_041712_NAR_30mM_plus2.8423.8423.2	2	7.58	0	7.55E+04		(K)QGGGG	(K)Q/G\G G/G/G G/G/S V|P G I E R(M)		98.27	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
15700	dirMS_041712_NAR_50mM_plus2.10920.10920.3	3	7.58	1	7.66E+05		(R)DISTNK	(R)D I|S T|N K V E Q\I/P Y G E R(I)		124.17	583.6304	1748.881	-0.0047	-2.7	4.68	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
15701	dirMS_041712_NAR_50mM_plus2.10983.10983.3	3	7.58	1	2.48E+05		(K)YGQISE	(K)Y/G Q I/S E V V/V/V K D R(E)		125.47	497.9426	1491.817	-0.0033	-2.2	6.07	28815.3	9.52	HUMAN	B4E2X2	Cold-inducible RNA-binding protein
15702	dirMS_041712_NAR_50mM_plus2.19701.19701.3	3	7.58	1	1.38E+05		(R)VAAKLE	(R)V A A K L E V|A|P I/S/D I I A I K(S)		171.43	584.3568	1751.068	-0.0119	-6.8	6.04	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
15703	dirMS_041712_NAR_50mM_plus2.21111.21111.3	3	7.58	0	3.42E+06		(R)AGKPVI	(R)A G K\P V/I C A|T Q/M/L E/S M/I K(K)	C:Carbamidomethylation	180.2	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
15704	dirMS_041712_NAR_50mM_plus2.8945.8945.3	3	7.58	0	1.22E+06		(R)LESGMC	(R)L/E|S G M Q/N M/S/I H T K(T)		113.45	492.5704	1475.698	-0.0015	-1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
15705	dirMS_041712_NAR_60mM_plus.10257.10257.3	3	7.58	1	5.26E+05		(R)LQEKED	(R)L Q|E/K E D L/Q/E/L/N D R(L)		111.75	543.9389	1629.808	-0.0057	-3.5	4.18	74423.5	6.57	HUMAN	P02545	Prelamin-A/C
15706	dirMS_041712_NAR_60mM_plus.15153.15153.3	3	7.58	1	2.70E+05		(K)KAEAAA	(K)K A E A A A S A|L|A/D A/D A D L E E/R(L)		135.37	639.6435	1916.92	-0.0036	-1.9	4.02	25103.6	5.88	HUMAN	O43633	Charged multivesicular body protein 2a
15707	dirMS_041712_NAR_30mM_minus2.5975.5975.2	2	7.57	0	1.11E+05		(K)SSSPLSS	(K)S S S/P L/S S T R(S)		86.53	461.2392	921.464	0.0075	8.2	9.47	55757.3	5.55	HUMAN	O94919	Endonuclease domain-containing 1 protein
15708	dirMS_041712_NAR_40mM_minus2.11639.11639.3	3	7.57	1	4.75E+04		(R)QVFGEA	(R)Q V/F G E A T K Q/P G I/T F/I A A K(F)		152.53	636.0167	1906.043	-0.0077	-4.1	8.59	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
15709	dirMS_041712_NAR_40mM_minus2.8249.8249.3	3	7.57	0	5.10E+02		(K)SLYVAEY	(K)S L/Y/V/A E Y H S E P V E D E K P(-)		130.12	664.6437	1991.923	-0.0067	-3.4	4.25	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
15710	dirMS_041712_NAR_50mM_minus2.10081.10081.3	3	7.57	0	1.78E+05	M392m	(K)EmNPAL	(K)E m/N/P A L|G I|D C L H K(G)	C:Carbamidomethylation m:Oxid	125.77	505.2416	1497.719	15.9914	-2.3	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
15711	dirMS_041712_NAR_50mM_minus2.10520.10520.3	3	7.57	0	1.72E+05		(K)VFEGNR	(K)V F/E/G N R P T N S I V F/T K(L)		128.63	570.3032	1708.902	-0.0066	-3.9	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
15712	dirMS_041712_NAR_50mM_minus2.15975.15975.3	3	7.57	0	3.39E+05		(K)LYGPTNI	(K)L Y G\P T N|F/S/P\I I N H V A R(F)		158.27	600.3221	1798.96	-0.0081	-4.5	8.75	60985.3	5.6	HUMAN	O75131	Copine-3
15713	dirMS_041712_NAR_50mM_minus2.7116.7116.3	3	7.57	1	2.74E+04		(R)LAEEKA	(R)L/A/E E K A Q A S S/I/P V G S R(C)		107.42	548.29	1642.876	-0.0204	-12.4	6.14	23811.2	6.78	HUMAN	A8MVD5	Tubulin-folding cofactor B
15714	dirMS_041712_NAR_50mM_minus2.8658.8658.3	3	7.57	1	2.43E+05		(R)AGTGVD	(R)A/G T|G V/D N V D L E/A A T R K(G)		116.55	539.6119	1616.824	-0.0027	-1.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
15715	dirMS_041712_NAR_60mM_minus.14564.14564.3	3	7.57	0	3.50E+05		(K)LPNLTHI	(K)L/P/N L/T/H L N/L S G N K(L)		140.87	474.2636	1420.791	-0.0144	-10.2	8.76	18070.1	3.52	HUMAN	Q5T6W8	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member B (Fragment)
15716	dirMS_041712_NAR_60mM_minus.15229.15229.3	3	7.57	1	3.39E+05		(K)AKLEQLI	(K)A K\L E Q L|F/Q D E/V A K(A)		144.37	506.9421	1518.816	-0.0045	-3	4.68	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
15717	dirMS_041712_NAR_60mM_minus.5880.5880.3	3	7.57	0	3.55E+05	N81n M89	(K)FnDPVV	(K)F/n D/P/V V Q A D m K(L)	n:N-acetylglucosamine (N) m	88.95	494.9008	1263.604	219.084	6.6	4.21	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
15718	dirMS_041712_NAR_60mM_minus.8430.8430.3	3	7.57	1	5.51E+04		(R)FEEEIKA	(R)F E|E E\I K A E/Q E E R(K)		107.07	512.9085	1536.718	-0.0067	-4.4	4.2	26810.9	5.15	HUMAN	Q96C19	EF-hand domain-containing protein D2
15719	dirMS_041712_NAR_120mM_plus.6154.6154.3	3	7.57	0	7.08E+05		(K)QRPQAT	(K)Q R P Q A/T/A/E Q I R(L)		85.93	433.2367	1297.697	-0.0016	-1.2	9.6	113668.7	6.2	HUMAN	F8W726	Ubiquitin-associated protein 2-like
15720	dirMS_041712_NAR_120mM_plus.8133.8133.3	3	7.57	0	2.72E+05		(K)HEQNID	(K)H E Q N\I\D/C/G G G Y V K(L)	C:Carbamidomethylation	96.22	492.8886	1476.654	-0.0024	-1.6	5.32	48311.8	4.29	HUMAN	P27797	Calreticulin
15721	dirMS_041712_NAR_120mM_plus.8652.8652.3	3	7.57	0	2.25E+06		(K)HTGPNS	(K)H T G\P N\S P/D/T/A|N/D G F V/R(L)		99.03	562.26	1684.767	-0.0019	-1.2	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
15722	dirMS_041712_NAR_20mM_plus.11998.11998.2	2	7.57	0	4.00E+04		(R)ETPIGLV	(R)E T/P I G L V/P K(E)		155.55	477.2872	953.567	0.0005	0.5	6.1	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
15723	dirMS_041712_NAR_20mM_plus.12013.12013.2	2	7.57	0	4.22E+04	M65m	(R)VLVFVm	(R)V/L|V|F V m G/K(E)	m:Oxidized methionine	155.75	454.7679	892.533	15.9961	1.3	8.72	9912.2	9.69	HUMAN	C9J712	Profilin-2
15724	dirMS_041712_NAR_20mM_plus.14694.14694.2	2	7.57	0	1.02E+05		(R)FIDTTLA	(R)F I D/T/T|L/A/I T S R(F)		172.52	619.3413	1237.679	-0.0034	-2.7	5.84	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
15725	dirMS_041712_NAR_20mM_plus.18601.18601.2	2	7.57	0	5.88E+04	S3142s	(R)TVLVSs	(R)T/V\L V/S s/G L R(E)	s:N-acetylglucosamine (S)	199.5	567.8286	931.557	203.0928	11.8	9.41	523482.6	5.17	HUMAN	Q07954	Prolow-density lipoprotein receptor-related protein 1
15726	dirMS_041712_NAR_20mM_plus.6832.6832.2	2	7.57	0	4.52E+05	M132m	(R)DmVGIA	(R)D m|V/G I/A/Q T G S G K(T)	m:Oxidized methionine	112.75	590.2864	1163.573	15.993	-1.6	5.84	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
15727	dirMS_041712_NAR_30mM_plus2.17183.17305.2	2	7.57	0	5.42E+05		(R)GLVGIE	(R)G L|V/G/I E/F K(E)		143.98	431.7495	862.503	-0.0116	-13.4	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
15728	dirMS_041712_NAR_30mM_plus2.6791.6791.2	2	7.57	0	9.23E+04		(R)GAEQLA	(R)G A\E\Q/L\A|E/G G R(M)		90.18	494.2448	987.485	-0.0031	-3.1	4.53	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b
15729	dirMS_041712_NAR_30mM_plus2.7274.7309.2	2	7.57	0	3.05E+05		(K)GSAITG	(K)G S|A|I|T/G P V A K(E)		92.77	450.7605	900.515	-0.0012	-1.3	8.75	8956.4	10.28	HUMAN	J3KTJ3	60S ribosomal protein L23
15730	dirMS_041712_NAR_40mM_plus2.12961.12961.3	3	7.57	0	3.01E+05		(K)NLPPSG	(K)N L/P P S G A V/P V T G I/P P/H V V K(V)		142.87	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
15731	dirMS_041712_NAR_60mM_plus.4789.4789.3	3	7.57	1	3.22E+05		(K)AGADEE	(K)A/G\A/D/E\E R/A E/T A/R(L)		79.42	425.868	1275.592	-0.0029	-2.3	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
15732	dirMS_041712_NAR_120mM_minus.12526.12526.3	3	7.56	1	3.39E+05	M316m	(R)ISEQFTA	(R)I/S E/Q/F\T A m F R/R(K)	m:Oxidized methionine	122.32	467.9028	1385.699	15.9944	-0.4	9.6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
15733	dirMS_041712_NAR_120mM_minus.18426.18426.3	3	7.56	0	1.60E+05		(R)FHQLDI	(R)F H\Q L D\I/D D|L/Q/S I R(A)		155.33	533.9425	1599.813	0.0004	0.3	4.41	24897.7	9.84	HUMAN	A8MTM1	Carbonyl reductase [NADPH] 1
15734	dirMS_041712_NAR_20mM_minus.9180.9180.2	2	7.56	0	5.67E+03		(R)VLQSFT	(R)V L|Q|S/F/T V D S S K(A)		141.55	605.8196	1210.631	0.0005	0.4	5.81	258215.9	5.48	HUMAN	E7EN95	Filamin-B
15735	dirMS_041712_NAR_30mM_minus2.10111.10165.2	2	7.56	0	1.66E+05		(R)GYAVLG	(R)G Y|A|V|L/G G E/R(G)		109.23	461.2392	921.479	-0.0077	-8.4	6	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
15736	dirMS_041712_NAR_30mM_minus2.10287.10287.2	2	7.56	0	1.33E+06		(R)LSIYEAR	(R)L S|I/Y E/A R(C)		110.6	426.2334	851.462	-0.0026	-3.1	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
15737	dirMS_041712_NAR_40mM_minus2.6152.6152.2	2	7.56	0	1.51E+05		(K)AQYEDI	(K)A Q|Y/E/D/I A N R(S)		101.52	540.2599	1079.512	0.0009	0.8	4.37	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
15738	dirMS_041712_NAR_60mM_minus.11131.11131.3	3	7.56	0	2.48E+05		(R)ALPESL	(R)A L/P E|S L G/Q H A L R(S)		121.55	431.2376	1291.712	-0.0135	-10.4	6.79	31463.6	5.53	HUMAN	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1
15739	dirMS_041712_NAR_60mM_minus.11504.11504.3	3	7.56	1	1.64E+05		(K)NVDILK	(K)N V/D/I/L K/D/P E T V K(Q)		124.33	457.5867	1370.753	-0.007	-5.1	4.56	124524.8	5.71	HUMAN	O14980	Exportin-1
15740	dirMS_041712_NAR_60mM_minus.16898.16898.3	3	7.56	1	2.51E+05		(K)YAVLYQ	(K)Y/A/V/L/Y Q/P L F D/K R(F)		154.53	504.9409	1512.821	-0.0128	-8.4	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
15741	dirMS_041712_NAR_60mM_minus.9804.9804.3	3	7.56	1	2.10E+05		(K)LQTRAA	(K)L Q T\R A A/N/L/E S K(F)		114.72	410.9037	1230.68	0.0165	13.4	8.75	52940.3	4.39	HUMAN	Q9ULW6	Nucleosome assembly protein 1-like 2
15742	dirMS_041712_NAR_120mM_plus.13286.13310.3	3	7.56	0	1.25E+05		(R)VLSAPP	(R)V L|S/A|P P H F H F G Q T N R(T)		122.77	569.9613	1707.871	-0.0021	-1.2	9.74	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
15743	dirMS_041712_NAR_120mM_plus.14973.14973.4	4	7.56	1	2.36E+06		(K)LDKSQI	(K)L D K S Q I H D I\V\L\V/G/G S/T R(I)		131.17	460.2603	1838.013	0.0063	3.4	6.75	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
15744	dirMS_041712_NAR_20mM_plus.13185.13185.2	2	7.56	0	2.89E+05		(K)LSELEAA	(K)L S/E/L/E A/A/L/Q/R(A)		162.33	565.3132	1129.621	-0.002	-1.8	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
15745	dirMS_041712_NAR_20mM_plus.14751.14751.2	2	7.56	0	1.09E+05	M72m	(R)TEmENE	(R)T E\m/E/N/E F|V/L I/K(K)	m:Oxidized methionine	172.97	684.8399	1352.677	15.9959	0.7	4.25	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
15746	dirMS_041712_NAR_20mM_plus.16341.16341.3	3	7.56	0	1.32E+05		(R)LLDAQL	(R)L L\D\A Q L|A\T G G I V D/P/R(L)		183.53	513.6218	1538.854	-0.0028	-1.8	4.21	533778	5.74	HUMAN	Q15149	Plectin
15747	dirMS_041712_NAR_20mM_plus.16868.16868.2	2	7.56	0	2.07E+05		(R)IVLLDSS	(R)I V|L L/D/S S L\E Y K(K)		187.33	640.36	1279.714	-0.0017	-1.3	4.37	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
15748	dirMS_041712_NAR_20mM_plus.8789.8789.3	3	7.56	0	1.41E+05	M224m	(K)GGKPEP	(K)G G K P E\P P\A\m\P Q|P V|P/T A(-)	m:Oxidized methionine	130.62	530.6038	1573.804	15.9926	-1.5	6	25541.5	9.92	HUMAN	E9PL09	40S ribosomal protein S3
15749	dirMS_041712_NAR_30mM_plus2.14370.14370.2	2	7.56	0	5.30E+05	M257m	(R)LmDLLG	(R)L m|D|L\L G E G L K(R)	m:Oxidized methionine	128.22	552.8032	1088.602	15.9971	2	4.37	52817.9	6.2	HUMAN	F5H3T8	Arginine--tRNA ligase, cytoplasmic
15750	dirMS_041712_NAR_30mM_plus2.17880.17880.2	2	7.56	0	5.11E+04		(R)MQFGV	(R)M Q|F/G|V/P L A R(N)		146.85	509.7774	1018.55	-0.0027	-2.7	9.5	43069.5	9.24	HUMAN	B4DK85	Glutaryl-CoA dehydrogenase, mitochondrial
15751	dirMS_041712_NAR_40mM_plus2.7215.7215.2	2	7.56	0	3.40E+04		(K)CNLLAE	(K)C N|L|L/A/E/K(Q)	C:Carbamidomethylation	102.42	424.216	847.434	-0.0095	-11.2	6	40209.9	5.43	HUMAN	C9JV77	Alpha-2-HS-glycoprotein
15752	dirMS_041712_NAR_50mM_plus2.10598.10598.3	3	7.56	1	2.32E+06		(R)MQKEIT	(R)M Q K E I T\A L/A|P S T M K(I)		123.97	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
15753	dirMS_041712_NAR_50mM_plus2.10730.10730.3	3	7.56	1	5.02E+05		(R)VAVEEV	(R)V/A|V/E E/V D E/E G K F V R(L)		124.33	535.9422	1605.812	0.0002	0.1	4.25	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
15754	dirMS_041712_NAR_50mM_plus2.15147.15147.3	3	7.56	1	4.10E+05		(R)LSQELEY	(R)L S/Q/E L E Y L/T/E D V K/R(L)		147.4	574.9669	1722.891	-0.0047	-2.7	4.41	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
15755	dirMS_041712_NAR_50mM_plus2.9309.9309.3	3	7.56	0	1.33E+05		(K)AEITLVA	(K)A/E I T L/V/A T K/P E K(L)		116.23	433.922	1299.752	-0.0004	-0.3	6.18	98761.7	5.56	HUMAN	Q9UBF2	Coatomer subunit gamma-2
15756	dirMS_041712_NAR_120mM_minus.10714.10714.3	3	7.55	1	7.24E+04		(K)LRETAE	(K)L R E T A E\A\D\V|A/S/L N R(R)		111.52	515.6051	1544.803	-0.002	-1.3	4.68	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
15757	dirMS_041712_NAR_20mM_minus.11104.11104.2	2	7.55	0	8.39E+04		(K)VIDPAT	(K)V/I/D/P A/T A\T S V D L R(D)		158.43	679.3706	1357.732	0.0018	1.3	4.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
15758	dirMS_041712_NAR_30mM_minus2.16510.16510.3	3	7.55	0	7.07E+05		(R)ASLEAAI	(R)A S L E/A A I/A/D/A E/Q R(G)		143.67	448.8965	1344.675	-0.0004	-0.3	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
15759	dirMS_041712_NAR_40mM_minus2.7388.7388.3	3	7.55	0	1.00E+05		(K)ASQEPSI	(K)A/S Q|E/P S P K P G T E V\I/P A A P R(K)		119.13	644.6737	1932.018	-0.012	-6.2	6.19	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
15760	dirMS_041712_NAR_50mM_minus2.9246.9246.3	3	7.55	0	1.89E+05	M778m	(R)mLTGPV	(R)m L/T/G/P V/Y/S Q S T A L/T H K(Q)	m:Oxidized methionine	121.02	583.963	1733.889	15.9854	-5.5	8.37	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
15761	dirMS_041712_NAR_60mM_minus.15436.15436.3	3	7.55	1	4.51E+05		(K)YQLDKD	(K)Y/Q|L D K D G V/V L F K(K)		146.28	475.5992	1424.778	0.0047	3.3	5.96	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
15762	dirMS_041712_NAR_60mM_minus.17815.17815.3	3	7.55	1	3.60E+05		(K)NLRDID	(K)N L R\D I D E\V/S/S/L L R(T)		160.9	510.6099	1529.828	-0.013	-8.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
15763	dirMS_041712_NAR_60mM_minus.17830.17830.3	3	7.55	1	3.65E+05		(K)NLRDID	(K)N L R D I D\E\V/S/S L L R(T)		160.92	510.6099	1529.828	-0.013	-8.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
15764	dirMS_041712_NAR_120mM_plus.12258.12258.3	3	7.55	0	9.91E+04		(R)HVFLTG	(R)H V\F L\T/G\P/P G V/G K(T)		116.27	403.562	1208.679	-0.0072	-5.9	8.76	25356.9	9.94	HUMAN	Q5TDF0	Cancer-related nucleoside-triphosphatase
15765	dirMS_041712_NAR_120mM_plus.14437.14437.2	2	7.55	0	6.00E+05		(R)HFDQFV	(R)H/F|D/Q F W S A A/K(T)		128.8	618.7928	1236.58	-0.0013	-1.1	6.74	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
15766	dirMS_041712_NAR_120mM_plus.17195.17195.4	4	7.55	0	6.14E+05	T76t	(R)VPtPSV	(R)V P t P/S V Q S D S D I T V L/R(H)	t:N-acetylglucosamine (T)	142.42	479.9954	1713.902	203.058	-11.1	4.21	43548	6.22	HUMAN	Q8IXN7	N-acetylaspartyl-glutamate synthetase A
15767	dirMS_041712_NAR_120mM_plus.17426.17464.3	3	7.55	1	4.15E+05		(R)RTVQSLI	(R)R T V Q S\L\E|I/D|L/D S M R(N)		144.22	554.9524	1662.848	-0.0053	-3.2	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
15768	dirMS_041712_NAR_20mM_plus.18764.18764.2	2	7.55	0	7.30E+04		(R)AYSDQA	(R)A Y\S D Q/A I V/N L/L K(M)		200.58	667.8685	1334.731	-0.0017	-1.3	5.88	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
15769	dirMS_041712_NAR_20mM_plus.6448.6448.2	2	7.55	0	2.02E+05	M216m	(R)DLmAC	(R)D L\m|A/C/A/Q T G/S G K(T)	C:Carbamidomethylation m:Oxid	107.72	627.776	1238.55	15.9943	-0.5	5.84	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
15770	dirMS_041712_NAR_20mM_plus.6793.6793.2	2	7.55	0	4.19E+05	M132m	(R)DmVGIA	(R)D m|V|G\I/A Q T G/S G K(T)	m:Oxidized methionine	112.65	590.2864	1163.573	15.993	-1.6	5.84	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
15771	dirMS_041712_NAR_30mM_plus2.8519.8519.2	2	7.55	0	3.58E+05		(R)AVVGV	(R)A V/V/G\V/V|A\G\G G R(I)		99.07	471.2779	941.553	-0.0042	-4.4	9.79	24115.6	11.59	HUMAN	E9PIZ3	60S ribosomal protein L8
15772	dirMS_041712_NAR_30mM_plus2.9709.9709.2	2	7.55	0	7.62E+05		(K)EAESSP	(K)E\A/E S/S/P F/V E R(L)		105.13	575.7726	1150.537	0.0004	0.4	4.25	92752.5	4.76	HUMAN	P14625	Endoplasmin
15773	dirMS_041712_NAR_50mM_plus2.10407.10407.2	2	7.55	1	1.50E+06		(R)DGKLVS	(R)D/G K\L\V|S\E S S D V\L|P K(-)		122.83	737.3925	1473.78	-0.0018	-1.2	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
15774	dirMS_041712_NAR_50mM_plus2.12014.12014.3	3	7.55	1	4.97E+05		(R)DNKQA	(R)D N K Q A\G\V|F E/P T I V K(V)		131.35	515.9483	1545.827	0.0032	2.1	6.07	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
15775	dirMS_041712_NAR_50mM_plus2.12700.12700.3	3	7.55	1	3.83E+05		(K)LPGGEL	(K)L/P/G G E L N/P G E/D/E/V E/G L K R(L)		134.28	636.9936	1908.966	0.0001	0.1	4.25	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
15776	dirMS_041712_NAR_50mM_plus2.8317.8317.3	3	7.55	1	1.41E+05	M258m	(K)TTDMA	(K)T/T|D/M/A/P S K E T E m A L/A/K(D)	m:Oxidized methionine	110.3	580.6104	1723.824	15.9925	-1.4	4.68	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
15777	dirMS_041712_NAR_50mM_plus2.9330.9330.3	3	7.55	0	1.33E+05		(K)AEITLVA	(K)A/E/I T L/V A/T K/P E K(L)		116.23	433.922	1299.752	-0.0004	-0.3	6.18	98761.7	5.56	HUMAN	Q9UBF2	Coatomer subunit gamma-2
15778	dirMS_041712_NAR_60mM_plus.9399.9399.3	3	7.55	0	6.10E+05		(K)SVIHSG	(K)S V/I/H S G P|F/T\E/S Q K(S)		107.38	472.9094	1416.712	0.0019	1.3	6.47	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
15779	dirMS_041712_NAR_20mM_minus.7695.7695.2	2	7.54	0	4.88E+05	M239m	(K)EVDEQ	(K)E V/D/E\Q/m L/N V/Q N/K(N)	m:Oxidized methionine	125.43	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
15780	dirMS_041712_NAR_30mM_minus2.13740.13740.2	2	7.54	0	5.77E+05		(K)TCTFILR	(K)T/C|T/F I/L R(G)	C:Carbamidomethylation	127.92	455.7458	910.481	0.0028	3.1	9.41	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
15781	dirMS_041712_NAR_30mM_minus2.15496.15496.2	2	7.54	2	3.27E+05		(K)TKAEGD	(K)T K/A/E\G D/R L K(E)		137.28	509.2945	1017.569	0.013	12.8	8.26	141476.1	5.99	HUMAN	O95239	Chromosome-associated kinesin KIF4A
15782	dirMS_041712_NAR_40mM_minus2.10996.10996.3	3	7.54	0	8.21E+04		(K)SPAPPL	(K)S P\A/P/P L L H\V A A L G Q K(Q)		148.12	500.2927	1498.874	-0.0105	-7	8.49	17549.1	10.39	HUMAN	E5RFJ3	DBIRD complex subunit KIAA1967 (Fragment)
15783	dirMS_041712_NAR_40mM_minus2.11739.11739.3	3	7.54	1	6.56E+04		(R)GDVVPK	(R)G D V/V/P K D V N A A/I A T I K(T)		152.95	537.6382	1610.911	-0.0112	-6.9	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
15784	dirMS_041712_NAR_40mM_minus2.12053.12053.3	3	7.54	1	1.22E+05		(K)LDVSNV	(K)L/D|V\S/N/V A T D T E R L E/L K(A)		153.9	601.6499	1802.949	-0.0143	-7.9	4.32	288852.1	5.33	HUMAN	E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein
15785	dirMS_041712_NAR_40mM_minus2.13549.13549.3	3	7.54	0	1.40E+05		(K)VAIVKP	(K)V/A I V K P G V/P M/E I V/L N/K(E)		163.27	569.6777	1707.024	-0.0052	-3	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
15786	dirMS_041712_NAR_40mM_minus2.9436.9436.3	3	7.54	1	2.72E+04		(K)IINADSE	(K)I I|N/A D S E D/P K Y I I N V K(Q)		138.1	611.3244	1831.98	-0.0214	-11.7	4.56	14693.3	4.69	HUMAN	C9JLS9	26S protease regulatory subunit 7 (Fragment)
15787	dirMS_041712_NAR_50mM_minus2.10454.10454.3	3	7.54	0	7.23E+04		(R)LTSPIVS	(R)L/T|S/P I V S/T H L D/T R(N)		127.37	480.6	1439.785	0.0002	0.1	6.74	58760.2	5.26	HUMAN	Q6ZTN6	Ankyrin repeat domain-containing protein 13D
15788	dirMS_041712_NAR_50mM_minus2.14466.14466.3	3	7.54	1	8.33E+04		(R)LSQELEY	(R)L/S|Q E L E Y L/T E/D V K R(L)		149.87	574.9724	1722.891	0.0118	6.8	4.41	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
15789	dirMS_041712_NAR_60mM_minus.16741.16741.3	3	7.54	0	1.02E+05		(K)ICDQW	(K)I C/D Q W D|A|L/G S L T H S R(R)	C:Carbamidomethylation	153.88	586.9446	1758.823	-0.0035	-2	5.21	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
15790	dirMS_041712_NAR_60mM_minus.7997.7997.3	3	7.54	1	3.76E+05	M230m M	(R)mSmKE	(R)m S m K E V D E|Q m|L N\V/Q/N K(N)	m:Oxidized methionine	103.85	657.9647	1923.897	47.9823	-1.3	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
15791	dirMS_041712_NAR_20mM_plus.11131.11131.2	2	7.54	0	1.49E+05		(K)YGVSGY	(K)Y G|V|S G/Y/P T L K(I)		149.72	542.7869	1084.567	-0.0008	-0.8	8.5	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
15792	dirMS_041712_NAR_20mM_plus.12135.12135.2	2	7.54	0	3.75E+04		(R)LCYYIGA	(R)L C\Y Y|I|G A T D\D A|A T K(I)	C:Carbamidomethylation	156.62	781.3622	1561.72	-0.0032	-2	4.21	21156.2	9.41	HUMAN	P55145	Mesencephalic astrocyte-derived neurotrophic factor
15793	dirMS_041712_NAR_30mM_plus2.17234.17288.2	2	7.54	0	3.48E+05		(R)LIVNVN	(R)L I|V/N\V/N D/L R(R)		143.97	528.3113	1055.621	-0.0054	-5.2	5.84	91606.8	5.53	HUMAN	P25205	DNA replication licensing factor MCM3
15794	dirMS_041712_NAR_40mM_plus2.19563.19563.3	3	7.54	0	3.40E+04		(K)GAEILEV	(K)G A E|I L/E\V/L H S L/P A V R(Q)		183.02	535.3088	1603.917	-0.0048	-3	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
15795	dirMS_041712_NAR_50mM_plus2.10819.10819.3	3	7.54	1	4.68E+05		(R)ALRETL	(R)A L R\E T\L|P\A\E Q D L T T K(N)		125.08	562.6377	1685.907	-0.0083	-4.9	4.68	26790	6.25	HUMAN	F5GX11	Proteasome subunit alpha type-1
15796	dirMS_041712_NAR_60mM_plus.18038.18038.3	3	7.54	1	4.97E+04		(R)ARFEEL	(R)A R\F E E\L N/A/D/L F R(G)		151.58	494.2554	1480.754	-0.0027	-1.8	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
15797	dirMS_041712_NAR_60mM_plus.19608.19608.3	3	7.54	0	1.33E+05		(R)NSVSNF	(R)N\S/V/S N F L/H/S L E/R(G)		161.23	468.2401	1402.707	-0.0016	-1.1	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
15798	dirMS_041712_NAR_120mM_minus.18175.18175.3	3	7.53	1	2.92E+05		(K)IESQAA	(K)I E S Q A A R|L/L S L E G R(T)		154.38	514.9655	1542.86	0.0221	14.3	6.14	19841.3	6.19	HUMAN	C9JNZ9	Zinc finger protein 746
15799	dirMS_041712_NAR_20mM_minus.10173.10173.2	2	7.53	0	1.24E+05		(R)YALYDA	(R)Y A/L/Y/D A T Y E T/K(E)		150.82	669.3156	1337.626	-0.0021	-1.5	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
15800	dirMS_041712_NAR_30mM_minus2.6859.6859.2	2	7.53	0	1.55E+05	M697m	(K)EGALCEI	(K)E G A/L|C/E E N m R(G)	C:Carbamidomethylation m:Oxid	91.9	612.7538	1208.503	15.9969	1.6	4.25	96306.4	6.41	HUMAN	P13639	Elongation factor 2

15801	dirMS_041712_NAR_30mM_minus2.8229.8229.2	2	7.53	0	3.89E+05		(K)SFQQSSI	(K)S/F/Q/Q|S S/L S R(D)		99.82	520.2591	1039.517	-0.0058	-5.6	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
15802	dirMS_041712_NAR_60mM_minus.15500.15500.3	3	7.53	1	2.23E+05		(R)GPIKFN\	(R)G P I K F\N V|W/D/T A G Q E K(F)		146.48	563.9575	1689.86	-0.0015	-0.9	6.07	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
15803	dirMS_041712_NAR_60mM_minus.15950.15950.3	3	7.53	1	3.04E+04		(K)LPFPIIDI	(K)L/P F/P I I/D/D R N R(E)		149.15	452.5849	1355.743	-0.0029	-2.1	5.96	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
15804	dirMS_041712_NAR_20mM_plus.16949.16949.3	3	7.53	0	3.00E+05		(K)VQIAVA	(K)V Q|I A\V\A N\A Q/E/L L Q/R(M)		187.88	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
15805	dirMS_041712_NAR_20mM_plus.18274.18274.2	2	7.53	0	1.04E+05		(K)LVLPSLIS	(K)L V|L/P S/L I S S R(I)		196.7	542.8388	1084.672	-0.0021	-2	9.75	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
15806	dirMS_041712_NAR_30mM_plus2.11393.11393.3	3	7.53	0	4.09E+05	M298m	(R)MGQmA	(R)M G Q/m A\M G G/A\M/G/I/N N R(G)	m:Oxidized methionine	113.05	518.8921	1538.67	15.9923	-1.7	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
15807	dirMS_041712_NAR_30mM_plus2.12041.12146.2	2	7.53	0	2.91E+05		(K)ENPLQFI	(K)E N|P/L Q/F K(F)		116.12	438.2344	875.462	-0.0006	-0.7	6.1	71218.8	6.3	HUMAN	A7YIJ8	Radixin
15808	dirMS_041712_NAR_30mM_plus2.15674.15674.2	2	7.53	0	3.60E+05		(R)QPTPPFI	(R)Q P T/P/P/F F/G R(D)		134.4	523.7794	1046.542	0.0097	9.3	9.75	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
15809	dirMS_041712_NAR_30mM_plus2.18428.18428.2	2	7.53	0	1.50E+05		(K)DVLSVAI	(K)D V/L S\V/A/F S S D N/R(Q)		149.78	655.3231	1309.638	0.0007	0.5	4.21	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
15810	dirMS_041712_NAR_30mM_plus2.22007.22007.2	2	7.53	0	1.76E+05		(R)WQFLTL	(R)W/Q|F|L/T L R(E)		170.85	482.2695	963.541	-0.0093	-9.7	9.75	132493.1	6.53	HUMAN	B4DER1	Leucine--tRNA ligase, cytoplasmic
15811	dirMS_041712_NAR_40mM_plus2.9444.9444.2	2	7.53	0	8.85E+04		(R)INVYYNI	(R)I N/V/Y/Y N E/A T/G G K(Y)		118.58	664.8248	1328.648	-0.0058	-4.4	6	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
15812	dirMS_041712_NAR_50mM_plus2.13460.13460.3	3	7.53	0	9.05E+05		(R)TVVTGIE	(R)T V|V/T/G I E/M/F H K(S)		138.55	421.225	1261.661	-0.0005	-0.4	6.41	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
15813	dirMS_041712_NAR_50mM_plus2.21202.21202.3	3	7.53	0	2.35E+06		(R)AGKPVI(	(R)A G K\P V\I C\A\T|Q/M/L E S M I K(K)	C:Carbamidomethylation	180.57	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
15814	dirMS_041712_NAR_50mM_plus2.21705.21705.3	3	7.53	1	2.08E+05		(R)KVPELM	(R)K V P/E L M|E M F L/P A T K(N)		185.52	545.2925	1633.869	-0.0063	-3.8	6.14	95051	6.63	HUMAN	B3KXW5	AP-1 complex subunit gamma-1
15815	dirMS_041712_NAR_50mM_plus2.8313.8313.3	3	7.53	0	2.33E+05		(K)VQQAEL	(K)V/Q|Q/A E L/H T G S L P R(I)		110.33	479.2607	1435.765	0.0023	1.6	6.72	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
15816	dirMS_041712_NAR_60mM_plus.11543.11543.3	3	7.53	2	2.88E+05		(K)EKFEAG(	(K)E K F E A G Q\F/E|P S E T T A K S(-)		117.53	629.2968	1885.881	-0.0056	-3	4.49	14458.2	9.22	HUMAN	Q5JTJ3	Cytochrome c oxidase assembly factor 6 homolog
15817	dirMS_041712_NAR_60mM_plus.17891.17891.3	3	7.53	1	1.04E+06		(R)ARFEELN	(R)A R F E\E\L|N\A/D L/F R(G)		150.85	494.2554	1480.754	-0.0027	-1.8	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
15818	dirMS_041712_NAR_120mM_minus.11162.11162.2	2	7.52	1	4.02E+05		(R)LASYLDF	(R)L A|S Y L D/R/V/R(S)		114.85	546.811	1092.616	-0.0013	-1.2	8.75	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
15819	dirMS_041712_NAR_120mM_minus.17248.17248.4	4	7.52	2	6.24E+05		(R)KVESLQI	(R)K\V E S L/Q/E E I A F/L K K(L)		148.93	416.2415	1661.947	-0.0031	-1.9	6.23	49709.6	5.19	HUMAN	B0YJC4	Vimentin
15820	dirMS_041712_NAR_120mM_minus.4217.4217.3	3	7.52	1	6.83E+05		(R)EPGPAG	(R)E P/G P/A G R G D/G/D/S G R(S)		70.47	443.2041	1327.599	-0.0008	-0.6	4.56	558007.1	5.44	HUMAN	P58107	Epiplakin
15821	dirMS_041712_NAR_20mM_minus.10778.10778.3	3	7.52	0	1.40E+05		(K)VNQIGS'	(K)V N Q\I G/S V T|E/S|I Q/A C K(L)	C:Carbamidomethylation	155.38	545.2807	1633.821	0.0062	3.8	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
15822	dirMS_041712_NAR_30mM_minus2.14753.14753.2	2	7.52	0	3.72E+05		(K)DLAGSII(	(K)D L|A/G/S I I G K(G)		133.25	437.2551	873.504	-0.0011	-1.2	5.84	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
15823	dirMS_041712_NAR_30mM_minus2.15591.15591.2	2	7.52	0	1.48E+05		(K)AMTGVI	(K)A M/T\G/V E Q W|P/Y/R(A)		138.33	669.3172	1337.631	-0.0036	-2.7	6.04	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
15824	dirMS_041712_NAR_40mM_minus2.10766.10766.3	3	7.52	0	1.27E+05	M56m	(K)VAIVKP(	(K)V A I/V K/P G V/P m E I V L N K(E)	m:Oxidized methionine	146.87	575.0112	1707.024	15.9953	0.2	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
15825	dirMS_041712_NAR_40mM_minus2.5870.5870.2	2	7.52	0	8.80E+05		(K)AGFAGD	(K)A G/F|A/G D D/A/P R(A)		97.85	488.7279	976.448	0.0002	0.2	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
15826	dirMS_041712_NAR_50mM_minus2.18213.18213.3	3	7.52	1	2.29E+05		(K)LKEAELL	(K)L K E A E L L|E|P L/M/P A I R(A)		172.8	574.9957	1722.982	-0.0097	-5.6	4.79	56164.6	6.01	HUMAN	E9PP73	Coatomer subunit beta (Fragment)
15827	dirMS_041712_NAR_20mM_plus.12246.12246.2	2	7.52	0	4.61E+04		(K)VALSSET	(K)V A|L|S/S E T E V A L A R(D)		157.62	673.3693	1345.732	-0.0008	-0.6	4.53	246695.2	5.91	HUMAN	E7EVA0	Microtubule-associated protein
15828	dirMS_041712_NAR_20mM_plus.9037.9037.2	2	7.52	0	5.20E+03		(R)LAAIAES	(R)L A|A|I/A/E S G V E R(Q)		132.4	558.303	1115.605	-0.0068	-6.1	4.53	25585.5	4.8	HUMAN	P28072	Proteasome subunit beta type-6
15829	dirMS_041712_NAR_30mM_plus2.19329.19329.2	2	7.52	0	2.16E+05		(K)NFSGAE	(K)N F|S/G\A|E L/E G L\V/R(A)		155.28	646.3361	1291.664	0.0008	0.6	4.53	71924.9	6.25	HUMAN	B4DFA2	Vesicle-fusing ATPase
15830	dirMS_041712_NAR_30mM_plus2.22165.22165.2	2	7.52	0	9.55E+04		(-)MLPLSLL	(-)M/L|P/L S/L L K(T)		171.75	457.7881	914.574	-0.0054	-5.9	8.5	15520.6	10.36	HUMAN	Q9Y4Z0	U6 snRNA-associated Sm-like protein LSm4
15831	dirMS_041712_NAR_30mM_plus2.22398.22398.2	2	7.52	0	3.90E+04		(R)WLLDFA	(R)W L/L/D F/A/S K(R)		173.55	490.2728	979.525	0.0136	13.9	5.84	59384	7.79	HUMAN	B7Z3Z9	Long-chain-fatty-acid--CoA ligase 1
15832	dirMS_041712_NAR_40mM_plus2.12664.12664.2	2	7.52	0	2.54E+04		(K)ICSWNV	(K)I/C|S W N|V/D/G L R(A)	C:Carbamidomethylation	140.23	610.297	1219.589	-0.0021	-1.7	5.84	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
15833	dirMS_041712_NAR_40mM_plus2.7128.7128.2	2	7.52	0	4.43E+04		(R)SSYLESP	(R)S S|Y L/E/S/P|R(G)		101.62	469.7347	938.458	0.0043	4.6	5.72	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
15834	dirMS_041712_NAR_50mM_plus2.12310.12310.3	3	7.52	1	4.91E+05		(K)ILDSVGII	(K)I/L/D/S V/G I E A D D/D R L N K(V)		132.85	591.6385	1772.902	-0.0015	-0.9	4.04	11664.7	4.42	HUMAN	P05387	60S acidic ribosomal protein P2
15835	dirMS_041712_NAR_50mM_plus2.14028.14028.3	3	7.52	0	1.16E+06	M457m	(R)mGPLGL	(R)m/G|P L/G L D H M/A S/S I E R(M)	m:Oxidized methionine	142.8	543.9304	1613.777	15.9992	2.6	5.3	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
15836	dirMS_041712_NAR_50mM_plus2.18174.18188.3	3	7.52	1	5.21E+05		(K)VIAATNI	(K)V I\A/A/T N R V D\I\L/D/P A L L R(S)		164.43	617.3645	1850.086	-0.0069	-3.7	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
15837	dirMS_041712_NAR_50mM_plus2.6949.6949.3	3	7.52	1	8.24E+05		(K)IVADKD'	(K)I/V|A D/K D Y S V/T A N S K(I)		101.55	504.2628	1510.775	-0.0009	-0.6	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
15838	dirMS_041712_NAR_60mM_plus.10610.10610.3	3	7.52	0	1.02E+06		(K)YAVTTG	(K)Y/A/V T/T G D/H G I I/R(T)		112.6	434.9004	1302.68	0.0066	5	6.74	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
15839	dirMS_041712_NAR_60mM_plus.7347.7347.3	3	7.52	0	9.36E+05		(R)AAHSEG	(R)A A H S E G N T\T/A/G/L/D|M R(E)		96.68	510.9035	1530.697	-0.0006	-0.4	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
15840	dirMS_041712_NAR_120mM_minus.20217.20217.3	3	7.51	0	1.72E+05	M195m	(R)LHFFmP	(R)L H F F m\P G|F\A/P L T S/R(G)	m:Oxidized methionine	165.67	546.2809	1620.835	15.9926	-1.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
15841	dirMS_041712_NAR_30mM_minus2.12360.12360.2	2	7.51	0	2.96E+05		(K)STLTDSL	(K)S T|L/T/D S L/V C/K(A)	C:Carbamidomethylation	120.75	562.2838	1123.566	-0.006	-5.4	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
15842	dirMS_041712_NAR_50mM_minus2.13962.13962.3	3	7.51	0	4.58E+04		(R)VAPEEH	(R)V A/P E/E H P V L L/T/E A/P L N P K(A)		147.42	652.0252	1954.064	-0.0034	-1.7	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
15843	dirMS_041712_NAR_50mM_minus2.16160.16160.3	3	7.51	1	4.43E+06		(R)VSFELFA	(R)V/S F E L F/A D K V/P K(T)		159.72	460.5908	1379.757	0.0009	0.7	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
15844	dirMS_041712_NAR_50mM_minus2.9274.9274.3	3	7.51	0	1.54E+05		(R)TPVIDAI	(R)T P/V|I/D A D/K/P V S S Q L R(V)		121.28	542.6354	1625.886	0.0059	3.7	5.62	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
15845	dirMS_041712_NAR_60mM_minus.10083.10083.3	3	7.51	1	6.76E+04		(K)ALDLDS!	(K)A L|D|L/D S S C K E A/A D/G Y Q R(C)	C:Carbamidomethylation	115.93	633.6235	1898.855	0.0011	0.6	4.23	60404.6	6.4	HUMAN	F5H0T1	Stress-induced-phosphoprotein 1
15846	dirMS_041712_NAR_60mM_minus.10897.10897.3	3	7.51	1	2.79E+05		(R)QSVEAD	(R)Q S V/E/A\D/I/N G\L R R(V)		120.8	453.2461	1357.718	0.0055	4	6.07	19213.2	4.66	HUMAN	K7EMD9	Keratin, type I cytoskeletal 13 (Fragment)
15847	dirMS_041712_NAR_20mM_plus.10451.10451.3	3	7.51	0	2.60E+05		(R)AQIFAN'	(R)A Q\I\F A\N/T/V/D/N A R(I)		145.25	440.5608	1319.67	-0.0024	-1.8	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
15848	dirMS_041712_NAR_20mM_plus.11057.11057.2	2	7.51	0	1.01E+05	M196m	(K)DAGTIA(	(K)D A G T|I/A|G L N V m R(I)	m:Oxidized methionine	148.68	617.3237	1217.631	16.0094	11.8	5.84	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
15849	dirMS_041712_NAR_20mM_plus.14578.14578.2	2	7.51	0	4.50E+04	M256m	(R)SLDmDS	(R)S L|D/m|D|S I I A E/V K(A)	m:Oxidized methionine	171.72	668.8371	1320.671	15.9954	0.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
15850	dirMS_041712_NAR_20mM_plus.9610.9610.2	2	7.51	0	1.16E+05		(K)VAGQD(	(K)V/A/G Q\D G S V V/Q F K(I)		137.93	617.8225	1234.643	-0.0049	-4	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
15851	dirMS_041712_NAR_30mM_plus2.21747.21747.2	2	7.51	0	2.25E+05		(R)TTNFAG	(R)T T N/F|A/G I L S Q G L/R(I)		169.37	689.3749	1377.748	-0.006	-4.3	9.41	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
15852	dirMS_041712_NAR_30mM_plus2.22177.22177.2	2	7.51	0	1.79E+05		(K)GLSSLLC	(K)G L|S\S/L/L/C N\F T K(S)	C:Carbamidomethylation	171.87	620.3199	1239.64	-0.0077	-6.2	8.75	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
15853	dirMS_041712_NAR_50mM_plus2.14437.14437.3	3	7.51	0	3.95E+05		(K)YYITIIDA	(K)Y Y/I T I/I/D/A/P G H R(D)		143.98	473.5865	1418.743	0.0023	1.6	6.74	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
15854	dirMS_041712_NAR_50mM_plus2.16882.16882.3	3	7.51	0	1.53E+06		(K)GSDHSA	(K)G S D H S A S L E|P G E/L/A/E L V R(S)		156.32	622.9846	1866.919	0.0201	10.7	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
15855	dirMS_041712_NAR_60mM_plus.10724.10724.3	3	7.51	1	3.23E+04		(K)KGENYV	(K)K\G E N Y V Y|I/N/E A T R(H)		114.25	519.5996	1556.77	0.0139	8.9	6.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
15856	dirMS_041712_NAR_60mM_plus.13263.13263.3	3	7.51	1	1.19E+05		(R)SEADSD	(R)S E|A D S D K N A T/I/L/E L/R(S)		126.82	554.615	1661.834	-0.0036	-2.2	4.32	334221.3	6.44	HUMAN	P15924	Desmoplakin
15857	dirMS_041712_NAR_60mM_plus.8370.8370.3	3	7.51	1	6.44E+05		(K)EPLYEKI	(K)E P/L/Y|E K D S|S V/A A/R(F)		102.25	488.9148	1464.733	-0.0031	-2.1	4.68	26283.8	8.96	HUMAN	O43809	Cleavage and polyadenylation specificity factor subunit 5
15858	dirMS_041712_NAR_120mM_minus.15846.15846.4	4	7.5	1	8.03E+04		(K)KPITDDI	(K)K P I T D\D D|V/D/R I S L C/L/K(V)	C:Carbamidomethylation	140.62	472.7486	1887.984	-0.0119	-6.3	4.58	108281.4	5.72	HUMAN	P53618	Coatomer subunit beta
15859	dirMS_041712_NAR_120mM_minus.8839.8839.3	3	7.5	1	6.10E+04		(R)VASSTLL	(R)V/A/S S\T L/L/D D/R/R(N)		102.7	411.5568	1232.659	-0.0035	-2.8	5.93	108806.2	4.84	HUMAN	O60763	General vesicular transport factor p115
15860	dirMS_041712_NAR_20mM_minus.11250.11250.3	3	7.5	1	4.32E+05		(K)EENKQV	(K)E/E N K Q V A/L/G\T S K(L)		159.85	435.2303	1303.685	-0.0089	-6.8	6.24	12945.6	9.79	HUMAN	H0YAR3	DNA topoisomerase I, mitochondrial (Fragment)
15861	dirMS_041712_NAR_20mM_minus.14038.14038.3	3	7.5	0	2.43E+05		(R)TTVPQLI	(R)T T V P Q\L|L/A/S V Q R(W)		192.72	438.2582	1312.758	0.0017	1.3	9.41	266161	5.68	HUMAN	E9PPU0	Epiplakin
15862	dirMS_041712_NAR_30mM_minus2.10051.10051.2	2	7.5	0	1.97E+05		(R)VPVDVA	(R)V/P/V/D\V/A Y Q R(G)		108.05	523.7834	1046.563	-0.0034	-3.2	5.8	533778	5.74	HUMAN	Q15149	Plectin
15863	dirMS_041712_NAR_30mM_minus2.16271.16271.2	2	7.5	0	9.66E+04		(K)SIELFYK(	(K)S I|E/L F Y K(F)		141.88	450.2494	899.487	0.0042	4.7	5.72	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
15864	dirMS_041712_NAR_30mM_minus2.20071.20071.2	2	7.5	0	8.03E+04		(K)SLNILTA	(K)S L|N|I/L T A F Q K(K)		169.83	567.8283	1134.652	-0.0024	-2.1	8.47	18172.6	7.77	HUMAN	F8VY02	Endoplasmic reticulum resident protein 29
15865	dirMS_041712_NAR_30mM_minus2.5080.5080.2	2	7.5	1	8.13E+05	S666s	(K)SQKVFsI	(K)S Q/K/V F s E/K(L)	s:Phosphorylated S	80.28	516.7465	952.51	79.9759	9.3	8.31	87498	6.43	HUMAN	C9J266	E3 ubiquitin-protein ligase RNF123
15866	dirMS_041712_NAR_40mM_minus2.9277.9277.3	3	7.5	0	1.31E+05		(K)VQASLA	(K)V Q|A/S/L/A/A N T F T I T G H A E T K(Q)		137.35	654.0087	1960.013	-0.0019	-1	6.72	11802.2	5.6	HUMAN	D6RDG3	Transcription factor BTF3 (Fragment)
15867	dirMS_041712_NAR_50mM_minus2.13856.13856.3	3	7.5	0	3.00E+04		(K)TGEEIFG	(K)T/G/E E/I/F/G/T I G M R P N A K(N)		146.93	574.2947	1720.869	0.0009	0.5	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
15868	dirMS_041712_NAR_50mM_minus2.14883.14883.3	3	7.5	0	3.07E+04		(K)GQYFGE	(K)G Q/Y F/G E L/A L/V T N K/P R(A)		152.52	564.9709	1692.907	-0.0086	-5.1	8.59	10305.6	6.94	HUMAN	H7C330	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
15869	dirMS_041712_NAR_50mM_minus2.14972.14972.3	3	7.5	1	2.60E+05		(K)NIYVLQI	(K)N I/Y\V/L\Q E/L D N P G A K R(I)		152.68	577.3116	1729.923	-0.0029	-1.7	6.07	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
15870	dirMS_041712_NAR_50mM_minus2.15116.15116.3	3	7.5	0	1.83E+05		(K)AETLASS	(K)A E|T|L A/S S L Q E D L/A/H T R(N)		154.87	581.2998	1741.872	0.0133	7.7	4.65	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
15871	dirMS_041712_NAR_50mM_minus2.15279.15279.3	3	7.5	1	2.37E+05		(K)LALDIEI/	(K)L/A/L\D I/E I A T Y R K(L)		154.55	469.2729	1405.805	-0.0008	-0.6	6.07	49564	5.84	HUMAN	E9PAX3	Glial fibrillary acidic protein
15872	dirMS_041712_NAR_60mM_minus.14261.14302.3	3	7.5	1	2.95E+05		(K)ALQQGL	(K)A L/Q Q/G L V/G L E L K/E K(L)		139.65	509.2999	1525.895	-0.0097	-6.3	6.18	266161	5.68	HUMAN	E9PPU0	Epiplakin
15873	dirMS_041712_NAR_60mM_minus.18367.18367.3	3	7.5	0	6.43E+04		(K)YAPLHL\	(K)Y A/P L H L\V/P L I E R(L)		163.73	474.2805	1420.831	-0.0041	-2.9	6.75	147553.6	6.73	HUMAN	E7EVF4	Cytoplasmic FMR1-interacting protein 2
15874	dirMS_041712_NAR_120mM_plus.14220.14220.4	4	7.5	1	7.08E+05		(R)ETNLDSI	(R)E T N L D S L/P/L/V D T H/S K R(T)		127.75	456.9906	1824.945	-0.0044	-2.4	5.38	53707.8	5.06	HUMAN	P08670	Vimentin
15875	dirMS_041712_NAR_120mM_plus.19144.19144.3	3	7.5	1	5.84E+04		(K)QLDDLK'	(K)Q L/D D/L K/V E/L/S/Q L R(V)		153.65	519.6254	1556.864	-0.0026	-1.7	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
15876	dirMS_041712_NAR_20mM_plus.15881.15881.2	2	7.5	0	4.98E+03		(R)SSFYVN(	(R)S S F Y|V/N G\L/T\L/G G Q K(C)		180.83	735.8818	1470.759	-0.0024	-1.6	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
15877	dirMS_041712_NAR_20mM_plus.17354.17354.2	2	7.5	0	2.38E+04	K25k	(R)IVALSSS	(R)I V/A/L S S S L S/N/A|k(D)	k:Ubiquitin-K	191.02	652.3664	1189.679	114.0468	3	8.75	68431.2	6.21	HUMAN	B4E0P5	U5 small nuclear ribonucleoprotein 200 kDa helicase
15878	dirMS_041712_NAR_20mM_plus.17687.17687.2	2	7.5	0	3.04E+05		(R)ILVATNL	(R)I L|V|A T/N L/F G R(G)		194.17	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
15879	dirMS_041712_NAR_20mM_plus.18294.18294.2	2	7.5	0	4.06E+04		(K)EGPAVV	(K)E G/P A|V|V|G Q F I Q D V K(N)		197.27	743.8975	1486.79	-0.0023	-1.5	4.37	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
15880	dirMS_041712_NAR_20mM_plus.7824.7824.2	2	7.5	0	8.55E+04		(K)AQAAAF	(K)A Q\A A|A/P A S V P A Q A P K(R)		123.6	689.3745	1377.748	-0.0068	-4.9	8.8	17808.8	11.77	HUMAN	P47914	60S ribosomal protein L29
15881	dirMS_041712_NAR_30mM_plus2.15540.15540.2	2	7.5	0	1.09E+06		(R)YIELLTR(	(R)Y I|E/L L/T R(S)		133.25	454.2621	907.525	-0.0078	-8.6	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
15882	dirMS_041712_NAR_30mM_plus2.5632.5632.2	2	7.5	0	2.38E+05	M154m M:	(R)mGYmD	(R)m G|Y/m D|P R(E)	m:Oxidized methionine	83.4	451.1814	869.364	31.9911	1.4	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
15883	dirMS_041712_NAR_40mM_plus2.13552.13552.3	3	7.5	1	2.44E+04		(R)IIEFVPTI	(R)I I|E F V|P T K T P Y D/P R(W)		146.22	559.3044	1675.905	-0.0067	-4	6.07	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
15884	dirMS_041712_NAR_40mM_plus2.6308.6308.2	2	7.5	1	2.84E+05		(R)YSGGNY	(R)Y S/G G N Y/R D\N Y|D N(-)		95.58	719.2857	1437.567	-0.0024	-1.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
15885	dirMS_041712_NAR_50mM_plus2.11272.11272.3	3	7.5	1	3.14E+05		(R)DLDRIA(	(R)D L D R I\A|G Q|V\A/A/A N/K(K)		126.77	481.2661	1441.776	0.008	5.5	5.96	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
15886	dirMS_041712_NAR_50mM_plus2.15067.15067.3	3	7.5	0	4.74E+05		(K)TTISVAH	(K)T/T/I/S/V A H L\L/A A/R(Q)		146.48	418.2499	1252.737	-0.002	-1.6	9.44	34143.2	10.07	HUMAN	B4DT23	Protein FAM98A
15887	dirMS_041712_NAR_60mM_plus.6518.6518.3	3	7.5	1	1.36E+05		(K)SAADDS	(K)S A|A|D D S E/A K S N E L T R(A)		92.62	531.9155	1593.735	-0.0031	-2	4.32	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
15888	dirMS_041712_NAR_120mM_minus.12143.12143.3	3	7.49	1	3.42E+05		(K)IRLENEI(	(K)I R L E N E|I/Q T\Y R(S)		120.18	478.9273	1434.77	-0.0026	-1.8	6.14	59054.3	5.14	HUMAN	P13645	Keratin, type I cytoskeletal 10
15889	dirMS_041712_NAR_120mM_minus.4989.4989.3	3	7.49	1	5.89E+05		(R)AAEEED	(R)A A|E/E E D\E A D/P K/R(Q)		79.32	453.8716	1359.602	-0.002	-1.5	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
15890	dirMS_041712_NAR_20mM_minus.7524.7524.2	2	7.49	0	6.67E+05	M239m	(K)EVDEQn	(K)E V|D E Q|m L N|V/Q/N K(N)	m:Oxidized methionine	123.65	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
15891	dirMS_041712_NAR_30mM_minus2.8608.8608.2	2	7.49	0	9.70E+04		(K)IDDVVN'	(K)I/D/D V/V N T R(-)		101.97	466.2472	931.484	0.0028	3	4.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
15892	dirMS_041712_NAR_50mM_minus2.13431.13431.3	3	7.49	0	1.45E+05		(R)IVATKPL	(R)I/V/A T K/P L Y V A\L A Q|R(K)		144.18	514.9821	1542.937	-0.0049	-3.2	9.99	65918.2	9.74	HUMAN	E7EQV3	Polyadenylate-binding protein 1
15893	dirMS_041712_NAR_50mM_minus2.17937.17937.3	3	7.49	0	4.27E+05	M203m	(R)DTGIFLI	(R)D T/G I/F L D L m H L K(K)	m:Oxidized methionine	170.33	473.5826	1402.74	15.9933	-1.1	5.21	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
15894	dirMS_041712_NAR_50mM_minus2.7277.7277.3	3	7.49	1	8.39E+04		(K)ELQAAG	(K)E L/Q/A/A G/K/S P E/D L E R(L)		108.02	514.9262	1542.776	-0.0118	-7.6	4.41	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
15895	dirMS_041712_NAR_60mM_minus.11270.11270.3	3	7.49	1	7.95E+05		(K)MKEIAE/	(K)M K/E I A|E|A/Y/L/G K(T)		122.48	418.226	1252.661	0.0029	2.3	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
15896	dirMS_041712_NAR_20mM_plus.12673.12673.3	3	7.49	0	7.26E+04		(K)GTIQVIT	(K)G T\I Q\V/I|T/Q/G T S L K(N)		160.1	449.261	1345.769	-0.0001	-0.1	8.75	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
15897	dirMS_041712_NAR_20mM_plus.9661.9661.2	2	7.49	0	6.17E+04		(K)ITLVSAA	(K)I T\L/V S/A/A/P G K(V)		137.98	478.793	956.577	0.0012	1.3	8.75	12480.3	9.05	HUMAN	F5H2L4	Acyl-coenzyme A thioesterase 13
15898	dirMS_041712_NAR_30mM_plus2.18221.18281.2	2	7.49	0	1.73E+05	M703m	(R)DILSVm/	(R)D I/L S/V/m A/K(A)	m:Oxidized methionine	149.23	446.7383	876.486	15.9834	-12.9	5.84	139489.6	6	HUMAN	P46019	Phosphorylase b kinase regulatory subunit alpha, liver isoform
15899	dirMS_041712_NAR_30mM_plus2.23647.23647.2	2	7.49	0	2.77E+04		(R)IAIYELLF	(R)I A|I/Y/E L L/F K(E)		192.48	555.3331	1109.661	-0.0016	-1.4	6	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
15900	dirMS_041712_NAR_40mM_plus2.15913.15913.3	3	7.49	0	2.77E+05		(K)VAIVKP(	(K)V/A|I V/K/P G V/P\M E I V L/N K(E)		160.87	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
15901	dirMS_041712_NAR_40mM_plus2.17959.17959.3	3	7.49	0	1.24E+05		(R)GFGFITF	(R)G F/G/F/I/T F/T N/P E H A S V A M R(A)		172.02	661.3289	1981.959	0.0133	6.7	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
15902	dirMS_041712_NAR_40mM_plus2.9003.9003.2	2	7.49	0	1.19E+05		(R)GYSFTTI	(R)G/Y|S/F/T/T T\A E R(E)		114.9	566.7672	1132.527	0.0002	0.2	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
15903	dirMS_041712_NAR_50mM_plus2.15462.15462.3	3	7.49	1	6.87E+05		(R)GFPTIYF	(R)G F/P T I Y F S P/A N K K(L)		149.05	490.5973	1469.779	-0.0014	-0.9	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
15904	dirMS_041712_NAR_50mM_plus2.17859.17859.3	3	7.49	1	2.25E+04		(R)EVLEAL(	(R)E V/L E/A/L G E V M V S R|P R E(-)		161.83	605.3151	1813.948	-0.0169	-9.3	4.69	59918.2	5.27	HUMAN	E9PC67	ATP-binding cassette sub-family F member 1
15905	dirMS_041712_NAR_50mM_plus2.19870.19870.3	3	7.49	1	4.19E+05		(R)LFLDRDI	(R)L F/L D R D L M T\L/P I Q\N K(L)		173.38	606.3362	1816.999	-0.0049	-2.7	5.96	18188.9	10.98	HUMAN	K7EKP7	Ferrochelatase, mitochondrial (Fragment)
15906	dirMS_041712_NAR_50mM_plus2.9196.9196.3	3	7.49	1	7.57E+05	M239m	(R)MQKEIT	(R)M Q K E I T/A\L\A/P S T m K(I)	m:Oxidized methionine	115.63	522.2726	1548.812	15.9908	-2.6	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
15907	dirMS_041712_NAR_60mM_plus.12942.12942.3	3	7.49	0	1.66E+05		(R)IFHTVTT	(R)I F H T V T T/T/D|D/P V I R(K)		124.48	538.9517	1614.849	-0.0081	-5	5.21	31956.7	9.73	HUMAN	B0QYA5	Eukaryotic translation initiation factor 3 subunit D (Fragment)
15908	dirMS_041712_NAR_60mM_plus.15676.15676.3	3	7.49	1	5.65E+05		(R)MSMKE'	(R)M S M K E V D E\Q\M/L/N/V Q/N K(N)		139.12	641.9696	1923.897	-0.003	-1.6	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
15909	dirMS_041712_NAR_60mM_plus.15930.15930.3	3	7.49	0	2.00E+05		(K)LLSTVPA	(K)L L/S T V P A|A S/S C L\R(Y)	C:Carbamidomethylation	140.07	458.9149	1374.741	-0.0108	-7.9	9.75	474806.9	5.78	HUMAN	F8VWT9	Probable E3 ubiquitin-protein ligase HECTD4

15910	dirMS_041712_NAR_60mM_plus.16762.16762.3	3	7.49	1	8.72E+05		(R)STNKGT	(R)S T N K G T A Y T/F F/T/P G N L K(Q)		144.73	616.3117	1846.933	-0.0128	-7	9.7	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
15911	dirMS_041712_NAR_120mM_minus.11448.11448.2	2	7.48	0	7.46E+05		(R)GSAVHC	(R)G S A\V/H|Q|L S/E E/L R(C)		116.68	663.3434	1325.681	-0.0013	-1	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
15912	dirMS_041712_NAR_120mM_minus.4253.4253.3	3	7.48	1	6.63E+05		(R)EPGPAG	(R)E P/G P/A G R G D/G D/S G/R(S)		70.5	443.2041	1327.599	-0.0008	-0.6	4.56	558007.1	5.44	HUMAN	P58107	Epiplakin
15913	dirMS_041712_NAR_120mM_minus.9621.9621.3	3	7.48	0	1.70E+06		(K)EFHLNE	(K)E F H L N\E/S/G D/P S S K(S)		106.18	482.8881	1446.65	0.0002	0.1	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
15914	dirMS_041712_NAR_40mM_minus2.12853.12853.3	3	7.48	0	1.34E+05		(K)GVTIIGP	(K)G V|T I/I/G/P A T V G G I K/P G C F K(I)	C:Carbamidomethylation	159.28	624.6828	1872.041	-0.0073	-3.9	10	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
15915	dirMS_041712_NAR_40mM_minus2.15306.15306.3	3	7.48	1	1.50E+05		(R)VISGVL	(R)V I/S/G\V L Q L G N I V F K K(E)		176.95	539.0017	1614.994	-0.0036	-2.2	10	227783.5	5.5	HUMAN	P35579	Myosin-9
15916	dirMS_041712_NAR_60mM_minus.14507.14507.3	3	7.48	0	7.73E+05		(K)SLTNDW	(K)S L|T|N D W E D H L A V K(H)		141.52	509.9191	1527.744	-0.0011	-0.7	4.53	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
15917	dirMS_041712_NAR_60mM_minus.8797.8797.3	3	7.48	0	1.23E+05		(K)NCPHIV	(K)N\C|P H/I\V V/G/T/P G/R(I)	C:Carbamidomethylation	109.35	436.2271	1306.669	-0.0017	-1.3	9.75	28185.1	10.76	HUMAN	B4DIJ6	Spliceosome RNA helicase DDX39B
15918	dirMS_041712_NAR_60mM_minus.9134.9134.3	3	7.48	0	2.84E+05		(K)ATAGDT	(K)A/T/A/G D/T H L G G E D F D/N R(L)		111.4	559.2488	1675.731	0.0012	0.7	4.22	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
15919	dirMS_041712_NAR_20mM_plus.10381.10381.2	2	7.48	0	2.28E+04		(K)LVSESSD	(K)L/V|S E/S S D V L/P K(-)		144.32	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
15920	dirMS_041712_NAR_20mM_plus.18961.18961.2	2	7.48	0	4.70E+04		(R)GLAVFIS	(R)G L|A/V F/I/S/D/I/R(N)		201.8	545.8154	1090.626	-0.002	-1.8	5.84	75530.1	6.04	HUMAN	E9PJJ7	AP-2 complex subunit alpha-2
15921	dirMS_041712_NAR_20mM_plus.7593.7593.2	2	7.48	0	2.49E+05		(K)VLTPTQ	(K)V/L|T/P T Q V K(N)		121.73	443.2734	885.54	-0.0009	-1	8.72	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
15922	dirMS_041712_NAR_20mM_plus.8465.8465.2	2	7.48	0	1.04E+05	M607m M	(R)mGLAm	(R)m G\L\A/m\G G/G G G A S F D/R(A)	m:Oxidized methionine	128.17	708.3061	1383.614	31.9905	0.5	5.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
15923	dirMS_041712_NAR_20mM_plus.8975.8975.2	2	7.48	0	2.20E+05		(R)VLTVIN	(R)V L|T\V I/N/Q T Q K(E)		132.83	572.3399	1143.673	-0.0007	-0.6	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
15924	dirMS_041712_NAR_30mM_plus2.10445.10445.2	2	7.48	0	5.36E+04		(K)TAVCDI	(K)T A|V/C D/I/P\P R(G)	C:Carbamidomethylation	108.98	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
15925	dirMS_041712_NAR_40mM_plus2.13229.13229.3	3	7.48	1	1.17E+05		(R)ETFEKT	(R)E T/F E K T P V/E V/P V/G G F K(G)		144.53	588.6444	1763.921	-0.0028	-1.6	4.79	533778	5.74	HUMAN	Q15149	Plectin
15926	dirMS_041712_NAR_50mM_plus2.11810.11810.3	3	7.48	0	3.17E+04		(K)SNMGH	(K)S N\M G H|P E P/A\S/G L|A A L A K(V)		130.23	550.9462	1650.827	-0.0028	-1.7	6.47	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
15927	dirMS_041712_NAR_50mM_plus2.15164.15164.3	3	7.48	1	7.72E+05		(K)TVGVEP	(K)T V/G V E/P A A D G K G V V V V I K(R)		147.63	580.0056	1738.011	-0.0087	-5	5.73	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
15928	dirMS_041712_NAR_50mM_plus2.5627.5627.3	3	7.48	0	2.03E+05		(K)SVSSASE	(K)S V|S S/A/S E H S T T E P S P/A A R(R)		91.42	600.9498	1800.836	-0.001	-0.6	5.38	133030.9	10.9	HUMAN	F5H1R7	Protein FLJ22184
15929	dirMS_041712_NAR_60mM_plus.7885.7885.3	3	7.48	1	1.16E+04		(K)LQWATK	(K)L Q|W/A/T/K I I Q E/K(Y)		100.17	453.2595	1357.784	-0.0199	-14.6	8.59	413444.1	10.73	HUMAN	Q8IZT6	Abnormal spindle-like microcephaly-associated protein
15930	dirMS_041712_NAR_120mM_minus.4220.4232.3	3	7.47	1	6.83E+05		(R)EPGPAG	(R)E P/G/P/A G R G D/G D/S G R(S)		70.47	443.2041	1327.599	-0.0008	-0.6	4.56	558007.1	5.44	HUMAN	P58107	Epiplakin
15931	dirMS_041712_NAR_120mM_minus.8234.8234.3	3	7.47	1	5.77E+05		(K)IQDKEGI	(K)I Q D K E G I|P/P D Q Q R(L)		98.82	508.5981	1523.781	-0.0015	-1	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
15932	dirMS_041712_NAR_20mM_minus.10992.10992.3	3	7.47	0	3.35E+03	M17m M2	(K)GAEEmE	(K)G A E E m\E T V I/P V D V m R(R)	m:Oxidized methionine	157.57	569.9352	1675.803	31.9881	-1	4	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
15933	dirMS_041712_NAR_20mM_minus.14087.14087.3	3	7.47	0	7.32E+05		(K)SYELPD	(K)S Y E L|P D G Q V/I/T/I G N E R(F)		193.9	597.6345	1790.892	-0.003	-1.7	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
15934	dirMS_041712_NAR_20mM_minus.14627.14627.3	3	7.47	0	3.68E+05		(K)LAVEAL	(K)L A\V\E A L\S S L/D G D/L/A G R(Y)		201.3	529.6163	1586.838	-0.0041	-2.6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
15935	dirMS_041712_NAR_30mM_minus2.11194.11194.2	2	7.47	0	1.32E+05		(R)AMGEQ	(R)A M/G E/Q/A/V A L A/R(A)		114.68	558.7916	1116.583	-0.0071	-6.3	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
15936	dirMS_041712_NAR_40mM_minus2.15842.15842.3	3	7.47	0	3.30E+05		(R)DLLDTVI	(R)D L|L|D T/V L/P H\L Y N E/T K(V)		185.33	590.9795	1770.927	-0.0033	-1.9	4.54	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
15937	dirMS_041712_NAR_50mM_minus2.12931.12931.3	3	7.47	0	5.01E+05	M347m	(R)LAEHIVS	(R)L A|E H\I V S m\L F/T S I A K(L)	m:Oxidized methionine	142.53	559.3044	1659.914	15.9848	-6	6.75	142131.9	5.5	HUMAN	H7C183	Ubiquitin carboxyl-terminal hydrolase 34 (Fragment)
15938	dirMS_041712_NAR_50mM_minus2.14699.14699.3	3	7.47	1	2.93E+05		(R)EAVTEIL	(R)E/A/V/T E/I/L G I E/P D R E K(G)		152.23	566.9683	1698.891	-0.0005	-0.3	4.25	25685.9	6.4	HUMAN	E9PGT1	Translin
15939	dirMS_041712_NAR_50mM_minus2.15770.15770.3	3	7.47	0	1.18E+05		(K)IEVIKPG	(K)I E/V/I/K/P G D L G V D/L T S K(L)		157.2	561.9884	1683.953	-0.0021	-1.2	4.56	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
15940	dirMS_041712_NAR_50mM_minus2.16977.16977.3	3	7.47	1	5.94E+04		(R)EFTRLEI	(R)E F T R L E\I C|N/L/T|P D A L K(S)	C:Carbamidomethylation	164.93	640.6675	1919.989	-0.0016	-0.8	4.68	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
15941	dirMS_041712_NAR_50mM_minus2.17560.17560.3	3	7.47	0	2.34E+05		(R)DVCTELI	(R)D V/C T/E L/L/P L I K P Q G R(V)	C:Carbamidomethylation	168.67	580.3212	1738.952	-0.003	-1.7	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
15942	dirMS_041712_NAR_50mM_minus2.18678.18678.3	3	7.47	0	3.42E+05		(R)AGKPVI	(R)A G K\P V I\C A T Q|M/L E/S M I K(K)	C:Carbamidomethylation	180.9	626.3309	1876.969	0.0088	4.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
15943	dirMS_041712_NAR_50mM_minus2.5861.5861.3	3	7.47	1	4.33E+04		(R)AIEAAP	(R)A I/E/A A/P Q|E/P E Q K R(S)		95.43	489.5922	1466.76	0.0023	1.5	4.79	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
15944	dirMS_041712_NAR_50mM_minus2.8996.8996.3	3	7.47	0	1.52E+05		(R)VMLGET	(R)V M/L/G E/T N P A D/S K P G T I R(G)		119.6	595.9744	1785.916	-0.0077	-4.3	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
15945	dirMS_041712_NAR_50mM_minus2.9825.9825.3	3	7.47	0	2.63E+05	M147m	(K)LQmEAP	(K)L Q/m E A|P/H|I/I/V G T P G/R(V)	m:Oxidized methionine	124.53	545.6267	1618.873	15.9922	-1.7	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
15946	dirMS_041712_NAR_60mM_minus.14826.14826.3	3	7.47	0	2.66E+05		(K)YYITIIDA	(K)Y Y/I T/I/I/D A/P G/H R(D)		142.87	473.5815	1418.743	-0.0127	-9	6.74	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
15947	dirMS_041712_NAR_60mM_minus.16686.16686.3	3	7.47	1	1.80E+05		(K)VSEQGL	(K)V/S/E/Q G L I E/I L K K(V)		152.83	452.9408	1356.81	-0.0018	-1.4	6.11	12899.6	6.59	HUMAN	K7EL31	Programmed cell death protein 5
15948	dirMS_041712_NAR_60mM_minus.4845.4845.3	3	7.47	1	1.28E+05	M75m M8	(R)mGPSG	(R)m G|P/S/G G E G m E/P E R R(D)	m:Oxidized methionine	80.42	507.8846	1489.652	31.987	-1.8	4.78	23181	4.83	HUMAN	B4DGQ0	LIM and SH3 domain protein 1
15949	dirMS_041712_NAR_120mM_plus.9093.9093.3	3	7.47	1	4.91E+05		(R)SGRGGN	(R)S G R G G N|F/G|F G D/S R(G)		101.07	438.538	1313.598	0.0013	1	9.32	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
15950	dirMS_041712_NAR_20mM_plus.14155.14155.2	2	7.47	0	9.91E+03		(K)GCSFLP	(K)G C\S/F/L|P D P Y Q/K(Q)	C:Carbamidomethylation	169.5	656.3061	1311.604	0.0011	0.9	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
15951	dirMS_041712_NAR_30mM_plus2.17415.17415.2	2	7.47	0	4.15E+05		(R)LIVNVN	(R)L I|V/N V N D/L R(R)		144.6	528.3113	1055.621	-0.0054	-5.2	5.84	91606.8	5.53	HUMAN	P25205	DNA replication licensing factor MCM3
15952	dirMS_041712_NAR_30mM_plus2.18757.18757.2	2	7.47	0	3.25E+05		(R)ESLEALL	(R)E\S/L/E/A L/L/Q R(A)		152.03	529.8026	1058.584	0.0139	13.1	4.53	107721.8	8.85	HUMAN	O94906	Pre-mRNA-processing factor 6
15953	dirMS_041712_NAR_30mM_plus2.20349.20349.3	3	7.47	0	4.68E+05		(K)SYELPD	(K)S Y E\L P D/G Q V/I/T I/G N E R(F)		159.97	597.6334	1790.892	-0.0063	-3.5	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
15954	dirMS_041712_NAR_30mM_plus2.23359.23359.2	2	7.47	0	7.85E+05		(R)ILDPFIIR	(R)I L/D P/F/I I R(T)		188.48	493.8049	986.603	-0.0008	-0.8	5.84	25765.6	9.49	HUMAN	C9IZL6	Type 2 lactosamine alpha-2,3-sialyltransferase (Fragment)
15955	dirMS_041712_NAR_30mM_plus2.5556.5556.2	2	7.47	0	5.86E+04		(K)FAETQP	(K)F/A/E/T Q/P/K(K)		83.25	410.7181	820.42	0.009	10.9	6	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
15956	dirMS_041712_NAR_40mM_plus2.12170.12170.3	3	7.47	1	2.24E+05		(R)VVDALG	(R)V V|D A L/G N A I/D G K G P I/G S K(T)		137.22	570.9838	1710.939	-0.0016	-1	5.93	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
15957	dirMS_041712_NAR_40mM_plus2.6090.6090.2	2	7.47	0	5.66E+04		(R)QAFPNT	(R)Q/A|F/P N T N R(W)		94.88	474.2383	947.469	0	0	9.75	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
15958	dirMS_041712_NAR_50mM_plus2.16370.16370.3	3	7.47	0	3.28E+04		(R)EVIDLLK	(R)E V|I/D/L/L K/P D Q V E G I Q K(S)		154.37	608.6724	1824.011	-0.0087	-4.7	4.32	156557.7	5.52	HUMAN	Q86UP2	Kinectin
15959	dirMS_041712_NAR_60mM_plus.12791.12791.3	3	7.47	0	3.02E+05		(R)ILHLLGQ	(R)I L/H L L/G Q E G P K(T)		123.6	402.2397	1204.705	-0.0003	-0.2	6.75	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
15960	dirMS_041712_NAR_60mM_plus.17033.17033.3	3	7.47	1	2.25E+05		(R)ASLISAV	(R)A S|L/I/S A/V S D K L R(W)		145.97	420.5832	1259.732	0.0033	2.6	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
15961	dirMS_041712_NAR_60mM_plus.8433.8433.4	4	7.47	2	2.34E+05	M4m S7s	(K)EmYQsA	(K)E m Y Q s/A E A K\V\S K S T G K(W)	m:Oxidized methionine s:N-a	102.1	491.4815	1743.858	219.046	-14.4	8.52	46774.9	5.8	HUMAN	A8MPV3	Putative uncharacterized protein ENSP00000344348
15962	dirMS_041712_NAR_120mM_minus.17630.17630.4	4	7.46	1	5.26E+05		(R)GFGHIG	(R)G F G H I G I A\V/P/D V Y S/A/C K R(F)	C:Carbamidomethylation	150.43	487.502	1946.991	-0.0044	-2.2	8.6	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
15963	dirMS_041712_NAR_120mM_minus.17765.17765.3	3	7.46	1	1.82E+05		(R)AGKLDP	(R)A G K L D|P H L V|L/D Q\L R(C)		151.52	525.6385	1574.901	-0.0004	-0.2	6.79	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
15964	dirMS_041712_NAR_20mM_minus.13491.13491.2	2	7.46	0	5.99E+05		(K)DAGTIA	(K)D A/G T\I|A/G L N V L R(I)		185.07	600.3403	1199.674	-0.0009	-0.8	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
15965	dirMS_041712_NAR_30mM_minus2.14132.14132.2	2	7.46	0	2.19E+05		(R)GANDF	(R)G A N D F|M|C D E M E/R(S)	C:Carbamidomethylation	130.03	737.7725	1474.54	-0.0018	-1.2	3.91	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
15966	dirMS_041712_NAR_30mM_minus2.18183.18225.2	2	7.46	0	9.25E+04		(R)LIEDFLA	(R)L I|E/D/F/L A R(S)		153.43	488.7803	976.546	0.0071	7.3	4.37	15119.1	4.81	HUMAN	A6NDN0	Trafficking protein particle complex 3, isoform CRA_a
15967	dirMS_041712_NAR_40mM_minus2.14259.14259.3	3	7.46	0	1.23E+05		(R)GTEDITS	(R)G T|E/D/I|T S/P/H G I/P L D|L\L D R(V)		168.55	650.3366	1948.997	-0.0022	-1.1	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
15968	dirMS_041712_NAR_50mM_minus2.10602.10602.3	3	7.46	0	2.31E+05		(K)VFEGNR	(K)V/F/E/G N R P T N S I V F/T/K(L)		128.93	570.3032	1708.902	-0.0066	-3.9	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
15969	dirMS_041712_NAR_50mM_minus2.13127.13127.3	3	7.46	0	3.30E+06	M84m	(K)YPIEHGI	(K)Y/P/I E H G I I\T|N|W/D D m E K(I)	m:Oxidized methionine	141.85	659.6398	1960.911	15.9939	-0.5	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
15970	dirMS_041712_NAR_50mM_minus2.13327.13327.3	3	7.46	1	1.92E+05	M26m	(K)GAEEME	(K)G/A E/E\M/E T V/I/P V D V m R R(A)	m:Oxidized methionine	143.83	616.6435	1831.904	16.0119	9.2	4.41	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
15971	dirMS_041712_NAR_50mM_minus2.5202.5202.3	3	7.46	0	8.95E+04		(R)AEAEAG	(R)A E|A\E A/G S P\R P D/P R(E)		87.28	451.5573	1352.655	0.002	1.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
15972	dirMS_041712_NAR_50mM_minus2.6698.6698.3	3	7.46	1	8.76E+04	M22m M2	(K)LAEQAE	(K)L/A E/Q/A/E R Y D D m A A/C m K(S)	C:Carbamidomethylation m:Oxid	104.8	645.2741	1901.819	31.9887	-0.6	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
15973	dirMS_041712_NAR_60mM_minus.10978.10978.3	3	7.46	1	2.36E+05		(K)VTVAGL	(K)V/T|V/A/G L/A G K D P V Q C S R(D)	C:Carbamidomethylation	121.1	553.2923	1657.869	-0.0067	-4	8.72	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
15974	dirMS_041712_NAR_60mM_minus.18598.18598.3	3	7.46	0	2.87E+05		(K)TFLVWV	(K)T F/L/V W/V/N E E D H L R(V)		165.77	553.2818	1657.833	-0.0024	-1.5	4.65	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
15975	dirMS_041712_NAR_60mM_minus.7303.7303.3	3	7.46	0	2.48E+06	M434m	(R)LESGm	(R)L E/S G m Q\N/M/S I H T K(T)	m:Oxidized methionine	98.97	497.9023	1475.698	15.9942	-0.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
15976	dirMS_041712_NAR_20mM_plus.13681.13681.2	2	7.46	0	2.77E+05		(R)GDLGIEI	(R)G D L/G/I|E I/P A E K(V)		166.72	571.3075	1141.61	-0.0022	-1.9	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
15977	dirMS_041712_NAR_20mM_plus.14367.14367.2	2	7.46	0	6.82E+04		(R)ELAQQV	(R)E L/A/Q Q/V/Q/Q V A\D D Y G K(C)		170.75	846.4161	1691.824	0.0014	0.8	4.03	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
15978	dirMS_041712_NAR_20mM_plus.19153.19153.3	3	7.46	0	2.10E+05		(R)LAGTQP	(R)L A G T Q P L E|V L/E/A/V Q R(S)		204.03	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
15979	dirMS_041712_NAR_30mM_plus2.21805.21805.2	2	7.46	0	3.88E+05		(R)FSWNV	(R)F S W/N/V W|P S/S R(L)		169.52	633.3085	1265.606	0.0035	2.8	9.75	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
15980	dirMS_041712_NAR_30mM_plus2.6328.6328.2	2	7.46	0	1.09E+05		(K)FNYSGS	(K)F/N|Y/S/G S G G R(S)		87.1	472.7087	944.422	-0.0119	-12.6	8.75	96205.6	9.06	HUMAN	G5E9M5	Interleukin enhancer binding factor 3, 90kDa, isoform CRA_b
15981	dirMS_041712_NAR_40mM_plus2.13458.13458.3	3	7.46	0	9.16E+03		(K)MVMIQ	(K)M V M I/Q|D G P L/P T G A D K P L R(I)		145.45	647.0084	1939.014	-0.0033	-1.7	5.71	61981.6	8.97	HUMAN	Q96I24	Far upstream element-binding protein 3
15982	dirMS_041712_NAR_40mM_plus2.5728.5728.2	2	7.46	0	1.12E+05		(R)FSSSSGY	(R)F S|S/S S/G/Y/G G G S/S R(V)		90.98	618.2686	1235.529	0.0012	1	8.75	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
15983	dirMS_041712_NAR_50mM_plus2.17218.17218.3	3	7.46	1	3.37E+05		(R)VSFELFA	(R)V/S\F E L/F A/D K/V/P K(T)		158.8	460.5906	1379.757	0.0003	0.2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
15984	dirMS_041712_NAR_50mM_plus2.20017.20017.3	3	7.46	1	1.59E+05		(K)EIEELKE	(K)E I E E L K E\L/L/P E/I/R(E)		173.57	537.6393	1610.9	0.0034	2.1	4.33	30121.3	4.2	HUMAN	E9PRH9	Nuclear autoantigenic sperm protein (Fragment)
15985	dirMS_041712_NAR_50mM_plus2.22274.22274.3	3	7.46	0	9.12E+05		(R)GGHPPA	(R)G G H P P A I Q S L/I|N L/L/A D N R(Y)		191.35	629.3448	1886.024	-0.0044	-2.3	6.74	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
15986	dirMS_041712_NAR_60mM_plus.11366.11366.3	3	7.46	1	1.87E+06		(K)LKGEAT	(K)L K G E A\T\V/S/F/D|D/P P S A K(A)		116.45	554.615	1661.838	-0.0076	-4.6	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
15987	dirMS_041712_NAR_120mM_minus.11962.11962.3	3	7.45	0	5.63E+05		(R)IVNHWA	(R)I V/N H/W A/S/P E/L R(Q)		118.8	441.2372	1321.701	-0.0041	-3.1	6.75	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
15988	dirMS_041712_NAR_120mM_minus.12003.12003.3	3	7.45	1	3.13E+05		(R)LKGYLIS	(R)L K G Y L\I/S/G S S Y A/R(S)		119.58	472.2599	1414.769	-0.0037	-2.6	9.7	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
15989	dirMS_041712_NAR_20mM_minus.14565.14565.3	3	7.45	0	1.76E+04		(K)LAVEAL	(K)L A V E A L\S S\L/D/G D/L/A G R(Y)		199.98	529.6163	1586.838	-0.0041	-2.6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
15990	dirMS_041712_NAR_30mM_minus2.11481.11481.2	2	7.45	1	1.42E+05		(K)LGLLRES	(K)L/G/L/L/R E S S(-)		115.87	437.7522	874.499	-0.0021	-2.4	6	24849.3	11.77	HUMAN	D3DRR9	Chromosome 10 open reading frame 47, isoform CRA_b
15991	dirMS_041712_NAR_30mM_minus2.14628.14628.2	2	7.45	0	2.85E+05		(R)VFDMLN	(R)V/F/D M/L/N R(R)		133.87	447.7317	894.45	0.0059	6.6	5.81	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
15992	dirMS_041712_NAR_40mM_minus2.9502.9502.3	3	7.45	0	9.99E+04		(K)AASDIA	(K)A A|S/D/I A M T E L/P P T H P I R(L)		138.25	607.3174	1819.937	0.0006	0.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
15993	dirMS_041712_NAR_50mM_minus2.9589.9589.3	3	7.45	1	7.56E+04		(R)LLQTSNI	(R)L L/Q/T S N|I T/K/L E Q K(K)		123.28	505.963	1515.874	0.0004	0.2	8.59	20207.3	8.69	HUMAN	B1AKS5	Serine/threonine-protein kinase PAK 3 (Fragment)
15994	dirMS_041712_NAR_60mM_minus.12678.12678.3	3	7.45	1	1.29E+05		(R)TPSDVK	(R)T P/S D V K/E\L|V|L/D N S R(S)		131.18	524.9451	1572.823	-0.002	-1.3	4.55	20111	4.47	HUMAN	H0YN26	Acidic leucine-rich nuclear phosphoprotein 32 family member A
15995	dirMS_041712_NAR_60mM_minus.9513.9513.3	3	7.45	1	5.38E+04		(K)VTLTSEE	(K)V/T/L T/S E E E A R L K(K)		112.88	459.2545	1375.743	0.0062	4.5	4.79	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
15996	dirMS_041712_NAR_120mM_plus.14666.14693.3	3	7.45	1	1.02E+06		(K)LDKSQI	(K)L D/K/S Q I H D|I V|L V|G G S T R(I)		130.55	613.3369	1838.013	-0.0169	-9.2	6.75	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
15997	dirMS_041712_NAR_120mM_plus.16303.16303.4	4	7.45	1	9.60E+05		(R)ALEHFT	(R)A L E H/F T/D L/Y/D/I/K/R(A)		138.37	405.9647	1620.838	-0.0011	-0.7	5.38	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
15998	dirMS_041712_NAR_20mM_plus.13899.13899.2	2	7.45	0	1.84E+04		(R)GLCAIA	(R)G L/C\A|I|A/Q/A E S L R(Y)	C:Carbamidomethylation	167.55	644.8389	1288.668	0.0027	2.1	6	18529.2	9.98	HUMAN	E9PL45	40S ribosomal protein S3
15999	dirMS_041712_NAR_20mM_plus.14228.14286.2	2	7.45	0	3.86E+04	M61m	(R)IIPGFm	(R)I/I/P G F/m C Q G G D F/T R(H)	C:Carbamidomethylation m:Oxid	170.9	807.8736	1598.745	15.9945	-0.2	5.84	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
16000	dirMS_041712_NAR_20mM_plus.14656.14656.2	2	7.45	0	9.93E+04		(K)FLDGIYV	(K)F L/D G/I/Y V S E K(G)		173.5	585.8066	1170.604	0.0018	1.5	4.37	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
16001	dirMS_041712_NAR_20mM_plus.18856.18856.2	2	7.45	0	2.42E+05		(K)IYVDDGI	(K)I Y V/D/D/G L/I/S L Q V K(Q)		200.75	731.9068	1462.815	-0.0088	-6	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
16002	dirMS_041712_NAR_30mM_plus2.15281.15281.2	2	7.45	0	7.55E+04		(K)TVPINLI	(K)T V|P I/N/L I K(D)		132.93	449.2894	897.577	-0.0053	-5.9	8.41	24497.1	9.3	HUMAN	O43708	Maleylacetoacetate isomerase
16003	dirMS_041712_NAR_30mM_plus2.16685.16685.2	2	7.45	0	3.85E+05		(K)QLQEM	(K)Q L/Q/E M\L/G L/S K(V)		140.38	573.8112	1146.619	-0.0036	-3.1	6	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
16004	dirMS_041712_NAR_30mM_plus2.19494.19494.2	2	7.45	0	9.05E+05		(R)ISEQFTA	(R)I/S\E/Q/F T/A/M F R(R)		156.75	615.3024	1229.598	-0.0008	-0.6	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
16005	dirMS_041712_NAR_40mM_plus2.14035.14035.3	3	7.45	0	1.98E+05		(K)VALLLLD	(K)V A L L/L/L D Q/G A/S P/H A A A K(N)		148.27	558.9886	1674.954	-0.0025	-1.5	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
16006	dirMS_041712_NAR_50mM_plus2.21866.21866.3	3	7.45	0	1.62E+04		(K)GHYTEG	(K)G H Y T E G A E\L V|D/S V/L D/V V R(K)		185.95	653.6688	1958.982	0.0101	5.1	4.31	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
16007	dirMS_041712_NAR_50mM_plus2.7559.7559.3	3	7.45	0	8.39E+04		(R)AGAISA	(R)A G A|I\S A/S G P E L Q G A/G/H S K(L)		105.82	546.6129	1637.824	0	0	6.79	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
16008	dirMS_041712_NAR_60mM_plus.16640.16640.3	3	7.45	1	6.93E+05		(R)STNKGT	(R)S T N K G T A Y T/F/F/T/P G N L K(Q)		144.48	616.3117	1846.933	-0.0128	-7	9.7	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
16009	dirMS_041712_NAR_60mM_plus.5141.5141.3	3	7.45	0	2.14E+04		(R)LENNEN	(R)L/E|N N E N K/P V|T N S R(D)		85.37	505.5852	1514.756	-0.0147	-9.7	6.14	62504.2	9.01	HUMAN	Q9Y5A9	YTH domain family protein 2
16010	dirMS_041712_NAR_20mM_minus.11206.11213.2	2	7.44	0	1.15E+05	M148m	(R)DLTDYL	(R)D L|T|D Y L/m/K(I)	m:Oxidized methionine	159.57	507.7443	998.486	15.995	0.1	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
16011	dirMS_041712_NAR_30mM_minus2.11396.11396.2	2	7.44	0	1.15E+06		(K)FSASGE	(K)F S|A/S|G E/L/G N G N\I\K(L)		115	647.3253	1293.643	0	0	6	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
16012	dirMS_041712_NAR_30mM_minus2.14394.14394.2	2	7.44	0	2.40E+05		(K)CCSGAII	(K)C C|S|G A/I I V L T K(S)	C:Carbamidomethylation	131.97	611.3188	1221.633	-0.0027	-2.2	8.75	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
16013	dirMS_041712_NAR_40mM_minus2.8898.8898.3	3	7.44	1	5.45E+04		(R)IVAPGK	(R)I V/A P G K G I L A A/D E/S T G S I A K(R)		135.25	633.355	1898.059	-0.0089	-4.7	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
16014	dirMS_041712_NAR_50mM_minus2.10873.10873.3	3	7.44	0	1.19E+05		(R)IMLFTN	(R)I M|L/F/T|N/E D N P H G/N D\S A K(A)		129.82	634.9586	1902.865	-0.0038	-2	4.54	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
16015	dirMS_041712_NAR_50mM_minus2.12460.12460.3	3	7.44	1	2.20E+05	M2709m	(K)ISmPDID	(K)I/S m|P D I/D/L N L/K G P K(V)	m:Oxidized methionine	139.4	519.6148	1540.84	15.9895	-3.5	5.96	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
16016	dirMS_041712_NAR_50mM_minus2.14520.14520.3	3	7.44	1	2.52E+05		(R)GFPTIYF	(R)G F/P T/I Y F S/P A N K K(L)		150.58	490.5972	1469.779	-0.0017	-1.1	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
16017	dirMS_041712_NAR_50mM_minus2.15151.15151.3	3	7.44	0	3.32E+05		(K)AETLAS	(K)A E|T|L/A/S S L Q/E D L A H T R(N)		154.6	581.2998	1741.872	0.0133	7.7	4.65	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
16018	dirMS_041712_NAR_60mM_minus.10936.10936.3	3	7.44	1	2.28E+05		(K)VTVAGL	(K)V T|V/A/G L A/G K D/P V Q C S R(D)	C:Carbamidomethylation	121.07	553.2923	1657.869	-0.0067	-4	8.72	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1

16019	dirMS_041712_NAR_60mM_minus.14702.14702.3	3	7.44	0	3.56E+05		(R)AVAIDLF	(R)A V/A I D L/P G/L G H/S K(E)		142.4	426.578	1277.721	-0.0018	-1.4	6.79	19983.6	8.14	HUMAN	B4DQI4	Alpha/beta hydrolase domain-containing protein 14B
16020	dirMS_041712_NAR_60mM_minus.15411.15411.3	3	7.44	1	4.44E+05		(K)YQLDKD	(K)Y Q|L/D K D G V/V L F/K(K)		146.27	475.5992	1424.778	0.0047	3.3	5.96	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
16021	dirMS_041712_NAR_60mM_minus.18586.18586.3	3	7.44	0	2.72E+05		(K)LHDNLII	(K)L H D N\L/I\I/S/D/L/E N T V K(K)		165.78	575.3117	1723.922	-0.0019	-1.1	4.54	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
16022	dirMS_041712_NAR_60mM_minus.6323.6367.2	2	7.44	1	1.72E+05		(K)IIAPPERI	(K)I/I|A|P/P E R K(Y)		94	462.287	923.567	-0.0006	-0.6	8.75	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
16023	dirMS_041712_NAR_120mM_plus.4404.4404.3	3	7.44	1	4.80E+04	S521s M52	(R)QDTsFm	(R)Q D T s/F/m K/K(N)	s:N-acetylglucosamine (S) m:	71.82	401.8588	984.482	219.08	4.7	8.59	93852.6	6.3	HUMAN	H9KV44	Protein EFR3 homolog A
16024	dirMS_041712_NAR_20mM_plus.10502.10502.2	2	7.44	0	3.12E+05		(K)VLQATV	(K)V L/Q|A\T V/V/A/V/G S/G S K(G)		145.67	658.3737	1315.758	-0.0179	-13.6	8.72	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
16025	dirMS_041712_NAR_20mM_plus.11230.11230.2	2	7.44	0	2.18E+05		(K)LITPAVV	(K)L I/T/P/A/V/V S E\R(L)		150.05	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
16026	dirMS_041712_NAR_30mM_plus2.20942.20942.2	2	7.44	0	4.39E+04		(R)EMVLEII	(R)E/M\V/L/E/I I/R(E)		163.4	501.7877	1002.565	0.0029	2.9	4.53	61981.6	8.97	HUMAN	Q96I24	Far upstream element-binding protein 3
16027	dirMS_041712_NAR_30mM_plus2.21806.21806.3	3	7.44	0	1.83E+05		(K)GLVQAL	(K)G L\V Q/A L G\L/S/N/F N S R(Q)		169.45	492.6036	1475.796	-0.0003	-0.2	9.75	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
16028	dirMS_041712_NAR_30mM_plus2.7758.7783.2	2	7.44	0	3.15E+05		(R)AQIDNL	(R)A Q|I/D/N/L T/R(E)		94.68	465.7534	930.5	-0.0008	-0.9	5.88	334221.3	6.44	HUMAN	P15924	Desmoplakin
16029	dirMS_041712_NAR_40mM_plus2.16104.16104.3	3	7.44	0	4.05E+05		(R)FGVPVI	(R)F G V/P V I A/D G G I/Q N V G H I A K(A)		162.12	631.3436	1892.039	-0.0226	-12	6.74	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
16030	dirMS_041712_NAR_50mM_plus2.19959.19959.3	3	7.44	0	5.26E+04		(K)GLCLLEC	(K)G L/C|L/L E/Q I/D S F K P P Q/R(S)	C:Carbamidomethylation	172.9	634.3344	1900.995	-0.0063	-3.3	6.07	45536.8	9.03	HUMAN	B7Z1K2	HBS1-like protein
16031	dirMS_041712_NAR_50mM_plus2.9310.9310.3	3	7.44	0	5.74E+05	M115m	(R)VmLGET	(R)V m/L/G E T N P A D/S K P G T I\R(G)	m:Oxidized methionine	115.57	601.3075	1785.916	15.9916	-1.8	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
16032	dirMS_041712_NAR_60mM_plus.10776.10776.3	3	7.44	1	1.18E+06		(R)TAAEND	(R)T A|A E\N D\F V/T/L/K K(D)		114.87	446.2368	1336.711	-0.0149	-11.1	5.73	65717	8.32	HUMAN	P35908	Keratin, type II cytoskeletal 2 epidermal
16033	dirMS_041712_NAR_60mM_plus.19463.19463.3	3	7.44	0	6.19E+05		(K)VSHLLGI	(K)V/S H L L\G I\N\V/T|D/F T R(G)		159.92	524.6233	1571.854	0.0013	0.8	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
16034	dirMS_041712_NAR_60mM_plus.7246.7246.3	3	7.44	1	4.31E+05		(K)VVSETN	(K)V/V/S E/T N D T K/V/L R(H)		95.93	454.2511	1360.743	-0.0043	-3.2	6.04	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
16035	dirMS_041712_NAR_60mM_plus.7309.7350.3	3	7.44	1	9.36E+05		(R)AVTGYK	(R)A V|T|G Y K D/P Y|S G K(L)		96.6	429.2193	1285.642	0.0011	0.8	8.47	533778	5.74	HUMAN	Q15149	Plectin
16036	dirMS_041712_NAR_20mM_minus.14367.14367.2	2	7.43	0	2.51E+05		(R)APGSGL	(R)A/P/G/S G L/A L/L/P L K(I)		198.32	568.8551	1136.704	-0.0008	-0.7	8.8	266161	5.68	HUMAN	E9PPU0	Epiplakin
16037	dirMS_041712_NAR_20mM_minus.14570.14570.2	2	7.43	0	7.28E+04	M332m	(R)IVSQLLT	(R)I V\S Q\L/L/T/L m D G L K(Q)	m:Oxidized methionine	200.32	723.9145	1430.829	15.993	-1.3	5.84	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
16038	dirMS_041712_NAR_30mM_minus2.8566.8586.2	2	7.43	0	2.24E+05		(R)NVLLNN	(R)N V|L|L/N N S E K(M)		101.18	515.7847	1030.553	0.0094	9.1	6	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b
16039	dirMS_041712_NAR_50mM_minus2.14339.14339.3	3	7.43	0	3.37E+05		(K)LHIIEVG	(K)L H I I E V G\T/P/P T/G N Q P F/P K(K)		149.9	649.0215	1945.054	-0.0042	-2.2	6.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
16040	dirMS_041712_NAR_50mM_minus2.5802.5802.3	3	7.43	1	4.10E+04		(R)ATEGM	(R)A/T/E/G M V/V/A D K N C S K(I)	C:Carbamidomethylation	94.57	503.9058	1509.704	-0.0007	-0.5	6.11	15607.8	9.99	HUMAN	B4E0P1	Proteasome (Prosome, macropain) subunit, beta type, 7, isoform CRA_b
16041	dirMS_041712_NAR_60mM_minus.10547.10547.3	3	7.43	1	1.64E+06		(K)TLQEVTI	(K)T L|Q E V/T/E M D S V K R(Y)		119.37	512.5957	1535.773	-0.0008	-0.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
16042	dirMS_041712_NAR_60mM_minus.18896.18896.3	3	7.43	0	1.29E+06		(R)IHFPLAT	(R)I H\F P L A T Y|A/P/V I S/A E K(A)		166.27	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
16043	dirMS_041712_NAR_60mM_minus.8481.8481.3	3	7.43	1	8.31E+03		(R)DPSNM	(R)D/P/S N M Y T/K Y Y/I/H/R(I)		107.72	563.2673	1687.79	-0.0024	-1.4	8.44	24435.4	9.58	HUMAN	Q96F25	UDP-N-acetylglucosamine transferase subunit ALG14 homolog
16044	dirMS_041712_NAR_120mM_plus.17965.17965.4	4	7.43	1	1.12E+05		(R)ILEFFGLI	(R)I L E F/F G/L K K E E C/P A V/R(L)	C:Carbamidomethylation	146.97	484.7638	1936.036	-0.0027	-1.4	6.23	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
16045	dirMS_041712_NAR_20mM_plus.18148.18148.2	2	7.43	0	6.87E+04	M78m	(K)LVSDEm	(K)L V|S D E/m V/V/E L/I E K(N)	m:Oxidized methionine	196.88	760.3973	1503.797	15.9899	-3.3	4	17727.3	6.31	HUMAN	F8VZG5	Adenylate kinase 2, mitochondrial
16046	dirMS_041712_NAR_20mM_plus.19240.19240.3	3	7.43	0	1.02E+04		(R)ALIAGG	(R)A L\I\A G G G A/P E/I/E|L A L R(L)		203.72	517.6345	1550.89	-0.0011	-0.7	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
16047	dirMS_041712_NAR_20mM_plus.8334.8334.2	2	7.43	0	1.32E+04		(R)LAAVDV	(R)L/A|A/V/D\V/S A R(A)		127.57	451.2557	901.51	-0.006	-6.7	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin
16048	dirMS_041712_NAR_30mM_plus2.11501.11501.2	2	7.43	0	3.61E+05		(R)NGDFLP	(R)N G|D/F/L/P T|R(L)		113.78	460.2391	919.463	0.0077	8.4	5.84	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
16049	dirMS_041712_NAR_30mM_plus2.15910.15910.2	2	7.43	0	4.35E+05		(R)MGPNIY	(R)M/G|P N I/Y E L/R(T)		136.43	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
16050	dirMS_041712_NAR_30mM_plus2.15967.15967.2	2	7.43	0	5.04E+05		(R)YLCGLG	(R)Y L/C G L/G A V G G V R(L)	C:Carbamidomethylation	137.02	611.3189	1221.641	-0.0103	-8.5	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
16051	dirMS_041712_NAR_30mM_plus2.7045.7045.2	2	7.43	0	1.34E+05		(K)YTQSNS	(K)Y T/Q/S N/S V\C Y/A K(N)	C:Carbamidomethylation	91.15	660.7963	1320.589	-0.0036	-2.7	8.5	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
16052	dirMS_041712_NAR_50mM_plus2.12708.12708.3	3	7.43	1	2.81E+05	S463s	(R)LRSsSEG	(R)L R S s/S E G T/A G/S/S R(M)	s:N-acetylglucosamine (S)	135.3	499.9106	1294.635	203.0827	2.2	9.6	73493.6	6.92	HUMAN	E7EUW0	Protein CCSER1
16053	dirMS_041712_NAR_50mM_plus2.16999.16999.3	3	7.43	1	3.71E+05		(K)LSKNEVL	(K)L S K N E V L M\V N\I/G/S/L/S/T G G R(V)		157	659.0229	1975.064	-0.0099	-5	8.75	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
16054	dirMS_041712_NAR_50mM_plus2.17651.17663.3	3	7.43	0	5.02E+05		(R)IMEIVD	(R)I M/E|I/V/D A I/T T T A Q S H Q R(T)		160.45	638.6636	1913.975	0.0013	0.7	5.32	94165.2	8.68	HUMAN	J3KNX3	6-phosphofructokinase
16055	dirMS_041712_NAR_50mM_plus2.5203.5203.3	3	7.43	0	5.44E+04	N22n	(K)AAAYPG	(K)A/A/A Y P/G V Y G S n G R(T)	n:N-acetylglucosamine (N)	86.15	495.9137	1282.618	203.1091	20	8.63	31114.6	5.53	HUMAN	B4DWS0	Nuclear receptor-binding factor 2
16056	dirMS_041712_NAR_50mM_plus2.6144.6144.3	3	7.43	1	1.12E+05		(R)VVSSIEC	(R)V V/S S I E Q K\T E/G A E K(K)		96.75	502.2651	1504.785	-0.0046	-3	4.79	8491.4	6.28	HUMAN	E5RIR4	14-3-3 protein zeta/delta (Fragment)
16057	dirMS_041712_NAR_50mM_plus2.7524.7524.3	3	7.43	0	1.09E+04		(K)VSYGIGI	(K)V/S Y/G/I/G D/E E H D/Q E G R(V)		105.67	564.2484	1690.73	0.0003	0.2	4.17	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
16058	dirMS_041712_NAR_50mM_plus2.7717.7717.3	3	7.43	0	6.60E+04	M378m M	(K)mIVDPV	(K)m/I/V D/P/V E/P H G/E m K(F)	m:Oxidized methionine	106.6	505.2419	1481.713	31.9984	5.7	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
16059	dirMS_041712_NAR_60mM_plus.13274.13274.3	3	7.43	1	5.62E+05		(R)LDDRVY	(R)L/D D/R V Y A|M C Q I K(S)	C:Carbamidomethylation	125.73	504.5817	1511.735	-0.0039	-2.6	5.96	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
16060	dirMS_041712_NAR_60mM_plus.13322.13322.3	3	7.43	1	2.72E+05		(K)YLPDIIKI	(K)Y/L|P D I/I K D Q K(A)		126.15	411.5685	1232.689	0.0024	2	5.96	59955.3	4.28	HUMAN	O15355	Protein phosphatase 1G
16061	dirMS_041712_NAR_120mM_minus.13504.13504.4	4	7.42	0	3.23E+05		(R)VLSAPPI	(R)V L S A/P P H F/H F G Q T N R(T)		127.85	427.7219	1707.871	-0.0056	-3.3	9.74	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
16062	dirMS_041712_NAR_120mM_minus.20413.20413.4	4	7.42	0	2.45E+05		(K)ALEHAF	(K)A L E H/A F\Q/L/E H I/M/D L/T R(L)		167.78	481.7478	1923.975	-0.0052	-2.7	5.27	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
16063	dirMS_041712_NAR_20mM_minus.13633.13633.2	2	7.42	0	2.30E+05		(K)LGGSAV	(K)L G G S|A V/I/S L E G K/P L(-)		187.87	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
16064	dirMS_041712_NAR_30mM_minus2.17048.17048.2	2	7.42	0	4.44E+04		(K)LGINSLC	(K)L/G I|N S/L/Q E L K(Q)		146.95	557.8242	1114.647	-0.0055	-5	6	25978.5	4.91	HUMAN	C9J502	Prostate leucine zipper variant 2
16065	dirMS_041712_NAR_30mM_minus2.6988.6988.2	2	7.42	0	2.66E+05	M169m	(R)MQSFG	(R)M Q|S F/G m/K(T)	m:Oxidized methionine	92.22	422.689	828.374	15.9965	1.8	8.5	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
16066	dirMS_041712_NAR_40mM_minus2.6013.6013.2	2	7.42	0	1.01E+06		(K)AGFAGD	(K)A G/F|A/G D/D A P R(A)		98.48	488.7279	976.448	0.0002	0.2	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
16067	dirMS_041712_NAR_40mM_minus2.6230.6230.3	3	7.42	0	5.09E+04		(R)EATNPP	(R)E A/T N/P/P V I Q E/E K P K(K)		102.47	527.2804	1579.833	-0.006	-3.8	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
16068	dirMS_041712_NAR_40mM_minus2.9177.9190.3	3	7.42	0	4.23E+05		(R)VAPDEH	(R)V A|P D E H\P I L L T E A/P L N P K(I)		137.07	652.0263	1954.064	-0.0001	0	4.65	42344.8	5.39	HUMAN	Q562R1	Beta-actin-like protein 2
16069	dirMS_041712_NAR_50mM_minus2.10121.10121.3	3	7.42	1	9.68E+04		(R)VGEPVA	(R)V G\E|P V/A/L S E E E R L K(L)		125.5	519.2824	1555.833	0	0	4.49	8516.9	5.1	HUMAN	E9PIL8	Splicing factor 3B subunit 2 (Fragment)
16070	dirMS_041712_NAR_50mM_minus2.14440.14440.3	3	7.42	1	1.40E+05		(R)GDVVPK	(R)G D V|V/P K D V N A A I A T I K(T)		150.42	537.6375	1610.911	-0.0133	-8.2	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
16071	dirMS_041712_NAR_50mM_minus2.16878.16878.3	3	7.42	0	2.46E+05		(R)LGIEGLS	(R)L/G\I/E G L/S L H N V L/K(L)		164.17	464.9452	1392.821	0.0001	0.1	6.75	177928	5.42	HUMAN	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1
16072	dirMS_041712_NAR_60mM_minus.14912.14912.3	3	7.42	0	3.31E+05		(R)AVAIDLF	(R)A V|A\I/D L/P/G L G H S K(E)		142.67	426.578	1277.721	-0.0018	-1.4	6.79	19983.6	8.14	HUMAN	B4DQI4	Alpha/beta hydrolase domain-containing protein 14B
16073	dirMS_041712_NAR_60mM_minus.17590.17590.3	3	7.42	1	4.27E+06		(R)VSFELFA	(R)V/S|F E L/F/A D K V/P K(T)		157.75	460.5911	1379.757	0.0018	1.3	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
16074	dirMS_041712_NAR_60mM_minus.4742.4742.3	3	7.42	1	6.70E+04		(K)DADSQ	(K)D A/D/S Q N/P/D/A P E G K R(S)		78.6	500.5629	1499.672	0.0021	1.4	4.23	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
16075	dirMS_041712_NAR_60mM_minus.8308.8308.3	3	7.42	1	8.21E+05	M174m	(R)VKYETEL	(R)V\K Y/E\T E|L/A m R(Q)	m:Oxidized methionine	106.05	419.2169	1239.64	15.996	0.8	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
16076	dirMS_041712_NAR_120mM_plus.10883.10883.3	3	7.42	0	3.79E+04		(K)NFYQEH	(K)N F/Y\Q E H/P/D L A/R(R)		110.25	463.8906	1389.655	0.0027	1.9	5.32	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
16077	dirMS_041712_NAR_120mM_plus.22581.22581.4	4	7.42	1	2.26E+05		(R)DTLYEA	(R)D T/L/Y E/A V R E/V L/H G N Q R(K)		171.92	475.7468	1899.967	-0.0018	-0.9	5.45	25002	10.06	HUMAN	P62906	60S ribosomal protein L10a
16078	dirMS_041712_NAR_20mM_plus.10869.10869.2	2	7.42	0	2.17E+05		(K)LVIITAG	(K)L V/I|I T A/G A R(Q)		147.98	457.2945	913.583	-0.0012	-1.3	9.75	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
16079	dirMS_041712_NAR_20mM_plus.13533.13533.2	2	7.42	0	4.19E+05	M148m	(R)DLTDYL	(R)D L|T/D/Y L m/K(I)	m:Oxidized methionine	164.95	507.7439	998.486	15.9942	-0.7	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
16080	dirMS_041712_NAR_20mM_plus.7712.7712.2	2	7.42	0	1.57E+05		(K)IAVAAQ	(K)I/A|V/A/A Q N C Y K(V)	C:Carbamidomethylation	122.43	569.2902	1137.572	0.001	0.9	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
16081	dirMS_041712_NAR_30mM_plus2.12923.12923.2	2	7.42	0	3.14E+05		(K)QQIQSI	(K)Q\Q/I|Q/S\I/Q/Q S I E R(L)		120.75	729.3893	1457.771	0.0006	0.4	6	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
16082	dirMS_041712_NAR_30mM_plus2.21038.21038.2	2	7.42	0	2.22E+05		(R)GVVQEL	(R)G V/V/Q E/L/Q|Q A I|S K(L)		165.42	650.3632	1299.727	-0.0076	-5.8	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
16083	dirMS_041712_NAR_30mM_plus2.6432.6432.2	2	7.42	0	2.52E+05		(K)GEGQLG	(K)G E|G Q|L/G/P A E R(A)		87.53	507.2537	1013.501	-0.0009	-0.9	4.53	96306.4	6.41	HUMAN	P13639	Elongation factor 2
16084	dirMS_041712_NAR_30mM_plus2.8981.8981.2	2	7.42	0	1.11E+05		(R)GVNTFS	(R)G V\N|T/F|S\P E G\R(L)		100.63	532.2579	1063.517	-0.0082	-7.7	6	26581.7	4.74	HUMAN	P28066	Proteasome subunit alpha type-5
16085	dirMS_041712_NAR_50mM_plus2.16225.16225.3	3	7.42	1	2.11E+06		(K)LLQDFF	(K)L L/Q/D F F/N/G K/E L\N K(S)		154.67	522.6137	1565.832	-0.0057	-3.6	6.07	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
16086	dirMS_041712_NAR_60mM_plus.11456.11456.3	3	7.42	1	1.93E+05		(K)TAVCDI	(K)T A|V/C/D/I/P P R G L K(M)	C:Carbamidomethylation	118	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
16087	dirMS_041712_NAR_60mM_plus.13005.13005.3	3	7.42	1	2.54E+05		(R)VVGAM	(R)V V|G|A M Q L/Y/S V D R K(V)		124.97	489.2643	1465.783	-0.0048	-3.3	8.56	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
16088	dirMS_041712_NAR_60mM_plus.15035.15035.3	3	7.42	0	5.61E+05		(R)YLDLHD	(R)Y/L/D/L/H D C Y L K(Y)	C:Carbamidomethylation	135	447.2169	1339.635	0.001	0.8	5.21	52796.2	5.19	HUMAN	E7EUT8	Splicing factor 3A subunit 3
16089	dirMS_041712_NAR_120mM_minus.20016.20016.3	3	7.41	1	2.47E+05		(R)AKFEEL	(R)A K\F E E\L|N/M/D/L/F R(S)		164.85	504.9216	1512.752	-0.0013	-0.8	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
16090	dirMS_041712_NAR_20mM_minus.8371.8371.2	2	7.41	0	1.25E+05		(K)VTADVI	(K)V T|A/D V|I N/A A E K(L)		132.47	565.8065	1130.605	0.0005	0.5	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
16091	dirMS_041712_NAR_30mM_minus2.7054.7054.2	2	7.41	0	1.24E+05		(K)CATITPD	(K)C A/T I/T/P D/E K(R)	C:Carbamidomethylation	93.68	517.7448	1034.482	0	0	4.37	17833.3	8.73	HUMAN	C9J4N6	Isocitrate dehydrogenase [NADP] cytoplasmic (Fragment)
16092	dirMS_041712_NAR_30mM_minus2.7220.7220.2	2	7.41	0	1.96E+04		(K)SAVLQE	(K)S A|V|L/Q\E A R(I)		93.53	437.2408	873.479	-0.0045	-5.2	5.72	28218.2	9.35	HUMAN	F6X838	Coatomer subunit gamma-2
16093	dirMS_041712_NAR_40mM_minus2.14477.14477.3	3	7.41	1	1.39E+05		(K)GTVPDD	(K)G T V/P D D A V/E A L/A D S L G K K(E)		170.27	595.9791	1785.923	-0.0001	-0.1	4.23	81397.3	4.99	HUMAN	B7Z468	Calpastatin
16094	dirMS_041712_NAR_50mM_minus2.12945.12945.3	3	7.41	1	5.62E+05		(K)VLAGDK	(K)V/L|A G D K N F I/T\A E E/L R(R)		142.62	559.3044	1675.901	-0.0027	-1.6	4.68	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
16095	dirMS_041712_NAR_50mM_minus2.9861.9861.3	3	7.41	1	8.96E+04		(R)ALRETLF	(R)A L R E T L|P/A E/Q\D L\T T K(N)		124.45	562.6354	1685.907	-0.0152	-9	4.68	26790	6.25	HUMAN	F5GX11	Proteasome subunit alpha type-1
16096	dirMS_041712_NAR_60mM_minus.12839.12839.3	3	7.41	1	1.97E+05		(K)LSAEKVE	(K)L/S/A E/K V E I A/T/L T R(E)		131.13	477.6112	1430.821	-0.0023	-1.6	6.14	26661.1	7.81	HUMAN	H0YL69	Proteasome subunit alpha type (Fragment)
16097	dirMS_041712_NAR_60mM_minus.13717.13717.3	3	7.41	0	3.78E+05		(-)MVNHFI	(-)M V/N/H/F/I A E|F K(R)		136.52	412.5461	1235.624	-0.0004	-0.3	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
16098	dirMS_041712_NAR_60mM_minus.15201.15201.2	2	7.41	0	4.20E+05		(R)EHALLA	(R)E H/A|L/L/A Y T L G V\K(Q)		144.65	657.873	1314.742	-0.0029	-2.2	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
16099	dirMS_041712_NAR_60mM_minus.6672.6672.3	3	7.41	0	4.07E+04		(K)VDCTAH	(K)V D/C/T A/H S D\V/C/S A Q G V R(G)	C:Carbamidomethylation	95.73	587.9248	1761.764	-0.0044	-2.5	5.21	41053.3	5.58	HUMAN	Q86UY0	TXNDC5 protein
16100	dirMS_041712_NAR_20mM_plus.13782.13782.2	2	7.41	0	4.19E+04		(K)IVLTNPV	(K)I V/L\T\N/P V/C T E V/G E K(I)	C:Carbamidomethylation	167.07	779.9082	1558.815	-0.0054	-3.5	4.53	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
16101	dirMS_041712_NAR_20mM_plus.14266.14266.2	2	7.41	0	8.76E+04		(K)GVVDSD	(K)G V V|D/S D D/L|P L N V S R(E)		170.28	743.3789	1485.754	-0.0038	-2.6	3.93	92752.5	4.76	HUMAN	P14625	Endoplasmin
16102	dirMS_041712_NAR_20mM_plus.15756.15756.3	3	7.41	0	8.77E+03		(R)SSFYVN	(R)S S F Y V N/G L/T/L G G/Q K(C)		179.37	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
16103	dirMS_041712_NAR_20mM_plus.17476.17476.3	3	7.41	0	6.85E+04		(K)LAAVDA	(K)L A A V D A T V/N Q V/L/A S R(Y)		192.37	509.9542	1527.849	-0.0009	-0.6	5.84	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
16104	dirMS_041712_NAR_20mM_plus.6870.6870.2	2	7.41	0	4.20E+05	M132m	(R)DmVGIA	(R)D m|V/G/I|A Q/T G S G K(T)	m:Oxidized methionine	112.85	590.2864	1163.573	15.993	-1.6	5.84	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
16105	dirMS_041712_NAR_30mM_plus2.12600.12600.2	2	7.41	0	6.43E+05		(R)LLVVTDI	(R)L L|V/V T D/P R(A)		119.08	456.779	912.551	-0.0006	-0.6	5.84	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
16106	dirMS_041712_NAR_40mM_plus2.14905.14905.3	3	7.41	0	8.33E+04		(R)LLIHQSL	(R)L L/I H Q\S L/A/G G I I/G V K(G)		154.33	506.9819	1518.937	-0.0055	-3.6	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
16107	dirMS_041712_NAR_40mM_plus2.15805.15805.3	3	7.41	0	1.62E+05		(K)VAIVKP	(K)V A|I V/K P G V|P M E I V L N K(E)		160.42	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
16108	dirMS_041712_NAR_40mM_plus2.15912.15912.3	3	7.41	1	7.42E+04		(K)VLDSGA	(K)V L/D S/G A/P I/K I\P V/G/P E/T L\G R(I)		160.05	640.3668	1919.096	-0.0102	-5.3	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
16109	dirMS_041712_NAR_40mM_plus2.16344.16344.3	3	7.41	1	3.74E+05		(R)CITDPQ	(R)C I/T D/P Q\T G L C L L/P L K E K(K)	C:Carbamidomethylation	163.12	662.6815	1986.04	-0.0099	-5	6.07	533778	5.74	HUMAN	Q15149	Plectin
16110	dirMS_041712_NAR_40mM_plus2.6417.6417.2	2	7.41	0	8.79E+03		(K)STMQEL	(K)S T/M/Q E L N S R(L)		96.93	533.2486	1065.499	-0.0094	-8.8	5.72	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
16111	dirMS_041712_NAR_40mM_plus2.6962.6962.2	2	7.41	0	7.26E+04		(R)LTEGCSI	(R)L/T|E/G C S/F R(R)	C:Carbamidomethylation	101	485.2217	969.446	-0.0097	-10	6	5988.9	10.55	HUMAN	C9J1C5	40S ribosomal protein S27
16112	dirMS_041712_NAR_40mM_plus2.9912.9912.2	2	7.41	0	2.38E+05		(K)EQFAWI	(K)E Q/F|A/W/R(H)		122.83	418.706	836.405	-0.0002	-0.3	6.1	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
16113	dirMS_041712_NAR_50mM_plus2.10156.10156.3	3	7.41	1	1.76E+05		(R)QELILSN	(R)Q E/L|I/L/S N S E/D K S I R(V)		121.43	544.624	1631.86	-0.0024	-1.5	4.68	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
16114	dirMS_041712_NAR_60mM_plus.13795.13795.3	3	7.41	0	7.04E+05		(K)VLSLNFS	(K)V L/S L/N F/S\E C H T K(I)	C:Carbamidomethylation	129.08	478.9108	1434.705	0.0133	9.3	6.72	16092.9	6.43	HUMAN	D6RAC7	Ras GTPase-activating protein-binding protein 2 (Fragment)
16115	dirMS_041712_NAR_60mM_plus.20916.20916.3	3	7.41	1	1.34E+05		(K)TFVNITP	(K)T F V|N/I T/P/A E V G V L V G K D R(S)		170.6	639.0248	1915.065	-0.0049	-2.6	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
16116	dirMS_041712_NAR_60mM_plus.21437.21437.3	3	7.41	1	3.68E+05		(R)ARDDLI	(R)A R D\D\L\I|T/D L/L N E A K(Q)		177.42	529.6165	1586.838	-0.0035	-2.2	4.23	23653.1	9.28	HUMAN	C9J8H1	V-type proton ATPase subunit E 1 (Fragment)
16117	dirMS_041712_NAR_120mM_minus.13149.13149.3	3	7.4	1	5.79E+05	M316m	(K)RISEQFT	(K)R I\S\E\Q/F/T/A m F\R(R)	m:Oxidized methionine	125.83	467.9028	1385.699	15.9944	-0.4	9.6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
16118	dirMS_041712_NAR_120mM_minus.9670.9670.3	3	7.4	1	3.82E+05		(K)YAGKDG	(K)Y/A|G K D G Y N/Y T L/S K(T)		107.43	493.9089	1479.711	0.0007	0.5	8.38	11854.4	6.57	HUMAN	P31949	Protein S100-A11
16119	dirMS_041712_NAR_20mM_minus.11748.11748.2	2	7.4	0	3.05E+05		(R)GALQNI	(R)G A L Q/N/I|I\P\A S T G A A K(A)		165.38	706.3976	1411.79	-0.0024	-1.7	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
16120	dirMS_041712_NAR_30mM_minus2.18456.18456.2	2	7.4	0	9.87E+03		(K)LNLGTV	(K)L N|L/G/T|V/G F Y R(T)		154.28	570.3115	1139.621	-0.005	-4.4	8.75	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
16121	dirMS_041712_NAR_30mM_minus2.8773.8773.2	2	7.4	0	2.07E+05		(K)QAEILQI	(K)Q A|E/I/L Q E/S/R(M)		102.72	537.2824	1073.559	-0.001	-1	4.53	15962.5	9.61	HUMAN	B4DT30	Tubulin-specific chaperone A
16122	dirMS_041712_NAR_40mM_minus2.7817.7817.3	3	7.4	0	8.08E+04		(K)TGVAVN	(K)T G V|A V/N K/P A E/F T V D/A K(H)		124.68	549.6354	1646.875	0.0168	10.2	5.73	283472.4	5.71	HUMAN	P21333	Filamin-A
16123	dirMS_041712_NAR_50mM_minus2.14609.14609.3	3	7.4	0	6.40E+04		(K)VVYTDVQ	(K)V/Y|T D\V/Q/Q/V A S S L/T H/P R(F)		151.52	600.976	1800.924	-0.0104	-5.8	6.71	74230.8	5.34	HUMAN	B1AH89	Tubulin tyrosine ligase-like family, member 12
16124	dirMS_041712_NAR_60mM_minus.10273.10273.3	3	7.4	1	1.31E+05		(K)TCVFEKI	(K)T C V/F/E K/E N D/P S V M/R(S)	C:Carbamidomethylation	117.3	571.2615	1711.778	-0.0079	-4.6	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
16125	dirMS_041712_NAR_60mM_minus.18505.18505.3	3	7.4	0	1.57E+05		(R)VTMLFL	(R)V T/M L/F/L G L H/N V R(Q)		164.85	467.2647	1399.788	-0.0083	-5.9	9.73	21721.5	5.37	HUMAN	H7BZ35	Aspartate--tRNA ligase, cytoplasmic (Fragment)
16126	dirMS_041712_NAR_120mM_plus.12882.12882.3	3	7.4	0	8.50E+05		(K)HYGPGV	(K)H Y G P G\W|V/S/M/A N A G K(D)		121.4	492.2383	1474.69	0.0108	7.3	8.6	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
16127	dirMS_041712_NAR_120mM_plus.18781.18781.3	3	7.4	2	4.45E+05		(R)KIEEIKDI	(R)K\I E\E/I K|D F L/L/T A R(R)		151.9	525.9746	1575.911	-0.0012	-0.8	6.18	2559	9.99	HUMAN	J3KSP2	60S ribosomal protein L38 (Fragment)

16128	dirMS_041712_NAR_120mM_plus.21173.21173.3	3	7.4	2	6.50E+05		(R)TLAEIAK	(R)T/L/A E I/A K V E L D N M/P L R G K(Q)		163.62	666.7047	1998.105	-0.0057	-2.8	5.85	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
16129	dirMS_041712_NAR_20mM_plus.10428.10428.2	2	7.4	0	1.08E+05		(K)VQISPDS	(K)V Q|I|S\P D S G G L/P E/R(S)		144.47	677.8458	1354.696	-0.0118	-8.7	4.37	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
16130	dirMS_041712_NAR_30mM_plus2.18531.18531.2	2	7.4	0	6.91E+05		(K)AAIDWF	(K)A A|I/D/W F/D G K(E)		150.73	511.7539	1022.494	0.0064	6.2	4.21	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
16131	dirMS_041712_NAR_30mM_plus2.20247.20247.2	2	7.4	0	3.58E+04		(R)TLMNLG	(R)T L/M/N/L/G G L A/V A/R(D)		159.42	608.3434	1215.688	-0.0083	-6.8	9.41	22562.2	8.8	HUMAN	P37802	Transgelin-2
16132	dirMS_041712_NAR_30mM_plus2.5602.5602.2	2	7.4	0	2.68E+05	M283m	(R)DYDDm	(R)D/Y|D\D m S\P R(R)	m:Oxidized methionine	84.22	507.6956	998.388	15.9955	0.6	3.93	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
16133	dirMS_041712_NAR_30mM_plus2.8540.8540.2	2	7.4	0	4.51E+05		(R)FAQIVQ	(R)F/A/Q/I V\Q K(G)		97.98	417.2466	833.488	-0.002	-2.4	8.75	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
16134	dirMS_041712_NAR_40mM_plus2.5729.5729.2	2	7.4	1	5.58E+04		(R)ARGDSE	(R)A R G D S E A L|D\E\E|S(-)		91.22	639.7736	1278.544	-0.0045	-3.5	3.83	74986.2	6.56	HUMAN	I3L080	Hepatoma-derived growth factor-related protein 2
16135	dirMS_041712_NAR_50mM_plus2.11425.11425.3	3	7.4	1	7.45E+05		(K)LAEQAE	(K)L/A|E/Q/A E R Y D\D M A A A M/K(A)		127.98	604.9469	1812.825	0.0007	0.4	4.32	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
16136	dirMS_041712_NAR_50mM_plus2.11524.11524.3	3	7.4	1	6.51E+05		(R)DVVICP	(R)D V|V/I/C/P D A S L E D A K K(E)	C:Carbamidomethylation	127.98	553.9467	1659.826	-0.0003	-0.2	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
16137	dirMS_041712_NAR_50mM_plus2.18863.18863.3	3	7.4	1	5.27E+05	M1m	(-)mDELQL	(-)m/D|E|L|Q L/F R/G D T V L L K(G)	m:Oxidized methionine	166.78	598.6527	1777.952	15.9919	-1.7	4.56	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
16138	dirMS_041712_NAR_50mM_plus2.20099.20099.3	3	7.4	0	5.36E+05		(R)QARPTY	(R)Q A R P T Y A/T|A M|L Q|S L/L K(-)		174.55	597.9962	1791.979	-0.0045	-2.5	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
16139	dirMS_041712_NAR_50mM_plus2.20629.20629.3	3	7.4	1	4.37E+04		(K)GKLPIV	(K)G K L\P I V\N E/D D E L\V|A/I/I A/R(T)		177.43	655.7032	1965.102	-0.0065	-3.3	4.32	30838.7	4.9	HUMAN	E7ETK5	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
16140	dirMS_041712_NAR_50mM_plus2.6648.6648.3	3	7.4	1	3.80E+05		(R)IVDGKV	(R)I/V\D/G/K/V/V/S E T N D/T K(V)		100.3	502.2651	1504.785	-0.0046	-3	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
16141	dirMS_041712_NAR_50mM_plus2.8950.8950.3	3	7.4	0	1.80E+05		(K)TPVEPE	(K)T P V E P E\V/A/I/H R(I)		113.98	416.5627	1247.674	-0.0007	-0.6	5.37	5429.1	9.6	HUMAN	E5RIP1	40S ribosomal protein S20
16142	dirMS_041712_NAR_50mM_plus2.8955.8955.3	3	7.4	1	2.37E+04		(R)GGSDDS	(R)G G\S\D D S S K D P\I|D/V/N Y E K(L)		114.08	609.2765	1825.809	0.0063	3.5	4.03	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
16143	dirMS_041712_NAR_60mM_plus.12208.12208.3	3	7.4	1	1.23E+06		(R)LNDSIL	(R)L/N|D/S/I L Q/A T E Q R R(R)		120.47	515.2771	1543.819	-0.0019	-1.3	6.07	334221.3	6.44	HUMAN	P15924	Desmoplakin
16144	dirMS_041712_NAR_60mM_plus.18916.18916.3	3	7.4	0	1.64E+05		(R)NHPGLL	(R)N H/P G L\L\L/M/D T|T F R(D)		156.68	505.6001	1514.778	0.0073	4.8	6.74	130372.9	6.37	HUMAN	P11498	Pyruvate carboxylase, mitochondrial
16145	dirMS_041712_NAR_120mM_minus.12755.12755.3	3	7.39	1	2.32E+05		(R)NKQEV	(R)N K Q E V M|I|S D|L E E/R(L)		123.53	530.9318	1590.779	0.0016	1	4.41	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
16146	dirMS_041712_NAR_120mM_minus.14920.14920.2	2	7.39	0	7.65E+05		(R)DWSHY	(R)D W/S/H/Y/F K(I)		135	491.725	982.442	0.001	1	6.74	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
16147	dirMS_041712_NAR_20mM_minus.11123.11123.2	2	7.39	0	1.10E+05	M316m	(R)ISEQFTA	(R)I/S|E Q F/T A m/F R(R)	m:Oxidized methionine	159.05	623.3005	1229.598	15.9954	0.4	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
16148	dirMS_041712_NAR_50mM_minus2.14183.14183.3	3	7.39	1	6.62E+05		(R)VEKIPG	(R)V/E\K I\P G G I\I/E/D S C V\L R(G)	C:Carbamidomethylation	149.1	595.6534	1784.958	-0.0118	-6.6	4.68	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
16149	dirMS_041712_NAR_50mM_minus2.18170.18170.3	3	7.39	1	2.53E+05		(K)LKEAELL	(K)L K E A E L\L|E|P L/M/P A I R(A)		172.67	574.9957	1722.982	-0.0097	-5.6	4.79	56164.6	6.01	HUMAN	E9PP73	Coatomer subunit beta (Fragment)
16150	dirMS_041712_NAR_60mM_minus.18316.18316.3	3	7.39	0	5.10E+03		(R)EYFSWE	(R)E Y F|S/W/E G A F Q|H V G K(A)		163.38	562.2608	1684.775	-0.0076	-4.5	5.4	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
16151	dirMS_041712_NAR_60mM_minus.7746.7746.3	3	7.39	1	5.37E+05		(R)YLAEVA	(R)Y/L/A E/V A/A G D D K K(G)		102.12	427.222	1279.653	-0.0014	-1.1	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
16152	dirMS_041712_NAR_120mM_plus.7839.7839.3	3	7.39	1	2.90E+05		(R)IADEDR	(R)I/A/D/E D R G N/W/R(H)		94.67	411.1986	1231.581	-0.0002	-0.1	4.56	163032.4	6.38	HUMAN	F5H335	Eukaryotic translation initiation factor 3 subunit A
16153	dirMS_041712_NAR_20mM_plus.10208.10208.3	3	7.39	0	1.21E+05	M281m M	(R)NmPQA	(R)N m/P Q A D\A m/V/L/V/A R(N)	m:Oxidized methionine	143.32	483.2393	1415.713	31.99	0.1	5.84	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
16154	dirMS_041712_NAR_20mM_plus.18359.18359.3	3	7.39	0	7.14E+04		(K)ITSEALL	(K)I T S E A L L|V|T Q Q L V K(A)		198.2	514.9762	1542.91	0.0039	2.5	6	50425	5.53	HUMAN	H0YH27	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
16155	dirMS_041712_NAR_20mM_plus.18973.18973.3	3	7.39	0	1.81E+05		(K)TLETQS	(K)T L E\T Q S A/L/G/P A L/Q A A F K(L)		202.42	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
16156	dirMS_041712_NAR_20mM_plus.19130.19130.2	2	7.39	0	1.45E+05		(R)EGDVLT	(R)E G\D V|L/T/L L/E/S E R(E)		203.45	680.8536	1360.696	0.0045	3.3	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
16157	dirMS_041712_NAR_30mM_plus2.10365.10365.2	2	7.39	0	4.28E+05		(K)EQVANS	(K)E Q|V/A/N S A/F/V/E R(C)		107.43	625.311	1249.617	-0.0024	-1.9	4.53	17664	8.77	HUMAN	H0Y6E4	Heat shock protein HSP 90-beta (Fragment)
16158	dirMS_041712_NAR_30mM_plus2.4266.4266.2	2	7.39	0	4.73E+05	M558m	(R)mGANN	(R)m/G\A/N N/L E R(M)	m:Oxidized methionine	70.22	460.7158	904.431	15.9938	-1.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
16159	dirMS_041712_NAR_40mM_plus2.14603.14603.3	3	7.39	1	8.74E+04	S48s	(K)VTAIKsL	(K)V T A/I/K s L S I E I G H E V K(T)	s:N-acetylglucosamine (S)	153.33	643.0301	1723.995	203.0805	0.6	6.73	11113.3	6.73	HUMAN	C9JTT8	BET1 homolog
16160	dirMS_041712_NAR_50mM_plus2.10959.10959.3	3	7.39	0	1.94E+05		(K)ADDGR	(K)A/D/D G R P F P Q V/I/K(S)		125.1	448.2419	1342.711	-0.0002	-0.2	6	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
16161	dirMS_041712_NAR_50mM_plus2.13283.13283.3	3	7.39	1	2.49E+05		(R)GYISPYF	(R)G Y/I|S/P Y F I N T S K G Q/K(C)		137.03	568.292	1702.88	-0.0185	-10.8	9.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
16162	dirMS_041712_NAR_60mM_plus.18969.18969.3	3	7.39	1	2.62E+05		(K)YGKLEV	(K)Y/G K L E V A/N L/L/L Q K(S)		156.68	496.9628	1488.878	-0.0046	-3.1	8.5	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
16163	dirMS_041712_NAR_60mM_plus.21156.21156.3	3	7.39	0	1.67E+05		(K)NGGLG	(K)N G\G L/G/H M N I\A/L/L/S D/L T K(Q)		174.03	585.3126	1753.927	-0.0033	-1.9	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
16164	dirMS_041712_NAR_60mM_plus.7161.7161.3	3	7.39	1	1.52E+07		(R)AAPGAE	(R)A A/P G A E F/A/P N K R(R)		96.27	410.2195	1228.643	0.0007	0.5	8.79	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
16165	dirMS_041712_NAR_20mM_minus.10961.10961.2	2	7.38	0	1.62E+05		(K)IDIIPNP	(K)I/D I|I/P/N P Q E R(T)		157.43	597.8271	1194.648	-0.0008	-0.7	4.37	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
16166	dirMS_041712_NAR_20mM_minus.14650.14650.2	2	7.38	0	5.20E+03		(K)TLFPLIE	(K)T L|F/P L/I E A K(K)		201.18	516.3086	1031.614	-0.0036	-3.5	5.66	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
16167	dirMS_041712_NAR_30mM_minus2.11543.11543.2	2	7.38	0	2.45E+04		(K)FSASGEL	(K)F/S|A/S G/E/L/G N G N I/K(L)		116.38	647.3253	1293.643	0	0	6	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
16168	dirMS_041712_NAR_30mM_minus2.8078.8078.2	2	7.38	0	4.16E+05		(K)IYSSEAI	(K)I/Y/S S/E A I K(S)		97.97	455.7458	910.488	-0.0037	-4.1	6	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
16169	dirMS_041712_NAR_30mM_minus2.8111.8111.2	2	7.38	0	1.83E+05		(K)GSGTAE	(K)G S|G T/A/E V/E L K(K)		98.32	495.7528	990.51	-0.0119	-12	4.53	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
16170	dirMS_041712_NAR_40mM_minus2.6916.6916.2	2	7.38	0	6.99E+04	M239m	(K)EITALAP	(K)E I T\A/L/A/P/S T m K(I)	m:Oxidized methionine	111.13	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
16171	dirMS_041712_NAR_50mM_minus2.13027.13027.3	3	7.38	1	1.05E+06	M320m	(K)YmACCL	(K)Y m|A C C L L Y/R G D\V V/P K(E)	C:Carbamidomethylation m:Oxid	141.47	620.9644	1844.886	15.9931	-1	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
16172	dirMS_041712_NAR_60mM_minus.10583.10583.3	3	7.38	0	2.57E+05		(R)SVIHSLA	(R)S V I/H/S L A\S/V/E A/Q K(S)		119.02	456.9195	1368.748	-0.0042	-3.1	6.47	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
16173	dirMS_041712_NAR_120mM_plus.14952.14952.2	2	7.38	0	3.41E+06		(R)DWSHY	(R)D/W/S H Y\F|K(I)		132.02	491.725	982.442	0.001	1	6.74	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
16174	dirMS_041712_NAR_20mM_plus.12860.12860.2	2	7.38	0	3.77E+05		(K)LSELEAA	(K)L S|E L/E A A|L Q/R(A)		161.72	565.3132	1129.621	-0.002	-1.8	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
16175	dirMS_041712_NAR_40mM_plus2.12061.12061.3	3	7.38	0	5.05E+04	T300t	(R)LLAGtQ	(R)L L/A G t Q D S E/I F E V I V R(E)	t:N-acetylglucosamine (T)	137.88	665.0257	1789.969	203.0931	6.9	4.14	220405.8	7.24	HUMAN	Q6ZMW3	Echinoderm microtubule-associated protein-like 6
16176	dirMS_041712_NAR_50mM_plus2.16805.16805.3	3	7.38	1	1.87E+05	M132m	(R)TLAEIAK	(R)T L|A\E\I/A K V E|L D N m P L R(G)	m:Oxidized methionine	155.92	610.3302	1812.989	15.9873	-4.2	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
16177	dirMS_041712_NAR_50mM_plus2.17417.17417.3	3	7.38	0	4.75E+05		(R)DLISHDE	(R)D L|I/S/H D E M F/S D I Y K(I)		160.08	571.5992	1712.784	-0.0006	-0.3	4.22	19709.1	4.83	HUMAN	P13693	Translationally-controlled tumor protein
16178	dirMS_041712_NAR_60mM_plus.14571.14796.3	3	7.38	1	1.26E+06		(K)FSIEDLK	(K)F/S/I/E D/L K A Q P K(Q)		132.38	425.898	1275.694	-0.0149	-11.7	6.07	13579.2	9.99	HUMAN	E9PPQ6	Thymocyte nuclear protein 1 (Fragment)
16179	dirMS_041712_NAR_60mM_plus.19903.19903.3	3	7.38	1	2.07E+05		(R)SLVQEM	(R)S L|V\Q/E/M V G S/F G K R(D)		164.38	479.9219	1437.752	-0.0007	-0.5	8.46	71929.1	5.1	HUMAN	C9JAQ9	U5 small nuclear ribonucleoprotein 200 kDa helicase
16180	dirMS_041712_NAR_60mM_plus.20633.20633.3	3	7.38	1	7.00E+05		(K)IKYPENF	(K)I/K/Y P E N F|F/L L R(G)		167.98	480.6056	1439.805	-0.0023	-1.6	8.59	33222.3	5.74	HUMAN	A6NNR3	Serine/threonine-protein phosphatase
16181	dirMS_041712_NAR_60mM_plus.21564.21564.3	3	7.38	1	5.66E+05		(K)EIIDLVL	(K)E I/I/D/L V L D R I R(K)		180.53	452.2733	1354.805	0.0001	0.1	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
16182	dirMS_041712_NAR_60mM_plus.9219.9219.3	3	7.38	1	9.57E+05		(K)YAGKDG	(K)Y/A/G K D G Y|N Y T/L S K(T)		106.32	493.9098	1479.711	0.0034	2.3	8.38	11854.4	6.57	HUMAN	P31949	Protein S100-A11
16183	dirMS_041712_NAR_30mM_minus2.5794.5937.2	2	7.37	0	7.31E+05		(K)YAEAVTI	(K)Y/A|E|A/V T/R(A)		86.68	405.2098	809.415	-0.0029	-3.5	6	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
16184	dirMS_041712_NAR_50mM_minus2.10700.10700.3	3	7.37	1	3.79E+05		(R)DVVICP	(R)D V|V I/C/P D A S/L E D A K K(E)	C:Carbamidomethylation	128.73	553.9474	1659.826	0.0018	1.1	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
16185	dirMS_041712_NAR_50mM_minus2.4939.4939.3	3	7.37	1	4.33E+05		(R)AAEDDE	(R)A/A\E/D D E/D D D V/D T K K(Q)		82.37	522.5522	1565.645	-0.0029	-1.8	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
16186	dirMS_041712_NAR_50mM_minus2.5619.5619.3	3	7.37	1	9.00E+03		(K)DSYVGD	(K)D S\Y/V/G D E A Q/S K R(G)		92.38	452.2119	1354.623	-0.0022	-1.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
16187	dirMS_041712_NAR_60mM_minus.13796.13796.3	3	7.37	0	1.42E+05		(K)ADFCIIH	(K)A D/F/C I I/H/Y/A G K(V)	C:Carbamidomethylation	137.43	432.2132	1294.625	0.0002	0.1	6.79	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
16188	dirMS_041712_NAR_60mM_minus.18443.18443.3	3	7.37	1	7.22E+04		(K)AKIGLIQ	(K)A K\I G L\I|Q/F/C L S/A P/K(T)	C:Carbamidomethylation	164.15	515.9647	1545.882	-0.0026	-1.7	10	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
16189	dirMS_041712_NAR_120mM_plus.11534.11534.4	4	7.37	2	5.81E+05		(K)KGEKDI	(K)K\G E K D I P G L\T D T/T/V/P/R(R)		113.53	432.4918	1726.933	0.012	6.9	6.12	25082	11.29	HUMAN	A2A3R5	40S ribosomal protein S6
16190	dirMS_041712_NAR_20mM_plus.18489.18489.2	2	7.37	0	7.71E+04		(R)VVVLGLI	(R)V V/V/L/G L\L P R(G)		198.88	483.3247	965.651	-0.0085	-8.8	9.72	25847.9	6.33	HUMAN	Q15102	Platelet-activating factor acetylhydrolase IB subunit gamma
16191	dirMS_041712_NAR_20mM_plus.18603.18603.2	2	7.37	0	1.51E+05		(R)IITLTGP	(R)I I/T L T/G/P T N/A I F K(A)		200.27	694.9091	1388.815	-0.0039	-2.8	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
16192	dirMS_041712_NAR_20mM_plus.6425.6425.2	2	7.37	0	2.02E+05	M216m	(R)DLmACA	(R)D L|m/A C A Q|T G S/G K(T)	C:Carbamidomethylation m:Oxid	107.72	627.776	1238.55	15.9943	-0.5	5.84	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
16193	dirMS_041712_NAR_30mM_plus2.15395.15395.2	2	7.37	0	9.68E+05		(K)LWNTLG	(K)L/W|N T L\G V/C/K(Y)	C:Carbamidomethylation	132.68	545.7923	1090.571	0.0059	5.5	8.75	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
16194	dirMS_041712_NAR_30mM_plus2.17171.17171.2	2	7.37	0	3.12E+05		(K)SFNLSAL	(K)S\F/N/L/S/A L E/K(H)		143.32	504.7726	1008.536	0.0019	1.9	5.72	82756.6	5.34	HUMAN	C9JIF9	Acylamino-acid-releasing enzyme
16195	dirMS_041712_NAR_50mM_plus2.10620.10620.3	3	7.37	0	4.86E+05		(K)MIVDPV	(K)M I|V D/P V E P H G E M/K(F)		123.28	494.5783	1481.713	0.0076	5.2	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
16196	dirMS_041712_NAR_50mM_plus2.17897.17898.3	3	7.37	1	1.98E+05		(K)VLTLSD	(K)V/L\T|L/S D D/L E R T I E E/R(V)		162.37	596.9838	1788.934	0.0031	1.7	4.18	49678.3	5.41	HUMAN	P55010	Eukaryotic translation initiation factor 5
16197	dirMS_041712_NAR_50mM_plus2.18340.18358.3	3	7.37	1	3.49E+05		(R)GDSVIV	(R)G D/S/V I/V V/L R N P L I/A/G K(-)		165.37	550.9999	1650.99	-0.005	-3	8.75	6144.3	10.23	HUMAN	K7EJB5	Small nuclear ribonucleoprotein Sm D2
16198	dirMS_041712_NAR_60mM_plus.7247.7247.3	3	7.37	1	4.98E+05		(K)TIIQNPT	(K)T I/I/Q/N/P T D Q Q K K(D)		95.72	471.9324	1413.77	0.013	9.2	8.26	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
16199	dirMS_041712_NAR_120mM_minus.13868.13868.4	4	7.36	1	1.62E+06		(K)ASIHEA	(K)A/S|I/H E A W/T D/G K E A M L K(H)		129.97	447.476	1786.879	0.0029	1.6	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
16200	dirMS_041712_NAR_30mM_minus2.12520.12520.2	2	7.36	0	7.59E+05		(R)GVVGPE	(R)G V|V/G/P E L Y G R(L)		122.5	523.7834	1046.563	-0.0034	-3.2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
16201	dirMS_041712_NAR_30mM_minus2.17213.17213.2	2	7.36	0	1.03E+05		(R)NGGQIL	(R)N G\G/Q/I/L I/A/D L R(G)		147.92	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
16202	dirMS_041712_NAR_30mM_minus2.5175.5175.2	2	7.36	0	5.62E+05		(R)TDTGEP	(R)T D|T|G E P M/G/R(G)		81.8	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
16203	dirMS_041712_NAR_30mM_minus2.7491.7491.2	2	7.36	0	5.49E+04		(R)GAEQLA	(R)G/A\E|Q/L\A|E G G R(M)		95.05	494.2466	987.485	0.0005	0.5	4.53	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b
16204	dirMS_041712_NAR_50mM_minus2.16059.16059.3	3	7.36	1	8.40E+04		(K)LQVDAL	(K)L Q/V D/A/L I/D T I K K(S)		159.23	452.9385	1356.81	-0.0087	-6.4	5.96	234333.2	6.01	HUMAN	J3KNX9	Unconventional myosin-XVIIIa
16205	dirMS_041712_NAR_60mM_minus.15623.15623.3	3	7.36	1	3.12E+05		(K)VAAIRGI	(K)V/A\A I R G E V\T A/A|D L/F N S/R(V)		147.35	597.3237	1789.956	0.001	0.6	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
16206	dirMS_041712_NAR_60mM_minus.15663.15663.3	3	7.36	1	1.72E+05		(R)GRLPLL	(R)G R L P\L\L|A/V/C D Y K(Q)	C:Carbamidomethylation	146.87	468.9273	1404.767	0.0006	0.4	8.59	533778	5.74	HUMAN	Q15149	Plectin
16207	dirMS_041712_NAR_60mM_minus.19948.19948.3	3	7.36	1	8.17E+05		(R)LIALLEVI	(R)L I|A\L L/E V L S Q K R(M)		182.02	461.6287	1382.873	-0.0014	-1	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
16208	dirMS_041712_NAR_60mM_minus.6372.6372.3	3	7.36	0	5.08E+04		(R)CPPGVV	(R)C P|P G V V/P A/C H N S K(D)	C:Carbamidomethylation	94.08	474.8938	1422.662	0.0052	3.6	8.76	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
16209	dirMS_041712_NAR_20mM_plus.13563.13563.2	2	7.36	0	2.03E+05		(R)GDLGIEI	(R)G D|L/G/I|E I/P/A E K(V)		166.5	571.3075	1141.61	-0.0022	-1.9	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
16210	dirMS_041712_NAR_20mM_plus.14884.14884.2	2	7.36	0	1.98E+05	M179m M	(K)mFVLDE	(K)m F V|L/D/E A D/E m L/S R(G)	m:Oxidized methionine	173.6	794.3555	1555.713	31.9906	0.5	3.91	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
16211	dirMS_041712_NAR_30mM_plus2.10409.10409.2	2	7.36	0	1.89E+04		(K)SMSTEG	(K)S M|S|T E G L M K(F)		108.35	492.2338	983.454	0.0067	6.8	5.72	50659.2	7.87	HUMAN	B4DJV2	Citrate synthase
16212	dirMS_041712_NAR_30mM_plus2.21952.21952.2	2	7.36	0	1.38E+05		(K)ETLLAM	(K)E T\L/L/A/M F/K(Y)		170.97	476.7621	952.517	-0.0003	-0.3	6.1	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
16213	dirMS_041712_NAR_30mM_plus2.4920.4920.2	2	7.36	0	7.22E+05		(R)MGQT	(R)M/G\Q|T/M E/R(I)		77.33	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
16214	dirMS_041712_NAR_30mM_plus2.9422.9422.2	2	7.36	0	5.75E+04		(K)TAVCDI	(K)T A|V/C/D/I/P\P/R(G)	C:Carbamidomethylation	104.02	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
16215	dirMS_041712_NAR_40mM_plus2.11001.11001.3	3	7.36	1	6.32E+04		(K)VAVVAG	(K)V/A|V|V A/G Y G D V G K G C A Q A\L R(G)	C:Carbamidomethylation	131.05	630.9981	1890.985	-0.0057	-3	8.56	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
16216	dirMS_041712_NAR_40mM_plus2.12907.12907.2	2	7.36	0	1.27E+05		(K)YMACCL	(K)Y/M|A|C|C L/L Y R(G)	C:Carbamidomethylation	141.87	625.28	1249.553	0.0001	0.1	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
16217	dirMS_041712_NAR_40mM_plus2.5796.5796.2	2	7.36	0	3.81E+04		(K)ESPQEIA	(K)E S/P/Q/E/I/A/R(K)		92.07	465.2357	929.469	-0.0046	-4.9	4.53	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
16218	dirMS_041712_NAR_50mM_plus2.14069.14069.3	3	7.36	1	4.33E+05		(R)NVIFQP	(R)N V/I F Q|P V A E L K K(Q)		142.2	462.6094	1385.815	-0.0015	-1.1	8.59	23167	8.94	HUMAN	B1APP8	6-phosphofructokinase type C
16219	dirMS_041712_NAR_50mM_plus2.15374.15374.3	3	7.36	1	1.09E+05		(R)VEKIPG	(R)V E K I P G G I|I/E/D/S C V|L R(G)	C:Carbamidomethylation	147.53	595.6548	1784.958	-0.0076	-4.3	4.68	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
16220	dirMS_041712_NAR_50mM_plus2.19897.19897.3	3	7.36	1	2.46E+05		(K)LLLEGVE	(K)L L/L/E/G V E N K L I/P/G L K(I)		172.92	546.0037	1636.004	-0.0078	-4.8	6.14	59384	7.79	HUMAN	B7Z3Z9	Long-chain-fatty-acid--CoA ligase 1
16221	dirMS_041712_NAR_50mM_plus2.20454.20454.3	3	7.36	1	2.58E+05		(R)GGPNIIT	(R)G G/P|N I I/T L\A D I/V K D P V S R(T)		176.63	622.3526	1865.049	-0.0058	-3.1	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
16222	dirMS_041712_NAR_60mM_plus.10317.10317.3	3	7.36	1	8.18E+05		(K)TAVCDI	(K)T A|V/C D I/P P R G L/K(M)	C:Carbamidomethylation	111.95	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
16223	dirMS_041712_NAR_60mM_plus.11730.11730.3	3	7.36	0	2.77E+05		(K)VAKPVV	(K)V A K\P V V\E M/D\G/D E M T R(I)		118.25	559.6022	1676.798	-0.0062	-3.7	4.32	35557.8	9.19	HUMAN	H0YL11	Isocitrate dehydrogenase [NADP], mitochondrial
16224	dirMS_041712_NAR_120mM_minus.11752.11752.4	4	7.35	1	3.82E+05		(R)DFTVSAI	(R)D F\T/V/S A M/H/G D M D Q K/E R(D)		118.4	467.458	1866.811	-0.0007	-0.4	4.66	26945.8	8.07	HUMAN	J3KSZ0	Eukaryotic initiation factor 4A-I (Fragment)
16225	dirMS_041712_NAR_20mM_minus.10295.10295.2	2	7.35	0	6.93E+04		(K)AVLSLYA	(K)A V|L/S/L/Y/A S\G R(T)		152.43	518.7929	1036.579	0	0	8.79	14579.3	5.13	HUMAN	K7EM38	Actin, cytoplasmic 2, N-terminally processed (Fragment)
16226	dirMS_041712_NAR_20mM_minus.13635.13635.2	2	7.35	0	8.82E+04		(K)FIIPNVV	(K)F I|I/P N V V K(Y)		186.48	465.294	929.582	-0.0011	-1.2	8.75	17529.3	9.3	HUMAN	F5GXY2	L-lactate dehydrogenase A chain (Fragment)
16227	dirMS_041712_NAR_20mM_minus.14522.14522.3	3	7.35	0	4.72E+03		(R)AAVEEG	(R)A A V E E G I|V/L/G G/G C/A L L R(C)	C:Carbamidomethylation	199.5	562.3053	1684.905	-0.0037	-2.2	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
16228	dirMS_041712_NAR_20mM_minus.14711.14711.2	2	7.35	0	8.96E+05		(K)EIIDLVL	(K)E I|I/D L V/L D R(I)		202.87	543.3133	1085.62	-0.0008	-0.7	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
16229	dirMS_041712_NAR_30mM_minus2.13783.13783.2	2	7.35	0	3.41E+05		(K)TIFQGIA	(K)T I|F Q/G I A/A K(V)		128.78	474.7782	948.551	-0.0022	-2.3	8.41	52385	7.18	HUMAN	B4DQJ8	6-phosphogluconate dehydrogenase, decarboxylating
16230	dirMS_041712_NAR_30mM_minus2.18020.18020.2	2	7.35	0	3.25E+04		(R)GLFIIDD	(R)G L F\I/I/D/D/K(G)		151.48	460.7585	920.509	0.001	1	4.21	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
16231	dirMS_041712_NAR_30mM_minus2.9302.9302.2	2	7.35	0	6.79E+04		(R)CSEQVQ	(R)C S/E/Q/V/Q/D|F\T K(C)	C:Carbamidomethylation	105.07	621.2773	1241.547	0.0006	0.5	4.37	13533.5	9.82	HUMAN	H7C3D8	COX assembly mitochondrial protein homolog (Fragment)
16232	dirMS_041712_NAR_30mM_minus2.9551.9551.2	2	7.35	0	1.74E+05		(K)QTTCW	(K)Q T/T/C/W/D\G V R(N)	C:Carbamidomethylation	106.35	561.7582	1122.5	0.0095	8.4	5.84	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1
16233	dirMS_041712_NAR_40mM_minus2.8053.8053.3	3	7.35	1	3.06E+05		(R)DGKLVS	(R)D G K L\V\S E/S\S D V L/P K(-)		128.17	491.9311	1473.78	-0.0008	-0.5	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
16234	dirMS_041712_NAR_50mM_minus2.10600.10600.3	3	7.35	0	1.70E+05		(R)LLELGPK	(R)L L/E/L G P K/P E V A Q Q T R(K)		128.62	560.3182	1678.949	-0.0086	-5.1	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
16235	dirMS_041712_NAR_50mM_minus2.10777.10777.3	3	7.35	1	2.03E+04		(K)ELALQP	(K)E L/A L Q/P K D D I/V/D R(A)		128.23	504.6068	1511.806	-0.0006	-0.4	4.23	83905.8	6.62	HUMAN	P41250	Glycine--tRNA ligase
16236	dirMS_041712_NAR_50mM_minus2.12750.12750.3	3	7.35	0	3.41E+06	M84m	(K)YPIEHGI	(K)Y/P I E H G I I\T/N|W D/D m E K(I)	m:Oxidized methionine	141.47	659.6398	1960.911	15.9939	-0.5	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle

16237	dirMS_041712_NAR_50mM_minus2.7062.7062.3	3	7.35	0	2.09E+05		(K)VSYGIG	(K)V/S|Y/G I G D E E H D Q E G R(V)		106.65	564.249	1690.73	0.0021	1.3	4.17	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
16238	dirMS_041712_NAR_60mM_minus.7576.7576.3	3	7.35	1	1.82E+05		(K)DSIKLD	(K)D S|I K L/D D/D/S E R(K)		101.43	431.5388	1292.597	0.0054	4.2	4.04	6116.1	5.2	HUMAN	F5H6I6	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
16239	dirMS_041712_NAR_120mM_plus.15311.15311.4	4	7.35	1	1.45E+06		(R)VKPAPD	(R)V K P A P D E/T/S F/S/E A L/L K/R(N)		133.42	472.7599	1888.017	0.0003	0.2	6.15	43289.6	5.19	HUMAN	Q12905	Interleukin enhancer-binding factor 2
16240	dirMS_041712_NAR_20mM_plus.10413.10413.2	2	7.35	0	1.05E+05	M267m	(R)LITLEEE	(R)L I/T|L/E E/E m T K(Y)	m:Oxidized methionine	145.1	611.8175	1206.629	15.9991	3.4	4.25	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
16241	dirMS_041712_NAR_20mM_plus.10987.10987.2	2	7.35	0	1.28E+05		(K)LAEYVIT	(K)L/A E/Y V I/T K(S)		148.33	468.7674	936.54	-0.0125	-13.4	6	236508.3	9.06	HUMAN	E7EUA9	Neuron navigator 3
16242	dirMS_041712_NAR_20mM_plus.11144.11144.2	2	7.35	0	1.22E+05		(K)TIVFVET	(K)T I|V/F/V E/T K(R)		148.37	468.7674	936.54	-0.0125	-13.4	5.66	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
16243	dirMS_041712_NAR_20mM_plus.15358.15358.3	3	7.35	0	5.59E+03		(K)VGINYQ	(K)V G I N Y Q/P/P T V/V/P G G D L A K(V)		178.02	608.9991	1824.985	-0.0027	-1.5	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
16244	dirMS_041712_NAR_20mM_plus.15741.15741.2	2	7.35	0	1.11E+05		(K)SILFVPT	(K)S I L/F V/P T S A P R(G)		180.28	594.3403	1187.678	-0.005	-4.2	9.47	92752.5	4.76	HUMAN	P14625	Endoplasmin
16245	dirMS_041712_NAR_20mM_plus.8206.8206.2	2	7.35	0	1.06E+05		(K)VTEDTS	(K)V/T|E/D/T S S V L R(S)		126.02	553.7889	1106.569	0.0017	1.6	4.37	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
16246	dirMS_041712_NAR_30mM_plus2.17125.17125.2	2	7.35	0	2.27E+05		(K)ACGNF	(K)A C|G N/F|G/I\P C E L R(V)	C:Carbamidomethylation	142.65	697.3237	1393.635	0.005	3.6	6.05	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
16247	dirMS_041712_NAR_30mM_plus2.21814.21814.2	2	7.35	0	8.69E+04		(K)GLVQAL	(K)G L V Q A|L/G L|S N F\N S R(Q)		169.52	738.3989	1475.796	-0.006	-4.1	9.75	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
16248	dirMS_041712_NAR_30mM_plus2.6280.6280.2	2	7.35	0	3.88E+05		(R)QIDNPD	(R)Q\I/D/N/P D/Y K(G)		87.23	496.7371	992.468	-0.0014	-1.4	4.21	28545.1	4.5	HUMAN	K7EJB9	Calreticulin (Fragment)
16249	dirMS_041712_NAR_50mM_plus2.14088.14088.3	3	7.35	1	4.19E+05		(R)NVIFQP	(R)N V/I/F\Q/P V A E L K K(Q)		142.28	462.6094	1385.815	-0.0015	-1.1	8.59	23167	8.94	HUMAN	B1APP8	6-phosphofructokinase type C
16250	dirMS_041712_NAR_50mM_plus2.15730.15730.3	3	7.35	1	7.42E+05		(R)AITGASL	(R)A I/T/G A S L/A/D I M A K/R(N)		150.28	473.2658	1417.783	-0.0003	-0.2	8.79	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
16251	dirMS_041712_NAR_50mM_plus2.20467.20467.3	3	7.35	1	1.87E+05		(K)SYLNMD	(K)S Y|L N M D A I M E A/I K K(T)		176.7	542.9473	1626.823	0.0044	2.7	5.79	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
16252	dirMS_041712_NAR_60mM_plus.11841.11841.3	3	7.35	0	9.22E+06		(R)FAQHGT	(R)F A Q H G T\F E\Y/E/Y S Q/R(W)		118.63	588.265	1762.782	-0.0015	-0.9	5.4	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
16253	dirMS_041712_NAR_60mM_plus.11999.11999.3	3	7.35	1	5.64E+05		(R)FSALQQ	(R)F S A L|Q/Q/A/V/P T E S T D N R R(V)		119.47	640.654	1919.957	-0.0095	-5	6.07	176357.7	5.25	HUMAN	D3DNT2	Eukaryotic translation initiation factor 4 gamma 1
16254	dirMS_041712_NAR_20mM_minus.10700.10700.3	3	7.34	0	1.40E+05		(K)VNQIGS	(K)V N Q\I/G S V|T/E|S/I/Q A C/K(L)	C:Carbamidomethylation	155.38	545.2807	1633.821	0.0062	3.8	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
16255	dirMS_041712_NAR_20mM_minus.13193.13193.2	2	7.34	0	2.38E+04	M329m	(K)ALELNm	(K)A L|E/L|N m L S L K(G)	m:Oxidized methionine	183.02	574.3232	1131.644	15.9949	0	6.05	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
16256	dirMS_041712_NAR_30mM_minus2.14367.14367.2	2	7.34	0	2.40E+05		(K)CCSGAII	(K)C/C|S G A I I|V L/T/K(S)	C:Carbamidomethylation	131.97	611.3188	1221.633	-0.0027	-2.2	8.75	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
16257	dirMS_041712_NAR_30mM_minus2.19005.19005.2	2	7.34	0	2.33E+05		(K)MAILQI	(K)M/A/I|L Q/I/M/K(E)		158.23	474.2745	947.542	0.0001	0.1	8.5	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
16258	dirMS_041712_NAR_50mM_minus2.10289.10289.3	3	7.34	0	1.66E+05		(K)LQAEAP	(K)L Q|A E A P H/I V V/G T P G R(V)		127.08	515.6179	1544.854	-0.0152	-9.8	6.75	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
16259	dirMS_041712_NAR_50mM_minus2.8949.8949.3	3	7.34	0	2.36E+05		(R)VMLGET	(R)V M/L G/E/T N/P A D S K/P G T I R(G)		118.3	595.9744	1785.916	-0.0077	-4.3	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
16260	dirMS_041712_NAR_60mM_minus.13463.13463.3	3	7.34	1	3.04E+05		(K)FSIEDLK	(K)F/S/I E D/L/K/A Q P K(Q)		135.1	425.9025	1275.694	-0.0014	-1.1	6.07	13579.2	9.99	HUMAN	E9PPQ6	Thymocyte nuclear protein 1 (Fragment)
16261	dirMS_041712_NAR_20mM_plus.14383.14383.3	3	7.34	0	1.08E+05	M174m	(K)AmGAA	(K)A m G\A\A Q V|V|V\T D L S/A T R(L)	m:Oxidized methionine	171.1	535.9457	1589.832	15.991	-2.5	5.88	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
16262	dirMS_041712_NAR_20mM_plus.14548.14548.2	2	7.34	0	3.89E+04	M185m	(K)LAVNm	(K)L/A|V N/m/V/P F P R(L)	m:Oxidized methionine	172.75	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
16263	dirMS_041712_NAR_20mM_plus.9717.9717.3	3	7.34	0	8.23E+04		(R)TPQAPA	(R)T P Q A P A\S A\N/L/V G P R(S)		138.37	460.2573	1378.744	0.0136	9.9	9.41	300351.7	12.1	HUMAN	Q9UQ35	Serine/arginine repetitive matrix protein 2
16264	dirMS_041712_NAR_30mM_plus2.21886.21886.2	2	7.34	0	2.21E+05		(R)NSILAQ	(R)N S I|L|A/Q V L/D Q\S A R(A)		170.18	707.8889	1414.765	0.0057	4	5.84	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
16265	dirMS_041712_NAR_30mM_plus2.8136.8136.2	2	7.34	0	3.24E+05		(K)IAVAAQ	(K)I/A|V|A/A/Q N C Y K(V)	C:Carbamidomethylation	96	569.2905	1137.572	0.0016	1.4	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
16266	dirMS_041712_NAR_30mM_plus2.8535.8535.2	2	7.34	0	8.93E+05		(R)LGLGEG	(R)L G/L/G E/G\A E E K(S)		98.92	501.7639	1002.51	0.0103	10.3	4.25	40096.8	9.24	HUMAN	C9JW69	Regulator of chromosome condensation (Fragment)
16267	dirMS_041712_NAR_40mM_plus2.15822.15822.3	3	7.34	0	1.85E+05		(K)VAIVKP	(K)V A/I V K P/G V/P M E/I V L N K(E)		160.55	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
16268	dirMS_041712_NAR_40mM_plus2.5460.5460.2	2	7.34	0	3.24E+04		(R)YYNQV	(R)Y Y/N/Q\V/G/R(K)		88.93	450.2218	899.437	-0.0007	-0.7	8.59	37238.2	9.57	HUMAN	K7ELX4	Ferrochelatase, mitochondrial (Fragment)
16269	dirMS_041712_NAR_50mM_plus2.10339.10339.3	3	7.34	0	2.06E+05	M277m	(R)GLGHQ	(R)G L\G H Q V A\T D A|L|V/A m E K(A)	m:Oxidized methionine	120.55	552.6181	1639.847	15.9925	-1.4	5.32	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
16270	dirMS_041712_NAR_50mM_plus2.11145.11145.3	3	7.34	1	3.14E+05		(R)DLDRIA	(R)D L/D R I A/G\Q V|A A A N K(K)		126.77	481.2661	1441.776	0.008	5.5	5.96	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
16271	dirMS_041712_NAR_50mM_plus2.13862.13862.3	3	7.34	0	1.45E+06		(K)DLAGCI	(K)D L|A/G C I/H G/L S N V/K(L)	C:Carbamidomethylation	140.48	461.9061	1383.705	-0.0012	-0.8	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
16272	dirMS_041712_NAR_60mM_plus.18226.18226.3	3	7.34	1	6.34E+05		(K)QLDDLK	(K)Q L|D D L/K V E/L/S\Q L R(V)		153.47	519.6254	1556.864	-0.0026	-1.7	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
16273	dirMS_041712_NAR_60mM_plus.5868.5868.3	3	7.34	1	8.35E+04		(R)CLSSAT	(R)C L|S S\A T D/P Q T K R(K)	C:Carbamidomethylation	88.43	455.226	1363.663	0	0	8.75	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
16274	dirMS_041712_NAR_20mM_minus.7324.7324.2	2	7.33	0	1.37E+05	M328m	(K)ALmDEV	(K)A/L/m/D E V/V K(A)	m:Oxidized methionine	120.6	460.7411	904.481	15.9941	-0.9	4.37	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
16275	dirMS_041712_NAR_20mM_minus.9470.9470.3	3	7.33	0	1.18E+04	M175m	(R)LEQGQ	(R)L E Q G Q A/I/D D|L/m P A Q K(-)	m:Oxidized methionine	144.5	558.2794	1656.826	15.9975	1.5	4.03	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
16276	dirMS_041712_NAR_30mM_minus2.14334.14443.2	2	7.33	0	2.20E+05		(R)ELAFQIS	(R)E L/A/F/Q I/S K(E)		131.8	468.2614	935.52	-0.0041	-4.4	6.1	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
16277	dirMS_041712_NAR_40mM_minus2.9364.9364.3	3	7.33	0	1.31E+05		(K)VQASLA	(K)V Q|A S L/A/A N T/F T\I/T G H A E T K(Q)		137.35	654.0087	1960.013	-0.0019	-1	6.72	11802.2	5.6	HUMAN	D6RDG3	Transcription factor BTF3 (Fragment)
16278	dirMS_041712_NAR_50mM_minus2.18277.18277.3	3	7.33	1	1.03E+06		(R)KAIIIFVP	(R)K A I I I\F\V|P V P Q L K(S)		173.78	489.3206	1465.95	-0.0032	-2.2	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
16279	dirMS_041712_NAR_50mM_minus2.4914.4914.3	3	7.33	1	4.33E+05		(R)AAEDDE	(R)A/A\E D D/E D D D V/D T K K(Q)		82.37	522.5522	1565.645	-0.0029	-1.8	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
16280	dirMS_041712_NAR_60mM_minus.13396.13396.3	3	7.33	1	1.40E+06		(R)QLREYQ	(R)Q L R E Y\Q/E/L/M/N V K(L)		135.27	517.6033	1550.8	-0.0042	-2.7	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
16281	dirMS_041712_NAR_120mM_plus.20195.20195.4	4	7.33	1	3.15E+05		(R)IDILDSA	(R)I/D I/L D S A/L L R P G R I D/R(K)		159.27	456.5157	1823.05	-0.0088	-4.8	6.04	44954.5	8.44	HUMAN	A8K3Z3	26S protease regulatory subunit 8
16282	dirMS_041712_NAR_20mM_plus.10217.10217.2	2	7.33	0	9.56E+04		(K)LEAEIAT	(K)L/E\A/E|I A T Y R(R)		143.43	533.2797	1065.557	-0.0054	-5	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
16283	dirMS_041712_NAR_20mM_plus.17364.17364.3	3	7.33	0	1.71E+05	M90m	(R)LFVGNLI	(R)L F/V G N L/P/P D I/T E E/E m R(K)	m:Oxidized methionine	191.48	625.9762	1859.921	15.9933	-0.9	4	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
16284	dirMS_041712_NAR_20mM_plus.17798.17798.2	2	7.33	0	1.59E+05		(K)GADFLV	(K)G A D F L/V|T/E/V E/N G G/S L G S K(K)		194.95	890.4414	1779.876	-0.0004	-0.2	4.14	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
16285	dirMS_041712_NAR_30mM_plus2.16934.16934.2	2	7.33	1	2.63E+05		(R)FVLSQAI	(R)F V|L|S Q A K D E|L(-)		141.48	575.3104	1149.615	-0.0015	-1.3	4.37	41053.3	5.58	HUMAN	Q86UY0	TXNDC5 protein
16286	dirMS_041712_NAR_30mM_plus2.4869.4869.2	2	7.33	0	3.09E+05	M71m	(K)ETmQSL	(K)E T/m\Q/S/L/N D R(L)	m:Oxidized methionine	77.37	555.2469	1093.494	15.9923	-2.4	4.37	48845.9	4.72	HUMAN	C4AM86	Keratin, type I cuticular Ha5
16287	dirMS_041712_NAR_60mM_plus.12673.12673.3	3	7.33	0	5.66E+05		(K)GSYSLS	(K)G S/Y|S L/S H\V/Y/T/P N D V R(M)		123.05	565.6098	1694.813	0.0016	0.9	6.74	63566.6	6.3	HUMAN	P07686	Beta-hexosaminidase subunit beta
16288	dirMS_041712_NAR_120mM_minus.18769.18769.4	4	7.32	1	4.42E+05		(K)FQIPPN	(K)F Q|I|P/P N/A E L K Y E L/H L K(S)		157.08	485.7686	1940.064	-0.0114	-5.9	6.75	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
16289	dirMS_041712_NAR_40mM_minus2.14175.14175.3	3	7.32	0	1.69E+05		(K)LQAVEV	(K)L Q|A\V E V V I T H L A/P G T K(H)		167.22	559.3273	1675.974	-0.0068	-4	6.75	16120	9.05	HUMAN	Q9Y2V2	Calcium-regulated heat stable protein 1
16290	dirMS_041712_NAR_50mM_minus2.11177.11177.3	3	7.32	1	3.77E+05		(R)VVDLM	(R)V/V/D L M A H/M A/S K E(-)		131.38	444.2213	1330.649	0	0	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
16291	dirMS_041712_NAR_60mM_minus.14462.14462.3	3	7.32	1	2.71E+05		(R)TEMENE	(R)T/E\M E/N E F V L/I/K K(D)		140.07	494.2594	1480.772	-0.0079	-5.4	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
16292	dirMS_041712_NAR_60mM_minus.14824.14824.3	3	7.32	0	3.86E+05		(K)AVGHPF	(K)A V G H|P F\V I/Q L/G/R(I)		142.08	431.9182	1293.743	-0.0026	-2	9.8	124524.8	5.71	HUMAN	O14980	Exportin-1
16293	dirMS_041712_NAR_60mM_minus.17761.17761.3	3	7.32	1	3.76E+05		(K)YGKLEV	(K)Y/G K\L\E\V A/N L/L/L Q/K(S)		159.57	496.9631	1488.878	-0.0037	-2.5	8.5	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
16294	dirMS_041712_NAR_60mM_minus.18326.18326.3	3	7.32	1	1.07E+05		(R)GMLRED	(R)G M/L R E\D A\V/L/E/Y L K(I)		162.98	512.9419	1536.809	0.0021	1.4	4.68	67933	6.08	HUMAN	P26038	Moesin
16295	dirMS_041712_NAR_60mM_minus.18740.18740.3	3	7.32	0	2.45E+05		(R)DFLLKPE	(R)D F/L L/K/P E L L R(A)		165.48	415.25	1243.741	-0.0054	-4.4	6.07	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
16296	dirMS_041712_NAR_120mM_plus.9454.9454.3	3	7.32	1	6.42E+05		(R)RMGESD	(R)R M\G E S\D D/S/I/L/R(L)		103.27	426.8756	1278.611	0.0016	1.2	4.56	9225.3	9.16	HUMAN	P63220	40S ribosomal protein S21
16297	dirMS_041712_NAR_20mM_plus.11747.11747.2	2	7.32	0	1.01E+05		(K)LVPVGY	(K)L V/P V/G Y G I K(K)		153.78	473.2909	945.577	-0.0023	-2.4	8.59	24934.4	4.5	HUMAN	P24534	Elongation factor 1-beta
16298	dirMS_041712_NAR_20mM_plus.12750.12750.2	2	7.32	0	2.63E+05	M316m	(R)ISEQFTA	(R)I S/E/Q|F/T|A m F/R(R)	m:Oxidized methionine	161.22	623.3012	1229.598	15.9968	1.5	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
16299	dirMS_041712_NAR_30mM_plus2.10619.10656.2	2	7.32	0	2.98E+05		(R)TYLPSQ	(R)T Y|L|P S Q V S/R(V)		109.15	525.7773	1050.558	-0.0105	-10	8.41	99900.1	5.04	HUMAN	B4DZI8	Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b
16300	dirMS_041712_NAR_30mM_plus2.12735.12735.2	2	7.32	0	3.22E+05		(K)SKPVFSE	(K)S\K|P V F S E|S L|S/D(-)		119.82	598.2946	1195.584	-0.0022	-1.8	4.67	11226.4	5.09	HUMAN	O60220	Mitochondrial import inner membrane translocase subunit Tim8 A
16301	dirMS_041712_NAR_30mM_plus2.19362.19362.2	2	7.32	0	5.76E+04		(R)QAQEYE	(R)Q\A/Q/E Y/E A L L|N\I K(V)		155.35	710.3766	1419.748	-0.0019	-1.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
16302	dirMS_041712_NAR_40mM_plus2.19367.19367.3	3	7.32	1	4.25E+05		(K)ALFEEV	(K)A/L|F E E V/P E L L T E A E K K(E)		181.68	615.9991	1845.984	-0.0017	-0.9	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
16303	dirMS_041712_NAR_50mM_plus2.11904.11904.3	3	7.32	1	3.00E+05		(K)FVQDTL	(K)F V/Q D T L/K/G D G V/T E I R(M)		130.55	559.9637	1677.881	-0.0041	-2.4	4.56	15119.1	4.81	HUMAN	A6NDN0	Trafficking protein particle complex 3, isoform CRA_a
16304	dirMS_041712_NAR_50mM_plus2.16870.16870.3	3	7.32	0	7.72E+05		(R)QYYTLL	(R)Q Y Y T/L/L N Q A/P D\M L H/R(K)		156.92	621.6447	1862.922	-0.0022	-1.2	6.74	4335.1	9.82	HUMAN	E5RH00	Ras GTPase-activating protein-binding protein 1
16305	dirMS_041712_NAR_50mM_plus2.18739.18739.3	3	7.32	0	7.77E+05		(R)CRPDQL	(R)C R P D Q L T\G L/S\L/L|P L S E K(A)	C:Carbamidomethylation	167.3	643.0148	1927.032	-0.0019	-1	6.07	533778	5.74	HUMAN	Q15149	Plectin
16306	dirMS_041712_NAR_60mM_plus.11930.11930.2	2	7.32	1	1.06E+06		(R)FPGQLN	(R)F/P/G/Q/L/N/A D|L R\K(L)		119.6	629.8482	1258.69	-0.0011	-0.9	8.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
16307	dirMS_041712_NAR_60mM_plus.16562.16562.3	3	7.32	1	6.81E+05		(R)TDGKVF	(R)T/D/G K V F/Q/F L N A K(C)		143.42	456.5782	1367.732	-0.0117	-8.6	8.26	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
16308	dirMS_041712_NAR_60mM_plus.18022.18022.3	3	7.32	0	1.53E+05		(K)ILLQPTS	(K)I L L Q P T S S|I/S T T K(T)		151.3	463.6084	1388.8	0.0111	8	8.75	192522.7	5.74	HUMAN	Q9P1Z9	Uncharacterized protein C9orf174
16309	dirMS_041712_NAR_60mM_plus.20449.20449.3	3	7.32	1	3.20E+04	S852s	(K)LGPNGE	(K)L G P/N\G E R s/A E L/L/L/G K(S)	s:N-acetylglucosamine (S)	167.23	586.3246	1553.865	203.0947	8.7	6.14	193289	6.79	HUMAN	Q7LBC6	Lysine-specific demethylase 3B
16310	dirMS_041712_NAR_60mM_plus.8712.8712.3	3	7.32	1	1.58E+06		(K)GGIMLP	(K)G G|I/M L/P E/K S Q G/K(V)		103.58	415.5607	1244.667	0.0008	0.7	8.59	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
16311	dirMS_041712_NAR_30mM_minus2.19690.19690.2	2	7.31	0	3.52E+05		(R)ASLSLW	(R)A/S L/S L/W Q/A M E K(G)		163.07	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
16312	dirMS_041712_NAR_40mM_minus2.13491.13491.3	3	7.31	0	1.27E+04		(R)DLKPSN	(R)D L K P S N\L\L|I\N T/T C D L K(I)	C:Carbamidomethylation	163.35	615.6649	1844.979	0.0015	0.8	5.96	30925	5.63	HUMAN	B3KR49	Mitogen-activated protein kinase 3
16313	dirMS_041712_NAR_40mM_minus2.7843.7843.3	3	7.31	1	1.59E+05		(R)DGKLVS	(R)D G K L V S E/S\S/D\V L/P K(-)		125.2	491.9311	1473.78	-0.0008	-0.5	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
16314	dirMS_041712_NAR_50mM_minus2.19026.19026.3	3	7.31	1	1.34E+06		(R)KEGGLG	(R)K E G G L G P L N|I|P\L/L/A D V T R(R)		187.5	621.6941	1863.07	-0.0021	-1.1	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
16315	dirMS_041712_NAR_60mM_minus.10599.10599.3	3	7.31	0	2.57E+05		(R)SVIHSLA	(R)S V|I H S\L A/S V E A Q K(S)		119.02	456.9195	1368.748	-0.0042	-3.1	6.47	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
16316	dirMS_041712_NAR_60mM_minus.14394.14394.3	3	7.31	1	1.30E+06		(R)MSMKE	(R)M S M K E V D\E Q|M/L/N/V\Q N K(N)		140.47	641.9701	1923.897	-0.0015	-0.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
16317	dirMS_041712_NAR_60mM_minus.18934.18934.3	3	7.31	1	1.98E+05		(K)ITQDIFQ	(K)I/T Q D I|F/Q/Q L L K R(G)		167.82	501.6268	1502.869	-0.0031	-2.1	8.75	72796.9	6.75	HUMAN	A6NC17	Methionine--tRNA ligase, cytoplasmic
16318	dirMS_041712_NAR_60mM_minus.5097.5097.3	3	7.31	1	6.90E+04		(K)EEASGS	(K)E E A/S/G S/S V/T A E E A K K(F)		83.3	508.2453	1522.723	-0.0018	-1.2	4.49	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
16319	dirMS_041712_NAR_120mM_plus.19197.19197.3	3	7.31	1	6.13E+05		(R)HGVQEL	(R)H/G V Q E\L\E\I\E|L/Q/S Q L S K K(A)		153.85	656.0237	1966.06	-0.0038	-2	5.5	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
16320	dirMS_041712_NAR_20mM_plus.10800.10800.2	2	7.31	0	8.63E+04		(R)FLEQQN	(R)F L\E/Q Q/N Q V L/Q/T K(W)		146.73	738.3942	1475.785	-0.0041	-2.8	6	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
16321	dirMS_041712_NAR_20mM_plus.15292.15292.2	2	7.31	0	7.05E+03		(K)DVLSVA	(K)D V\L|S V/A/F/S S D N R(Q)		176.72	655.3293	1309.638	0.0131	10	4.21	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
16322	dirMS_041712_NAR_20mM_plus.16748.16748.3	3	7.31	0	2.85E+05		(K)VQIAVA	(K)V Q\I A V A\N A/Q/E/L/L/Q R(M)		186.82	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
16323	dirMS_041712_NAR_20mM_plus.17501.17501.3	3	7.31	0	3.61E+04	M74m	(R)mIAGQV	(R)m I A G Q V|L|D|I N L A/A E P K(V)	m:Oxidized methionine	193.18	566.9751	1682.915	15.9962	0.7	4.37	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
16324	dirMS_041712_NAR_20mM_plus.8945.8945.2	2	7.31	0	1.96E+05		(K)VTADVI	(K)V T|A D\V/I/N A\A E K(L)		132.52	565.806	1130.605	-0.0005	-0.4	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
16325	dirMS_041712_NAR_30mM_plus2.13336.13336.2	2	7.31	0	5.70E+05		(K)CPFTGN	(K)C/P/F/T|G\N V S I R(G)	C:Carbamidomethylation	122.88	575.7876	1150.567	0.0006	0.5	9.75	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
16326	dirMS_041712_NAR_30mM_plus2.15631.15903.2	2	7.31	0	7.19E+05		(R)YPVNSV	(R)Y/P|V|N S V N I L/K(A)		134.63	573.8278	1146.652	-0.0034	-3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
16327	dirMS_041712_NAR_30mM_plus2.16757.16757.2	2	7.31	0	3.63E+05		(K)QLQEMI	(K)Q L/Q/E/M/L/G/L/S K(V)		140.63	573.8112	1146.619	-0.0036	-3.1	6	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
16328	dirMS_041712_NAR_30mM_plus2.16823.16823.2	2	7.31	0	3.49E+05		(K)QLQEMI	(K)Q/L|Q/E/M L G L S K(V)		140.92	573.8112	1146.619	-0.0036	-3.1	6	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
16329	dirMS_041712_NAR_30mM_plus2.19425.19425.2	2	7.31	0	2.87E+05		(K)TVDNFV	(K)T V|D\N\F|V/A/L A T/G E K(G)		155.25	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
16330	dirMS_041712_NAR_30mM_plus2.5455.5455.2	2	7.31	0	3.75E+04		(K)SAAQAA	(K)S A/A Q A\A/A/Q T/N\S N A A G K(Q)		82.75	730.8568	1460.709	-0.0025	-1.7	8.47	45021.6	8.74	HUMAN	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein
16331	dirMS_041712_NAR_30mM_plus2.6304.6593.2	2	7.31	0	1.64E+06		(R)LGCQSV	(R)L/G/C Q S V/R(G)	C:Carbamidomethylation	87.92	410.2146	819.414	0.0078	9.5	9.75	52835.4	9.64	HUMAN	H7C0W7	Hyccin (Fragment)
16332	dirMS_041712_NAR_40mM_plus2.11563.11563.3	3	7.31	0	3.79E+05		(R)MPLPAP	(R)M P/L/P A\P S L S H Q|P P P A P R(V)		133.63	598.3202	1792.953	-0.0066	-3.7	9.52	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
16333	dirMS_041712_NAR_40mM_plus2.9522.9522.2	2	7.31	0	7.31E+04		(R)GGGGNI	(R)G G G/G N F/G/P G P/G S N F R(G)		119.27	689.3182	1377.629	-0.0003	-0.2	9.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
16334	dirMS_041712_NAR_60mM_plus.17616.17616.3	3	7.31	1	5.15E+05		(R)LMDLLG	(R)L M/D L|L/G E|G L K R(S)		149.03	415.5712	1244.703	-0.0041	-3.3	6.07	52817.9	6.2	HUMAN	F5H3T8	Arginine--tRNA ligase, cytoplasmic
16335	dirMS_041712_NAR_120mM_minus.7677.7677.3	3	7.3	1	1.61E+05		(K)DGGFCE	(K)D G/G/F/C/E V C K K(L)	C:Carbamidomethylation	96.37	400.5128	1199.518	0.0055	4.6	6.07	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
16336	dirMS_041712_NAR_20mM_minus.14500.14500.3	3	7.3	0	4.72E+03		(R)AAVEEG	(R)A A V E\E\G I|V L/G/G G C A L L R(C)	C:Carbamidomethylation	199.5	562.3053	1684.905	-0.0037	-2.2	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
16337	dirMS_041712_NAR_20mM_minus.9805.9805.2	2	7.3	0	1.05E+05		(R)IVLQIDN	(R)I/V/L Q/I/D/N A R(L)		148.63	521.3059	1041.605	-0.0006	-0.6	5.84	20842.9	5.32	HUMAN	C9JM50	Keratin, type I cytoskeletal 19 (Fragment)
16338	dirMS_041712_NAR_30mM_minus2.14439.14440.2	2	7.3	0	4.86E+05	M494m	(R)GAHImN	(R)G A/H/I m N S\T C/A A M\P K(L)	C:Carbamidomethylation m:Oxid	132.68	752.8364	1488.676	15.9899	-3.3	8.76	114220.9	9.14	HUMAN	O43303	Centriolar coiled-coil protein of 110 kDa
16339	dirMS_041712_NAR_30mM_minus2.15399.15399.2	2	7.3	0	7.68E+04		(K)WSLLQC	(K)W/S|L|L/Q Q Q K(T)		137.75	515.7847	1030.568	-0.0059	-5.7	8.75	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
16340	dirMS_041712_NAR_30mM_minus2.16890.16908.2	2	7.3	0	2.98E+05		(R)FFMGN	(R)F/F|M|G N Q V L\K(V)		145.83	542.2866	1083.566	0.0004	0.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
16341	dirMS_041712_NAR_40mM_minus2.7450.7450.3	3	7.3	0	2.98E+03	M180m	(R)VVVLmC	(R)V V\V/L/m/G S T S D\L G H C E K(I)	C:Carbamidomethylation m:Oxid	120.22	583.2806	1731.84	15.9868	-4.6	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
16342	dirMS_041712_NAR_50mM_minus2.13655.13655.3	3	7.3	0	4.59E+04		(K)MLDAED	(K)M L|D A E D I/V/N T A R P\D E K(A)		144.98	606.2965	1816.875	0.0004	0.2	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
16343	dirMS_041712_NAR_50mM_minus2.15958.15958.3	3	7.3	1	1.14E+05		(R)VSFELFA	(R)V/S/F E/L F/A D K/V P K(T)		159.03	460.5908	1379.757	0.0009	0.7	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
16344	dirMS_041712_NAR_50mM_minus2.17566.17566.3	3	7.3	0	2.60E+05		(R)LLLDGAI	(R)L L\L D G A/P L/I A I H K(A)		168.5	458.6218	1373.852	-0.0007	-0.5	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
16345	dirMS_041712_NAR_50mM_minus2.17905.17905.3	3	7.3	0	2.19E+05		(R)LGFHLPI	(R)L G F H L P L\E|V/A/Y Q R(G)		170.25	514.953	1542.843	0.0017	1.1	6.75	533778	5.74	HUMAN	Q15149	Plectin

16346	dirMS_041712_NAR_50mM_minus2.8703.8703.3	3	7.3	1	5.39E+04		(R)AIAGND	(R)A/I/A\G N D/D V K/D/A I V/R(A)		117.52	486.2632	1456.775	-0.0004	-0.3	4.43	45030.9	6.31	HUMAN	B4E1N1	Armadillo repeat-containing protein 6
16347	dirMS_041712_NAR_60mM_minus.14410.14410.3	3	7.3	1	1.17E+05		(R)KLVILEG	(R)K L V\I|L\E/G E/L E/R(A)		139.83	433.5934	1298.768	-0.0022	-1.7	4.79	12073.4	4.67	HUMAN	K7EMU5	Tropomyosin alpha-4 chain (Fragment)
16348	dirMS_041712_NAR_60mM_minus.20010.20010.3	3	7.3	1	7.54E+05		(R)LIALLEVI	(R)L/I|A L/L E/V/L S Q K R(M)		182.12	461.6287	1382.873	-0.0014	-1	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
16349	dirMS_041712_NAR_120mM_plus.15184.15184.2	2	7.3	0	2.87E+06		(R)DWSHYF	(R)D W|S/H Y F\K(I)		132.17	491.725	982.442	0.001	1	6.74	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
16350	dirMS_041712_NAR_120mM_plus.5460.5460.3	3	7.3	0	1.03E+05		(R)RPDQQL	(R)R P D Q\Q\L/Q/G E G K(I)		81.82	419.2172	1255.639	-0.0019	-1.5	6.07	45021.6	8.74	HUMAN	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein
16351	dirMS_041712_NAR_20mM_plus.10436.10436.3	3	7.3	0	1.35E+05	M592m M5	(R)mGPAm	(R)m G/P A m G P/A|L|G A G I E R(M)	m:Oxidized methionine	144.65	487.2418	1427.713	31.9975	5.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
16352	dirMS_041712_NAR_20mM_plus.16535.16535.2	2	7.3	0	1.48E+05		(K)VQIAVA	(K)V Q I/A\V|A N A Q E/L/L Q R(M)		185.98	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
16353	dirMS_041712_NAR_30mM_plus2.16556.16866.2	2	7.3	0	4.52E+05		(R)LWDLTT	(R)L/W|D|L/T T/G T T T R(R)		140.32	632.8304	1264.653	0.0003	0.3	5.84	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
16354	dirMS_041712_NAR_30mM_plus2.17099.17099.2	2	7.3	0	2.27E+05		(K)ACGNFG	(K)A C|G/N F/G I\P C E/L/R(V)	C:Carbamidomethylation	142.65	697.3237	1393.635	0.005	3.6	6.05	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
16355	dirMS_041712_NAR_30mM_plus2.4880.4880.2	2	7.3	0	5.57E+05		(K)QASEGP	(K)Q A/S E G/P L K(G)		77.53	415.225	829.441	0.0013	1.6	6	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
16356	dirMS_041712_NAR_50mM_plus2.13192.13192.3	3	7.3	1	1.52E+05		(R)GYSFTTT	(R)G Y|S F/T T T/A E R E I V R(D)		137.1	543.9455	1629.823	-0.0012	-0.7	6.14	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
16357	dirMS_041712_NAR_50mM_plus2.14170.14170.3	3	7.3	1	1.04E+06		(K)ALQQGL	(K)A L/Q|Q G L V|G L E/L K E K(L)		142.23	509.3022	1525.895	-0.0028	-1.8	6.18	266161	5.68	HUMAN	E9PPU0	Epiplakin
16358	dirMS_041712_NAR_50mM_plus2.15412.15412.3	3	7.3	0	1.07E+06		(R)QVLIASH	(R)Q V/L I/A S H L/P S Y E L R(H)		149.58	542.6394	1625.901	0.0027	1.6	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
16359	dirMS_041712_NAR_50mM_plus2.8890.8890.3	3	7.3	1	6.36E+04		(K)ATFIKVP	(K)A/T/F I/K V/P Q/N Q N G K(S)		113.77	482.2676	1444.791	-0.0024	-1.7	10	32503.1	5.29	HUMAN	H7BY16	Nucleolin (Fragment)
16360	dirMS_041712_NAR_60mM_plus.17227.17227.3	3	7.3	1	4.06E+05		(R)GFPTIYF	(R)G F\P T I/Y/F S/P A N/K K(L)		147.08	490.5979	1469.779	0.0004	0.3	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
16361	dirMS_041712_NAR_60mM_plus.17977.17977.3	3	7.3	1	3.13E+04		(R)LKLPAVV	(R)L K L P A V\V/T/A/D/L R(L)		151.27	432.6056	1295.805	-0.0023	-1.8	8.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
16362	dirMS_041712_NAR_60mM_plus.6006.6006.2	2	7.3	1	9.20E+04	Y31y	(K)SGKYVLG	(K)S G K/Y|V|L G y K(Q)	y:Phosphorylated Y	89.87	547.7628	1014.562	79.9565	-9	9.52	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
16363	dirMS_041712_NAR_120mM_minus.10069.10069.3	3	7.29	0	5.96E+05		(R)HGESAW	(R)H G E S A\W|N/L/E N R(F)		109.4	438.2098	1312.603	0.012	9.1	5.4	28917.5	6.68	HUMAN	P18669	Phosphoglycerate mutase 1
16364	dirMS_041712_NAR_30mM_minus2.13092.13178.2	2	7.29	0	2.52E+05		(R)FTVAELK	(R)F/T|V A/E/L K(Q)		125.05	404.2383	807.461	0.0082	10.2	6	98282.7	5.49	HUMAN	E9PPJ0	Splicing factor 3B subunit 2
16365	dirMS_041712_NAR_30mM_minus2.17323.17323.2	2	7.29	0	1.15E+04		(K)VIVPNM	(K)V I|V/P N M E F R(A)		147.4	552.7932	1104.587	-0.0079	-7.2	5.97	86098.8	5.31	HUMAN	B4DUC5	Exportin-2
16366	dirMS_041712_NAR_50mM_minus2.12683.12683.3	3	7.29	0	7.34E+03		(R)DLEIERP	(R)D\L|E/I E/R P I L G Q N D N/K(S)		141.55	585.3067	1753.908	-0.0024	-1.3	4.32	30062.6	5.35	HUMAN	B7Z341	Protein NDRG3
16367	dirMS_041712_NAR_50mM_minus2.12696.12696.3	3	7.29	0	2.16E+05		(R)LVVVLCN	(R)L V|V/V|L C N L K/P Q K(M)	C:Carbamidomethylation	140.23	470.9508	1410.85	-0.0123	-8.7	10	59484.7	6.61	HUMAN	P54577	Tyrosine--tRNA ligase, cytoplasmic
16368	dirMS_041712_NAR_60mM_minus.11031.11031.3	3	7.29	1	1.31E+04		(K)TAVCDIP	(K)T A V/C D I/P/P/R G L K(M)	C:Carbamidomethylation	121.85	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
16369	dirMS_041712_NAR_120mM_plus.16946.16946.3	3	7.29	1	1.33E+06		(K)LKVPEW	(K)L K V/P E W|V D\T V/K(L)		141.93	438.5868	1313.746	-0.0005	-0.4	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
16370	dirMS_041712_NAR_120mM_plus.19901.19901.3	3	7.29	0	1.23E+04		(K)SFLIWVN	(K)S/F|L I/W V N E E D/H T R(V)		157.53	549.2711	1645.797	0.0019	1.1	4.65	29478.9	6.26	HUMAN	E9PCP8	Creatine kinase U-type, mitochondrial
16371	dirMS_041712_NAR_20mM_plus.10750.10750.2	2	7.29	0	3.14E+04		(K)IGGIGTV	(K)I/G/G\I/G|T V P V G/R(V)		146.8	513.3057	1025.61	-0.0061	-5.9	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
16372	dirMS_041712_NAR_20mM_plus.17201.17201.3	3	7.29	0	1.17E+04		(R)LTVEDPV	(R)L\T V E\D P V/T\V/E/Y I T R(Y)		189.77	545.6246	1634.864	-0.0043	-2.6	4.14	21330	9.14	HUMAN	H0Y586	Proteasome subunit alpha type-7 (Fragment)
16373	dirMS_041712_NAR_20mM_plus.19161.19161.3	3	7.29	0	2.19E+05		(R)LAGTQP	(R)L A/G\T Q P L|E V\L E/A/V Q R(S)		204.08	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
16374	dirMS_041712_NAR_20mM_plus.19259.19259.3	3	7.29	0	2.77E+05		(R)LAGTQP	(R)L A G T Q\P L/E\V L/E/A V Q R(S)		204.3	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
16375	dirMS_041712_NAR_30mM_plus2.20852.20852.3	3	7.29	2	6.31E+05	N565n	(K)LKASENS	(K)L K A S E N S/R/E\n R(L)	n:N-acetylglucosamine (N)	162.7	502.9201	1303.671	203.0744	-3.3	8.75	71155.9	9.54	HUMAN	Q7Z2Q7	Leucine-rich repeat-containing protein 70
16376	dirMS_041712_NAR_30mM_plus2.6617.6617.2	2	7.29	0	1.98E+05		(K)TLNAGA	(K)T L|N A/G A Y/S K(V)		89.15	462.7408	924.479	-0.0042	-4.5	8.26	30197.4	7.91	HUMAN	E9PMG2	Palmitoyl-protein thioesterase 1 (Fragment)
16377	dirMS_041712_NAR_40mM_plus2.7229.7229.2	2	7.29	0	9.78E+04		(R)SGYFDEI	(R)S G/Y/F D/E R(Y)		102.85	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
16378	dirMS_041712_NAR_40mM_plus2.8259.8259.2	2	7.29	0	1.92E+05		(R)AVVIVDI	(R)A V V/I/V/D/D/R(G)		108.33	443.7528	886.499	-0.0009	-1.1	4.21	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
16379	dirMS_041712_NAR_50mM_plus2.13664.13664.3	3	7.29	0	1.41E+06		(K)STTSDIP	(K)S T|T/S D I P H/M L N Q V E/S K(V)		140.28	596.2908	1786.864	-0.0061	-3.4	5.3	11532.2	6.34	HUMAN	H0YNA1	Protein FAM98B (Fragment)
16380	dirMS_041712_NAR_50mM_plus2.13803.13803.3	3	7.29	1	5.68E+05		(K)GGELVYT	(K)G G E\L/V|Y/T/D S/E A R D V F E K(A)		141.23	638.9735	1914.908	-0.002	-1.1	4.18	533778	5.74	HUMAN	Q15149	Plectin
16381	dirMS_041712_NAR_50mM_plus2.20582.20582.3	3	7.29	1	2.51E+05		(R)GGPNIIT	(R)G G/P\N I/I T L A/D/I V K D P V S R(T)		176.95	622.3526	1865.049	-0.0058	-3.1	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
16382	dirMS_041712_NAR_50mM_plus2.9951.9951.3	3	7.29	1	9.24E+05	M2806m	(R)LEGDLSL	(R)L E G\D L S L A D/K G/m T A K(D)	m:Oxidized methionine	119.38	522.2726	1548.794	16.0095	9.3	4.56	617759.6	5.2	HUMAN	Q8IVF2	Protein AHNAK2
16383	dirMS_041712_NAR_60mM_plus.10107.10107.3	3	7.29	1	2.64E+05	M142m	(K)VKEGMN	(K)V K E G M N\I\V/E/A m E R(F)	m:Oxidized methionine	111.27	507.9187	1505.745	15.9965	1	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
16384	dirMS_041712_NAR_60mM_plus.17386.17386.3	3	7.29	1	8.46E+05		(R)DKLNNL	(R)D K L N N\L/V/L/F D/K(A)		148.4	440.2499	1318.737	-0.0014	-1	5.96	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
16385	dirMS_041712_NAR_60mM_plus.6627.6627.3	3	7.29	1	7.24E+04		(K)IYEDGDD	(K)I Y/E/D G/D D/D M K R(T)		93.07	452.8641	1356.574	0.0041	3	4.03	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
16386	dirMS_041712_NAR_60mM_plus.7127.7147.2	2	7.29	0	4.34E+05		(K)SVPADLS	(K)S V|P|A/D/L S R P K(S)		95.35	535.3025	1069.6	-0.0023	-2.2	8.46	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
16387	dirMS_041712_NAR_120mM_minus.11711.11711.3	3	7.28	2	3.38E+05		(R)SGKYDLI	(R)S G K/Y D L D|F K/S/P D D|P S R(Y)		117.87	609.6226	1826.855	-0.0023	-1.3	4.58	47510.4	7.04	HUMAN	P06733	Alpha-enolase
16388	dirMS_041712_NAR_120mM_minus.14626.14626.4	4	7.28	2	3.97E+05		(K)IANILKD	(K)I A N I L K D K D P\P I/P V/A/K(I)		133.75	433.764	1732.037	-0.0026	-1.5	8.5	73273.4	4.96	HUMAN	P13667	Protein disulfide-isomerase A4
16389	dirMS_041712_NAR_120mM_minus.5174.5174.3	3	7.28	1	3.17E+05		(R)LRAETEQ	(R)L R A E T E|Q/G E Q Q R(Q)		81.13	482.2432	1444.714	0.0012	0.8	4.79	533778	5.74	HUMAN	Q15149	Plectin
16390	dirMS_041712_NAR_20mM_minus.11651.11651.2	2	7.28	0	4.27E+05		(R)GALQNI	(R)G A L Q/N/I/I\P A S T G A A K(A)		164.78	706.3976	1411.79	-0.0024	-1.7	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
16391	dirMS_041712_NAR_20mM_minus.14102.14102.2	2	7.28	0	1.20E+06		(K)SYELPDG	(K)S Y E|L|P D G/Q V I T/I G N E R(F)		194	895.9481	1790.892	-0.003	-1.7	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
16392	dirMS_041712_NAR_30mM_minus2.5273.5273.2	2	7.28	0	6.10E+05		(R)TDTGEP	(R)T D|T G/E\P M/G R(G)		82.42	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
16393	dirMS_041712_NAR_40mM_minus2.11285.11285.3	3	7.28	0	4.48E+04		(R)EALAEA	(R)E A\L/A E/A/A L E S P R P A L V R(S)		149.25	598.3347	1792.992	-0.002	-1.1	4.79	22148.2	5.87	HUMAN	B3KY21	Na(+)/H(+) exchange regulatory cofactor NHE-RF1
16394	dirMS_041712_NAR_50mM_minus2.10350.10350.3	3	7.28	0	1.32E+05		(K)NAQLNI	(K)N A|Q/L N I/E|L E A A H H(-)		127.2	487.2478	1459.729	0	0	5.23	13452	8.89	HUMAN	F5H246	Protein NAMPTL
16395	dirMS_041712_NAR_50mM_minus2.5270.5270.3	3	7.28	0	8.24E+05		(K)TATPQQ	(K)T A|T/P Q/Q A/Q E V/H\E K(L)		88.02	489.5768	1466.723	-0.0075	-5.1	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
16396	dirMS_041712_NAR_50mM_minus2.8438.8438.3	3	7.28	1	6.15E+04		(R)DYQDNK	(R)D Y/Q/D/N K/A D V I/L K(Y)		115.68	474.5792	1421.727	-0.004	-2.8	4.43	16556.2	5.07	HUMAN	O14602	Eukaryotic translation initiation factor 1A, Y-chromosomal
16397	dirMS_041712_NAR_50mM_minus2.8480.8480.3	3	7.28	1	2.45E+04		(R)LGGSPFG	(R)L/G G/S|P/F G/P A/G T G K T E S V K(A)		116.02	563.9636	1689.881	-0.0044	-2.6	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
16398	dirMS_041712_NAR_60mM_minus.13296.13296.3	3	7.28	0	4.41E+05		(K)IDISAVM	(K)I/D I S/A V M S V H/S/A V K(E)		133.55	486.2642	1456.783	-0.0048	-3.3	6.74	80122.6	4.88	HUMAN	Q5H9M0	PWWP domain-containing protein MUM1L1
16399	dirMS_041712_NAR_60mM_minus.14845.14845.3	3	7.28	1	3.69E+05		(R)LQDFKLI	(R)L/Q/D F/K/L/D F G N S Q G K(T)		142.8	532.935	1596.802	-0.0112	-7	5.96	18626.5	5.64	HUMAN	B8ZZK2	Gamma-glutamylcyclotransferase
16400	dirMS_041712_NAR_120mM_plus.4148.4148.3	3	7.28	1	1.89E+06	M54m	(K)SLDEmE	(K)S L|D/E m E/K Q/Q R(E)	m:Oxidized methionine	70.13	427.2032	1263.6	15.9953	0.3	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
16401	dirMS_041712_NAR_20mM_plus.16900.16900.3	3	7.28	0	1.80E+05		(R)AIVAIEN	(R)A I V A\I E N/P/A D V S V I S S R(N)		188.67	580.9864	1740.949	-0.0044	-2.5	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
16402	dirMS_041712_NAR_20mM_plus.17844.17844.2	2	7.28	0	9.16E+04		(K)VDFPQD	(K)V D F/P Q D Q L T/A L/T/G R(I)		194.83	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
16403	dirMS_041712_NAR_20mM_plus.18680.18680.3	3	7.28	0	1.06E+05	M80m	(R)APLPDLY	(R)A P/L P D L\Y|P/F G T m R(G)	m:Oxidized methionine	200.23	498.5865	1477.751	15.9941	-0.5	5.88	81122.9	9.03	HUMAN	H3BLZ8	Probable ATP-dependent RNA helicase DDX17
16404	dirMS_041712_NAR_30mM_plus2.20851.20851.2	2	7.28	0	3.65E+05		(R)QINWTV	(R)Q\I/N|W/T/V/L/Y R(R)		163.18	596.8315	1192.647	0.0084	7	8.75	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
16405	dirMS_041712_NAR_30mM_plus2.22670.22670.3	3	7.28	0	5.00E+05		(R)ALTVPEL	(R)A L T V/P E L T Q/Q V/F D A K(N)		175.77	553.9697	1659.895	-0.0007	-0.4	4.37	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
16406	dirMS_041712_NAR_30mM_plus2.6069.6069.2	2	7.28	0	1.50E+05		(R)VGSTSEN	(R)V/G\S|T/S\E N I T Q\K(V)		85.97	582.2983	1163.59	-0.0009	-0.8	5.97	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
16407	dirMS_041712_NAR_40mM_plus2.11374.11374.3	3	7.28	0	4.54E+04		(R)VYNVTQ	(R)V/Y/N/V\T Q/H/A/V/G I V V N K(Q)		132.98	547.642	1640.912	-0.0004	-0.3	8.57	10000.5	10.56	HUMAN	G3V1B3	60S ribosomal protein L21
16408	dirMS_041712_NAR_40mM_plus2.9721.9721.3	3	7.28	0	2.39E+05		(R)AAEDPV	(R)A A|E/D/P/V A/A/A P R P L P A G G R(L)		121.07	572.6438	1715.919	-0.0019	-1.1	6.12	73966.7	10.21	HUMAN	B3KWK6	Alpha-L-iduronidase
16409	dirMS_041712_NAR_50mM_plus2.14539.14539.3	3	7.28	1	5.40E+05		(R)QAIKELP	(R)Q A I\K E L/P Q F/A/T/G E N L P R(V)		144.47	638.0091	1912.029	-0.0159	-8.3	6.14	58250.7	8.99	HUMAN	B4E283	Apoptosis inhibitor 5
16410	dirMS_041712_NAR_50mM_plus2.15349.15349.3	3	7.28	1	1.10E+05		(R)VEKIPGG	(R)V E/K I/P G G I|I/E/D S/C/V\L R(G)	C:Carbamidomethylation	147.42	595.6548	1784.958	-0.0076	-4.3	4.68	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
16411	dirMS_041712_NAR_50mM_plus2.18035.18035.3	3	7.28	1	1.57E+06		(R)ELIKVLEI	(R)E L I K V L E E\A N Q|A|I|N\P K(L)		163.35	603.6741	1809.012	-0.0039	-2.2	4.79	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
16412	dirMS_041712_NAR_50mM_plus2.18902.18902.3	3	7.28	1	4.41E+05	M1m	(-)mDELQLI	(-)m/D/E/L/Q L/F R G D T V L L K(G)	m:Oxidized methionine	166.93	598.6527	1777.952	15.9919	-1.7	4.56	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
16413	dirMS_041712_NAR_50mM_plus2.5174.5174.3	3	7.28	0	5.02E+05	M434m M4	(R)LESGmC	(R)L E\S G/m Q N m S I/H T/K(T)	m:Oxidized methionine	86.25	503.2336	1475.698	31.9881	-1.1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
16414	dirMS_041712_NAR_50mM_plus2.6683.6683.3	3	7.28	0	1.30E+04		(K)TIEAEAA	(K)T I|E A/E A/A/H/G T V T R(H)		100.13	452.5685	1355.691	-0.0004	-0.3	5.37	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
16415	dirMS_041712_NAR_50mM_plus2.6932.6932.3	3	7.28	1	1.65E+05		(R)EGVLTGS	(R)E G V/L/T/G S P E Q K E E A/A K(A)		100.93	558.2837	1672.839	-0.0023	-1.4	4.49	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
16416	dirMS_041712_NAR_60mM_plus.7201.7201.3	3	7.28	0	7.57E+05		(K)LMELHG	(K)L/M/E/L/H G E G S S S\G K(A)		95.93	444.5486	1331.626	0.0053	3.9	5.4	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
16417	dirMS_041712_NAR_60mM_plus.7668.7668.2	2	7.28	1	1.09E+06		(R)AVVIVDI	(R)A V|V|I|V D/D R G R(S)		98.32	550.3143	1099.622	-0.0005	-0.5	6.01	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
16418	dirMS_041712_NAR_120mM_minus.5600.5600.3	3	7.27	1	1.23E+05		(K)CDSSPDS	(K)C/D/S S|P D/S A E/D/V R K(V)	C:Carbamidomethylation	83.98	489.2132	1465.622	0.0027	1.8	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
16419	dirMS_041712_NAR_120mM_minus.8773.8773.3	3	7.27	0	7.85E+05		(R)SNTENLS	(R)S N/T/E/N L/S Q/H F/R(K)		102.12	444.8813	1332.629	0.0002	0.2	6.47	43303.4	8.7	HUMAN	F8VRN8	LIM domain and actin-binding protein 1
16420	dirMS_041712_NAR_30mM_minus2.16143.16143.2	2	7.27	0	1.35E+05		(R)SLVSGLI	(R)S L|V/S/G/L/I R(L)		141.88	422.7649	844.525	-0.0026	-3	9.47	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
16421	dirMS_041712_NAR_40mM_minus2.10767.10767.3	3	7.27	0	1.27E+05	M56m	(K)VAIVKPG	(K)V A|I/V K P G V|P/m E I V L/N K(E)	m:Oxidized methionine	146.87	575.0112	1707.024	15.9953	0.2	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
16422	dirMS_041712_NAR_50mM_minus2.12197.12197.3	3	7.27	1	9.13E+04		(R)IAVVSEK	(R)I A/V V S E K G I/Y/S K(T)		137.27	431.9219	1293.741	0.0099	7.6	8.5	5163.5	4.49	HUMAN	Q9BXN2-8	Isoform 8 of C-type lectin domain family 7 member A
16423	dirMS_041712_NAR_50mM_minus2.7715.7731.3	3	7.27	1	4.75E+04		(K)TTSPPEV	(K)T T\S/P/P E/V/S G Y S Y E K/T E/R(S)		110.92	644.3067	1930.903	0.0027	1.4	4.78	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
16424	dirMS_041712_NAR_60mM_minus.12333.12333.3	3	7.27	1	4.18E+05		(R)INVYYNE	(R)I/N|V|Y Y|N E A T G G K/Y V/P R(A)		127.75	615.3145	1843.934	-0.0048	-2.6	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
16425	dirMS_041712_NAR_60mM_minus.15187.15187.3	3	7.27	1	1.80E+05		(K)IKDLSTV	(K)I K D L S T V|E/A L/Q N/L K(N)		144.25	524.6378	1571.9	-0.0015	-0.9	6.07	13242.4	4.17	HUMAN	E9PPH5	Acidic leucine-rich nuclear phosphoprotein 32 family member E (Fragment)
16426	dirMS_041712_NAR_60mM_minus.15235.15235.3	3	7.27	1	3.13E+05		(R)LLDAQLA	(R)L L/D|A Q/L/A T G G L V C P A R R(L)	C:Carbamidomethylation	145.53	604.3344	1810.996	-0.007	-3.8	9.6	266161	5.68	HUMAN	E9PPU0	Epiplakin
16427	dirMS_041712_NAR_60mM_minus.16981.16981.3	3	7.27	1	2.40E+05		(R)GQFSTD	(R)G Q|F S/T D E L/V/A E V E/K R(N)		154.08	569.9569	1707.855	0.0013	0.8	4.41	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
16428	dirMS_041712_NAR_60mM_minus.8584.8584.3	3	7.27	0	3.02E+05		(K)EFHLNES	(K)E F H L\N\E S/G D/P/S S K(S)		108.08	482.8882	1446.65	0.0005	0.3	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
16429	dirMS_041712_NAR_60mM_minus.9765.9765.3	3	7.27	1	1.01E+06		(K)TAVCDIP	(K)T A|V|C D/I/P P R G L K(M)	C:Carbamidomethylation	114.77	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
16430	dirMS_041712_NAR_120mM_plus.10379.10657.3	3	7.27	1	8.75E+05		(K)IKGEHPG	(K)I/K/G E H/P/G\L S I G D\V\A/K(K)		108.22	507.6167	1520.843	-0.0076	-5	6.75	24408.7	5.92	HUMAN	B2RPK0	Putative high mobility group protein B1-like 1
16431	dirMS_041712_NAR_120mM_plus.15719.15719.3	3	7.27	0	2.58E+05		(R)HTMMF	(R)H T M\M|F/S\A/T F/P K(E)		135.93	433.2091	1297.607	0.006	4.6	8.76	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
16432	dirMS_041712_NAR_20mM_plus.11481.11481.2	2	7.27	0	1.82E+05		(R)YALYDAT	(R)Y A\L|Y/D/A T Y E T K(E)		151.48	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
16433	dirMS_041712_NAR_20mM_plus.13477.13477.2	2	7.27	0	1.49E+05	M273m	(K)mISDAIP	(K)m I/S\D A I/P/E L K(A)	m:Oxidized methionine	165.25	566.7967	1116.597	15.9892	-5	4.37	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
16434	dirMS_041712_NAR_20mM_plus.17073.17073.3	3	7.27	0	1.36E+05		(R)AVLVDLE	(R)A V L V D L E/P/G T M D S V|R(S)		189.37	534.6105	1601.82	-0.0034	-2.1	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
16435	dirMS_041712_NAR_20mM_plus.7709.7709.2	2	7.27	0	3.70E+04		(R)VAIEPGA	(R)V/A/I E/P G A P R(E)		123.08	455.26	909.515	-0.0025	-2.8	5.97	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
16436	dirMS_041712_NAR_30mM_plus2.13380.13380.2	2	7.27	0	5.70E+05		(K)CPFTGN	(K)C/P/F|T|G N/V S I R(G)	C:Carbamidomethylation	122.88	575.7876	1150.567	0.0006	0.5	9.75	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
16437	dirMS_041712_NAR_30mM_plus2.21845.21845.2	2	7.27	0	2.28E+05		(R)TTNFAG	(R)T T|N|F/A/G I L/S/Q G L R(I)		169.48	689.3749	1377.748	-0.006	-4.3	9.41	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
16438	dirMS_041712_NAR_30mM_plus2.9664.9664.2	2	7.27	0	1.36E+06		(R)QLSSGVS	(R)Q L/S S G V/S/E/I/R(H)		104.9	538.2855	1075.574	-0.0105	-9.8	6	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
16439	dirMS_041712_NAR_40mM_plus2.10984.10984.3	3	7.27	0	6.82E+04		(R)LLELGPK	(R)L L|E/L|G P K P E V/A Q Q T R(K)		131.02	560.318	1678.949	-0.0092	-5.5	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
16440	dirMS_041712_NAR_50mM_plus2.16204.16204.3	3	7.27	0	1.05E+06		(R)LSFQHD	(R)L/S F Q H D P E/T\S/V/L/V L R(K)		152.42	580.9801	1740.928	-0.0022	-1.2	5.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
16441	dirMS_041712_NAR_50mM_plus2.21439.21439.3	3	7.27	0	4.25E+06		(R)LHFFMP	(R)L H\F F\M P G\F|A|P\L T S R(G)		182.13	540.9498	1620.835	-0.0007	-0.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
16442	dirMS_041712_NAR_50mM_plus2.8747.8747.3	3	7.27	1	2.21E+05		(K)TTSPPEV	(K)T T|S P/P/E V S/G Y/S Y E K/T E/R(S)		113.33	644.3093	1930.903	0.0105	5.4	4.78	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
16443	dirMS_041712_NAR_60mM_plus.16262.16262.3	3	7.27	1	2.20E+05		(K)GIDRYNI	(K)G I D R Y N|P\E/N/L A/T L E R(Y)		141.9	587.635	1760.893	-0.0021	-1.2	4.68	24768.8	4.76	HUMAN	B7ZAM9	Eukaryotic translation initiation factor 3 subunit K
16444	dirMS_041712_NAR_60mM_plus.19243.19243.3	3	7.27	1	4.20E+05		(R)TRIEGLL	(R)T R\I E G\L\L/A A/F/P K(L)		159.27	439.262	1315.773	-0.0018	-1.4	8.41	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
16445	dirMS_041712_NAR_60mM_plus.20695.20695.3	3	7.27	1	4.77E+05		(R)DSIVAEL	(R)D S/I/V/A E L D/R E M S R(S)		168.38	507.5883	1520.737	0.013	8.6	4.32	34709.6	4.98	HUMAN	O14579	Coatomer subunit epsilon
16446	dirMS_041712_NAR_120mM_minus.15614.15614.4	4	7.26	2	2.58E+05		(R)EDLRLPE	(R)E D L R L/P E G D/L/G K E I E Q K(Y)		138.85	493.0108	1969.024	-0.0023	-1.2	4.36	16346.3	4.85	HUMAN	I3L397	Eukaryotic translation initiation factor 5A-1 (Fragment)
16447	dirMS_041712_NAR_120mM_minus.5535.5557.2	2	7.26	1	6.56E+05		(K)CDVDIRK	(K)C/D|V/D|I R\K(D)	C:Carbamidomethylation	84.02	453.2291	905.451	0	0	5.96	42675.9	5.9	HUMAN	I3L3I4	Actin, cytoplasmic 2, N-terminally processed
16448	dirMS_041712_NAR_120mM_minus.7616.7616.3	3	7.26	1	7.89E+05		(K)IQDKEGI	(K)I Q D K E G\I|P/P D Q Q/R(L)		94.92	508.5981	1523.781	-0.0015	-1	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
16449	dirMS_041712_NAR_20mM_minus.11109.11109.2	2	7.26	0	1.31E+05	M92m	(R)ImNTFSV	(R)I m/N/T/F/S V/V/P S P K(V)	m:Oxidized methionine	158.32	668.3513	1319.703	15.9925	-1.8	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
16450	dirMS_041712_NAR_20mM_minus.14158.14158.2	2	7.26	0	7.07E+03		(R)YLTVAAV	(R)Y L|T/V A/A V F R(G)		195.1	520.3009	1039.593	0.001	1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
16451	dirMS_041712_NAR_30mM_minus2.10054.10054.2	2	7.26	0	6.98E+04	M1026m	(K)QVSVFQ	(K)Q V/S/V|F/Q/A m K(K)	m:Oxidized methionine	109.02	527.2782	1037.545	16.0043	8.9	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
16452	dirMS_041712_NAR_30mM_minus2.13163.13163.2	2	7.26	0	1.50E+05		(K)VPVNLLI	(K)V/P/V/N L L/R(A)		125.33	405.7631	810.52	-0.0007	-0.8	9.72	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
16453	dirMS_041712_NAR_30mM_minus2.17755.17755.2	2	7.26	0	2.08E+05		(R)TEMDW	(R)T/E|M/D/W V L/K(H)		151.1	511.2565	1021.502	0.0034	3.4	4.37	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
16454	dirMS_041712_NAR_40mM_minus2.8315.8315.3	3	7.26	0	3.89E+03		(R)LLELGPK	(R)L L|E/L/G P K P E V A\Q/Q T R(K)		129.42	560.3204	1678.949	-0.002	-1.2	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha

16455	dirMS_041712_NAR_50mM_minus2.11168.11168.3	3	7.26	0	1.66E+04		(R)VVVLMC	(R)V V|V|L/M/G S\T S D/L G H C E K(I)	C:Carbamidomethylation	132.28	577.9535	1731.84	0.0055	3.2	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
16456	dirMS_041712_NAR_50mM_minus2.7971.7971.3	3	7.26	1	1.81E+05		(R)IITEGFE	(R)I/I|T E/G F E A A/K E K(A)		112.27	445.912	1335.716	0.006	4.5	4.79	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
16457	dirMS_041712_NAR_60mM_minus.11269.11269.3	3	7.26	1	1.43E+05		(R)DGKLVS	(R)D G K L V\S E|S/S D V/L/P K(-)		123.12	491.927	1473.78	-0.0131	-8.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
16458	dirMS_041712_NAR_60mM_minus.11297.11297.3	3	7.26	1	9.28E+05	M232m	(R)MSmKE	(R)M/S m K E V D E/Q|M/L/N V/Q N K(N)	m:Oxidized methionine	122.78	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
16459	dirMS_041712_NAR_120mM_plus.22532.22532.4	4	7.26	1	5.59E+05		(K)SKGLAPI	(K)S\K/G L A P D\L/P E D L Y H L I/K(K)		171.52	478.0137	1909.043	-0.01	-5.2	5.36	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
16460	dirMS_041712_NAR_120mM_plus.4169.4169.2	2	7.26	1	1.45E+06	M310m	(R)TKTEISE	(R)T K|T/E\I/S E m/N R(N)	m:Oxidized methionine	69.8	612.7976	1208.594	15.994	-0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
16461	dirMS_041712_NAR_120mM_plus.7490.7490.2	2	7.26	0	1.77E+05		(R)LYVHEA	(R)L/Y|V/H E/A V K(A)		93.27	479.7757	958.536	0.0085	8.8	6.75	533778	5.74	HUMAN	Q15149	Plectin
16462	dirMS_041712_NAR_20mM_plus.12970.12970.2	2	7.26	0	3.19E+05	M316m	(R)ISEQFTA	(R)I S\E/Q/F/T/A m F R(R)	m:Oxidized methionine	161.53	623.3012	1229.598	15.9968	1.5	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
16463	dirMS_041712_NAR_20mM_plus.13517.13517.2	2	7.26	0	1.51E+05		(R)GDLGIEI	(R)G D L/G I/E/I/P A E/K(V)		166.22	571.3075	1141.61	-0.0022	-1.9	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
16464	dirMS_041712_NAR_20mM_plus.17635.17635.2	2	7.26	0	3.49E+04	M199m	(K)SmVPVC	(K)S m|V/P/V\Q V Q L D/V/P V V K(V)	m:Oxidized methionine	192.93	827.4624	1637.93	15.988	-4.2	5.55	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
16465	dirMS_041712_NAR_20mM_plus.17865.17865.2	2	7.26	0	9.78E+04		(K)VDFPQD	(K)V D/F/P Q\D/Q L T A L\T G R(I)		194.95	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
16466	dirMS_041712_NAR_20mM_plus.6020.6020.3	3	7.26	0	1.02E+06	M295m M:	(R)mGQmA	(R)m\G Q m\A\m G G|A|m/G/I/N N R(G)	m:Oxidized methionine	100.27	534.8861	1538.67	63.9743	-3.4	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
16467	dirMS_041712_NAR_20mM_plus.6951.6951.2	2	7.26	0	8.44E+04	M29m	(K)IVQmTE	(K)I\V/Q/m/T\E A/E V R(G)	m:Oxidized methionine	114.35	596.3035	1175.609	15.9908	-3.4	4.53	14493.5	5.23	HUMAN	C9J9S3	Serine/threonine-protein phosphatase (Fragment)
16468	dirMS_041712_NAR_20mM_plus.7483.7483.2	2	7.26	0	2.70E+05		(K)TGQAPC	(K)T G\Q|A|P/G Y|S Y T A A N K(N)		119.58	714.8394	1428.675	-0.0039	-2.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
16469	dirMS_041712_NAR_40mM_plus2.12510.12510.2	2	7.26	0	2.54E+04		(K)ICSWNV	(K)I C|S W N V D/G L/R(A)	C:Carbamidomethylation	140.23	610.297	1219.589	-0.0021	-1.7	5.84	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
16470	dirMS_041712_NAR_40mM_plus2.6815.6815.2	2	7.26	0	5.30E+03		(R)FLNAEN	(R)F L|N A/E N/A Q/K(F)		99.83	517.7656	1034.526	-0.0026	-2.5	6	20592.3	9.75	HUMAN	B3KUP2	RAN binding protein 1, isoform CRA_f
16471	dirMS_041712_NAR_50mM_plus2.11450.11450.3	3	7.26	0	5.84E+04		(K)SLYVAEY	(K)S L\Y/V/A E Y H S E P V E D/E K/P(-)		127.85	664.6463	1991.923	0.0011	0.5	4.25	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
16472	dirMS_041712_NAR_50mM_plus2.9790.9790.3	3	7.26	0	8.80E+04		(R)AVIEHNI	(R)A V/I/E H N L L S A\S K(L)		119.05	427.9124	1281.716	0.0065	5.1	6.79	40481.5	6.48	HUMAN	B3KST5	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis), isoform CRA_a
16473	dirMS_041712_NAR_60mM_plus.14427.14427.3	3	7.26	1	1.86E+03		(R)TVENIKD	(R)T/V|E N I\K D/P L F R(F)		133.2	444.5813	1331.732	-0.0024	-1.8	5.74	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
16474	dirMS_041712_NAR_60mM_plus.16491.16491.3	3	7.26	0	2.67E+05		(R)HSVGM	(R)H S V G M\A\V L/G/Q/L A R(R)		142.93	446.9171	1338.731	0.0057	4.2	9.75	20278.4	11.86	HUMAN	C9J7Z1	Probable peptidyl-tRNA hydrolase
16475	dirMS_041712_NAR_60mM_plus.6454.6454.2	2	7.26	1	1.46E+05		(K)GSGTAE	(K)G S|G\T/A/E V E\L K/K(G)		92.38	559.806	1118.605	-0.0005	-0.4	6.14	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
16476	dirMS_041712_NAR_60mM_plus.8065.8065.3	3	7.26	1	2.40E+06	M174m	(R)VKYETEL	(R)V/K Y E T E|L/A/m/R(Q)	m:Oxidized methionine	101.42	419.2169	1239.64	15.996	0.8	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
16477	dirMS_041712_NAR_120mM_minus.9755.9755.3	3	7.25	1	3.16E+05		(K)YIDENQI	(K)Y/I/D/E/N Q D R\Y/I K(K)		108.1	486.2403	1456.707	-0.0003	-0.2	4.56	6412.4	9.52	HUMAN	J3KSS4	Cytosolic non-specific dipeptidase (Fragment)
16478	dirMS_041712_NAR_30mM_minus2.16699.16699.2	2	7.25	0	2.35E+05		(K)NAAGAL	(K)N A|A/G A|L D L L K(E)		144.27	493.2881	985.568	0.0013	1.3	5.84	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
16479	dirMS_041712_NAR_40mM_minus2.12226.12226.3	3	7.25	1	2.85E+05		(K)DVAIKEF	(K)D V|A I\K E P\L/V/D/V V D P K(Q)		156.08	546.3068	1636.916	-0.0098	-6	4.23	24376.8	6.08	HUMAN	E9PIX6	Protein arginine N-methyltransferase 1 (Fragment)
16480	dirMS_041712_NAR_50mM_minus2.18156.18156.3	3	7.25	0	1.01E+06		(K)ALESPEF	(K)A L/E/S/P E R P F L A I L G G A K(V)		173.62	590.3356	1768.996	-0.0033	-1.9	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
16481	dirMS_041712_NAR_60mM_minus.12048.12048.3	3	7.25	1	2.54E+03		(R)VIDRELY	(R)V/I|D R E L\Y/Q/Q L Q R(G)		128.12	520.9529	1560.849	-0.0051	-3.3	6.04	533778	5.74	HUMAN	Q15149	Plectin
16482	dirMS_041712_NAR_60mM_minus.6391.6391.3	3	7.25	0	5.08E+04		(R)CPPGVV	(R)C P/P G V V|P A C/H N S K(D)	C:Carbamidomethylation	94.08	474.8938	1422.662	0.0052	3.6	8.76	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
16483	dirMS_041712_NAR_120mM_plus.18030.18030.3	3	7.25	1	3.70E+05		(R)ARFEELN	(R)A R F E E L/N|A/D/L F|R(G)		147.85	494.2571	1480.754	0.0024	1.7	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
16484	dirMS_041712_NAR_20mM_plus.12640.12640.2	2	7.25	1	1.21E+05	S1216s	(K)VKGDVD	(K)V K G D/V|D V/s V P K(V)	s:N-acetylglucosamine (S)	160.13	673.3693	1142.642	203.0898	7.7	5.93	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
16485	dirMS_041712_NAR_30mM_plus2.6836.6836.2	2	7.25	0	1.17E+05		(R)EMDEQI	(R)E/M/D/E/Q I/R(L)		90.27	460.7158	920.414	0.0101	11	4.14	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
16486	dirMS_041712_NAR_40mM_plus2.13605.13605.3	3	7.25	0	1.65E+05		(K)NLPPSG	(K)N L P P S\G A V/P\V T G I/P P H V V K(V)		146.07	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
16487	dirMS_041712_NAR_50mM_plus2.7709.7709.3	3	7.25	1	2.65E+05		(K)GGIMLP	(K)G G|I/M/L/P E K S Q G K(V)		106.62	415.5609	1244.667	0.0014	1.1	8.59	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
16488	dirMS_041712_NAR_50mM_plus2.8233.8233.3	3	7.25	0	6.80E+04		(K)LDSPAG	(K)L/D S/P A G T A\L/S/P/S G H T K(L)		109.98	513.5973	1538.781	-0.0036	-2.3	6.74	36208.1	7.21	HUMAN	B4DMU0	Pyrroline-5-carboxylate reductase
16489	dirMS_041712_NAR_50mM_plus2.9712.9712.3	3	7.25	0	7.45E+04		(K)GAVDGC	(K)G A V|D/G G L/S I/P/H S T K(R)		118.58	446.9057	1338.701	0.0013	1	6.74	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
16490	dirMS_041712_NAR_60mM_plus.11382.11382.3	3	7.25	0	3.70E+05		(R)SLGTAD	(R)S L/G/T/A/D/V H/F E/R(K)		116.88	411.2075	1231.607	0.0014	1.1	5.3	27557.2	11.05	HUMAN	E9PB61	THO complex subunit 4
16491	dirMS_041712_NAR_60mM_plus.18329.18329.3	3	7.25	1	5.41E+05		(R)IRIDSLSA	(R)I R I D S L\S\A Q/L/S Q/L Q/K(Q)		153.63	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
16492	dirMS_041712_NAR_30mM_minus2.15371.15371.2	2	7.24	0	1.76E+04		(R)IGGGID	(R)I G\G\G I/D/V\P V P R(H)		137.17	540.3087	1079.621	-0.0106	-9.9	5.84	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
16493	dirMS_041712_NAR_30mM_minus2.8398.8398.2	2	7.24	0	1.09E+05		(K)CAMTAL	(K)C A/M/T/A L/S/S K(L)	C:Carbamidomethylation	100.45	484.7299	968.454	-0.0014	-1.5	8.75	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
16494	dirMS_041712_NAR_50mM_minus2.10544.10544.3	3	7.24	0	1.12E+05	M271m	(R)DLSYCLS	(R)D L|S/Y/C L S G m Y D/H R(Y)	C:Carbamidomethylation m:Oxid	128.07	544.8966	1616.683	15.9921	-1.7	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
16495	dirMS_041712_NAR_50mM_minus2.11442.11442.3	3	7.24	0	2.35E+04		(R)LIAEQPF	(R)L I A E Q/P P H L T P/G I R(E)		133.68	514.6309	1541.88	-0.0017	-1.1	6.75	20915.7	6.45	HUMAN	C9JBI3	Phosphoserine phosphatase (Fragment)
16496	dirMS_041712_NAR_50mM_minus2.12103.12103.3	3	7.24	1	2.47E+04		(K)SSPVDL	(K)S S|P V/D L V T/A T D Q K V E K(M)		136.9	572.9736	1716.901	0.0048	2.8	4.56	17343.9	8.78	HUMAN	E5RG13	Inositol monophosphatase 1 (Fragment)
16497	dirMS_041712_NAR_50mM_minus2.6197.6197.3	3	7.24	0	4.44E+05	M434m	(R)LESGmC	(R)L E|S G m\Q N/M S I H T/K(T)	m:Oxidized methionine	97.77	497.9018	1475.698	15.9927	-1.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
16498	dirMS_041712_NAR_50mM_minus2.6870.6870.3	3	7.24	1	2.02E+04	S154s	(R)SQKLSIs	(R)S Q|K/L S I|s A V/I S(-)	s:N-acetylglucosamine (S)	105.67	445.926	1132.657	203.1062	20.1	8.47	17917.3	5.86	HUMAN	C9JLE9	Kelch-like protein 22 (Fragment)
16499	dirMS_041712_NAR_60mM_minus.14182.14182.3	3	7.24	0	1.71E+05		(R)NFDLTA	(R)N F/D L T A I/P C A/N H K(M)	C:Carbamidomethylation	139.13	500.914	1500.726	0.0011	0.7	6.74	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
16500	dirMS_041712_NAR_60mM_minus.19661.19661.3	3	7.24	1	3.15E+05		(R)ARDDLIT	(R)A R\D D\L\I T/D|L L/N/E A K(Q)		176.95	529.6145	1586.838	-0.0095	-6	4.23	23653.1	9.28	HUMAN	C9J8H1	V-type proton ATPase subunit E 1 (Fragment)
16501	dirMS_041712_NAR_60mM_minus.8128.8128.3	3	7.24	1	6.51E+04		(K)SLVSDKT	(K)S L|V/S D/K T S I S E K(V)		105.47	431.9006	1293.69	-0.0024	-1.8	5.79	58791	9.93	HUMAN	E9PDI4	Ladinin-1
16502	dirMS_041712_NAR_60mM_minus.9851.9851.3	3	7.24	1	9.10E+04		(K)KTGCNV	(K)K T G C\N V/L/L\I/Q K(S)	C:Carbamidomethylation	114.63	425.2478	1273.73	-0.0008	-0.6	10	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
16503	dirMS_041712_NAR_60mM_minus.9968.9968.3	3	7.24	1	2.53E+05		(K)QTLENEI	(K)Q/T L/E/N E R G E/L A\N E V K(V)		115.13	577.2903	1729.872	-0.0152	-8.8	4.49	227783.5	5.5	HUMAN	P35579	Myosin-9
16504	dirMS_041712_NAR_120mM_plus.4703.4703.3	3	7.24	0	3.30E+05		(K)ISRPGDS	(K)I/S/R P G D/S D/D/S R(S)		75.02	402.1896	1204.555	-0.001	-0.8	4.43	64759.2	8.88	HUMAN	P14866	Heterogeneous nuclear ribonucleoprotein L
16505	dirMS_041712_NAR_20mM_plus.11542.11542.2	2	7.24	0	1.16E+05		(R)ANTFVA	(R)A N/T/F/V/A/E/L K(G)		152.8	496.7735	992.541	-0.0014	-1.4	6.05	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
16506	dirMS_041712_NAR_20mM_plus.13304.13304.2	2	7.24	0	9.69E+04		(R)AELIVQF	(R)A E/L|I/V Q|P E L\K(Y)		164.3	570.3361	1139.667	-0.0021	-1.9	4.53	334221.3	6.44	HUMAN	P15924	Desmoplakin
16507	dirMS_041712_NAR_20mM_plus.7724.7724.2	2	7.24	0	3.70E+04		(R)VAIEPGA	(R)V A|I/E/P G A P R(E)		123.08	455.26	909.515	-0.0025	-2.8	5.97	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
16508	dirMS_041712_NAR_30mM_plus2.11415.11415.2	2	7.24	0	2.32E+05		(-)MMEVA	(-)M/M/E|V\A A A D V/K(Q)		113.63	532.7609	1064.512	0.003	2.9	4.37	9475.6	4.64	HUMAN	J3KRD5	Cytosolic non-specific dipeptidase (Fragment)
16509	dirMS_041712_NAR_30mM_plus2.5427.5427.2	2	7.24	0	5.67E+04		(R)TDTGEP	(R)T D/T|G/E P M G R(G)		81.95	482.2128	963.42	-0.0017	-1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
16510	dirMS_041712_NAR_40mM_plus2.10032.10032.2	2	7.24	0	9.42E+04		(K)YEELQV	(K)Y E|E|L/Q V T A/G K(H)		123.57	569.2912	1137.579	-0.0035	-3.1	4.53	58119.8	6.75	HUMAN	Q5XKE5	Keratin, type II cytoskeletal 79
16511	dirMS_041712_NAR_40mM_plus2.9559.9559.2	2	7.24	0	5.93E+04		(R)NYYEQW	(R)N Y|Y/E Q/W G K(L)		119.3	544.2469	1087.484	0.0022	2	6	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
16512	dirMS_041712_NAR_50mM_plus2.11165.11165.3	3	7.24	1	1.15E+05		(K)VGDKVL	(K)V G\D K V L L|P/E/Y/G G T K(V)		125.85	492.6069	1475.81	-0.0043	-2.9	6.04	5189.9	4.56	HUMAN	B8ZZ54	10 kDa heat shock protein, mitochondrial
16513	dirMS_041712_NAR_120mM_minus.13257.13257.3	3	7.23	2	2.61E+05		(R)AQKDEE	(R)A Q/K/D E E K M E I/Q\E\I Q L K(E)		126.68	654.0058	1960.006	-0.0027	-1.4	4.58	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
16514	dirMS_041712_NAR_120mM_minus.13404.13404.3	3	7.23	0	2.41E+04	M1m	(-)mVNHFI	(-)m V N H\F/I/A E F/K(R)	m:Oxidized methionine	126.85	417.8786	1235.624	15.9971	1.8	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
16515	dirMS_041712_NAR_120mM_minus.20073.20073.3	3	7.23	0	4.35E+05	M195m	(R)LHFFmP	(R)L H\F F m|P G F/A/P L T S R(G)	m:Oxidized methionine	166.03	546.2809	1620.835	15.9926	-1.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
16516	dirMS_041712_NAR_20mM_minus.14365.14365.2	2	7.23	0	1.70E+05		(K)LVLPSLIS	(K)L V|L/P S L I S S R(I)		198.08	542.8402	1084.672	0.0007	0.6	9.75	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
16517	dirMS_041712_NAR_30mM_minus2.19365.19365.2	2	7.23	0	2.42E+05		(R)FEELNAI	(R)F E|E|L/N A/D\L F|R(G)		160.88	627.3141	1253.616	0.0048	3.9	4.14	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
16518	dirMS_041712_NAR_40mM_minus2.14310.14310.3	3	7.23	0	1.23E+05		(R)GTEDITS	(R)G T|E/D/I/T S P H G I/P L D\L\L D R(V)		168.55	650.3366	1948.997	-0.0022	-1.1	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
16519	dirMS_041712_NAR_40mM_minus2.9426.9426.3	3	7.23	0	2.15E+05	M114m M:	(R)AGKPVI	(R)A G K\P V I|C\A T/Q/m|L E/S m I K(K)	C:Carbamidomethylation m:Oxid	138.18	636.9906	1876.969	31.9879	-1	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
16520	dirMS_041712_NAR_50mM_minus2.17408.17408.3	3	7.23	0	2.39E+05		(R)LLLDGAI	(R)L L/L D G A/P/L I A I/H K(A)		168.43	458.6218	1373.852	-0.0007	-0.5	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
16521	dirMS_041712_NAR_60mM_minus.13444.13444.3	3	7.23	1	3.04E+05		(K)FSIEDLK	(K)F/S/I/E D L K A Q/P K(Q)		135.1	425.9025	1275.694	-0.0014	-1.1	6.07	13579.2	9.99	HUMAN	E9PPQ6	Thymocyte nuclear protein 1 (Fragment)
16522	dirMS_041712_NAR_60mM_minus.18134.18134.3	3	7.23	1	4.95E+04		(K)SLLGKD	(K)S L|L G/K/D V\L F L K(D)		162.28	411.5912	1232.761	-0.0022	-1.8	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
16523	dirMS_041712_NAR_60mM_minus.6477.6477.3	3	7.23	1	1.99E+05		(R)AIEAAP	(R)A I/E A/A|P\Q E P E Q K R(S)		95.33	489.5907	1466.76	-0.0022	-1.5	4.79	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
16524	dirMS_041712_NAR_120mM_plus.9077.9077.2	2	7.23	0	6.58E+04		(K)HVVFIA	(K)H/V|V/F I A Q/R(R)		100.83	485.2849	969.563	-0.0003	-0.3	9.75	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
16525	dirMS_041712_NAR_20mM_plus.10677.10677.3	3	7.23	0	2.82E+04		(K)SQLLAPI	(K)S Q\L L A/P/P|P/P S A P P G N K(T)		146.3	524.2902	1570.859	-0.0027	-1.7	8.47	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
16526	dirMS_041712_NAR_20mM_plus.18662.18796.2	2	7.23	0	1.68E+05		(R)IITLTGP	(R)I I|T\L/T|G|P T N A I F K(A)		200.4	694.9091	1388.815	-0.0039	-2.8	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
16527	dirMS_041712_NAR_20mM_plus.9480.9480.2	2	7.23	0	1.43E+05		(R)GTGIVS	(R)G T G\I/V/S A P V P/K(K)		136.92	513.3057	1025.599	0.0052	5	8.75	21898	11.33	HUMAN	E9PM36	40S ribosomal protein S2
16528	dirMS_041712_NAR_30mM_plus2.19915.19915.2	2	7.23	0	2.21E+05		(K)GFAFVQ	(K)G F\A|F/V|Q/Y V N E R(N)		157.65	665.3326	1329.659	-0.0007	-0.5	6	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
16529	dirMS_041712_NAR_40mM_plus2.11839.11839.3	3	7.23	2	6.86E+04	K413k	(K)LDDLFSD	(K)L D/D/L|F S/D N G R V R A k(L)	k:Ubiquitin-K	136.07	573.9644	1605.834	114.0443	0.8	6.04	116716.6	9.41	HUMAN	F5H3X0	CLIP-associating protein 2
16530	dirMS_041712_NAR_40mM_plus2.12537.12537.2	2	7.23	0	2.11E+05		(R)YIEIFK(S	(R)Y/I|E I/F K(S)		140.35	406.7302	812.455	-0.0021	-2.6	6	24249.1	6.99	HUMAN	D6RBM0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
16531	dirMS_041712_NAR_40mM_plus2.13847.13847.3	3	7.23	0	2.23E+05		(K)VALLLLD	(K)V A\L L/L|L D Q/G A/S P H A A A K(N)		148.13	558.9886	1674.954	-0.0025	-1.5	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
16532	dirMS_041712_NAR_40mM_plus2.16309.16309.2	2	7.23	0	1.50E+05		(R)YLTVAA	(R)Y L|T/V|A\A V F R(G)		162.03	520.2997	1039.593	-0.0014	-1.3	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
16533	dirMS_041712_NAR_40mM_plus2.9669.9669.3	3	7.23	0	1.82E+05		(R)AAEDPV	(R)A A|E/D/P/V A A A\P R P L P A G G R(L)		120.85	572.6438	1715.919	-0.0019	-1.1	6.12	73966.7	10.21	HUMAN	B3KWK6	Alpha-L-iduronidase
16534	dirMS_041712_NAR_50mM_plus2.12983.12983.3	3	7.23	0	5.97E+05		(R)FDAERP	(R)F/D/A E R\P V D\C/S/V I V V/N K(Q)	C:Carbamidomethylation	135.82	616.6476	1847.932	-0.0038	-2	4.56	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
16535	dirMS_041712_NAR_60mM_plus.10102.10102.2	2	7.23	0	2.03E+06		(K)GIVEFSG	(K)G I/V|E|F/S G K/P A A R(K)		111.3	616.3425	1231.679	-0.0016	-1.3	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
16536	dirMS_041712_NAR_60mM_plus.11879.11879.3	3	7.23	1	5.04E+05		(R)SEQEFQ	(R)S E|Q|E/F Q/E Q L E S A R R(E)		119.45	579.6102	1736.82	-0.0038	-2.2	4.49	66923.1	6.88	HUMAN	E9PG35	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (Fragment)
16537	dirMS_041712_NAR_60mM_plus.5803.5803.3	3	7.23	0	2.06E+04		(R)AVTNHS	(R)A V/T N H\S V Y/C/S T K(G)	C:Carbamidomethylation	88.8	456.2187	1366.642	-0.0004	-0.3	8.64	15120.3	9.29	HUMAN	J3KRZ4	L-xylulose reductase (Fragment)
16538	dirMS_041712_NAR_120mM_minus.11082.11082.3	3	7.22	0	9.62E+05		(R)GFCLPPI	(R)G F\C L/P/P H C S R(G)	C:Carbamidomethylation	113.83	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
16539	dirMS_041712_NAR_20mM_minus.12541.12541.2	2	7.22	0	3.92E+05	M185m	(K)LAVNm	(K)L A\V/N/m V/P\F|P R(L)	m:Oxidized methionine	172.97	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
16540	dirMS_041712_NAR_40mM_minus2.10784.10784.3	3	7.22	0	1.27E+05	M56m	(K)VAIVKPC	(K)V A/I V K P G V/P m\E I/V/L N K(E)	m:Oxidized methionine	146.87	575.0112	1707.024	15.9953	0.2	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
16541	dirMS_041712_NAR_50mM_minus2.6590.6590.3	3	7.22	0	1.34E+05	M185m M:	(R)DFTVSA	(R)D F\T V/S A\m H G D m D Q/K(E)	m:Oxidized methionine	103.42	538.5571	1581.667	31.9895	-0.2	4.41	26945.8	8.07	HUMAN	J3KSZ0	Eukaryotic initiation factor 4A-I (Fragment)
16542	dirMS_041712_NAR_60mM_minus.16833.16833.3	3	7.22	0	1.02E+05		(K)ICDQWD	(K)I/C|D Q|W D A/L G S L/T H S/R(R)	C:Carbamidomethylation	153.88	586.9446	1758.823	-0.0035	-2	5.21	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
16543	dirMS_041712_NAR_60mM_minus.8421.8421.3	3	7.22	1	6.45E+04		(K)QGIETPE	(K)Q G I/E/T/P E D/Q/N D L R K(M)		106.97	548.2737	1642.803	0.0034	2.1	4.32	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
16544	dirMS_041712_NAR_120mM_plus.14001.14001.3	3	7.22	1	4.03E+05		(K)WKDSDE	(K)W\K D S D E|A/D\L V/L/A K(E)		126.42	497.2584	1489.753	0.0073	4.9	4.23	20982.2	5.23	HUMAN	Q13185	Chromobox protein homolog 3
16545	dirMS_041712_NAR_120mM_plus.21133.21133.4	4	7.22	0	3.26E+05		(K)ALEHAF	(K)A L/E H A/F Q L E H/I/M D L T R(L)		163.93	481.7493	1923.975	0.0008	0.4	5.27	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
16546	dirMS_041712_NAR_20mM_plus.18417.18417.3	3	7.22	0	2.23E+05		(R)LSVEEA	(R)L S V E E A V\A A G\V/V/G/G E I Q E K(L)		198.5	629.0001	1884.991	-0.0056	-2.9	4.09	266161	5.68	HUMAN	E9PPU0	Epiplakin
16547	dirMS_041712_NAR_30mM_plus2.12545.12545.2	2	7.22	0	2.50E+05		(R)NCSSFLI	(R)N C|S/S F L/I/K(R)	C:Carbamidomethylation	118.65	484.7469	968.487	-0.0005	-0.5	8.75	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
16548	dirMS_041712_NAR_30mM_plus2.16078.16078.2	2	7.22	0	1.85E+04		(K)TDTVLIL	(K)T D|T|V/L I L/C R(K)	C:Carbamidomethylation	135.78	545.7923	1090.593	-0.0152	-13.9	5.5	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
16549	dirMS_041712_NAR_30mM_plus2.19745.19745.2	2	7.22	0	2.35E+05		(K)APDFVF	(K)A P D/F|V/F/Y A P R(L)		156.72	591.8008	1182.594	0.0001	0.1	5.88	71218.8	6.3	HUMAN	A7YIJ8	Radixin
16550	dirMS_041712_NAR_30mM_plus2.9065.9065.2	2	7.22	0	4.34E+05	M176m	(K)VLEGmE	(K)V/L|E/G m E V V/R(K)	m:Oxidized methionine	100.57	524.279	1031.555	15.9953	0.4	4.53	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
16551	dirMS_041712_NAR_30mM_plus2.9161.9161.2	2	7.22	0	3.70E+05		(K)ATFDAIS	(K)A/T|F D A I/S K(T)		101.83	426.7266	852.446	-0.0002	-0.3	5.88	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
16552	dirMS_041712_NAR_40mM_plus2.12649.12649.3	3	7.22	0	4.95E+03		(K)LTGDVEI	(K)L T/G D V E/E L E I Q/E K P A L K(V)		140.8	638.0075	1912.027	-0.0194	-10.1	4.25	74103.6	5.35	HUMAN	G5E9W3	Cleavage and polyadenylation specific factor 3, 73kDa, isoform CRA_b
16553	dirMS_041712_NAR_40mM_plus2.13599.13599.3	3	7.22	0	3.25E+05		(K)SIEIPRP	(K)S I|E I/P R\P V D G V E/V|P G C G K(I)	C:Carbamidomethylation	146	637.0002	1908.985	0.0013	0.7	4.68	34243.5	4.88	HUMAN	K7ENG2	Splicing factor U2AF 65 kDa subunit
16554	dirMS_041712_NAR_40mM_plus2.17982.17982.3	3	7.22	0	1.71E+05		(K)ISSIQSIV	(K)I/S S I/Q S I V/P A L E I/A N/A H R(K)		172.4	640.3668	1919.071	0.015	7.8	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
16555	dirMS_041712_NAR_40mM_plus2.6307.6307.2	2	7.22	1	2.84E+05		(R)YSGGNY	(R)Y S|G G N/Y R D N Y|D\N(-)		95.58	719.2857	1437.567	-0.0024	-1.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
16556	dirMS_041712_NAR_40mM_plus2.6908.6908.2	2	7.22	0	5.95E+04		(K)CCTESLV	(K)C/C|T\E S L/V N/R(R)	C:Carbamidomethylation	100.58	569.7569	1138.498	0.0086	7.5	6	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
16557	dirMS_041712_NAR_50mM_plus2.10856.10856.3	3	7.22	0	1.82E+05		(K)GYAEVV	(K)G Y|A E/V/V V A/S E N S V/H K(L)		124.73	530.2702	1588.797	-0.0005	-0.3	5.4	16170.5	4.37	HUMAN	C9J286	Cleavage and polyadenylation-specificity factor subunit 7 (Fragment)
16558	dirMS_041712_NAR_50mM_plus2.13626.13626.3	3	7.22	0	1.38E+06		(K)STTSDIP	(K)S T/T/S/D I P H/M L N/Q V E/S K(V)		140.25	596.2908	1786.864	-0.0061	-3.4	5.3	11532.2	6.34	HUMAN	H0YNA1	Protein FAM98B (Fragment)
16559	dirMS_041712_NAR_50mM_plus2.13700.13700.3	3	7.22	0	8.59E+05		(K)AASDIAI	(K)A/A|S/D I|A\M/T E L/P/P T H P I R(L)		140.1	607.3177	1819.937	0.0015	0.8	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
16560	dirMS_041712_NAR_50mM_plus2.15038.15038.3	3	7.22	1	2.05E+05		(R)QVFGEA	(R)Q\V/F/G/E A T K Q/P G I T F I A A K(F)		147.35	636.0141	1906.043	-0.0155	-8.1	8.59	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
16561	dirMS_041712_NAR_50mM_plus2.19182.19182.3	3	7.22	1	2.06E+05		(K)LALFQAI	(K)L A|L F/Q/A/I G K E V V D/R(A)		168.82	520.3019	1558.895	-0.004	-2.6	6.07	266161	5.68	HUMAN	E9PPU0	Epiplakin
16562	dirMS_041712_NAR_60mM_plus.12944.12944.3	3	7.22	0	1.66E+05		(R)IFHTVTT	(R)I F H T V T T/T/D/D/P V I R(K)		124.48	538.9517	1614.849	-0.0081	-5	5.21	31956.7	9.73	HUMAN	B0QYA5	Eukaryotic translation initiation factor 3 subunit D (Fragment)
16563	dirMS_041712_NAR_60mM_plus.21286.21286.3	3	7.22	1	1.34E+05		(R)TLAEIAK	(R)T L|A/E I/A K V/E/L D N M P L R(G)		175.47	604.9996	1812.989	-0.0045	-2.5	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)

16564	dirMS_041712_NAR_30mM_minus2.18050.18050.2	2	7.21	0	4.01E+05		(R)GLFIIDD	(R)G L|F|I/I D/D K(G)		153.42	460.7585	920.509	0.001	1	4.21	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
16565	dirMS_041712_NAR_40mM_minus2.14249.14249.3	3	7.21	0	1.90E+04		(R)VSAAVLI	(R)V/S\A A V L/P L V H/P L P E/G L R(A)		167.98	590.0205	1768.048	-0.001	-0.6	6.72	63124.2	9.53	HUMAN	E7EVU5	Nuclear receptor corepressor 1 (Fragment)
16566	dirMS_041712_NAR_50mM_minus2.11208.11208.3	3	7.21	0	5.57E+03		(R)ISLGMP	(R)I/S L G M/P V/G/P N A H/K(V)		132.17	440.9072	1320.709	-0.0022	-1.7	8.76	98282.7	5.49	HUMAN	E9PPJ0	Splicing factor 3B subunit 2
16567	dirMS_041712_NAR_50mM_minus2.15487.15487.3	3	7.21	0	2.99E+05	M118m	(R)AGKPVI	(R)A G K\P V I\C A T/Q|M/L/E S m I/K(K)	C:Carbamidomethylation m:Oxid	155.8	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
16568	dirMS_041712_NAR_50mM_minus2.18362.18362.3	3	7.21	0	4.62E+05		(K)ALIEVLQ	(K)A L\I|E V/L Q/P L I A E H Q A R(R)		175.42	601.0139	1801.033	-0.0059	-3.3	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
16569	dirMS_041712_NAR_60mM_minus.11994.11994.3	3	7.21	1	2.62E+05		(R)GLAGLG	(R)G L/A/G L/G D V A/E V R K(S)		126.95	428.9126	1284.727	-0.0038	-2.9	6.07	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
16570	dirMS_041712_NAR_60mM_minus.15183.15183.3	3	7.21	1	3.39E+05		(K)AKLEQL	(K)A K\L\E Q L|F/Q/D E V A K(A)		144.37	506.9421	1518.816	-0.0045	-3	4.68	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
16571	dirMS_041712_NAR_60mM_minus.16793.16793.3	3	7.21	1	2.85E+05		(R)GQFSTD	(R)G Q|F/S T D E L V A E V/E K/R(N)		153.92	569.9569	1707.855	0.0013	0.8	4.41	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
16572	dirMS_041712_NAR_120mM_plus.5386.5386.3	3	7.21	1	7.52E+04		(R)GSQGG	(R)G S/Q/G/G N F/E/G P N K R(R)		81.23	449.8829	1347.64	-0.0059	-4.3	8.75	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
16573	dirMS_041712_NAR_20mM_plus.14758.14758.2	2	7.21	0	2.03E+05	M73m	(R)AVLVDLI	(R)A V L/V/D L\E|P G T m D S V R(S)	m:Oxidized methionine	172.45	809.4082	1601.82	15.9888	-3.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
16574	dirMS_041712_NAR_20mM_plus.16696.16696.2	2	7.21	0	1.35E+05		(K)IAFAITAI	(K)I/A|F A I/T A/I/K(G)		185.77	474.2987	947.592	-0.0023	-2.4	8.75	17718.4	10.99	HUMAN	P62269	40S ribosomal protein S18
16575	dirMS_041712_NAR_20mM_plus.18319.18319.2	2	7.21	0	2.71E+04		(K)SSGPTSL	(K)S S G P T S L/F/A/V\T V/A/P P G A R(Q)		197.6	857.9559	1714.912	-0.0077	-4.5	9.47	91324.5	5.75	HUMAN	Q00839	Heterogeneous nuclear ribonucleoprotein U
16576	dirMS_041712_NAR_30mM_plus2.10402.10402.2	2	7.21	0	2.95E+05		(R)SLSYSPV	(R)S L|S/Y/S\P V E/R(R)		108.27	519.2668	1037.526	0.0001	0.1	5.72	9057.8	12.09	HUMAN	I3L4U6	Serine/arginine repetitive matrix protein 2 (Fragment)
16577	dirMS_041712_NAR_30mM_plus2.16121.16121.2	2	7.21	0	6.56E+05		(K)GVLFYGI	(K)G V/L|F/Y/G/P P G C G K(T)	C:Carbamidomethylation	137.93	626.3175	1251.619	0.0087	6.9	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
16578	dirMS_041712_NAR_30mM_plus2.17335.17335.2	2	7.21	0	8.32E+04		(K)VFQFLN	(K)V F|Q/F/L/N A K(C)		143.97	483.7736	966.541	-0.0008	-0.8	8.72	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
16579	dirMS_041712_NAR_30mM_plus2.20354.20354.2	2	7.21	0	1.91E+05		(K)LGLENAI	(K)L/G/L E/N/A E A/L I R(L)		161	599.8397	1198.679	-0.0069	-5.7	4.53	61411.3	8.74	HUMAN	P10155	60 kDa SS-A/Ro ribonucleoprotein
16580	dirMS_041712_NAR_30mM_plus2.9118.9118.2	2	7.21	0	2.25E+05		(R)ALELEQ	(R)A/L|E/L E/Q E/R(K)		101.35	494.2566	987.511	-0.0046	-4.7	4.25	67933	6.08	HUMAN	P26038	Moesin
16581	dirMS_041712_NAR_40mM_plus2.13456.13456.3	3	7.21	0	9.16E+03		(K)MVMIQI	(K)M V\M\I/Q|D/G P/L P/T G A D K P L R(I)		145.45	647.0084	1939.014	-0.0033	-1.7	5.71	61981.6	8.97	HUMAN	Q96I24	Far upstream element-binding protein 3
16582	dirMS_041712_NAR_40mM_plus2.9010.9010.2	2	7.21	0	6.13E+04		(K)QEAFSIR	(K)Q E/A/F/S I R(M)		114.47	425.7237	850.442	-0.0016	-1.9	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
16583	dirMS_041712_NAR_50mM_plus2.15443.15443.3	3	7.21	1	9.72E+05		(R)KVPGVT	(R)K\V P G V T A I/E/L/D E/D/T G/T/F R(I)		149.82	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
16584	dirMS_041712_NAR_50mM_plus2.17978.17978.3	3	7.21	0	2.80E+05		(R)FGNQAI	(R)F/G/N Q A/D H/F L/G S L A F A K(L)		162.53	574.9575	1722.86	-0.0019	-1.1	6.74	44411.4	9.19	HUMAN	Q9H488	GDP-fucose protein O-fucosyltransferase 1
16585	dirMS_041712_NAR_50mM_plus2.19139.19139.3	3	7.21	0	5.40E+05		(K)HLLQAP	(K)H L L Q A\P L D\D A\Q/E|I|L Q A/R(F)		169.5	644.3484	1931.035	-0.0039	-2	4.54	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
16586	dirMS_041712_NAR_50mM_plus2.20874.20874.3	3	7.21	0	6.20E+05		(R)LHFFMP	(R)L H\F F M P G F/A|P\L/T/S R(G)		179.62	540.9498	1620.835	-0.0007	-0.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
16587	dirMS_041712_NAR_50mM_plus2.4822.4822.3	3	7.21	1	2.29E+05		(R)AAEDDE	(R)A/A|E/D\D E/D D D V D T K K(Q)		80.78	522.5519	1565.645	-0.0038	-2.4	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
16588	dirMS_041712_NAR_60mM_plus.7065.7065.3	3	7.21	0	3.92E+05		(K)YELGRP	(K)Y/E|L G R P A A N T K(I)		95.2	407.2199	1219.643	0.0022	1.8	8.59	24490	10.56	HUMAN	P62241	40S ribosomal protein S8
16589	dirMS_041712_NAR_120mM_minus.12006.12006.2	2	7.2	1	3.39E+05		(K)MKEIAE	(K)M/K|E|I\A E/A/Y L/G K(T)		119.63	626.8305	1252.661	-0.0069	-5.5	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
16590	dirMS_041712_NAR_30mM_minus2.15133.15133.2	2	7.2	0	5.54E+05	M316m	(R)ISEQFTA	(R)I S/E Q/F/T/A m F R(R)	m:Oxidized methionine	135.18	623.3014	1229.598	15.9972	1.8	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
16591	dirMS_041712_NAR_30mM_minus2.19492.19492.2	2	7.2	0	3.54E+05		(R)ASLSLW	(R)A S/L/S L/W Q/A M E K(G)		162.45	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
16592	dirMS_041712_NAR_50mM_minus2.17938.17938.3	3	7.2	1	4.40E+04		(R)GLFIIDD	(R)G L/F|I/I/D D K G I L R(Q)		170.97	453.9381	1359.8	0.0003	0.2	5.96	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
16593	dirMS_041712_NAR_50mM_minus2.6800.6800.3	3	7.2	0	5.92E+05		(R)EATNPP	(R)E A T N/P P V I Q E E K/P K(K)		105.52	527.2846	1579.833	0.0066	4.2	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
16594	dirMS_041712_NAR_50mM_minus2.6922.6922.3	3	7.2	1	6.78E+04		(R)TESTPIT	(R)T E/S T/P I|T A V|K Q P E K(V)		105.98	510.2775	1528.822	-0.0038	-2.5	5.81	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
16595	dirMS_041712_NAR_60mM_minus.15172.15172.3	3	7.2	1	1.80E+05		(K)IKDLSTV	(K)I K D L S T\V/E/A\L Q N L K(N)		144.25	524.6378	1571.9	-0.0015	-0.9	6.07	13242.4	4.17	HUMAN	E9PPH5	Acidic leucine-rich nuclear phosphoprotein 32 family member E (Fragment)
16596	dirMS_041712_NAR_60mM_minus.18581.18581.3	3	7.2	0	1.21E+05		(R)IDILDSA	(R)I/D|I/L/D S A L L R P G R(I)		165.13	480.2832	1438.838	-0.0026	-1.8	5.96	44954.5	8.44	HUMAN	A8K3Z3	26S protease regulatory subunit 8
16597	dirMS_041712_NAR_60mM_minus.9721.9721.3	3	7.2	0	5.63E+05		(K)VFEHDS	(K)V/F/E H D\S V/E/L/N C K(M)	C:Carbamidomethylation	112.98	492.8981	1476.679	0.001	0.7	4.65	31975.7	6.55	HUMAN	P10768	S-formylglutathione hydrolase
16598	dirMS_041712_NAR_120mM_plus.10800.10800.2	2	7.2	1	3.17E+05		(R)EKLEME	(R)E K/L\E|M|E M E A A R(H)		109.58	668.8148	1336.623	-0.0012	-0.9	4.49	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)
16599	dirMS_041712_NAR_20mM_plus.12323.12323.2	2	7.2	0	6.68E+04		(R)DLAPIGI	(R)D L/A/P I/G I/R(V)		158.02	427.7587	854.509	0.0007	0.8	5.84	27150.8	7.95	HUMAN	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2
16600	dirMS_041712_NAR_20mM_plus.7618.7618.2	2	7.2	0	1.57E+05		(K)IAVAAQ	(K)I/A/V|A|A Q N C Y K(V)	C:Carbamidomethylation	122.43	569.2902	1137.572	0.001	0.9	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
16601	dirMS_041712_NAR_20mM_plus.8195.8195.2	2	7.2	0	4.72E+03	M239m	(K)EVDEQm	(K)E V/D E Q/m L N|V/Q|N K(N)	m:Oxidized methionine	126.32	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
16602	dirMS_041712_NAR_20mM_plus.9636.9636.2	2	7.2	0	6.10E+04		(K)ITLVSAA	(K)I/T|L/V\S A A/P G K(V)		137.97	478.793	956.577	0.0012	1.3	8.75	12480.3	9.05	HUMAN	F5H2L4	Acyl-coenzyme A thioesterase 13
16603	dirMS_041712_NAR_30mM_plus2.11413.11413.3	3	7.2	0	4.08E+05	M300m	(R)MGQM	(R)M G Q\M A m G/G/A\M/G I/N N R(G)	m:Oxidized methionine	113.1	518.8921	1538.67	15.9923	-1.7	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
16604	dirMS_041712_NAR_30mM_plus2.20571.20571.2	2	7.2	0	1.54E+05		(K)LGLENAI	(K)L G L/E N/A E|A L I/R(L)		161.3	599.8397	1198.679	-0.0069	-5.7	4.53	61411.3	8.74	HUMAN	P10155	60 kDa SS-A/Ro ribonucleoprotein
16605	dirMS_041712_NAR_30mM_plus2.21686.21686.2	2	7.2	0	2.07E+05		(R)NIPMLF	(R)N I|P/M/L F V/R(G)		168	495.2847	989.56	0.002	2.1	9.75	11845.2	4.58	HUMAN	P62310	U6 snRNA-associated Sm-like protein LSm3
16606	dirMS_041712_NAR_30mM_plus2.4355.4355.2	2	7.2	0	2.74E+05		(R)SYTSGP	(R)S Y/T\S/G P G S/R(I)		71.83	456.2155	911.422	0.002	2.2	8.46	19288.4	10.19	HUMAN	F8VQY3	Keratin, type II cytoskeletal 8 (Fragment)
16607	dirMS_041712_NAR_40mM_plus2.14591.14591.3	3	7.2	0	2.16E+04		(K)IYGADDI	(K)I Y G/A D D I E L\L/P E A Q H/K(A)		153.4	604.6467	1811.917	0.0081	4.5	4.31	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
16608	dirMS_041712_NAR_40mM_plus2.17945.17945.3	3	7.2	0	7.68E+04		(K)DMTVPI	(K)D M/T\V/P I L V S K P P V F T G K(D)		173.37	610.3443	1829.024	-0.0058	-3.2	8.59	53885.5	9	HUMAN	P11182	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial
16609	dirMS_041712_NAR_40mM_plus2.9303.9303.2	2	7.2	0	4.84E+05		(R)GGNFGI	(R)G G N|F|G F/G D/S R(G)		116.53	507.2256	1013.444	0.0004	0.4	5.84	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
16610	dirMS_041712_NAR_50mM_plus2.16811.16811.3	3	7.2	0	7.42E+05		(R)QYYTLLI	(R)Q Y Y/T/L L|N Q A/P D\M L H R(K)		156.87	621.6447	1862.922	-0.0022	-1.2	6.74	4335.1	9.82	HUMAN	E5RH00	Ras GTPase-activating protein-binding protein 1
16611	dirMS_041712_NAR_50mM_plus2.20331.20331.3	3	7.2	1	1.54E+05		(R)YLPDTLL	(R)Y L/P D T L L L/E/E C G L L R K(G)	C:Carbamidomethylation	175.18	645.0183	1933.046	-0.006	-3.1	4.68	25180.2	5.34	HUMAN	E7EMS6	Catechol O-methyltransferase (Fragment)
16612	dirMS_041712_NAR_50mM_plus2.8603.8603.3	3	7.2	1	7.17E+04		(R)LATNTS	(R)L/A\T/N T S/A/P D/L/K N V R(S)		112.28	500.6117	1499.818	0.0029	1.9	8.75	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
16613	dirMS_041712_NAR_60mM_plus.9296.9296.3	3	7.2	2	1.07E+06	Y192y	(K)QPVRGY	(K)Q P V R G Y/y R G|A V G G T F D R(L)	y:Phosphorylated Y	106.6	660.3045	1898.962	79.9369	-14.9	9.98	23942.2	9.26	HUMAN	K7EN91	Bifunctional coenzyme A synthase (Fragment)
16614	dirMS_041712_NAR_120mM_minus.10659.10659.3	3	7.19	0	2.17E+05		(K)ALHQTV	(K)A L H Q T V T/E A N/G/K(L)		111.63	423.557	1268.659	-0.0029	-2.3	6.79	229367.3	5.87	HUMAN	Q9P219	Protein Daple
16615	dirMS_041712_NAR_120mM_minus.11205.11205.3	3	7.19	0	2.93E+05		(K)SAKPTKI	(K)S A K/P T K P A A S D|L|P V/P A E G V R(N)		115.03	664.3662	1991.092	-0.008	-4	8.31	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
16616	dirMS_041712_NAR_120mM_minus.4385.4385.3	3	7.19	1	1.50E+07	M310m	(R)TKTEISE	(R)T\K/T E/I/S/E/m N/R(N)	m:Oxidized methionine	72.87	408.8693	1208.594	15.9994	3.7	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
16617	dirMS_041712_NAR_120mM_minus.7851.7851.3	3	7.19	0	3.77E+05		(R)AFHNEA	(R)A F/H N E A Q/V/N/P E/R(K)		96.77	471.229	1411.671	0.0011	0.8	5.4	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
16618	dirMS_041712_NAR_20mM_minus.14671.14671.3	3	7.19	0	7.26E+04		(K)IYVDDGI	(K)I Y V D D G L/I/S L Q/V K(Q)		201.57	488.2771	1462.815	0.0016	1.1	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
16619	dirMS_041712_NAR_20mM_minus.8242.8242.2	2	7.19	0	1.66E+05	M161m	(K)LLIEmEC	(K)L L|I/E m E/Q R(L)	m:Oxidized methionine	132.15	524.2783	1031.555	15.9939	-0.9	4.53	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
16620	dirMS_041712_NAR_30mM_minus2.16516.16516.2	2	7.19	0	2.43E+05		(K)NAAGAL	(K)N/A/A|G A L D L L K(E)		143.58	493.2881	985.568	0.0013	1.3	5.84	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
16621	dirMS_041712_NAR_60mM_minus.17342.17342.3	3	7.19	1	3.46E+05		(R)KAPSDL	(R)K\A P S D|L/Y Q/I I/L K(A)		156.37	463.6095	1388.815	-0.0008	-0.6	8.5	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
16622	dirMS_041712_NAR_60mM_minus.9276.9276.3	3	7.19	0	2.51E+05		(K)QADNPI	(K)Q A D|N P H/V/A L/Y Q A/R(F)		111.68	494.9197	1482.745	-0.0003	-0.2	6.74	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
16623	dirMS_041712_NAR_120mM_plus.14880.14880.4	4	7.19	1	6.41E+04	M251m	(K)FSHEEIA	(K)F S H E\E\I/A/m/A/T/V T A/L R R(T)	m:Oxidized methionine	131.28	462.7409	1831.948	15.9934	-0.8	6.76	39795.8	9.08	HUMAN	H3BQN4	Fructose-bisphosphate aldolase
16624	dirMS_041712_NAR_120mM_plus.5573.5573.3	3	7.19	1	7.62E+04		(R)YGEDNR	(R)Y/G/E D/N R G Y G G S Q\G G G R(G)		82.97	543.9055	1629.7	0.0019	1.2	6.07	26157.9	4.57	HUMAN	K7EL85	TATA-binding protein-associated factor 2N (Fragment)
16625	dirMS_041712_NAR_20mM_plus.11967.11967.2	2	7.19	0	7.97E+04		(K)ILQDGG	(K)I L|Q D G G\L Q/V V/E/K(Q)		155.62	649.8662	1298.731	-0.0063	-4.9	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
16626	dirMS_041712_NAR_20mM_plus.7906.7906.2	2	7.19	0	9.11E+04	M21m	(K)ATAVmI	(K)A T/A/V|m|P D G Q F K(D)	m:Oxidized methionine	124.52	590.7861	1164.572	15.9932	-1.5	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
16627	dirMS_041712_NAR_30mM_plus2.13068.13068.2	2	7.19	0	6.45E+05		(R)GVVGPE	(R)G V|V|G P E L/Y G R(L)		122.37	523.7794	1046.563	-0.0114	-10.9	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
16628	dirMS_041712_NAR_30mM_plus2.6616.6728.2	2	7.19	0	2.20E+05		(K)TLNAGA	(K)T L|N/A/G A Y S K(V)		89.32	462.7408	924.479	-0.0042	-4.5	8.26	30197.4	7.91	HUMAN	E9PMG2	Palmitoyl-protein thioesterase 1 (Fragment)
16629	dirMS_041712_NAR_40mM_plus2.7036.7036.2	2	7.19	0	1.61E+05		(R)QLETLG	(R)Q L/E|T/L/G Q E K(L)		101.52	523.282	1045.552	0.0043	4.1	4.53	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
16630	dirMS_041712_NAR_40mM_plus2.7169.7169.2	2	7.19	0	1.60E+04		(R)VGFAEA	(R)V/G/F A/E/A A R(L)		101.97	410.7186	820.431	-0.0013	-1.5	5.97	20599.3	9.19	HUMAN	H7C1V0	Cathepsin D light chain (Fragment)
16631	dirMS_041712_NAR_50mM_plus2.15992.15992.3	3	7.19	1	7.39E+04		(K)LGINSLC	(K)L/G\I/N/S L Q E L K Q N I A/K(G)		151.78	556.9915	1668.964	-0.0043	-2.6	8.59	25978.5	4.91	HUMAN	C9J502	Prostate leucine zipper variant 2
16632	dirMS_041712_NAR_50mM_plus2.16176.16176.3	3	7.19	1	4.90E+04		(R)EGIVTAT	(R)E G I/V/T/A T E Q E/V K E D I A K(L)		152.25	620.658	1859.96	-0.0002	-0.1	4.25	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
16633	dirMS_041712_NAR_50mM_plus2.8311.8311.3	3	7.19	0	2.33E+05		(K)VQQAEL	(K)V Q|Q A E L/H/T G S L P R(I)		110.33	479.2607	1435.765	0.0023	1.6	6.72	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
16634	dirMS_041712_NAR_60mM_plus.11764.11764.3	3	7.19	1	2.93E+06		(K)KAEAGA	(K)K A E A G A G S\A/T/E/F Q F R(G)		118.23	523.9277	1569.766	0.003	1.9	6.14	18897.4	10.15	HUMAN	P46783	40S ribosomal protein S10
16635	dirMS_041712_NAR_60mM_plus.21289.21289.3	3	7.19	1	1.34E+05		(R)TLAEIAK	(R)T L/A/E/I A K/V E L D N M/P L R(G)		175.47	604.9996	1812.989	-0.0045	-2.5	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
16636	dirMS_041712_NAR_60mM_plus.5155.5173.3	3	7.19	1	4.46E+04		(K)GNSPPS	(K)G N|S|P/P/S S G E A C R E E K(G)	C:Carbamidomethylation	84.52	535.5678	1604.697	-0.0081	-5	4.79	24954.4	5.33	HUMAN	A6NM98	ARD1 homolog A, N-acetyltransferase (S. cerevisiae), isoform CRA_b
16637	dirMS_041712_NAR_60mM_plus.8549.8549.3	3	7.19	1	8.53E+05		(K)EGYADK	(K)E G Y/A D K/N L/I/A/K(W)		102.45	407.889	1221.647	0.0051	4.1	6.17	12475.2	9.39	HUMAN	C9JCD9	Protein BUD31 homolog
16638	dirMS_041712_NAR_120mM_minus.11035.11035.3	3	7.18	0	5.83E+05		(R)GLHQSII	(R)G L/H\Q S\I|E/E F/R(A)		114.27	405.8796	1215.612	0.0126	10.4	5.4	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
16639	dirMS_041712_NAR_120mM_minus.13453.13453.4	4	7.18	2	7.08E+05	M100m	(K)KQGGLG	(K)K Q G G\L G\P m N I/P L/V S D/P K\R(T)	m:Oxidized methionine	128.4	481.5173	1907.053	15.9942	-0.3	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
16640	dirMS_041712_NAR_120mM_minus.20212.20212.3	3	7.18	0	1.72E+05	M195m	(R)LHFFmP	(R)L H F F m P G|F\A/P L/T S R(G)	m:Oxidized methionine	165.67	546.2809	1620.835	15.9926	-1.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
16641	dirMS_041712_NAR_30mM_minus2.8820.8820.2	2	7.18	0	4.89E+05		(K)SDPVVS	(K)S D|P/V/V S Y/R(E)		102.55	461.7315	922.463	-0.0071	-7.7	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
16642	dirMS_041712_NAR_40mM_minus2.14267.14267.3	3	7.18	0	2.72E+05		(R)DVCTELI	(R)D V/C T/E L L/P L I K P Q/G R(V)	C:Carbamidomethylation	168.95	580.3211	1738.952	-0.0033	-1.9	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
16643	dirMS_041712_NAR_40mM_minus2.7830.7830.3	3	7.18	0	7.49E+04	M47m M5	(K)SGTGIA	(K)S G T/G/I|A/A M S V m R P E Q I m K(S)	m:Oxidized methionine	125.22	646.9867	1906.955	31.9908	0.5	8.46	8797.3	9.3	HUMAN	H3BR50	V-type proton ATPase 16 kDa proteolipid subunit
16644	dirMS_041712_NAR_50mM_minus2.11648.11648.3	3	7.18	1	4.52E+05		(K)ILIANTG	(K)I L/I A/N T G M D T D/K I/K(I)		133.55	511.6179	1532.835	0.0039	2.5	5.96	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
16645	dirMS_041712_NAR_50mM_minus2.8990.8990.3	3	7.18	0	1.31E+05	N460n	(K)IVFEDGI	(K)I V F\E D G N/I/N/V n K(G)	n:N-acetylglucosamine (N)	119.48	522.2727	1361.706	203.0976	11.6	4.37	62370.8	6.26	HUMAN	E9PD68	Dihydropyrimidinase-related protein 1
16646	dirMS_041712_NAR_60mM_minus.13743.13743.3	3	7.18	1	7.02E+04	T546t	(R)IAKNEA	(R)I A/K\N/E A/A t N E L M R(W)	t:N-acetylglucosamine (T)	136.33	555.2761	1460.753	203.0612	-10.9	6.14	111159.1	9.59	HUMAN	Q8TC59	Piwi-like protein 2
16647	dirMS_041712_NAR_60mM_minus.6270.6270.3	3	7.18	1	4.66E+04		(R)LTQEPE	(R)L/T Q E/P E/S I R K(W)		93.75	400.8938	1200.658	0.0086	7.1	6.14	8409.9	4.52	HUMAN	H0Y9Q6	Clathrin light chain B (Fragment)
16648	dirMS_041712_NAR_60mM_minus.8839.8839.3	3	7.18	1	1.14E+05		(K)YAGKDG	(K)Y/A/G/K D/G Y N Y T L/S K(T)		109.12	493.9126	1479.711	0.0118	8	8.38	11854.4	6.57	HUMAN	P31949	Protein S100-A11
16649	dirMS_041712_NAR_120mM_plus.14413.14413.2	2	7.18	0	6.18E+05		(R)HFDQFV	(R)H|F|D Q F|W S A A/K(T)		128.75	618.7928	1236.58	-0.0013	-1.1	6.74	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
16650	dirMS_041712_NAR_20mM_plus.10029.10029.2	2	7.18	0	2.16E+05		(K)VASGCLI	(K)V/A/S/G/C/L D I/N S S V K(G)	C:Carbamidomethylation	140.05	675.3376	1349.673	-0.005	-3.7	5.81	56837	7.19	HUMAN	E7ETT1	Propionyl-CoA carboxylase beta chain, mitochondrial
16651	dirMS_041712_NAR_20mM_plus.18443.18443.2	2	7.18	0	6.88E+04		(R)VVVLGLI	(R)V V|V/L/G L L P R(G)		198.75	483.3247	965.651	-0.0085	-8.8	9.72	25847.9	6.33	HUMAN	Q15102	Platelet-activating factor acetylhydrolase IB subunit gamma
16652	dirMS_041712_NAR_20mM_plus.18683.18683.2	2	7.18	0	8.18E+04	M80m	(R)APLPDL	(R)A P L|P D L Y P F G T m R(G)	m:Oxidized methionine	200.35	747.3751	1477.751	15.9921	-1.9	5.88	81122.9	9.03	HUMAN	H3BLZ8	Probable ATP-dependent RNA helicase DDX17
16653	dirMS_041712_NAR_30mM_plus2.11414.11414.3	3	7.18	0	4.08E+05	M304m	(R)MGQM	(R)M G Q M A\M/G G\A/m/G I/N N R(G)	m:Oxidized methionine	113.1	518.8921	1538.67	15.9923	-1.7	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
16654	dirMS_041712_NAR_30mM_plus2.11686.11686.2	2	7.18	0	6.20E+05		(R)AMGEQ	(R)A M/G\E/Q/A/V/A L A/R(A)		114.52	558.7944	1116.583	-0.0015	-1.3	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
16655	dirMS_041712_NAR_40mM_plus2.9953.9953.2	2	7.18	0	7.96E+04		(R)AQIFAN	(R)A Q\I/F/A/N T/V D N A R(I)		122.82	660.3347	1319.67	-0.0081	-6.1	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
16656	dirMS_041712_NAR_50mM_plus2.21247.21247.3	3	7.18	0	1.87E+06		(R)AGKPVI	(R)A G K\P V I C A|T\Q\M L E/S M I/K(K)	C:Carbamidomethylation	180.72	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
16657	dirMS_041712_NAR_50mM_plus2.8322.8322.3	3	7.18	0	3.62E+04		(R)AVTGTH	(R)A/V/T G T H/T L A L A A/K(H)		110.58	418.5793	1253.721	0.0021	1.7	8.8	9213.8	9.99	HUMAN	H0YK01	Translation initiation factor eIF-2B subunit beta (Fragment)
16658	dirMS_041712_NAR_50mM_plus2.8400.8400.3	3	7.18	1	8.78E+04		(R)DYVAPT	(R)D Y/V/A/P T A N L/D Q K D K(Q)		111.07	526.5923	1577.781	-0.0182	-11.6	4.43	102679.8	6.75	HUMAN	Q7KZF4	Staphylococcal nuclease domain-containing protein 1
16659	dirMS_041712_NAR_60mM_plus.12861.12861.3	3	7.18	1	8.89E+05	M232m	(R)MSmKE	(R)M S m K E V D\E\Q/M|L/N V\Q N K(N)	m:Oxidized methionine	123.58	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
16660	dirMS_041712_NAR_60mM_plus.17015.17015.3	3	7.18	0	3.40E+05		(K)EGHVEV	(K)E G H V E V\V/S/E L/L/Q/R(E)		145.97	498.9326	1494.791	-0.0078	-5.2	4.75	48586.6	9.32	HUMAN	D6RCB2	Ankyrin-3
16661	dirMS_041712_NAR_60mM_plus.9105.9106.3	3	7.18	1	8.68E+05	M827m M8	(K)YAmmF	(K)Y/A/m m F A E L K S T/R(M)	m:Oxidized methionine	106.2	493.9098	1447.707	32.0076	12	8.59	376926.5	4.99	HUMAN	H0Y5W0	E3 ubiquitin-protein ligase HUWE1 (Fragment)
16662	dirMS_041712_NAR_60mM_plus.9553.9553.3	3	7.18	0	1.08E+06		(R)IQFKPDI	(R)I Q|F/K/P D D G T T/P E R(I)		107.58	501.923	1503.744	0.0106	7.1	4.56	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
16663	dirMS_041712_NAR_120mM_minus.18236.18236.4	4	7.17	1	1.95E+05		(K)YYITIIDA	(K)Y Y I T I I/D/A/P G H R D F I K(N)		154.23	481.2594	1922.017	-0.0013	-0.7	6.75	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
16664	dirMS_041712_NAR_120mM_minus.19482.19482.3	3	7.17	0	7.14E+05		(R)NSVSNF	(R)N S/V\S N F L/H S L E R(G)		162.22	468.2346	1402.707	-0.0181	-12.9	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
16665	dirMS_041712_NAR_20mM_minus.14545.14545.3	3	7.17	0	5.23E+03		(K)VVVQVL	(K)V V\V Q V L/A/E E/P E A V L K(G)		199.73	541.6469	1622.936	-0.0102	-6.3	4.26	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
16666	dirMS_041712_NAR_50mM_minus2.7021.7021.3	3	7.17	0	1.74E+05		(R)SAEEEA	(R)S A/E/E E A A D/L/P T K/P\T/K(I)		106.92	529.6012	1586.791	-0.0018	-1.1	4.41	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
16667	dirMS_041712_NAR_50mM_minus2.9411.9411.3	3	7.17	0	6.17E+04		(R)DLSKPIG	(R)D L\S K/P I/G/A/L N P K(R)		121.75	418.2465	1252.726	-0.001	-0.8	8.59	84798.4	5.92	HUMAN	B7Z2H9	Neurobeachin
16668	dirMS_041712_NAR_60mM_minus.12514.12514.3	3	7.17	1	3.69E+05		(R)EMDRET	(R)E M D R E T|L|I/D/V A R(T)		129.4	483.2454	1447.721	0.0007	0.5	4.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
16669	dirMS_041712_NAR_60mM_minus.14572.14572.3	3	7.17	1	1.51E+05		(R)KTTLQVI	(R)K T T\L/Q V D T L N\A|E/L/A/A E R(S)		140.6	625.0044	1873.003	-0.0039	-2.1	4.68	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
16670	dirMS_041712_NAR_60mM_minus.15611.15611.3	3	7.17	1	1.83E+05		(R)ASLISAV	(R)A/S/L I S A/V/S D K L R(W)		146.25	420.5811	1259.732	-0.003	-2.4	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
16671	dirMS_041712_NAR_60mM_minus.18268.18268.3	3	7.17	1	5.28E+05		(K)IKTLFPLI	(K)I K T L F|P L/I E/A/K(K)		162.75	424.9345	1272.793	-0.0036	-2.9	8.59	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
16672	dirMS_041712_NAR_60mM_minus.19193.19193.3	3	7.17	1	1.61E+04		(R)GLFIIDD	(R)G L/F I/I D/D/K/G I L R(Q)		169.72	453.9368	1359.8	-0.0036	-2.7	5.96	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)

16673	dirMS_041712_NAR_60mM_minus.6119.6119.3	3	7.17	1	2.99E+05		(K)ETEGDV	(K)E|T\E/G D/V T S V/K D A K(I)		92.5	460.2267	1378.67	-0.0041	-3	4.32	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
16674	dirMS_041712_NAR_120mM_plus.10470.10470.3	3	7.17	1	5.50E+05		(R)NSKIEIS	(R)N/S K I E I/S E/L/N/R(V)		108.33	434.9023	1302.701	-0.0089	-6.8	6.14	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
16675	dirMS_041712_NAR_120mM_plus.12881.12881.3	3	7.17	0	8.50E+05		(K)HYGPGV	(K)H Y G P G\W|V|S M/A N A G/K(D)		121.4	492.2383	1474.69	0.0108	7.3	8.6	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
16676	dirMS_041712_NAR_120mM_plus.18685.18685.4	4	7.17	0	3.80E+05		(K)APIRPDI	(K)A/P/I R P D I V N F V/H T N L R(K)		151.27	466.2639	1862.04	-0.0058	-3.1	9.65	18988.7	11.2	HUMAN	H3BTP7	60S ribosomal protein L4 (Fragment)
16677	dirMS_041712_NAR_20mM_plus.10589.10589.2	2	7.17	0	2.04E+05		(K)NAGVE	(K)N/A|G V/E/G S L I/V/E\K(I)		146.07	608.3304	1215.658	-0.0044	-3.6	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
16678	dirMS_041712_NAR_20mM_plus.11592.11592.3	3	7.17	0	3.27E+04	M596m	(R)MGPAm	(R)M G P A m G\P A|L/G/A/G I E/R(M)	m:Oxidized methionine	152.82	481.9117	1427.713	16.0072	8.5	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
16679	dirMS_041712_NAR_20mM_plus.12645.12645.3	3	7.17	0	6.37E+04		(K)AINQQT	(K)A I N Q Q T/G A/F/V/E I S R(Q)		159.7	511.9382	1533.802	-0.0019	-1.3	6.05	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
16680	dirMS_041712_NAR_20mM_plus.13948.13948.2	2	7.17	0	1.01E+05	M2232m	(R)SLLVNP	(R)S L L V/N/P E G P T L m R(L)	m:Oxidized methionine	167.43	721.8852	1426.772	15.9909	-2.8	5.72	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
16681	dirMS_041712_NAR_20mM_plus.18016.18016.2	2	7.17	0	1.49E+05		(R)TVQSLEI	(R)T V|Q/S L/E/I D/L D S M R(N)		195.15	753.8776	1506.747	0.0011	0.7	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
16682	dirMS_041712_NAR_30mM_plus2.13536.13536.2	2	7.17	0	7.56E+05		(R)SSMTFL	(R)S/S/M/T/F L T|R(Q)		124.75	471.7412	942.471	0.0038	4	9.47	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
16683	dirMS_041712_NAR_30mM_plus2.16807.16807.2	2	7.17	0	3.33E+05		(R)LWDLTT	(R)L W|D|L/T/T/G T T T R(R)		140.72	632.8304	1264.653	0.0003	0.3	5.84	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
16684	dirMS_041712_NAR_40mM_plus2.19907.19907.3	3	7.17	0	4.60E+05	M166m	(K)VLDFEHI	(K)V/L/D F E H F|L|P m L Q T/V A/K(N)	m:Oxidized methionine	187.63	635.3379	1888.004	15.9954	0.3	5.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
16685	dirMS_041712_NAR_60mM_plus.14879.14899.3	3	7.17	0	1.05E+05		(K)MHGGG	(K)M H G G G P T\V|T/A/G L/P L/P K(A)		134.4	511.6089	1532.825	-0.0132	-8.6	8.52	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
16686	dirMS_041712_NAR_60mM_plus.20523.20523.3	3	7.17	1	4.08E+05		(K)NAAGAL	(K)N A\A/G A L D/L/L/K E/L K(N)		166.95	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
16687	dirMS_041712_NAR_120mM_minus.13168.13168.4	4	7.16	2	1.41E+06		(R)AQKDEE	(R)A Q K D\E E/K M E\I\Q/E|I Q/L K(E)		126.52	490.7539	1960.006	-0.0118	-6	4.58	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
16688	dirMS_041712_NAR_30mM_minus2.18920.18920.2	2	7.16	0	1.32E+04		(R)NTWLY	(R)N T|W|L Y/Q A L/R(E)		157.48	582.8109	1164.616	-0.0015	-1.3	8.75	49457.5	6.47	HUMAN	P56545	C-terminal-binding protein 2
16689	dirMS_041712_NAR_30mM_minus2.19261.19261.2	2	7.16	0	2.53E+05		(R)LTIAILR	(R)L T|I/A I L R(H)		159.35	400.2731	799.54	-0.0011	-1.3	9.75	87498	6.43	HUMAN	C9J266	E3 ubiquitin-protein ligase RNF123
16690	dirMS_041712_NAR_50mM_minus2.15909.15909.3	3	7.16	1	8.21E+04		(K)DANAKL	(K)D A N A/K L\S E\L/E|A/A L Q R(A)		158.97	543.6248	1628.86	-0.0004	-0.2	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
16691	dirMS_041712_NAR_50mM_minus2.18813.18813.3	3	7.16	0	2.37E+05		(K)GAEILEV	(K)G A E/I/L/E/V/L H/S/L/P A V R(Q)		183.2	535.3101	1603.917	-0.0009	-0.5	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
16692	dirMS_041712_NAR_60mM_minus.9462.9462.3	3	7.16	1	2.46E+05		(R)QERYEIE	(R)Q E R Y E\I E|E/T E/T V T K(S)		112.57	585.6185	1754.844	-0.0034	-1.9	4.32	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
16693	dirMS_041712_NAR_120mM_plus.8645.8645.3	3	7.16	1	4.30E+04		(R)RQQEEL	(R)R Q Q E E/L|L\A|E E N Q R(L)		99.1	548.2767	1642.814	0.0012	0.7	4.49	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
16694	dirMS_041712_NAR_20mM_plus.10989.10989.3	3	7.16	0	1.01E+05		(K)ALIAAQ	(K)A L/I A A Q/Y/S G/A Q V R(V)		147.88	449.9174	1347.738	-0.0003	-0.2	8.79	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
16695	dirMS_041712_NAR_20mM_plus.14067.14067.3	3	7.16	0	3.05E+04	S68s	(K)sFLEGT	(K)s F L E G T/M Q V A Q S R(M)	s:N-acetylglucosamine (S)	168.3	552.9426	1453.71	203.1029	14.2	5.72	16739.9	9.44	HUMAN	C9JM66	FCH and double SH3 domains protein 2 (Fragment)
16696	dirMS_041712_NAR_20mM_plus.14301.14301.3	3	7.16	0	7.24E+03		(R)VPTANV	(R)V P T A N\V S\V|V|D/L T C R(L)	C:Carbamidomethylation	169.75	510.9348	1530.795	-0.0046	-3	5.81	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
16697	dirMS_041712_NAR_20mM_plus.17071.17071.3	3	7.16	0	1.97E+05		(K)VQIAVA	(K)V Q\I A V|A\N A/Q/E L/L Q/R(M)		188.3	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
16698	dirMS_041712_NAR_20mM_plus.17965.17965.3	3	7.16	0	1.93E+05		(R)TVQSLEI	(R)T V\Q S L E I|D L/D S M R(N)		195.03	502.9236	1506.747	0.0094	6.2	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
16699	dirMS_041712_NAR_20mM_plus.8279.8279.2	2	7.16	0	9.35E+04		(R)LATNTS	(R)L A|T/N/T/S A\P D L K(N)		127.33	565.806	1130.605	-0.0005	-0.4	5.84	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
16700	dirMS_041712_NAR_30mM_plus2.11564.11643.2	2	7.16	0	4.18E+05		(R)GLNISA	(R)G L|N|I/S/A V/R(L)		114.3	415.2469	829.489	-0.0025	-3	9.75	69753.6	5.49	HUMAN	E7EX17	Eukaryotic translation initiation factor 4B
16701	dirMS_041712_NAR_30mM_plus2.13600.13640.2	2	7.16	0	3.14E+05		(R)LLEEGVL	(R)L/L|E|E/G V/L/R(Q)		124.53	464.7736	928.546	-0.0063	-6.8	4.53	77401.7	5.34	HUMAN	E7EMH5	Pyridoxal-dependent decarboxylase domain-containing protein 1
16702	dirMS_041712_NAR_30mM_plus2.17078.17078.2	2	7.16	0	3.76E+05		(K)NCIGDFI	(K)N/C|I/G\D/F L K(T)	C:Carbamidomethylation	142.4	483.7442	966.471	0.0098	10.1	5.84	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
16703	dirMS_041712_NAR_30mM_plus2.9266.9266.2	2	7.16	0	7.68E+05		(K)TAVCDIF	(K)T A V|C/D/I/P|P R(G)	C:Carbamidomethylation	101.15	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
16704	dirMS_041712_NAR_40mM_plus2.9475.9475.2	2	7.16	0	8.89E+04		(R)LVDMM	(R)L/V/D M M/E R(G)		118.72	447.2146	893.422	0	0	4.37	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
16705	dirMS_041712_NAR_50mM_plus2.13680.13680.3	3	7.16	0	4.46E+05		(K)FLSDPQ	(K)F/L|S D/P Q V H/T V L V E R(S)		140.13	547.2984	1639.88	0.0004	0.3	5.32	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
16706	dirMS_041712_NAR_60mM_plus.13357.13357.3	3	7.16	0	6.62E+05	M1m	(-)mVNHFI	(-)m/V/N\H F/I A E/F K(R)	m:Oxidized methionine	126.13	417.8778	1235.624	15.9947	-0.2	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
16707	dirMS_041712_NAR_60mM_plus.17426.17597.3	3	7.16	1	8.46E+05		(R)DKLNNL	(R)D K L N N\L|V|L/F/D K(A)		148.4	440.2499	1318.737	-0.0014	-1	5.96	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
16708	dirMS_041712_NAR_60mM_plus.17936.17936.3	3	7.16	1	2.50E+05		(R)GQFSTD	(R)G Q|F/S T/D E L V/A E V E K/R(N)		150.63	569.9588	1707.855	0.007	4.1	4.41	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
16709	dirMS_041712_NAR_60mM_plus.6502.6502.3	3	7.16	1	1.72E+06		(R)TKTEISEI	(R)T\K T E I|S/E/M N R(N)		92.8	403.5374	1208.594	0.0037	3	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
16710	dirMS_041712_NAR_20mM_minus.7697.7697.2	2	7.15	0	2.04E+05		(K)TVPVEA	(K)T V|P V/E A V/T S K(T)		125.87	515.7883	1030.578	-0.0086	-8.3	5.66	35720	5.34	HUMAN	B4E358	Src substrate cortactin
16711	dirMS_041712_NAR_20mM_minus.7951.7951.3	3	7.15	0	4.94E+04		(R)EGQGE	(R)E G Q G E G E T Q\E A A/A/A/T A A A R(R)		128.8	606.6126	1817.826	-0.0028	-1.5	4.09	558007.1	5.44	HUMAN	P58107	Epiplakin
16712	dirMS_041712_NAR_20mM_minus.8116.8116.2	2	7.15	0	1.00E+05		(R)ATTGYPI	(R)A T/T/G\Y|P D P Y G G E K(L)		130.42	678.3078	1355.611	-0.0031	-2.3	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
16713	dirMS_041712_NAR_20mM_minus.8307.8307.2	2	7.15	0	1.41E+05		(K)DVGSLA	(K)D V|G S L/A S V/Q R(Y)		132.33	516.2772	1031.548	-0.0009	-0.8	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin
16714	dirMS_041712_NAR_30mM_minus2.10629.10647.2	2	7.15	0	3.22E+05		(K)YSGTLNI	(K)Y/S|G T/L/N L/D R(V)		111.55	519.7639	1038.521	-0.0009	-0.9	5.83	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
16715	dirMS_041712_NAR_30mM_minus2.5822.5822.2	2	7.15	0	9.22E+04	M57m	(K)EmGTPD	(K)E m/G T/P/D/V/R(I)	m:Oxidized methionine	85.88	460.7171	904.419	16.0076	13.8	4.37	15175.4	10.46	HUMAN	B7Z4C8	60S ribosomal protein L31
16716	dirMS_041712_NAR_40mM_minus2.6015.6015.2	2	7.15	0	1.00E+06		(K)AGFAGD	(K)A G F|A|G D D A/P R(A)		98.48	488.7279	976.448	0.0002	0.2	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
16717	dirMS_041712_NAR_50mM_minus2.17055.17055.3	3	7.15	0	1.55E+05		(R)LLEVLSG	(R)L L/E V/L/S G E I L P K/P T/K(G)		165.35	546.3329	1636.988	-0.0042	-2.6	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
16718	dirMS_041712_NAR_50mM_minus2.9728.9728.3	3	7.15	0	7.38E+04		(R)ELTLEKP	(R)E L/T/L/E K/P E/L K(A)		123.72	400.5678	1199.688	0.0007	0.6	4.79	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
16719	dirMS_041712_NAR_60mM_minus.12648.13163.3	3	7.15	0	9.18E+05		(K)GIHPTIIS	(K)G I H\P T\I|I|S E/S F Q K(A)		132.28	486.2642	1456.78	-0.0014	-1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
16720	dirMS_041712_NAR_60mM_minus.13634.13634.3	3	7.15	0	1.41E+05		(R)MVIPGG	(R)M V/I/P/G G\I D V H T R(F)		135.72	432.2409	1294.694	0.0145	11.2	6.49	18330.7	11.54	HUMAN	E5RFU4	Dihydropyrimidinase-related protein 2 (Fragment)
16721	dirMS_041712_NAR_60mM_minus.14739.14739.3	3	7.15	0	2.58E+05		(K)YYITIIDA	(K)Y Y\I/T I I/D/A P G H R(D)		142.85	473.5815	1418.743	-0.0127	-9	6.74	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
16722	dirMS_041712_NAR_60mM_minus.17813.17813.3	3	7.15	1	3.60E+05		(K)NLRDID	(K)N L/R D I D\E/V/S/S L L/R(T)		160.9	510.6099	1529.828	-0.013	-8.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
16723	dirMS_041712_NAR_60mM_minus.8198.8198.3	3	7.15	1	1.32E+05		(R)KQSTDE	(R)K Q S T D\E E|V/T/S/L A K(S)		105.82	479.2451	1435.728	-0.0067	-4.7	4.68	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
16724	dirMS_041712_NAR_120mM_plus.15254.15254.3	3	7.15	1	5.50E+05		(K)KKELEEI	(K)K\K E L E E|I/V Q/P I I/S K(L)		133.28	551.998	1653.978	0.0009	0.5	6.23	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
16725	dirMS_041712_NAR_120mM_plus.15490.15490.4	4	7.15	2	5.00E+05		(R)KTVGVE	(R)K\T V G V\E/P A/A D G K G V V V V I/K(R)		134.83	467.2783	1866.106	-0.0145	-7.8	8.5	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
16726	dirMS_041712_NAR_20mM_plus.15930.15930.2	2	7.15	0	9.49E+04		(R)GLFIIDG	(R)G L/F/I I/D G K(G)		181.63	431.7544	862.503	-0.0018	-2	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
16727	dirMS_041712_NAR_20mM_plus.17531.17531.3	3	7.15	0	1.96E+05		(K)SYELPD	(K)S Y E|L P D G Q V|I\T/I/G N E R(F)		193.17	597.6357	1790.892	0.0006	0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
16728	dirMS_041712_NAR_20mM_plus.6943.6943.2	2	7.15	0	8.44E+04	M29m	(K)IVQmTE	(K)I V/Q/m/T E/A E/V R(G)	m:Oxidized methionine	114.35	596.3035	1175.609	15.9908	-3.4	4.53	14493.5	5.23	HUMAN	C9J9S3	Serine/threonine-protein phosphatase (Fragment)
16729	dirMS_041712_NAR_20mM_plus.7966.7966.2	2	7.15	0	4.82E+04		(K)YIDQEEL	(K)Y/I|D/Q E/E L N K(T)		124.37	576.2845	1151.558	0.0038	3.3	4.14	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
16730	dirMS_041712_NAR_20mM_plus.9309.9309.2	2	7.15	0	1.86E+05		(K)SVTNED	(K)S V/T\N\E D/V/T Q E E L G G A K(T)		136	838.9014	1676.797	-0.0018	-1.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
16731	dirMS_041712_NAR_20mM_plus.9824.9824.2	2	7.15	0	7.77E+04		(K)AIADTG	(K)A I|A D T/G A/N V V/V T G G K(V)		139.1	686.874	1372.743	-0.0023	-1.7	5.88	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
16732	dirMS_041712_NAR_30mM_plus2.19410.19410.2	2	7.15	0	1.85E+04		(K)MNEFLE	(K)M N\E|F|L|E N F E K(N)		155.87	650.7974	1300.588	-0.0003	-0.2	4.25	28580.2	9.35	HUMAN	Q9UFN0	Protein NipSnap homolog 3A
16733	dirMS_041712_NAR_30mM_plus2.8327.8327.2	2	7.15	0	3.66E+05		(K)TAVCDIF	(K)T A|V C D I/P P/R(G)	C:Carbamidomethylation	97.88	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
16734	dirMS_041712_NAR_40mM_plus2.7127.7127.2	2	7.15	0	2.31E+05		(K)NMMAA	(K)N M/M|A/A/C D/P\R(H)	C:Carbamidomethylation	101.42	533.2182	1065.427	0.0017	1.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
16735	dirMS_041712_NAR_50mM_plus2.10248.10300.3	3	7.15	1	1.76E+05		(R)QELILSN	(R)Q E L/I/L/S/N S E D/K S I R(V)		121.43	544.624	1631.86	-0.0024	-1.5	4.68	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
16736	dirMS_041712_NAR_60mM_plus.14097.14364.3	3	7.15	1	1.57E+06		(R)LVGIFEN	(R)L V G/I F|E N Q\E R K(H)		131.05	444.917	1332.727	0.0094	7.1	6.14	19641.8	5.99	HUMAN	O95989	Diphosphoinositol polyphosphate phosphohydrolase 1
16737	dirMS_041712_NAR_60mM_plus.6765.6765.3	3	7.15	1	1.11E+06		(R)NTEEEG	(R)N T/E|E E/G L K/Y K(S)		93.37	404.2017	1210.595	-0.0045	-3.7	4.79	83344.9	10.18	HUMAN	E9PK09	Bcl-2-associated transcription factor 1 (Fragment)
16738	dirMS_041712_NAR_60mM_plus.8073.8284.3	3	7.15	1	6.10E+05		(K)ALSRQEI	(K)A L/S R Q E M/Q/E V\Q/S S R(S)		100.33	550.2735	1648.807	-0.0012	-0.7	6.19	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
16739	dirMS_041712_NAR_60mM_plus.9286.9286.3	3	7.15	1	1.49E+06		(R)SRAEAE	(R)S R A E A\E|S/M/Y Q I K(Y)		105.95	471.5691	1412.684	0.0089	6.3	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
16740	dirMS_041712_NAR_120mM_minus.11043.11043.3	3	7.14	0	2.80E+04		(K)GSYVSIH	(K)G S/Y/V/S I/H/S S G F R(D)		114.25	432.8784	1296.633	-0.0125	-9.6	8.75	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
16741	dirMS_041712_NAR_120mM_minus.5661.5702.2	2	7.14	1	6.56E+05		(R)CAEELK	(R)C/A E/E/L/K/R(Q)	C:Carbamidomethylation	84.02	453.2291	905.451	0	0	6.14	137011.4	5.71	HUMAN	F5H1N7	Uncharacterized protein KIAA1211
16742	dirMS_041712_NAR_120mM_minus.6540.6540.3	3	7.14	1	8.36E+05		(R)TEERAEI	(R)T E|E R A/E L/A E/S/R(C)		89.2	430.8806	1290.628	-0.0012	-0.9	4.49	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
16743	dirMS_041712_NAR_20mM_minus.10377.10377.2	2	7.14	0	4.57E+04	M145m	(R)VVLFEm	(R)V V|L/F/E/m E A R(K)	m:Oxidized methionine	152.52	555.2868	1093.571	15.9953	0.3	4.53	27142.4	5.34	HUMAN	E5RG68	Copine-3 (Fragment)
16744	dirMS_041712_NAR_20mM_minus.12121.12121.3	3	7.14	0	4.21E+05	M256m	(R)SLDmDS	(R)S L D m D S\I/I A/E/V K(A)	m:Oxidized methionine	170.58	446.227	1320.671	15.9949	0	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
16745	dirMS_041712_NAR_20mM_minus.8334.8334.2	2	7.14	0	1.25E+05		(K)VTADVI	(K)V T|A/D/V/I N A A E K(L)		132.47	565.8065	1130.605	0.0005	0.5	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
16746	dirMS_041712_NAR_30mM_minus2.8281.8281.2	2	7.14	0	1.96E+04		(R)QLEEAEI	(R)Q L/E/E/A/E\E/E A Q\R(A)		99.67	666.3076	1331.607	0.0006	0.4	3.98	227783.5	5.5	HUMAN	P35579	Myosin-9
16747	dirMS_041712_NAR_50mM_minus2.13515.13515.3	3	7.14	1	2.38E+05		(K)ITDIIGKE	(K)I T/D\I|I G K E E G I/G/P E N L R(G)		145.2	618.665	1853.997	-0.0163	-8.8	4.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
16748	dirMS_041712_NAR_60mM_minus.16180.16180.3	3	7.14	1	1.63E+05	M84m	(K)ETmQSL	(K)E T m/Q/S/L\N D R L A S/Y L D R(V)	m:Oxidized methionine	150.25	643.3097	1911.923	15.9916	-1.7	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
16749	dirMS_041712_NAR_60mM_minus.17018.17018.3	3	7.14	1	2.43E+05		(K)YAVLYQ	(K)Y A/V/L Y Q/P L F D/K R(F)		154.65	504.9409	1512.821	-0.0128	-8.4	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
16750	dirMS_041712_NAR_60mM_minus.19795.19795.3	3	7.14	1	1.59E+06		(K)EIIDLVL	(K)E/I I/D/L/V/L D R I R(K)		179.72	452.2739	1354.805	0.0019	1.4	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
16751	dirMS_041712_NAR_120mM_plus.12781.12781.3	3	7.14	0	5.21E+05		(K)HLSVND	(K)H L\S V\N\D\L/P V G/R(S)		119.9	402.8906	1206.659	-0.0017	-1.4	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
16752	dirMS_041712_NAR_120mM_plus.18085.18085.3	3	7.14	1	3.70E+05		(R)ARFEEL	(R)A R F E\E\L/N A D/L/F/R(G)		147.85	494.2571	1480.754	0.0024	1.7	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
16753	dirMS_041712_NAR_120mM_plus.8141.8160.3	3	7.14	1	5.48E+05		(K)IVSGKD	(K)I/V|S G K D Y N V/T/A N S K(L)		96.75	499.263	1495.775	-0.0007	-0.4	8.5	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
16754	dirMS_041712_NAR_120mM_plus.9030.9030.3	3	7.14	0	1.41E+06		(K)HTGPNS	(K)H T\G P N/S P\D\T A/N/D/G F V R(L)		100.03	562.26	1684.767	-0.0019	-1.2	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
16755	dirMS_041712_NAR_20mM_plus.14092.14092.2	2	7.14	0	2.09E+05	M256m	(R)SLDmDS	(R)S L|D m D/S I I A/E V/K(A)	m:Oxidized methionine	168.68	668.8371	1320.671	15.9954	0.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
16756	dirMS_041712_NAR_20mM_plus.14192.14192.2	2	7.14	0	5.25E+04		(K)LIINSLY	(K)L/I/I/N/S L Y K(N)		169.95	482.2962	963.587	-0.0022	-2.3	8.59	5582.4	4.81	HUMAN	F8W026	Endoplasmin (Fragment)
16757	dirMS_041712_NAR_30mM_plus2.19701.19701.2	2	7.14	0	2.35E+05		(K)APDFVF	(K)A/P/D/F/V|F Y A P R(L)		156.72	591.8008	1182.594	0.0001	0.1	5.88	71218.8	6.3	HUMAN	A7YIJ8	Radixin
16758	dirMS_041712_NAR_30mM_plus2.8401.8401.2	2	7.14	0	1.29E+06		(K)QGGGG	(K)Q G G G G/G G/G/S V/P G I E/R(M)		97.22	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
16759	dirMS_041712_NAR_40mM_plus2.8904.8904.2	2	7.14	0	1.05E+05		(K)FYEQFS	(K)F/Y|E/Q F S K(N)		115.03	474.7301	948.446	0.0068	7.1	6	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
16760	dirMS_041712_NAR_50mM_plus2.18104.18104.3	3	7.14	0	2.25E+05		(R)VTMLFL	(R)V T|M/L/F/L/G L H N V R(Q)		162.9	467.267	1399.788	-0.0014	-1	9.73	21721.5	5.37	HUMAN	H7BZ35	Aspartate--tRNA ligase, cytoplasmic (Fragment)
16761	dirMS_041712_NAR_50mM_plus2.21136.21136.3	3	7.14	0	2.87E+05		(K)HSQFIG	(K)H S Q\F I G\Y|P I/T L F V E K(E)		180.25	593.6536	1778.948	-0.0013	-0.8	6.75	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
16762	dirMS_041712_NAR_50mM_plus2.5644.5644.3	3	7.14	1	1.06E+06		(K)TAGPIA	(K)T/A|G P/I A S A Q K Q/P A G K(V)		91.9	475.5987	1424.786	-0.0041	-2.8	10	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
16763	dirMS_041712_NAR_50mM_plus2.8862.8862.3	3	7.14	0	7.69E+05		(R)AALAHS	(R)A A L A H S E E\V|T|A S Q V A/A T K(T)		113.47	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
16764	dirMS_041712_NAR_60mM_plus.13164.13164.3	3	7.14	1	9.77E+05		(R)ISVYYNE	(R)I/S/V/Y/Y N E A T G G K Y V P R(A)		125.9	606.3113	1816.923	-0.0035	-1.9	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
16765	dirMS_041712_NAR_60mM_plus.15836.15836.3	3	7.14	0	2.03E+05		(K)NFDLRP	(K)N/F/D/L/R/P/G V I V R(-)		140.08	429.248	1285.738	-0.0081	-6.3	9.6	33192.3	6.77	HUMAN	B4DN45	S-adenosylmethionine synthase
16766	dirMS_041712_NAR_60mM_plus.16000.16000.3	3	7.14	1	2.52E+05		(R)TSFLDD	(R)T S F/L/D/D/A/F R K(N)		139.92	400.5399	1199.605	-0.0004	-0.3	5.62	21195.7	6.97	HUMAN	H0YJ21	Cytoplasmic dynein 1 heavy chain 1 (Fragment)
16767	dirMS_041712_NAR_60mM_plus.17176.17176.3	3	7.14	0	2.26E+05		(K)EGHVEV	(K)E G H V E V\V/S/E/L/L Q R(E)		146.07	498.9326	1494.791	-0.0078	-5.2	4.75	48586.6	9.32	HUMAN	D6RCB2	Ankyrin-3
16768	dirMS_041712_NAR_60mM_plus.17873.17873.3	3	7.14	1	8.12E+05		(R)LKLPAV	(R)L K/L|P A V\V/T/A D/L R(L)		150.67	432.6056	1295.805	-0.0023	-1.8	8.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
16769	dirMS_041712_NAR_30mM_minus2.16428.16428.3	3	7.13	0	6.11E+05		(R)ASLEAAI	(R)A S L E A A\I/A/D/A/E Q R(G)		143.53	448.8965	1344.675	-0.0004	-0.3	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
16770	dirMS_041712_NAR_30mM_minus2.19029.19029.2	2	7.13	0	2.34E+05		(R)TLLAILR	(R)T L/L/A I L R(L)		159.05	400.2731	799.54	-0.0011	-1.3	9.41	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
16771	dirMS_041712_NAR_30mM_minus2.7347.7347.2	2	7.13	0	3.01E+05	M514m M5	(K)NEEmm	(K)N E/E/m/m E Q/K(E)	m:Oxidized methionine	94.68	535.7092	1038.423	31.9881	-1.6	4.25	67721.3	5.54	HUMAN	P32456	Interferon-induced guanylate-binding protein 2
16772	dirMS_041712_NAR_50mM_minus2.12889.12889.3	3	7.13	1	1.80E+05		(K)GGELVY	(K)G G E\L|V/Y/T D S E/A R D V/F E K(A)		141.5	638.9739	1914.908	-0.0008	-0.4	4.18	533778	5.74	HUMAN	Q15149	Plectin
16773	dirMS_041712_NAR_60mM_minus.19737.19737.3	3	7.13	0	2.93E+05		(K)HSQFIG	(K)H S Q F I G\Y/P/I/T L F V E K(E)		178.25	593.6533	1778.948	-0.0022	-1.3	6.75	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
16774	dirMS_041712_NAR_120mM_plus.15648.15648.3	3	7.13	1	5.16E+04		(K)VKEGM	(K)V K E G M N\I|V/E/A M E R(F)		135.1	502.5857	1505.745	-0.0025	-1.7	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
16775	dirMS_041712_NAR_120mM_plus.18086.18086.3	3	7.13	1	3.70E+05		(R)ARFEEL	(R)A R F E\E\L|N\A/D/L F R(G)		147.85	494.2571	1480.754	0.0024	1.7	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
16776	dirMS_041712_NAR_20mM_plus.10609.10609.2	2	7.13	0	5.11E+04		(R)ELAEDG	(R)E L\A E|D/G Y/S/G V/E V R(V)		145.7	712.3373	1423.67	-0.0026	-1.9	4	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
16777	dirMS_041712_NAR_20mM_plus.12308.12350.2	2	7.13	0	1.41E+05		(K)TIIFVET	(K)T I|I/F V/E/T K(R)		158.63	475.7818	950.556	0.0006	0.6	5.66	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
16778	dirMS_041712_NAR_20mM_plus.18797.18797.2	2	7.13	0	1.91E+05		(R)VFIGNL	(R)V F|I/G/N L N\T L V\V K(K)		200.17	658.8999	1316.794	-0.0011	-0.9	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
16779	dirMS_041712_NAR_20mM_plus.9794.9794.2	2	7.13	0	7.67E+04		(K)AIADTG	(K)A I/A D/T/G A N V V\V/T G/G K(V)		139.02	686.874	1372.743	-0.0023	-1.7	5.88	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
16780	dirMS_041712_NAR_30mM_plus2.4847.4847.2	2	7.13	1	2.39E+05		(R)NTKGG	(R)N T K G G D A P A|A/G E/D/A(-)		76.97	637.286	1273.565	-0.0008	-0.6	4.03	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
16781	dirMS_041712_NAR_30mM_plus2.6768.6768.2	2	7.13	0	2.32E+05		(R)SPDNPM	(R)S/P|D|N/P M N Q/R(A)		89.32	529.7357	1058.468	-0.0042	-4	5.55	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124

16782	dirMS_041712_NAR_30mM_plus2.9676.9697.2	2	7.13	0	2.43E+06		(K)VGVNGF	(K)V/G|V/N/G\F G\R(I)		104.07	403.2192	805.432	-0.0004	-0.5	9.72	36223.7	8.79	HUMAN	P04406	Glyceraldehyde-3-phosphate dehydrogenase
16783	dirMS_041712_NAR_40mM_plus2.17984.17984.3	3	7.13	0	1.66E+05		(K)LAKPLSS	(K)L A|K P L S\S L/T|P L|I M A A K(E)		171.7	552.0052	1653.997	0.0039	2.3	10	24711.4	5.19	HUMAN	H7C1X3	PAK-2p34 (Fragment)
16784	dirMS_041712_NAR_40mM_plus2.7323.7323.2	2	7.13	0	1.54E+05		(R)SGYFDEI	(R)S/G/Y|F D/E R(Y)		103.57	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
16785	dirMS_041712_NAR_60mM_plus.18727.18727.3	3	7.13	1	1.60E+05		(R)KAPSDL	(R)K\A\P S D\L\Y/Q|I I L/K(A)		155.1	463.6084	1388.815	-0.0041	-3	8.5	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
16786	dirMS_041712_NAR_60mM_plus.5149.5149.3	3	7.13	1	4.46E+04		(K)GNSPPS	(K)G N|S/P/P S S G E A C R E E K(G)	C:Carbamidomethylation	84.52	535.5678	1604.697	-0.0081	-5	4.79	24954.4	5.33	HUMAN	A6NM98	ARD1 homolog A, N-acetyltransferase (S. cerevisiae), isoform CRA_b
16787	dirMS_041712_NAR_120mM_minus.16830.16830.3	3	7.12	0	4.28E+05		(R)EHALLA	(R)E H A L L\A|Y T/L/G V/K(Q)		145.83	438.9186	1314.742	-0.0004	-0.3	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
16788	dirMS_041712_NAR_20mM_minus.11766.11766.2	2	7.12	0	8.32E+04		(R)GGIVDE	(R)G G I|V/D E G A L L R(A)		166.5	550.3071	1099.611	-0.0037	-3.3	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
16789	dirMS_041712_NAR_30mM_minus2.6295.6295.2	2	7.12	0	1.88E+05	M796m	(R)mNEAF	(R)m N|E/A/F/G D/T K(F)	m:Oxidized methionine	88.07	514.726	1012.44	16.0043	9.1	4.37	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
16790	dirMS_041712_NAR_30mM_minus2.7173.7173.2	2	7.12	0	3.86E+05		(K)QQTLEA	(K)Q Q|T/L/E/A E E\A K(R)		93.4	573.7846	1146.564	-0.0018	-1.6	4.25	76925.9	4.46	HUMAN	A8MV58	Drebrin
16791	dirMS_041712_NAR_50mM_minus2.17742.17742.3	3	7.12	0	3.21E+05		(K)VAHALA	(K)V A H A L A E G L/G|V|I|A C I G E/K(L)	C:Carbamidomethylation	169.02	603.3247	1807.974	-0.0139	-7.7	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
16792	dirMS_041712_NAR_50mM_minus2.9263.9263.3	3	7.12	0	1.99E+05		(K)VGQEIE	(K)V/G|Q/E/I E V R P G I V S K(D)		120.43	504.2902	1510.859	-0.0027	-1.8	6.11	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
16793	dirMS_041712_NAR_60mM_minus.10593.10593.3	3	7.12	0	9.70E+04		(R)NRPPFG	(R)N R P P F\G/Q|G Y T/Q|P G/P G Y R(-)		118.75	631.3087	1891.92	-0.0083	-4.4	9.99	43076.8	5.01	HUMAN	G5E9V1	Protein TFG
16794	dirMS_041712_NAR_60mM_minus.18338.18338.3	3	7.12	1	1.35E+05		(R)SELELTL	(R)S E|L/E/L T L G K L E Q V R(S)		163.07	538.9724	1614.906	-0.0035	-2.1	4.78	533778	5.74	HUMAN	Q15149	Plectin
16795	dirMS_041712_NAR_20mM_plus.15546.15546.2	2	7.12	0	3.73E+05		(R)GNPTVE	(R)G N|P T\V/E/V D L F T S K(G)		179.47	703.861	1406.716	-0.0015	-1	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
16796	dirMS_041712_NAR_20mM_plus.16539.16539.2	2	7.12	0	1.75E+05		(R)LLEAQIA	(R)L L E A/Q I|A/T\G/G I\I D|P K(E)		185.47	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
16797	dirMS_041712_NAR_20mM_plus.16713.16713.2	2	7.12	0	1.65E+05		(K)TVDNFV	(K)T V|D N F V/A/L\A T G E K(G)		186.22	682.8565	1364.706	0.0001	0.1	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
16798	dirMS_041712_NAR_20mM_plus.9151.9151.2	2	7.12	0	5.96E+05	M239m	(K)EITALAP	(K)E I/T A|L/A/P S T m K(I)	m:Oxidized methionine	133.15	589.309	1161.618	15.9923	-2.2	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
16799	dirMS_041712_NAR_20mM_plus.9574.9574.2	2	7.12	0	5.05E+05		(R)ISVYYNE	(R)I/S V Y/Y/N E|A T G G K(Y)		138.18	651.3211	1301.637	-0.0023	-1.8	6	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
16800	dirMS_041712_NAR_40mM_plus2.8362.8362.2	2	7.12	0	2.86E+05		(R)FGSGM	(R)F/G|S/G/M N/M|G R(I)		109.45	478.706	956.408	-0.003	-3.1	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
16801	dirMS_041712_NAR_50mM_plus2.12364.12364.3	3	7.12	1	2.80E+05		(R)ESDVPL	(R)E S D V/P/L K/T/E E F E V T K(T)		132.68	584.2981	1750.874	0.0052	3	4.25	18909	6.21	HUMAN	Q969H8	UPF0556 protein C19orf10
16802	dirMS_041712_NAR_50mM_plus2.14307.14308.3	3	7.12	0	8.72E+04		(R)VAPEEH	(R)V A\P E E H P T L L/T/E A/P L N/P K(A)		143.4	652.6835	1956.044	-0.0077	-3.9	4.75	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
16803	dirMS_041712_NAR_50mM_plus2.8214.8214.3	3	7.12	1	3.09E+05		(R)NTVSQS	(R)N T|V\S Q S I/S G D/P E I D/K K(I)		110.27	573.2915	1717.86	-0.0003	-0.2	4.56	58392.6	9.36	HUMAN	B4DF96	Eukaryotic translation initiation factor 2A
16804	dirMS_041712_NAR_60mM_plus.10246.10246.2	2	7.12	0	2.03E+06		(K)GIVEFSG	(K)G I/V E F|S G/K/P A A/R(K)		111.3	616.3425	1231.679	-0.0016	-1.3	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
16805	dirMS_041712_NAR_60mM_plus.16091.16091.3	3	7.12	1	5.53E+05		(R)IKIGDPL	(R)I K I G D\P L|L/E D T/R(M)		141.48	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
16806	dirMS_041712_NAR_60mM_plus.8754.8817.3	3	7.12	1	1.52E+06		(K)GGIMLP	(K)G G|I/M/L/P E K S Q G K(V)		103.63	415.5607	1244.667	0.0008	0.7	8.59	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
16807	dirMS_041712_NAR_20mM_minus.10302.10302.2	2	7.11	0	9.30E+04		(R)NTGIICT	(R)N T\G I\I/C/T|I/G\P A S R(S)	C:Carbamidomethylation	152.63	680.3561	1359.705	0	0	9.75	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
16808	dirMS_041712_NAR_20mM_minus.11175.11175.2	2	7.11	0	3.44E+05	M1m N6n	(-)mPLFPnL	(-)m P|L F/P n L/P/R(L)	m:Oxidized methionine n:N-	159.62	652.3395	1084.597	219.0745	0.2	9.5	39133.5	4.5	HUMAN	Q8TD91-2	Isoform 2 of Melanoma-associated antigen C3
16809	dirMS_041712_NAR_50mM_minus2.13179.13179.3	3	7.11	1	2.32E+04		(R)TQVELL	(R)T Q|V/E L/L\E/A P T/P A L K R(T)		143.82	555.9883	1665.953	-0.003	-1.8	5.81	18460.6	5.48	HUMAN	C9IYM4	Glycogen [starch] synthase, muscle (Fragment)
16810	dirMS_041712_NAR_50mM_minus2.13578.13578.3	3	7.11	1	8.23E+04		(K)ITDIIGK	(K)I/T D I/I/G K E E/G\I G/P E N L R(G)		144.9	618.665	1853.997	-0.0163	-8.8	4.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
16811	dirMS_041712_NAR_50mM_minus2.18789.18789.3	3	7.11	1	1.98E+06		(R)LIALLEVI	(R)L I/A L/L E V/L S Q K R(M)		183.63	461.6289	1382.873	-0.0008	-0.6	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
16812	dirMS_041712_NAR_60mM_minus.19362.19362.3	3	7.11	0	4.51E+05	S14s	(-)XDGVFLS	(-)X D|G V F L/S N/S F/Q P P s A K(A)	s:Phosphorylated S	171.95	596.2923	1706.875	79.9875	11.9	5.84	13361.5	9.89	HUMAN	H0Y8U8	Afadin (Fragment)
16813	dirMS_041712_NAR_20mM_plus.11401.11401.2	2	7.11	0	3.45E+05		(K)LITPAVV	(K)L I/T|P A V V S E R(L)		151	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
16814	dirMS_041712_NAR_20mM_plus.11494.11494.2	2	7.11	0	1.72E+05		(R)YALYDA	(R)Y A/L|Y|D/A T Y E T/K(E)		151.55	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
16815	dirMS_041712_NAR_20mM_plus.19037.19037.2	2	7.11	0	1.05E+05		(K)DTSYLF	(K)D T/S Y L/F/I/T/G/P D V V/K(S)		201.92	777.9049	1554.805	-0.0025	-1.6	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
16816	dirMS_041712_NAR_20mM_plus.7963.7963.2	2	7.11	0	2.04E+05		(R)FGQGG	(R)F G/Q/G/G/A/G P V G G Q/G P R(G)		125.17	671.3361	1341.666	-0.0009	-0.7	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
16817	dirMS_041712_NAR_30mM_plus2.5704.5704.2	2	7.11	0	1.39E+04	S326s Y32	(R)VLsLGyR	(R)V/L/s/L G/y/R(T)	s:Phosphorylated S y:Phosph	84.02	484.2042	807.472	159.9288	-4	8.72	63795.9	9.27	HUMAN	O00219	Hyaluronan synthase 3
16818	dirMS_041712_NAR_30mM_plus2.6409.6409.2	2	7.11	0	2.52E+05		(K)GEGQLG	(K)G E\G Q/L/G/P/A E R(A)		87.53	507.2537	1013.501	-0.0009	-0.9	4.53	96306.4	6.41	HUMAN	P13639	Elongation factor 2
16819	dirMS_041712_NAR_30mM_plus2.7622.7622.2	2	7.11	0	6.83E+05		(R)VNTELM	(R)V/N|T E/L/M/K(A)		94.05	417.7282	834.439	0.0102	12.2	5.97	61760.3	6.01	HUMAN	O14773	Tripeptidyl-peptidase 1
16820	dirMS_041712_NAR_40mM_plus2.10616.10616.3	3	7.11	0	1.85E+05		(K)VGSLDN	(K)V/G S L/D N V/G H|L P A/G G A V K(I)		128.15	530.9567	1590.86	-0.0043	-2.7	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
16821	dirMS_041712_NAR_40mM_plus2.19013.19013.3	3	7.11	0	1.41E+05		(R)ETSSDV	(R)E T|S S/D/V A|L/A S H/I L T A L R(E)		178.6	595.3161	1783.955	-0.0211	-11.8	5.32	36920.6	4.68	HUMAN	O00273	DNA fragmentation factor subunit alpha
16822	dirMS_041712_NAR_40mM_plus2.19273.19273.3	3	7.11	1	1.93E+05		(K)TSAQVV	(K)T|S/A Q V|V\L D G L V D K I G D/V K(C)		180.37	619.6811	1857.033	-0.004	-2.2	4.43	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
16823	dirMS_041712_NAR_40mM_plus2.5651.5651.2	2	7.11	0	1.12E+05		(R)FSSSSGY	(R)F S S S S/G Y/G/G G S S R(V)		90.98	618.2686	1235.529	0.0012	1	8.75	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
16824	dirMS_041712_NAR_50mM_plus2.12478.12478.3	3	7.11	0	2.04E+05		(K)AIIKPQY	(K)A I|I K/P Q|Y\V D Q I/P K(A)		133.23	504.9637	1512.878	-0.0019	-1.3	8.54	47949	9.16	HUMAN	D6R9I9	ATP-binding cassette sub-family E member 1
16825	dirMS_041712_NAR_50mM_plus2.12709.12709.3	3	7.11	0	3.28E+05		(K)LQELPD	(K)L Q|E L/P D A V P H/G E M P R(H)		134.3	563.6145	1688.843	-0.0135	-8	4.65	78390.7	9.27	HUMAN	B1AHB1	DNA replication licensing factor MCM5
16826	dirMS_041712_NAR_50mM_plus2.18147.18147.3	3	7.11	0	2.51E+05		(R)DIKPDNI	(R)D I K P D N\F|L/M/G I G R(H)		163.28	492.5943	1475.767	0.0008	0.6	5.96	27968.7	9.69	HUMAN	D6REM4	Casein kinase I isoform alpha
16827	dirMS_041712_NAR_50mM_plus2.9478.9478.3	3	7.11	1	4.84E+05		(K)LTSDDVI	(K)L/T/S D D/V/K E Q I/Y/K(L)		117.45	480.2521	1438.742	-0.0007	-0.5	4.56	12573.5	10.39	HUMAN	E9PS50	40S ribosomal protein S13 (Fragment)
16828	dirMS_041712_NAR_60mM_plus.12034.12034.3	3	7.11	0	5.62E+05		(K)CPNLTH	(K)C/P N L T H\L/N L/S G N/K(I)	C:Carbamidomethylation	119.98	489.9162	1467.737	-0.0032	-2.2	8.76	20111	4.47	HUMAN	H0YN26	Acidic leucine-rich nuclear phosphoprotein 32 family member A
16829	dirMS_041712_NAR_60mM_plus.16218.16218.3	3	7.11	0	5.80E+05		(K)MTHLPE	(K)M T H L|P E\L\D T L/S|S E/R(A)		142.22	543.6023	1628.795	-0.0025	-1.5	4.65	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
16830	dirMS_041712_NAR_60mM_plus.17139.17139.3	3	7.11	1	2.25E+05		(K)IKAIPQL	(K)I/K A I/P Q/L/Q/G Y L R(S)		146.2	467.2842	1399.842	-0.0039	-2.8	9.99	25891.4	10.67	HUMAN	F8W181	60S ribosomal protein L6 (Fragment)
16831	dirMS_041712_NAR_60mM_plus.17204.17204.3	3	7.11	1	4.07E+05		(R)GFPTIYF	(R)G F/P/T/I Y F S/P A N K K(L)		147.05	490.5979	1469.779	0.0004	0.3	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
16832	dirMS_041712_NAR_60mM_plus.21275.21275.3	3	7.11	1	5.45E+05		(R)SKALGS	(R)S K A L G S D H C P I T\L Y\L|A|L(-)	C:Carbamidomethylation	175.57	620.326	1858.973	-0.0097	-5.2	6.46	5634.5	9.82	HUMAN	G3V574	DNA-(apurinic or apyrimidinic site) lyase
16833	dirMS_041712_NAR_60mM_plus.5737.5737.3	3	7.11	0	1.87E+05		(R)STFETE	(R)S T|F E/T/E/H A G Q R(D)		88.4	421.5294	1262.576	-0.0024	-1.9	5.38	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
16834	dirMS_041712_NAR_60mM_plus.9472.9472.3	3	7.11	0	4.80E+05		(K)QADNP	(K)Q A/D N/P H/V/A L Y/Q A R(F)		107.52	494.9186	1482.745	-0.0036	-2.4	6.74	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
16835	dirMS_041712_NAR_120mM_minus.10341.10341.3	3	7.1	0	1.52E+05	S970s T981	(R)sPEASAS	(R)s P E/A S A S\A|S\P H/t P/R(E)	s:Phosphorylated S t:Phosph	110.45	518.8751	1394.666	159.9449	7.8	6.47	218451.1	8.24	HUMAN	Q8TF72	Protein Shroom3
16836	dirMS_041712_NAR_120mM_minus.11348.11348.3	3	7.1	0	2.31E+05		(R)GFCLPP	(R)G F C/L/P/P/H C S R(G)	C:Carbamidomethylation	116.42	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
16837	dirMS_041712_NAR_20mM_minus.7995.7995.2	2	7.1	0	9.09E+03		(R)AAAGYP	(R)A A A/G\Y|P D/P Y/S R(A)		129.45	584.2733	1167.543	-0.0036	-3.1	5.88	266161	5.68	HUMAN	E9PPU0	Epiplakin
16838	dirMS_041712_NAR_30mM_minus2.14729.14729.2	2	7.1	0	5.00E+05		(R)TFEDFV	(R)T F|E/D/F V/R(I)		133.23	457.2246	913.441	0.0005	0.6	4.37	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
16839	dirMS_041712_NAR_50mM_minus2.14435.14435.3	3	7.1	0	4.26E+05		(R)QIFHPE	(R)Q I F H/P/E Q L I/T G K(E)		149.72	470.9286	1410.774	-0.0027	-1.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
16840	dirMS_041712_NAR_50mM_minus2.9560.9560.3	3	7.1	1	2.04E+05	M183m	(R)VEVERD	(R)V E|V/E R D N L/A/E D I m R(L)	m:Oxidized methionine	122.12	568.9459	1688.827	15.9959	0.6	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
16841	dirMS_041712_NAR_60mM_minus.17793.17793.3	3	7.1	1	2.22E+05		(R)LGLSTLG	(R)L/G/L/S\T L/G E L K Q N L S R(S)		159.6	543.6476	1628.933	-0.0047	-2.9	8.75	22294.4	5.26	HUMAN	O43399	Tumor protein D54
16842	dirMS_041712_NAR_60mM_minus.6370.6370.3	3	7.1	1	1.15E+05		(K)DSYVGD	(K)D/S Y V/G D/E/A Q S K R(G)		93.23	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
16843	dirMS_041712_NAR_120mM_plus.7496.7496.3	3	7.1	1	2.02E+06	M281m	(R)SRAEAE	(R)S R A E\A\E|S m/Y Q\I K(Y)	m:Oxidized methionine	93.02	476.8977	1412.684	15.9947	-0.1	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
16844	dirMS_041712_NAR_20mM_plus.10258.10258.3	3	7.1	0	1.36E+05	M281m M	(R)NmPQA	(R)N m|P Q A D A|m/V L/V/A R(N)	m:Oxidized methionine	143.47	483.2393	1415.713	31.99	0.1	5.84	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
16845	dirMS_041712_NAR_20mM_plus.16197.16197.2	2	7.1	0	7.18E+04		(R)LLDAQL	(R)L L D/A Q L|A/T G G I V D/P R(L)		183.93	769.9362	1538.854	0.0114	7.4	4.21	533778	5.74	HUMAN	Q15149	Plectin
16846	dirMS_041712_NAR_30mM_plus2.20710.20710.2	2	7.1	0	5.75E+04		(K)YLEHLVI	(K)Y/L/E H/L/V I D K(R)		163.05	565.3227	1129.625	0.0129	11.5	5.32	98297.1	6.1	HUMAN	Q8WUH2	Transforming growth factor-beta receptor-associated protein 1
16847	dirMS_041712_NAR_60mM_plus.11346.11362.3	3	7.1	1	6.05E+05	M477m	(R)TLKIPA	(R)T L/K I/P A m T I A K(N)	m:Oxidized methionine	116.93	401.5768	1186.723	15.9931	-1.5	10	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
16848	dirMS_041712_NAR_60mM_plus.19934.19934.3	3	7.1	1	1.46E+05		(R)SELELTL	(R)S E/L/E/L/T L G K L/E Q V R(S)		163.83	538.9738	1614.906	0.0007	0.5	4.78	533778	5.74	HUMAN	Q15149	Plectin
16849	dirMS_041712_NAR_60mM_plus.21143.21143.3	3	7.1	1	4.03E+05		(R)KAIIIFVP	(R)K A I I\I\F\V|P V P Q L K(S)		174.23	489.3205	1465.95	-0.0035	-2.4	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
16850	dirMS_041712_NAR_60mM_plus.5395.5395.3	3	7.1	1	7.94E+04		(K)VSQGVE	(K)V/S|Q/G V E D/G/P D T K R(A)		85.7	463.233	1387.681	0.0032	2.3	4.56	33726	7.84	HUMAN	B3KNJ4	SUMO-1 activating enzyme subunit 1, isoform CRA_a
16851	dirMS_041712_NAR_120mM_minus.17921.17921.3	3	7.09	1	1.87E+05		(R)ARFEEL	(R)A R F E\E L N/A|D/L F/R(G)		152.87	494.2561	1480.754	-0.0006	-0.4	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
16852	dirMS_041712_NAR_20mM_minus.12300.12300.2	2	7.09	0	8.72E+05	M313m	(R)TVQSLEI	(R)T V|Q/S/L E|I D/L D S m R(N)	m:Oxidized methionine	171.22	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
16853	dirMS_041712_NAR_30mM_minus2.9087.9087.2	2	7.09	0	6.56E+05		(K)LAAIGE	(K)L A|A/I/G E|A T R(L)		103.43	451.2537	901.51	-0.01	-11.1	6	533778	5.74	HUMAN	Q15149	Plectin
16854	dirMS_041712_NAR_40mM_minus2.14331.14331.3	3	7.09	0	6.10E+05		(R)IHFPLAT	(R)I H\F P L A\T Y\A/P\V/I S A E K(A)		167.93	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
16855	dirMS_041712_NAR_50mM_minus2.15218.15218.3	3	7.09	0	1.67E+05		(R)NSSHAG	(R)N S S H A\G A F V\I/V/T/E E A\I A K(G)		154.53	615.3184	1843.955	-0.0142	-7.7	5.4	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
16856	dirMS_041712_NAR_50mM_minus2.15405.15405.3	3	7.09	1	1.08E+05		(K)YAVLYQ	(K)Y A/V/L Y Q/P L F D/K R(F)		155.62	504.9453	1512.821	0.0004	0.3	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
16857	dirMS_041712_NAR_50mM_minus2.16796.16796.3	3	7.09	0	2.54E+05		(K)ALVSHN	(K)A/L\V S H N G S L\I/N\V|G S L L Q R(A)		163.8	626.6879	1878.056	-0.0064	-3.4	9.8	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
16858	dirMS_041712_NAR_60mM_minus.13976.13976.3	3	7.09	1	3.38E+05		(R)SLIANLA	(R)S L|I/A N L/A A/A|N C Y K K(E)	C:Carbamidomethylation	138.2	512.9419	1536.82	-0.0091	-5.9	9.7	36978.6	6.33	HUMAN	B7Z800	Adenosine kinase
16859	dirMS_041712_NAR_60mM_minus.15935.15935.3	3	7.09	1	3.69E+05		(R)AEGAIA	(R)A/E/G/A\I A/G F R D P F/S G K(Q)		148.08	508.2601	1522.765	0.0009	0.6	6.12	266161	5.68	HUMAN	E9PPU0	Epiplakin
16860	dirMS_041712_NAR_60mM_minus.6353.6353.3	3	7.09	1	6.26E+04		(R)VEEKEGI	(R)V E\E K E G I|P/P Q Q Q R(L)		93.95	513.2702	1537.797	-0.0008	-0.6	4.79	19593.1	6.86	HUMAN	E9PL57	Protein NEDD8-MDP1 (Fragment)
16861	dirMS_041712_NAR_20mM_plus.13213.13213.2	2	7.09	0	6.43E+04		(R)IGGGID	(R)I/G|G G I/D/V/P V/P R(H)		163.25	540.3131	1079.621	-0.0018	-1.7	5.84	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
16862	dirMS_041712_NAR_30mM_plus2.17946.17946.3	3	7.09	0	1.70E+05		(R)MADAL	(R)M A\D\A L D N/Y/V/I/R(G)		146.95	427.5478	1280.63	-0.0015	-1.2	4.21	15838.9	7.03	HUMAN	H0Y5U0	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
16863	dirMS_041712_NAR_30mM_plus2.21128.21128.2	2	7.09	0	1.02E+05		(K)VFSIGPV	(K)V F/S|I/G/P V F/R(A)		164.3	511.2941	1021.583	-0.002	-2	9.72	57534.6	6.11	HUMAN	P14868	Aspartate--tRNA ligase, cytoplasmic
16864	dirMS_041712_NAR_30mM_plus2.21210.21210.2	2	7.09	0	3.48E+03		(R)GAFQNL	(R)G A F\Q/N/L/F/Q/S V R(E)		164.47	633.8315	1266.659	-0.0032	-2.5	9.75	68629.9	5.59	HUMAN	E7EVX6	Androgen receptor
16865	dirMS_041712_NAR_30mM_plus2.21251.21251.2	2	7.09	0	4.50E+03		(K)SCSLLSL	(K)S C S\L/L/S L A T/I/K(V)	C:Carbamidomethylation	164.7	596.8315	1192.661	-0.0049	-4.1	8.47	84619.4	5.7	HUMAN	Q6UWE0	E3 ubiquitin-protein ligase LRSAM1
16866	dirMS_041712_NAR_30mM_plus2.21519.21519.2	2	7.09	0	3.38E+05		(R)NSYLEVI	(R)N S|Y|L/E V/L L K(L)		167.87	539.8092	1078.614	-0.0032	-2.9	6	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
16867	dirMS_041712_NAR_40mM_plus2.5722.5722.2	2	7.09	0	1.12E+05		(R)FSSSSGY	(R)F/S\S/S S/G/Y/G G G\S S R(V)		90.98	618.2686	1235.529	0.0012	1	8.75	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
16868	dirMS_041712_NAR_50mM_plus2.11562.11562.3	3	7.09	1	8.20E+04	M72m	(R)TEmENE	(R)T E/m E N E\F/V L I/K/K(D)	m:Oxidized methionine	128.73	499.5943	1480.772	15.9968	1.2	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
16869	dirMS_041712_NAR_50mM_plus2.19848.19848.3	3	7.09	1	9.47E+05		(R)GDLGIEI	(R)G D L/G/I|E/I/P A E K/V F L A Q K(M)		171.95	610.0104	1828.022	-0.0048	-2.6	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
16870	dirMS_041712_NAR_50mM_plus2.20207.20207.3	3	7.09	0	1.38E+05		(R)FAGLHFI	(R)F/A|G L H F F N P V/P V/M K(L)		175.03	535.2885	1603.845	0.0056	3.5	8.76	35407.1	6.73	HUMAN	E9PF18	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial
16871	dirMS_041712_NAR_50mM_plus2.21166.21166.3	3	7.09	1	3.98E+05	M145m	(R)GVmLA	(R)G V/m/L/A V D A V I/A E/L K K(Q)	m:Oxidized methionine	181.48	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
16872	dirMS_041712_NAR_50mM_plus2.6757.6757.3	3	7.09	1	1.25E+05		(K)EETQPP	(K)E E/T Q/P/P V A L K/K(E)		100.83	413.9019	1239.694	-0.0032	-2.6	6.24	45021.6	8.74	HUMAN	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein
16873	dirMS_041712_NAR_50mM_plus2.8794.8794.3	3	7.09	0	2.04E+05		(K)VVQVSA	(K)V V|Q V S A/G D/S H T A A L T D/D G R(V)		113.45	633.6509	1898.92	0.0179	9.4	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
16874	dirMS_041712_NAR_50mM_plus2.9802.9802.3	3	7.09	1	2.02E+05		(R)AESGPD	(R)A E|S G P D/L R Y E V/T/S/G G G G T S R(M)		119.13	665.9843	1995.937	0.0017	0.9	4.68	334221.3	6.44	HUMAN	P15924	Desmoplakin
16875	dirMS_041712_NAR_60mM_plus.11877.11877.3	3	7.09	0	4.38E+05		(R)MVQVH	(R)M/V/Q/V H E L S C E G I S K(S)	C:Carbamidomethylation	119.42	539.5969	1616.777	-0.0009	-0.6	5.38	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
16876	dirMS_041712_NAR_60mM_plus.8161.8161.3	3	7.09	0	3.20E+05	S338s	(R)sGWVSI	(R)s G/W V S I M A E/A M K(S)	s:N-acetylglucosamine (S)	100.78	504.907	1309.628	203.0785	-0.5	5.72	74944.9	7.85	HUMAN	Q96JX3	Protein SERAC1
16877	dirMS_041712_NAR_120mM_minus.18382.18382.3	3	7.08	0	1.59E+05		(R)FHQLDI	(R)F H/Q L\D\I D D|L/Q S I R(A)		155.27	533.9425	1599.813	0.0004	0.3	4.41	24897.7	9.84	HUMAN	A8MTM1	Carbonyl reductase [NADPH] 1
16878	dirMS_041712_NAR_120mM_minus.7618.7618.3	3	7.08	1	7.89E+05		(K)IQDKEGI	(K)I Q D K E G\I/P/P D/Q Q/R(L)		94.92	508.5981	1523.781	-0.0015	-1	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
16879	dirMS_041712_NAR_40mM_minus2.14241.14241.3	3	7.08	1	1.61E+05		(K)TGISDVF	(K)T G\I/S/D V F A K N D\L/A V/V D/V R(I)		168.48	640.3454	1919.023	-0.0016	-0.8	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
16880	dirMS_041712_NAR_50mM_minus2.13997.14123.3	3	7.08	1	3.62E+05		(K)VIDPAT	(K)V/I|D|P A T A/T S V D/L R D I K(I)		148.08	571.9822	1713.938	-0.0061	-3.6	4.43	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
16881	dirMS_041712_NAR_60mM_minus.15351.15351.3	3	7.08	0	1.17E+05		(R)QIFHPE	(R)Q I/F H/P E Q L/I/T G K(E)		145.13	470.9285	1410.774	-0.003	-2.1	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
16882	dirMS_041712_NAR_60mM_minus.16633.16633.2	2	7.08	1	4.84E+04		(K)LALDIEI	(K)L A/L/D/I E/I/A T/Y R K(L)		152.73	703.4027	1405.805	-0.0068	-4.9	6.07	49564	5.84	HUMAN	E9PAX3	Glial fibrillary acidic protein
16883	dirMS_041712_NAR_60mM_minus.7485.7485.3	3	7.08	1	3.94E+04		(R)TVEKELT	(R)T V/E K E L T/Y E/K(F)		101.13	413.8839	1239.647	-0.0096	-7.7	4.78	42963.5	5.19	HUMAN	P35237	Serpin B6
16884	dirMS_041712_NAR_120mM_plus.10952.10952.3	3	7.08	0	7.91E+05		(K)NFYVEH	(K)N F/Y/V/E H/P E V A R(L)		111.32	454.2277	1360.664	0.0041	3	5.4	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
16885	dirMS_041712_NAR_120mM_plus.20526.20526.3	3	7.08	1	1.03E+06		(K)AAIDWF	(K)A/A/I/D/W/F/D G K E F H G N I I K(V)		160.12	654.3334	1960.992	-0.0059	-3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
16886	dirMS_041712_NAR_120mM_plus.5295.5295.3	3	7.08	1	1.54E+05		(R)NDDDEE	(R)N/D/D/D/E/E E A A\R E R(R)		81.02	483.5401	1448.588	0.0173	12	3.95	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
16887	dirMS_041712_NAR_120mM_plus.9437.9437.3	3	7.08	1	1.26E+05		(R)SRAEAE	(R)S R A\E\A\E/S\M/Y/Q I K(Y)		104.18	471.5662	1412.684	0.0002	0.1	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
16888	dirMS_041712_NAR_120mM_plus.9670.9670.3	3	7.08	1	1.40E+05		(R)RLDECEI	(R)R L D\E C\E|E/A/F Q G T K(V)	C:Carbamidomethylation	104.07	528.2449	1582.717	0.0036	2.2	4.41	22568.6	6.35	HUMAN	B3KQ25	Proteasome activator complex subunit 3
16889	dirMS_041712_NAR_20mM_plus.10077.10077.2	2	7.08	0	6.29E+05		(K)LVSESSD	(K)L V|S E/S S D V L/P K(-)		141.55	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
16890	dirMS_041712_NAR_20mM_plus.16166.16166.2	2	7.08	0	4.99E+04		(R)LIDFLES	(R)L I|D/F/L E S/G K(T)		183.38	511.28	1021.556	-0.0037	-3.6	4.37	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17

16891	dirMS_041712_NAR_20mM_plus.19033.19033.2	2	7.08	0	1.91E+05		(R)STGEAF	(R)S T G E\A|F V/Q/F A\S Q/E I/A E K(A)		202.2	921.4477	1841.892	-0.0035	-1.9	4.25	24249.1	6.99	HUMAN	D6RBM0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
16892	dirMS_041712_NAR_20mM_plus.19359.19359.2	2	7.08	0	1.41E+05		(R)TGAIVD	(R)T G A\I/V|D V|P V G E E L L G R(V)		204.68	812.9497	1624.891	0.0017	1	4.14	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
16893	dirMS_041712_NAR_30mM_plus2.14453.14453.2	2	7.08	0	2.58E+05		(K)IVVLLQR	(K)I V|V/L\L Q R(L)		128.37	420.7864	840.567	-0.001	-1.2	9.75	28772.3	6.28	HUMAN	A6NJG9	Proteasome activator complex subunit 1
16894	dirMS_041712_NAR_30mM_plus2.21895.21895.2	2	7.08	0	1.56E+05		(R)QSSFALL	(R)Q S S F/A/L/L/G/D L/T K(A)		170.63	640.3472	1279.689	-0.0021	-1.7	5.84	46579.3	4.96	HUMAN	E5RI07	Transportin-1
16895	dirMS_041712_NAR_30mM_plus2.4555.4555.2	2	7.08	0	3.66E+05		(R)SYTSGP	(R)S Y/T|S G P G S R(I)		73.6	456.2155	911.422	0.002	2.2	8.46	19288.4	10.19	HUMAN	F8VQY3	Keratin, type II cytoskeletal 8 (Fragment)
16896	dirMS_041712_NAR_50mM_plus2.11825.11825.3	3	7.08	1	3.79E+05		(K)IGRIEDV	(K)I G R I E D V T/P\I|P/S D S T R(R)		130.28	585.9784	1755.924	-0.0029	-1.7	4.56	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
16897	dirMS_041712_NAR_50mM_plus2.11834.11834.3	3	7.08	0	3.17E+04		(K)SNMGH	(K)S N\M/G H\P\E/P A/S G L/A A L A K(V)		130.23	550.9462	1650.827	-0.0028	-1.7	6.47	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
16898	dirMS_041712_NAR_50mM_plus2.19735.19735.3	3	7.08	1	1.82E+05		(R)TSLLTLE	(R)T S|L/L/T L E\D V/K Q E L I/K(L)		172.17	577.3359	1729.995	-0.0014	-0.8	4.68	156316.8	8.61	HUMAN	Q7Z478	ATP-dependent RNA helicase DHX29
16899	dirMS_041712_NAR_60mM_plus.17016.17016.3	3	7.08	0	3.40E+05		(K)EGHVEV	(K)E G H V E\V\V/S/E/L/L/Q R(E)		145.97	498.9326	1494.791	-0.0078	-5.2	4.75	48586.6	9.32	HUMAN	D6RCB2	Ankyrin-3
16900	dirMS_041712_NAR_60mM_plus.7274.7315.3	3	7.08	0	3.00E+05		(K)ITPAHD	(K)I T|P A H\D Q/N D Y E/V/G Q R(H)		96.68	581.6074	1742.809	-0.0016	-0.9	4.54	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
16901	dirMS_041712_NAR_120mM_minus.17614.17614.4	4	7.07	2	2.50E+05		(R)NLKASLE	(R)N L K A S\L/E/N S L R E V E/A R(Y)		150.27	458.0011	1828.988	-0.005	-2.7	6.23	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
16902	dirMS_041712_NAR_20mM_minus.10963.10963.2	2	7.07	0	1.01E+05		(K)GTIQVIT	(K)G T I/Q V/I/T Q G T S L K(N)		157.17	673.3789	1345.769	-0.018	-13.4	8.75	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
16903	dirMS_041712_NAR_20mM_minus.8715.8715.3	3	7.07	0	6.96E+04		(R)SPSDSST	(R)S P\S D S S T A S T|P|V/A/E Q I E\R(A)		136.63	621.2935	1861.877	-0.0114	-6.1	4.14	76925.9	4.46	HUMAN	A8MV58	Drebrin
16904	dirMS_041712_NAR_30mM_minus2.12270.12270.2	2	7.07	0	1.51E+05		(R)MLVELS	(R)M/L/V E/L/S K(A)		121.08	410.242	819.465	0.0123	15	5.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
16905	dirMS_041712_NAR_30mM_minus2.18308.18308.2	2	7.07	0	1.57E+05		(K)FGAYIVD	(K)F/G|A|Y|I/V D G L\R(Q)		153.6	555.7984	1110.594	-0.0047	-4.2	5.83	269989.9	5.92	HUMAN	F8W8T8	Acetyl-CoA carboxylase 2
16906	dirMS_041712_NAR_40mM_minus2.5381.5381.2	2	7.07	0	1.03E+05		(K)DSYVGD	(K)D S Y|V/G D/E A Q S K(R)		89.65	599.7638	1198.522	-0.0019	-1.6	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
16907	dirMS_041712_NAR_50mM_minus2.12385.12385.3	3	7.07	1	8.70E+03	M124m M	(K)SYLNmD	(K)S Y/L/N m D\A I m E A I K/K(T)	m:Oxidized methionine	137.73	553.6091	1626.823	31.9898	0	5.79	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
16908	dirMS_041712_NAR_50mM_minus2.15835.15835.3	3	7.07	0	9.69E+04		(K)INLEAAE	(K)I N/L E/A A E L G E I S D I H/T K(L)		158.72	618.326	1852.965	-0.0016	-0.9	4.4	84268.2	6.32	HUMAN	Q9UHD2	Serine/threonine-protein kinase TBK1
16909	dirMS_041712_NAR_50mM_minus2.16738.16738.3	3	7.07	0	3.77E+04		(K)TVSGVN	(K)T V/S/G V N G\P L V/I/L D H V K(V)		164.65	549.9835	1647.943	-0.0069	-4.2	6.41	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
16910	dirMS_041712_NAR_50mM_minus2.5961.5961.3	3	7.07	0	3.55E+04		(R)ATAPQT	(R)A T|A/P Q/T Q H V/S P M R(Q)		96.35	475.244	1423.711	0.0064	4.5	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
16911	dirMS_041712_NAR_50mM_minus2.7640.7640.3	3	7.07	2	6.65E+04	T112t	(R)LQELERE	(R)L Q E/L/E R/E M R t E/R(E)	t:N-acetylglucosamine (T)	110.55	598.2978	1589.806	203.0724	-3.9	4.95	35626.3	6.14	HUMAN	H0YIZ9	Centrosomal protein of 128 kDa (Fragment)
16912	dirMS_041712_NAR_60mM_minus.16317.16317.3	3	7.07	0	1.58E+05		(R)FQSGDF	(R)F Q/S G D F H V|I/N G V L R(T)		150.83	530.2846	1588.823	0.0162	10.2	6.74	104619	5.75	HUMAN	F8W904	Exportin-2
16913	dirMS_041712_NAR_60mM_minus.17056.17056.3	3	7.07	1	1.90E+05		(K)LLQDFF	(K)L/L/Q|D F/F N G R D L N K(S)		155.28	527.277	1579.823	-0.0063	-4	5.96	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
16914	dirMS_041712_NAR_60mM_minus.9951.9951.3	3	7.07	1	5.63E+05	M230m M	(R)mSmKE	(R)m S m K E V D E/Q\M|L N V/Q N K(N)	m:Oxidized methionine	114.97	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
16915	dirMS_041712_NAR_120mM_plus.10190.10190.2	2	7.07	0	4.61E+05		(R)VHIEIGP	(R)V/H|I|E/I G/P/D G R(V)		105.95	546.7931	1092.58	-0.0007	-0.6	5.32	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
16916	dirMS_041712_NAR_120mM_plus.10420.10420.3	3	7.07	0	9.64E+05		(R)GFCLPP	(R)G F/C|L/P/P H C S/R(G)	C:Carbamidomethylation	107.67	410.8593	1230.551	0.0127	10.3	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
16917	dirMS_041712_NAR_20mM_plus.16769.16769.3	3	7.07	0	3.01E+05		(K)VQIAVA	(K)V Q\I A\V\A N A|Q/E L L/Q R(M)		186.93	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
16918	dirMS_041712_NAR_20mM_plus.19336.19336.3	3	7.07	0	9.30E+04		(R)ALIAGG	(R)A L I A G G G A/P E I/E L/A L R(L)		205.05	517.6345	1550.89	-0.0011	-0.7	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
16919	dirMS_041712_NAR_20mM_plus.6927.6927.2	2	7.07	0	1.59E+05		(K)TTTAAA	(K)T T T A A|A|V|A S/T G|P S S R(S)		114.18	689.3492	1377.697	-0.0057	-4.2	9.41	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
16920	dirMS_041712_NAR_20mM_plus.9978.9978.2	2	7.07	0	6.91E+04		(R)ALGQNF	(R)A L/G Q/N\P/T N/A\E V L K(V)		140.02	677.8702	1354.733	0.0006	0.5	6.05	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
16921	dirMS_041712_NAR_40mM_plus2.12116.12116.2	2	7.07	0	3.28E+03		(K)LYANMF	(K)L/Y|A N M/F E R(L)		137.6	522.2521	1043.498	-0.001	-0.9	6	9740.1	10.08	HUMAN	H0YFG2	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed (Fragment)
16922	dirMS_041712_NAR_40mM_plus2.19441.19441.3	3	7.07	1	4.58E+05		(K)ALFEEVF	(K)A L|F E/E V/P E L L T E A E K K(E)		181.77	615.9991	1845.984	-0.0017	-0.9	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
16923	dirMS_041712_NAR_40mM_plus2.5716.5716.2	2	7.07	1	5.58E+04		(R)ARGDSE	(R)A R G D S E A L\D\E|E S(-)		91.22	639.7736	1278.544	-0.0045	-3.5	3.83	74986.2	6.56	HUMAN	I3L080	Hepatoma-derived growth factor-related protein 2
16924	dirMS_041712_NAR_50mM_plus2.11357.11357.3	3	7.07	0	5.84E+04		(K)SLYVAEY	(K)S L|Y/V/A E Y H S E P V E D E K P(-)		127.85	664.6463	1991.923	0.0011	0.5	4.25	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
16925	dirMS_041712_NAR_50mM_plus2.17628.17628.3	3	7.07	0	5.02E+05		(R)IMEIVD	(R)I/M|E/I V/D/A I/T T T A Q S H Q R(T)		160.45	638.6636	1913.975	0.0013	0.7	5.32	94165.2	8.68	HUMAN	J3KNX3	6-phosphofructokinase
16926	dirMS_041712_NAR_50mM_plus2.19593.19593.3	3	7.07	1	9.25E+04		(K)TFVNITP	(K)T F/V/N I/T/P A E V G/V L V G K/D R(S)		171.23	639.0247	1915.065	-0.0052	-2.7	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
16927	dirMS_041712_NAR_50mM_plus2.7162.7162.3	3	7.07	1	6.93E+04		(K)EASKQA	(K)E A/S K Q\A\D V N/L V/N A K(L)		103.3	496.2658	1486.786	-0.0032	-2.1	6.17	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
16928	dirMS_041712_NAR_50mM_plus2.8131.8131.3	3	7.07	1	7.45E+03		(K)CLDENL	(K)C L/D E N L/E D/A/S Q C K K(L)	C:Carbamidomethylation	109.32	570.587	1709.747	-0.0005	-0.3	4.32	14458.2	9.22	HUMAN	Q5JTJ3	Cytochrome c oxidase assembly factor 6 homolog
16929	dirMS_041712_NAR_60mM_plus.15656.15656.3	3	7.07	1	3.64E+04		(K)KTSFVN	(K)K\T S F V N F/T/D I C K(L)	C:Carbamidomethylation	138.42	487.2426	1459.725	-0.0117	-8	8.59	38730.1	5.6	HUMAN	P20042	Eukaryotic translation initiation factor 2 subunit 2
16930	dirMS_041712_NAR_60mM_plus.15727.15727.3	3	7.07	1	4.04E+05		(K)KSDIDE	(K)K S D I D E\I\V|L\V/G\G S T/R(I)		138.4	530.2831	1588.854	-0.0193	-12.2	4.56	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
16931	dirMS_041712_NAR_60mM_plus.20450.20450.3	3	7.07	0	3.20E+04		(R)IHFPLAT	(R)I H F P L A T\Y A/P/V/I S A E/K(A)		167.23	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
16932	dirMS_041712_NAR_60mM_plus.6837.6837.2	2	7.07	1	2.58E+05		(K)SLDEME	(K)S/L/D E/M E/K Q|Q R(E)		94.13	632.3035	1263.6	-0.0001	0	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
16933	dirMS_041712_NAR_120mM_minus.17703.17703.3	3	7.06	1	1.82E+05		(R)AGKLDP	(R)A G K L D|P H|L/V/L D Q\L R(C)		151.47	525.6385	1574.901	-0.0004	-0.2	6.79	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
16934	dirMS_041712_NAR_20mM_minus.11666.11666.2	2	7.06	0	1.77E+05		(R)GDLGIEI	(R)G D L/G/I/E|I/P A E K(V)		164.15	571.3078	1141.61	-0.0016	-1.4	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
16935	dirMS_041712_NAR_20mM_minus.14421.14421.2	2	7.06	0	2.52E+05		(R)APGSGL	(R)A/P\G\S G L|A L L/P L\K(I)		198.32	568.8551	1136.704	-0.0008	-0.7	8.8	266161	5.68	HUMAN	E9PPU0	Epiplakin
16936	dirMS_041712_NAR_30mM_minus2.15318.15318.2	2	7.06	0	5.64E+05	M2249m	(K)MSIYQA	(K)M/S|I/Y\Q/A m W K(G)	m:Oxidized methionine	135.95	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
16937	dirMS_041712_NAR_40mM_minus2.5852.5852.2	2	7.06	0	6.85E+05		(K)AGFAGD	(K)A G/F|A/G D/D/A P R(A)		97.7	488.7279	976.448	0.0002	0.2	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
16938	dirMS_041712_NAR_50mM_minus2.10479.10479.3	3	7.06	0	1.52E+05		(K)SQIHDIV	(K)S Q I/H D I V|L/V/G G S T R(I)		128.4	494.6068	1481.807	-0.0012	-0.8	6.46	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
16939	dirMS_041712_NAR_50mM_minus2.11427.11427.3	3	7.06	1	1.24E+05		(K)LSAEKVE	(K)L/S/A E K V E I/A/T/L/T R(E)		133.37	477.6106	1430.821	-0.0041	-2.8	6.14	26661.1	7.81	HUMAN	H0YL69	Proteasome subunit alpha type (Fragment)
16940	dirMS_041712_NAR_50mM_minus2.16310.16310.3	3	7.06	0	1.08E+05	M463m	(K)mLNIHP	(K)m L N I/H/P S L/L/P S F/K(G)	m:Oxidized methionine	160.95	504.9453	1496.829	15.992	-1.9	8.52	60871.9	6.3	HUMAN	B4DJ93	Phosphoribosylformylglycinamidine cyclo-ligase
16941	dirMS_041712_NAR_50mM_minus2.16485.16485.3	3	7.06	0	8.79E+04		(R)LLLDIPL	(R)L L L D/I P L Q T/P H K(L)		162.33	463.2805	1387.831	-0.0038	-2.7	6.74	198852.6	5.95	HUMAN	A6NKT7	RanBP2-like and GRIP domain-containing protein 3
16942	dirMS_041712_NAR_50mM_minus2.7059.7059.3	3	7.06	0	2.09E+05		(K)VSYGIG	(K)V/S Y G\I/G D E E/H/D Q E G R(V)		106.65	564.249	1690.73	0.0021	1.3	4.17	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
16943	dirMS_041712_NAR_50mM_minus2.7705.7705.3	3	7.06	1	3.49E+04	M198m	(R)VFDKEG	(R)V F D K E G N G T/V/m/G/A/E/I R(H)	m:Oxidized methionine	110.87	580.2847	1722.848	15.9916	-1.9	4.68	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
16944	dirMS_041712_NAR_50mM_minus2.9012.9012.3	3	7.06	1	4.90E+04		(R)SATKVT	(R)S A|T K V T A/D/V|I/N/A A E K(L)		119.6	506.6094	1517.817	-0.0033	-2.2	5.79	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
16945	dirMS_041712_NAR_50mM_minus2.9143.9143.3	3	7.06	0	5.92E+04		(R)ASSLNE	(R)A/S/S\L/N E N V D H S A/L L K(L)		119.95	533.2774	1597.818	-0.0004	-0.2	5.32	89361.6	4.91	HUMAN	Q96SB3	Neurabin-2
16946	dirMS_041712_NAR_60mM_minus.12582.12582.3	3	7.06	1	9.01E+05		(K)AVLFCLS	(K)A V/L/F/C L/S E D K K(N)	C:Carbamidomethylation	130.78	437.2334	1309.682	0.0036	2.7	6.11	22956	8.8	HUMAN	E9PK25	Cofilin-1
16947	dirMS_041712_NAR_60mM_minus.14981.14981.3	3	7.06	0	5.83E+04		(R)DLSYCLS	(R)D L/S/Y/C L/S G M Y/D/H R(Y)	C:Carbamidomethylation	143.88	539.566	1616.683	0.0003	0.2	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
16948	dirMS_041712_NAR_60mM_minus.6512.6512.3	3	7.06	1	8.87E+04		(K)SESPKEP	(K)S E|S/P K E/P E Q L/R(K)		94.9	433.8887	1299.654	-0.0024	-1.8	4.78	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
16949	dirMS_041712_NAR_60mM_minus.8152.8152.3	3	7.06	1	2.70E+05		(K)IQDKEGI	(K)I Q/D K E G I|P P/D Q Q R(L)		105.15	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
16950	dirMS_041712_NAR_120mM_plus.14295.14295.3	3	7.06	1	2.78E+05		(R)KFNALF	(R)K\F\N A L F\A Q/G N|Y/S E A A/K(V)		127.67	586.9652	1758.881	0.0001	0	8.5	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
16951	dirMS_041712_NAR_120mM_plus.9186.9186.3	3	7.06	2	3.66E+05	M49m	(R)TIEKFEK	(R)T I/E K/F E K E\A/A E m G K(G)	m:Oxidized methionine	101.48	542.94	1610.809	15.996	0.7	4.94	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
16952	dirMS_041712_NAR_20mM_plus.15800.15800.3	3	7.06	0	1.73E+05		(R)GNPTVE	(R)G N/P/T/V E\V/D L F T S K(G)		180.2	469.577	1406.716	0.0003	0.2	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
16953	dirMS_041712_NAR_20mM_plus.17935.17935.2	2	7.06	0	1.10E+05		(K)VDFPQD	(K)V D F/P Q|D\Q L|T A L T|G R(I)		195.27	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
16954	dirMS_041712_NAR_30mM_plus2.11888.11927.2	2	7.06	0	1.27E+06		(K)ACTILLR	(K)A/C|T/I L/L/R(G)	C:Carbamidomethylation	115.35	423.7454	846.487	-0.0031	-3.6	9.79	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
16955	dirMS_041712_NAR_30mM_plus2.13160.13160.2	2	7.06	0	2.54E+05	S59s	(R)AIETLsG	(R)A/I/E T L\s G K(V)	s:Phosphorylated S	122.07	449.7242	818.462	79.9793	14.5	6.05	66899.1	8.59	HUMAN	F8W930	Insulin-like growth factor 2 mRNA-binding protein 2
16956	dirMS_041712_NAR_30mM_plus2.16631.16631.2	2	7.06	0	3.67E+05		(K)QLQEMI	(K)Q L|Q/E M L/G L S K(V)		140.15	573.8112	1146.619	-0.0036	-3.1	6	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
16957	dirMS_041712_NAR_30mM_plus2.17990.17990.2	2	7.06	0	3.47E+05		(R)MADALI	(R)M/A|D\A/L|D|N/Y V/I R(G)		147.02	640.8182	1280.63	-0.0012	-1	4.21	15838.9	7.03	HUMAN	H0Y5U0	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
16958	dirMS_041712_NAR_30mM_plus2.9708.9708.2	2	7.06	0	7.62E+05		(K)EAESSPF	(K)E A/E|S S/P F V E R(L)		105.13	575.7726	1150.537	0.0004	0.4	4.25	92752.5	4.76	HUMAN	P14625	Endoplasmin
16959	dirMS_041712_NAR_40mM_plus2.10638.10638.3	3	7.06	1	3.62E+05		(R)DGKLVS	(R)D G K L V S E/S/S D/V L/P/K(-)		128.45	491.9315	1473.78	0.0004	0.3	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
16960	dirMS_041712_NAR_50mM_plus2.13764.13764.3	3	7.06	0	6.35E+05		(K)EGKPTIV	(K)E G K\P T I\V/E/E D D/P E L F/K(Q)		140.55	615.9744	1845.912	-0.003	-1.6	4.08	29841.1	9.04	HUMAN	O75937	DnaJ homolog subfamily C member 8
16961	dirMS_041712_NAR_50mM_plus2.15294.15294.3	3	7.06	0	2.43E+04		(K)VALLLLD	(K)V A L/L L L D/Q/G/A S P/H A A A K(N)		147.53	558.9877	1674.954	-0.0052	-3.1	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
16962	dirMS_041712_NAR_50mM_plus2.8622.8622.3	3	7.06	1	1.01E+05		(K)TAVCDIF	(K)T A|V C D/I/P/P R G L/K(M)	C:Carbamidomethylation	112.57	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
16963	dirMS_041712_NAR_60mM_plus.15627.15627.3	3	7.06	0	3.64E+05	M867m	(R)AmGIET	(R)A m G/I E T S D I|A D V P S D T S/K(N)	m:Oxidized methionine	138.7	618.2833	1836.853	15.9822	-6.9	3.84	136983.7	6.37	HUMAN	E2QRH8	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-4
16964	dirMS_041712_NAR_60mM_plus.8267.8267.3	3	7.06	1	2.56E+05	M258m	(R)LMEEIm	(R)L/M|E E I m/S E K E N K(T)	m:Oxidized methionine	101.32	499.5719	1480.702	15.999	2.7	4.49	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
16965	dirMS_041712_NAR_120mM_minus.4937.4937.3	3	7.05	1	4.16E+05		(K)AGADEE	(K)A/G/A/D E/E R A/E T A R(L)		78.27	425.8687	1275.592	-0.0008	-0.7	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
16966	dirMS_041712_NAR_20mM_minus.8026.8026.2	2	7.05	0	8.63E+04		(R)DQVTYC	(R)D Q|V/T|Y/Q Q/L R(E)		129.78	575.7953	1150.585	-0.0018	-1.6	5.83	266161	5.68	HUMAN	E9PPU0	Epiplakin
16967	dirMS_041712_NAR_30mM_minus2.17825.17825.2	2	7.05	0	8.73E+04		(K)MFGMV	(K)M/F/G M V/L/E/K(I)		151.13	477.745	954.479	0.004	4.2	5.75	86098.8	5.31	HUMAN	B4DUC5	Exportin-2
16968	dirMS_041712_NAR_30mM_minus2.5122.5122.2	2	7.05	0	4.63E+05		(R)TDTGEP	(R)T/D|T/G/E\P M\G R(G)		81.5	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
16969	dirMS_041712_NAR_30mM_minus2.5824.5824.2	2	7.05	0	8.23E+04		(R)QLEDGD	(R)Q L|E/D/G\D|Q/P E S K(K)		85.63	623.284	1245.559	0.0014	1.1	3.91	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
16970	dirMS_041712_NAR_30mM_minus2.7043.7043.2	2	7.05	0	1.24E+05		(K)CATITPD	(K)C/A|T I/T|P D/E K(R)	C:Carbamidomethylation	93.68	517.7448	1034.482	0	0	4.37	17833.3	8.73	HUMAN	C9J4N6	Isocitrate dehydrogenase [NADP] cytoplasmic (Fragment)
16971	dirMS_041712_NAR_40mM_minus2.8085.8085.3	3	7.05	0	1.77E+05	M35m	(K)AASDIAr	(K)A A/S/D\I/A m T E|L/P P T H/P I R(L)	m:Oxidized methionine	128.23	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
16972	dirMS_041712_NAR_50mM_minus2.10042.10042.3	3	7.05	0	1.79E+05	M392m	(K)EmNPAL	(K)E m/N|P A\L|G\I|D C\L H K(G)	C:Carbamidomethylation m:Oxid	125.67	505.2416	1497.719	15.9914	-2.3	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
16973	dirMS_041712_NAR_50mM_minus2.16756.16756.3	3	7.05	0	4.18E+05		(K)NILFVIT	(K)N I|L F/V/I T K/P D V Y/K(S)		164.02	517.2991	1549.899	-0.0161	-10.4	8.5	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
16974	dirMS_041712_NAR_50mM_minus2.16840.16840.3	3	7.05	0	1.36E+05		(K)TVSGVN	(K)T V/S\G V/N G P L/V/I L D H V K(V)		164.97	549.9835	1647.943	-0.0069	-4.2	6.41	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
16975	dirMS_041712_NAR_50mM_minus2.8478.8478.3	3	7.05	1	1.42E+05		(K)LTSDDVI	(K)L/T/S/D/D/V/K E Q I Y/K(L)		115.98	480.252	1438.742	-0.001	-0.7	4.56	12573.5	10.39	HUMAN	E9PS50	40S ribosomal protein S13 (Fragment)
16976	dirMS_041712_NAR_60mM_minus.14867.14867.3	3	7.05	0	3.47E+05		(R)AVAIDLF	(R)A V|A\I D L/P G L G H/S K(E)		142.62	426.578	1277.721	-0.0018	-1.4	6.79	19983.6	8.14	HUMAN	B4DQI4	Alpha/beta hydrolase domain-containing protein 14B
16977	dirMS_041712_NAR_60mM_minus.15412.15412.3	3	7.05	0	2.13E+05		(K)EGHVEV	(K)E G H V E V\V/S E/L/L Q/R(E)		145.9	498.9349	1494.791	-0.0009	-0.6	4.75	48586.6	9.32	HUMAN	D6RCB2	Ankyrin-3
16978	dirMS_041712_NAR_60mM_minus.19411.19411.3	3	7.05	1	6.95E+05		(K)LASDLLE	(K)L/A/S D/L L E|W I R\R(T)		172.9	457.9288	1371.774	-0.0025	-1.8	6.07	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
16979	dirMS_041712_NAR_60mM_minus.6121.6121.3	3	7.05	0	6.51E+03		(K)DTTEVA	(K)D/T T E V A E N S H\H L K(I)		93.05	494.235	1480.703	-0.0122	-8.2	5.28	136109.7	6.2	HUMAN	E7EWU5	Calmodulin-binding transcription activator 2
16980	dirMS_041712_NAR_120mM_plus.6996.6996.3	3	7.05	1	1.61E+05		(R)NKQTYS	(R)N K\Q T Y\S T E|P N N L K(A)		90.15	512.9261	1536.765	-0.0015	-1	8.5	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
16981	dirMS_041712_NAR_30mM_plus2.19559.19559.2	2	7.05	0	1.85E+04		(K)MNEFLE	(K)M N\E|F/L/E N\F E K(N)		155.87	650.7974	1300.588	-0.0003	-0.2	4.25	28580.2	9.35	HUMAN	Q9UFN0	Protein NipSnap homolog 3A
16982	dirMS_041712_NAR_30mM_plus2.19930.19930.2	2	7.05	0	2.31E+05		(K)LALFQAI	(K)L/A|L|F/Q A I G/K(E)		158.42	480.795	960.588	-0.005	-5.2	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
16983	dirMS_041712_NAR_40mM_plus2.6534.6534.2	2	7.05	0	6.37E+04		(R)SDYDGI	(R)S D/Y/D/G/I/G S R(G)		97.52	485.2217	969.427	0.0089	9.2	4.21	15031.5	6.72	HUMAN	B4DLA0	ATP-dependent RNA helicase DDX3X
16984	dirMS_041712_NAR_40mM_plus2.8962.8962.2	2	7.05	0	1.19E+05		(R)GYSFTT	(R)G/Y|S F/T/T/T A E R(E)		114.9	566.7672	1132.527	0.0002	0.2	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
16985	dirMS_041712_NAR_50mM_plus2.12586.12586.3	3	7.05	0	2.08E+05		(K)TVTSATI	(K)T V|T/S/A T I V/Y H L A R(Q)		133.68	477.9357	1431.795	-0.0029	-2	8.44	125655.3	6.18	HUMAN	Q92900	Regulator of nonsense transcripts 1
16986	dirMS_041712_NAR_50mM_plus2.7742.7742.3	3	7.05	0	3.39E+04		(K)EQEPMF	(K)E Q/E/P M/P T V D S H E P R(L)		106.75	551.2532	1651.738	0.007	4.2	4.4	18962.9	9.6	HUMAN	A6NGP5	Hematological and neurological-expressed 1-like protein
16987	dirMS_041712_NAR_120mM_minus.11824.11824.4	4	7.04	1	3.82E+05		(R)DFTVSAI	(R)D F|T V/S A/M/H G D M D/Q K E/R(D)		118.4	467.458	1866.811	-0.0007	-0.4	4.66	26945.8	8.07	HUMAN	J3KSZ0	Eukaryotic initiation factor 4A-I (Fragment)
16988	dirMS_041712_NAR_20mM_minus.12667.12667.2	2	7.04	0	1.62E+05	M185m	(K)LAVNm	(K)L/A|V N m|V/P F P R(L)	m:Oxidized methionine	175.1	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
16989	dirMS_041712_NAR_20mM_minus.8099.8099.2	2	7.04	0	1.02E+05		(R)ATTGYP	(R)A T T/G Y|P D P Y/G/G E\K(L)		130.38	678.3078	1355.611	-0.0031	-2.3	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
16990	dirMS_041712_NAR_30mM_minus2.16772.16772.2	2	7.04	1	2.05E+05		(K)NAVIRD	(K)N A|V I R D/L G K(K)		144.6	493.2881	985.579	-0.01	-10.1	8.75	146921.1	6.29	HUMAN	F5GWA6	Myopalladin
16991	dirMS_041712_NAR_40mM_minus2.13178.13178.3	3	7.04	0	2.03E+04		(R)DQPAFT	(R)D Q/P A/F T P S G I L T/P H A L G S R(N)		160.88	655.6773	1965.019	-0.0015	-0.8	6.74	103213.3	7.77	HUMAN	B4DZC3	5'-3' exoribonuclease 2
16992	dirMS_041712_NAR_50mM_minus2.16689.16689.3	3	7.04	1	1.55E+05		(K)NIPIPTL	(K)N I|P I/P T L K D F A K(A)		163.33	452.9385	1356.789	0.0124	9.1	8.59	20960.6	7.05	HUMAN	H0YKU1	Tropomodulin-3 (Fragment)
16993	dirMS_041712_NAR_60mM_minus.11500.11500.3	3	7.04	1	2.76E+06		(R)MQKEIT	(R)M Q K E I T/A|L|A|P S T M K(I)		123.4	516.9421	1548.812	-0.0007	-0.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
16994	dirMS_041712_NAR_60mM_minus.15039.15039.3	3	7.04	0	5.83E+04		(R)DLSYCLS	(R)D L|S/Y/C L/S G M Y D/H R(Y)	C:Carbamidomethylation	143.88	539.566	1616.683	0.0003	0.2	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
16995	dirMS_041712_NAR_60mM_minus.7555.7555.3	3	7.04	0	4.90E+04		(R)QSLGHP	(R)Q S L/G H P P/P E/P G P D R(V)		101.33	495.2483	1483.729	0.0015	1	5.32	12758.7	4.21	HUMAN	C9J830	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
16996	dirMS_041712_NAR_120mM_plus.15309.15309.4	4	7.04	2	1.76E+06		(R)FKGQIL	(R)F K G Q I\L/M/P/N I G Y/G S N K K(T)		133.53	474.5115	1895.021	0.0034	1.8	10	15730.4	11.67	HUMAN	D3YTB1	60S ribosomal protein L32 (Fragment)
16997	dirMS_041712_NAR_120mM_plus.5708.5708.3	3	7.04	2	1.45E+05		(R)KTGQAP	(R)K/T G Q A/P G\Y|S Y/T A A N K N\K(G)		83.47	600.3013	1798.908	-0.0189	-10.5	9.83	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
16998	dirMS_041712_NAR_20mM_plus.11314.11314.2	2	7.04	0	7.91E+04		(R)IASLEVE	(R)I/A/S L E V/E/N Q S L/R(G)		150.47	679.8662	1358.727	-0.0023	-1.7	4.53	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
16999	dirMS_041712_NAR_20mM_plus.18927.18927.2	2	7.04	0	4.27E+04		(R)SIQLDGI	(R)S I/Q L\D/G L V/W/G A S K(L)		201.65	687.3716	1373.742	-0.0064	-4.7	5.55	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta

17000	dirMS_041712_NAR_20mM_plus.7626.7626.2	2	7.04	0	1.57E+05		(K)IAVAAQ	(K)I A\V|A/A\Q|N C/Y K(V)	C:Carbamidomethylation	122.43	569.2902	1137.572	0.001	0.9	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
17001	dirMS_041712_NAR_30mM_plus2.19120.19120.2	2	7.04	0	1.87E+05		(K)LNLGTV	(K)L N|L\G/T/V/G F Y R(T)		152.8	570.3123	1139.621	-0.0034	-3	8.75	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
17002	dirMS_041712_NAR_30mM_plus2.4480.4480.2	2	7.04	0	2.92E+05		(K)EDAANN	(K)E D/A/A/N N/Y A R(G)		72.9	512.2281	1023.449	-0.0001	-0.1	4.37	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
17003	dirMS_041712_NAR_40mM_plus2.16070.16070.3	3	7.04	2	6.09E+03	T253t	(R)IRCCtHC	(R)I/R C C t H/C K/D T L L K(R)	C:Carbamidomethylation t:N-ace	161.35	636.6425	1704.834	203.0787	-0.3	9.99	89666.9	5.37	HUMAN	Q9H1K0	Rabenosyn-5
17004	dirMS_041712_NAR_40mM_plus2.7909.7909.2	2	7.04	0	1.43E+05		(K)ASLENS	(K)A/S/L/E/N S L R(E)		106.82	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
17005	dirMS_041712_NAR_50mM_plus2.18007.18007.3	3	7.04	0	4.88E+04		(R)ATAAFIL	(R)A T/A\A|F/I L/A N E H N V A L/F K(H)		162.67	610.6671	1829.991	-0.0041	-2.2	6.79	125399.7	4.93	HUMAN	H0Y8C6	Importin-5 (Fragment)
17006	dirMS_041712_NAR_50mM_plus2.6430.6430.3	3	7.04	0	4.20E+04		(K)TQAYQD	(K)T Q|A/Y Q D Q K/P G T S G L R(K)		98.43	550.6127	1649.824	-0.0006	-0.4	8.25	61733.3	6.3	HUMAN	P36871	Phosphoglucomutase-1
17007	dirMS_041712_NAR_50mM_plus2.8416.8416.3	3	7.04	0	5.53E+05		(R)ASGNYA	(R)A/S|G N Y A T V I/S H/N P E T K(K)		111.85	563.6145	1688.824	0.0051	3	6.79	24115.6	11.59	HUMAN	E9PIZ3	60S ribosomal protein L8
17008	dirMS_041712_NAR_60mM_plus.14137.14137.3	3	7.04	1	8.21E+05		(K)TTVKDL	(K)T T V/K D L S E|L|G S V R(T)		130.38	468.9268	1404.769	-0.0034	-2.4	5.74	533778	5.74	HUMAN	Q15149	Plectin
17009	dirMS_041712_NAR_60mM_plus.14834.14834.3	3	7.04	1	3.95E+05		(K)NKDQG	(K)N K D Q G T\Y E D|Y V/E/G L/R(V)		134.12	596.2816	1786.824	0.006	3.4	4.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
17010	dirMS_041712_NAR_60mM_plus.18310.18310.3	3	7.04	1	5.11E+05		(R)IRIDSLS	(R)I R I D\S\L S A|Q|L/S Q L\Q K(Q)		153.58	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
17011	dirMS_041712_NAR_60mM_plus.19539.19539.3	3	7.04	1	1.62E+05		(K)SLLGKD	(K)S L|L\G/K/D V L F L K(D)		161.2	411.5915	1232.761	-0.0013	-1.1	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
17012	dirMS_041712_NAR_60mM_plus.6979.6979.3	3	7.04	1	1.77E+05		(K)VQVYQE	(K)V Q|V/Y Q E P N/R E T R(V)		94.82	506.9252	1518.766	-0.0049	-3.2	6.11	35946.5	9.41	HUMAN	B7ZKZ1	Phosphoribosyl pyrophosphate synthase-associated protein 2
17013	dirMS_041712_NAR_60mM_plus.8498.8498.2	2	7.04	1	2.61E+05		(R)VVASDK	(R)V V/A S D\K/E/T Y E/L R(Y)		102.87	705.3658	1409.727	-0.0028	-2	4.68	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
17014	dirMS_041712_NAR_60mM_plus.9630.9630.3	3	7.04	0	8.97E+05		(R)LGGPGD	(R)L/G/G/P G D/S\F H T P P R(S)		108.53	446.56	1337.66	0.0058	4.3	6.74	73966.7	10.21	HUMAN	B3KWK6	Alpha-L-iduronidase
17015	dirMS_041712_NAR_120mM_minus.13322.13322.4	4	7.03	2	2.79E+05	M100m	(K)KQGGLG	(K)K\Q G G L G\P/m N I/P L V S D/P\K R(T)	m:Oxidized methionine	128.03	481.5173	1907.053	15.9942	-0.3	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
17016	dirMS_041712_NAR_120mM_minus.16746.16746.3	3	7.03	0	4.87E+05		(R)EHALLA	(R)E H\A\L\L\A|Y/T/L/G V K(Q)		145.7	438.9186	1314.742	-0.0004	-0.3	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
17017	dirMS_041712_NAR_30mM_minus2.16481.16481.2	2	7.03	0	1.48E+05		(K)SQLLSYI	(K)S Q|L|L/S Y/I\D/R(L)		143.12	547.7949	1094.584	-0.0015	-1.4	5.55	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
17018	dirMS_041712_NAR_30mM_minus2.17850.17850.2	2	7.03	0	2.10E+05		(K)EGMNIV	(K)E G M/N/I/V E/A M E/R(F)		152.27	639.7955	1278.582	0.002	1.6	4.25	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
17019	dirMS_041712_NAR_50mM_minus2.8760.8760.3	3	7.03	0	1.19E+06		(R)EIVHIQA	(R)E I V H I Q A\G Q\C/G N Q I|G\A K(F)	C:Carbamidomethylation	117.03	608.3087	1822.923	-0.0113	-6.2	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
17020	dirMS_041712_NAR_60mM_minus.7640.7640.3	3	7.03	1	5.65E+05		(R)YLAEVA	(R)Y L/A E V/A/A/G D D K K(G)		102.07	427.222	1279.653	-0.0014	-1.1	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
17021	dirMS_041712_NAR_20mM_plus.10956.10956.2	2	7.03	0	2.62E+04		(K)ALIAAQ	(K)A L\I A/A/Q/Y/S G A Q/V R(V)		147.72	674.3695	1347.738	-0.0062	-4.6	8.79	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
17022	dirMS_041712_NAR_20mM_plus.16215.16215.2	2	7.03	0	5.36E+03		(R)ADLIAYL	(R)A D\L|I/A/Y\L K(K)		183.32	453.7678	906.529	-0.0012	-1.3	5.88	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
17023	dirMS_041712_NAR_20mM_plus.7775.7775.2	2	7.03	0	1.97E+05		(R)ALANSL	(R)A L|A|N/S\L A C Q G K(Y)	C:Carbamidomethylation	123.78	566.7967	1132.578	0.0082	7.2	8.8	13951.6	9.48	HUMAN	H3BR68	Fructose-bisphosphate aldolase A (Fragment)
17024	dirMS_041712_NAR_30mM_plus2.17313.17313.2	2	7.03	0	6.98E+04		(K)WPLYM	(K)W/P L|Y M S T/K(N)		144.88	513.2647	1025.513	0.0097	9.4	8.59	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
17025	dirMS_041712_NAR_30mM_plus2.19760.19760.2	2	7.03	0	3.56E+05		(K)SNNVEN	(K)S N|N|V/E|M D W V L K(H)		156.95	667.8205	1334.641	-0.0072	-5.4	4.37	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
17026	dirMS_041712_NAR_30mM_plus2.7568.7568.2	2	7.03	0	6.31E+05		(K)SFQQSSI	(K)S F/Q/Q/S\S/L S R(D)		93.8	520.2659	1039.517	0.0078	7.5	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
17027	dirMS_041712_NAR_50mM_plus2.10102.10102.3	3	7.03	0	4.13E+05		(R)MVQVH	(R)M/V|Q V/H/E L/G|C E G/I S K(S)	C:Carbamidomethylation	120.23	529.5984	1586.767	0.0141	8.9	5.38	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
17028	dirMS_041712_NAR_50mM_plus2.15178.15178.3	3	7.03	1	1.27E+06		(R)GDVVPK	(R)G D V|V|P K D V N/A A/I/A T I K(T)		148.17	537.6393	1610.911	-0.0079	-4.9	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
17029	dirMS_041712_NAR_50mM_plus2.8682.8682.3	3	7.03	1	9.99E+04		(R)SCMLTG	(R)S C|M/L|T G/T P E S V/Q S A K R(L)	C:Carbamidomethylation	112.52	584.6157	1751.842	-0.0089	-5.1	8.46	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
17030	dirMS_041712_NAR_60mM_plus.15058.15058.3	3	7.03	1	2.99E+04		(R)ELAFQIS	(R)E L/A/F/Q/I/S K E Y E R(F)		135.27	504.9258	1512.769	-0.0064	-4.3	4.79	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
17031	dirMS_041712_NAR_60mM_plus.19367.19367.3	3	7.03	0	6.28E+05		(K)VSHLLGI	(K)V/S H L L G\I/N|V|T/D F T R(G)		159.65	524.6233	1571.854	0.0013	0.8	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
17032	dirMS_041712_NAR_60mM_plus.19536.19536.3	3	7.03	1	6.35E+05		(K)TVTAMD	(K)T V/T/A M/D V/V/Y A L K R(Q)		160.75	489.6071	1466.804	0.0032	2.2	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
17033	dirMS_041712_NAR_60mM_plus.9502.9502.2	2	7.03	1	3.03E+05		(K)VVWVEE	(K)V V/W|V/E E S D/K R(S)		107.45	623.8223	1246.643	-0.0053	-4.3	4.68	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
17034	dirMS_041712_NAR_120mM_minus.10182.10182.3	3	7.02	0	5.18E+05		(R)LESGMC	(R)L/E/S G M Q/N M/S I/H/T K(T)		110.2	492.571	1475.698	0.0003	0.2	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
17035	dirMS_041712_NAR_120mM_minus.10999.10999.3	3	7.02	0	6.08E+05		(R)ISNRPAF	(R)I/S/N R P A F\M/P S E/G K(M)		113.93	478.5776	1433.721	-0.0023	-1.6	8.75	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
17036	dirMS_041712_NAR_30mM_minus2.18761.18780.2	2	7.02	0	3.33E+04		(R)ALLFIPR	(R)A L|L/F I/P R(R)		156.77	415.2685	829.529	0.0003	0.3	9.79	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
17037	dirMS_041712_NAR_40mM_minus2.11336.11336.3	3	7.02	0	7.68E+04		(K)SIEIPRP	(K)S I|E/I/P R P V D G V E/V P G C G K(I)	C:Carbamidomethylation	149.55	637.0036	1908.985	0.0115	6	4.68	34243.5	4.88	HUMAN	K7ENG2	Splicing factor U2AF 65 kDa subunit
17038	dirMS_041712_NAR_40mM_minus2.15783.15783.3	3	7.02	0	6.75E+05		(K)GLAPDLI	(K)G L|A/P D/L/P E D L Y H L I K(K)		184.4	565.3111	1693.916	0.0028	1.7	4.54	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
17039	dirMS_041712_NAR_50mM_minus2.10905.10905.3	3	7.02	0	1.79E+05	M35m	(K)AASDIA	(K)A A S D/I A/m/T E/L/P P T H P I R(L)	m:Oxidized methionine	130.27	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
17040	dirMS_041712_NAR_50mM_minus2.17008.17008.3	3	7.02	1	4.79E+04		(K)LVGQSI	(K)L V/G Q/S I/I A Y L Q K/K(G)		165.03	487.6328	1460.883	0.0003	0.2	9.7	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
17041	dirMS_041712_NAR_50mM_minus2.17172.17172.3	3	7.02	1	1.20E+05		(K)VIAATN	(K)V I/A/A\T N R V D I L D/P A/L L R(S)		166.75	617.366	1850.086	-0.0024	-1.3	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
17042	dirMS_041712_NAR_60mM_minus.11553.11553.3	3	7.02	0	2.25E+05		(K)ADDGRF	(K)A/D/D/G R P F/P Q V/I/K(S)		124.53	448.2371	1342.711	-0.0146	-10.9	6	15633.5	9.15	HUMAN	H3BMQ8	Fructose-bisphosphate aldolase A (Fragment)
17043	dirMS_041712_NAR_60mM_minus.9772.9772.3	3	7.02	0	9.17E+04		(K)YAVTTG	(K)Y A/V/T T/G D/H/G I I R(T)		114.47	434.9021	1302.68	0.0117	9	6.74	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
17044	dirMS_041712_NAR_120mM_plus.16445.16445.4	4	7.02	2	4.05E+05		(K)IQQLVK	(K)I Q/Q L V K/E F/F|N G K E/P S R(G)		138.98	480.7631	1920.034	-0.0032	-1.7	8.59	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
17045	dirMS_041712_NAR_120mM_plus.8747.8747.2	2	7.02	0	1.70E+05		(K)HTGPNS	(K)H/T|G P N S P D T A N D G F V R(L)		99.13	842.8861	1684.767	-0.0025	-1.5	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
17046	dirMS_041712_NAR_20mM_plus.15639.15639.2	2	7.02	0	6.50E+04		(K)VFLENVI	(K)V/F|L/E N/V I R(D)		179.55	495.2908	989.578	-0.0035	-3.6	5.97	11367.1	11.36	HUMAN	P62805	Histone H4
17047	dirMS_041712_NAR_20mM_plus.17934.17934.2	2	7.02	0	1.10E+05		(K)VDFPQD	(K)V/D/F/P Q D Q/L T A/L T/G R(I)		195.27	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
17048	dirMS_041712_NAR_20mM_plus.18783.18783.2	2	7.02	0	1.04E+05		(K)LTVYTTL	(K)L T|V/Y/T/T L I D V T K(G)		200.83	683.8948	1366.783	-0.0005	-0.4	5.83	42194.9	8.75	HUMAN	E7EMM4	Acid ceramidase
17049	dirMS_041712_NAR_20mM_plus.7945.7945.2	2	7.02	0	1.98E+05		(R)FGQGG	(R)F G Q|G\G A/G P V G G Q/G P R(G)		125.15	671.3361	1341.666	-0.0009	-0.7	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
17050	dirMS_041712_NAR_20mM_plus.8570.8570.2	2	7.02	0	3.02E+05		(K)DVNQQI	(K)D V/N Q/Q E/F V R(A)		129.47	567.7865	1134.554	0.0119	10.5	4.37	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
17051	dirMS_041712_NAR_20mM_plus.9462.9462.2	2	7.02	0	1.42E+05		(R)GTGIVS	(R)G T G\I/V/S A/P V/P\K(K)		136.92	513.3057	1025.599	0.0052	5	8.75	21898	11.33	HUMAN	E9PM36	40S ribosomal protein S2
17052	dirMS_041712_NAR_30mM_plus2.15805.15805.2	2	7.02	0	2.64E+05		(R)FDVSGY	(R)F D|V|S/G Y P T I K(I)		136.02	563.7923	1126.578	-0.0006	-0.5	5.83	73273.4	4.96	HUMAN	P13667	Protein disulfide-isomerase A4
17053	dirMS_041712_NAR_40mM_plus2.6897.6897.2	2	7.02	0	2.64E+04		(R)DYDDM	(R)D Y/D/D M S P R(R)		100.75	499.6964	998.388	-0.0029	-2.9	3.93	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
17054	dirMS_041712_NAR_50mM_plus2.18931.18931.3	3	7.02	1	1.55E+05		(K)QLKLDP	(K)Q L K L D P S I/F|E S L Q K(E)		167.52	549.3076	1645.916	-0.0077	-4.7	6.07	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
17055	dirMS_041712_NAR_50mM_plus2.21834.21834.3	3	7.02	1	2.08E+05		(R)KVPELM	(R)K\V P E L M|E|M/F\L/P A T K(N)		185.52	545.2925	1633.869	-0.0063	-3.8	6.14	95051	6.63	HUMAN	B3KXW5	AP-1 complex subunit gamma-1
17056	dirMS_041712_NAR_50mM_plus2.5987.5987.3	3	7.02	0	4.82E+04		(K)LVDQSG	(K)L V/D Q S/G/P P H/E P K(F)		95.7	435.2256	1303.664	-0.0018	-1.4	5.32	142137.5	9.17	HUMAN	E7ENU4	Double-stranded RNA-specific adenosine deaminase
17057	dirMS_041712_NAR_60mM_plus.11500.11500.3	3	7.02	1	4.52E+05		(K)TCVFEK	(K)T C|V/F E K E N D|P S V M R(S)	C:Carbamidomethylation	117.33	571.2635	1711.778	-0.0019	-1.1	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
17058	dirMS_041712_NAR_60mM_plus.18873.18873.3	3	7.02	1	2.59E+05		(K)YGKLEV	(K)Y G K L\E V A/N/L/L/L Q/K(S)		156.67	496.9628	1488.878	-0.0046	-3.1	8.5	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
17059	dirMS_041712_NAR_60mM_plus.6288.6288.3	3	7.02	0	2.56E+05	M480m	(R)AAHSEG	(R)A A H S E G N T T/A|G|L D m R(E)	m:Oxidized methionine	91.37	516.2346	1530.697	15.9927	-1.4	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
17060	dirMS_041712_NAR_60mM_plus.9807.9807.3	3	7.02	1	7.09E+05		(R)TPGKEA	(R)T/P G K E A\V/A/M/E/S Y A K(A)		109.58	494.5808	1481.73	-0.0026	-1.8	5.81	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
17061	dirMS_041712_NAR_120mM_minus.15824.15824.4	4	7.01	1	3.85E+05		(R)ALEHFT	(R)A L E H F T D L/Y|D/I K R(A)		140.32	405.9646	1620.838	-0.0015	-0.9	5.38	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
17062	dirMS_041712_NAR_120mM_minus.8016.8016.3	3	7.01	0	2.04E+05		(K)HEQNID	(K)H E Q N\I/D\C/G G/G Y V K(L)	C:Carbamidomethylation	97.95	492.8901	1476.654	0.0021	1.5	5.32	48311.8	4.29	HUMAN	P27797	Calreticulin
17063	dirMS_041712_NAR_20mM_minus.12503.12503.3	3	7.01	0	6.75E+05	M73m	(R)AVLVDLI	(R)A V L\V D L E/P G T/m D S V R(S)	m:Oxidized methionine	172.85	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
17064	dirMS_041712_NAR_20mM_minus.13830.13830.2	2	7.01	0	2.50E+05		(R)IVLLDSS	(R)I V/L/L D S S L E/Y K(K)		189.3	640.3594	1279.714	-0.0029	-2.2	4.37	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
17065	dirMS_041712_NAR_20mM_minus.8739.8739.2	2	7.01	0	1.91E+04	M149m	(K)ITLDNA	(K)I/T/L/D/N/A Y m E/K(C)	m:Oxidized methionine	136.55	607.2934	1197.582	15.9975	2.1	4.37	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
17066	dirMS_041712_NAR_30mM_minus2.12550.12904.2	2	7.01	0	6.57E+05		(K)NQAVN	(K)N|Q|A|V/N F L/R(M)		122.92	481.2669	961.521	0.0051	5.3	9.75	22166.1	7.91	HUMAN	Q7LBR1	Charged multivesicular body protein 1b
17067	dirMS_041712_NAR_30mM_minus2.16692.16692.2	2	7.01	0	9.34E+04		(R)IMNTFS	(R)I M N/T\F/S V V/P S P K(V)		144.8	660.3534	1319.703	-0.0033	-2.5	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
17068	dirMS_041712_NAR_30mM_minus2.17610.17610.2	2	7.01	0	1.73E+05		(R)NGGQIL	(R)N G/G Q|I|L I/A D L R(G)		149.53	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
17069	dirMS_041712_NAR_50mM_minus2.10907.10907.3	3	7.01	0	1.79E+05	M35m	(K)AASDIA	(K)A A|S D I/A m/T E L/P P T H/P I/R(L)	m:Oxidized methionine	130.27	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
17070	dirMS_041712_NAR_50mM_minus2.14864.14864.3	3	7.01	1	6.81E+04	M84m	(K)ETmQSL	(K)E T m Q/S/L/N D R L A S Y L D R(V)	m:Oxidized methionine	152.25	643.3122	1911.923	15.9991	2.2	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
17071	dirMS_041712_NAR_60mM_minus.14630.14630.3	3	7.01	1	2.82E+04		(R)MSMKE	(R)M S/M K E V D E Q|M/L|N V Q N K(N)		141.58	641.9701	1923.897	-0.0015	-0.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
17072	dirMS_041712_NAR_60mM_minus.7839.7839.3	3	7.01	2	3.82E+05	S224s	(K)SVDGED	(K)S V/D G E|D A K s E\A T K/S C G/K(I)	C:Carbamidomethylation s:N-ace	103.83	657.9647	1768.802	203.0778	-0.8	4.78	58008.6	8.96	HUMAN	Q5T7P8	Synaptotagmin-6
17073	dirMS_041712_NAR_120mM_plus.15952.15952.3	3	7.01	1	8.08E+04		(K)THLPGF	(K)T/H|L|P G F\V E\Q\A E A L K A K(G)		137.02	580.3208	1738.949	-0.0008	-0.5	6.42	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
17074	dirMS_041712_NAR_120mM_plus.20229.20229.3	3	7.01	0	2.78E+05		(R)INLWHL	(R)I/N L/W/H L E I T D/R(S)		159.48	470.5889	1409.754	-0.0014	-1	5.32	52204.6	5.82	HUMAN	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
17075	dirMS_041712_NAR_20mM_plus.11976.11976.2	2	7.01	0	4.00E+04		(R)ETPIGLV	(R)E T/P I G L/V/P K(E)		155.55	477.2872	953.567	0.0005	0.5	6.1	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
17076	dirMS_041712_NAR_30mM_plus2.8746.8790.2	2	7.01	0	2.26E+05		(R)SGYFDEI	(R)S G|Y|F D/E/R(Y)		99.62	437.1915	873.374	0.002	2.3	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
17077	dirMS_041712_NAR_40mM_plus2.10252.10252.2	2	7.01	0	6.93E+04		(R)EYQELM	(R)E Y/Q E/L/M/N V/K(L)		125.03	577.2823	1153.556	0.0015	1.3	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
17078	dirMS_041712_NAR_50mM_plus2.8795.8795.3	3	7.01	0	2.04E+05		(K)VVQVSA	(K)V V|Q\V/S/A/G D S H\T A A L T D D G R(V)		113.45	633.6509	1898.92	0.0179	9.4	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
17079	dirMS_041712_NAR_60mM_plus.11404.11404.3	3	7.01	0	4.84E+05		(K)NFYVEH	(K)N F/Y/V/E/H/P E V A R(L)		117.65	454.2286	1360.664	0.0068	5	5.4	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
17080	dirMS_041712_NAR_60mM_plus.12350.12350.3	3	7.01	1	9.36E+05		(R)LSFDKD	(R)L/S/F D K/D A/M/V A R(A)		121.18	418.2158	1252.635	-0.0026	-2.1	5.96	35556.4	9.3	HUMAN	F2Z393	Transaldolase
17081	dirMS_041712_NAR_20mM_minus.11157.11157.2	2	7	0	6.98E+04		(R)DFTPVC	(R)D F/T|P/V C T/T E L G/R(A)	C:Carbamidomethylation	159.32	698.3303	1395.657	-0.004	-2.8	4.37	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
17082	dirMS_041712_NAR_20mM_minus.11664.11664.2	2	7	0	1.67E+05		(R)VEVTEF	(R)V E/V/T|E F E/D/I K(S)		164.8	604.8043	1208.604	-0.0032	-2.6	4	30992.3	4.14	HUMAN	B2REB8	Protein SET
17083	dirMS_041712_NAR_40mM_minus2.10983.10983.3	3	7	0	4.88E+05		(R)DAGEGL	(R)D A|G E/G L L A V Q I/T D Q/E G|K P K(R)		147.97	657.0157	1969.024	0.0089	4.5	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
17084	dirMS_041712_NAR_40mM_minus2.11736.11736.3	3	7	1	1.31E+05		(K)TVGVEP	(K)T V|G V E/P A A D G K G V V V/V I K(R)		152.07	580.008	1738.011	-0.0015	-0.8	5.73	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
17085	dirMS_041712_NAR_50mM_minus2.16585.16585.3	3	7	0	1.74E+05		(R)GGYVLH	(R)G G/Y\V L/H I/G T I/Y/G D L K(V)		161.8	535.9583	1605.863	-0.0032	-2	6.74	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
17086	dirMS_041712_NAR_50mM_minus2.16787.16787.3	3	7	1	1.45E+05		(K)TVTAMD	(K)T V/T/A M/D V/V Y A L K R(Q)		162.88	489.6051	1466.804	-0.0028	-1.9	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
17087	dirMS_041712_NAR_60mM_minus.16236.16236.3	3	7	1	4.22E+05	T123t	(K)AtGDET	(K)A t G D E T G/A K/V E R(A)	t:N-acetylglucosamine (T)	151.08	479.5624	1233.607	203.0657	-9.5	4.68	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
17088	dirMS_041712_NAR_60mM_minus.8118.8118.3	3	7	0	1.29E+05		(K)EAYPDH	(K)E A Y/P/D H T Q F E/K(N)		105.03	455.5427	1364.612	0.0018	1.3	4.65	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1
17089	dirMS_041712_NAR_120mM_plus.11872.11872.3	3	7	1	4.39E+05		(K)MKEIAE	(K)M K E I/A E|A/Y/L/G K(T)		115.82	418.2253	1252.661	0.0008	0.6	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
17090	dirMS_041712_NAR_20mM_plus.10814.10814.2	2	7	0	8.05E+03		(R)LAEVEA	(R)L/A|E|V/E A A\L E K(Q)		146.92	536.7941	1072.589	-0.0075	-7	4.25	533778	5.74	HUMAN	Q15149	Plectin
17091	dirMS_041712_NAR_20mM_plus.5819.5819.3	3	7	0	2.94E+04		(K)SAAQAA	(K)S A\A Q/A A/A Q/T/N/S/N A A G K(Q)		97	487.5747	1460.709	0.0007	0.5	8.47	45021.6	8.74	HUMAN	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein
17092	dirMS_041712_NAR_20mM_plus.7476.7476.2	2	7	0	1.84E+05		(K)VLTPTQ	(K)V L|T/P/T/Q V K(N)		120.93	443.2734	885.54	-0.0009	-1	8.72	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
17093	dirMS_041712_NAR_20mM_plus.8838.8838.2	2	7	0	1.30E+05		(K)VLEEAN	(K)V L/E/E|A\N Q/A|I/N/P K(L)		131.6	663.353	1325.706	-0.0072	-5.5	4.53	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
17094	dirMS_041712_NAR_40mM_plus2.11043.11043.2	2	7	0	7.20E+03		(R)GDFCIQ	(R)G D/F/C I/Q V/G R(-)	C:Carbamidomethylation	131.12	526.2539	1051.499	0.0016	1.5	5.84	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
17095	dirMS_041712_NAR_40mM_plus2.16776.16776.3	3	7	0	8.98E+04		(R)LLEVLSG	(R)L L|E V/L S G E/I L/P K P T K(G)		166	546.3323	1636.988	-0.006	-3.7	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
17096	dirMS_041712_NAR_60mM_plus.11429.11431.3	3	7	0	4.84E+05		(K)NFYVEH	(K)N F/Y/V/E H/P E V/A R(L)		117.65	454.2286	1360.664	0.0068	5	5.4	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
17097	dirMS_041712_NAR_60mM_plus.12125.12125.3	3	7	1	2.47E+05		(K)IDKTDY	(K)I D K T D\Y\M|V/G S Y/G P/R(A)		120.28	534.5906	1601.763	-0.0056	-3.5	5.96	21671	5.37	HUMAN	J3KTF8	Rho GDP-dissociation inhibitor 1 (Fragment)
17098	dirMS_041712_NAR_60mM_plus.7473.7473.3	3	7	0	8.43E+05		(R)AAHSEG	(R)A A H S E G\N T|T/A/G L D/M R(E)		96.8	510.9035	1530.697	-0.0006	-0.4	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
17099	dirMS_041712_NAR_60mM_plus.7646.7646.2	2	7	1	1.09E+06		(R)AVVIVDI	(R)A V V|I\V/D/D/R/G R(S)		98.32	550.3143	1099.622	-0.0005	-0.5	6.01	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
17100	dirMS_041712_NAR_20mM_minus.9750.9750.2	2	6.99	0	2.44E+05		(K)LVIITAG	(K)L V|I/I/T A G A R(Q)		147.62	457.2947	913.583	-0.0008	-0.9	9.75	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
17101	dirMS_041712_NAR_20mM_minus.9771.9771.2	2	6.99	0	3.36E+05		(K)IGGIGTV	(K)I G/G I/G/T V/P/V G R(V)		147.47	513.3075	1025.61	-0.0025	-2.4	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
17102	dirMS_041712_NAR_30mM_minus2.12308.12308.2	2	6.99	0	5.09E+05		(R)EYQELM	(R)E Y Q/E L/M/N V K(L)		119.68	577.2825	1153.556	0.0019	1.7	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
17103	dirMS_041712_NAR_30mM_minus2.5197.5197.2	2	6.99	0	5.99E+05		(R)TDTGEP	(R)T\D|T/G E P M G R(G)		81.93	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
17104	dirMS_041712_NAR_50mM_minus2.10607.10607.3	3	6.99	1	2.03E+04		(K)ELALQP	(K)E L/A L Q/P K D D I V/D/R(A)		128.23	504.6068	1511.806	-0.0006	-0.4	4.23	83905.8	6.62	HUMAN	P41250	Glycine--tRNA ligase
17105	dirMS_041712_NAR_50mM_minus2.14608.14608.3	3	6.99	0	6.40E+04		(K)VYTDVQ	(K)V Y|T D V Q Q V A/S/S L T/H P R(F)		151.52	600.976	1800.924	-0.0104	-5.8	6.71	74230.8	5.34	HUMAN	B1AH89	Tubulin tyrosine ligase-like family, member 12
17106	dirMS_041712_NAR_50mM_minus2.6030.6030.3	3	6.99	0	4.74E+04		(R)LQVEQA	(R)L Q|V E Q/A/P H S S P G A K(L)		96.7	483.5881	1448.749	0.0005	0.4	6.75	16834.6	6.3	HUMAN	H0YKT9	Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase MESH1 (Fragment)
17107	dirMS_041712_NAR_120mM_plus.7469.7469.2	2	6.99	0	1.55E+05		(R)LYVHEA	(R)L Y/V|H E A V/K(A)		93.12	479.7757	958.536	0.0085	8.8	6.75	533778	5.74	HUMAN	Q15149	Plectin
17108	dirMS_041712_NAR_20mM_plus.14648.14648.2	2	6.99	0	3.89E+04	M185m	(K)LAVNm	(K)L A|V/N/m V|P\F/P R(L)	m:Oxidized methionine	172.75	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377

17109	dirMS_041712_NAR_20mM_plus.17134.17134.2	2	6.99	0	8.41E+04		(K)VNIIPIIA	(K)V/N\I|I/P I I A K(A)		189.33	490.8283	980.65	-0.001	-1	8.72	51212	5.84	HUMAN	A6NFQ9	Septin-8
17110	dirMS_041712_NAR_20mM_plus.17564.17564.3	3	6.99	0	2.13E+05	M90m	(R)LFVGNLI	(R)L F\V G N L|P/P D I T/E/E E m R(K)	m:Oxidized methionine	192.73	625.9762	1859.921	15.9933	-0.9	4	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
17111	dirMS_041712_NAR_20mM_plus.18438.18438.2	2	6.99	0	1.76E+05		(R)NIPGITL	(R)N I|P G I T/L L N V/S K(L)		198.82	634.8801	1268.757	-0.0043	-3.4	8.75	37884.5	11.27	HUMAN	H3BM89	60S ribosomal protein L4
17112	dirMS_041712_NAR_20mM_plus.7923.7923.2	2	6.99	0	1.89E+05		(R)FGQGG	(R)F G Q|G/G\A/G\P V\G/G Q G P R(G)		125.1	671.3361	1341.666	-0.0009	-0.7	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
17113	dirMS_041712_NAR_50mM_plus2.8736.8736.3	3	6.99	0	7.40E+05		(R)AALAHS	(R)A A L/A H S E E V T|A/S Q V A A T K(T)		113.43	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
17114	dirMS_041712_NAR_60mM_plus.18315.18315.3	3	6.99	0	1.94E+05		(K)DHGLEV	(K)D H G\L E\V\L/G L V R(V)		153.45	403.2318	1207.679	0.0015	1.2	5.32	17732.8	5.85	HUMAN	F5GYJ1	U8 snoRNA-decapping enzyme
17115	dirMS_041712_NAR_60mM_plus.7429.7429.3	3	6.99	1	1.93E+06		(R)SEEKISD	(R)S E|E K I\S/D/S/E G/F K(A)		96.8	452.5501	1355.632	0.0032	2.4	4.41	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
17116	dirMS_041712_NAR_60mM_plus.9704.9704.2	2	6.99	0	2.23E+05		(R)FATHAA	(R)F A/T/H/A/A/A L S V R(N)		108.87	572.3143	1143.627	-0.0056	-4.9	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
17117	dirMS_041712_NAR_30mM_minus2.12054.12054.2	2	6.98	0	3.05E+05		(K)GLVQAL	(K)G L|V|Q/A|L Q T K(V)		118.83	479.288	957.573	-0.004	-4.2	8.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
17118	dirMS_041712_NAR_30mM_minus2.17791.17791.2	2	6.98	0	3.01E+05		(K)EAFQLF	(K)E A/F/Q|L/F D R(T)		151.63	513.2571	1025.505	0.0019	1.8	4.37	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
17119	dirMS_041712_NAR_30mM_minus2.9601.9601.2	2	6.98	0	1.22E+05		(K)AVTEVL	(K)A V/T/E/V L A R(T)		106.07	429.7546	858.504	-0.0024	-2.8	6.05	36474.5	5.04	HUMAN	E7EVZ4	Endophilin-A2
17120	dirMS_041712_NAR_40mM_minus2.13514.13514.3	3	6.98	1	3.72E+04		(K)VTLVVG	(K)V T/L V/V G A/S Q D I I/P Q L K\K(K)		163.58	603.696	1809.084	-0.011	-6.1	8.56	25180.2	5.34	HUMAN	E7EMS6	Catechol O-methyltransferase (Fragment)
17121	dirMS_041712_NAR_40mM_minus2.6982.6982.2	2	6.98	0	5.85E+05		(R)GYSFTT	(R)G Y\S/F|T/T T A E R(E)		111.95	566.7661	1132.527	-0.002	-1.8	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
17122	dirMS_041712_NAR_60mM_minus.11023.11023.3	3	6.98	1	9.23E+04		(R)DGKLVS	(R)D G K L\V S\E/S\S/D V/L/P K(-)		121.25	491.927	1473.78	-0.0131	-8.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
17123	dirMS_041712_NAR_60mM_minus.13922.13922.3	3	6.98	0	4.32E+05		(K)DCGATV	(K)D C|G A T W V/V L/G H S E R(R)	C:Carbamidomethylation	137.98	529.5838	1586.738	-0.0012	-0.7	5.32	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
17124	dirMS_041712_NAR_120mM_plus.15629.15629.4	4	6.98	2	1.86E+05		(K)VGLQVV	(K)V/G L Q V V/A V K A/P G/F G D/N R K(N)		134.55	464.5161	1855.055	-0.0123	-6.6	9.99	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
17125	dirMS_041712_NAR_120mM_plus.8096.8096.3	3	6.98	2	2.08E+05	M53m	(K)LTDCVV	(K)L T/D/C V V m R D/P A S K/R(S)	C:Carbamidomethylation m:Oxid	95.88	555.2807	1647.831	15.997	1.3	8.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
17126	dirMS_041712_NAR_20mM_plus.12873.12873.2	2	6.98	0	1.44E+05		(R)LVVPAS	(R)L V|V/P/A S\Q C G S L I G K(G)	C:Carbamidomethylation	161.58	714.8991	1428.788	0.003	2.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
17127	dirMS_041712_NAR_20mM_plus.13297.13534.2	2	6.98	0	4.95E+05	M148m	(R)DLTDYL	(R)D L|T/D/Y/L m K(I)	m:Oxidized methionine	164.77	507.7439	998.486	15.9942	-0.7	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
17128	dirMS_041712_NAR_20mM_plus.16340.16340.2	2	6.98	0	8.43E+04		(R)AYILNLV	(R)A Y|I/L N/L/V K(Q)		183.77	467.2905	933.577	-0.0031	-3.3	8.63	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
17129	dirMS_041712_NAR_20mM_plus.18062.18062.2	2	6.98	0	2.89E+05		(R)ILVATNL	(R)I L|V|A T N L/F G R(G)		195.07	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
17130	dirMS_041712_NAR_20mM_plus.18405.18405.3	3	6.98	1	1.88E+05		(K)IAVISGV	(K)I A\V I S G/V G T\R N Y Y/R(K)		198.77	523.617	1568.854	-0.0179	-11.4	9.99	49803.3	9.21	HUMAN	B4DE19	Elongator complex protein 3
17131	dirMS_041712_NAR_20mM_plus.18962.18962.3	3	6.98	0	6.34E+04		(K)DTSYLF	(K)D T S|Y L\F I/T/G/P D V V K(S)		201.93	518.9378	1554.805	-0.0062	-4	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
17132	dirMS_041712_NAR_30mM_plus2.10486.10486.2	2	6.98	0	5.44E+05		(K)ACQIFV	(K)A/C|Q/I/F V R(N)	C:Carbamidomethylation	108.75	447.2386	893.466	0.0037	4.2	9.79	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
17133	dirMS_041712_NAR_30mM_plus2.11286.11286.2	2	6.98	0	5.16E+04		(R)MGESD	(R)M/G E S|D/D S I/L R(L)		112.17	561.7585	1122.51	0.0002	0.1	4.03	9225.3	9.16	HUMAN	P63220	40S ribosomal protein S21
17134	dirMS_041712_NAR_30mM_plus2.12484.12803.2	2	6.98	0	3.68E+05		(R)IFYDMK	(R)I/F/Y D/M/K(V)		119.08	408.702	816.396	0.0007	0.8	5.83	15739.2	9.3	HUMAN	F6RFD5	Destrin
17135	dirMS_041712_NAR_30mM_plus2.21792.21792.2	2	6.98	0	2.13E+05		(R)NSILAQ	(R)N S I/L|A|Q V L/D Q\S/A R(A)		170.13	707.8889	1414.765	0.0057	4	5.84	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
17136	dirMS_041712_NAR_40mM_plus2.12528.12528.2	2	6.98	0	2.54E+04		(K)ICSWNV	(K)I C|S/W/N/V D/G L R(A)	C:Carbamidomethylation	140.23	610.297	1219.589	-0.0021	-1.7	5.84	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
17137	dirMS_041712_NAR_50mM_plus2.13377.13377.3	3	6.98	0	1.99E+05		(K)LVRPPV	(K)L V/R/P P V\Q\V/Y/G I E G/R(Y)		138.6	528.3069	1582.906	-0.0002	-0.2	8.75	8249.6	10.2	HUMAN	H7C086	ATP synthase subunit O, mitochondrial (Fragment)
17138	dirMS_041712_NAR_50mM_plus2.14049.14049.3	3	6.98	1	4.02E+05		(K)TSIAIDTI	(K)T S I/A/I/D/T/I I N Q K R(F)		142.52	491.6191	1472.843	-0.0004	-0.3	8.41	48851.3	9.2	HUMAN	K7EK63	ATP synthase subunit alpha, mitochondrial
17139	dirMS_041712_NAR_50mM_plus2.21130.21130.3	3	6.98	0	2.87E+05		(K)HSQFIG	(K)H S Q F I G Y|P I/T L F V/E K(E)		180.25	593.6536	1778.948	-0.0013	-0.8	6.75	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
17140	dirMS_041712_NAR_50mM_plus2.4984.4984.3	3	6.98	1	1.04E+05		(K)VSSAEG	(K)V/S|S A E G A A K E/E/P K(R)		83.1	434.8891	1302.654	-0.0008	-0.6	4.79	4801.6	11.17	HUMAN	F2Z2W6	Non-histone chromosomal protein HMG-14
17141	dirMS_041712_NAR_50mM_plus2.5163.5163.3	3	6.98	0	7.90E+04		(R)AEAEAG	(R)A E|A\E/A/G S P R P D/P\R(E)		85.77	451.5555	1352.655	-0.0034	-2.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
17142	dirMS_041712_NAR_50mM_plus2.5746.5746.3	3	6.98	1	1.51E+05	M254m M	(R)LmEEIm	(R)L m|E\E I m S E/K/E|N K(T)	m:Oxidized methionine	93.27	504.9014	1480.702	31.9875	-1.6	4.49	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
17143	dirMS_041712_NAR_50mM_plus2.7471.7471.3	3	6.98	0	1.03E+04		(R)ASAPSP	(R)A S\A/P S/P N A Q V/A C D H C L K(E)	C:Carbamidomethylation	105.13	609.2765	1825.832	-0.017	-9.3	6.79	72626.7	9.13	HUMAN	Q14258	E3 ubiquitin/ISG15 ligase TRIM25
17144	dirMS_041712_NAR_50mM_plus2.9261.9261.3	3	6.98	1	7.57E+05	M239m	(R)MQKEIT	(R)M Q K E\I T A\L/A|P S T m K(I)	m:Oxidized methionine	115.63	522.2726	1548.812	15.9908	-2.6	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
17145	dirMS_041712_NAR_60mM_plus.16635.16635.3	3	6.98	1	6.23E+05		(R)TDGKV	(R)T/D G K V/F/Q/F L/N A K(C)		143.53	456.5782	1367.732	-0.0117	-8.6	8.26	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
17146	dirMS_041712_NAR_60mM_plus.20540.20540.3	3	6.98	0	6.34E+05		(R)LGFHLP	(R)L G F H L P/L E|V/A/Y Q R(G)		168.5	514.9568	1542.843	0.0131	8.5	6.75	533778	5.74	HUMAN	Q15149	Plectin
17147	dirMS_041712_NAR_60mM_plus.5761.5761.3	3	6.98	1	1.91E+05		(R)SSGGGY	(R)S S/G/G G/Y/S G D R S G G G Y G G D\R(S)		88.07	583.5777	1748.722	-0.0033	-1.9	5.68	21563.9	10.01	HUMAN	K7EKB2	TATA-binding protein-associated factor 2N (Fragment)
17148	dirMS_041712_NAR_60mM_plus.6554.6554.3	3	6.98	1	6.89E+05		(R)NKQTYS	(R)N K Q\T Y/S T/E/P N N L K(A)		92.93	512.9257	1536.765	-0.0027	-1.8	8.5	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
17149	dirMS_041712_NAR_60mM_plus.8825.8825.3	3	6.98	1	5.73E+05		(K)ELKSPD	(K)E L/K S P D E/G/F/E/G K(S)		104.5	445.8862	1335.643	0.0014	1	4.41	84557.3	6.5	HUMAN	Q04609	Glutamate carboxypeptidase 2
17150	dirMS_041712_NAR_20mM_minus.13188.13188.3	3	6.97	0	1.06E+05		(R)GVVDSE	(R)G V\V D S E D\I/P L N L S\R(E)		183	505.266	1513.786	-0.0022	-1.5	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
17151	dirMS_041712_NAR_30mM_minus2.11839.11839.2	2	6.97	0	1.01E+05		(R)SGYLLP	(R)S G/Y/L/L|P D/T K(A)		116.68	497.265	993.525	-0.0024	-2.4	5.55	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
17152	dirMS_041712_NAR_30mM_minus2.15180.15180.2	2	6.97	0	4.88E+05		(R)YPVNSV	(R)Y/P|V/N S V/N I L/K(A)		136.3	573.8282	1146.652	-0.0026	-2.3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
17153	dirMS_041712_NAR_30mM_minus2.6801.6801.2	2	6.97	0	1.51E+04		(K)AMEAV	(K)A M|E/A V/A A\Q G K(A)		91.35	488.2495	975.493	-0.0011	-1.1	6.05	28936.8	9.22	HUMAN	P15259	Phosphoglycerate mutase 2
17154	dirMS_041712_NAR_40mM_minus2.14640.14640.3	3	6.97	0	1.63E+05	M159m	(R)SVAAIH	(R)S V|A A I H P S L E I P m L I/P/K(E)	m:Oxidized methionine	171.28	611.3477	1816.04	15.9884	-3.5	6.47	31606.3	6.72	HUMAN	B4E329	Phosphoribosyl pyrophosphate synthase-associated protein 2
17155	dirMS_041712_NAR_50mM_minus2.7017.7017.3	3	6.97	1	2.04E+05		(K)GAVAED	(K)G A V|A/E/D G D E L/R T E P E A K(K)		106.92	596.2904	1786.845	0.0113	6.3	4.08	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
17156	dirMS_041712_NAR_50mM_minus2.8984.8984.3	3	6.97	0	2.36E+05		(R)VMLGET	(R)V M|L|G E T N/P A D/S K P G T I R(G)		118.3	595.9744	1785.916	-0.0077	-4.3	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
17157	dirMS_041712_NAR_50mM_minus2.9554.9554.2	2	6.97	1	7.15E+05		(R)DGKLVS	(R)D/G/K L|V|S E S S D V\L|P/K(-)		121.97	737.3927	1473.78	-0.0014	-0.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
17158	dirMS_041712_NAR_60mM_minus.16263.16263.3	3	6.97	0	2.78E+05		(R)HDPTSE	(R)H D\P T\S E/N/I/L Q L V/K(A)		150.57	498.6051	1493.796	0.0049	3.3	5.32	13564.4	5.9	HUMAN	F8VZ98	Serine/threonine-protein kinase D1 (Fragment)
17159	dirMS_041712_NAR_120mM_plus.17982.17982.3	3	6.97	1	2.78E+05		(K)LALDIEI	(K)L/A/L\D/I E/I/A T Y R K(L)		147.47	469.2696	1405.805	-0.0107	-7.6	6.07	49564	5.84	HUMAN	E9PAX3	Glial fibrillary acidic protein
17160	dirMS_041712_NAR_120mM_plus.4128.4128.3	3	6.97	1	1.52E+07	M310m	(R)TKTEISE	(R)T K T E\I|S|E/m N R(N)	m:Oxidized methionine	69.72	408.8687	1208.594	15.9976	2.2	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
17161	dirMS_041712_NAR_120mM_plus.5345.5345.3	3	6.97	0	3.85E+04		(R)TGIYSST	(R)T G|I/Y S S/T S/C H K(T)	C:Carbamidomethylation	81.43	414.1962	1240.563	0.0114	9.2	8.28	38077.6	8.9	HUMAN	P09668	Pro-cathepsin H
17162	dirMS_041712_NAR_20mM_plus.8285.8285.2	2	6.97	0	9.35E+04		(R)LATNTS	(R)L A|T/N T S A P D/L K(N)		127.33	565.806	1130.605	-0.0005	-0.4	5.84	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
17163	dirMS_041712_NAR_30mM_plus2.16931.17315.2	2	6.97	0	7.05E+05		(K)FFVGGN	(K)F F|V/G/G N/W K(M)		142.57	477.7447	954.483	-0.0011	-1.1	8.75	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
17164	dirMS_041712_NAR_30mM_plus2.8392.8392.2	2	6.97	0	2.24E+05		(R)VAIEPG	(R)V A/I|E/P/G A\P R(E)		97.73	455.2602	909.515	-0.0021	-2.3	5.97	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
17165	dirMS_041712_NAR_40mM_plus2.11467.11467.2	2	6.97	1	8.88E+04		(K)QRIDEF	(K)Q R I D\E\F E|A|M(-)		133.8	569.7569	1138.52	-0.0132	-11.6	4.14	52734.7	5.88	HUMAN	F5H1A7	Radixin
17166	dirMS_041712_NAR_40mM_plus2.11935.11935.3	3	6.97	1	6.43E+04		(R)FGEVVD	(R)F/G\E V|V/D C T I K T D/P\V T G R(S)	C:Carbamidomethylation	136.33	631.9821	1893.938	-0.0057	-3	4.56	46607.8	9.68	HUMAN	O14979	Heterogeneous nuclear ribonucleoprotein D-like
17167	dirMS_041712_NAR_40mM_plus2.17907.17907.3	3	6.97	0	2.41E+04		(K)DMTVP	(K)D M|T/V/P I L V/S K P P V F T G K(D)		173.15	610.3443	1829.024	-0.0058	-3.2	8.59	53885.5	9	HUMAN	P11182	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial
17168	dirMS_041712_NAR_50mM_plus2.20338.20338.3	3	6.97	1	1.04E+04		(K)SSVLESL	(K)S S V/L E S L V/G/R D L/L P R(G)		175.6	547.6436	1640.933	-0.0167	-10.2	5.79	19884.2	4.87	HUMAN	B4DDQ3	Dynamin-1-like protein
17169	dirMS_041712_NAR_50mM_plus2.21260.21260.3	3	6.97	1	5.54E+05	M145m	(R)GVmLA	(R)G V/m L/A/V/D A V/I A E L K K(Q)	m:Oxidized methionine	181.93	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
17170	dirMS_041712_NAR_60mM_plus.11097.11097.2	2	6.97	1	6.40E+05		(R)QQEGF	(R)Q/Q E G/F|K/G T F P D|A/R(E)		115.62	740.8612	1480.718	-0.0028	-1.9	6.07	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
17171	dirMS_041712_NAR_60mM_plus.19933.19933.3	3	6.97	1	1.53E+05		(R)GMLRE	(R)G M/L R E D\A\V|L/E Y L/K(I)		163.87	512.9411	1536.809	-0.0003	-0.2	4.68	67933	6.08	HUMAN	P26038	Moesin
17172	dirMS_041712_NAR_60mM_plus.21511.21511.3	3	6.97	0	1.09E+05		(R)LHFFMP	(R)L/H F F M P G F/A/P\L T S R(G)		179.2	540.9492	1620.835	-0.0025	-1.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
17173	dirMS_041712_NAR_60mM_plus.9563.9563.3	3	6.97	0	2.94E+04	S266s	(K)IHNGsV	(K)I H/N G s V F/T/K(N)	s:N-acetylglucosamine (S)	108.13	402.5452	1002.537	203.0843	4.1	8.76	36470.7	5.59	HUMAN	P46736	Lys-63-specific deubiquitinase BRCC36
17174	dirMS_041712_NAR_20mM_minus.13163.13163.2	2	6.96	0	2.34E+05		(R)GVVDSE	(R)G V/V\D\S\E/D I/P L N L/S R(E)		183.02	757.3944	1513.786	-0.0041	-2.7	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
17175	dirMS_041712_NAR_50mM_minus2.10441.10441.3	3	6.96	1	1.84E+04		(R)TEMEDL	(R)T E|M/E/D L/M S S K D D V G K(S)		127.38	562.2507	1684.74	-0.0029	-1.7	4.1	227783.5	5.5	HUMAN	P35579	Myosin-9
17176	dirMS_041712_NAR_50mM_minus2.12066.12066.3	3	6.96	1	2.49E+04		(R)ELISNSS	(R)E L/I/S/N S S D A L D K I R(Y)		137.62	520.9445	1560.823	-0.0038	-2.5	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
17177	dirMS_041712_NAR_50mM_minus2.5302.5302.3	3	6.96	0	7.53E+05	M434m M	(R)LESGmC	(R)L/E|S G m Q N m S I H/T/K(T)	m:Oxidized methionine	87.88	503.2361	1475.698	31.9956	3.9	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
17178	dirMS_041712_NAR_50mM_minus2.6032.6032.3	3	6.96	1	6.40E+05	M286m M	(R)VVDLm	(R)V/V|D/L m/A H m A S K E(-)	m:Oxidized methionine	97.23	454.8842	1330.649	31.9887	-0.8	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
17179	dirMS_041712_NAR_60mM_minus.6929.6966.3	3	6.96	1	1.90E+05	M153m	(K)mIYASS	(K)m/I/Y A S/S K D/A I/K(K)	m:Oxidized methionine	97.3	414.886	1226.645	15.9985	2.9	8.26	22956	8.8	HUMAN	E9PK25	Cofilin-1
17180	dirMS_041712_NAR_60mM_minus.9278.9278.3	3	6.96	0	8.83E+04		(R)EVEEEP	(R)E V E/E E/P G I H S L K(H)		111.42	456.229	1366.685	-0.0124	-9.1	4.48	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
17181	dirMS_041712_NAR_120mM_plus.18177.18177.4	4	6.96	1	1.29E+05		(K)YYITIIDA	(K)Y Y I T I I/D/A/P G H R D F I K(N)		148.22	481.2587	1922.017	-0.0041	-2.1	6.75	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
17182	dirMS_041712_NAR_120mM_plus.19050.19050.4	4	6.96	1	5.99E+05		(K)ALERLE	(K)A L/E R L E G/V E G V A H I I D/P/K(A)		153.18	487.2719	1946.071	-0.0048	-2.5	4.83	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
17183	dirMS_041712_NAR_120mM_plus.21370.21370.4	4	6.96	2	4.44E+05	M145m	(R)RGVmL	(R)R G V\m\L\A/V D|A V I/A E L K K(Q)	m:Oxidized methionine	166.2	433.0059	1713.009	15.9926	-1.3	8.59	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
17184	dirMS_041712_NAR_20mM_plus.10437.10437.3	3	6.96	0	5.88E+04		(K)EVDEQ	(K)E V D\E Q\M\L/N V/Q/N K(N)		144.9	482.9	1446.689	-0.0039	-2.7	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
17185	dirMS_041712_NAR_20mM_plus.15799.15799.3	3	6.96	0	1.71E+05		(R)GVVDSE	(R)G V V/D\S E D I\P L N/L S R(E)		179.57	505.2667	1513.786	-0.0001	-0.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
17186	dirMS_041712_NAR_20mM_plus.16941.16941.2	2	6.96	0	1.34E+05		(K)LGGSAV	(K)L G G S A/V\I|S L E G K|P\L(-)		187.28	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
17187	dirMS_041712_NAR_20mM_plus.7055.7055.3	3	6.96	0	1.33E+05	M295m M	(R)mGQmA	(R)m G Q\m\A m\G G\A|M/G I N N R(G)	m:Oxidized methionine	115.02	529.5557	1538.67	47.9831	-1.1	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
17188	dirMS_041712_NAR_20mM_plus.7474.7474.2	2	6.96	0	1.25E+05		(K)AQYEDI	(K)A/Q|Y/E D I/A N R(S)		120.48	540.2601	1079.512	0.0013	1.2	4.37	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
17189	dirMS_041712_NAR_40mM_plus2.18860.18860.3	3	6.96	0	2.79E+04		(K)ALESPEF	(K)A L/E/S/P E R P F L A I L G G A K(V)		176.58	590.3359	1768.996	-0.0024	-1.4	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
17190	dirMS_041712_NAR_50mM_plus2.8266.8266.3	3	6.96	1	3.09E+05		(R)NTVSQS	(R)N T/V/S Q S I S G D/P E I D K K(I)		110.27	573.2915	1717.86	-0.0003	-0.2	4.56	58392.6	9.36	HUMAN	B4DF96	Eukaryotic translation initiation factor 2A
17191	dirMS_041712_NAR_60mM_plus.10297.10297.3	3	6.96	1	4.39E+05		(R)RQQEQ	(R)R Q Q/E\Q Q\V|P I/L E K(F)		111.5	499.2786	1495.823	-0.0015	-1	6.14	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
17192	dirMS_041712_NAR_60mM_plus.13906.13906.3	3	6.96	1	9.19E+05		(K)TTVKDL	(K)T T V K D L\S E/L/G/S V R(T)		129.45	468.9268	1404.769	-0.0034	-2.4	5.74	533778	5.74	HUMAN	Q15149	Plectin
17193	dirMS_041712_NAR_60mM_plus.5034.5034.3	3	6.96	1	3.95E+05		(R)AAEDDE	(R)A A|E|D D E D D D V D T/K K(Q)		83.53	522.5529	1565.645	-0.0008	-0.5	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
17194	dirMS_041712_NAR_60mM_plus.7232.7232.3	3	6.96	1	4.23E+05		(R)FSEGTS	(R)F/S/E/G T S A D R E I Q/R(T)		96.42	499.2424	1495.714	-0.0009	-0.6	4.68	7809.8	5.24	HUMAN	H0YJX2	26S protease regulatory subunit 10B (Fragment)
17195	dirMS_041712_NAR_60mM_plus.9330.9330.3	3	6.96	0	1.44E+05		(R)IEPADA	(R)I E\P A D/A H V L Q/K(N)		106.87	407.5532	1220.663	-0.0183	-15	5.32	11018.4	8.89	HUMAN	B0AZT5	N-alpha-acetyltransferase 50
17196	dirMS_041712_NAR_120mM_minus.5011.5011.3	3	6.95	1	2.26E+05		(K)AGADEE	(K)A/G\A/D E/E R A E/T A/R(L)		78.83	425.8687	1275.592	-0.0008	-0.7	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
17197	dirMS_041712_NAR_120mM_minus.9265.9265.3	3	6.95	0	4.27E+05		(K)ASIHEA	(K)A/S I/H E/A W/T D/G K(E)		105.02	405.5322	1214.58	0.002	1.7	5.32	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
17198	dirMS_041712_NAR_120mM_minus.9693.9693.3	3	6.95	1	5.92E+04		(R)AREQAE	(R)A R E Q\A\E A E\V|A|S/L N R(R)		107	515.2649	1543.782	-0.0022	-1.4	4.79	11017	4.8	HUMAN	D6R904	Tropomyosin alpha-3 chain
17199	dirMS_041712_NAR_20mM_minus.12111.12111.3	3	6.95	0	4.05E+05	M256m	(R)SLDmDS	(R)S L D m D S/I/I/A E/V K(A)	m:Oxidized methionine	170.55	446.227	1320.671	15.9949	0	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
17200	dirMS_041712_NAR_20mM_minus.7398.7398.2	2	6.95	0	9.88E+04		(K)VEIIAND	(K)V E/I|I/A/N\D Q G N R(T)		122.23	614.8166	1228.628	-0.0021	-1.7	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
17201	dirMS_041712_NAR_30mM_minus2.9714.9714.2	2	6.95	0	1.92E+05		(R)LGYTPV	(R)L/G Y|T/P V C R(A)	C:Carbamidomethylation	107.18	483.2423	965.487	-0.01	-10.3	8.75	25847.9	6.33	HUMAN	Q15102	Platelet-activating factor acetylhydrolase IB subunit gamma
17202	dirMS_041712_NAR_40mM_minus2.6912.6912.2	2	6.95	0	5.65E+05		(R)GYSFTT	(R)G Y|S/F/T/T T A E R(E)		111.92	566.7661	1132.527	-0.002	-1.8	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
17203	dirMS_041712_NAR_50mM_minus2.12108.12108.3	3	6.95	1	6.84E+04		(R)IAAAILN	(R)I/A|A A I/L/N T/P D L R K(Q)		137.2	465.9459	1395.832	-0.0087	-6.2	8.75	43371.1	9.64	HUMAN	E7ERW2	Aspartate aminotransferase
17204	dirMS_041712_NAR_50mM_minus2.7955.7955.2	2	6.95	1	1.27E+05	M239m	(R)MQKEIT	(R)M Q K\E I T/A\L A|P S T m/K(I)	m:Oxidized methionine	112.32	782.9062	1548.812	15.9927	-1.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
17205	dirMS_041712_NAR_60mM_minus.15392.15392.3	3	6.95	1	4.39E+05		(K)YQLDKD	(K)Y Q|L D K D G V V L/F/K(K)		146.25	475.5992	1424.778	0.0047	3.3	5.96	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
17206	dirMS_041712_NAR_120mM_plus.5841.5862.3	3	6.95	1	4.06E+05		(R)LNGTLR	(R)L/N|G/T L R E D D/N/R(I)		83.5	434.8849	1302.64	0.0005	0.4	4.56	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
17207	dirMS_041712_NAR_120mM_plus.8789.8789.3	3	6.95	1	4.30E+04		(R)RQQEEL	(R)R Q Q\E E\L\L/A/E E N/Q R(L)		99.1	548.2767	1642.814	0.0012	0.7	4.49	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
17208	dirMS_041712_NAR_20mM_plus.18979.18979.2	2	6.95	0	2.13E+04		(K)LLVYEAL	(K)L/L|V/Y E A L E/Y A K(R)		201.67	656.3664	1311.719	0.006	4.6	4.53	32535.6	9.19	HUMAN	B4DZW6	Regulator of microtubule dynamics protein 1
17209	dirMS_041712_NAR_20mM_plus.8436.8436.2	2	6.95	0	2.56E+04		(R)NDAPTP	(R)N D A/P/T/P G T S\T T P G L R(S)		127.98	742.8666	1484.734	-0.008	-5.4	5.84	83912.5	6.73	HUMAN	E9PD64	Transducin-like enhancer protein 3
17210	dirMS_041712_NAR_20mM_plus.9466.9466.2	2	6.95	0	9.50E+04		(R)ALEESN	(R)A L\E|E S N Y E L E/G K(I)		136.5	691.3246	1381.648	-0.0062	-4.5	4.09	59054.3	5.14	HUMAN	P13645	Keratin, type I cytoskeletal 10
17211	dirMS_041712_NAR_30mM_plus2.10693.10693.2	2	6.95	0	4.20E+05		(K)QGYVIY	(K)Q/G/Y/V I/Y/R(I)		109.18	449.7424	898.478	-0.0006	-0.7	8.59	20608.6	11.48	HUMAN	E7ENU7	Ribosomal protein L15 (Fragment)
17212	dirMS_041712_NAR_30mM_plus2.17626.17626.3	3	6.95	1	6.98E+05		(R)LENGNC	(R)L E N G N Q/A/R S/E A R(R)		144.98	448.8963	1344.661	0.0129	9.6	6.14	185718.4	8.45	HUMAN	F5GX68	Cytosine-specific methyltransferase
17213	dirMS_041712_NAR_30mM_plus2.19728.19728.2	2	6.95	0	2.35E+05		(K)APDFVF	(K)A/P/D/F\V|F|Y A|P R(L)		156.72	591.8008	1182.594	0.0001	0.1	5.88	71218.8	6.3	HUMAN	A7YIJ8	Radixin
17214	dirMS_041712_NAR_40mM_plus2.14347.14347.3	3	6.95	1	1.80E+05		(K)IMASSP	(K)I/M|A S S P/D M D L A T/V S A/L R K(M)		151.18	635.9975	1905.977	0.0007	0.4	5.96	36208.1	7.21	HUMAN	B4DMU0	Pyrroline-5-carboxylate reductase
17215	dirMS_041712_NAR_50mM_plus2.15713.15713.3	3	6.95	1	8.95E+05		(R)KVPGVT	(R)K\V\P G V T A\I/E\L/D E D/T G T F R(I)		149.98	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
17216	dirMS_041712_NAR_50mM_plus2.19027.19027.3	3	6.95	0	8.17E+05		(R)CRPDQL	(R)C R P D Q\L T/G\L\S/L/L/P L S E K(A)	C:Carbamidomethylation	167.72	643.0148	1927.032	-0.0019	-1	6.07	533778	5.74	HUMAN	Q15149	Plectin
17217	dirMS_041712_NAR_50mM_plus2.21500.21500.3	3	6.95	0	1.01E+05		(K)THLPLA	(K)T H L P L A L\L/P Q|T L/L D Q K(V)		183.97	601.0191	1801.058	-0.0154	-8.6	6.41	22243.5	7.91	HUMAN	E9PKR8	Sulfotransferase 1A2 (Fragment)

17218	dirMS_041712_NAR_50mM_plus2.9507.9507.3	3	6.95	1	1.95E+05		(K)NVSEEL	(K)N V/S\E/E L D/R T P P E V S K(K)		117.07	567.2893	1699.85	0.0036	2.1	4.41	136658.9	5.13	HUMAN	Q15393	Splicing factor 3B subunit 3
17219	dirMS_041712_NAR_60mM_plus.11474.11474.3	3	6.95	1	2.36E+05		(K)TAVCDI	(K)T A|V/C D/I/P P R G L|K(M)	C:Carbamidomethylation	118.73	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
17220	dirMS_041712_NAR_60mM_plus.13665.13665.3	3	6.95	1	5.41E+05		(R)FQNSLK	(R)F/Q/N/S L K E L Q L Q K(Q)		128.32	492.6101	1475.822	-0.0059	-4	8.59	334221.3	6.44	HUMAN	P15924	Desmoplakin
17221	dirMS_041712_NAR_60mM_plus.9484.9484.3	3	6.95	1	3.92E+05		(K)VGIRET	(K)V/G/I R E T|P E N L A/K(L)		107.65	442.9125	1326.738	-0.0146	-11	6.11	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
17222	dirMS_041712_NAR_60mM_plus.9774.9774.2	2	6.95	0	1.96E+05		(R)FATHAA	(R)F A/T/H/A/A A L S V R(N)		108.95	572.3143	1143.627	-0.0056	-4.9	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
17223	dirMS_041712_NAR_20mM_minus.13156.13156.2	2	6.94	0	2.34E+05		(R)GVVDSE	(R)G V/V D S/E/D/I/P L N L S R(E)		183.02	757.3944	1513.786	-0.0041	-2.7	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
17224	dirMS_041712_NAR_30mM_minus2.19072.19072.2	2	6.94	0	1.22E+05		(R)ALLFIPR	(R)A L L|F/I|P/R(R)		158.7	415.2685	829.529	0.0003	0.3	9.79	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
17225	dirMS_041712_NAR_30mM_minus2.6085.6085.2	2	6.94	0	1.54E+05		(R)AQAEQ	(R)A Q|A/E Q/A/A L/R(Q)		87.55	479.2592	957.511	-0.0001	-0.1	6.05	533778	5.74	HUMAN	Q15149	Plectin
17226	dirMS_041712_NAR_30mM_minus2.6212.6212.2	2	6.94	0	1.72E+05		(R)AQAEQ	(R)A/Q|A/E Q/A A/L R(Q)		88.18	479.2592	957.511	-0.0001	-0.1	6.05	533778	5.74	HUMAN	Q15149	Plectin
17227	dirMS_041712_NAR_40mM_minus2.11755.11755.3	3	6.94	1	1.29E+05		(K)TVGVEP	(K)T V|G V/E/P A A D G K G V V V V I K(R)		152.08	580.008	1738.011	-0.0015	-0.8	5.73	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
17228	dirMS_041712_NAR_60mM_minus.18085.18085.3	3	6.94	0	2.43E+05		(R)VLDPFTI	(R)V L|D/P F T I/K P L D R(K)		161.4	471.9394	1413.81	-0.0064	-4.5	5.93	63448.4	7.29	HUMAN	B4E022	Transketolase
17229	dirMS_041712_NAR_20mM_plus.15895.15895.2	2	6.94	0	2.02E+05		(R)GVVDSE	(R)G V V D S E/D I/P/L N L/S R(E)		180.07	757.3956	1513.786	-0.0017	-1.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
17230	dirMS_041712_NAR_30mM_plus2.13489.13489.2	2	6.94	0	8.55E+05		(K)EITALAP	(K)E I|T|A/L/A P S T M K(I)		123.35	581.307	1161.618	-0.0117	-10	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
17231	dirMS_041712_NAR_30mM_plus2.19500.19500.2	2	6.94	0	2.88E+04		(R)FLLADNI	(R)F/L|L|A/D N/L/Y C K(A)	C:Carbamidomethylation	155.03	628.8226	1256.634	0.0036	2.8	5.83	22400.1	6.19	HUMAN	F5H2A7	Prefoldin subunit 3
17232	dirMS_041712_NAR_30mM_plus2.6161.6161.2	2	6.94	0	6.96E+04		(R)SAEEGEI	(R)S A/E E/G E L A E/S K(S)		86.42	575.2667	1149.527	-0.0009	-0.8	4.09	182819.3	4.77	HUMAN	Q9C0C2	182 kDa tankyrase-1-binding protein
17233	dirMS_041712_NAR_30mM_plus2.9537.9537.2	2	6.94	0	8.52E+04		(K)VCNPIIT	(K)V/C|N/P I I\T K(L)	C:Carbamidomethylation	104.22	472.7711	944.523	0.0116	12.2	8.72	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
17234	dirMS_041712_NAR_40mM_plus2.10133.10133.3	3	6.94	0	5.15E+04		(K)EVVKPV	(K)E V V K P V/P I/T S/P A V S K(V)		123.87	517.6421	1550.915	-0.0035	-2.2	8.69	65142.1	9.24	HUMAN	Q96HC4	PDZ and LIM domain protein 5
17235	dirMS_041712_NAR_40mM_plus2.10323.10323.2	2	6.94	0	9.40E+04		(K)IGGIGTV	(K)I/G/G|I/G T V/P V G R(V)		125.75	513.3081	1025.61	-0.0013	-1.2	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
17236	dirMS_041712_NAR_50mM_plus2.13525.13525.3	3	6.94	0	1.54E+06		(R)VLVVHD	(R)V/L|V/V/H D/G F E G L A K(G)		139.83	461.9229	1383.763	-0.0089	-6.5	5.32	18719.9	6.91	HUMAN	F8VP00	6-phosphofructokinase, muscle type (Fragment)
17237	dirMS_041712_NAR_50mM_plus2.14277.14277.3	3	6.94	1	6.66E+05		(R)MSMKE	(R)M/S M K E V D\E Q/M|L/N V Q N K(N)		142.87	641.9706	1923.897	0	0	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
17238	dirMS_041712_NAR_50mM_plus2.21459.21459.3	3	6.94	0	1.01E+05		(K)THLPLAL	(K)T H L P L A L\L/P Q/T L L D Q K(V)		183.97	601.0191	1801.058	-0.0154	-8.6	6.41	22243.5	7.91	HUMAN	E9PKR8	Sulfotransferase 1A2 (Fragment)
17239	dirMS_041712_NAR_50mM_plus2.8768.8953.3	3	6.94	1	2.21E+05		(K)TTSPPEV	(K)T T|S/P/P E V S G Y S Y E K/T E R(S)		113.33	644.3093	1930.903	0.0105	5.4	4.78	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
17240	dirMS_041712_NAR_60mM_plus.15594.15594.3	3	6.94	0	2.27E+05		(R)NFDLTA	(R)N F/D\L T A I/P C/A N H K(M)	C:Carbamidomethylation	138.13	500.9145	1500.726	0.0026	1.7	6.74	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
17241	dirMS_041712_NAR_60mM_plus.19342.19342.3	3	6.94	1	2.50E+04		(K)RSIQFVD	(K)R S I Q F\V/D/W C/P T G F K(V)	C:Carbamidomethylation	159.1	580.9558	1740.853	0.0002	0.1	8.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
17242	dirMS_041712_NAR_60mM_plus.5736.5736.3	3	6.94	0	1.87E+05		(R)STFETEH	(R)S T|F/E/T E/H A/G Q R(D)		88.4	421.5294	1262.576	-0.0024	-1.9	5.38	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
17243	dirMS_041712_NAR_120mM_minus.12150.12150.3	3	6.93	1	4.14E+04		(R)FPGQLN	(R)F/P G\Q L N/A D L R K(L)		120.47	420.2348	1258.69	-0.0004	-0.3	8.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
17244	dirMS_041712_NAR_120mM_minus.13495.13495.3	3	6.93	0	6.42E+04	M46m M4	(R)HQGVm	(R)H Q/G\V\m|V|G\m/G Q/K(D)	m:Oxidized methionine	127.75	401.8604	1171.571	31.9956	4.8	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
17245	dirMS_041712_NAR_20mM_minus.9794.9794.2	2	6.93	0	3.36E+05		(K)IGGIGTV	(K)I G/G|I/G/T V P V G R(V)		147.47	513.3075	1025.61	-0.0025	-2.4	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
17246	dirMS_041712_NAR_30mM_minus2.5740.5740.2	2	6.93	0	4.13E+04		(R)AAEDDE	(R)A A/E\D D\E\D D D/V/D T K(K)		85.35	719.2778	1437.55	-0.0016	-1.1	3.5	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
17247	dirMS_041712_NAR_50mM_minus2.14130.14130.3	3	6.93	0	1.50E+05		(K)SIEIPRP	(K)S I|E/I/P R P V D G V\E V/P G C G K(I)	C:Carbamidomethylation	148.28	636.9917	1908.985	-0.0242	-12.7	4.68	34243.5	4.88	HUMAN	K7ENG2	Splicing factor U2AF 65 kDa subunit
17248	dirMS_041712_NAR_50mM_minus2.18004.18004.3	3	6.93	1	1.77E+05		(R)ALSAQA	(R)A L S/A Q A Y L/L F Y E R V L(-)		171	586.3248	1756.963	-0.0034	-1.9	6.04	87539.7	7.78	HUMAN	E2QRF0	Ubiquitin carboxyl-terminal hydrolase
17249	dirMS_041712_NAR_50mM_minus2.6074.6074.3	3	6.93	0	5.24E+03	M145m	(K)EQEPmP	(K)E Q E/P m/P T V/D/S H E/P R(L)	m:Oxidized methionine	97.45	556.5819	1651.738	15.9931	-1.1	4.4	18962.9	9.6	HUMAN	A6NGP5	Hematological and neurological-expressed 1-like protein
17250	dirMS_041712_NAR_60mM_minus.5590.5590.3	3	6.93	1	2.78E+05		(K)EAEGAP	(K)E A E/G A/P Q/V E A G K R(L)		87.38	447.8959	1341.676	-0.0026	-1.9	4.79	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
17251	dirMS_041712_NAR_60mM_minus.9660.9660.3	3	6.93	0	1.70E+06		(K)VFEHDS	(K)V F E H D/S V/E/L/N C/K(M)	C:Carbamidomethylation	112.55	492.8981	1476.679	0.001	0.7	4.65	31975.7	6.55	HUMAN	P10768	S-formylglutathione hydrolase
17252	dirMS_041712_NAR_120mM_plus.10996.10996.3	3	6.93	0	5.51E+05		(R)GFCLPP	(R)G F\C L/P/P/H C S/R(G)	C:Carbamidomethylation	109.88	410.8593	1230.551	0.0127	10.3	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
17253	dirMS_041712_NAR_120mM_plus.21202.21202.4	4	6.93	1	2.30E+05		(K)AAIDWF	(K)A A\I D/W/F D G K/E/F H G N I I K(V)		164.62	491.0027	1960.992	-0.0026	-1.3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
17254	dirMS_041712_NAR_120mM_plus.6280.6280.3	3	6.93	0	7.73E+05		(K)QRPQAT	(K)Q R/P Q A\T|A/E Q/I/R(L)		86.05	433.2367	1297.697	-0.0016	-1.2	9.6	113668.7	6.2	HUMAN	F8W726	Ubiquitin-associated protein 2-like
17255	dirMS_041712_NAR_20mM_plus.10176.10176.2	2	6.93	0	2.01E+05		(K)LSDGVA	(K)L/S/D/G/V A V L K(V)		143.02	451.2712	901.535	-0.0002	-0.2	5.84	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
17256	dirMS_041712_NAR_20mM_plus.10802.10802.2	2	6.93	0	8.63E+04		(R)FLEQQN	(R)F L/E Q Q\N Q V\L/Q|T K(W)		146.73	738.3942	1475.785	-0.0041	-2.8	6	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
17257	dirMS_041712_NAR_20mM_plus.12541.12541.2	2	6.93	0	2.98E+04	M92m	(R)ImNTFS	(R)I m|N T\F/S V V/P S\P K(V)	m:Oxidized methionine	159.52	668.3516	1319.703	15.9931	-1.3	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
17258	dirMS_041712_NAR_20mM_plus.13866.13866.2	2	6.93	0	3.96E+04		(R)LQTSSVI	(R)L Q/T/S S V/L V S/G L R(G)		167.4	630.3666	1259.732	-0.0059	-4.6	9.75	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
17259	dirMS_041712_NAR_20mM_plus.7371.7371.2	2	6.93	0	2.44E+05		(R)TVGIVGI	(R)T V|G I|V G N Q/P K(V)		119.85	506.7922	1012.579	-0.0014	-1.4	8.41	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
17260	dirMS_041712_NAR_30mM_plus2.10274.10274.2	2	6.93	0	4.96E+05		(R)GVNVSA	(R)G V|N/V/S A L S R(D)		106.6	451.7509	902.505	-0.0109	-12.1	9.75	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
17261	dirMS_041712_NAR_30mM_plus2.4686.4686.2	2	6.93	0	2.80E+05		(R)MDDYCI	(R)M/D|D/Y C R(R)	C:Carbamidomethylation	75.32	430.1579	859.307	0.0012	1.4	4.21	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
17262	dirMS_041712_NAR_40mM_plus2.10968.10968.3	3	6.93	0	9.41E+04	M35m	(K)AASDIA	(K)A A S D I A|m/T E L/P P T H P I R(L)	m:Oxidized methionine	130.8	612.652	1819.937	16.0044	5.1	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
17263	dirMS_041712_NAR_40mM_plus2.17431.17431.3	3	6.93	1	2.55E+04		(R)NAAALS	(R)N A/A\A L/S/Q/A L R L/E A/P E L P V/K(V)		169.55	664.3784	1991.128	-0.0078	-3.9	6.14	10558	9.4	HUMAN	H0YE28	Protein C11orf31 (Fragment)
17264	dirMS_041712_NAR_40mM_plus2.20136.20136.3	3	6.93	0	1.76E+05		(R)DALSDL	(R)D A|L/S D L/A L H F L N K(M)		190.72	486.2654	1456.78	0.0022	1.5	5.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
17265	dirMS_041712_NAR_40mM_plus2.7134.7134.2	2	6.93	0	3.50E+04		(K)LDSLTYK	(K)L D/S/L T Y/K(I)		102.03	420.2265	839.451	-0.0052	-6.2	5.83	30810.8	4.73	HUMAN	Q5T1P5	Chloride channel CLIC-like 1
17266	dirMS_041712_NAR_50mM_plus2.18571.18571.3	3	6.93	0	1.81E+05	M195m	(R)LHFFmP	(R)L H\F\F\m|P G|F|A/P L T S/R(G)	m:Oxidized methionine	164.68	546.2803	1620.835	15.9908	-2.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
17267	dirMS_041712_NAR_50mM_plus2.19809.19809.3	3	6.93	0	3.74E+05		(K)NGGLGH	(K)N/G G/L G\H M N\I A|L/L\S D L T K(Q)		173.03	585.311	1753.927	-0.0081	-4.6	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
17268	dirMS_041712_NAR_50mM_plus2.8080.8080.3	3	6.93	0	7.80E+04		(K)QEYDES	(K)Q E\Y D\E/S/G/P/S/I V H R(K)		109.4	506.2382	1516.703	-0.0026	-1.7	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
17269	dirMS_041712_NAR_50mM_plus2.9456.9456.3	3	6.93	1	1.73E+05		(R)DYQDN	(R)D Y/Q/D N K A D V I L/K(Y)		116.97	474.5801	1421.727	-0.0013	-0.9	4.43	16556.2	5.07	HUMAN	O14602	Eukaryotic translation initiation factor 1A, Y-chromosomal
17270	dirMS_041712_NAR_50mM_plus2.9931.9931.3	3	6.93	0	1.78E+05	M72m	(K)STTSDIP	(K)S T/T/S/D I P H m L N Q V E S K(V)	m:Oxidized methionine	119.57	601.6245	1786.864	15.995	0	5.3	11532.2	6.34	HUMAN	H0YNA1	Protein FAM98B (Fragment)
17271	dirMS_041712_NAR_60mM_plus.11264.11264.2	2	6.93	1	3.54E+05		(K)LTSDDVI	(K)L T/S/D|D\V K E\Q\I/Y/K(L)		116.4	719.8737	1438.742	-0.0023	-1.6	4.56	12573.5	10.39	HUMAN	E9PS50	40S ribosomal protein S13 (Fragment)
17272	dirMS_041712_NAR_60mM_plus.12908.12908.3	3	6.93	1	5.25E+05		(K)ESNGPV	(K)E/S N/G P V\K V/W G S I/K(G)		124.25	467.5853	1400.753	-0.0119	-8.5	8.69	16163.7	5.7	HUMAN	P00441	Superoxide dismutase [Cu-Zn]
17273	dirMS_041712_NAR_20mM_minus.14696.14696.2	2	6.92	0	1.37E+05		(R)IITLAGP	(R)I I T/L/A/G\P T N A I F K(A)		202.15	679.9047	1358.804	-0.0021	-1.5	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
17274	dirMS_041712_NAR_30mM_minus2.11193.11193.2	2	6.92	0	3.89E+05		(R)NTDEM	(R)N T|D/E|M V/E L/R(I)		115.05	553.7611	1106.515	0.0003	0.2	4.14	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
17275	dirMS_041712_NAR_30mM_minus2.12515.12515.2	2	6.92	0	1.25E+05		(R)TIGISVD	(R)T\I/G|I|S V D|P R(R)		121.77	479.2746	957.536	0.0056	5.8	5.5	14749.1	12.2	HUMAN	J3QSB4	60S ribosomal protein L13 (Fragment)
17276	dirMS_041712_NAR_30mM_minus2.13223.13223.2	2	6.92	0	4.80E+05		(K)IYFMAG	(K)I/Y/F|M A/G S S R(K)		126.58	516.2552	1031.498	0.0052	5.1	8.75	92752.5	4.76	HUMAN	P14625	Endoplasmin
17277	dirMS_041712_NAR_30mM_minus2.15657.15657.2	2	6.92	0	3.51E+05		(K)LLYNNV	(K)L/L|Y/N/N V|S N/F G R(L)		137.97	648.8355	1296.67	-0.0058	-4.5	8.75	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
17278	dirMS_041712_NAR_30mM_minus2.4553.4553.2	2	6.92	0	8.93E+05		(K)QASEGP	(K)Q A/S/E G/P/L/K(G)		75.68	415.2235	829.441	-0.0017	-2	6	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
17279	dirMS_041712_NAR_30mM_minus2.5514.5514.2	2	6.92	0	1.16E+05		(R)QLAAEE	(R)Q/L/A/A/E/E/E R(R)		84.25	473.2359	945.464	0.0009	1	4.25	533778	5.74	HUMAN	Q15149	Plectin
17280	dirMS_041712_NAR_40mM_minus2.12776.12776.3	3	6.92	0	3.09E+05		(R)DVQIGD	(R)D V Q\I/G/D I V/T V G E C R P L S K(T)	C:Carbamidomethylation	159.6	662.684	1986.033	0.005	2.5	4.56	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
17281	dirMS_041712_NAR_50mM_minus2.10684.10684.3	3	6.92	0	2.71E+05		(K)VFEGNR	(K)V/F/E/G N R P/T N S I V F T K(L)		129.15	570.3032	1708.902	-0.0066	-3.9	8.72	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
17282	dirMS_041712_NAR_50mM_minus2.16614.16614.3	3	6.92	0	4.48E+05		(R)VLDPFTI	(R)V/L D/P F T I K/P L D/R(K)		162	471.9411	1413.81	-0.0013	-0.9	5.93	63448.4	7.29	HUMAN	B4E022	Transketolase
17283	dirMS_041712_NAR_60mM_minus.15212.15212.3	3	6.92	1	4.91E+04		(K)YMACCL	(K)Y M/A C C L L/Y R G D V V/P K(E)	C:Carbamidomethylation	145.53	615.6321	1844.886	-0.0038	-2.1	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
17284	dirMS_041712_NAR_60mM_minus.15440.15440.3	3	6.92	1	1.77E+05		(R)ASLISAV	(R)A/S/L/I/S/A V/S D K L R(W)		146.23	420.5811	1259.732	-0.003	-2.4	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
17285	dirMS_041712_NAR_60mM_minus.5571.5571.3	3	6.92	1	6.15E+04	M22m	(K)EmDEED	(K)E m/D E/E D K/A/F/K(Q)	m:Oxidized methionine	87.2	419.8485	1241.535	15.9955	0.5	4.18	7066.2	10	HUMAN	Q9Y2S6	Translation machinery-associated protein 7
17286	dirMS_041712_NAR_20mM_plus.18079.18079.2	2	6.92	0	1.71E+05		(K)DAGVIA	(K)D A G\V/I/A/G L\N V L R(I)		196.7	599.3505	1197.695	-0.0013	-1.1	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
17287	dirMS_041712_NAR_20mM_plus.19237.19237.3	3	6.92	0	2.77E+05		(R)LAGTQP	(R)L A\G T Q P\L E V L/E/A\V Q/R(S)		204.3	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
17288	dirMS_041712_NAR_30mM_plus2.19536.19536.2	2	6.92	0	1.85E+04		(K)MNEFLE	(K)M N\E\F|L/E/N F E\K(N)		155.87	650.7974	1300.588	-0.0003	-0.2	4.25	28580.2	9.35	HUMAN	Q9UFN0	Protein NipSnap homolog 3A
17289	dirMS_041712_NAR_40mM_plus2.13319.13319.3	3	6.92	1	1.17E+05		(R)ETFEKTP	(R)E T/F E K T P V\E/V/P V G G F/K(G)		144.53	588.6444	1763.921	-0.0028	-1.6	4.79	533778	5.74	HUMAN	Q15149	Plectin
17290	dirMS_041712_NAR_40mM_plus2.7790.7790.2	2	6.92	0	1.91E+04		(R)SEGFDT	(R)S E/G/F|D\T Y R(C)		105.63	487.7152	974.421	0.0017	1.8	4.37	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
17291	dirMS_041712_NAR_50mM_plus2.11756.11756.3	3	6.92	0	3.17E+04		(K)SNMGH	(K)S N/M G H P E P A/S/G L|A/A L A K(V)		130.23	550.9462	1650.827	-0.0028	-1.7	6.47	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
17292	dirMS_041712_NAR_50mM_plus2.17566.17566.3	3	6.92	0	1.52E+05		(K)VSHLLGI	(K)V S H L L G I|N|V/T D F T R(G)		160.52	524.6245	1571.854	0.0049	3.1	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
17293	dirMS_041712_NAR_50mM_plus2.18855.18855.3	3	6.92	1	4.36E+05		(K)AAIDWF	(K)A/A/I/D/W F D\G K E F S G N P I K(V)		167.18	632.3186	1894.933	0.0079	4.1	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
17294	dirMS_041712_NAR_60mM_plus.13436.13602.3	3	6.92	1	6.19E+06		(R)VVDLM	(R)V/V/D\L M\A H M A S/K/E(-)		127.22	444.2219	1330.649	0.0018	1.3	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
17295	dirMS_041712_NAR_60mM_plus.17369.17369.3	3	6.92	1	3.74E+05		(R)KVPGVT	(R)K\V P G V T A I E/L/D E D T/G T F R(I)		148.18	650.0017	1948.002	-0.0117	-6	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
17296	dirMS_041712_NAR_60mM_plus.18438.18438.3	3	6.92	0	2.09E+05		(K)DHGLEV	(K)D H G\L\E\V|L/G\L V R(V)		153.65	403.2318	1207.679	0.0015	1.2	5.32	17732.8	5.85	HUMAN	F5GYJ1	U8 snoRNA-decapping enzyme
17297	dirMS_041712_NAR_120mM_minus.10960.10960.3	3	6.91	1	2.36E+05		(R)TNEKVE	(R)T N/E K V E L Q/E L/N D R(F)		114.1	529.9368	1587.797	-0.0014	-0.9	4.41	49709.6	5.19	HUMAN	B0YJC4	Vimentin
17298	dirMS_041712_NAR_30mM_minus2.15356.15356.2	2	6.91	0	4.30E+05	M2249m	(K)MSIYQA	(K)M/S|I/Y/Q/A m W K(G)	m:Oxidized methionine	136.15	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
17299	dirMS_041712_NAR_30mM_minus2.18322.18322.2	2	6.91	0	4.28E+05		(R)QAQEYE	(R)Q\A Q E/Y/E/A L L/N/I K(V)		154.63	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
17300	dirMS_041712_NAR_50mM_minus2.11606.11606.3	3	6.91	1	1.89E+04		(R)IVLANDI	(R)I/V|L/A N D P D A D R L A V A E K(Q)		134.4	603.9924	1809.97	-0.0079	-4.3	4.23	32837.5	6.16	HUMAN	B4E0G8	Phosphoglucomutase-2
17301	dirMS_041712_NAR_50mM_minus2.8458.8458.3	3	6.91	1	1.02E+05		(R)YESLTDF	(R)Y E|S L/T/D\P S K L D S G K(E)		116.12	513.9233	1539.754	0.0017	1.1	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
17302	dirMS_041712_NAR_60mM_minus.18477.18477.3	3	6.91	1	8.06E+03	K1374k	(R)IGNGVP	(R)I/G N G V P S T/P L I L/E R/T/k(D)	k:Ubiquitin-K	164.4	603.6759	1694.98	114.0332	-5.4	8.75	240963.9	5.95	HUMAN	F8W6X9	Protein sidekick-1
17303	dirMS_041712_NAR_120mM_plus.11319.11319.3	3	6.91	1	1.75E+05	M406m	(R)QLREYQ	(R)Q/L R E Y\Q/E/L m N V/K(L)	m:Oxidized methionine	112.53	522.9357	1550.8	15.993	-1.2	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
17304	dirMS_041712_NAR_120mM_plus.16143.16226.4	4	6.91	1	1.23E+06		(R)YAEIVHL	(R)Y A|E I V/H L T L/P\D/G T K/R(S)		138.9	428.9885	1712.933	-0.0008	-0.5	6.75	21230	6.36	HUMAN	H0YC04	V-type proton ATPase subunit B, brain isoform (Fragment)
17305	dirMS_041712_NAR_120mM_plus.18249.18249.4	4	6.91	1	6.11E+05		(K)ILGSGIS	(K)I L G S G I S/S/S S V L H G M/V F K K(E)		148.82	487.5232	1947.073	-0.0022	-1.1	10	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
17306	dirMS_041712_NAR_120mM_plus.21235.21235.3	3	6.91	2	3.96E+05		(R)TLAEIAK	(R)T L|A E/I/A K V E L/D N M P L R G K(Q)		164.18	666.7047	1998.105	-0.0057	-2.8	5.85	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
17307	dirMS_041712_NAR_20mM_plus.14197.14197.2	2	6.91	0	8.67E+04		(K)GVVDSD	(K)G V|V/D S/D D/L|P L\N V\S R(E)		170.27	743.3789	1485.754	-0.0038	-2.6	3.93	92752.5	4.76	HUMAN	P14625	Endoplasmin
17308	dirMS_041712_NAR_20mM_plus.7667.7667.2	2	6.91	0	5.63E+04	M1614m	(R)VmGLVF	(R)V/m/G L V/P A K(G)	m:Oxidized methionine	122.17	415.7382	814.486	15.9836	-13.6	8.72	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
17309	dirMS_041712_NAR_30mM_plus2.14413.14413.2	2	6.91	0	2.58E+05		(R)ELFEMA	(R)E/L/F/E/M A\R(T)		128.82	448.2205	895.434	-0.0005	-0.5	4.53	33615.3	9.15	HUMAN	B7Z5E2	26S protease regulatory subunit 7
17310	dirMS_041712_NAR_30mM_plus2.21126.21126.2	2	6.91	0	3.28E+05		(K)TIFAYFT	(K)T I|F\A/Y F T G S K(D)		165.13	567.7949	1134.583	-0.0005	-0.4	8.26	8599.5	5.51	HUMAN	I3L0K2	Thioredoxin domain-containing protein 17
17311	dirMS_041712_NAR_30mM_plus2.5750.5750.2	2	6.91	0	5.89E+05		(R)QQEEMI	(R)Q\Q/E/E/M M/R(R)		83.88	476.2056	951.402	0.0017	1.7	4.53	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
17312	dirMS_041712_NAR_40mM_plus2.11006.11006.3	3	6.91	0	1.70E+04		(R)MLTGPV	(R)M L/T/G P V Y/S Q S/T A L T/H K(Q)		130.95	578.6331	1733.889	-0.0043	-2.5	8.37	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
17313	dirMS_041712_NAR_40mM_plus2.13427.13427.3	3	6.91	0	2.43E+05		(K)SIEIPRP	(K)S I|E/I/P R\P V D G V E V|P G C G K(I)	C:Carbamidomethylation	145.88	637.0002	1908.985	0.0013	0.7	4.68	34243.5	4.88	HUMAN	K7ENG2	Splicing factor U2AF 65 kDa subunit
17314	dirMS_041712_NAR_40mM_plus2.20079.20079.3	3	6.91	1	5.86E+05		(K)EGGLGP	(K)E G G L/G/P L/N I/P L L A D V T R R(L)		189.82	631.0288	1891.076	-0.0041	-2.2	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
17315	dirMS_041712_NAR_50mM_plus2.10574.10574.3	3	6.91	0	5.27E+05		(K)MIVDPV	(K)M I\V D/P V E/P H/G E M K(F)		123.17	494.5783	1481.713	0.0076	5.2	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
17316	dirMS_041712_NAR_50mM_plus2.5944.5944.3	3	6.91	0	8.73E+04		(K)AVTEQG	(K)A V/T E/Q G H/E L/S N E E R(N)		95.48	533.5846	1598.741	-0.0013	-0.8	4.48	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
17317	dirMS_041712_NAR_60mM_plus.20674.20674.3	3	6.91	1	2.54E+05		(R)KVESLW	(R)K V E S L W/P I/F R(I)		169.53	425.5789	1274.726	-0.0034	-2.7	8.75	14138.1	9.89	HUMAN	C9JNV2	Protein BUD31 homolog
17318	dirMS_041712_NAR_120mM_minus.12207.12403.4	4	6.9	2	1.34E+06		(R)EGPEEP	(R)E G P E E/P G L A K/Q D S/F R S R(L)		120.08	476.4927	1902.93	0.0185	9.7	4.87	96735.1	9.2	HUMAN	J3KPS2	Protein FAM83H (Fragment)
17319	dirMS_041712_NAR_120mM_minus.7157.7157.3	3	6.9	1	3.75E+05	M71m	(R)VNEARE	(R)V/N/E/A R E E L/m\R(M)	m:Oxidized methionine	92.97	421.542	1246.621	15.9906	-3.4	4.79	16201.6	6.74	HUMAN	B7ZB63	ADP-ribosylation factor 3
17320	dirMS_041712_NAR_30mM_minus2.9118.9118.2	2	6.9	0	1.04E+05		(K)LSTHLG	(K)L/S/T H L G G/R(C)		103.95	420.7416	840.469	0.0073	8.7	9.75	6001.7	10.27	HUMAN	F8WED2	CTD small phosphatase-like protein
17321	dirMS_041712_NAR_50mM_minus2.10774.10774.3	3	6.9	1	2.88E+05		(K)NQVAM	(K)N Q/V|A M/N/P T/N T V F D A K R(L)		129.02	602.6379	1805.896	0.0029	1.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
17322	dirMS_041712_NAR_50mM_minus2.9762.9762.3	3	6.9	0	2.46E+05		(K)TSEVDL	(K)T/S|E V D L A K/P L V K(F)		123.2	433.9205	1299.752	-0.0049	-3.8	5.73	17178.3	5.63	HUMAN	C9IZF9	Programmed cell death 6-interacting protein (Fragment)
17323	dirMS_041712_NAR_60mM_minus.11371.11371.3	3	6.9	1	2.49E+05		(K)NQLTSN	(K)N Q|L/T/S/N/P E N T V/F D A K R(L)		123.97	611.9739	1833.909	-0.0018	-1	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
17324	dirMS_041712_NAR_60mM_minus.18473.18473.3	3	6.9	0	6.05E+04		(R)HATALEI	(R)H A\T A L\E\E|L\S/E/Q L/E Q A K(R)		164.37	599.64	1796.902	0.003	1.6	4.48	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
17325	dirMS_041712_NAR_60mM_minus.9599.9599.3	3	6.9	0	2.26E+04		(R)ENVFQE	(R)E N/V/F Q E H Q/T L/K(E)		111.92	458.2344	1372.686	0.0031	2.3	5.4	25153.2	6.6	HUMAN	H7C314	Src substrate cortactin (Fragment)
17326	dirMS_041712_NAR_120mM_plus.14143.14143.4	4	6.9	1	5.79E+05		(R)LEAPELP	(R)L E|A P E/L/P V K V N P T K P R(R)		127.33	447.7616	1788.038	-0.0132	-7.4	8.59	10558	9.4	HUMAN	H0YE28	Protein C11orf31 (Fragment)

17327	dirMS_041712_NAR_120mM_plus.4204.4204.2	2	6.9	1	1.40E+06	M310m	(R)TKTEISE	(R)T/K|T|E/I S E m N R(N)	m:Oxidized methionine	69.85	612.7976	1208.594	15.994	-0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
17328	dirMS_041712_NAR_120mM_plus.4455.4455.3	3	6.9	1	3.00E+05		(R)AAEEED	(R)A A\E/E E/D/E A D/P K R(Q)		72.4	453.8721	1359.602	-0.0005	-0.4	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
17329	dirMS_041712_NAR_20mM_plus.11480.11480.2	2	6.9	0	2.08E+05		(K)VGLQVV	(K)V G L/Q|V V/A V/K(A)		151.53	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
17330	dirMS_041712_NAR_20mM_plus.19038.19038.3	3	6.9	0	6.34E+04		(K)DTSYLFI	(K)D T S Y L F I/T/G/P D V V K(S)		201.93	518.9378	1554.805	-0.0062	-4	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
17331	dirMS_041712_NAR_20mM_plus.5986.5986.3	3	6.9	0	1.02E+06	M295m M	(R)mGQmA	(R)m G Q\m A\m G G|A|m|G\I/N N R(G)	m:Oxidized methionine	100.27	534.8861	1538.67	63.9743	-3.4	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
17332	dirMS_041712_NAR_20mM_plus.7439.7439.2	2	6.9	0	1.14E+05		(K)AQYEDI	(K)A Q/Y/E/D I|A N R(S)		120.38	540.2601	1079.512	0.0013	1.2	4.37	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
17333	dirMS_041712_NAR_20mM_plus.9298.9298.3	3	6.9	0	3.09E+04		(R)SVSLTG	(R)S V S L T G A/P E/S V/Q K(A)		135.52	434.9007	1302.69	-0.0024	-1.9	5.72	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
17334	dirMS_041712_NAR_30mM_plus2.12887.12887.2	2	6.9	0	3.40E+05		(R)LLVVTD	(R)L L|V/V T D/P/R(A)		120.38	456.779	912.551	-0.0006	-0.6	5.84	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
17335	dirMS_041712_NAR_30mM_plus2.20167.20167.2	2	6.9	0	1.43E+05		(K)NIEDVIA	(K)N I/E/D/V|I/A Q G I/G K(L)		160.3	628.8445	1256.685	-0.0028	-2.2	4.37	9098.8	4.38	HUMAN	H0YDD8	60S acidic ribosomal protein P2 (Fragment)
17336	dirMS_041712_NAR_30mM_plus2.20718.20718.2	2	6.9	0	2.45E+05		(R)YLTVAA	(R)Y L/T\V/A A V F R(G)		162.38	520.2996	1039.593	-0.0016	-1.5	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
17337	dirMS_041712_NAR_30mM_plus2.22519.22519.2	2	6.9	0	6.10E+04		(R)LEGLTD	(R)L E/G L/T/D E I N/F L R(Q)		174.63	710.3766	1419.748	-0.0019	-1.3	4.14	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
17338	dirMS_041712_NAR_30mM_plus2.5208.5208.2	2	6.9	0	4.06E+05		(K)VSSFEEK	(K)V/S/S F E|E K(M)		81.18	413.203	825.399	-0.0002	-0.2	4.53	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
17339	dirMS_041712_NAR_30mM_plus2.6038.6038.2	2	6.9	0	1.72E+05		(R)GGSGGS	(R)G G S G\G S Y/G G G/G/S/G/G G Y G G G S G S R(G)		85.83	896.3659	1791.728	-0.0032	-1.8	8.59	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
17340	dirMS_041712_NAR_40mM_plus2.10396.10396.2	2	6.9	0	2.39E+04		(R)CNNVLY	(R)C N\N|V/L/Y/I/R(G)	C:Carbamidomethylation	125.85	526.2705	1051.535	-0.0016	-1.5	8.75	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F
17341	dirMS_041712_NAR_40mM_plus2.5554.5554.2	2	6.9	0	2.45E+05	M299m	(K)NmMAA	(K)N m/M/A/A C D|P R(H)	C:Carbamidomethylation m:Oxid	89.2	541.2145	1065.427	15.9943	-0.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
17342	dirMS_041712_NAR_50mM_plus2.14046.14046.3	3	6.9	0	1.58E+06	M457m	(R)mGPLGL	(R)m/G P L/G L/D H M/A S S I E/R(M)	m:Oxidized methionine	142.5	543.9304	1613.777	15.9992	2.6	5.3	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
17343	dirMS_041712_NAR_50mM_plus2.16249.16249.3	3	6.9	0	2.89E+05		(K)ACQSIYF	(K)A C/Q/S I Y/P/L H D V F V R(K)	C:Carbamidomethylation	154.4	568.9562	1704.853	0.0014	0.8	6.79	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
17344	dirMS_041712_NAR_50mM_plus2.18082.18082.3	3	6.9	1	4.26E+05		(K)ASIAQA	(K)A S/I/A Q A/V R D G L\L/P T G L\G/Q R(L)		162.9	641.6959	1923.077	-0.0039	-2	9.64	266161	5.68	HUMAN	E9PPU0	Epiplakin
17345	dirMS_041712_NAR_50mM_plus2.18615.18615.3	3	6.9	0	1.81E+05		(K)ASVITQ	(K)A S/V/I/T Q V F H V/P\L E E R(K)		166.42	575.6533	1724.933	0.0124	7.2	5.4	24511.6	6.62	HUMAN	C9J5E5	Vigilin (Fragment)
17346	dirMS_041712_NAR_50mM_plus2.7396.7396.3	3	6.9	1	1.18E+05		(K)AAIAQL	(K)A/A/I/A/Q L N G K E/V K(G)		104.82	414.5758	1241.721	-0.0084	-6.7	8.64	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
17347	dirMS_041712_NAR_60mM_plus.10904.10904.3	3	6.9	0	6.53E+05		(R)ISNRPAF	(R)I/S/N R P A\F\M|P S/E G K(M)		114.83	478.578	1433.721	-0.0011	-0.8	8.75	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
17348	dirMS_041712_NAR_60mM_plus.11463.11463.3	3	6.9	1	8.44E+05	M406m	(R)QLREYQ	(R)Q L/R E Y Q/E/L m N V/K(L)	m:Oxidized methionine	116.7	522.9381	1550.8	16.0002	3.4	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
17349	dirMS_041712_NAR_60mM_plus.18795.18795.3	3	6.9	0	7.04E+04		(R)LYDLNH	(R)L/Y/D\L/N H N E I G/E L\I R(M)		155.95	566.9611	1698.881	-0.0122	-7.2	4.65	246157.8	5.73	HUMAN	O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase
17350	dirMS_041712_NAR_60mM_plus.18846.18846.3	3	6.9	1	3.96E+06		(R)VSFELFA	(R)V/S|F E L F A D K V/P/K(T)		155.83	460.5914	1379.757	0.0027	2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
17351	dirMS_041712_NAR_120mM_minus.15384.15384.3	3	6.89	2	9.57E+05		(R)ALKDEEI	(R)A L K|D E E K M E/L|Q E I|Q/L K(E)		137.72	649.0139	1945.031	-0.0039	-2	4.58	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
17352	dirMS_041712_NAR_120mM_minus.7764.7764.2	2	6.89	1	7.85E+04		(K)TKFENL	(K)T/K/F E|N L/C K(I)	C:Carbamidomethylation	96.7	520.2689	1039.524	0.0064	6.2	8.26	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
17353	dirMS_041712_NAR_120mM_minus.8665.8665.3	3	6.89	0	6.78E+05		(R)SNTENL	(R)S N/T/E N L/S/Q H/F|R(K)		101.78	444.8813	1332.629	0.0002	0.2	6.47	43303.4	8.7	HUMAN	F8VRN8	LIM domain and actin-binding protein 1
17354	dirMS_041712_NAR_120mM_minus.9860.9860.3	3	6.89	1	2.01E+05		(R)SRSGEG	(R)S R S G E G E\V/S/G L M R(K)		108.07	455.559	1364.659	0.0038	2.8	5.87	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
17355	dirMS_041712_NAR_30mM_minus2.11406.11406.2	2	6.89	0	1.40E+05		(R)AATSPA	(R)A A|T S/P/A L/F N R(C)		115.4	524.2789	1047.558	-0.0076	-7.3	9.79	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
17356	dirMS_041712_NAR_30mM_minus2.12271.12271.2	2	6.89	0	1.51E+05		(K)LMVELSI	(K)L M|V/E/L S K(S)		121.08	410.242	819.465	0.0123	15	6	55804.4	5.33	HUMAN	B7ZAR1	T-complex protein 1 subunit epsilon
17357	dirMS_041712_NAR_30mM_minus2.13895.13895.2	2	6.89	0	3.41E+05		(R)LAGLFNI	(R)L/A|G L/F/N E Q/R(K)		129.18	524.2789	1047.558	-0.0076	-7.3	6	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
17358	dirMS_041712_NAR_40mM_minus2.10883.10883.3	3	6.89	1	1.14E+05	M362m	(R)EGSVmL	(R)E G/S V/m|L Q/V D V D T V K G G L K(L)	m:Oxidized methionine	147.85	630.9989	1874.989	15.993	-1	4.56	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
17359	dirMS_041712_NAR_50mM_minus2.15149.15149.3	3	6.89	0	2.79E+05	M118m	(R)AGKPVI	(R)A G K\P V I/C A|T/Q M/L/E S m I K(K)	C:Carbamidomethylation m:Oxid	154.6	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
17360	dirMS_041712_NAR_50mM_minus2.15400.15400.3	3	6.89	0	3.84E+05	M118m	(R)AGKPVI	(R)A G K P V I C A T\Q/M/L|E|S/m I K(K)	C:Carbamidomethylation m:Oxid	155.5	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
17361	dirMS_041712_NAR_50mM_minus2.16540.16540.3	3	6.89	0	9.06E+04		(R)LLLDIPL	(R)L L|L D I/P L/Q T P/H K(L)		162.37	463.2805	1387.831	-0.0038	-2.7	6.74	198852.6	5.95	HUMAN	A6NKT7	RanBP2-like and GRIP domain-containing protein 3
17362	dirMS_041712_NAR_60mM_minus.11914.11914.3	3	6.89	1	4.82E+04		(K)TLGTMI	(K)T L|G|T/M I A G D/T S G D Y R R(L)		126.4	571.9448	1713.823	-0.0026	-1.5	5.63	38089.6	6.79	HUMAN	B4DT77	Annexin
17363	dirMS_041712_NAR_60mM_minus.17542.17542.3	3	6.89	0	2.41E+05		(K)GSDHSA	(K)G S D H S A S L E|P/G E L/A/E L/V R(S)		157.1	622.9764	1866.919	-0.0045	-2.4	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
17364	dirMS_041712_NAR_120mM_plus.18805.18805.4	4	6.89	0	3.69E+05		(K)APIRPDI	(K)A/P I R P D I/V N F V H T N L R(K)		151.55	466.2639	1862.04	-0.0058	-3.1	9.65	18988.7	11.2	HUMAN	H3BTP7	60S ribosomal protein L4 (Fragment)
17365	dirMS_041712_NAR_120mM_plus.4061.4061.3	3	6.89	0	3.37E+05		(R)FAGHSE	(R)F A G H S E A/G/G/G S G/D R(R)		67.78	435.5253	1304.561	-0.0001	-0.1	5.32	64356.2	9.96	HUMAN	O96013	Serine/threonine-protein kinase PAK 4
17366	dirMS_041712_NAR_120mM_plus.5420.5420.3	3	6.89	0	3.85E+04		(R)TGIYSST	(R)T/G I/Y/S S T S C H K(T)	C:Carbamidomethylation	81.43	414.1962	1240.563	0.0114	9.2	8.28	38077.6	8.9	HUMAN	P09668	Pro-cathepsin H
17367	dirMS_041712_NAR_20mM_plus.6708.6708.2	2	6.89	0	2.51E+04		(R)AAPTAA	(R)A A/P T/A\A\S D Q P D S A A T T E K(A)		110.9	866.4036	1731.803	-0.0032	-1.9	4.03	22655.1	9.45	HUMAN	Q9BRP8	Partner of Y14 and mago
17368	dirMS_041712_NAR_20mM_plus.8388.8388.2	2	6.89	0	4.09E+04	M105m	(K)mADEA	(K)m A D\E/A|V C V|G\P A|P T S K(S)	C:Carbamidomethylation m:Oxid	127.8	774.8589	1532.708	16.0022	4.7	4.37	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
17369	dirMS_041712_NAR_30mM_plus2.12424.12424.2	2	6.89	0	4.61E+05		(K)SIYYITGE	(K)S I/Y/Y/I T G E S K(E)		118.45	580.796	1160.583	0.0013	1.2	5.72	16789.1	8.77	HUMAN	H0Y5S7	Heat shock protein HSP 90-beta (Fragment)
17370	dirMS_041712_NAR_30mM_plus2.17355.17355.2	2	6.89	0	4.30E+05		(K)SFNLSAL	(K)S F/N/L/S A L E K(H)		144.1	504.7726	1008.536	0.0019	1.9	5.72	82756.6	5.34	HUMAN	C9JIF9	Acylamino-acid-releasing enzyme
17371	dirMS_041712_NAR_30mM_plus2.18674.18674.3	3	6.89	0	4.97E+05		(R)SSFYVN	(R)S S F Y V N/G L/T L/G G Q/K(C)		150.95	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
17372	dirMS_041712_NAR_30mM_plus2.18717.18717.2	2	6.89	0	3.04E+05		(R)FVNVVP	(R)F V|N\V/V P T F G K(K)		151.4	554.3087	1107.62	-0.0096	-8.7	8.75	10904.6	11.56	HUMAN	E9PR30	40S ribosomal protein S30
17373	dirMS_041712_NAR_30mM_plus2.9080.9224.2	2	6.89	0	4.02E+05		(K)SFYMQR	(K)S F|Y/M Q/R(C)		101.32	416.1955	831.382	0.0019	2.3	8.46	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
17374	dirMS_041712_NAR_40mM_plus2.5655.5655.2	2	6.89	0	1.12E+05		(R)FSSSSGY	(R)F S S/S S/G Y/G G G/S S/R(V)		90.98	618.2686	1235.529	0.0012	1	8.75	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
17375	dirMS_041712_NAR_40mM_plus2.6489.6489.2	2	6.89	1	7.06E+04		(R)YSGGNY	(R)Y/S/G G/N Y R D N Y\D N(-)		96.7	719.2857	1437.567	-0.0024	-1.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
17376	dirMS_041712_NAR_40mM_plus2.7470.7470.3	3	6.89	0	6.28E+03	T40t	(K)HAEAtL	(K)H A\E A\t L/G S/G/N L R(M)	t:Phosphorylated T	104.08	435.8697	1225.628	79.9662	-0.1	6.75	14802.4	4.98	HUMAN	D6RCK3	MOB kinase activator 1B (Fragment)
17377	dirMS_041712_NAR_50mM_plus2.6035.6035.3	3	6.89	1	4.14E+04	M625m M	(K)AQALRD	(K)A Q|A/L R D N\S\T/m G Y m A A K(K)	m:Oxidized methionine	95.82	587.2736	1727.82	31.9859	-2.2	8.63	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
17378	dirMS_041712_NAR_50mM_plus2.8617.8617.3	3	6.89	1	7.17E+04		(R)LATNTS	(R)L/A|T N/T/S A/P D/L K N V R(S)		112.28	500.6117	1499.818	0.0029	1.9	8.75	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
17379	dirMS_041712_NAR_60mM_plus.13635.13635.3	3	6.89	0	6.09E+05		(K)LIHPDED	(K)L I H\P D E D\I|S/L/E E R(R)		128.45	522.6019	1565.781	0.0106	6.8	4.17	53035.1	9.47	HUMAN	E1P660	Zinc finger protein 207
17380	dirMS_041712_NAR_60mM_plus.20453.20453.3	3	6.89	1	7.78E+04		(R)LFVGNLI	(R)L F V/G/N/L/P A D/I T E D E F K R(L)		167.3	655.3407	1964.012	-0.0048	-2.5	4.32	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
17381	dirMS_041712_NAR_60mM_plus.20553.20553.3	3	6.89	1	7.78E+04		(R)LFVGNLI	(R)L F/V G/N/L/P A D I T E D E F K R(L)		167.3	655.3407	1964.012	-0.0048	-2.5	4.32	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
17382	dirMS_041712_NAR_60mM_plus.7245.7245.2	2	6.89	0	5.06E+05		(R)IGKPAP	(R)I G K/P A/P D|F\K(A)		95.78	486.7793	972.551	0	0	8.59	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
17383	dirMS_041712_NAR_30mM_minus2.12787.12787.2	2	6.88	0	2.37E+05		(R)CGYFDE	(R)C/G/Y|F/D E E/M/N/R(I)	C:Carbamidomethylation	122.97	660.7538	1320.498	0.002	1.5	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
17384	dirMS_041712_NAR_30mM_minus2.20079.20079.2	2	6.88	0	8.03E+04		(K)SLNILTA	(K)S L\N\I/L/T A/F Q K(K)		169.83	567.8283	1134.652	-0.0024	-2.1	8.47	18172.6	7.77	HUMAN	F8VY02	Endoplasmic reticulum resident protein 29
17385	dirMS_041712_NAR_50mM_minus2.10225.10225.3	3	6.88	0	1.54E+05	M392m	(K)EmNPAL	(K)E m N/P A L|G I|D C L H K(G)	C:Carbamidomethylation m:Oxid	126	505.2416	1497.719	15.9914	-2.3	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
17386	dirMS_041712_NAR_50mM_minus2.10733.10733.3	3	6.88	0	2.42E+05	M35m	(K)AASDIA	(K)A A/S/D I A/m T/E L P P T H P I R(L)	m:Oxidized methionine	129.05	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
17387	dirMS_041712_NAR_50mM_minus2.12662.12662.3	3	6.88	1	2.07E+05	M2709m	(K)ISmPDID	(K)I/S m/P D/I D L N L K G P K(V)	m:Oxidized methionine	139.82	519.6148	1540.84	15.9895	-3.5	5.96	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
17388	dirMS_041712_NAR_50mM_minus2.17911.17911.3	3	6.88	0	2.29E+05		(R)IHFPLAT	(R)I H F\P L A T Y/A|P/V I S A E K(A)		169.75	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
17389	dirMS_041712_NAR_50mM_minus2.6109.6109.3	3	6.88	0	1.34E+04		(K)TQAYQD	(K)T Q|A/Y Q D Q/K/P G T S G L R(K)		97.55	550.6108	1649.824	-0.0063	-3.8	8.25	61733.3	6.3	HUMAN	P36871	Phosphoglucomutase-1
17390	dirMS_041712_NAR_120mM_plus.10905.10905.4	4	6.88	1	5.61E+05		(K)AVEHINI	(K)A V E H I\N K T I/A|P A L V/S K(K)		110.72	423.5016	1690.985	-0.0005	-0.3	8.64	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
17391	dirMS_041712_NAR_120mM_plus.5278.5278.3	3	6.88	1	1.54E+05		(R)NDDDEE	(R)N D\D/D/E/E E/A/A\R E/R(R)		81.02	483.5401	1448.588	0.0173	12	3.95	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
17392	dirMS_041712_NAR_20mM_plus.10753.10753.2	2	6.88	0	1.38E+04	M33m	(K)VAGmD	(K)V A|G m D/V|E/L T V E E R(N)	m:Oxidized methionine	146.43	732.3555	1447.71	15.994	-0.6	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
17393	dirMS_041712_NAR_20mM_plus.13485.13485.2	2	6.88	0	4.02E+03		(K)SPILVAT	(K)S P I\L|V|A/T A V A A R(G)		165.7	584.8517	1168.705	-0.0087	-7.5	9.47	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
17394	dirMS_041712_NAR_20mM_plus.6757.6757.3	3	6.88	0	1.25E+05	M136m	(R)LVAGEm	(R)L V\A\G/E m G Q N E/P D/Q G G Q R(G)	m:Oxidized methionine	111.45	601.2753	1785.818	15.9929	-1.1	4.14	17508.7	8.03	HUMAN	Q5H928	3-hydroxyacyl-CoA dehydrogenase type-2
17395	dirMS_041712_NAR_20mM_plus.7431.7431.2	2	6.88	0	7.51E+04	M33m	(R)IDEmPE	(R)I/D E|m/P E A A V/K(S)	m:Oxidized methionine	120.15	559.7742	1102.545	15.9962	1.2	4.14	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
17396	dirMS_041712_NAR_20mM_plus.9743.9743.2	2	6.88	0	1.21E+05		(K)VAGQD	(K)V/A|G\Q/D/G S V/V Q F K(I)		138.27	617.8225	1234.643	-0.0049	-4	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
17397	dirMS_041712_NAR_30mM_plus2.20181.20181.2	2	6.88	0	1.43E+05		(K)TVALWD	(K)T V/A|L/W D/L R(N)		159.08	487.2769	973.547	0	0	5.5	19598	4.45	HUMAN	B4DRT0	Histone-binding protein RBBP4
17398	dirMS_041712_NAR_30mM_plus2.5907.5907.2	2	6.88	0	2.05E+05		(R)STSYGYS	(R)S T|S/Y G Y\S/R(S)		85.28	460.7158	920.411	0.0135	14.7	8.31	25655.9	8.94	HUMAN	Q13242	Serine/arginine-rich splicing factor 9
17399	dirMS_041712_NAR_40mM_plus2.9835.9835.3	3	6.88	0	1.23E+05		(R)VMLGET	(R)V M/L|G/E/T N/P A/D S K/P G T I R(G)		122.05	595.9778	1785.916	0.0025	1.4	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
17400	dirMS_041712_NAR_50mM_plus2.21174.21174.3	3	6.88	1	4.22E+05	M145m	(R)GVmLA	(R)G V|m/L A\V D A V I/A E L K K(Q)	m:Oxidized methionine	181.53	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
17401	dirMS_041712_NAR_50mM_plus2.7224.7224.3	3	6.88	1	1.94E+05		(R)DSFDGR	(R)D S|F/D/G R G P P/G/P E S Q S R(A)		103.85	563.592	1688.762	-0.0009	-0.5	4.56	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
17402	dirMS_041712_NAR_60mM_plus.10296.10296.3	3	6.88	1	4.39E+05		(R)RQQEQ	(R)R/Q\Q E Q\Q\V/P I L E/K(F)		111.5	499.2786	1495.823	-0.0015	-1	6.14	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
17403	dirMS_041712_NAR_60mM_plus.12656.12656.3	3	6.88	1	7.43E+05		(K)VFDGIPF	(K)V/F/D G I/P P P/Y D K K(K)		122.93	459.2464	1375.726	-0.001	-0.7	5.93	23633.9	11.02	HUMAN	P40429	60S ribosomal protein L13a
17404	dirMS_041712_NAR_60mM_plus.14389.14389.3	3	6.88	1	1.17E+06		(R)TATWKI	(R)T/A T/W K I Q V E T R(K)		131.55	444.917	1332.727	0.0094	7.1	8.41	57228.3	6.07	HUMAN	Q6AZZ1	E3 ubiquitin-protein ligase TRIM68
17405	dirMS_041712_NAR_60mM_plus.21568.21568.3	3	6.88	1	5.79E+05		(K)EIIDLVL	(K)E I/I/D/L V L D R I R(K)		180.55	452.2733	1354.805	0.0001	0.1	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
17406	dirMS_041712_NAR_60mM_plus.7493.7493.3	3	6.88	1	2.58E+05		(R)AAPGAE	(R)A A/P G A E F/A/P N/K/R(R)		97.4	410.2195	1228.643	0.0007	0.5	8.79	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
17407	dirMS_041712_NAR_120mM_minus.19341.19341.3	3	6.87	1	3.72E+05		(K)NLRDIDI	(K)N L R D I\D\E\V/S S/L L R(T)		161.42	510.614	1529.828	-0.0007	-0.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
17408	dirMS_041712_NAR_120mM_minus.7208.7208.3	3	6.87	1	1.58E+05		(K)DSYVGD	(K)D S|Y/V/G D E/A Q S K R(G)		92.85	452.2134	1354.623	0.0023	1.7	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
17409	dirMS_041712_NAR_20mM_minus.10103.10103.2	2	6.87	0	8.14E+04		(K)STGGAP	(K)S T|G G A|P T F N V/T/V T K(T)		150.73	690.3599	1379.717	-0.004	-2.9	8.47	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
17410	dirMS_041712_NAR_20mM_minus.7465.7465.2	2	6.87	0	1.18E+05		(K)VEIIAND	(K)V E/I/I/A N D Q G N R(T)		122.48	614.8166	1228.628	-0.0021	-1.7	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
17411	dirMS_041712_NAR_50mM_minus2.16104.16275.3	3	6.87	0	2.66E+06	T314t M31	(K)LLASANI	(K)L L/A S A N\L\E/E V t/m K(Q)	t:N-acetylglucosamine (T) m:	159.65	546.6098	1418.756	219.0589	-9.4	4.53	39728.1	8.78	HUMAN	B4DFG0	Protein DEK
17412	dirMS_041712_NAR_60mM_minus.15599.15599.3	3	6.87	1	3.52E+05	S383s	(K)LDsQGK	(K)L/D s Q G K\Y T/L|F R(C)	s:N-acetylglucosamine (S)	147.02	510.9286	1327.7	203.0708	-5.6	8.59	67392.8	5.23	HUMAN	B4DJ85	Glomulin
17413	dirMS_041712_NAR_60mM_minus.17622.17622.3	3	6.87	1	1.41E+05		(R)LGLSTLG	(R)L/G\L\S/T L/G E L K/Q/N L S R(S)		159.27	543.6476	1628.933	-0.0047	-2.9	8.75	22294.4	5.26	HUMAN	O43399	Tumor protein D54
17414	dirMS_041712_NAR_60mM_minus.5870.5870.2	2	6.87	1	2.61E+06		(K)DSYVGD	(K)D/S Y|V/G D/E\A/Q S K\R(G)		88.52	677.8144	1354.623	-0.0018	-1.3	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
17415	dirMS_041712_NAR_20mM_plus.10500.10500.2	2	6.87	0	2.77E+03	M28m	(R)VFQVEY	(R)V/F Q|V/E Y A/m K(A)	m:Oxidized methionine	144.78	565.7823	1114.56	15.9972	2	5.97	3930.3	4.78	HUMAN	G3V3W4	Proteasome subunit alpha type-3
17416	dirMS_041712_NAR_20mM_plus.14567.14567.2	2	6.87	0	3.89E+04	M185m	(K)LAVNm	(K)L/A/V N m/V/P F P R(L)	m:Oxidized methionine	172.75	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
17417	dirMS_041712_NAR_20mM_plus.16323.16323.3	3	6.87	0	1.77E+05		(R)QAQEYE	(R)Q A\Q E\Y E/A/L/L N I K(V)		184.65	473.9191	1419.748	-0.0051	-3.6	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
17418	dirMS_041712_NAR_20mM_plus.7765.7765.3	3	6.87	0	1.06E+05		(K)AQAAA	(K)A Q A A\A\P A/S\V/P A Q A/P K(R)		123.6	459.9204	1377.748	-0.0018	-1.3	8.8	17808.8	11.77	HUMAN	P47914	60S ribosomal protein L29
17419	dirMS_041712_NAR_30mM_plus2.12618.12618.2	2	6.87	0	6.56E+05		(R)TIGISVD	(R)T I/G|I|S V D|P R(R)		118.43	479.2725	957.536	0.0014	1.4	5.5	14749.1	12.2	HUMAN	J3QSB4	60S ribosomal protein L13 (Fragment)
17420	dirMS_041712_NAR_30mM_plus2.15685.15732.2	2	6.87	0	4.57E+05		(R)QMSLLL	(R)Q M/S/L/L/L/R(R)		135.37	430.7564	860.502	0.0033	3.8	9.75	48851.3	9.2	HUMAN	K7EK63	ATP synthase subunit alpha, mitochondrial
17421	dirMS_041712_NAR_30mM_plus2.5514.5514.2	2	6.87	0	6.24E+04		(K)QSQDEP	(K)Q S/Q/D/E/P L R(S)		83.02	486.741	972.475	0.0002	0.2	4.37	33803.8	6.12	HUMAN	B1AKP7	TAR DNA binding protein
17422	dirMS_041712_NAR_30mM_plus2.7257.7257.2	2	6.87	0	6.90E+04		(R)SQLQIS	(R)S Q|L/Q/I/S N N R(T)		92.6	530.2783	1059.554	-0.0048	-4.6	9.47	334221.3	6.44	HUMAN	P15924	Desmoplakin
17423	dirMS_041712_NAR_40mM_plus2.15673.15673.3	3	6.87	1	3.51E+04		(R)IILPPEKE	(R)I I/L/P\P E K E L\A\M/P G E D L K(F)		158.55	631.6874	1893.04	0.0075	4	4.41	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
17424	dirMS_041712_NAR_50mM_plus2.12996.12996.3	3	6.87	1	1.51E+06	M356m	(K)VGEVIV	(K)V/G|E/V/I V T K D D/A m L L K(G)	m:Oxidized methionine	137.12	549.6381	1630.908	15.9913	-2.2	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
17425	dirMS_041712_NAR_50mM_plus2.21194.21194.3	3	6.87	1	4.45E+05	M145m	(R)GVmLA	(R)G V|m/L/A/V D A/V/I/A E L K K(Q)	m:Oxidized methionine	181.6	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
17426	dirMS_041712_NAR_50mM_plus2.21447.21447.3	3	6.87	1	8.47E+04		(K)ITPENLP	(K)I T/P E N L/P Q I L/L Q L K/R(R)		183.3	592.694	1776.074	-0.0067	-3.8	8.75	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
17427	dirMS_041712_NAR_50mM_plus2.7703.7703.3	3	6.87	0	6.60E+04	M378m M	(K)mIVDPV	(K)m I V/D/P V/E P\H/G E m K(F)	m:Oxidized methionine	106.6	505.2419	1481.713	31.9984	5.7	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
17428	dirMS_041712_NAR_50mM_plus2.9166.9166.3	3	6.87	0	1.50E+05		(R)NDIASHI	(R)N D/I/A S H/P/P V E G S Y\A/P R(R)		114.92	570.6114	1709.824	-0.0045	-2.6	5.32	26398.4	5.21	HUMAN	H7C597	Staphylococcal nuclease domain-containing protein 1 (Fragment)
17429	dirMS_041712_NAR_60mM_plus.12734.12734.3	3	6.87	1	9.60E+05	M230m	(R)mSMKE	(R)m S M K E V D E/Q|M|L/N V Q N K(N)	m:Oxidized methionine	123.5	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
17430	dirMS_041712_NAR_60mM_plus.15830.15830.3	3	6.87	0	4.38E+05		(R)VWYVS	(R)V W|Y V S N I/D/G T H I A K(T)		139.73	534.9464	1602.828	-0.0028	-1.8	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
17431	dirMS_041712_NAR_60mM_plus.21288.21288.3	3	6.87	0	2.23E+05		(R)QARPTY	(R)Q/A R P T Y/A\T|A|M L/Q S L L K(-)		175.57	597.9953	1791.979	-0.0072	-4	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
17432	dirMS_041712_NAR_60mM_plus.21449.21449.3	3	6.87	1	3.68E+05		(R)ARDDLI	(R)A R D D L\I|T/D/L L/N E A K(Q)		177.42	529.6165	1586.838	-0.0035	-2.2	4.23	23653.1	9.28	HUMAN	C9J8H1	V-type proton ATPase subunit E 1 (Fragment)
17433	dirMS_041712_NAR_60mM_plus.8107.8107.3	3	6.87	1	6.02E+05		(R)KQSTDE	(R)K Q S T D\E\E|V|T/S L A/K(S)		100.85	479.2461	1435.728	-0.0037	-2.6	4.68	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
17434	dirMS_041712_NAR_120mM_minus.19750.19750.3	3	6.86	1	1.48E+05		(K)GTKHLSI	(K)G T K H|L/S/P Y A T L T V G D S S H K(T)		163.12	667.0203	1999.024	0.022	11	8.51	123367.7	5.57	HUMAN	Q9BSJ8	Extended synaptotagmin-1
17435	dirMS_041712_NAR_40mM_minus2.12819.12819.3	3	6.86	1	2.01E+05		(K)DVLFLK	(K)D V/L/F|L K D C\V G P E V E K(A)	C:Carbamidomethylation	158.43	583.3021	1747.893	-0.0018	-1	4.32	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase

17436	dirMS_041712_NAR_40mM_minus2.9389.9389.3	3	6.86	0	9.99E+04		(K)AASDIAI	(K)A A|S D I/A/M T E L/P/P T H P I R(L)		138.25	607.3174	1819.937	0.0006	0.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
17437	dirMS_041712_NAR_60mM_minus.11548.11548.3	3	6.86	0	2.97E+05	T120t	(K)MPEGtF	(K)M P/E/G t/F L/V/R(D)	t:N-acetylglucosamine (T)	123.92	418.2174	1049.545	203.0928	10.7	5.75	31075.9	5.99	HUMAN	G5E9R1	Cytokine inducible SH2-containing protein, isoform CRA_c
17438	dirMS_041712_NAR_60mM_minus.6318.6318.3	3	6.86	1	1.97E+04	M172m	(K)ALmAAE	(K)A L|m/A A/E D/K/Y S Q K(E)	m:Oxidized methionine	93.85	457.5567	1354.667	15.9884	-4.7	6.11	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
17439	dirMS_041712_NAR_120mM_plus.7773.7773.3	3	6.86	0	4.73E+05		(R)SGSMDF	(R)S G\S\M/D/P/S/G A H P S V R(Q)		94.1	462.218	1384.627	0.0121	8.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
17440	dirMS_041712_NAR_20mM_plus.8634.8634.2	2	6.86	0	6.29E+04		(R)LDAEPRI	(R)L D A\E/P R|P P P T Q E\A\A(-)		129.63	746.3743	1491.744	-0.0025	-1.7	4.14	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
17441	dirMS_041712_NAR_30mM_plus2.5714.5714.2	2	6.86	0	6.89E+04		(R)QLEDGD	(R)Q L/E\D G D Q/P\E/S|K(K)		83.85	623.2808	1245.559	-0.005	-4	3.91	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
17442	dirMS_041712_NAR_30mM_plus2.6493.6493.2	2	6.86	0	1.82E+05		(K)TLNAGA	(K)T L/N/A/G A/Y S K(V)		88.78	462.7408	924.479	-0.0042	-4.5	8.26	30197.4	7.91	HUMAN	E9PMG2	Palmitoyl-protein thioesterase 1 (Fragment)
17443	dirMS_041712_NAR_40mM_plus2.6074.6074.2	2	6.86	0	1.78E+04		(R)NGYDYG	(R)N G Y|D/Y/G/Q|C R(L)	C:Carbamidomethylation	94.57	566.7355	1132.448	0.0161	14.2	5.83	25655.9	8.94	HUMAN	Q13242	Serine/arginine-rich splicing factor 9
17444	dirMS_041712_NAR_50mM_plus2.11364.11364.3	3	6.86	1	4.13E+05		(R)MLFKDD	(R)M L/F K D D Y|P S S/P P K(C)		127.05	508.9188	1524.74	0.0016	1	5.71	20685.4	9.18	HUMAN	B0QYN7	SUMO-conjugating enzyme UBC9
17445	dirMS_041712_NAR_50mM_plus2.11696.11696.3	3	6.86	1	1.31E+05		(K)IGRIEDV	(K)I G R I E D V\T/P I/P S D/S T R(R)		128.73	585.9784	1755.924	-0.0029	-1.7	4.56	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
17446	dirMS_041712_NAR_50mM_plus2.17982.17982.3	3	6.86	0	9.05E+04		(R)TIRPMD	(R)T I R P M D\M\E/T|I/E A S V M/K(T)		162.53	617.9711	1851.901	-0.0026	-1.4	4.68	39089.4	7.08	HUMAN	C9J634	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial
17447	dirMS_041712_NAR_60mM_plus.10207.10207.2	2	6.86	0	2.03E+06		(K)GIVEFSG	(K)G I/V|E|F S/G K P A A/R(K)		111.3	616.3425	1231.679	-0.0016	-1.3	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
17448	dirMS_041712_NAR_60mM_plus.15855.15855.3	3	6.86	0	4.00E+04		(K)NFDLRP	(K)N/F/D/L R/P G V/I V R(-)		138.1	429.248	1285.738	-0.0081	-6.3	9.6	33192.3	6.77	HUMAN	B4DN45	S-adenosylmethionine synthase
17449	dirMS_041712_NAR_120mM_minus.10769.10769.3	3	6.85	0	9.20E+05		(R)GFCLPPI	(R)G F C L/P/P/H C S/R(G)	C:Carbamidomethylation	113.52	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
17450	dirMS_041712_NAR_30mM_minus2.5827.5827.2	2	6.85	0	1.23E+05		(K)TSEVNC	(K)T/S/E/V/N C/Y R(C)	C:Carbamidomethylation	86.58	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
17451	dirMS_041712_NAR_30mM_minus2.7366.7366.2	2	6.85	0	3.01E+05	M514m M5	(K)NEEmm	(K)N E/E m/m E Q/K(E)	m:Oxidized methionine	94.68	535.7092	1038.423	31.9881	-1.6	4.25	67721.3	5.54	HUMAN	P32456	Interferon-induced guanylate-binding protein 2
17452	dirMS_041712_NAR_40mM_minus2.6618.6618.2	2	6.85	0	4.02E+05		(K)LAADDF	(K)L/A/A/D/D F R(T)		107.5	404.2037	807.399	0.0006	0.7	4.21	48845.9	4.72	HUMAN	C4AM86	Keratin, type I cuticular Ha5
17453	dirMS_041712_NAR_50mM_minus2.14445.14445.3	3	6.85	1	8.33E+04		(R)LSQELEY	(R)L S/Q/E L E/Y L/T E D V K R(L)		149.87	574.9724	1722.891	0.0118	6.8	4.41	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
17454	dirMS_041712_NAR_50mM_minus2.15301.15301.3	3	6.85	1	2.27E+05		(K)LALDIEI	(K)L/A/L D I/E\I A T Y R K(L)		154.58	469.2729	1405.805	-0.0008	-0.6	6.07	49564	5.84	HUMAN	E9PAX3	Glial fibrillary acidic protein
17455	dirMS_041712_NAR_60mM_minus.10866.10866.3	3	6.85	1	2.16E+05		(K)VTVAGL	(K)V T/V|A/G/L/A G K/D P V Q C S R(D)	C:Carbamidomethylation	121	553.2923	1657.869	-0.0067	-4	8.72	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
17456	dirMS_041712_NAR_60mM_minus.10996.11041.3	3	6.85	1	5.49E+05	M112m	(R)EmDRET	(R)E m D R E T L|I/D/V A R(T)	m:Oxidized methionine	121.17	488.5781	1447.721	15.9988	2.6	4.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
17457	dirMS_041712_NAR_60mM_minus.13216.13216.3	3	6.85	1	2.81E+05	M194m	(R)KLQEEEI	(R)K L Q E E E\L L|A/T/Q V D m/R(A)	m:Oxidized methionine	133.93	606.9793	1802.932	15.9917	-1.8	4.41	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
17458	dirMS_041712_NAR_60mM_minus.14831.14831.3	3	6.85	1	2.72E+05		(R)KLQEEEI	(R)K L Q E E E\L\L|A|T/Q V D\M/R(A)		142.8	601.6438	1802.932	-0.0148	-8.2	4.41	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
17459	dirMS_041712_NAR_60mM_minus.15604.15604.3	3	6.85	1	3.29E+05		(R)GPIKFN	(R)G P I K F N V|W/D\T|A/G Q E K(F)		146.37	563.9575	1689.86	-0.0015	-0.9	6.07	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
17460	dirMS_041712_NAR_60mM_minus.17935.17935.3	3	6.85	1	1.25E+04		(K)RSIQFVD	(K)R S I Q F|V|D/W C/P T G F K(V)	C:Carbamidomethylation	161.33	580.9568	1740.853	0.0032	1.8	8.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
17461	dirMS_041712_NAR_60mM_minus.18195.18195.3	3	6.85	1	5.46E+05		(K)IKTLFPLI	(K)I K T L F/P L/I/E A/K(K)		162.7	424.9345	1272.793	-0.0036	-2.9	8.59	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
17462	dirMS_041712_NAR_60mM_minus.18562.18562.3	3	6.85	0	1.19E+05		(R)IDILDSA	(R)I/D/I/L/D/S A L L R P G R(I)		165.08	480.2832	1438.838	-0.0026	-1.8	5.96	44954.5	8.44	HUMAN	A8K3Z3	26S protease regulatory subunit 8
17463	dirMS_041712_NAR_60mM_minus.5500.5500.3	3	6.85	0	1.22E+05	M480m	(R)AAHSEG	(R)A A H\S E G N T|T|A/G L D\m R(E)	m:Oxidized methionine	86.85	516.235	1530.697	15.9939	-0.6	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
17464	dirMS_041712_NAR_120mM_plus.10210.10443.3	3	6.85	1	1.43E+05		(R)RGVVGF	(R)R G V V\G|P E|L/Y G R(L)		107.48	401.5586	1202.664	-0.0028	-2.3	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
17465	dirMS_041712_NAR_120mM_plus.11284.11284.3	3	6.85	1	2.23E+05		(K)FGQYNK	(K)F/G\Q\Y N/K/E D|P T/S F R(L)		112.6	530.2516	1588.739	0.0012	0.8	6.07	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
17466	dirMS_041712_NAR_120mM_plus.6140.6140.2	2	6.85	1	3.38E+05		(K)DSYVGD	(K)D S Y/V/G/D E A Q/S K R(G)		86.27	677.815	1354.623	-0.0006	-0.5	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
17467	dirMS_041712_NAR_20mM_plus.9686.9686.2	2	6.85	0	6.34E+04		(K)ITLVSAA	(K)I T L/V/S A A P/G K(V)		138.03	478.793	956.577	0.0012	1.3	8.75	12480.3	9.05	HUMAN	F5H2L4	Acyl-coenzyme A thioesterase 13
17468	dirMS_041712_NAR_40mM_plus2.9507.9507.3	3	6.85	0	3.47E+04		(R)GGGGNI	(R)G G G G N F G|P G/P/G/S N F/R(G)		119.3	459.8801	1377.629	-0.0037	-2.7	9.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
17469	dirMS_041712_NAR_50mM_plus2.10141.10141.3	3	6.85	1	1.76E+05		(R)QELILSN	(R)Q E L I/L/S/N S E D/K S/I R(V)		121.43	544.624	1631.86	-0.0024	-1.5	4.68	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
17470	dirMS_041712_NAR_50mM_plus2.13777.13777.3	3	6.85	0	3.05E+05		(K)ASLASLP	(K)A S L A|S L/P/P L/H V A K(L)		140.47	435.2622	1303.773	-0.0012	-0.9	8.8	141626	5.5	HUMAN	A8MY36	Dynactin subunit 1
17471	dirMS_041712_NAR_50mM_plus2.14207.14207.3	3	6.85	1	3.51E+05		(R)NVIFQP	(R)N V/I F Q/P V A/E L K/K(Q)		142.5	462.6094	1385.815	-0.0015	-1.1	8.59	23167	8.94	HUMAN	B1APP8	6-phosphofructokinase type C
17472	dirMS_041712_NAR_50mM_plus2.15483.15483.3	3	6.85	1	6.66E+05		(R)GFPTIYF	(R)G F/P/T I Y F/S/P/A N K K(L)		149.08	490.5973	1469.779	-0.0014	-0.9	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
17473	dirMS_041712_NAR_50mM_plus2.16956.16956.3	3	6.85	1	5.24E+05		(K)LSKNEVI	(K)L S K N E V L M V N I|G/S L/S T G G R(V)		157.05	659.0229	1975.064	-0.0099	-5	8.75	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
17474	dirMS_041712_NAR_50mM_plus2.5765.5765.3	3	6.85	1	9.72E+04		(R)AAPTAA	(R)A/A P\T/A/A S D Q/P D S A A T T E K A K(K)		93.32	644.3093	1930.935	-0.0219	-11.3	4.56	22655.1	9.45	HUMAN	Q9BRP8	Partner of Y14 and mago
17475	dirMS_041712_NAR_50mM_plus2.9105.9105.3	3	6.85	0	1.91E+05		(K)TAVEHA	(K)T/A V E H A/T D E/D/I/L A K(G)		115.42	504.9238	1512.754	0.0028	1.9	4.31	288852.1	5.33	HUMAN	E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein
17476	dirMS_041712_NAR_60mM_plus.12770.12770.3	3	6.85	1	1.06E+06		(R)DLDRIA	(R)D L/D R I\A\G Q\V|A/A A/N K(K)		123.83	481.263	1441.776	-0.0013	-0.9	5.96	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
17477	dirMS_041712_NAR_60mM_plus.16575.16575.3	3	6.85	0	3.86E+05		(R)EAYPGD	(R)E A Y/P/G D V/F Y/L/H S R(L)		142.97	518.5855	1553.738	0.0036	2.3	5.32	48851.3	9.2	HUMAN	K7EK63	ATP synthase subunit alpha, mitochondrial
17478	dirMS_041712_NAR_120mM_minus.17473.17632.3	3	6.84	1	3.26E+05		(R)RAPFDLI	(R)R A\P F\D\L|F/E/N K(K)		150.78	412.8849	1236.637	0.003	2.4	6.07	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
17479	dirMS_041712_NAR_20mM_minus.7293.7293.2	2	6.84	0	3.99E+04		(K)AVTEQG	(K)A V/T E/Q\G A|E L\S N E/E R(N)		120.98	766.8612	1532.719	-0.0036	-2.3	4.09	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
17480	dirMS_041712_NAR_20mM_minus.9325.9325.2	2	6.84	0	2.79E+05		(R)AQIFAN	(R)A Q|I/F/A/N T V D N A R(I)		142.32	660.3388	1319.67	0.0001	0.1	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
17481	dirMS_041712_NAR_30mM_minus2.15215.15215.2	2	6.84	0	6.94E+05		(K)LYANMF	(K)L Y|A N M/F/E R(L)		135.35	522.2529	1043.498	0.0006	0.6	6	9740.1	10.08	HUMAN	H0YFG2	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed (Fragment)
17482	dirMS_041712_NAR_30mM_minus2.15685.15685.2	2	6.84	0	2.70E+04	M1342m	(R)ASLSLW	(R)A S L/S/L/W Q A m E K(G)	m:Oxidized methionine	138.55	640.3185	1263.64	15.9895	-4.2	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
17483	dirMS_041712_NAR_30mM_minus2.5102.5102.2	2	6.84	0	2.07E+05		(K)VSSFEEK	(K)V/S|S/F E/E K(M)		80.68	413.2023	825.399	-0.0016	-1.9	4.53	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
17484	dirMS_041712_NAR_30mM_minus2.7636.7636.2	2	6.84	0	8.48E+05		(R)FSNISAA	(R)F/S|N I/S A/A/K(A)		95.77	419.2279	837.447	0.002	2.4	8.75	55232.1	8.4	HUMAN	F5H5W3	T-complex protein 1 subunit delta
17485	dirMS_041712_NAR_40mM_minus2.14434.14434.3	3	6.84	1	2.00E+05		(R)GLLPGLI	(R)G L|L/P G L/L/P A P A D K L T P K(G)		169.47	567.6813	1701.031	-0.0016	-0.9	8.59	153084.9	5.55	HUMAN	Q6P2E9	Enhancer of mRNA-decapping protein 4
17486	dirMS_041712_NAR_50mM_minus2.10868.10868.3	3	6.84	1	2.14E+05		(R)DVVICPI	(R)D V|V\I/C/P D A/S L E D A K K(E)	C:Carbamidomethylation	129.57	553.9474	1659.826	0.0018	1.1	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
17487	dirMS_041712_NAR_50mM_minus2.17576.17576.3	3	6.84	0	2.60E+05		(R)LLLDGAI	(R)L L/L D G A/P L I A I H K(A)		168.5	458.6218	1373.852	-0.0007	-0.5	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
17488	dirMS_041712_NAR_60mM_minus.10327.10327.3	3	6.84	0	2.76E+05		(K)HVGNQ	(K)H V G N\Q Q Y/N V/T/Y V/V K(E)		116.92	550.2838	1648.844	-0.0073	-4.4	8.51	258215.9	5.48	HUMAN	E7EN95	Filamin-B
17489	dirMS_041712_NAR_60mM_minus.14238.14238.3	3	6.84	0	1.71E+05		(R)NFDLTA	(R)N F|D L T/A I/P C A N H K(M)	C:Carbamidomethylation	139.13	500.914	1500.726	0.0011	0.7	6.74	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
17490	dirMS_041712_NAR_120mM_plus.23963.23963.3	3	6.84	1	3.41E+05	M145m	(R)GVmLA	(R)G V/m L/A V D A V\I A E L K K(Q)	m:Oxidized methionine	179.88	524.9713	1556.908	15.9913	-2.3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
17491	dirMS_041712_NAR_20mM_plus.12290.12290.2	2	6.84	0	6.30E+04		(R)DLAPIGI	(R)D L|A/P I G I/R(V)		157.88	427.7587	854.509	0.0007	0.8	5.84	27150.8	7.95	HUMAN	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2
17492	dirMS_041712_NAR_20mM_plus.14512.14512.2	2	6.84	1	6.87E+04		(K)ITEVKIN	(K)I/T|E/V K I/N E A R(E)		170.72	586.8315	1172.663	-0.0076	-6.5	6.14	512542.6	5.52	HUMAN	K7EK91	Dynein heavy chain 17, axonemal
17493	dirMS_041712_NAR_20mM_plus.15035.15035.2	2	6.84	0	2.08E+04		(R)IAAAILN	(R)I A|A A\I L/N T/P D L/R(K)		175.3	634.3708	1267.737	-0.0025	-2	5.84	43371.1	9.64	HUMAN	E7ERW2	Aspartate aminotransferase
17494	dirMS_041712_NAR_20mM_plus.7844.7844.2	2	6.84	0	6.38E+04		(K)LITEDVC	(K)L I|T/E D V/Q|G K(N)		123.35	501.7728	1002.547	-0.0083	-8.3	4.37	14616.7	10.16	HUMAN	D6RAS7	40S ribosomal protein S3a (Fragment)
17495	dirMS_041712_NAR_30mM_plus2.22135.22135.2	2	6.84	0	1.73E+05		(K)GLSSLLC	(K)G L/S S|L/L/C N F/T K(S)	C:Carbamidomethylation	171.82	620.3199	1239.64	-0.0077	-6.2	8.75	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
17496	dirMS_041712_NAR_40mM_plus2.14052.14052.3	3	6.84	0	1.09E+05		(R)LVLEVA	(R)L V|L E V A/Q H L G E/S T V R(T)		149.12	550.9762	1650.917	-0.0033	-2	5.4	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
17497	dirMS_041712_NAR_40mM_plus2.7044.7044.2	2	6.84	0	3.88E+04		(R)QGYGEG	(R)Q G/Y/G/E/G F/R(W)		101.27	457.2098	913.416	-0.0039	-4.3	6	17613.9	5.58	HUMAN	B4DQ19	GTP-binding protein SAR1a
17498	dirMS_041712_NAR_40mM_plus2.7064.7064.2	2	6.84	0	2.07E+04		(K)STCIYGG	(K)S T/C/I/Y G G A P K(G)	C:Carbamidomethylation	101.43	527.2536	1053.503	-0.0034	-3.3	8.31	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
17499	dirMS_041712_NAR_50mM_plus2.19135.19135.3	3	6.84	0	4.79E+05		(R)CRPDQL	(R)C R P D\Q\L T/G\L/S|L L/P L S E K(A)	C:Carbamidomethylation	168.18	643.0148	1927.032	-0.0019	-1	6.07	533778	5.74	HUMAN	Q15149	Plectin
17500	dirMS_041712_NAR_50mM_plus2.21104.21104.3	3	6.84	1	3.21E+05	M145m	(R)GVmLA	(R)G V/m L/A/V\D A/V I A E L K K(Q)	m:Oxidized methionine	180.98	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
17501	dirMS_041712_NAR_50mM_plus2.8735.8735.3	3	6.84	0	7.40E+05		(R)AALAHS	(R)A A\L A H S E E\V|T/A/S Q V A/A T K(T)		113.43	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
17502	dirMS_041712_NAR_60mM_plus.13720.13720.3	3	6.84	1	4.08E+05		(K)SGYLAGI	(K)S G/Y/L/A/G D K L L/P Q R(V)		128.58	473.2654	1417.78	0.0019	1.3	8.31	67933	6.08	HUMAN	P26038	Moesin
17503	dirMS_041712_NAR_30mM_minus2.7908.8077.2	2	6.83	0	8.56E+05		(R)NTNPNF	(R)N/T|N/P N F V/R(C)		97.67	481.2466	961.485	0.0009	1	9.75	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
17504	dirMS_041712_NAR_30mM_minus2.8650.8650.2	2	6.83	0	4.53E+04		(K)QVIEYAF	(K)Q\V/I/E/Y A/R(Q)		101.48	439.737	878.473	-0.0063	-7.2	6	39896.4	9.92	HUMAN	P48556	26S proteasome non-ATPase regulatory subunit 8
17505	dirMS_041712_NAR_50mM_minus2.13279.13279.3	3	6.83	0	5.21E+05		(K)SLTNDW	(K)S L|T/N D W E D H L A V K(H)		144.18	509.9192	1527.744	-0.0008	-0.5	4.53	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
17506	dirMS_041712_NAR_50mM_minus2.16757.16757.3	3	6.83	0	4.18E+05		(K)NILFVITI	(K)N I|L/F V/I T K P D V/Y K(S)		164.02	517.2991	1549.899	-0.0161	-10.4	8.5	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
17507	dirMS_041712_NAR_50mM_minus2.18080.18080.3	3	6.83	1	3.85E+04	S100s	(K)VLELKFP	(K)V L E/L/K F P A S S s L K(-)	s:N-acetylglucosamine (S)	171.9	541.3004	1418.825	203.0613	-11.1	8.56	11491.7	6.15	HUMAN	H7C4X6	Coiled-coil domain-containing protein 39 (Fragment)
17508	dirMS_041712_NAR_50mM_minus2.5613.5613.3	3	6.83	1	9.00E+03		(K)DSYVGD	(K)D S/Y/V G D/E A/Q S K R(G)		92.38	452.2119	1354.623	-0.0022	-1.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
17509	dirMS_041712_NAR_60mM_minus.15463.15463.3	3	6.83	0	3.72E+05		(K)THLPGF	(K)T H\L\P G F\V/E Q A\E A/L/K(A)		146.35	513.947	1539.817	0.0099	6.4	5.37	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
17510	dirMS_041712_NAR_60mM_minus.18198.18198.3	3	6.83	1	1.54E+05		(R)IRVESLL	(R)I R V E S\L\L/V/T/A I/S K(A)		162.6	476.9628	1428.878	-0.0046	-3.2	8.75	91730	7.16	HUMAN	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15
17511	dirMS_041712_NAR_60mM_minus.9736.9736.2	2	6.83	1	4.41E+05		(R)LQAEIEG	(R)L Q/A/E|I E G L K/G Q/R(A)		114.13	671.3768	1341.748	-0.0022	-1.6	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
17512	dirMS_041712_NAR_120mM_plus.16490.16490.4	4	6.83	1	1.15E+06		(R)YAEIVHL	(R)Y/A E I V\H L T L/P/D/G T K/R(S)		139.08	428.9885	1712.933	-0.0008	-0.5	6.75	21230	6.36	HUMAN	H0YC04	V-type proton ATPase subunit B, brain isoform (Fragment)
17513	dirMS_041712_NAR_120mM_plus.18843.18843.4	4	6.83	1	1.08E+06		(K)FQIPPN	(K)F Q|I/P P N/A E L K Y E L/H L K(S)		151.82	485.7703	1940.064	-0.0046	-2.4	6.75	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
17514	dirMS_041712_NAR_120mM_plus.22759.22759.4	4	6.83	1	9.32E+03		(K)LRELSEL	(K)L R E L S\E\L/S/L L/S\L/Y G I H K(Q)		172.15	493.5345	1971.127	-0.0112	-5.7	6.75	44907.6	5.84	HUMAN	P15309	Prostatic acid phosphatase
17515	dirMS_041712_NAR_20mM_plus.12825.12825.2	2	6.83	0	4.13E+05	M1m N6n	(-)mPLFPnL	(-)m P|L F|P n L/P R(L)	m:Oxidized methionine n:N-	161.62	652.3439	1084.597	219.0833	6.9	9.5	39133.5	4.5	HUMAN	Q8TD91-2	Isoform 2 of Melanoma-associated antigen C3
17516	dirMS_041712_NAR_20mM_plus.15150.15150.2	2	6.83	0	9.87E+04		(K)AILFVPR	(K)A I|L/F V/P R(R)		176.13	408.2606	815.514	0.0001	0.2	9.79	57660.2	6.38	HUMAN	Q9NQH7	Probable Xaa-Pro aminopeptidase 3
17517	dirMS_041712_NAR_30mM_plus2.14207.14207.2	2	6.83	0	5.53E+05		(K)CCSGAII	(K)C\C/S G A/I I V L T K(S)	C:Carbamidomethylation	128.18	611.3189	1221.633	-0.0025	-2	8.75	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
17518	dirMS_041712_NAR_30mM_plus2.15373.15373.2	2	6.83	0	5.90E+05		(R)YPVNSV	(R)Y/P|V/N S V N I L K(A)		133.4	573.8278	1146.652	-0.0034	-3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
17519	dirMS_041712_NAR_30mM_plus2.17925.17925.2	2	6.83	0	1.39E+05		(K)SCYEDG	(K)S C|Y/E D G W/L I K(M)	C:Carbamidomethylation	147.02	635.7922	1270.577	-0.0001	-0.1	4.37	19112.4	4.9	HUMAN	P23434	Glycine cleavage system H protein, mitochondrial
17520	dirMS_041712_NAR_30mM_plus2.21815.21815.2	2	6.83	0	1.55E+05		(K)ANFLQN	(K)A N\F|L/Q/N M I E D R(T)		170.25	675.8282	1350.647	0.0021	1.5	4.37	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
17521	dirMS_041712_NAR_30mM_plus2.21816.21816.2	2	6.83	0	7.95E+03		(R)DLLFQAI	(R)D L|L/F/Q A/L G R(T)		169.52	516.7959	1032.584	0.0009	0.8	5.84	66742	6.4	HUMAN	Q9NSD9	Phenylalanine--tRNA ligase beta subunit
17522	dirMS_041712_NAR_30mM_plus2.7126.7126.2	2	6.83	0	1.37E+05		(R)TTTGSYI	(R)T T|T/G S/Y/I A N/R(V)		91.82	542.274	1083.543	-0.0022	-2	8.41	10799.8	5.07	HUMAN	I3L3X7	Proteasome subunit beta type-6 (Fragment)
17523	dirMS_041712_NAR_40mM_plus2.6231.6231.2	2	6.83	0	4.28E+05		(K)NAGFTP	(K)N A|G F/T/P/Q E R(Q)		96.22	510.2487	1019.491	-0.0004	-0.4	6	29474.8	6.94	HUMAN	G3V3M6	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
17524	dirMS_041712_NAR_50mM_plus2.9043.9043.3	3	6.83	1	2.70E+05		(K)AQALRD	(K)A Q|A\L/R D\N S T/M/G Y M A A K(K)		115.12	576.611	1727.82	-0.0019	-1.1	8.63	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
17525	dirMS_041712_NAR_30mM_minus2.15132.15132.2	2	6.82	0	5.54E+05	M316m	(R)ISEQFTA	(R)I/S\E\Q|F/T/A m F R(R)	m:Oxidized methionine	135.18	623.3014	1229.598	15.9972	1.8	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
17526	dirMS_041712_NAR_30mM_minus2.18965.18965.2	2	6.82	0	2.38E+05		(K)MAILQIN	(K)M/A/I/L/Q/I/M K(E)		158.15	474.2745	947.542	0.0001	0.1	8.5	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
17527	dirMS_041712_NAR_30mM_minus2.5006.5006.2	2	6.82	0	3.01E+05		(R)TDTGEP	(R)T D|T G|E/P M G R(G)		80.93	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
17528	dirMS_041712_NAR_30mM_minus2.5542.5542.2	2	6.82	0	1.77E+05		(R)LYQAGE	(R)L Y|Q|A G E/G R(L)		84.58	447.2217	893.448	-0.0114	-12.8	6	38089.6	6.79	HUMAN	B4DT77	Annexin
17529	dirMS_041712_NAR_50mM_minus2.12776.12776.3	3	6.82	1	2.33E+05		(R)QATKDA	(R)Q A T K D A G\T I/A/G L N V/L/R(I)		140.57	543.3085	1627.913	-0.0016	-1	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
17530	dirMS_041712_NAR_50mM_minus2.16316.16316.3	3	6.82	1	2.05E+05		(R)SSGISLG	(R)S S G/I/S L G\Y\D Q/R H G S P R(S)		160.35	572.9609	1716.841	0.0269	15.7	8.49	46549.6	9.68	HUMAN	A6NIX2	Wilms tumor protein 1-interacting protein
17531	dirMS_041712_NAR_50mM_minus2.16793.16793.3	3	6.82	0	2.43E+05		(R)LGIEGLS	(R)L/G I E G L/S L H N V L/K(L)		164.17	464.9452	1392.821	0.0001	0.1	6.75	177928	5.42	HUMAN	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1
17532	dirMS_041712_NAR_50mM_minus2.17169.17169.3	3	6.82	1	2.93E+04		(K)IILDLISE	(K)I I|L D/L I/S E S/P I/K G R(A)		166.75	518.6444	1553.926	-0.0075	-4.8	6.07	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
17533	dirMS_041712_NAR_50mM_minus2.17432.17432.3	3	6.82	2	1.46E+04		(K)EVGEASI	(K)E V\G/E A S I K/V P Q L K M E I(-)		167.3	590.9853	1770.967	-0.0257	-14.5	4.79	45692.5	9.38	HUMAN	Q9H4B0	Probable tRNA threonylcarbamoyladenosine biosynthesis protein OSGEPL1
17534	dirMS_041712_NAR_60mM_minus.13214.13214.3	3	6.82	1	2.20E+03		(R)LQDEIQI	(R)L Q/D E I Q/N M K E E M/A R(H)		132.78	578.9425	1734.815	-0.002	-1.1	4.41	49709.6	5.19	HUMAN	B0YJC4	Vimentin
17535	dirMS_041712_NAR_60mM_minus.14400.14400.3	3	6.82	1	2.95E+05		(K)ALQQGL	(K)A L|Q Q/G L/V G L E L K E K(L)		139.65	509.2999	1525.895	-0.0097	-6.3	6.18	266161	5.68	HUMAN	E9PPU0	Epiplakin
17536	dirMS_041712_NAR_120mM_plus.18274.18301.4	4	6.82	0	6.08E+05		(R)ASVLFDT	(R)A S/V L/F/D/T M Q H/H L A L N R(D)		148.98	463.9921	1852.949	-0.0021	-1.1	6.96	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
17537	dirMS_041712_NAR_20mM_plus.12158.12158.2	2	6.82	0	3.37E+04		(K)LQAFSA	(K)L Q\A F S/A/A/I|E S C N K(A)	C:Carbamidomethylation	156.67	719.8475	1438.699	-0.0118	-8.2	6	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
17538	dirMS_041712_NAR_20mM_plus.14511.14511.2	2	6.82	0	5.49E+04	S185s	(R)GLVsLSA	(R)G L/V s L/S A K(I)	s:N-acetylglucosamine (S)	171.77	489.2861	774.472	203.0929	13.9	8.75	44720.5	9.74	HUMAN	Q8TBH0	Arrestin domain-containing protein 2
17539	dirMS_041712_NAR_20mM_plus.7755.7755.2	2	6.82	0	5.08E+03		(K)TAVCDIF	(K)T A|V|C D I/P|P R(G)	C:Carbamidomethylation	123.92	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
17540	dirMS_041712_NAR_30mM_plus2.13978.13999.2	2	6.82	0	2.80E+05		(K)INLIAPPI	(K)I N|L|I A/P P R(Y)		126.12	447.2813	893.557	-0.0014	-1.6	9.75	31604.9	6.88	HUMAN	G3V4T5	Eukaryotic translation initiation factor 2 subunit 1 (Fragment)
17541	dirMS_041712_NAR_30mM_plus2.20822.20822.2	2	6.82	0	1.90E+05		(K)EGLLLW	(K)E/G L/L/L/W/C Q R(K)	C:Carbamidomethylation	163.18	587.8038	1174.604	-0.0034	-2.9	6.1	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
17542	dirMS_041712_NAR_30mM_plus2.5509.5509.2	2	6.82	0	7.35E+04		(R)QMSGA	(R)Q M|S/G A Q|I/K(I)		82.95	431.7254	862.445	-0.0016	-1.8	8.75	34267.8	9.05	HUMAN	B4DXP5	Poly(rC)-binding protein 2
17543	dirMS_041712_NAR_30mM_plus2.6135.6135.2	2	6.82	0	3.03E+05	M299m	(K)NmMAA	(K)N m\M/A/A C D|P R(H)	C:Carbamidomethylation m:Oxid	86.65	541.2163	1065.427	15.9979	2.8	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
17544	dirMS_041712_NAR_50mM_plus2.13535.13535.3	3	6.82	1	3.73E+05		(R)SLIANLA	(R)S L/I/A N/L|A/A A/N C Y K K(E)	C:Carbamidomethylation	138.97	512.9444	1536.82	-0.0016	-1.1	9.7	36978.6	6.33	HUMAN	B7Z800	Adenosine kinase

17545	dirMS_041712_NAR_50mM_plus2.17803.17803.3	3	6.82	0	6.69E+05		(K)ALVSHN	(K)A/L V S H N G S L I|N|V|G S L L Q R(A)		161.37	626.6872	1878.056	-0.0085	-4.5	9.8	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
17546	dirMS_041712_NAR_50mM_plus2.21441.21441.3	3	6.82	1	4.09E+05	M145m	(R)GVmLA\	(R)G V/m L A/V D A V I A/E L K K(Q)	m:Oxidized methionine	182.55	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
17547	dirMS_041712_NAR_50mM_plus2.7450.7450.3	3	6.82	0	2.28E+04		(R)LIQSHPE	(R)L/I/Q S/H P E S A/E D L Q E K(C)		105.13	575.2802	1723.85	-0.0237	-13.7	4.4	285798.6	5.23	HUMAN	A6NG51	Spectrin alpha chain, non-erythrocytic 1
17548	dirMS_041712_NAR_50mM_plus2.8267.8267.3	3	6.82	1	3.49E+05		(R)VAVEAK	(R)V/A/V/E A/K N/P A D\L/P/K(L)		110.53	451.2563	1351.758	-0.0036	-2.7	6.04	96306.4	6.41	HUMAN	P13639	Elongation factor 2
17549	dirMS_041712_NAR_60mM_plus.10247.10247.2	2	6.82	0	2.03E+06		(K)GIVEFSG	(K)G I|V/E F/S G K/P A A R(K)		111.3	616.3425	1231.679	-0.0016	-1.3	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
17550	dirMS_041712_NAR_60mM_plus.15151.15151.3	3	6.82	1	1.45E+05		(R)VFDKDG	(R)V F D K\D G N/G Y I/S/A A E L R(H)		135.57	585.6281	1754.871	-0.001	-0.6	4.56	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
17551	dirMS_041712_NAR_60mM_plus.19434.19434.3	3	6.82	0	6.32E+05		(K)VSHLLGI	(K)V/S H L L\G I|N/V/T/D/F T R(G)		159.85	524.6233	1571.854	0.0013	0.8	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
17552	dirMS_041712_NAR_30mM_minus2.10440.10440.2	2	6.81	0	1.26E+06		(R)ANIQAV	(R)A N|I/Q/A/V S L K(I)		110.72	472.2815	943.557	-0.0014	-1.5	8.8	25103.6	5.88	HUMAN	O43633	Charged multivesicular body protein 2a
17553	dirMS_041712_NAR_30mM_minus2.6809.6809.2	2	6.81	0	3.43E+04		(R)VGSTSEI	(R)V/G|S\T\S E N I/T/Q/K(V)		91.57	582.2977	1163.59	-0.0021	-1.8	5.97	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
17554	dirMS_041712_NAR_40mM_minus2.11848.11848.3	3	6.81	0	2.32E+05		(K)DAGEGL	(K)D A|G/E/G L L A V Q\I T D P E G\K\P K(K)		153.8	646.6785	1938.018	0.0031	1.6	4.32	283472.4	5.71	HUMAN	P21333	Filamin-A
17555	dirMS_041712_NAR_60mM_minus.12886.12886.3	3	6.81	0	4.82E+05		(K)GIHPTIIS	(K)G I H P T I|I/S E S F Q/K(A)		131.55	486.2642	1456.78	-0.0014	-1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
17556	dirMS_041712_NAR_60mM_minus.19386.19386.3	3	6.81	1	1.89E+05		(R)KAIIIFVP	(R)K A I\I I F\V|P/V P Q L K(S)		172.82	489.3209	1465.95	-0.0023	-1.6	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
17557	dirMS_041712_NAR_60mM_minus.6893.6893.3	3	6.81	1	2.98E+04		(R)AAEEAE	(R)A A/E/E/A E/E A R V Q A E R(E)		97.23	520.2566	1558.746	0.0097	6.2	4.33	533778	5.74	HUMAN	Q15149	Plectin
17558	dirMS_041712_NAR_30mM_plus2.11774.11774.2	2	6.81	0	4.85E+05		(R)AMGEQ	(R)A/M|G E|Q/A/V A L A R(A)		114.22	558.7944	1116.583	-0.0015	-1.3	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
17559	dirMS_041712_NAR_30mM_plus2.21846.21846.3	3	6.81	0	1.80E+05		(K)GLVQAL	(K)G L|V Q A\L/G/L/S N/F/N S R(Q)		169.47	492.6036	1475.796	-0.0003	-0.2	9.75	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
17560	dirMS_041712_NAR_40mM_plus2.10285.10285.2	2	6.81	0	2.87E+04		(K)YNNCWI	(K)Y/N|N/C W/L A/R(T)	C:Carbamidomethylation	125.6	548.7522	1096.499	-0.0022	-2	8.75	55416	8.63	HUMAN	H0YM31	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
17561	dirMS_041712_NAR_40mM_plus2.12318.12318.3	3	6.81	0	3.63E+04		(R)VLTEDEI	(R)V L|T/E/D E M G H P E I/G D A I A R(L)		138.75	651.6493	1952.938	-0.0049	-2.5	4.17	40874	5.06	HUMAN	E9PCI9	Farnesyl pyrophosphate synthase
17562	dirMS_041712_NAR_40mM_plus2.16182.16182.3	3	6.81	0	3.01E+05		(K)VAIVKPC	(K)V A\I\V/K P G V/P M E I V L N K(E)		161.5	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
17563	dirMS_041712_NAR_40mM_plus2.5823.5823.2	2	6.81	1	2.68E+05		(R)WDGVSI	(R)W|D G V S/K K(A)		92.68	410.2256	819.436	0.008	9.8	8.59	119452.8	9.16	HUMAN	Q8NFZ0	F-box only protein 18
17564	dirMS_041712_NAR_50mM_plus2.13601.13601.3	3	6.81	0	2.07E+06		(K)AGVVGF	(K)A G V/V/G P E L H E Q L L/S A E/K(A)		138.73	592.986	1776.949	-0.0056	-3.1	4.75	533778	5.74	HUMAN	Q15149	Plectin
17565	dirMS_041712_NAR_50mM_plus2.15188.15188.3	3	6.81	1	3.82E+05		(R)MGLAIS	(R)M/G\L|A I S/L/V/A T/E K E\K(V)		147.7	497.2822	1489.829	0.0026	1.7	5.9	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
17566	dirMS_041712_NAR_60mM_plus.14640.14640.3	3	6.81	1	1.99E+05		(K)KVPQVS	(K)K V P Q V S T|P T L/V E/V S R(N)		132.83	547.3173	1639.938	-0.0004	-0.2	8.75	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
17567	dirMS_041712_NAR_60mM_plus.18122.18122.3	3	6.81	1	8.15E+05		(K)EVNKFQ	(K)E V/N K/F Q M/A Y/S/N/L L R(A)		152.58	571.6293	1712.879	-0.0055	-3.2	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
17568	dirMS_041712_NAR_60mM_plus.18658.18658.3	3	6.81	1	6.14E+05		(R)IRIDSLSA	(R)I R I D\S\L S\A Q/L/S Q L Q/K(Q)		154.62	567.3254	1699.97	-0.0085	-5	8.75	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
17569	dirMS_041712_NAR_60mM_plus.8170.8170.3	3	6.81	1	4.47E+05		(K)KDLSGSE	(K)K/D/L/S G S E E D V I E G K(T)		100.28	502.5849	1505.733	0.0072	4.8	4.18	27728.2	9.22	HUMAN	Q8IZU3	Synaptonemal complex protein 3
17570	dirMS_041712_NAR_60mM_plus.9384.9384.2	2	6.81	0	5.11E+05		(K)QEYDES	(K)Q/E/Y D/E/S/G P S I/V\H/R(K)		107.15	758.8546	1516.703	-0.0007	-0.5	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
17571	dirMS_041712_NAR_120mM_minus.10051.10051.3	3	6.8	0	5.96E+05		(R)HGESAV	(R)H G\E S A\W|N/L/E/N R(F)		109.4	438.2098	1312.603	0.012	9.1	5.4	28917.5	6.68	HUMAN	P18669	Phosphoglycerate mutase 1
17572	dirMS_041712_NAR_120mM_minus.5138.5138.3	3	6.8	1	1.60E+05		(R)LKQSAEI	(R)L/K Q S A\E/E/Q/A/Q A R(A)		80.68	453.5713	1358.702	-0.0029	-2.1	6.14	533778	5.74	HUMAN	Q15149	Plectin
17573	dirMS_041712_NAR_20mM_minus.12184.12184.2	2	6.8	0	5.27E+05	M185m	(K)LAVNm\	(K)L\A|V N/m/V P/F P R(L)	m:Oxidized methionine	171.1	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
17574	dirMS_041712_NAR_30mM_minus2.18955.18955.2	2	6.8	0	8.39E+05		(K)LAVNM\	(K)L A/V/N/M/V/P/F P R(L)		158.8	572.3143	1143.634	-0.013	-11.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
17575	dirMS_041712_NAR_40mM_minus2.10964.10964.3	3	6.8	1	1.14E+05	M362m	(R)EGSVmL	(R)E G S/V m/L Q V/D/V D/T V K G G L/K(L)	m:Oxidized methionine	147.85	630.9989	1874.989	15.993	-1	4.56	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
17576	dirMS_041712_NAR_60mM_minus.16696.16696.3	3	6.8	1	2.30E+05		(R)KGFSEGI	(R)K G F S E G\L W E\I E/N N|P T V K(A)		153.68	649.9986	1947.981	0.0002	0.1	4.79	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
17577	dirMS_041712_NAR_60mM_minus.7948.7948.3	3	6.8	1	1.27E+05		(K)FEDKTV	(K)F E D/K T V|A/Y T/E Q K(M)		104.43	486.908	1458.711	-0.0017	-1.1	4.68	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
17578	dirMS_041712_NAR_60mM_minus.8208.8208.3	3	6.8	0	1.27E+04	M354m	(R)LSNRPAI	(R)L S\N R/P A F\m|P S E G R(M)	m:Oxidized methionine	105.97	493.2448	1461.727	15.9931	-1.2	9.6	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
17579	dirMS_041712_NAR_120mM_plus.8558.8558.3	3	6.8	2	1.41E+05		(R)KVVGCS	(R)K|V/V/G C S C V V/V K D|Y G K(E)	C:Carbamidomethylation	97.98	566.6258	1697.871	-0.0085	-5	9.53	14914.1	6.84	HUMAN	P25398	40S ribosomal protein S12
17580	dirMS_041712_NAR_30mM_plus2.11454.11454.2	2	6.8	0	3.67E+05		(R)NGDFLP	(R)N G\D/F|L/P T|R(L)		113.58	460.2391	919.463	0.0077	8.4	5.84	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
17581	dirMS_041712_NAR_40mM_plus2.12200.12200.3	3	6.8	0	1.49E+05		(K)QLTEEDI	(K)Q L/T/E/E D G V H S V I E/E N I K(C)		138.65	647.3228	1939.961	-0.0069	-3.5	4.25	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
17582	dirMS_041712_NAR_40mM_plus2.17385.17385.3	3	6.8	1	8.46E+04		(R)NAAALS	(R)N/A|A|A|L/S Q A L R L E A P E L P V K(V)		168.6	664.3784	1991.128	-0.0078	-3.9	6.14	10558	9.4	HUMAN	H0YE28	Protein C11orf31 (Fragment)
17583	dirMS_041712_NAR_50mM_plus2.13878.13878.3	3	6.8	1	2.00E+06	M320m	(K)YmACCL	(K)Y/m/A C C L/L Y R G D V V/P K(E)	C:Carbamidomethylation m:Oxid	140.55	620.9622	1844.886	15.9865	-4.5	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
17584	dirMS_041712_NAR_50mM_plus2.19679.19679.3	3	6.8	0	9.67E+04		(R)QGDTGI	(R)Q G/D T/G/D W I/G T F L G H K(G)		171.7	544.6001	1631.781	0.0045	2.8	5.21	40119.4	5.14	HUMAN	B4DNJ6	Serine-threonine kinase receptor-associated protein
17585	dirMS_041712_NAR_60mM_plus.11501.11501.3	3	6.8	1	4.52E+05		(K)TCVFEKE	(K)T\C|V/F E/K E N D/P S V M R(S)	C:Carbamidomethylation	117.33	571.2635	1711.778	-0.0019	-1.1	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
17586	dirMS_041712_NAR_60mM_plus.20528.20528.3	3	6.8	0	6.17E+05		(R)LGFHLPI	(R)L G\F H L P L\E/V/A Y Q R(G)		168.48	514.9568	1542.843	0.0131	8.5	6.75	533778	5.74	HUMAN	Q15149	Plectin
17587	dirMS_041712_NAR_60mM_plus.21122.21122.3	3	6.8	1	1.07E+05		(K)TIRDIIAL	(K)T I R D\I I A\L/N/P/L/Y R(E)		173.7	519.9722	1557.911	-0.0091	-5.8	8.41	86039.3	5.74	HUMAN	F5GZ27	Lon protease homolog
17588	dirMS_041712_NAR_60mM_plus.6844.6844.3	3	6.8	0	5.16E+05		(R)ATAPQT	(R)A T|A/P/Q|T Q H V S P M R(Q)		94.17	475.2423	1423.711	0.0013	0.9	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
17589	dirMS_041712_NAR_60mM_plus.7588.7588.2	2	6.8	1	1.09E+06		(R)AVVIVDI	(R)A V|V\I|V D/D R G/R(S)		98.32	550.3143	1099.622	-0.0005	-0.5	6.01	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
17590	dirMS_041712_NAR_60mM_plus.7674.7674.3	3	6.8	1	7.88E+05		(K)TPKGPSS	(K)T P K G P S/S/V/E/D/I/K(A)		98.27	419.894	1257.669	-0.0011	-0.8	5.73	32745.6	4.64	HUMAN	P06748	Nucleophosmin
17591	dirMS_041712_NAR_120mM_minus.11005.11005.3	3	6.79	1	1.13E+06		(K)KGENYV	(K)K G E N Y V|Y\I/N E A T R(H)		113.53	519.5935	1556.77	-0.0044	-2.8	6.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
17592	dirMS_041712_NAR_30mM_minus2.14207.14207.2	2	6.79	0	4.17E+05		(K)MFLYAD	(K)M/F|L|Y/A D N/E D R(A)		131.08	637.2806	1273.552	0.0022	1.7	4.03	24724.1	5.17	HUMAN	E7ETQ7	Vacuolar protein sorting-associated protein VTA1 homolog
17593	dirMS_041712_NAR_30mM_minus2.7330.7330.2	2	6.79	0	7.25E+04		(R)GAGSIA	(R)G A\G S I/A|G A/S A S/P K(E)		94.4	537.2824	1073.559	-0.001	-1	8.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
17594	dirMS_041712_NAR_40mM_minus2.14095.14095.3	3	6.79	0	3.46E+05		(R)LLEVLSG	(R)L/L/E V L S/G E I\L/P K P T K(G)		166.62	546.333	1636.988	-0.0039	-2.4	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
17595	dirMS_041712_NAR_40mM_minus2.9279.9279.2	2	6.79	0	3.31E+04		(K)LSELEAA	(K)L S E|L/E A/A L Q R(A)		137.03	565.3111	1129.621	-0.0062	-5.5	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
17596	dirMS_041712_NAR_50mM_minus2.13011.13011.3	3	6.79	0	3.40E+05		(R)ETNLDSI	(R)E T N L/D S L/P L/V D T H S K(R)		142.38	556.9529	1668.844	0.0002	0.1	4.53	53707.8	5.06	HUMAN	P08670	Vimentin
17597	dirMS_041712_NAR_50mM_minus2.16694.16694.3	3	6.79	0	3.35E+05		(K)NILFVITI	(K)N\I/L F V I T K/P D V Y K(S)		163.85	517.2991	1549.899	-0.0161	-10.4	8.5	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
17598	dirMS_041712_NAR_50mM_minus2.17429.17429.3	3	6.79	0	3.42E+05		(K)VAHALA	(K)V A H\A L A\E G\L G\V|I/A/C I G E K(L)	C:Carbamidomethylation	168.57	603.3247	1807.974	-0.0139	-7.7	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
17599	dirMS_041712_NAR_60mM_minus.11948.11948.3	3	6.79	0	1.92E+05		(R)ILHLLGQ	(R)I/L/H|L\L\G Q\E G P K(T)		126.37	402.2384	1204.705	-0.0042	-3.5	6.75	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
17600	dirMS_041712_NAR_60mM_minus.12182.12182.3	3	6.79	0	3.77E+05		(K)VTNEFV	(K)V/T/N E F V/H I N N L K(L)		127.53	476.5974	1427.764	0.0135	9.5	6.72	18317.8	6.19	HUMAN	B7Z3E2	Serine/threonine-protein phosphatase 6 catalytic subunit
17601	dirMS_041712_NAR_60mM_minus.15821.15821.3	3	6.79	0	1.65E+04		(K)LFCIPVH	(K)L/F C/I/P V H G I R(S)	C:Carbamidomethylation	148.82	404.5628	1211.672	0.0021	1.7	9.75	29040.9	5.88	HUMAN	H0YBL1	Inositol monophosphatase 1 (Fragment)
17602	dirMS_041712_NAR_60mM_minus.19065.19065.3	3	6.79	0	5.73E+05		(R)LGFHLPI	(R)L G F H L\P L E\V/A/Y Q/R(G)		168.62	514.9512	1542.843	-0.0037	-2.4	6.75	533778	5.74	HUMAN	Q15149	Plectin
17603	dirMS_041712_NAR_60mM_minus.7045.7045.3	3	6.79	1	2.62E+05		(R)VKVEPA	(R)V K/V E P\A|V/D T/S R(I)		97.47	400.8938	1200.658	0.0086	7.1	6.04	258215.9	5.48	HUMAN	E7EN95	Filamin-B
17604	dirMS_041712_NAR_120mM_plus.20978.20978.3	3	6.79	2	1.39E+06		(R)TLAEIAK	(R)T L|A E I/A K V E L D/N/M P L R G K(Q)		162.92	666.7047	1998.105	-0.0057	-2.8	5.85	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
17605	dirMS_041712_NAR_20mM_plus.14902.14902.2	2	6.79	0	1.26E+05		(R)LLDAQLS	(R)L L D/A Q|L\S/T G G I V D P S K(S)		174.67	807.4389	1613.874	-0.004	-2.5	4.21	533778	5.74	HUMAN	Q15149	Plectin
17606	dirMS_041712_NAR_20mM_plus.16979.16979.2	2	6.79	0	2.55E+05		(K)VQIAVA	(K)V Q/I|A|V/A/N A\Q E L/L Q R(M)		188.03	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
17607	dirMS_041712_NAR_30mM_plus2.16076.16076.2	2	6.79	0	1.26E+05		(K)LALASLG	(K)L A|L/A|S L G Y E K(S)		136.85	532.8002	1064.599	-0.0055	-5.2	6	96649	6.13	HUMAN	Q8WUM4	Programmed cell death 6-interacting protein
17608	dirMS_041712_NAR_40mM_plus2.16238.16238.2	2	6.79	0	1.50E+05		(R)YLTVAA	(R)Y L/T/V/A A V F/R(G)		162.03	520.2997	1039.593	-0.0014	-1.3	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
17609	dirMS_041712_NAR_40mM_plus2.9759.9759.2	2	6.79	0	3.18E+05		(K)SCNCLLL	(K)S C/N C L/L/L/K(V)	C:Carbamidomethylation	120.88	504.2542	1007.501	-0.0001	-0.1	8.47	47510.4	7.04	HUMAN	P06733	Alpha-enolase
17610	dirMS_041712_NAR_50mM_plus2.18882.18882.3	3	6.79	1	1.70E+05		(K)LALFQAI	(K)L/A|L\F Q A I G K E/V V D R(A)		168.03	520.3019	1558.895	-0.004	-2.6	6.07	266161	5.68	HUMAN	E9PPU0	Epiplakin
17611	dirMS_041712_NAR_60mM_plus.16704.16704.3	3	6.79	1	2.29E+04		(R)YRSDGA	(R)Y R S D G A L L|L/G A S/S/L/S G R(C)		143.73	574.9718	1722.913	-0.0125	-7.2	8.75	30278.5	5.29	HUMAN	B4DP38	Methylosome protein 50
17612	dirMS_041712_NAR_60mM_plus.5647.5647.3	3	6.79	0	2.96E+04		(R)IIECTHC	(R)I I/E/C T H C G C/R(G)	C:Carbamidomethylation	87.63	435.8559	1305.55	0.0035	2.7	6.75	12475.2	9.39	HUMAN	C9JCD9	Protein BUD31 homolog
17613	dirMS_041712_NAR_60mM_plus.9033.9033.3	3	6.79	0	1.59E+06		(K)EFHLNES	(K)E\F H L N\E/S/G D/P/S S K(S)		105.52	482.8882	1446.65	0.0005	0.3	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
17614	dirMS_041712_NAR_30mM_minus2.16960.16960.2	2	6.78	0	1.11E+05		(K)NLYIISVI	(K)N L|Y/I I S V K(G)		145.92	475.2872	949.572	-0.0046	-4.8	8.59	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
17615	dirMS_041712_NAR_30mM_minus2.17176.17176.2	2	6.78	0	1.03E+05		(R)NGGQIL	(R)N G G\Q|I/L I/A D/L R(G)		147.92	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
17616	dirMS_041712_NAR_30mM_minus2.7484.7484.2	2	6.78	1	6.47E+05		(K)DELKSTS	(K)D/E/L K S T S K(A)		95.2	454.2433	907.473	0.0062	6.9	6.07	66873	4.98	HUMAN	Q8IXH7	Negative elongation factor C/D
17617	dirMS_041712_NAR_50mM_minus2.12041.12041.3	3	6.78	1	1.88E+05		(R)LATALQI	(R)L/A/T\A/L Q K/L E E A E K(A)		136.98	481.9385	1443.805	-0.0044	-3	4.79	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
17618	dirMS_041712_NAR_50mM_minus2.13964.13964.3	3	6.78	1	3.23E+04		(R)VTPTRTE	(R)V T|P T R T E I/I I|L/A T R(T)		147.73	528.653	1583.948	-0.0035	-2.2	9.57	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
17619	dirMS_041712_NAR_50mM_minus2.16512.16512.3	3	6.78	0	8.79E+04		(K)VSHLLGI	(K)V S H L L\G\I N\V/T|D F T R(G)		162.08	524.6237	1571.854	0.0025	1.6	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
17620	dirMS_041712_NAR_60mM_minus.10783.10783.3	3	6.78	0	5.06E+04		(R)AYADSY	(R)A Y/A/D/S\Y Y Y/E D G G M K P R(V)		119.78	629.2712	1885.806	-0.0071	-3.8	4.56	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
17621	dirMS_041712_NAR_60mM_minus.17958.17958.3	3	6.78	1	1.25E+04		(K)RSIQFVD	(K)R S I Q|F\V|D|W C/P T G F K(V)	C:Carbamidomethylation	161.33	580.9568	1740.853	0.0032	1.8	8.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
17622	dirMS_041712_NAR_60mM_minus.5869.5869.2	2	6.78	1	2.61E+06		(K)DSYVGD	(K)D S Y|V/G/D E A Q S K R(G)		88.52	677.8144	1354.623	-0.0018	-1.3	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
17623	dirMS_041712_NAR_60mM_minus.7633.7633.3	3	6.78	1	7.96E+05		(K)IQDKEGI	(K)I Q D K E G I|P/P/D Q Q R(L)		101.62	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
17624	dirMS_041712_NAR_20mM_plus.15253.15253.2	2	6.78	0	5.88E+04		(R)EQLAIAE	(R)E Q|L|A/I/A E F A R(S)		176.1	574.312	1147.611	0.0061	5.3	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
17625	dirMS_041712_NAR_30mM_plus2.21554.21554.2	2	6.78	0	1.58E+05		(R)VFIGNLN	(R)V F|I/G N L N T L V\V K(K)		167.38	658.8983	1316.794	-0.0043	-3.3	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
17626	dirMS_041712_NAR_30mM_plus2.22582.22582.3	3	6.78	0	5.00E+05		(R)ALTVPEL	(R)A L\T V/P E L T/Q Q/V F D A K(N)		175.77	553.9697	1659.895	-0.0007	-0.4	4.37	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
17627	dirMS_041712_NAR_30mM_plus2.5777.5777.2	2	6.78	0	1.37E+05		(R)TVQCLSI	(R)T/V|Q C/L/S R(E)	C:Carbamidomethylation	85.03	432.2218	863.44	-0.004	-4.7	9.41	14357.1	4.94	HUMAN	H0Y4B9	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
17628	dirMS_041712_NAR_40mM_plus2.6896.6896.2	2	6.78	0	5.56E+03		(R)LSVAAQ	(R)L S/V/A/A Q/E/A\A R(L)		100.35	508.2775	1015.553	-0.0054	-5.3	6	533778	5.74	HUMAN	Q15149	Plectin
17629	dirMS_041712_NAR_50mM_plus2.10294.10294.3	3	6.78	0	8.80E+04	M778m	(R)mLTGPV	(R)m L|T/G P V|Y/S Q/S T A L T H K(Q)	m:Oxidized methionine	121.92	583.9631	1733.889	15.9857	-5.3	8.37	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
17630	dirMS_041712_NAR_50mM_plus2.18511.18511.3	3	6.78	0	1.20E+06		(R)DFLLKPE	(R)D F|L/L/K/P E L/L R(A)		164.68	415.2519	1243.741	0.0003	0.2	6.07	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
17631	dirMS_041712_NAR_60mM_plus.9904.9904.3	3	6.78	1	3.09E+05		(K)ALTSELA	(K)A L|T/S E L/A N A R D E/S K(K)		109.5	502.2639	1504.76	0.017	11.3	4.68	67933	6.08	HUMAN	P26038	Moesin
17632	dirMS_041712_NAR_120mM_minus.8669.8669.3	3	6.77	1	2.00E+05		(R)KQSTDE	(R)K Q S T D\E E/V/T/S L/A K(S)		101.68	479.2478	1435.728	0.0014	1	4.68	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
17633	dirMS_041712_NAR_20mM_minus.7380.7380.2	2	6.77	0	1.37E+05	M21m	(K)ATAVmF	(K)A T/A\V/m|P D G Q F K(D)	m:Oxidized methionine	122.1	590.7864	1164.572	15.9938	-1	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
17634	dirMS_041712_NAR_30mM_minus2.12184.12184.2	2	6.77	0	2.43E+05		(R)TIGISVD	(R)T I/G|I/S V D|P R(R)		119.08	479.2746	957.536	0.0056	5.8	5.5	14749.1	12.2	HUMAN	J3QSB4	60S ribosomal protein L13 (Fragment)
17635	dirMS_041712_NAR_40mM_minus2.12042.12042.3	3	6.77	0	2.87E+04	M202m	(K)ILGSGIS	(K)I L|G/S G\I/S S S S V L H G m V/F K(K)	m:Oxidized methionine	154.1	612.3321	1818.978	16.0035	4.7	8.76	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
17636	dirMS_041712_NAR_40mM_minus2.12330.12330.3	3	6.77	1	1.79E+04		(K)VVEEAP	(K)V V|E E/A P S I F L D/A E T R R(A)		155.72	611.3244	1831.955	0.0038	2.1	4.41	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
17637	dirMS_041712_NAR_50mM_minus2.18036.18036.3	3	6.77	0	8.78E+04		(R)EAVELPI	(R)E/A\V/E L/P L/T H F E L/Y K(Q)		171.98	563.634	1688.889	-0.002	-1.2	4.75	47479.5	5.09	HUMAN	P43686	26S protease regulatory subunit 6B
17638	dirMS_041712_NAR_60mM_minus.10791.10791.3	3	6.77	0	2.07E+05		(K)TGNLGN	(K)T/G/N/L|G N V/V/H I E R(F)		120.15	436.9057	1308.702	0.0007	0.5	6.41	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
17639	dirMS_041712_NAR_60mM_minus.20000.20000.3	3	6.77	0	2.25E+05		(R)EGGFLLI	(R)E G G F/L/L L/H T L L R(G)		182.45	456.9372	1368.8	-0.0027	-2	6.85	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
17640	dirMS_041712_NAR_60mM_minus.8246.8246.3	3	6.77	1	1.32E+05		(R)KQSTDE	(R)K Q S T D\E E|V/T/S L/A/K(S)		105.82	479.2451	1435.728	-0.0067	-4.7	4.68	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
17641	dirMS_041712_NAR_60mM_minus.8447.8447.3	3	6.77	1	5.51E+04		(R)FEEEIKA	(R)F/E/E E I/K A\E Q/E E R(K)		107.07	512.9085	1536.718	-0.0067	-4.4	4.2	26810.9	5.15	HUMAN	Q96C19	EF-hand domain-containing protein D2
17642	dirMS_041712_NAR_120mM_plus.10704.10704.3	3	6.77	1	3.49E+05		(R)KLDPGSI	(R)K\L D/P G S/E E/T/Q T/L\V R(E)		109	524.9451	1572.823	-0.002	-1.3	4.68	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
17643	dirMS_041712_NAR_120mM_plus.15506.15506.4	4	6.77	2	6.93E+05		(K)VGLQVV	(K)V G L Q V/V A V/K/A/P G F G D N R K(N)		135.03	464.5161	1855.055	-0.0123	-6.6	9.99	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
17644	dirMS_041712_NAR_120mM_plus.6026.6026.2	2	6.77	1	2.29E+06		(K)IREEYPD	(K)I R\E E/Y P D|R(I)		84.93	539.2694	1077.532	-0.0008	-0.8	4.68	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
17645	dirMS_041712_NAR_120mM_plus.8346.8346.3	3	6.77	0	2.20E+05	M80m	(R)TICSHVC	(R)T/I/C S/H V Q N m I K(G)	C:Carbamidomethylation m:Oxid	97.45	449.5568	1330.661	15.9952	0.2	8.44	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
17646	dirMS_041712_NAR_120mM_plus.8418.8418.2	2	6.77	0	2.62E+05		(K)EFHGNII	(K)E F/H/G N I\I/K(V)		97.6	479.2612	957.515	-0.0001	-0.1	6.85	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
17647	dirMS_041712_NAR_20mM_plus.12046.12046.2	2	6.77	0	5.20E+04		(K)VVLVLA(	(K)V V|L/V L A/G/R(Y)		156.4	413.778	826.551	-0.0022	-2.6	9.72	4480.4	11.2	HUMAN	K7ERY7	60S ribosomal protein L27
17648	dirMS_041712_NAR_20mM_plus.12393.12393.3	3	6.77	0	3.15E+04		(K)IISNASC	(K)I I\S N\A\S C T T/N C L/A/P L A K(V)	C:Carbamidomethylation	157.65	611.9768	1833.92	-0.0039	-2.1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
17649	dirMS_041712_NAR_20mM_plus.9007.9007.2	2	6.77	0	2.37E+05		(R)VLTVINC	(R)V L|T|V/I|N Q T Q K(E)		132.92	572.3399	1143.673	-0.0007	-0.6	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
17650	dirMS_041712_NAR_30mM_plus2.6727.6727.2	2	6.77	0	1.86E+05		(K)TLNAGA	(K)T\L|N/A G A Y S K(V)		89.6	462.7408	924.479	-0.0042	-4.5	8.26	30197.4	7.91	HUMAN	E9PMG2	Palmitoyl-protein thioesterase 1 (Fragment)
17651	dirMS_041712_NAR_30mM_plus2.7206.7206.2	2	6.77	0	2.52E+05		(R)FVDPNT	(R)F/V/D|P N T Q E K(V)		91.67	539.2643	1077.521	0.0002	0.2	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
17652	dirMS_041712_NAR_40mM_plus2.10441.10441.2	2	6.77	0	9.40E+04		(K)IGGIGTV	(K)I/G|G I|G T V P/V G R(V)		125.75	513.3081	1025.61	-0.0013	-1.2	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
17653	dirMS_041712_NAR_50mM_plus2.14189.14189.3	3	6.77	0	1.87E+06	M457m	(R)mGPLGL	(R)m/G/P L/G L D H M/A/S S I E R(M)	m:Oxidized methionine	143.02	543.9304	1613.777	15.9992	2.6	5.3	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M

17654	dirMS_041712_NAR_60mM_plus.16474.16474.3	3	6.77	0	3.49E+05		(R)VHIGQV	(R)V H\I G Q V|I/M/S I R(T)		144.05	418.2478	1252.719	0.0094	7.5	9.73	18819.6	10.31	HUMAN	F8W7C6	60S ribosomal protein L10
17655	dirMS_041712_NAR_60mM_plus.6865.6865.2	2	6.77	0	2.45E+05		(R)MEELHN	(R)M E/E|L/H/N Q E M/Q|K(R)		94.28	708.8155	1416.625	-0.0009	-0.6	4.75	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
17656	dirMS_041712_NAR_20mM_minus.10375.10375.2	2	6.76	0	1.44E+05		(R)IYVVDV	(R)I Y/V/V/D V G S E/P R(A)		152.93	617.3216	1233.647	-0.0115	-9.3	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
17657	dirMS_041712_NAR_30mM_minus2.4544.4544.2	2	6.76	0	9.20E+05		(K)QASEGP	(K)Q A/S E G/P L/K(G)		75.6	415.2235	829.441	-0.0017	-2	6	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
17658	dirMS_041712_NAR_30mM_minus2.7880.7880.2	2	6.76	0	5.46E+05		(K)TQLAVC	(K)T Q|L/A/V/C Q Q R(I)	C:Carbamidomethylation	96.65	552.2842	1103.563	-0.0015	-1.3	9.41	9740.1	10.08	HUMAN	H0YFG2	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed (Fragment)
17659	dirMS_041712_NAR_30mM_minus2.9255.9255.2	2	6.76	0	3.53E+05		(K)CAADLG	(K)C A|A|D/L G L N/K(G)	C:Carbamidomethylation	104.88	481.2466	961.477	0.0088	9.1	5.84	13915.8	6.43	HUMAN	P49773	Histidine triad nucleotide-binding protein 1
17660	dirMS_041712_NAR_50mM_minus2.10655.10655.3	3	6.76	0	5.37E+03		(K)HCASQY	(K)H C A/S Q Y S E L L/E T\T E/T/P K(R)	C:Carbamidomethylation	127.82	665.3162	1993.917	0.0169	8.5	4.75	95816.5	4.57	HUMAN	B5MCW3	Bromodomain-containing protein 8
17661	dirMS_041712_NAR_50mM_minus2.11685.11685.3	3	6.76	1	1.81E+04		(R)ELISNSSI	(R)E L/I/S/N/S S D A L/D K I R(Y)		134.55	520.9445	1560.823	-0.0038	-2.5	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
17662	dirMS_041712_NAR_50mM_minus2.13631.13631.3	3	6.76	0	5.40E+05		(K)LQMEAF	(K)L Q|M E/A P H\I/I V G T/P G R(V)		145.62	540.2947	1618.873	-0.0038	-2.4	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
17663	dirMS_041712_NAR_60mM_minus.15063.15063.3	3	6.76	0	3.51E+04		(K)AFSLNSN	(K)A F|S L N|S N L/V/L H Q R(I)		143.9	500.2735	1498.813	-0.0065	-4.4	9.8	40178.9	9.55	HUMAN	B3KRF7	Zinc finger protein with KRAB and SCAN domains 1
17664	dirMS_041712_NAR_120mM_plus.10003.10003.3	3	6.76	2	2.75E+05		(K)MQASIE	(K)M Q|A S I E K/G G S L P K V E/A K(F)		105.42	591.657	1772.958	-0.001	-0.6	8.25	32745.6	4.64	HUMAN	P06748	Nucleophosmin
17665	dirMS_041712_NAR_120mM_plus.11282.11282.3	3	6.76	0	5.91E+05		(R)SIFQHIQ	(R)S I/F Q/H I Q S A Q S Q R(S)		112.63	510.5986	1529.782	-0.0007	-0.4	9.49	108720.9	10.17	HUMAN	Q9Y2W1	Thyroid hormone receptor-associated protein 3
17666	dirMS_041712_NAR_20mM_plus.6763.6763.2	2	6.76	0	2.68E+05	S224s	(K)AILDsK(	(K)A I|L|D s K(R)	s:N-acetylglucosamine (S)	111.43	425.2226	646.377	203.0609	-21.7	5.88	26203.6	8.83	HUMAN	Q9NPB1	5'(3')-deoxyribonucleotidase, mitochondrial
17667	dirMS_041712_NAR_20mM_plus.8995.9049.2	2	6.76	0	4.43E+05		(K)VIPELNG	(K)V I|P/E L N G K(L)		133.17	435.2573	869.509	-0.0018	-2	5.97	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
17668	dirMS_041712_NAR_30mM_plus2.12275.12537.2	2	6.76	0	1.24E+06		(R)IGAVGQ	(R)I G|A/V G/Q A V S R(T)		118.1	479.2725	957.548	-0.0099	-10.3	9.75	109422.9	8.68	HUMAN	A4D2Q0	SUN domain-containing protein 1
17669	dirMS_041712_NAR_30mM_plus2.20128.20128.2	2	6.76	0	2.07E+04		(R)SPTWFG	(R)S P|T/W/F/G I\P R(L)		159.2	530.785	1060.557	0.0053	5	9.47	112927.8	6.09	HUMAN	P78347	General transcription factor II-I
17670	dirMS_041712_NAR_30mM_plus2.9413.9413.2	2	6.76	0	4.50E+05		(K)ATFDAIS	(K)A T|F/D A/I S K(T)		103.12	426.7266	852.446	-0.0002	-0.3	5.88	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
17671	dirMS_041712_NAR_40mM_plus2.9860.9860.2	2	6.76	0	2.29E+05		(K)EQFAW	(K)E Q|F/A/W R(H)		122.8	418.706	836.405	-0.0002	-0.3	6.1	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
17672	dirMS_041712_NAR_50mM_plus2.11421.11421.3	3	6.76	1	2.61E+05		(K)CATITPD	(K)C A/T|I/T/P/D E/A R V E E F K(L)	C:Carbamidomethylation	127.75	589.2842	1765.843	-0.0045	-2.5	4.41	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
17673	dirMS_041712_NAR_50mM_plus2.19025.19025.3	3	6.76	0	8.54E+05		(R)CRPDQL	(R)C R P D Q L T\G\L/S\L/L/P L S E K(A)	C:Carbamidomethylation	167.68	643.0148	1927.032	-0.0019	-1	6.07	533778	5.74	HUMAN	Q15149	Plectin
17674	dirMS_041712_NAR_50mM_plus2.20352.20352.3	3	6.76	1	1.04E+04		(K)SSVLESL	(K)S S/V/L/E/S L V G R D/L L P\R(G)		175.6	547.6436	1640.933	-0.0167	-10.2	5.79	19884.2	4.87	HUMAN	B4DDQ3	Dynamin-1-like protein
17675	dirMS_041712_NAR_60mM_plus.11015.11015.3	3	6.76	0	6.44E+05		(K)GSYVSIH	(K)G S/Y/V/S I/H S S G F R(D)		115.62	432.8835	1296.633	0.0028	2.2	8.75	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
17676	dirMS_041712_NAR_20mM_minus.13129.13129.2	2	6.75	0	2.35E+05		(R)GNPTVE	(R)G N/P T/V/E V D/L F/T S K(G)		183.13	703.8605	1406.716	-0.0025	-1.8	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
17677	dirMS_041712_NAR_40mM_minus2.8128.8128.3	3	6.75	1	3.18E+05		(R)DGKLVS	(R)D G\K L V\S\E/S/S D\V L/P K(-)		128.2	491.9311	1473.78	-0.0008	-0.5	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
17678	dirMS_041712_NAR_50mM_minus2.10527.10527.3	3	6.75	1	7.84E+04		(K)VIQEIVD	(K)V I/Q E/I V/D K/S G V V R(V)		128.13	481.2838	1441.837	-0.0005	-0.3	6.04	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
17679	dirMS_041712_NAR_50mM_minus2.12318.12318.3	3	6.75	0	1.00E+05		(K)IVLDNSV	(K)I V/L/D N S\V/F S E H R(N)		138.13	472.5813	1415.728	0.0016	1.1	5.32	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
17680	dirMS_041712_NAR_50mM_minus2.17094.17094.3	3	6.75	0	1.55E+05		(R)LLEVLSG	(R)L L/E/V\L S/G E I L/P/K P T/K(G)		165.35	546.3329	1636.988	-0.0042	-2.6	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
17681	dirMS_041712_NAR_60mM_minus.12810.12810.3	3	6.75	1	1.50E+05		(R)TPSDVKI	(R)T|P S D V/K E L/V/L D N S/R(S)		131.37	524.9451	1572.823	-0.002	-1.3	4.55	20111	4.47	HUMAN	H0YN26	Acidic leucine-rich nuclear phosphoprotein 32 family member A
17682	dirMS_041712_NAR_60mM_minus.17835.17835.3	3	6.75	1	5.88E+05		(R)KVESLQI	(R)K\V E S\L\Q\E E|I/A/F L K(K)		159.98	511.9529	1533.852	-0.0081	-5.3	4.79	49709.6	5.19	HUMAN	B0YJC4	Vimentin
17683	dirMS_041712_NAR_20mM_plus.8013.8013.2	2	6.75	0	4.21E+05	M239m	(K)EVDEQm	(K)E V D E/Q m\L|N V|Q/N K(N)	m:Oxidized methionine	125.1	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
17684	dirMS_041712_NAR_30mM_plus2.19386.19553.2	2	6.75	0	1.93E+05		(K)CALDFFF	(K)C/A|L/D/F F R(Q)	C:Carbamidomethylation	155.83	464.7242	928.434	0.0066	7.1	5.84	15387.4	6.92	HUMAN	F5H7V7	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8
17685	dirMS_041712_NAR_30mM_plus2.5715.5715.2	2	6.75	0	6.89E+04		(R)QLEDGD	(R)Q L|E D|G D Q/P E S K(K)		83.85	623.2808	1245.559	-0.005	-4	3.91	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
17686	dirMS_041712_NAR_30mM_plus2.6406.6489.2	2	6.75	0	2.26E+05		(R)CAYVYK	(R)C A|Y/V/Y/K(A)	C:Carbamidomethylation	87.97	402.1948	803.376	0.0067	8.3	8.5	10702.2	10.89	HUMAN	C9K025	60S ribosomal protein L35a (Fragment)
17687	dirMS_041712_NAR_30mM_plus2.6978.6978.2	2	6.75	0	2.46E+05		(R)FVDPNT	(R)F V|D|P N T Q E\K(V)		91.57	539.2643	1077.521	0.0002	0.2	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
17688	dirMS_041712_NAR_40mM_plus2.10239.10239.2	2	6.75	0	1.25E+05		(K)AAVLTE	(K)A A V/L T E/T/P/R(T)		124.93	479.2747	957.536	0.0058	6	6.05	114409.9	5.99	HUMAN	Q3ZCV1	Ubiquitin carboxyl-terminal hydrolase
17689	dirMS_041712_NAR_40mM_plus2.17597.17597.3	3	6.75	0	5.36E+04		(K)ASVITQ	(K)A S|V/I/T Q V F H/V/P L E E R(K)		170.05	575.6528	1724.933	0.0109	6.3	5.4	24511.6	6.62	HUMAN	C9J5E5	Vigilin (Fragment)
17690	dirMS_041712_NAR_50mM_plus2.11963.11963.3	3	6.75	1	3.33E+06		(R)VVDLM	(R)V V|D L\M/A H/M A S K/E(-)		130.52	444.2215	1330.649	0.0006	0.4	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
17691	dirMS_041712_NAR_50mM_plus2.7754.7754.3	3	6.75	1	1.36E+05		(R)LGTPELS	(R)L/G\T/P/E L/S T A E R K(E)		106.72	434.5738	1301.706	0.0009	0.7	6.14	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
17692	dirMS_041712_NAR_50mM_plus2.9186.9186.3	3	6.75	1	6.63E+04		(R)NTNSVP	(R)N T|N/S V/P E T A P A A I/P E T K R(N)		115.33	632.6588	1895.982	-0.0203	-10.7	6.14	142137.5	9.17	HUMAN	E7ENU4	Double-stranded RNA-specific adenosine deaminase
17693	dirMS_041712_NAR_60mM_plus.8883.8883.3	3	6.75	1	7.11E+05		(R)QLQLAQ	(R)Q L/Q L A Q/E/A A Q K R(L)		104.87	461.9268	1383.77	-0.0044	-3.2	8.75	533778	5.74	HUMAN	Q15149	Plectin
17694	dirMS_041712_NAR_120mM_minus.15551.15551.3	3	6.74	1	3.00E+05		(R)MSMKE	(R)M/S M K E V D\E Q/M/L/N V/Q/N K(N)		138.97	641.9706	1923.897	0	0	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
17695	dirMS_041712_NAR_30mM_minus2.16247.16247.2	2	6.74	0	2.52E+04		(R)VFSGLV	(R)V/F/S G/L/V\S T G L K(V)		141.38	554.3215	1107.641	-0.0051	-4.6	8.72	96306.4	6.41	HUMAN	P13639	Elongation factor 2
17696	dirMS_041712_NAR_30mM_minus2.18782.18782.2	2	6.74	0	3.44E+04		(K)YPQLLP	(K)Y/P Q/L\L/P G I R(G)		157.48	528.816	1056.62	0.0047	4.4	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
17697	dirMS_041712_NAR_40mM_minus2.9192.9192.3	3	6.74	0	1.57E+05	M26m	(R)LSAmLV	(R)L S\A m L V\P V/T|P E V/K P K(R)	m:Oxidized methionine	136.37	542.315	1608.939	15.9911	-2.3	8.59	31524.1	4.5	HUMAN	P82970	High mobility group nucleosome-binding domain-containing protein 5
17698	dirMS_041712_NAR_50mM_minus2.14757.14757.3	3	6.74	0	8.03E+04	M1280m	(R)QARPTY	(R)Q A R P T Y A/T/A m/L Q S L L K(-)	m:Oxidized methionine	151.87	603.3247	1791.979	15.981	-7.7	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
17699	dirMS_041712_NAR_60mM_minus.4735.4735.3	3	6.74	1	1.35E+06		(R)AAEEED	(R)A/A/E E/E/D E A D/P K R(Q)		78.07	453.872	1359.602	-0.0008	-0.6	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
17700	dirMS_041712_NAR_120mM_plus.17668.17668.4	4	6.74	1	1.40E+05		(K)KTTIENI	(K)K T T I E\N\I Q L/P H T L/L S R(F)		145.95	466.7655	1864.065	-0.0249	-13.4	8.76	95792.4	6.36	HUMAN	J3KPV4	DNA replication licensing factor MCM4
17701	dirMS_041712_NAR_120mM_plus.8668.8668.3	3	6.74	1	1.57E+05		(R)RTEEGP	(R)R T E E G\P/T L/S Y G/R(D)		99.07	455.8929	1365.676	-0.0116	-8.5	6.14	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
17702	dirMS_041712_NAR_20mM_plus.18827.18827.2	2	6.74	0	1.03E+05		(K)LTVYTTL	(K)L T|V|Y/T T/L/I D V T K(G)		200.85	683.8948	1366.783	-0.0005	-0.4	5.83	42194.9	8.75	HUMAN	E7EMM4	Acid ceramidase
17703	dirMS_041712_NAR_20mM_plus.19364.19364.3	3	6.74	0	2.22E+05		(R)LAGTQP	(R)L A G T Q P L|E\V L|E A/V Q R(S)		204.52	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
17704	dirMS_041712_NAR_20mM_plus.8182.8182.2	2	6.74	0	3.29E+05	M176m	(K)VLEGmE	(K)V/L/E\G/m E V V R(K)	m:Oxidized methionine	126.93	524.278	1031.555	15.9933	-1.5	4.53	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
17705	dirMS_041712_NAR_30mM_plus2.14230.14230.3	3	6.74	0	3.23E+05		(R)LNDSILC	(R)L N D S I L/Q/A/T/E Q R(R)		127.15	463.2439	1387.718	-0.0004	-0.3	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
17706	dirMS_041712_NAR_30mM_plus2.16028.16028.2	2	6.74	0	1.59E+06		(K)ICSWNV	(K)I/C|S/W N/V D/G L R(A)	C:Carbamidomethylation	137.75	610.3003	1219.589	0.0045	3.7	5.84	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
17707	dirMS_041712_NAR_30mM_plus2.20862.21124.2	2	6.74	0	3.43E+05		(K)FIIPQIVK	(K)F I|I|P Q I V\K(Y)		164.53	479.3092	957.613	-0.002	-2.1	8.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
17708	dirMS_041712_NAR_30mM_plus2.21039.21039.2	2	6.74	0	3.90E+04		(R)EMVLEII	(R)E M|V L/E/I/I/R(E)		163.43	501.7877	1002.565	0.0029	2.9	4.53	61981.6	8.97	HUMAN	Q96I24	Far upstream element-binding protein 3
17709	dirMS_041712_NAR_40mM_plus2.10829.10829.3	3	6.74	0	2.22E+05		(R)LLEAQA	(R)L L/E A/Q/A C/T G G I I/H P T T G Q K(L)	C:Carbamidomethylation	128.95	665.6807	1995.033	-0.0052	-2.6	6.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
17710	dirMS_041712_NAR_40mM_plus2.9826.9826.3	3	6.74	0	1.23E+05		(R)VMLGET	(R)V M/L/G E T N P A D S K/P G T I R(G)		122.05	595.9778	1785.916	0.0025	1.4	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
17711	dirMS_041712_NAR_50mM_plus2.12806.12806.3	3	6.74	1	4.76E+05		(K)VQQTVC	(K)V Q|Q/T/V Q/D L F G R A P S K(A)		134.77	558.6425	1673.897	0.016	9.6	8.72	73964.5	5.87	HUMAN	P38646	Stress-70 protein, mitochondrial
17712	dirMS_041712_NAR_50mM_plus2.6010.6010.3	3	6.74	1	2.40E+04		(R)GTDDSP	(R)G T D D\S/P K D S Q E D L/Q/E\R(H)		95.62	607.2766	1819.794	0.0212	11.6	3.96	23420.8	4.74	HUMAN	Q5H9L2	Transcription elongation factor A protein-like 5
17713	dirMS_041712_NAR_30mM_minus2.15344.15344.2	2	6.73	0	1.76E+04		(R)IGGGID	(R)I/G\G G/I|D V/P/V P R(H)		137.17	540.3087	1079.621	-0.0106	-9.9	5.84	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
17714	dirMS_041712_NAR_30mM_minus2.20465.20465.2	2	6.73	0	4.58E+05		(R)FLTWILN	(R)F L|T/W I L N R(Y)		175.92	531.8089	1062.61	0.001	1	9.75	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
17715	dirMS_041712_NAR_50mM_minus2.10862.10862.3	3	6.73	1	4.82E+05		(K)QQEAAL	(K)Q Q/E/A A/L E L E E L|K K(K)		131.02	510.2775	1528.822	-0.0038	-2.5	4.49	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
17716	dirMS_041712_NAR_60mM_minus.10661.10661.3	3	6.73	0	3.44E+03	M722m	(K)AGNNm	(K)A/G N N m/L L/V/G V/H/G P R(T)	m:Oxidized methionine	119.93	484.257	1434.763	15.993	-1.3	9.8	83264.1	6.04	HUMAN	E9PHF0	Filamin-A
17717	dirMS_041712_NAR_60mM_minus.16878.16878.3	3	6.73	1	2.46E+05		(K)YAVLYQ	(K)Y A|V/L Y/Q/P/L F D/K R(F)		154.5	504.9409	1512.821	-0.0128	-8.4	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
17718	dirMS_041712_NAR_60mM_minus.16996.16996.3	3	6.73	1	2.47E+05		(K)YAVLYQ	(K)Y A|V/L Y Q/P L F D K/R(F)		154.63	504.9409	1512.821	-0.0128	-8.4	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
17719	dirMS_041712_NAR_60mM_minus.19282.19282.3	3	6.73	0	1.04E+06		(R)SLHDAL	(R)S L H\D\A/L\C|V|L/A Q T V K(D)	C:Carbamidomethylation	171.22	518.9484	1554.831	-0.0002	-0.1	6.46	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
17720	dirMS_041712_NAR_120mM_plus.16521.16521.4	4	6.73	1	2.10E+05		(R)QLLASEL	(R)Q L L A S E/L/P M G P G/L\P/R D P R(A)		139.6	487.5113	1947.048	-0.0247	-12.7	6.07	96157.7	9.19	HUMAN	A6PVC2	Protein monoglycylase TTLL8
17721	dirMS_041712_NAR_20mM_plus.16015.16015.2	2	6.73	0	2.40E+05		(K)DAGTIA	(K)D A\G\T I/A/G L N V L R(I)		182.48	600.3422	1199.674	0.0029	2.4	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
17722	dirMS_041712_NAR_30mM_plus2.20569.20569.2	2	6.73	0	1.75E+05		(R)ASLSLW	(R)A S L/S L/W/Q/A M E/K(G)		162.6	632.3231	1263.64	-0.0013	-1	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
17723	dirMS_041712_NAR_30mM_plus2.4735.4735.2	2	6.73	0	8.59E+05	M571m	(R)mGANSI	(R)m G A|N/S L/E/R(M)	m:Oxidized methionine	75.82	447.2119	877.42	15.9969	2.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
17724	dirMS_041712_NAR_40mM_plus2.11127.11127.3	3	6.73	0	9.07E+04		(R)VLVASS	(R)V/L|V|A S/S V V A G E S Q\K/P E L K(A)		131.88	614.3443	1841.038	-0.0195	-10.6	6.11	61441.6	5.93	HUMAN	G8JLE9	Fragile X mental retardation protein 1
17725	dirMS_041712_NAR_40mM_plus2.12273.12273.3	3	6.73	0	1.60E+05		(K)QLTEED	(K)Q L/T/E E/D/G V H S V I E E N I K(C)		138.73	647.3228	1939.961	-0.0069	-3.5	4.25	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
17726	dirMS_041712_NAR_40mM_plus2.13661.13661.3	3	6.73	1	1.31E+04		(K)DMELPT	(K)D M|E L/P T E K E V A L V K(D)		146.4	534.6192	1601.845	-0.0024	-1.5	4.41	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
17727	dirMS_041712_NAR_50mM_plus2.10800.10800.3	3	6.73	1	1.08E+05		(R)EIAQDF	(R)E I/A/Q D F K T/D/L R(F)		124.48	445.9079	1335.69	0.0188	14.1	4.56	14166.5	11.62	HUMAN	B4DEB1	Histone H3
17728	dirMS_041712_NAR_50mM_plus2.7732.7732.3	3	6.73	1	1.36E+05		(R)LGTPELS	(R)L/G\T/P E/L/S T A E R K(E)		106.72	434.5738	1301.706	0.0009	0.7	6.14	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
17729	dirMS_041712_NAR_60mM_plus.11620.11620.3	3	6.73	0	1.15E+06		(K)AYPLAD	(K)A Y/P L/A/D/A H L\T K(K)		118.4	400.5518	1199.642	-0.0011	-0.9	6.79	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
17730	dirMS_041712_NAR_60mM_plus.12611.12611.3	3	6.73	1	1.17E+06		(K)DLFPYEE	(K)D L/F/P Y|E E S K E/K(F)		123.58	462.2281	1384.663	0.0067	4.8	4.41	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
17731	dirMS_041712_NAR_60mM_plus.14412.14412.3	3	6.73	0	2.46E+05		(R)VNAIEH	(R)V/N/A/I/E H V/I I P R(I)		132	420.9182	1260.742	-0.0022	-1.8	6.72	21920.7	5.63	HUMAN	G3V2S6	V-type proton ATPase subunit D
17732	dirMS_041712_NAR_60mM_plus.17592.17592.3	3	6.73	0	3.49E+05	T485t	(K)GNHFQ	(K)G N/H F Q D|G t I T K(T)	t:N-acetylglucosamine (T)	148.95	474.2311	1217.591	203.0878	5.9	6.74	75261.9	5.96	HUMAN	Q99467	CD180 antigen
17733	dirMS_041712_NAR_60mM_plus.8277.8277.3	3	6.73	1	4.58E+05		(K)AALSEEE	(K)A/A|L/S/E E E L E/K K(S)		101.08	416.221	1246.652	-0.0041	-3.3	4.49	176357.7	5.25	HUMAN	D3DNT2	Eukaryotic translation initiation factor 4 gamma 1
17734	dirMS_041712_NAR_120mM_minus.10507.10702.3	3	6.72	1	7.08E+05		(K)VKRAGE	(K)V K\R A\G E\I/L/S D/R(K)		111.15	415.2436	1243.712	0.0045	3.6	8.72	990583.7	9.16	HUMAN	F8WCL5	Nebulin
17735	dirMS_041712_NAR_120mM_minus.17044.17044.3	3	6.72	1	4.97E+05		(K)RISEQFT	(K)R I S E\Q|F|T|A/M F R(R)		147.8	462.5714	1385.699	0.0002	0.2	9.6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
17736	dirMS_041712_NAR_120mM_minus.5741.5741.3	3	6.72	0	1.05E+05	M434m M4	(R)LESGmC	(R)L E/S G m Q N/m S I H T K(T)	m:Oxidized methionine	85.03	503.2345	1475.698	31.9908	0.7	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
17737	dirMS_041712_NAR_30mM_minus2.17644.17644.3	3	6.72	0	1.27E+05		(R)SLAALSC	(R)S L A A L S\Q/I/A/Y Q R(N)		150.78	440.9139	1320.727	0.0001	0.1	8.46	64225	6.66	HUMAN	E7EX44	Caldesmon
17738	dirMS_041712_NAR_30mM_minus2.8649.8694.2	2	6.72	0	1.81E+05		(R)VVFDSA	(R)V/V|F/D S A Q R(S)		101.52	461.2392	921.479	-0.0077	-8.4	5.81	82756.6	5.34	HUMAN	C9JIF9	Acylamino-acid-releasing enzyme
17739	dirMS_041712_NAR_40mM_minus2.14592.14592.3	3	6.72	1	9.03E+05		(K)TFVNITP	(K)T F/V|N I/T P A E V G V L V G K D R(S)		171.48	639.0252	1915.065	-0.0037	-1.9	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
17740	dirMS_041712_NAR_50mM_minus2.11084.11084.3	3	6.72	1	8.06E+04		(K)LIPDSIGI	(K)L/I P/D S I/G K D\I E/K(A)		130.97	443.2546	1327.747	0.0025	1.9	4.56	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
17741	dirMS_041712_NAR_50mM_minus2.11630.11630.3	3	6.72	0	1.65E+05		(R)GETFRP	(R)G E|T/F R P S|P A|L/N E F Q K(M)		134.55	574.2947	1720.865	0.0042	2.5	6.14	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
17742	dirMS_041712_NAR_50mM_minus2.6771.6771.3	3	6.72	1	1.42E+04		(R)LGAGGC	(R)L/G A|G G G/S P E K S P S A/Q E L K(E)		105	571.6268	1712.881	-0.0155	-9.1	6.14	24827.2	5.74	HUMAN	H3BS86	E3 ubiquitin-protein ligase CHIP (Fragment)
17743	dirMS_041712_NAR_60mM_minus.11895.11895.3	3	6.72	1	2.47E+04		(R)VQSVEQ	(R)V/Q/S/V/E Q I R E V/A S G A A R(I)		126.18	567.3057	1699.909	-0.006	-3.5	6.11	20631.5	6.98	HUMAN	D6RAX2	C-terminal-binding protein 1 (Fragment)
17744	dirMS_041712_NAR_60mM_minus.18197.18197.3	3	6.72	1	4.80E+05		(K)TQLNLL	(K)T Q|L N L/L/L D/K L R(S)		163.37	442.9403	1326.81	-0.004	-3	8.41	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
17745	dirMS_041712_NAR_20mM_plus.12078.12078.2	2	6.72	0	3.75E+04		(R)LCYYIGA	(R)L C/Y/Y|I|G A T D D A A T K(I)	C:Carbamidomethylation	156.62	781.3622	1561.72	-0.0032	-2	4.21	21156.2	9.41	HUMAN	P55145	Mesencephalic astrocyte-derived neurotrophic factor
17746	dirMS_041712_NAR_20mM_plus.13642.13642.2	2	6.72	0	2.77E+05		(R)GDLGIEI	(R)G D/L/G|I/E I/P A E K(V)		166.72	571.3075	1141.61	-0.0022	-1.9	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
17747	dirMS_041712_NAR_20mM_plus.14322.14322.3	3	6.72	0	7.24E+03		(R)VPTANV	(R)V P T A N V S V|V/D|L T C/R(L)	C:Carbamidomethylation	169.75	510.9348	1530.795	-0.0046	-3	5.81	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
17748	dirMS_041712_NAR_20mM_plus.16312.16312.2	2	6.72	0	8.43E+04		(R)AYILNLV	(R)A Y|I/L N L V K(Q)		183.77	467.2905	933.577	-0.0031	-3.3	8.63	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
17749	dirMS_041712_NAR_20mM_plus.16865.16865.3	3	6.72	0	3.42E+05		(K)VQIAVA	(K)V Q/I\A V\A\N/A/Q E/L L/Q R(M)		187.55	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
17750	dirMS_041712_NAR_20mM_plus.16911.16911.3	3	6.72	0	1.80E+05		(R)AIVAIEN	(R)A I\V/A I E N\P A/D V S V/I/S S/R(N)		188.67	580.9864	1740.949	-0.0044	-2.5	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
17751	dirMS_041712_NAR_20mM_plus.16984.16984.3	3	6.72	0	2.33E+05		(R)AIVAIEN	(R)A I V\A I\E N/P A/D V/S/V/I S S R(N)		188.87	580.9864	1740.949	-0.0044	-2.5	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
17752	dirMS_041712_NAR_30mM_plus2.12593.12593.2	2	6.72	0	3.44E+05		(K)SKPVFSE	(K)S K|P V F S E|S|L|S D(-)		119.12	598.2946	1195.584	-0.0022	-1.8	4.67	11226.4	5.09	HUMAN	O60220	Mitochondrial import inner membrane translocase subunit Tim8 A
17753	dirMS_041712_NAR_30mM_plus2.16135.16135.2	2	6.72	0	3.11E+05		(R)MGPNIY	(R)M/G|P N I|Y E L R(T)		136.67	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
17754	dirMS_041712_NAR_30mM_plus2.4831.4831.2	2	6.72	0	2.51E+05		(R)MDDYC	(R)M/D/D|Y C R(R)	C:Carbamidomethylation	76.48	430.1579	859.307	0.0012	1.4	4.21	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
17755	dirMS_041712_NAR_30mM_plus2.9043.9043.2	2	6.72	0	2.40E+05		(R)SGQGAF	(R)S G|Q|G A/F/G/N M C R(G)	C:Carbamidomethylation	100.87	592.7504	1184.494	0	0	9.47	18988.7	11.2	HUMAN	H3BTP7	60S ribosomal protein L4 (Fragment)
17756	dirMS_041712_NAR_60mM_plus.10695.10695.3	3	6.72	1	7.41E+05		(R)DMQLR	(R)D/M Q L R/V I/P A E V K(F)		112.92	466.9362	1398.777	0.0167	11.9	6.07	111607	8.89	HUMAN	Q6ZTR5	Uncharacterized protein CXorf22
17757	dirMS_041712_NAR_60mM_plus.15122.15122.3	3	6.72	1	1.45E+05		(R)VFDKDG	(R)V F/D K D G N/G\Y\I/S A/A E L R(H)		135.57	585.6281	1754.871	-0.001	-0.6	4.56	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
17758	dirMS_041712_NAR_120mM_minus.16689.16689.3	3	6.71	0	3.35E+05		(K)HLEINPD	(K)H L/E I/N P D H S/I/I/E T L R(Q)		146.33	596.3176	1786.945	-0.0064	-3.6	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
17759	dirMS_041712_NAR_120mM_minus.18755.18755.4	4	6.71	1	3.26E+05		(R)HATALEI	(R)H A\T A\L E/E L/S/E Q L E/Q A K/R(F)		157.77	489.0065	1953.004	0.0006	0.3	4.91	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
17760	dirMS_041712_NAR_20mM_minus.13057.13057.2	2	6.71	0	9.72E+05	M73m	(R)AILVDLE	(R)A I L V/D L/E|P G T m D S V/R(S)	m:Oxidized methionine	182.58	816.4184	1615.836	15.9935	-0.8	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
17761	dirMS_041712_NAR_40mM_minus2.13253.13253.3	3	6.71	0	9.33E+04		(K)VAIVKP	(K)V/A I V\K/P G V|P M/E/I V L N K(E)		162.12	569.6777	1707.024	-0.0052	-3	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
17762	dirMS_041712_NAR_60mM_minus.13304.13304.3	3	6.71	1	5.11E+05		(R)KLVIIEGI	(R)K L V I\I|E|G/D L E R(T)		135.05	428.9221	1284.752	-0.0004	-0.3	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain

17763	dirMS_041712_NAR_120mM_plus.10483.10483.3	3	6.71	1	8.28E+05		(R)LKYENE\	(R)L K Y/E N E/V/A/L/R(Q)		107.98	412.2295	1234.679	-0.0051	-4.1	6.14	59054.3	5.14	HUMAN	P13645	Keratin, type I cytoskeletal 10
17764	dirMS_041712_NAR_120mM_plus.5972.5972.4	4	6.71	2	5.37E+05		(R)KTGQAP	(R)K T G Q\A|P/G/Y S Y/T A A\N K/N K(G)		83.92	450.4826	1798.908	0.0003	0.2	9.83	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
17765	dirMS_041712_NAR_20mM_plus.15874.15874.3	3	6.71	0	8.77E+03		(R)SSFYVN(	(R)S S\F Y V N G L/T L/G G/Q K(C)		179.37	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
17766	dirMS_041712_NAR_20mM_plus.8963.8963.2	2	6.71	0	2.07E+05		(K)VTADVII	(K)V/T|A/D/V I N A A E K(L)		132.57	565.806	1130.605	-0.0005	-0.4	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
17767	dirMS_041712_NAR_30mM_plus2.22176.22176.2	2	6.71	0	1.79E+05		(K)GLSSLLC	(K)G L/S S/L/L/C/N F/T K(S)	C:Carbamidomethylation	171.87	620.3199	1239.64	-0.0077	-6.2	8.75	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
17768	dirMS_041712_NAR_30mM_plus2.7483.7483.2	2	6.71	1	2.75E+05		(K)GGCGG(	(K)G G C/G G Q|W R A/P Q D/R(T)	C:Carbamidomethylation	93.63	722.8266	1444.65	-0.0039	-2.7	9.6	130198.3	9.94	HUMAN	E7EXA6	Chromosome transmission fidelity protein 18 homolog
17769	dirMS_041712_NAR_40mM_plus2.9526.9526.3	3	6.71	0	3.47E+04		(R)GGGGNI	(R)G G G G N F G/P G/P G/S N F/R(G)		119.3	459.8801	1377.629	-0.0037	-2.7	9.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
17770	dirMS_041712_NAR_40mM_plus2.9892.9892.2	2	6.71	0	2.34E+05		(K)EQFAWI	(K)E Q/F/A/W/R(H)		122.82	418.706	836.405	-0.0002	-0.3	6.1	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
17771	dirMS_041712_NAR_50mM_plus2.10347.10347.3	3	6.71	0	1.74E+04		(R)TIVITSHI	(R)T I/V/I/T S H/P G Q I V K(H)		121.95	464.946	1392.821	0.0025	1.8	8.44	27999.4	5.61	HUMAN	B7Z5C0	DnaJ homolog subfamily A member 1
17772	dirMS_041712_NAR_50mM_plus2.14110.14110.3	3	6.71	1	6.91E+04		(K)VVSSSIV	(K)V V|S S S I V/D/K Y I G/E S A R(L)		142.2	570.6392	1709.907	-0.0038	-2.2	6.04	29938.9	6.07	HUMAN	H0YJC0	26S protease regulatory subunit 10B (Fragment)
17773	dirMS_041712_NAR_50mM_plus2.17794.17794.3	3	6.71	0	1.46E+05		(K)SPILLGSI	(K)S P/I|L|L G S L A H/Q I Y/R(M)		161.63	523.3008	1567.896	-0.0076	-4.9	8.49	35727.7	8.87	HUMAN	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial
17774	dirMS_041712_NAR_50mM_plus2.18378.18378.3	3	6.71	0	2.22E+05		(R)IDILDSA	(R)I/D/I/L/D S A L/L R P G R(I)		164.5	480.2828	1438.838	-0.0038	-2.6	5.96	44954.5	8.44	HUMAN	A8K3Z3	26S protease regulatory subunit 8
17775	dirMS_041712_NAR_50mM_plus2.19162.19162.3	3	6.71	0	4.19E+05		(R)CRPDQL	(R)C R P D Q L T/G\L|S/L L/P L S E K(A)	C:Carbamidomethylation	168.33	643.0148	1927.032	-0.0019	-1	6.07	533778	5.74	HUMAN	Q15149	Plectin
17776	dirMS_041712_NAR_60mM_plus.12075.12075.3	3	6.71	0	1.43E+05		(R)EQLQLLI	(R)E Q/L/Q L/L/E/E Q H R(A)		119.22	474.9161	1422.734	0.0002	0.1	4.75	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
17777	dirMS_041712_NAR_60mM_plus.18718.18718.3	3	6.71	1	3.96E+06		(R)VSFELFA	(R)V/S F E L/F A D K V/P K(T)		155.83	460.5914	1379.757	0.0027	2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
17778	dirMS_041712_NAR_120mM_minus.12292.12292.4	4	6.7	2	4.00E+05		(K)KGTVEG	(K)K G T V E G F\E/P A D/N K/C L L R(A)	C:Carbamidomethylation	120.57	484.251	1933.98	0.0021	1.1	6.18	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
17779	dirMS_041712_NAR_120mM_minus.6797.6797.2	2	6.7	0	4.89E+05		(K)HQPTAII	(K)H/Q|P T A|I\I|A K(T)		91.83	489.7898	978.573	-0.0008	-0.8	8.76	63448.4	7.29	HUMAN	B4E022	Transketolase
17780	dirMS_041712_NAR_20mM_minus.12446.12446.3	3	6.7	0	2.98E+05	M256m	(R)SLDmDS	(R)S L D m D S/I/I\A E/V K(A)	m:Oxidized methionine	172.23	446.227	1320.671	15.9949	0	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
17781	dirMS_041712_NAR_30mM_minus2.12374.12374.2	2	6.7	0	2.35E+04		(K)GDYPLE/	(K)G D/Y/P/L/E A V R(M)		119.97	510.2598	1019.516	-0.0033	-3.2	4.37	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
17782	dirMS_041712_NAR_30mM_minus2.17660.17660.2	2	6.7	0	1.24E+05		(K)TTFEDLI(	(K)T T|F/E/D/L/I Q R(C)		150.5	561.7944	1122.579	0.0026	2.3	4.37	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
17783	dirMS_041712_NAR_50mM_minus2.15274.15274.3	3	6.7	0	5.45E+05		(R)DGLAFN	(R)D/G\L/A F/N/A L/I H/R(H)		155.45	409.5594	1226.664	-0.0004	-0.3	6.74	146974	5.55	HUMAN	C9JRP8	Spectrin beta chain, non-erythrocytic 4
17784	dirMS_041712_NAR_50mM_minus2.15497.15497.3	3	6.7	1	8.63E+04	S8s	(R)LTsGFEC	(R)L/T/s G F E/G R V L S L A K(V)	s:N-acetylglucosamine (S)	155.97	560.9824	1477.837	203.0953	9.5	8.75	9330.1	12.31	HUMAN	K7EJ17	Ran-binding protein 3
17785	dirMS_041712_NAR_50mM_minus2.8611.8611.3	3	6.7	1	1.42E+05		(K)TAVCDIF	(K)T A/V/C/D I/P/P R G L K(M)	C:Carbamidomethylation	116.92	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
17786	dirMS_041712_NAR_60mM_minus.11069.11069.3	3	6.7	1	1.61E+05		(K)LLEDKN(	(K)L L|E/D|K N G E V Q N L/A V K(C)		121.37	557.3065	1669.912	-0.007	-4.2	4.68	6116.1	5.2	HUMAN	F5H6I6	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
17787	dirMS_041712_NAR_60mM_minus.13940.13940.3	3	6.7	0	3.54E+05		(K)LHLGTT(	(K)L H L\G T T Q N S\L/T/E/A D/F R(E)		137.45	601.6438	1802.903	0.0137	7.6	5.32	49472.3	6.75	HUMAN	O75351	Vacuolar protein sorting-associated protein 4B
17788	dirMS_041712_NAR_60mM_minus.14650.14650.3	3	6.7	1	2.82E+04		(R)MSMKE'	(R)M S\M K E V D E Q\M|L N\V/Q/N K(N)		141.58	641.9701	1923.897	-0.0015	-0.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
17789	dirMS_041712_NAR_120mM_plus.12438.12438.4	4	6.7	1	1.78E+06		(K)TLTTVQ(	(K)T L\T T V Q/G I/A D D Y D/K K K(L)		117.78	449.7412	1795.944	-0.0006	-0.4	5.71	13778.5	7.96	HUMAN	K7EM18	Eukaryotic translation initiation factor 1
17790	dirMS_041712_NAR_120mM_plus.21411.21411.4	4	6.7	2	4.53E+05	M145m	(R)RGVmLA	(R)R G V\m L\A/V/D/A V/I A E L/K K(Q)	m:Oxidized methionine	166.22	433.0059	1713.009	15.9926	-1.3	8.59	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
17791	dirMS_041712_NAR_20mM_plus.14949.14949.2	2	6.7	0	1.45E+05		(K)VLEQLT(	(K)V L/E Q\L\T G Q/T/P V/F\S|K(A)		174.65	773.9244	1546.848	-0.006	-3.9	5.97	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
17792	dirMS_041712_NAR_20mM_plus.9435.9435.2	2	6.7	0	1.41E+05		(R)GTGIVS/	(R)G T G I/V|S A P V/P K(K)		136.92	513.3057	1025.599	0.0052	5	8.75	21898	11.33	HUMAN	E9PM36	40S ribosomal protein S2
17793	dirMS_041712_NAR_30mM_plus2.20207.20207.3	3	6.7	0	1.14E+05		(R)SQNVM/	(R)S Q N V M/A/A|A/S/I/A N I V K(S)		159.13	506.2751	1516.815	-0.0044	-2.9	8.47	47423	5.43	HUMAN	E7ERF2	T-complex protein 1 subunit alpha
17794	dirMS_041712_NAR_30mM_plus2.4181.4181.2	2	6.7	0	1.24E+06	M299m M:	(K)NmmAA	(K)N m m A|A C D|P R(H)	C:Carbamidomethylation m:Oxid	69.55	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
17795	dirMS_041712_NAR_40mM_plus2.12246.12246.3	3	6.7	0	1.90E+05		(K)AASDIAI	(K)A A|S/D I A M T E/L/P P T H P I R(L)		139.08	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
17796	dirMS_041712_NAR_40mM_plus2.13805.13805.2	2	6.7	0	3.40E+05		(K)LLCGLLA	(K)L/L/C/G/L/L A E R(L)	C:Carbamidomethylation	148.58	522.7962	1044.587	-0.0019	-1.8	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
17797	dirMS_041712_NAR_40mM_plus2.19517.19517.3	3	6.7	1	1.39E+05		(R)TEGLSVI	(R)T E/G L S V L S|Q A M A V I/K E K(I)		181.93	602.0005	1803.988	-0.0015	-0.8	5.81	31604.9	6.88	HUMAN	G3V4T5	Eukaryotic translation initiation factor 2 subunit 1 (Fragment)
17798	dirMS_041712_NAR_50mM_plus2.10232.10232.3	3	6.7	1	5.63E+05	N394n	(R)TGKDSE'	(R)T/G K/D S E V S G S n S L D L K(H)	n:N-acetylglucosamine (N)	120.2	613.9672	1636.802	203.0846	2.8	4.55	121357	10.03	HUMAN	P59923	Zinc finger protein 445
17799	dirMS_041712_NAR_50mM_plus2.17181.17181.3	3	6.7	0	7.10E+05	T170t	(R)VILAGNI	(R)V I|L/A G N L L S H/S t Q/S R(D)	t:N-acetylglucosamine (T)	159.15	600.3189	1595.886	203.0558	-13.1	9.73	28051.3	5.84	HUMAN	C9JHC7	DNA polymerase delta subunit 2 (Fragment)
17800	dirMS_041712_NAR_50mM_plus2.9208.9208.3	3	6.7	0	1.33E+05		(K)AEITLVA	(K)A E I T/L/V A T K/P E K(L)		116.23	433.922	1299.752	-0.0004	-0.3	6.18	98761.7	5.56	HUMAN	Q9UBF2	Coatomer subunit gamma-2
17801	dirMS_041712_NAR_120mM_minus.18831.18831.4	4	6.69	1	3.78E+05		(K)ALERLEC	(K)A L\E R L E G\V/E G V A H I/I D/P K(A)		157.9	487.2717	1946.071	-0.0056	-2.9	4.83	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
17802	dirMS_041712_NAR_120mM_minus.18873.18873.4	4	6.69	1	4.11E+05		(R)HATALEI	(R)H A T A\L\E E\L/S/E Q L/E Q A K R(F)		158.23	489.0065	1953.004	0.0006	0.3	4.91	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
17803	dirMS_041712_NAR_40mM_minus2.9374.9374.3	3	6.69	1	6.96E+05	M356m	(K)VGEVIV'	(K)V/G|E\V|I/V/T K D D A m L L K(G)	m:Oxidized methionine	136.93	549.6354	1630.908	15.9832	-7.1	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
17804	dirMS_041712_NAR_50mM_minus2.10316.10316.3	3	6.69	1	9.57E+03		(K)AELEIQK	(K)A E|L\E\I/Q K/D A L E/P/G Q R(V)		126.97	566.2988	1696.886	-0.0046	-2.7	4.41	14613.6	6.73	HUMAN	G5E9J2	Adenine phosphoribosyltransferase
17805	dirMS_041712_NAR_50mM_minus2.15442.15442.3	3	6.69	0	6.57E+05		(R)LLIHQSL	(R)L/L I/H Q S\L/A/G G I/I G V K(G)		155.1	506.9833	1518.937	-0.0013	-0.8	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
17806	dirMS_041712_NAR_50mM_minus2.15718.15718.3	3	6.69	0	1.04E+05	M55m	(R)DIKPDNI	(R)D I K P D\N F|L/m G I/G R(H)	m:Oxidized methionine	157.97	497.9267	1475.767	15.998	2.1	5.96	27968.7	9.69	HUMAN	D6REM4	Casein kinase I isoform alpha
17807	dirMS_041712_NAR_50mM_minus2.15825.15825.3	3	6.69	0	2.23E+04		(R)GFGHIG	(R)G F G H\I G I A\V|P/D V/Y/S A/C K(R)	C:Carbamidomethylation	158	597.6337	1790.889	-0.0029	-1.6	6.74	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
17808	dirMS_041712_NAR_60mM_minus.10425.10425.3	3	6.69	1	1.06E+05		(K)TCVFEKE	(K)T C|V/F E K E/N D|P/S V M R(S)	C:Carbamidomethylation	117.67	571.2615	1711.778	-0.0079	-4.6	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
17809	dirMS_041712_NAR_60mM_minus.8567.8567.3	3	6.69	1	1.25E+05		(R)QLQLAC	(R)Q\L Q/L A Q/E A/A Q/K/R(L)		107.87	461.9241	1383.77	-0.0125	-9.1	8.75	533778	5.74	HUMAN	Q15149	Plectin
17810	dirMS_041712_NAR_120mM_plus.11404.11404.2	2	6.69	0	8.82E+05	K76k	(R)YFSQSDI	(R)Y/F/S Q S D k(S)	k:Ubiquitin-K	113.12	494.7156	874.394	114.0298	-13.3	5.83	16602.4	6.3	HUMAN	F8W8C9	Immunoglobulin iota chain
17811	dirMS_041712_NAR_20mM_plus.12510.12510.3	3	6.69	0	3.48E+05		(K)IISNASC	(K)I I\S N A\S C T T/N/C L/A P L A/K(V)	C:Carbamidomethylation	159.53	611.9768	1833.92	-0.0039	-2.1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
17812	dirMS_041712_NAR_20mM_plus.15530.15530.2	2	6.69	0	7.27E+04		(R)AVLNPL(	(R)A V/L|N|P L C Q V D|Y R(A)	C:Carbamidomethylation	178.62	724.3735	1447.736	0.0035	2.4	5.88	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
17813	dirMS_041712_NAR_40mM_plus2.9422.9422.2	2	6.69	0	9.68E+04		(R)ISVYYNE	(R)I/S|V/Y Y N/E A T G G K(Y)		118.55	651.3206	1301.637	-0.0033	-2.5	6	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
17814	dirMS_041712_NAR_50mM_plus2.12342.12342.3	3	6.69	0	6.29E+05		(K)GIHPTIIS	(K)G I H P T I\I/S E/S F Q K(A)		132.97	486.2644	1456.78	-0.0008	-0.6	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
17815	dirMS_041712_NAR_50mM_plus2.13735.13735.3	3	6.69	1	1.98E+06	M320m	(K)YmACCL	(K)Y/m|A C/C L L Y R G D V\V/P K(E)	C:Carbamidomethylation m:Oxid	140.55	620.9622	1844.886	15.9865	-4.5	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
17816	dirMS_041712_NAR_50mM_plus2.14332.14332.3	3	6.69	1	4.62E+05	M17m	(K)GAEEmE	(K)G A\E/E/m/E/T V I/P V D V M\R R(A)	m:Oxidized methionine	143.47	616.6377	1831.904	15.9945	-0.2	4.41	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
17817	dirMS_041712_NAR_50mM_plus2.9168.9168.3	3	6.69	0	8.29E+04		(R)LNQLKP(	(R)L/N/Q\L/K/P G L Q Y K(L)		115.55	434.5895	1301.758	-0.0037	-2.8	9.7	96205.6	9.06	HUMAN	G5E9M5	Interleukin enhancer binding factor 3, 90kDa, isoform CRA_b
17818	dirMS_041712_NAR_60mM_plus.8071.8071.3	3	6.69	1	4.67E+05		(K)EFVPGV	(K)E F|V P G V K/Y|G N I(-)		100.8	408.2176	1222.647	-0.0084	-6.9	6.1	7698.3	4.63	HUMAN	D6R9Y1	Polyadenylate-binding protein-interacting protein 2
17819	dirMS_041712_NAR_120mM_minus.9690.9690.3	3	6.68	0	3.99E+05		(K)NCPHIV'	(K)N\C|P H I/V|V/G T P G R(I)	C:Carbamidomethylation	107.5	436.2293	1306.669	0.0049	3.7	9.75	28185.1	10.76	HUMAN	B4DIJ6	Spliceosome RNA helicase DDX39B
17820	dirMS_041712_NAR_30mM_minus2.5866.5866.2	2	6.68	0	8.23E+04		(R)QLEDGD	(R)Q L E/D/G D/Q|P E S K(K)		85.63	623.284	1245.559	0.0014	1.1	3.91	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
17821	dirMS_041712_NAR_30mM_minus2.7478.7478.2	2	6.68	0	1.58E+05		(R)GNPFEN	(R)G N|P/F E N K(G)		95.22	403.1988	805.384	0.0064	8	6	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
17822	dirMS_041712_NAR_40mM_minus2.11050.11050.3	3	6.68	1	1.14E+05	M362m	(R)EGSVmL	(R)E G S V/m/L Q/V/D V/D/T V K G G/L K(L)	m:Oxidized methionine	147.85	630.9989	1874.989	15.993	-1	4.56	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
17823	dirMS_041712_NAR_50mM_minus2.11233.11233.3	3	6.68	1	1.28E+05		(K)TLTTVQ(	(K)T L|T T V Q/G I A/D D Y D K K(K)		132.02	556.6208	1667.849	-0.0008	-0.5	4.43	13778.5	7.96	HUMAN	K7EM18	Eukaryotic translation initiation factor 1
17824	dirMS_041712_NAR_50mM_minus2.18090.18090.3	3	6.68	1	2.51E+04		(R)LARGGG	(R)L A|R G G|G L G S/P G E G G A L P R(C)		172.18	541.3004	1621.877	0.0098	6	9.6	37248.1	11.03	HUMAN	Q7Z7A3	Cytoplasmic tRNA 2-thiolation protein 1
17825	dirMS_041712_NAR_50mM_minus2.5729.5729.3	3	6.68	1	3.05E+04		(K)DSYVGD	(K)D S/Y/V/G D E/A/Q/S K R(G)		93.88	452.2119	1354.623	-0.0022	-1.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
17826	dirMS_041712_NAR_60mM_minus.11573.11573.3	3	6.68	1	1.59E+05		(K)EIADYLA	(K)E\I/A/D/Y L A A G K D E R(A)		124.38	484.2432	1450.717	-0.0022	-1.5	4.32	41736.1	5.41	HUMAN	A8KAH5	IST1 homolog
17827	dirMS_041712_NAR_60mM_minus.17884.17884.3	3	6.68	1	3.70E+05		(K)NLRDIDE	(K)N/L R\D I D E\V/S S/L/L/R(T)		160.93	510.6099	1529.828	-0.013	-8.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
17828	dirMS_041712_NAR_60mM_minus.18240.18240.3	3	6.68	0	8.73E+03		(K)EFSHIAF	(K)E F/S/H I/A|F L T I K(G)		162.55	435.9153	1305.72	0.0112	8.6	6.85	54978.6	6.16	HUMAN	P10619	Lysosomal protective protein
17829	dirMS_041712_NAR_120mM_plus.18279.18279.4	4	6.68	1	6.11E+05		(K)ILGSGIS	(K)I L G S G I S/S/S S V L H G M V F K K(E)		148.82	487.5232	1947.073	-0.0022	-1.1	10	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
17830	dirMS_041712_NAR_20mM_plus.12131.12131.2	2	6.68	0	5.20E+04		(K)VVLVLA(	(K)V/V|L V L/A G/R(Y)		156.4	413.778	826.551	-0.0022	-2.6	9.72	4480.4	11.2	HUMAN	K7ERY7	60S ribosomal protein L27
17831	dirMS_041712_NAR_20mM_plus.17568.17568.2	2	6.68	0	8.56E+04		(R)GDGPICI	(R)G/D G P I C L|V/L/A/P T R(E)	C:Carbamidomethylation	193.13	684.8681	1368.73	-0.0015	-1.1	5.84	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
17832	dirMS_041712_NAR_20mM_plus.7019.7019.2	2	6.68	0	1.53E+05	M108m M:	(K)VEmmnI	(K)V/E|m m/n E K(N)	m:Oxidized methionine n:N-	115.48	558.2383	880.39	235.079	8.8	4.53	54841.6	5.8	HUMAN	Q969S3	Zinc finger protein 622
17833	dirMS_041712_NAR_20mM_plus.8099.8099.2	2	6.68	0	5.37E+04		(K)SVTEQG	(K)S V\T E/Q/G A/E\L|S N E\E R(N)		124.97	774.8589	1548.714	-0.0031	-2	4.09	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
17834	dirMS_041712_NAR_30mM_plus2.19243.19243.2	2	6.68	0	1.96E+05		(R)LTAEDLF	(R)L/T|A E/D L/F E A R(I)		153.5	582.796	1164.59	-0.0048	-4.1	4.14	533778	5.74	HUMAN	Q15149	Plectin
17835	dirMS_041712_NAR_40mM_plus2.12670.12670.2	2	6.68	0	8.84E+04		(R)INEILSN/	(R)I/N|E|I/L/S N A L K(R)		140.95	557.8263	1114.647	-0.0013	-1.2	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
17836	dirMS_041712_NAR_40mM_plus2.18385.18385.3	3	6.68	1	2.56E+04		(R)IAEVGG'	(R)I A E/V/G|G V P Y L/L P L V N Q K K(V)		174.58	646.716	1938.142	-0.0088	-4.5	8.5	18803.3	5.55	HUMAN	E9PIP1	Ester hydrolase C11orf54 (Fragment)
17837	dirMS_041712_NAR_50mM_plus2.11731.11731.3	3	6.68	1	1.31E+05		(K)IGRIEDV	(K)I G R I E D\V T|P\I|P S/D S T R(R)		128.73	585.9784	1755.924	-0.0029	-1.7	4.56	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
17838	dirMS_041712_NAR_50mM_plus2.18676.18676.3	3	6.68	1	2.23E+05		(K)IGEEFLT	(K)I/G/E E/F L T|D L S Q L K K(L)		167.02	540.965	1620.884	-0.0039	-2.4	4.68	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
17839	dirMS_041712_NAR_50mM_plus2.4849.4849.3	3	6.68	1	2.29E+05		(R)AAEDDE	(R)A A|E D D E/D D D V D T K K(Q)		80.78	522.5519	1565.645	-0.0038	-2.4	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
17840	dirMS_041712_NAR_50mM_plus2.7123.7123.3	3	6.68	1	4.68E+04		(K)LAQYEPI	(K)L/A\Q/Y/E/P/P Q E E K R A E(-)		103.17	563.2809	1687.829	-0.0004	-0.3	4.69	11966.5	5.71	HUMAN	Q99417	C-Myc-binding protein
17841	dirMS_041712_NAR_60mM_plus.17029.17029.3	3	6.68	0	3.51E+05		(K)EGHVEV	(K)E G H V E V\V\S/E/L/L|Q R(E)		146.07	498.9326	1494.791	-0.0078	-5.2	4.75	48586.6	9.32	HUMAN	D6RCB2	Ankyrin-3
17842	dirMS_041712_NAR_20mM_minus.10941.10941.2	2	6.67	0	1.01E+05		(K)GTIQVIT	(K)G T I/Q V|I|T Q G T S L K(N)		157.17	673.3789	1345.769	-0.018	-13.4	8.75	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
17843	dirMS_041712_NAR_20mM_minus.9688.9688.2	2	6.67	0	1.23E+05		(R)AGTGVD	(R)A G T G\V/D N/V/D L|E/A A T R(K)		146.8	744.8662	1488.729	-0.0038	-2.5	4.03	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
17844	dirMS_041712_NAR_20mM_minus.9893.9893.3	3	6.67	0	1.49E+04		(K)ALIAAQ'	(K)A L I\A A\Q Y/S/G/A/Q V/R(V)		148.72	449.916	1347.738	-0.0045	-3.3	8.79	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
17845	dirMS_041712_NAR_30mM_minus2.13038.13038.2	2	6.67	2	3.55E+05		(K)KSFKSPE	(K)K S|F/K/S P E P R(L)		124.82	538.2931	1075.59	-0.0105	-9.8	9.99	31183.3	5.86	HUMAN	P21583	Kit ligand
17846	dirMS_041712_NAR_40mM_minus2.8945.8945.3	3	6.67	0	7.64E+04	M237m	(R)LSSPCIm	(R)L S|S/P/C I m V V/N H D A S S\I P R(L)	C:Carbamidomethylation m:Oxid	135.02	666.9949	1982.979	15.9915	-1.7	6.74	87267.9	6.33	HUMAN	Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase
17847	dirMS_041712_NAR_40mM_minus2.9046.9046.3	3	6.67	0	2.56E+04		(K)AASAGV	(K)A A S/A/G V/P Y/H G E V P V S L\A R(A)		135.53	594.3141	1780.934	-0.0063	-3.5	6.79	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
17848	dirMS_041712_NAR_50mM_minus2.10629.10629.3	3	6.67	0	1.23E+05		(R)IMLFTNI	(R)I M\L\F/T N E D N/P/H G N D S A K(A)		129	634.9586	1902.865	-0.0038	-2	4.54	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
17849	dirMS_041712_NAR_50mM_minus2.8746.8746.3	3	6.67	1	2.45E+04		(R)LALGDD	(R)L A|L/G D D S/P/A L K E K(R)		117.67	452.917	1356.737	-0.0005	-0.3	4.56	44431.6	8.52	HUMAN	B7Z7E9	Aspartate aminotransferase
17850	dirMS_041712_NAR_60mM_minus.15874.15874.3	3	6.67	1	3.23E+05		(R)IDTRNEI	(R)I D/T R N E\L|E/S|Y/A/Y S L K(N)		148.27	601.3049	1801.897	0.0035	1.9	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
17851	dirMS_041712_NAR_120mM_plus.10815.10879.4	4	6.67	0	6.52E+05		(K)SAKPTKI	(K)S A K P T K P A A/S D\L\P\V|P A E G V R(N)		109.95	498.5226	1991.092	-0.0234	-11.8	8.31	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
17852	dirMS_041712_NAR_120mM_plus.11054.11054.2	2	6.67	1	6.38E+05		(R)ALAAFLI	(R)A/L/A/A F L K/K(S)		111.98	431.2797	861.556	-0.0035	-4.1	10	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
17853	dirMS_041712_NAR_20mM_plus.14606.14606.2	2	6.67	0	1.56E+05		(K)LVILANN	(K)L V\I/L/A\N N C/P A L R(K)	C:Carbamidomethylation	172.43	677.3851	1353.767	-0.0042	-3.1	9.75	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
17854	dirMS_041712_NAR_20mM_plus.16485.16485.2	2	6.67	0	1.40E+05		(R)QAQEYE	(R)Q A|Q\E\Y/E A/L L/N I K(V)		184.52	710.3754	1419.748	-0.0043	-3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
17855	dirMS_041712_NAR_20mM_plus.16938.16938.3	3	6.67	0	3.07E+05		(K)VQIAVA	(K)V Q I A V\A/N|A\Q/E/L/L Q/R(M)		187.85	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
17856	dirMS_041712_NAR_40mM_plus2.6568.6568.2	2	6.67	0	2.94E+04		(K)AGFAGD	(K)A G/F|A|G D D/A P R(A)		97.9	488.728	976.448	0.0004	0.4	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
17857	dirMS_041712_NAR_50mM_plus2.15475.15475.3	3	6.67	1	9.88E+05		(R)KVPGVT	(R)K\V P G\V T A\I E\L/D/E/D\T/G T F R(I)		149.83	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
17858	dirMS_041712_NAR_50mM_plus2.15507.15507.3	3	6.67	1	6.37E+05		(R)GFPTIYF	(R)G F/P T I/Y/F/S/P A N K K(L)		149.13	490.5973	1469.779	-0.0014	-0.9	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
17859	dirMS_041712_NAR_50mM_plus2.7124.7124.3	3	6.67	1	2.89E+04	M22m M2	(K)LAEQAE	(K)L/A|E/Q/A E R Y/D D m A T/C m K(A)	C:Carbamidomethylation m:Oxid	103.15	655.2828	1931.83	32.0043	7.3	4.32	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
17860	dirMS_041712_NAR_60mM_plus.11951.11951.3	3	6.67	0	3.16E+05		(K)CCLTYCF	(K)C C/L/T/Y C F N K/P E/D/K(-)	C:Carbamidomethylation	119.6	578.9149	1734.728	0.0017	1	6.07	18306.9	9.97	HUMAN	P62979	Ubiquitin-40S ribosomal protein S27a
17861	dirMS_041712_NAR_60mM_plus.14789.14789.3	3	6.67	1	9.63E+04		(R)KFLDGIY	(R)K F L D/G\I|Y/V/S E/K(G)		133.93	433.5671	1298.699	-0.0123	-9.5	6.07	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
17862	dirMS_041712_NAR_60mM_plus.15234.15234.3	3	6.67	1	3.21E+05		(R)FGDRFP.	(R)F/G D R F P A\M|S/D\A Y D R(T)		136.2	549.9126	1647.722	0.0012	0.7	4.43	16961.8	5.36	HUMAN	G3V308	Purine nucleoside phosphorylase (Fragment)
17863	dirMS_041712_NAR_60mM_plus.5172.5172.3	3	6.67	1	4.46E+04		(K)GNSPPS:	(K)G N|S/P/P/S S G E A C R E E K(G)	C:Carbamidomethylation	84.52	535.5678	1604.697	-0.0081	-5	4.79	24954.4	5.33	HUMAN	A6NM98	ARD1 homolog A, N-acetyltransferase (S. cerevisiae), isoform CRA_b
17864	dirMS_041712_NAR_120mM_minus.13515.13515.4	4	6.66	1	8.19E+05		(K)SVHSSVI	(K)S V H S S V/P\L|L/N S K D/P I D R(I)		127.75	466.7525	1863.992	-0.0041	-2.2	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
17865	dirMS_041712_NAR_20mM_minus.13615.13615.3	3	6.66	0	1.68E+05		(R)ETTDTD'	(R)E T T D T D/T A D/Q/V I/A/S F/K(V)		186.47	581.2735	1741.813	-0.0067	-3.9	3.84	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
17866	dirMS_041712_NAR_20mM_minus.9765.9765.2	2	6.66	0	1.57E+05		(K)LSELEPG	(K)L/S\E\L/E/P\G T G D L R(F)		147.78	643.8318	1286.659	-0.0023	-1.8	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
17867	dirMS_041712_NAR_30mM_minus2.11992.12013.2	2	6.66	0	3.50E+05		(R)TLLSDPT	(R)T L|L|S/D/P T Y R(E)		118.32	533.2797	1065.557	-0.0054	-5	5.5	60404.6	6.4	HUMAN	F5H0T1	Stress-induced-phosphoprotein 1
17868	dirMS_041712_NAR_30mM_minus2.20181.20181.2	2	6.66	0	5.54E+05		(K)IGFPWSI	(K)I/G/F/P W S E I R(N)		171.7	552.7932	1104.584	-0.0045	-4.1	6	71218.8	6.3	HUMAN	A7YIJ8	Radixin
17869	dirMS_041712_NAR_40mM_minus2.5754.5754.2	2	6.66	1	9.06E+04		(R)YSGGNY	(R)Y/S|G\G N Y/R D N Y|D\N(-)		95.47	719.2874	1437.567	0.001	0.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
17870	dirMS_041712_NAR_50mM_minus2.17107.17107.3	3	6.66	1	7.23E+04		(R)YDEIVKE	(R)Y/D\E/I V K\E V/S A Y/I K(K)		166.08	519.6148	1556.821	0.0092	5.9	4.68	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
17871	dirMS_041712_NAR_120mM_plus.16572.16716.3	3	6.66	0	2.20E+06		(R)EHALLA'	(R)E\H A\L L\A|Y/T/L/G V K(Q)		141.53	438.9167	1314.742	-0.0061	-4.6	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1

17872	dirMS_041712_NAR_20mM_plus.16414.16414.3	3	6.66	0	1.35E+05		(R)QAQEYE	(R)Q A Q\E Y E|A L/L/N I K(V)		184.45	473.9191	1419.748	-0.0051	-3.6	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
17873	dirMS_041712_NAR_20mM_plus.18679.18679.2	2	6.66	0	1.52E+05	M332m	(R)IVSQLLT	(R)I V|S Q L|L/T/L m D G L K(Q)	m:Oxidized methionine	199.53	723.9145	1430.829	15.993	-1.3	5.84	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
17874	dirMS_041712_NAR_20mM_plus.18967.18967.2	2	6.66	0	1.39E+04		(R)LVLVNA	(R)L V|L V/N A/V Y F R(G)		201.6	597.3545	1193.704	-0.0024	-2	8.75	42963.5	5.19	HUMAN	P35237	Serpin B6
17875	dirMS_041712_NAR_20mM_plus.8817.8817.2	2	6.66	0	2.37E+05		(R)VPPPPPI	(R)V/P/P\P P P I A R(A)		130.68	472.2851	943.572	-0.0094	-10	9.72	32085.2	8.93	HUMAN	B4DY08	Heterogeneous nuclear ribonucleoproteins C1/C2
17876	dirMS_041712_NAR_30mM_plus2.11979.11979.2	2	6.66	0	1.09E+05		(R)TPVSED	(R)T/P|V|S/E D M L G R(V)		115.97	552.7679	1104.535	-0.0069	-6.2	4.37	27142.6	6.66	HUMAN	C9J5E3	V-type proton ATPase subunit B, kidney isoform
17877	dirMS_041712_NAR_30mM_plus2.19927.19927.2	2	6.66	0	4.29E+04		(R)ISEQFTA	(R)I/S\E/Q/F/T A\M/F/R(R)		158.45	615.3024	1229.598	-0.0008	-0.6	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
17878	dirMS_041712_NAR_30mM_plus2.20189.20189.2	2	6.66	0	1.73E+05		(R)ALFLIPR	(R)A L/F/L/I P R(N)		159.33	415.2703	829.529	0.0039	4.7	9.79	40728.4	6.05	HUMAN	C9J338	TRAF2 and NCK-interacting protein kinase (Fragment)
17879	dirMS_041712_NAR_30mM_plus2.21680.21680.2	2	6.66	0	2.12E+05		(R)TTNFAG	(R)T T N F/A/G/I L/S/Q G L/R(I)		169.3	689.3749	1377.748	-0.006	-4.3	9.41	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
17880	dirMS_041712_NAR_30mM_plus2.4138.4138.2	2	6.66	0	1.26E+06	M299m M:	(K)NmmAA	(K)N m\m/A\A C D|P R(H)	C:Carbamidomethylation m:Oxid	69.2	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
17881	dirMS_041712_NAR_40mM_plus2.18507.18507.3	3	6.66	1	3.08E+04		(K)LLLEGVE	(K)L L|L E G/V E/N K L I P/G\L K(I)		175.08	546.0066	1636.004	0.0009	0.5	6.14	59384	7.79	HUMAN	B7Z3Z9	Long-chain-fatty-acid--CoA ligase 1
17882	dirMS_041712_NAR_50mM_plus2.11806.11806.3	3	6.66	1	1.87E+05		(R)SEADSD	(R)S E|A D S\D K N A T|I L E L R(S)		130.43	554.6155	1661.834	-0.0021	-1.3	4.32	334221.3	6.44	HUMAN	P15924	Desmoplakin
17883	dirMS_041712_NAR_50mM_plus2.16292.16292.3	3	6.66	1	8.77E+05		(K)CEFQDA	(K)C E/F Q D\A Y V L/L S E/K K(I)	C:Carbamidomethylation	152.52	577.2866	1729.847	-0.0013	-0.8	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
17884	dirMS_041712_NAR_50mM_plus2.20613.20613.3	3	6.66	1	4.35E+04		(R)QALQDL	(R)Q A/L/Q/D/L L/S E Y M/G N\A G R K(E)		176.63	631.9902	1893.949	0.0073	3.9	6.07	89360.3	5.63	HUMAN	F8W845	Catenin alpha-1
17885	dirMS_041712_NAR_60mM_plus.11049.11049.4	4	6.66	0	1.17E+06		(K)YPTPPS	(K)Y P T P P S Q H S\Y A S/S/N/A/A E R(T)		115.1	491.4815	1962.894	0.0101	5.2	6.75	279264.6	4.96	HUMAN	Q04721	Neurogenic locus notch homolog protein 2
17886	dirMS_041712_NAR_60mM_plus.6473.6473.3	3	6.66	0	2.42E+05		(R)VHPAM	(R)V H P\A M A T/A|A/G G C R(S)	C:Carbamidomethylation	92.4	433.5425	1298.609	0.0037	2.9	9.73	18923.5	9.99	HUMAN	H7C0N4	Splicing factor 1 (Fragment)
17887	dirMS_041712_NAR_120mM_minus.7341.7341.2	2	6.65	1	1.06E+05		(K)IIAPPER	(K)I I|A/P/P E R K(Y)		94.52	462.2871	923.567	-0.0004	-0.4	8.75	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
17888	dirMS_041712_NAR_120mM_minus.8647.8647.3	3	6.65	1	2.56E+05	S133s	(R)AGDLLE	(R)A/G|D|L/L/E D s P K R\P\K(E)	s:Phosphorylated S	101.53	502.5853	1425.77	79.9717	3.6	6.17	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
17889	dirMS_041712_NAR_30mM_minus2.19158.19158.3	3	6.65	0	1.74E+05		(K)SYELPD	(K)S Y E/L P D G Q V|I/T I/G N E R(F)		158.92	597.6343	1790.892	-0.0036	-2	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
17890	dirMS_041712_NAR_30mM_minus2.9596.9596.2	2	6.65	0	7.35E+05		(K)EAESSP	(K)E A E/S/S/P F V/E R(L)		107.13	575.7705	1150.537	-0.0038	-3.3	4.25	92752.5	4.76	HUMAN	P14625	Endoplasmin
17891	dirMS_041712_NAR_50mM_minus2.11878.11878.3	3	6.65	1	1.65E+05		(K)TVNVV	(K)T V/N V/V Q F E/P S K G A I G K(A)		135.95	558.6442	1673.922	-0.004	-2.4	8.26	83905.8	6.62	HUMAN	P41250	Glycine--tRNA ligase
17892	dirMS_041712_NAR_50mM_minus2.13542.13542.3	3	6.65	0	1.54E+04		(K)TGEEIFG	(K)T G/E\E I/F/G T I G M R P N A/K(N)		144.92	574.2947	1720.869	0.0009	0.5	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
17893	dirMS_041712_NAR_50mM_minus2.14443.14443.3	3	6.65	0	4.40E+05		(R)QVLIAS	(R)Q V/L I\A S/H\L/P S Y E L R(H)		150.95	542.6354	1625.901	-0.0093	-5.7	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
17894	dirMS_041712_NAR_60mM_minus.13920.13920.3	3	6.65	1	1.94E+05	M870m	(R)GEETGN	(R)G E/E T/G/N I R/G S m K(V)	m:Oxidized methionine	137.33	432.2132	1278.611	16.0144	15	6.14	139395	6.11	HUMAN	O15357	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2
17895	dirMS_041712_NAR_60mM_minus.15015.15015.3	3	6.65	1	2.62E+05		(K)NLKVTA	(K)N L K V T A\V/P T L L K(Y)		143.9	432.9457	1296.825	-0.0024	-1.9	10	11462.8	5.18	HUMAN	I3L2R6	Thioredoxin domain-containing protein 17
17896	dirMS_041712_NAR_60mM_minus.7894.7894.3	3	6.65	0	9.10E+04		(K)STGEPL	(K)S T/G E/P/L/G H V/P A R(M)		103.75	407.5515	1220.638	0.0017	1.4	6.47	9840	8.09	HUMAN	C9J1K7	Lipoma-preferred partner (Fragment)
17897	dirMS_041712_NAR_120mM_plus.4592.4592.3	3	6.65	0	6.19E+05		(R)THSQGG	(R)T H\S Q G G Y/G S Q/G Y/K(Y)		74.07	457.2092	1369.613	-0.0001	-0.1	8.2	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
17898	dirMS_041712_NAR_120mM_plus.8131.8131.2	2	6.65	0	4.29E+05		(K)AGEVFI	(K)A G/E/V/F/I/H\K(D)		96.3	450.7531	900.494	0.0051	5.7	6.79	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
17899	dirMS_041712_NAR_20mM_plus.11317.11317.2	2	6.65	0	1.61E+04		(R)GCITIIG	(R)G C I T I/I/G/G/G D T A T C C A|K(W)	C:Carbamidomethylation	150	877.8947	1754.787	-0.0049	-2.8	5.84	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
17900	dirMS_041712_NAR_20mM_plus.13747.13747.3	3	6.65	0	3.01E+04		(K)IFVGNV	(K)I F V G N V S/A/A/C T S/Q E L R(S)	C:Carbamidomethylation	167.02	584.6279	1751.874	-0.0053	-3.1	6	37433.2	9.17	HUMAN	B0LM41	Protein RBM14-RBM4
17901	dirMS_041712_NAR_20mM_plus.17015.17015.2	2	6.65	0	9.35E+04		(R)AIVAIEN	(R)A I V A\I/E/N/P|A\D V\S V I S\S R(N)		188.92	870.9764	1740.949	-0.0035	-2	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
17902	dirMS_041712_NAR_30mM_plus2.11184.11476.2	2	6.65	0	9.27E+05	S273s	(R)VSLAsR	(R)V S|L/A s/R(A)	s:N-acetylglucosamine (S)	111.03	418.2293	632.373	203.0787	-0.8	9.72	57002.6	8.29	HUMAN	Q9BTF0	THUMP domain-containing protein 2
17903	dirMS_041712_NAR_30mM_plus2.7888.7888.2	2	6.65	0	4.04E+05		(K)SDPVVS	(K)S D/P\V/V/S Y/R(E)		94.55	461.7327	922.463	-0.0047	-5.1	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
17904	dirMS_041712_NAR_40mM_plus2.13788.13788.2	2	6.65	0	5.62E+04		(K)AILFVPR	(K)A I|L F/V/P R(R)		147.9	408.2603	815.514	-0.0005	-0.6	9.79	57660.2	6.38	HUMAN	Q9NQH7	Probable Xaa-Pro aminopeptidase 3
17905	dirMS_041712_NAR_40mM_plus2.5549.5549.2	2	6.65	0	1.07E+05		(R)NQGGY	(R)N Q G G Y/G G S S/S/S S S/Y G S G R(R)		90.3	847.8525	1694.7	-0.0024	-1.4	8.59	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
17906	dirMS_041712_NAR_60mM_plus.14974.14974.3	3	6.65	1	1.74E+05	T117t	(K)IVDQNT	(K)I V/D Q N T K L A/P E/t/K(A)	t:N-acetylglucosamine (T)	134.78	553.9525	1456.801	203.0424	-22.3	6.07	16652.6	5.83	HUMAN	C9JE88	Carboxypeptidase E (Fragment)
17907	dirMS_041712_NAR_60mM_plus.15173.15173.3	3	6.65	0	3.00E+04	M1m	(-)mPVIPAF	(-)m P/V I P A F W/E A E/A A R(S)	m:Oxidized methionine	135.8	535.2618	1587.799	15.972	-14.3	4.53	25685.9	6.4	HUMAN	E9PGT1	Translin
17908	dirMS_041712_NAR_60mM_plus.8028.8028.3	3	6.65	1	3.68E+05		(K)DISTNYY	(K)D I/S/T N Y/Y A S Q K K(T)		99.77	473.2367	1417.696	-0.0002	-0.2	8.43	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
17909	dirMS_041712_NAR_120mM_minus.10482.10482.3	3	6.64	1	4.00E+04	M86m	(K)mKEIAE	(K)m K E\I A E|A/Y/L/G K(T)	m:Oxidized methionine	109.95	423.557	1252.661	15.9959	0.7	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
17910	dirMS_041712_NAR_120mM_minus.11248.11248.3	3	6.64	0	1.74E+05		(R)GFCLPP	(R)G/F C L/P/P H C S R(G)	C:Carbamidomethylation	114.25	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
17911	dirMS_041712_NAR_120mM_minus.8330.8330.3	3	6.64	1	4.70E+05		(R)ASRDEIF	(R)A S R D\E\I|F/A Q/S/K(E)		99.97	417.8786	1251.633	-0.0115	-9.2	6.12	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
17912	dirMS_041712_NAR_30mM_minus2.11507.11507.2	2	6.64	1	5.79E+04		(R)LDRLSE	(R)L/D/R/L S E A A K(V)		115.77	501.7874	1002.558	0.0097	9.7	6.07	112705.1	5.99	HUMAN	P12036	Neurofilament heavy polypeptide
17913	dirMS_041712_NAR_30mM_minus2.12254.12254.2	2	6.64	0	2.84E+05		(K)STLTDSL	(K)S T\L/T D S L V/C K(A)	C:Carbamidomethylation	120.08	562.2838	1123.566	-0.006	-5.4	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
17914	dirMS_041712_NAR_60mM_minus.10844.10844.3	3	6.64	0	7.56E+04		(R)TIVITSH	(R)T/I|V I T S H/P G Q I V K(H)		120.03	464.9423	1392.821	-0.0086	-6.2	8.44	27999.4	5.61	HUMAN	B7Z5C0	DnaJ homolog subfamily A member 1
17915	dirMS_041712_NAR_60mM_minus.11597.11597.3	3	6.64	0	1.81E+05		(R)YASINA	(R)Y/A|S I N A/H/L G I E Q S R(R)		124.27	520.269	1558.797	-0.0048	-3.1	6.75	27968.7	9.69	HUMAN	D6REM4	Casein kinase I isoform alpha
17916	dirMS_041712_NAR_60mM_minus.13064.13064.3	3	6.64	0	2.69E+05		(K)AQIHDL	(K)A Q I H D L V\L|V G/G S T/R(I)		132.78	489.2745	1465.812	-0.0032	-2.2	6.79	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
17917	dirMS_041712_NAR_60mM_minus.16768.16768.3	3	6.64	0	2.45E+06		(R)DGLAFN	(R)D G L|A/F/N/A/L I H R(H)		154.08	409.5576	1226.664	-0.0058	-4.7	6.74	146974	5.55	HUMAN	C9JRP8	Spectrin beta chain, non-erythrocytic 4
17918	dirMS_041712_NAR_60mM_minus.9429.9429.3	3	6.64	1	1.78E+05		(K)IFRDGEE	(K)I F R D G E\E\A/G A\Y D/G P R(T)		112.25	551.5934	1652.766	-0.0007	-0.4	4.32	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
17919	dirMS_041712_NAR_120mM_plus.4087.4087.3	3	6.64	1	9.51E+06	M310m	(R)TKTEISE	(R)T K T E\I/S/E/m/N R(N)	m:Oxidized methionine	69.42	408.8687	1208.594	15.9976	2.2	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
17920	dirMS_041712_NAR_120mM_plus.4424.4424.3	3	6.64	1	3.08E+05		(K)AGADEE	(K)A/G/A/D/E/E/R A E T A R(L)		71.55	425.869	1275.592	0.0001	0.1	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
17921	dirMS_041712_NAR_20mM_plus.15990.15990.2	2	6.64	0	1.15E+05		(R)GTPLISP	(R)G T/P/L/I S P L I K(W)		181.3	519.8306	1038.656	-0.0018	-1.8	8.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
17922	dirMS_041712_NAR_20mM_plus.18441.18441.3	3	6.64	0	5.84E+03		(K)VVVQVL	(K)V V V\Q V L A E E/P/E A V L K(G)		199.15	541.6507	1622.936	0.0012	0.7	4.26	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
17923	dirMS_041712_NAR_20mM_plus.7332.7332.2	2	6.64	0	2.85E+05		(K)TGQAPG	(K)T G Q|A|P G/Y\S Y T A A N K(N)		119.52	714.8394	1428.675	-0.0039	-2.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
17924	dirMS_041712_NAR_20mM_plus.7604.7604.2	2	6.64	0	2.49E+05		(K)VLTPTQ	(K)V L\T/P T/Q V K(N)		121.73	443.2734	885.54	-0.0009	-1	8.72	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
17925	dirMS_041712_NAR_30mM_plus2.10194.10194.2	2	6.64	0	3.98E+04		(R)NAMGS	(R)N A/M|G S L A|S Q A/T/K(D)		106.68	589.7934	1178.583	-0.0039	-3.3	8.75	21119.9	4.34	HUMAN	H0Y3Y9	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
17926	dirMS_041712_NAR_30mM_plus2.11402.11402.2	2	6.64	0	6.49E+05		(R)MGESD	(R)M/G E|S/D D\S I L R(L)		113.72	561.7585	1122.51	0.0002	0.1	4.03	9225.3	9.16	HUMAN	P63220	40S ribosomal protein S21
17927	dirMS_041712_NAR_40mM_plus2.9677.9677.2	2	6.64	0	2.93E+05		(K)SCNCLLL	(K)S C|N/C L|L/L K(V)	C:Carbamidomethylation	120.75	504.2542	1007.501	-0.0001	-0.1	8.47	47510.4	7.04	HUMAN	P06733	Alpha-enolase
17928	dirMS_041712_NAR_50mM_plus2.20304.20304.3	3	6.64	1	3.58E+05		(R)FLDKALE	(R)F/L/D K/A L E L N\M/L|S L K(G)		174.9	545.6431	1634.919	-0.0038	-2.4	6.07	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
17929	dirMS_041712_NAR_50mM_plus2.8125.8125.3	3	6.64	0	1.26E+05		(K)QLAVAE	(K)Q\L/A V/A E G K P P E/A/P K(G)		109.72	478.9337	1434.795	-0.0086	-6	6.14	24364.9	9.64	HUMAN	H0YIP0	Methionine--tRNA ligase, cytoplasmic (Fragment)
17930	dirMS_041712_NAR_60mM_plus.7368.7368.3	3	6.64	1	1.93E+06		(R)SEEKISD	(R)S E|E\K I/S D\S/E/G F K(A)		96.8	452.5501	1355.632	0.0032	2.4	4.41	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
17931	dirMS_041712_NAR_30mM_minus2.13366.13366.2	2	6.63	0	2.45E+05		(K)QYGNEV	(K)Q/Y/G N E V/F/L/A K(L)		126.23	584.7961	1168.6	-0.0148	-12.6	6	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
17932	dirMS_041712_NAR_30mM_minus2.6336.6336.2	2	6.63	0	1.60E+05		(K)MQASIE	(K)M/Q/A/S/I E K(G)		88.68	403.7074	806.408	-0.0001	-0.2	5.75	32745.6	4.64	HUMAN	P06748	Nucleophosmin
17933	dirMS_041712_NAR_50mM_minus2.7632.7632.3	3	6.63	1	9.63E+03		(R)TTKSPS	(R)T T K S\P S D\S G|Y/S/Y/E/T I/G K(T)		110.67	607.6254	1820.855	0.0068	3.7	5.74	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
17934	dirMS_041712_NAR_60mM_minus.17453.17453.3	3	6.63	0	1.17E+05		(R)GGHVVE	(R)G G H\V V E\G\L/A/G E/L E Q L/R(A)		158.32	555.2959	1663.876	-0.0031	-1.8	4.75	106088.3	5.78	HUMAN	P10275	Androgen receptor
17935	dirMS_041712_NAR_60mM_minus.4712.4712.3	3	6.63	1	5.58E+04		(K)DSYVGD	(K)D S Y/V/G D E A Q S K/R(G)		78.23	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
17936	dirMS_041712_NAR_120mM_plus.15214.15214.4	4	6.63	2	6.40E+05		(K)TVGVEP	(K)T\V/G V E/P A A D G K G V V/V V I K R(R)		132.5	474.2836	1894.112	0.0005	0.3	8.26	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
17937	dirMS_041712_NAR_120mM_plus.15351.15351.4	4	6.63	2	1.70E+06		(R)FKGQIL	(R)F K G Q\I\L|M/P N I/G Y G S N K K(T)		133.57	474.5115	1895.021	0.0034	1.8	10	15730.4	11.67	HUMAN	D3YTB1	60S ribosomal protein L32 (Fragment)
17938	dirMS_041712_NAR_120mM_plus.18175.18175.4	4	6.63	1	6.11E+05		(K)ILGSGIS	(K)I\L G S G I|S/S/S S V L H G M V F K K(E)		148.82	487.5232	1947.073	-0.0022	-1.1	10	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
17939	dirMS_041712_NAR_20mM_plus.13695.13695.3	3	6.63	0	1.01E+05		(K)IFVGNV	(K)I F V G N V\S A A C|T S Q E/L R(S)	C:Carbamidomethylation	166.62	584.6279	1751.874	-0.0053	-3.1	6	37433.2	9.17	HUMAN	B0LM41	Protein RBM14-RBM4
17940	dirMS_041712_NAR_20mM_plus.18923.18923.3	3	6.63	0	1.57E+05		(K)TLETQS	(K)T L\E T Q S A\L/G P/A/L Q A A F K(L)		202.28	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
17941	dirMS_041712_NAR_20mM_plus.19142.19142.2	2	6.63	0	2.70E+04		(R)STGEAF	(R)S T G E A F/V/Q/F A S Q\E\I/A/E K(A)		203.23	921.4477	1841.892	-0.0035	-1.9	4.25	24249.1	6.99	HUMAN	D6RBM0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
17942	dirMS_041712_NAR_30mM_plus2.10700.10700.2	2	6.63	0	3.62E+05		(K)ATAVVD	(K)A T/A|V/V D/G A F K(E)		109.45	489.7656	978.525	-0.0015	-1.6	5.88	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
17943	dirMS_041712_NAR_30mM_plus2.10953.10953.2	2	6.63	0	5.80E+05		(R)LASFYER	(R)L/A/S F Y E R(A)		110.9	443.2301	885.447	0.0064	7.3	6	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
17944	dirMS_041712_NAR_30mM_plus2.11215.11477.2	2	6.63	0	4.88E+05		(K)TTDGYL	(K)T T|D/G/Y L L/R(L)		112.43	469.75	938.494	-0.0014	-1.5	5.5	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
17945	dirMS_041712_NAR_30mM_plus2.6446.6446.2	2	6.63	0	1.64E+05		(R)AVVISG	(R)A V|V|I/S/G A G K(M)		87.83	401.2461	801.483	0.002	2.6	8.8	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
17946	dirMS_041712_NAR_40mM_plus2.12784.12925.2	2	6.63	1	1.22E+05		(R)RTPDYF	(R)R T P D\Y|F|L(-)		141.87	456.2358	911.462	0.0022	2.4	5.83	6212.9	6.77	HUMAN	H0YBN9	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform (Fragment)
17947	dirMS_041712_NAR_50mM_plus2.21768.21768.3	3	6.63	1	1.26E+05		(K)TENPLIL	(K)T E|N/P L I/L/I/D E V D K\I G R(G)		185.57	609.0045	1825.007	-0.0076	-4.2	4.32	86039.3	5.74	HUMAN	F5GZ27	Lon protease homolog
17948	dirMS_041712_NAR_50mM_plus2.7110.7110.3	3	6.63	1	3.65E+04	M92m	(K)LGEGEG	(K)L/G E/G E G/S m T K E/E F T K(M)	m:Oxidized methionine	103.2	553.5925	1642.763	16.0001	3.1	4.49	14591.3	4.63	HUMAN	G3V2U1	Sorting nexin-6
17949	dirMS_041712_NAR_50mM_plus2.8407.8407.3	3	6.63	1	5.15E+05		(K)NANKSP	(K)N A N K S/P N P L/L T\F S V K(T)		110.33	543.9631	1629.896	-0.0211	-13	10	87330.7	5.85	HUMAN	E9PGF6	Pleckstrin homology-like domain family B member 2
17950	dirMS_041712_NAR_120mM_minus.16891.16891.3	3	6.62	0	4.33E+05		(K)HLEINPD	(K)H/L/E I N|P/D H|S\I/I E T L R(Q)		146.72	596.3176	1786.945	-0.0064	-3.6	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
17951	dirMS_041712_NAR_120mM_minus.7342.7342.3	3	6.62	0	4.15E+05		(K)NNRPSE	(K)N N R P S E\G|P|L/Q T R(L)		94.1	456.9036	1368.698	-0.0016	-1.2	9.6	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
17952	dirMS_041712_NAR_120mM_minus.8829.8829.2	2	6.62	1	1.51E+06	M174m	(R)VKYETEL	(R)V K|Y/E T/E/L A m R(Q)	m:Oxidized methionine	101.97	628.3209	1239.64	15.9943	-0.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
17953	dirMS_041712_NAR_20mM_minus.11460.11460.2	2	6.62	1	2.35E+05		(R)DDSLRC	(R)D D/S L R\C H/K(K)	C:Carbamidomethylation	162.25	515.7416	1030.474	0.0025	2.4	6.75	74612	9.63	HUMAN	Q9NTW7	Zinc finger protein 64 homolog, isoforms 3 and 4
17954	dirMS_041712_NAR_30mM_minus2.5378.5378.2	2	6.62	0	2.15E+05		(R)SNAEDT	(R)S/N|A|E/D T L/R(S)		83.33	453.2209	905.432	0.0022	2.5	4.37	533778	5.74	HUMAN	Q15149	Plectin
17955	dirMS_041712_NAR_60mM_minus.5667.5667.2	2	6.62	0	5.36E+03		(K)NPAFDD	(K)N P A/F D D Y P L G L Q T V S(-)		87.55	818.8981	1636.785	0.0036	2.2	3.56	80211.1	6.85	HUMAN	Q8WUT4	Leucine-rich repeat neuronal protein 4
17956	dirMS_041712_NAR_60mM_minus.6622.6622.3	3	6.62	0	5.20E+04		(R)ATAPQT	(R)A T/A/P Q T Q H V/S P M/R(Q)		95.48	475.2404	1423.711	-0.0044	-3.1	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
17957	dirMS_041712_NAR_60mM_minus.7858.7858.3	3	6.62	1	3.82E+05	M230m M:	(R)mSmKE	(R)m S m K E V D E\Q/m\L/N/V|Q/N K(N)	m:Oxidized methionine	103.83	657.9647	1923.897	47.9823	-1.3	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
17958	dirMS_041712_NAR_120mM_plus.12326.12326.4	4	6.62	1	2.29E+06		(K)TLTTVQ	(K)T L\T T V/Q G/I A D D Y D K K/K(L)		117.52	449.7412	1795.944	-0.0006	-0.4	5.71	13778.5	7.96	HUMAN	K7EM18	Eukaryotic translation initiation factor 1
17959	dirMS_041712_NAR_120mM_plus.18129.18129.4	4	6.62	1	6.50E+05		(R)ILEFFGL	(R)I L E/F F/G L K K E E C/P A V/R(L)	C:Carbamidomethylation	148.63	484.7638	1936.036	-0.0027	-1.4	6.23	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
17960	dirMS_041712_NAR_120mM_plus.5086.5086.3	3	6.62	1	1.25E+05		(K)MSSPED	(K)M S/S/P E/D D/S D T K R(L)		79.22	456.5294	1367.574	-0.0007	-0.5	4.23	103309.5	5.34	HUMAN	A0AV56	SAFB protein
17961	dirMS_041712_NAR_20mM_plus.10698.10698.3	3	6.62	0	2.82E+04		(K)SQLLAP	(K)S Q L L/A/P/P P/P S A P/P G N K(T)		146.3	524.2902	1570.859	-0.0027	-1.7	8.47	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
17962	dirMS_041712_NAR_20mM_plus.13056.13056.2	2	6.62	0	9.65E+04		(K)TAVVVG	(K)T A V|V/V/G T I/T D D/V R(V)		162.18	673.3693	1345.732	-0.0008	-0.6	4.21	14643	11.93	HUMAN	F8VUA6	60S ribosomal protein L18 (Fragment)
17963	dirMS_041712_NAR_20mM_plus.16028.16028.2	2	6.62	0	1.06E+05		(R)GTPLISP	(R)G T/P L/I S P L I K(W)		181.38	519.8306	1038.656	-0.0018	-1.8	8.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
17964	dirMS_041712_NAR_20mM_plus.16709.16709.2	2	6.62	0	2.48E+05		(K)VQIAVA	(K)V Q|I\A V/A/N A Q/E L/L\Q R(M)		186.6	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
17965	dirMS_041712_NAR_20mM_plus.9568.9568.2	2	6.62	0	4.68E+05		(R)ISVYYNE	(R)I/S/V|Y|Y N E A T G G K(Y)		138.13	651.3211	1301.637	-0.0023	-1.8	6	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
17966	dirMS_041712_NAR_30mM_plus2.16111.16111.2	2	6.62	0	3.24E+05		(R)MGPNIY	(R)M G/P N/I/Y E L R(T)		136.63	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
17967	dirMS_041712_NAR_30mM_plus2.16159.16225.2	2	6.62	0	2.91E+04	M148m	(R)DLTDYL	(R)D L|T|D Y L m/K(I)	m:Oxidized methionine	137.32	507.7505	998.486	16.0074	12.3	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
17968	dirMS_041712_NAR_30mM_plus2.17211.17527.2	2	6.62	0	1.27E+05		(K)GPLMM	(K)G/P|L|M/M Y/I S K(M)		144.93	520.2659	1039.532	-0.007	-6.7	8.59	96306.4	6.41	HUMAN	P13639	Elongation factor 2
17969	dirMS_041712_NAR_40mM_plus2.10102.10115.2	2	6.62	0	1.11E+05		(R)LQIDEQ	(R)L/Q|I/D E/Q L R(Q)		123.92	507.7806	1014.558	-0.0039	-3.9	4.37	66105.7	7.3	HUMAN	A8MQB8	Fragile X mental retardation protein 1
17970	dirMS_041712_NAR_40mM_plus2.10719.10719.3	3	6.62	1	9.26E+03		(R)VAVEYL	(R)V/A V E/Y/L D/P S P E V Q K K(K)		128.35	567.9729	1701.906	-0.0016	-1	4.68	28637.7	6.66	HUMAN	B4DDM6	Mitotic checkpoint protein BUB3
17971	dirMS_041712_NAR_40mM_plus2.7183.7183.2	2	6.62	0	1.22E+04		(K)IAVAAQ	(K)I A|V/A/A/Q N C Y/K(V)	C:Carbamidomethylation	102.25	569.2912	1137.572	0.003	2.7	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
17972	dirMS_041712_NAR_50mM_plus2.18573.18573.3	3	6.62	0	9.05E+04		(R)FTARPL	(R)F T/A/R P L V\E\T I F E R(G)		165.57	526.9527	1578.864	-0.0203	-12.9	6.14	78432.3	6.17	HUMAN	E9PB70	Kinesin-like protein KIF2A
17973	dirMS_041712_NAR_50mM_plus2.21568.21568.3	3	6.62	1	1.91E+05		(R)LIALLEV	(R)L I|A\L/L E/V L/S Q K R(M)		183.28	461.6293	1382.873	0.0004	0.3	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
17974	dirMS_041712_NAR_50mM_plus2.8632.8632.3	3	6.62	0	5.53E+05		(R)ASGNYA	(R)A/S/G N Y/A T V I S/H N P E/T K(K)		111.85	563.6145	1688.824	0.0051	3	6.79	24115.6	11.59	HUMAN	E9PIZ3	60S ribosomal protein L8
17975	dirMS_041712_NAR_60mM_plus.10433.10433.3	3	6.62	1	1.61E+06		(R)TNAENE	(R)T/N|A E N E F V T/I/K\K(D)		112.27	465.2512	1393.732	0.0069	4.9	5.81	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
17976	dirMS_041712_NAR_60mM_plus.12257.12257.3	3	6.62	1	1.07E+05		(K)KVEEAE	(K)K V E E\A\E/P/E/E/F V V E K(V)		120.87	554.615	1661.827	0.0036	2.2	4.2	11857.8	9.63	HUMAN	B8ZZ43	Chromobox homolog 3 (HP1 gamma homolog, Drosophila), isoform CRA_b
17977	dirMS_041712_NAR_60mM_plus.13183.13183.3	3	6.62	1	3.19E+06		(R)VVDLM	(R)V/V\D/L M/A H M A S K/E(-)		126.52	444.2219	1330.649	0.0018	1.3	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
17978	dirMS_041712_NAR_60mM_plus.16587.16587.3	3	6.62	1	6.61E+05		(R)TDGKVF	(R)T/D|G K V F Q/F L N A K(C)		143.45	456.5782	1367.732	-0.0117	-8.6	8.26	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
17979	dirMS_041712_NAR_120mM_minus.8385.8502.2	2	6.61	0	2.25E+05		(R)HSVGVV	(R)H/S|V/G V V/I G R(S)		100.23	462.2742	923.542	-0.001	-1.1	9.75	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
17980	dirMS_041712_NAR_120mM_minus.8519.8519.3	3	6.61	1	2.08E+05		(R)LREDEN	(R)L R E D\E N\A\E/P V/G T T Y Q K(T)		100.38	617.3002	1849.893	-0.0066	-3.6	4.41	76925.9	4.46	HUMAN	A8MV58	Drebrin

17981	dirMS_041712_NAR_20mM_minus.14243.14243.2	2	6.61	0	2.59E+05		(K)VTDDLV	(K)V/T|D D/L/V/C L V\Y K(T)	C:Carbamidomethylation	195.25	662.8445	1324.682	0	0	4.21	10225.7	7.97	HUMAN	P49458	Signal recognition particle 9 kDa protein
17982	dirMS_041712_NAR_20mM_minus.8212.8212.2	2	6.61	0	5.74E+03		(K)DQVANS	(K)D Q|V\A|N S A F V/E/R(L)		131.7	618.3098	1235.602	0.0108	8.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
17983	dirMS_041712_NAR_30mM_minus2.14131.14131.2	2	6.61	0	1.25E+05		(K)CAGNED	(K)C/A|G N E/D I I/T L R(A)	C:Carbamidomethylation	130.12	631.315	1261.621	0.0022	1.8	4.37	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
17984	dirMS_041712_NAR_30mM_minus2.7998.7998.2	2	6.61	0	1.83E+05		(K)GSGTAE	(K)G/S|G/T/A/E V E/L/K(K)		98.32	495.7528	990.51	-0.0119	-12	4.53	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
17985	dirMS_041712_NAR_50mM_minus2.13981.13981.3	3	6.61	1	3.62E+05		(K)VIDPATA	(K)V/I/D/P A T A T S V D/L R D I\K(I)		148.08	571.9822	1713.938	-0.0061	-3.6	4.43	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
17986	dirMS_041712_NAR_50mM_minus2.8479.8479.3	3	6.61	0	4.10E+04		(R)DNIQGIT	(R)D N|I|Q G I/T K/P A I R(R)		116.12	442.5888	1325.754	-0.0017	-1.3	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
17987	dirMS_041712_NAR_120mM_plus.14724.14724.3	3	6.61	0	1.05E+06		(-)MVNHFIA	(-)M/V/N/H F I A E/F K(R)		131.35	412.5446	1235.624	-0.0049	-4	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
17988	dirMS_041712_NAR_20mM_plus.17029.17029.2	2	6.61	0	1.99E+05		(K)LFLVQLQ	(K)L F|L|V/Q L Q E K(A)		189.4	559.3342	1117.662	-0.0004	-0.4	6	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
17989	dirMS_041712_NAR_20mM_plus.17039.17039.2	2	6.61	0	8.06E+04		(K)VNIIPIIA	(K)V/N I|I/P I/I A K(A)		189.2	490.8283	980.65	-0.001	-1	8.72	51212	5.84	HUMAN	A6NFQ9	Septin-8
17990	dirMS_041712_NAR_20mM_plus.17974.17974.2	2	6.61	0	1.12E+05		(K)VDFPQD	(K)V/D F/P Q D Q/L T A L T/G R(I)		195.42	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
17991	dirMS_041712_NAR_20mM_plus.9115.9115.2	2	6.61	0	4.34E+05		(K)VIPELNG	(K)V I/P E L N/G K(L)		133.42	435.2573	869.509	-0.0018	-2	5.97	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
17992	dirMS_041712_NAR_30mM_plus2.11773.11773.2	2	6.61	0	4.85E+05		(R)AMGEQ	(R)A M|G E/Q A/V A/L/A/R(A)		114.22	558.7944	1116.583	-0.0015	-1.3	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
17993	dirMS_041712_NAR_30mM_plus2.15462.15462.2	2	6.61	0	7.11E+05		(R)YPVNSV	(R)Y/P V|N/S|V N I L K(A)		133.82	573.8278	1146.652	-0.0034	-3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
17994	dirMS_041712_NAR_40mM_plus2.17841.17841.3	3	6.61	1	2.31E+06		(R)LFVGNLI	(R)L F|V/G N/L/P A D I T E D E F K R(L)		170.33	655.3421	1964.012	-0.0006	-0.3	4.32	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
17995	dirMS_041712_NAR_50mM_plus2.13792.13792.3	3	6.61	1	4.77E+05		(R)SILKIDDV	(R)S I/L K I D\D\V/V N/T R(-)		140.5	458.2605	1372.78	-0.0125	-9.1	5.68	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
17996	dirMS_041712_NAR_50mM_plus2.16862.16862.3	3	6.61	0	1.55E+06		(K)GSDHSA	(K)G S D H S A S L\E|P G E\L A/E/L V R(S)		156.3	622.9846	1866.919	0.0201	10.7	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
17997	dirMS_041712_NAR_30mM_minus2.11105.11292.2	2	6.6	0	5.48E+04		(K)MLVIEQ	(K)M/L|V|I/E Q/C K(N)	C:Carbamidomethylation	114.78	510.7635	1020.522	-0.0019	-1.9	5.75	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
17998	dirMS_041712_NAR_30mM_minus2.11385.11385.2	2	6.6	0	9.79E+04		(R)NTDEMV	(R)N T|D/E/M|V E L/R(I)		117.07	553.7611	1106.515	0.0003	0.2	4.14	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
17999	dirMS_041712_NAR_30mM_minus2.16919.16919.2	2	6.6	0	1.27E+05		(K)NLYIISVK	(K)N/L/Y/I/I S V/K(G)		145.65	475.2872	949.572	-0.0046	-4.8	8.59	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
18000	dirMS_041712_NAR_50mM_minus2.10524.10524.2	2	6.6	1	1.03E+05	M72m	(R)TEmENE	(R)T E/m E/N E F V/L\I\K K(D)	m:Oxidized methionine	128.6	748.8859	1480.772	15.9929	-1.3	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
18001	dirMS_041712_NAR_50mM_minus2.10605.10605.3	3	6.6	0	1.90E+05		(K)SQIHDIV	(K)S Q\I H D I\V\L/V/G/G S T R(I)		128.67	494.6068	1481.807	-0.0012	-0.8	6.46	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
18002	dirMS_041712_NAR_50mM_minus2.9308.9308.3	3	6.6	1	1.36E+05		(R)QEEELQ	(R)Q E E E/L/Q A K/D E E/L L\K(V)		121.4	567.9554	1701.854	-0.0025	-1.5	4.14	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
18003	dirMS_041712_NAR_120mM_plus.22951.22951.4	4	6.6	1	3.99E+06		(K)GLAPDLI	(K)G L\A P/D L/P/E/D L Y/H L I K K(A)		174.1	456.259	1822.011	0.0033	1.8	5.38	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
18004	dirMS_041712_NAR_120mM_plus.7830.7830.3	3	6.6	1	2.26E+05	M316m	(R)RAmGEQ	(R)R A m G E Q/A|V A/L A R(A)	m:Oxidized methionine	94.5	430.2316	1272.684	15.9961	0.9	9.6	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
18005	dirMS_041712_NAR_20mM_plus.15165.15165.3	3	6.6	0	9.35E+04		(K)DVLSVAI	(K)D V\L S V A/F S S/D/N R(Q)		176.23	437.2168	1309.638	-0.0024	-1.9	4.21	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
18006	dirMS_041712_NAR_20mM_plus.16722.16722.2	2	6.6	1	1.90E+05		(R)RAQILEI	(R)R A Q/I/L/E|I L R(R)		186.3	556.3437	1111.695	-0.0145	-13	9.6	92192.1	9.13	HUMAN	O75173	A disintegrin and metalloproteinase with thrombospondin motifs 4
18007	dirMS_041712_NAR_30mM_plus2.19468.19468.2	2	6.6	0	2.19E+05		(K)NFSGAE	(K)N F|S/G/A|E/L E G L/V/R(A)		155.58	646.3361	1291.664	0.0008	0.6	4.53	71924.9	6.25	HUMAN	B4DFA2	Vesicle-fusing ATPase
18008	dirMS_041712_NAR_30mM_plus2.8473.8473.2	2	6.6	0	7.92E+05		(K)TAVCDIP	(K)T A|V C/D/I/P P R(G)	C:Carbamidomethylation	99.28	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
18009	dirMS_041712_NAR_30mM_plus2.8831.8831.2	2	6.6	0	2.39E+05		(K)SGTSEFL	(K)S G T/S/E/F L N/K(M)		99.58	491.7468	982.484	0.0023	2.4	5.72	92752.5	4.76	HUMAN	P14625	Endoplasmin
18010	dirMS_041712_NAR_40mM_plus2.17627.17627.3	3	6.6	1	1.96E+05		(R)LKLPSIPI	(R)L K L P S I/P L\V/P V S A Q K(R)		170.73	530.671	1589.999	-0.0004	-0.3	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
18011	dirMS_041712_NAR_40mM_plus2.5309.5309.2	2	6.6	0	1.31E+05		(R)DYSGYQ	(R)D Y/S|G Y Q R(D)		87.43	444.6967	888.385	0.0015	1.7	5.83	70523.3	4.94	HUMAN	G3V153	Caprin-1
18012	dirMS_041712_NAR_40mM_plus2.5905.5905.2	2	6.6	0	2.43E+04		(K)GEGQLG	(K)G E/G Q L/G P A E R(A)		92.77	507.2532	1013.501	-0.0019	-1.9	4.53	96306.4	6.41	HUMAN	P13639	Elongation factor 2
18013	dirMS_041712_NAR_40mM_plus2.9936.9936.3	3	6.6	1	1.48E+04		(K)VESLDVI	(K)V E S/L D V/D S/E A K K(L)		122.43	440.561	1319.669	-0.0005	-0.3	4.32	28309.6	4.17	HUMAN	E9PI86	Nuclear autoantigenic sperm protein (Fragment)
18014	dirMS_041712_NAR_50mM_plus2.10468.10468.2	2	6.6	1	1.53E+06		(R)DGKLVS	(R)D G/K L/V|S E S S/D V\L\P K(-)		122.85	737.3925	1473.78	-0.0018	-1.2	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
18015	dirMS_041712_NAR_50mM_plus2.13963.13963.3	3	6.6	1	6.41E+05		(K)GGELVYT	(K)G G/E\L/V|Y T/D S E A R D V F E K(A)		141.47	638.9735	1914.908	-0.002	-1.1	4.18	533778	5.74	HUMAN	Q15149	Plectin
18016	dirMS_041712_NAR_50mM_plus2.14273.14273.3	3	6.6	0	2.31E+06		(K)VEPVALA	(K)V E/P V A L A P S/P V I P R(L)		143.27	482.2828	1444.852	-0.0184	-12.7	5.97	104321.6	9.31	HUMAN	Q5VWG9	Transcription initiation factor TFIID subunit 3
18017	dirMS_041712_NAR_50mM_plus2.15445.15445.3	3	6.6	1	9.72E+05		(R)KVPGVT	(R)K V\P G V T A I E|L/D E/D/T/G T F R(I)		149.82	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
18018	dirMS_041712_NAR_50mM_plus2.18444.18444.3	3	6.6	1	3.94E+05		(K)VCSTND	(K)V/C/S/T N\D/L K/E L L I F N K(Q)	C:Carbamidomethylation	166.02	598.6527	1793.947	-0.0031	-1.7	6.04	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
18019	dirMS_041712_NAR_60mM_plus.16387.16387.3	3	6.6	1	1.84E+05		(K)KAPDFV	(K)K\A P D F\V/F/Y/A P R(L)		141.8	437.5685	1310.689	0.0018	1.3	8.59	71218.8	6.3	HUMAN	A7YIJ8	Radixin
18020	dirMS_041712_NAR_60mM_plus.19044.19044.3	3	6.6	0	1.44E+04		(R)LFGHSST	(R)L F G H S\S T S A\L/S A/I/L R(S)		157.23	520.622	1559.854	-0.0026	-1.6	9.75	376926.5	4.99	HUMAN	H0Y5W0	E3 ubiquitin-protein ligase HUWE1 (Fragment)
18021	dirMS_041712_NAR_60mM_plus.7608.7608.3	3	6.6	0	4.52E+05	S5s	(-)VTSAsPA	(-)V T\S A s P/A/P/S T A S A S R(W)	s:N-acetylglucosamine (S)	97.93	531.6013	1389.697	203.0925	8.2	9.72	4018.6	11.1	HUMAN	K7ERJ5	116 kDa U5 small nuclear ribonucleoprotein component (Fragment)
18022	dirMS_041712_NAR_60mM_plus.8341.8341.3	3	6.6	1	6.44E+05		(K)EPLYEKD	(K)E P/L/Y|E\K D S|S/V A A R(F)		102.25	488.9148	1464.733	-0.0031	-2.1	4.68	26283.8	8.96	HUMAN	O43809	Cleavage and polyadenylation specificity factor subunit 5
18023	dirMS_041712_NAR_120mM_minus.13862.13862.3	3	6.59	0	9.19E+04		(K)LPSDSGD	(K)L P\S D S G D|L E A L E G K(D)		129.58	477.5658	1430.701	-0.0181	-12.6	3.91	114417.4	5.61	HUMAN	G3V5V3	Nuclear export mediator factor NEMF (Fragment)
18024	dirMS_041712_NAR_120mM_minus.17487.17487.3	3	6.59	1	2.89E+05		(R)RAPFDLI	(R)R A\P F\D|L/F/E N K(K)		150.65	412.8849	1236.637	0.003	2.4	6.07	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
18025	dirMS_041712_NAR_120mM_minus.4584.4584.3	3	6.59	1	4.46E+05	M310m	(R)TKTEISE	(R)T|K T E\I/S E m N/R(N)	m:Oxidized methionine	73.98	408.8693	1208.594	15.9994	3.7	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
18026	dirMS_041712_NAR_20mM_minus.10391.10391.2	2	6.59	0	1.44E+05		(R)IYVVDVG	(R)I Y|V|V/D V G S E P R(A)		152.93	617.3216	1233.647	-0.0115	-9.3	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
18027	dirMS_041712_NAR_30mM_minus2.18833.18833.2	2	6.59	0	5.41E+04		(R)CGGIQY	(R)C G G I/Q/Y/L\Q|N A I\E S R(Q)	C:Carbamidomethylation	157.12	804.8951	1608.78	0.0031	1.9	6	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
18028	dirMS_041712_NAR_30mM_minus2.6064.6064.2	2	6.59	0	2.64E+05		(K)TSEVNCY	(K)T\S|E/V/N C Y R(C)	C:Carbamidomethylation	87.3	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
18029	dirMS_041712_NAR_30mM_minus2.7603.7603.2	2	6.59	0	6.58E+05		(R)EQALAV	(R)E Q/A\L A/V/S R(N)		96.32	437.2408	873.479	-0.0045	-5.2	6.1	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
18030	dirMS_041712_NAR_40mM_minus2.15678.15678.3	3	6.59	0	1.90E+05		(K)GAEILEV	(K)G A\E I L/E V/L H/S/L P A V/R(Q)		182.13	535.3104	1603.917	0	0	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
18031	dirMS_041712_NAR_50mM_minus2.14320.14320.3	3	6.59	1	8.33E+04		(R)LSQELEY	(R)L/S\Q/E L E/Y/L/T E D V K R(L)		149.87	574.9724	1722.891	0.0118	6.8	4.41	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
18032	dirMS_041712_NAR_50mM_minus2.8576.8576.3	3	6.59	1	8.87E+04		(R)YESLTDP	(R)Y E/S L T D/P S K L D/S G K(E)		116.3	513.9233	1539.754	0.0017	1.1	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
18033	dirMS_041712_NAR_60mM_minus.11722.11744.3	3	6.59	1	7.51E+05	M546m	(K)QmADTG	(K)Q m/A D/T G K/L N/T L L Q R(A)	m:Oxidized methionine	124.67	535.6216	1588.848	16.0027	4.8	8.75	91324.5	5.75	HUMAN	Q00839	Heterogeneous nuclear ribonucleoprotein U
18034	dirMS_041712_NAR_60mM_minus.5842.5842.3	3	6.59	1	8.37E+04	M1m	(-)mDSETD	(-)m D S/E T/D M V R Q/I/R(A)	m:Oxidized methionine	88.38	499.5724	1480.688	16.0144	13	4.56	28693	5.27	HUMAN	E9PJ36	Vacuolar protein sorting-associated protein 51 homolog (Fragment)
18035	dirMS_041712_NAR_120mM_plus.14045.14045.4	4	6.59	1	3.79E+05		(R)VVLIGGK	(R)V V|L/I/G G K P D R V V E C I K(I)	C:Carbamidomethylation	126.58	446.2597	1782.031	-0.0136	-7.6	8.56	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
18036	dirMS_041712_NAR_120mM_plus.9471.9471.3	3	6.59	1	6.74E+05		(R)RMGESD	(R)R M\G\E\S D\D|S/I/L R(L)		103.33	426.8756	1278.611	0.0016	1.2	4.56	9225.3	9.16	HUMAN	P63220	40S ribosomal protein S21
18037	dirMS_041712_NAR_20mM_plus.18459.18459.3	3	6.59	0	3.15E+05		(R)AAVEEG	(R)A A V\E E G I\V L|G/G G C A/L L R(C)	C:Carbamidomethylation	198.02	562.3058	1684.905	-0.0022	-1.3	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
18038	dirMS_041712_NAR_20mM_plus.18649.18649.2	2	6.59	0	1.60E+05	M332m	(R)IVSQLLT	(R)I V|S Q L/L/T L m D G L/K(Q)	m:Oxidized methionine	199.48	723.9145	1430.829	15.993	-1.3	5.84	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
18039	dirMS_041712_NAR_20mM_plus.19154.19154.3	3	6.59	0	2.10E+05		(R)LAGTQP	(R)L A G T Q|P L/E V/L/E/A V Q R(S)		204.03	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
18040	dirMS_041712_NAR_30mM_plus2.16994.17103.2	2	6.59	0	3.09E+05		(K)YYTLFGF	(K)Y/Y|T L/F/G/R(S)		142.35	460.2391	919.467	0.0037	4	8.59	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
18041	dirMS_041712_NAR_30mM_plus2.19096.19096.2	2	6.59	0	3.09E+05		(R)SVLQETF	(R)S V L|Q E T F/P/R(L)		152.67	538.7881	1076.574	-0.0046	-4.2	5.72	29114	5.19	HUMAN	A1L170	Uncharacterized protein C1orf226
18042	dirMS_041712_NAR_40mM_plus2.11280.11280.3	3	6.59	0	2.83E+04		(K)AGVSISV	(K)A G V/S|I|S V V H/G N L S E E A A K(Q)		132.63	589.9796	1767.924	0.0007	0.4	5.4	50949.8	9.28	HUMAN	P36551	Coproporphyrinogen-III oxidase, mitochondrial
18043	dirMS_041712_NAR_40mM_plus2.14479.14479.3	3	6.59	1	1.17E+05		(K)LDVSNV	(K)L D/V/S N V A/T D T E R L E L/K(A)		152.35	601.6538	1802.949	-0.0026	-1.4	4.32	288852.1	5.33	HUMAN	E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein
18044	dirMS_041712_NAR_50mM_plus2.17991.17991.3	3	6.59	1	1.26E+06		(K)GPVREG	(K)G P V R E G D\V\L/T/L L/E/S E/R(E)		162.92	590.6519	1769.939	0.0019	1.1	4.41	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
18045	dirMS_041712_NAR_50mM_plus2.18336.18336.3	3	6.59	1	5.56E+05		(R)LFVGNLI	(R)L F/V/G N L/P T/D I T E E D F K R(L)		163.85	665.3443	1994.023	-0.0046	-2.3	4.32	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
18046	dirMS_041712_NAR_50mM_plus2.18419.18419.3	3	6.59	1	3.95E+05		(R)IAKEEIFG	(R)I A K E E I F G|P V Q/P L F K(F)		164.93	572.6586	1715.973	-0.0118	-6.9	6.14	57661.7	6.36	HUMAN	P30837	Aldehyde dehydrogenase X, mitochondrial
18047	dirMS_041712_NAR_50mM_plus2.21821.21821.3	3	6.59	0	1.62E+04		(K)GHYTEG	(K)G H Y T E G A E\L\V/D S V/L/D V V/R(K)		185.95	653.6688	1958.982	0.0101	5.1	4.31	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
18048	dirMS_041712_NAR_50mM_plus2.9525.9525.3	3	6.59	1	6.42E+04		(K)MSKSLG	(K)M/S K/S L\G N V/V D\P\R(T)		117.02	434.9012	1302.683	0.0056	4.3	8.5	67502.5	9.02	HUMAN	Q96GW9	Methionine--tRNA ligase, mitochondrial
18049	dirMS_041712_NAR_60mM_plus.20602.20602.3	3	6.59	0	4.44E+05		(R)CRPDQL	(R)C R\P D Q L\T\G L|S/L/L P L/S E K(A)	C:Carbamidomethylation	168.32	643.0146	1927.032	-0.0025	-1.3	6.07	533778	5.74	HUMAN	Q15149	Plectin
18050	dirMS_041712_NAR_20mM_minus.13067.13067.2	2	6.58	0	1.08E+06	M73m	(R)AILVDLE	(R)A I L\V D|L/E|P G T m D S V R(S)	m:Oxidized methionine	182.65	816.4184	1615.836	15.9935	-0.8	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
18051	dirMS_041712_NAR_30mM_minus2.10670.10670.2	2	6.58	0	2.25E+05		(K)VLEFNCF	(K)V L|E/F N C R(F)	C:Carbamidomethylation	111.92	469.2383	937.456	0.0133	14.2	5.97	32853.1	5.92	HUMAN	F8WD69	Phosphoribosylformylglycinamidine cyclo-ligase
18052	dirMS_041712_NAR_50mM_minus2.14696.14696.3	3	6.58	0	4.00E+05		(K)QLEAIDQ	(K)Q L/E A I D Q L/H L E Y/A/K(R)		152.4	557.6327	1670.875	0.0087	5.2	4.65	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
18053	dirMS_041712_NAR_60mM_minus.10713.10713.3	3	6.58	1	7.29E+05		(K)TAVCDIP	(K)T/A V/C D I/P P/R G L K(M)	C:Carbamidomethylation	118.92	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
18054	dirMS_041712_NAR_120mM_plus.9616.9616.3	3	6.58	1	5.26E+04		(R)GSNKLV	(R)G S N K L V/I|E/E A E/R(S)		103.52	448.9084	1344.712	-0.0011	-0.8	4.79	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
18055	dirMS_041712_NAR_20mM_plus.14119.14119.2	2	6.58	0	7.30E+03	M185m	(K)LAVNmV	(K)L/A\V N m/V/P F\P R(L)	m:Oxidized methionine	169.3	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
18056	dirMS_041712_NAR_20mM_plus.15111.15111.2	2	6.58	0	9.21E+04		(K)AILFVPR	(K)A I/L|F/V/P\R(R)		176.05	408.2606	815.514	0.0001	0.2	9.79	57660.2	6.38	HUMAN	Q9NQH7	Probable Xaa-Pro aminopeptidase 3
18057	dirMS_041712_NAR_20mM_plus.19166.19166.2	2	6.58	0	1.16E+05		(R)TGAIVDV	(R)T G\A I/V/D\V|P V G E E L L G R(V)		204.07	812.9497	1624.891	0.0017	1	4.14	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
18058	dirMS_041712_NAR_20mM_plus.7587.7587.2	2	6.58	0	1.52E+05	M328m	(K)ALmDEV	(K)A/L/m/D E V V K(A)	m:Oxidized methionine	122.15	460.741	904.481	15.9939	-1.1	4.37	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
18059	dirMS_041712_NAR_30mM_plus2.4541.4541.2	2	6.58	0	2.63E+05		(K)EDAANN	(K)E D\A/A|N N Y A R(G)		73.3	512.2281	1023.449	-0.0001	-0.1	4.37	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
18060	dirMS_041712_NAR_50mM_plus2.9895.9895.3	3	6.58	1	1.46E+05		(K)IIEEAPAI	(K)I/I/E/E A/P A P G I K/S E V R(K)		119.47	536.9673	1608.896	-0.0082	-5.1	4.79	66923.1	6.88	HUMAN	E9PG35	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (Fragment)
18061	dirMS_041712_NAR_60mM_plus.12354.12354.3	3	6.58	1	2.56E+04		(R)VFDKEG	(R)V F|D K E G\N G T V/M/G A E I/R(H)		120.43	574.9548	1722.848	0.0019	1.1	4.68	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
18062	dirMS_041712_NAR_60mM_plus.20224.20224.3	3	6.58	0	1.07E+05		(R)IDILDSA	(R)I/D|I/L/D S A L L R P G R(I)		165.42	480.2825	1438.838	-0.0047	-3.3	5.96	44954.5	8.44	HUMAN	A8K3Z3	26S protease regulatory subunit 8
18063	dirMS_041712_NAR_60mM_plus.5521.5521.3	3	6.58	0	4.17E+05	M21m	(R)SGSmDP	(R)S G\S m/D/P/S G A H/P S V R(Q)	m:Oxidized methionine	86.32	467.5464	1384.627	15.9973	1.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
18064	dirMS_041712_NAR_60mM_plus.7966.7966.3	3	6.58	1	5.46E+05		(K)ALSRQEI	(K)A L|S R Q E M\Q/E V/Q S S R(S)		100.22	550.2735	1648.807	-0.0012	-0.7	6.19	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
18065	dirMS_041712_NAR_120mM_minus.14832.14832.2	2	6.57	0	7.65E+05		(R)DWSHYF	(R)D/W|S H/Y F K(I)		135	491.725	982.442	0.001	1	6.74	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18066	dirMS_041712_NAR_120mM_minus.9076.9076.3	3	6.57	2	6.33E+03		(R)RYNENT	(R)R/Y/N E N T E L/R K(T)		102.9	441.5597	1322.681	-0.0166	-12.5	8.59	66675.8	8.53	HUMAN	F8W6D7	Protein CBFA2T2
18067	dirMS_041712_NAR_20mM_minus.14117.14117.3	3	6.57	0	9.87E+05		(K)SYELPDG	(K)S Y\E L P D G Q\V/I/T I G N E/R(F)		194.13	597.6345	1790.892	-0.003	-1.7	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
18068	dirMS_041712_NAR_20mM_minus.14368.14368.2	2	6.57	0	2.34E+05		(K)DAGVIAG	(K)D A G\V|I/A/G L N V L R(I)		198.12	599.3503	1197.695	-0.0017	-1.4	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
18069	dirMS_041712_NAR_30mM_minus2.10123.10123.2	2	6.57	0	1.41E+05		(R)SPSTLLP	(R)S/P/S/T L L/P K(K)		109.23	421.7586	842.498	0.0117	13.9	8.47	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
18070	dirMS_041712_NAR_30mM_minus2.15389.15389.2	2	6.57	0	2.46E+05		(R)IDYIAGL	(R)I/D|Y\I|A/G L D S/R(G)		137.68	561.7944	1122.579	0.0026	2.3	4.21	14613.6	6.73	HUMAN	G5E9J2	Adenine phosphoribosyltransferase
18071	dirMS_041712_NAR_60mM_minus.10788.10788.3	3	6.57	1	1.38E+06		(R)FPGQLN	(R)F/P/G Q L N/A/D L R K(L)		120.53	420.2346	1258.69	-0.001	-0.8	8.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
18072	dirMS_041712_NAR_60mM_minus.13756.13756.3	3	6.57	1	2.57E+05		(K)KAEAAA	(K)K A E A A A\S A L|A/D/A/D\A/D L E/E R(L)		136.4	639.6429	1916.92	-0.0054	-2.8	4.02	25103.6	5.88	HUMAN	O43633	Charged multivesicular body protein 2a
18073	dirMS_041712_NAR_60mM_minus.19902.19902.3	3	6.57	1	6.04E+05		(R)LIALLEVI	(R)L I\A|L/L E/V L S Q K R(M)		181.8	461.6287	1382.873	-0.0014	-1	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
18074	dirMS_041712_NAR_60mM_minus.8480.8480.3	3	6.57	1	1.00E+05		(R)VVASDK	(R)V V/A S D K/E/T Y E L R(Y)		107.3	470.5828	1409.727	0.0068	4.8	4.68	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
18075	dirMS_041712_NAR_120mM_plus.11966.11966.4	4	6.57	1	5.36E+04		(R)LLHVAVS	(R)L L H V A V S/D/V N D D V R/R(A)		114.37	427.7382	1707.914	0.0173	10.1	5.3	20886.7	7.04	HUMAN	H7C378	26S proteasome non-ATPase regulatory subunit 1 (Fragment)
18076	dirMS_041712_NAR_120mM_plus.4792.4792.3	3	6.57	0	4.66E+03	M77m M7	(R)LTNSMm	(R)L/T/N/S M m m H/G R(N)	m:Oxidized methionine	77.6	403.8446	1177.527	31.9918	1.6	9.75	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
18077	dirMS_041712_NAR_120mM_plus.7924.7924.2	2	6.57	0	1.36E+05		(R)VNGGYS	(R)V N|G\G Y S G L R(D)		95.12	461.7364	922.474	-0.0086	-9.3	8.72	73195.4	6.04	HUMAN	P33908	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA
18078	dirMS_041712_NAR_20mM_plus.13835.13835.2	2	6.57	0	3.21E+04	M178m	(K)GGIVGm	(K)G/G\I|V/G/m\T L\P I\A R(D)	m:Oxidized methionine	167.35	600.8402	1184.682	15.9911	-3.1	9.75	27150.8	7.95	HUMAN	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2
18079	dirMS_041712_NAR_20mM_plus.7728.7728.2	2	6.57	0	5.36E+04		(K)LAAIGEA	(K)L/A\A\I/G/E/A T R(L)		123.2	451.2557	901.51	-0.006	-6.7	6	533778	5.74	HUMAN	Q15149	Plectin
18080	dirMS_041712_NAR_20mM_plus.7769.7769.2	2	6.57	0	5.08E+03		(K)TAVCDIP	(K)T A|V|C D/I P|P R(G)	C:Carbamidomethylation	123.92	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
18081	dirMS_041712_NAR_20mM_plus.7905.7905.2	2	6.57	0	4.82E+04		(K)YIDQEEL	(K)Y I/D|Q E\E L N K(T)		124.37	576.2845	1151.558	0.0038	3.3	4.14	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
18082	dirMS_041712_NAR_20mM_plus.9399.9399.2	2	6.57	0	6.25E+04		(R)GLTSVIN	(R)G L|T/S/V/I N Q K(L)		136.35	480.2806	959.552	0.0019	2	8.75	36923.1	5.71	HUMAN	P07195	L-lactate dehydrogenase B chain
18083	dirMS_041712_NAR_30mM_plus2.11396.11396.2	2	6.57	0	2.05E+05		(R)LTWHSC	(R)L T W H S C/P E D E|A|Q(-)	C:Carbamidomethylation	112.65	736.8094	1472.611	0.0005	0.3	4.13	20982.2	5.23	HUMAN	Q13185	Chromobox protein homolog 3
18084	dirMS_041712_NAR_50mM_plus2.12456.12456.3	3	6.57	0	6.29E+05		(K)GIHPTIIS	(K)G I H|P T I\I|S E/S/F Q K(A)		132.97	486.2644	1456.78	-0.0008	-0.6	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
18085	dirMS_041712_NAR_50mM_plus2.13745.13745.3	3	6.57	0	6.26E+05		(K)EGKPTIV	(K)E G K P T I V/E/E/D D/P E L/F K(Q)		140.52	615.9744	1845.912	-0.003	-1.6	4.08	29841.1	9.04	HUMAN	O75937	DnaJ homolog subfamily C member 8
18086	dirMS_041712_NAR_50mM_plus2.18483.18483.3	3	6.57	1	5.52E+05		(K)NAAGAL	(K)N A|A G/A L/D L L K E/L K(N)		165.92	452.601	1355.789	-0.0008	-0.6	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
18087	dirMS_041712_NAR_50mM_plus2.22149.22149.3	3	6.57	1	8.49E+05		(R)ELAILLG	(R)E L A/I/L/L G M/L D P A E K D E K(G)		190.5	629.004	1884.999	-0.0012	-0.7	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
18088	dirMS_041712_NAR_50mM_plus2.6863.6863.3	3	6.57	1	7.99E+05		(K)IVADKDY	(K)I/V/A/D K D Y S V/T A N S K(I)		101.35	504.2628	1510.775	-0.0009	-0.6	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
18089	dirMS_041712_NAR_40mM_minus2.14486.14486.3	3	6.56	1	1.42E+05		(K)GTVPDD	(K)G T V/P/D D A V E/A L A D/S L/G K K(E)		170.28	595.9791	1785.923	-0.0001	-0.1	4.23	81397.3	4.99	HUMAN	B7Z468	Calpastatin

18090	dirMS_041712_NAR_50mM_minus2.12470.12470.3	3	6.56	0	1.77E+05		(R)TTTGDV	(R)T T|T G D V Q/V|L G\L V/H T Q K(L)		138.75	566.3109	1696.923	-0.0047	-2.8	6.41	281330.5	5.64	HUMAN	P11717	Cation-independent mannose-6-phosphate receptor
18091	dirMS_041712_NAR_60mM_minus.10035.10035.3	3	6.56	0	2.95E+04		(R)ISNRPA	(R)I/S N R P A F|M/P S/E|G K(M)		115.67	478.5785	1433.721	0.0004	0.3	8.75	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
18092	dirMS_041712_NAR_60mM_minus.5529.5529.3	3	6.56	1	8.08E+04	S224s	(K)LEsKPSN	(K)L E/s K P S/N G D R S M(-)	s:N-acetylglucosamine (S)	86.2	508.5661	1320.621	203.0625	-11.1	6.07	27740.8	10.07	HUMAN	Q5HYJ3-2	Isoform 2 of Protein FAM76B
18093	dirMS_041712_NAR_120mM_plus.10359.10359.4	4	6.56	2	9.39E+05		(K)MQASIE	(K)M Q/A S I E/K/G G S L P K V/E A K(F)		106.77	443.9944	1772.958	-0.0017	-1	8.25	32745.6	4.64	HUMAN	P06748	Nucleophosmin
18094	dirMS_041712_NAR_120mM_plus.11539.11539.3	3	6.56	1	7.51E+05		(R)QREADL	(R)Q R E A D L L\A A/Q S L V R(E)		112.65	523.9602	1569.871	-0.0047	-3	6.07	120070.8	6.22	HUMAN	O75146	Huntingtin-interacting protein 1-related protein
18095	dirMS_041712_NAR_120mM_plus.5843.5843.4	4	6.56	2	5.86E+05		(R)KTGQAP	(R)K\T G Q A/P/G Y S Y T/A A N K N K(G)		83.75	450.4826	1798.908	0.0003	0.2	9.83	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
18096	dirMS_041712_NAR_120mM_plus.7416.7416.2	2	6.56	0	2.27E+05		(K)NAKPLS	(K)N A|K/P L S F/K(V)		92.32	452.767	904.525	0.0016	1.8	10	25233.4	9.34	HUMAN	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3
18097	dirMS_041712_NAR_20mM_plus.19333.19333.2	2	6.56	0	4.97E+03		(R)ASVILA	(R)A S V I|L A G L/G F\T/P K(M)		205.17	637.3763	1273.751	-0.0061	-4.8	8.8	80142.6	5.95	HUMAN	Q9NUQ8	ATP-binding cassette sub-family F member 3
18098	dirMS_041712_NAR_40mM_plus2.12421.12421.3	3	6.56	0	3.25E+05		(K)AASDIA	(K)A A/S D I/A/M T E L/P P T H P I R(L)		139.55	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
18099	dirMS_041712_NAR_60mM_plus.21144.21144.3	3	6.56	0	1.67E+05		(K)NGGLG	(K)N G G L/G H M\N I/A/L L S D/L/T K(Q)		174.03	585.3126	1753.927	-0.0033	-1.9	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
18100	dirMS_041712_NAR_120mM_minus.18791.18791.4	4	6.55	1	3.55E+05		(R)HATALE	(R)H A T A L\E|E\L/S E/Q L E Q A K R(F)		157.92	489.0065	1953.004	0.0006	0.3	4.91	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
18101	dirMS_041712_NAR_120mM_minus.7976.7976.3	3	6.55	1	4.27E+04		(K)GKGGEI	(K)G K\G\G E I\Q|P/V S V K(V)		98.08	400.229	1198.679	-0.0066	-5.5	8.59	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
18102	dirMS_041712_NAR_20mM_minus.13542.13542.2	2	6.55	0	1.30E+05		(K)DIYALIS	(K)D/I/Y A/L I/S D Q K(H)		186.42	583.3076	1165.61	-0.002	-1.7	4.21	266161	5.68	HUMAN	E9PPU0	Epiplakin
18103	dirMS_041712_NAR_30mM_minus2.15538.15538.2	2	6.55	0	1.83E+05		(K)EILFYDR	(K)E I/L/F/Y/D R(I)		137.63	478.2479	955.488	0.0002	0.2	4.37	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b
18104	dirMS_041712_NAR_30mM_minus2.15789.15789.2	2	6.55	1	9.54E+05		(R)LDGRNF	(R)L D|G R N/F H/R(F)		138.55	507.7594	1014.523	-0.0113	-11.1	9.61	14826.8	9.86	HUMAN	E5RIQ8	Probable tRNA(His) guanylyltransferase
18105	dirMS_041712_NAR_30mM_minus2.8753.8753.2	2	6.55	0	1.17E+05		(R)TSVETAL	(R)T/S/V/E/T/A\L\R(A)		101.98	438.7375	876.479	-0.0108	-12.3	5.66	19945.8	4.97	HUMAN	B4DG50	F-actin-capping protein subunit alpha-2
18106	dirMS_041712_NAR_30mM_minus2.8987.9030.2	2	6.55	0	1.92E+04		(R)GTQGAE	(R)G T/Q/G A/E E V/L R(A)		102.58	530.2724	1059.543	-0.0054	-5.1	4.53	533778	5.74	HUMAN	Q15149	Plectin
18107	dirMS_041712_NAR_40mM_minus2.13439.13439.3	3	6.55	0	1.46E+05		(K)VAIVKP	(K)V A I V K P G V|P M/E I V L N K(E)		163.22	569.6777	1707.024	-0.0052	-3	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
18108	dirMS_041712_NAR_40mM_minus2.7020.7020.2	2	6.55	0	5.73E+05		(R)GYSFTT	(R)G Y|S|F/T T T A/E R(E)		111.97	566.7661	1132.527	-0.002	-1.8	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
18109	dirMS_041712_NAR_50mM_minus2.10788.10788.3	3	6.55	1	7.44E+03		(K)VAVVA	(K)V A/V|V/A/G Y G D V G K G C A Q A L R(G)	C:Carbamidomethylation	129.78	630.9952	1890.985	-0.0144	-7.6	8.56	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
18110	dirMS_041712_NAR_50mM_minus2.18825.18825.3	3	6.55	0	2.32E+05		(K)GAEILEV	(K)G A\E|I L E/V/L H/S L P A V R(Q)		183.23	535.3101	1603.917	-0.0009	-0.5	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
18111	dirMS_041712_NAR_60mM_minus.15064.15064.3	3	6.55	1	3.39E+05		(K)AKLEQL	(K)A K L E\Q\L\F/Q|D\E V A K(A)		144.37	506.9421	1518.816	-0.0045	-3	4.68	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
18112	dirMS_041712_NAR_60mM_minus.19178.19178.3	3	6.55	1	1.74E+04		(K)GVPTGF	(K)G V P/T G F I L/P I R D/I R(A)		170.03	518.6442	1553.916	0.0018	1.2	9.6	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
18113	dirMS_041712_NAR_60mM_minus.5348.5348.3	3	6.55	1	1.52E+04		(K)DSYVGD	(K)D S/Y V/G D/E A Q S K R(G)		85.35	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
18114	dirMS_041712_NAR_60mM_minus.8895.8895.3	3	6.55	0	1.23E+05		(K)NCPHIV	(K)N C/P H I\V/V/G/T P G R(I)	C:Carbamidomethylation	109.35	436.2271	1306.669	-0.0017	-1.3	9.75	28185.1	10.76	HUMAN	B4DIJ6	Spliceosome RNA helicase DDX39B
18115	dirMS_041712_NAR_120mM_plus.21388.21388.4	4	6.55	1	7.39E+05		(R)DYLHLP	(R)D Y L H\L\P|P|E I V/P A T L R/R(S)		165.12	473.2689	1890.06	-0.0058	-3.1	6.75	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
18116	dirMS_041712_NAR_120mM_plus.4197.4197.3	3	6.55	0	5.81E+04	M46m M4	(R)HQGVm	(R)H Q G V\m|V G/m/G/Q K(D)	m:Oxidized methionine	70.08	401.8588	1171.571	31.9908	0.8	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
18117	dirMS_041712_NAR_20mM_plus.12923.12923.2	2	6.55	0	3.27E+05	M316m	(R)ISEQFTA	(R)I S E/Q|F T/A m\F R(R)	m:Oxidized methionine	161.47	623.3012	1229.598	15.9968	1.5	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
18118	dirMS_041712_NAR_20mM_plus.14150.14150.2	2	6.55	0	1.98E+05		(R)AALQEL	(R)A A|L/Q/E L L S K(G)		169	486.789	972.572	-0.0017	-1.7	6.05	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
18119	dirMS_041712_NAR_20mM_plus.15235.15235.3	3	6.55	0	1.07E+05		(K)DVLSVA	(K)D V\L/S V A/F S/S D/N R(Q)		176.42	437.2168	1309.638	-0.0024	-1.9	4.21	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
18120	dirMS_041712_NAR_20mM_plus.19067.19067.3	3	6.55	0	6.34E+04		(K)DTSYLF	(K)D T S Y L F/I/T/G/P D V V K(S)		201.93	518.9378	1554.805	-0.0062	-4	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
18121	dirMS_041712_NAR_20mM_plus.7123.7123.2	2	6.55	0	6.83E+04		(R)VLANPG	(R)V L\A/N|P G/N S Q V A R(V)		116.42	613.3355	1225.665	-0.001	-0.8	9.72	16598.6	5.48	HUMAN	J3QR48	Importin subunit beta-1 (Fragment)
18122	dirMS_041712_NAR_30mM_plus2.10253.10253.2	2	6.55	0	6.41E+05		(K)EQVANS	(K)E Q|V/A/N/S/A/F V E/R(C)		106.73	625.311	1249.617	-0.0024	-1.9	4.53	17664	8.77	HUMAN	H0Y6E4	Heat shock protein HSP 90-beta (Fragment)
18123	dirMS_041712_NAR_30mM_plus2.17322.17322.3	3	6.55	0	1.07E+06		(R)ASLEAA	(R)A S L E A\A I|A/D/A E Q R(G)		144.2	448.8963	1344.675	-0.001	-0.8	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
18124	dirMS_041712_NAR_30mM_plus2.17486.17486.2	2	6.55	0	9.20E+04		(K)VFQFLN	(K)V F/Q/F L/N\A K(C)		144.02	483.7736	966.541	-0.0008	-0.8	8.72	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
18125	dirMS_041712_NAR_40mM_plus2.18506.18506.3	3	6.55	1	3.14E+04		(K)GALPLD	(K)G A/L/P L/D T V/T F Y K V/I P K(S)		175	588.0112	1762.015	0.0041	2.3	8.5	29049.9	6.78	HUMAN	P30040	Endoplasmic reticulum resident protein 29
18126	dirMS_041712_NAR_40mM_plus2.7037.7037.2	2	6.55	0	4.94E+04		(R)YLSNAY	(R)Y L/S/N A Y/A R(E)		101.45	479.2437	957.479	0.0013	1.3	8.59	27264.5	5.09	HUMAN	O00299	Chloride intracellular channel protein 1
18127	dirMS_041712_NAR_50mM_plus2.8933.8933.3	3	6.55	0	1.77E+05		(K)VVQVSA	(K)V V|Q/V/S A G D S H/T A A/L T D D G R(V)		113.63	633.6509	1898.92	0.0179	9.4	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
18128	dirMS_041712_NAR_50mM_plus2.9396.9396.3	3	6.55	0	7.29E+04		(K)SLEIQKP	(K)S L/E|I Q K/P A V\A/P R(H)		116.55	436.9248	1308.763	-0.0036	-2.7	8.46	227602.2	9.63	HUMAN	C9J1F6	Protein PRRC2A
18129	dirMS_041712_NAR_60mM_plus.13282.13282.3	3	6.55	0	1.94E+05		(K)LSLGTY	(K)L S\L/G T Y/A S L/H G R(I)		125.72	425.563	1274.685	-0.0107	-8.4	8.75	67446.5	5.63	HUMAN	F8VQE1	LIM domain and actin-binding protein 1
18130	dirMS_041712_NAR_60mM_plus.20788.20788.3	3	6.55	1	2.14E+05		(K)LIQLME	(K)L/I|Q/L M E E I M A E/K E N K(T)		169.95	606.9819	1818.934	-0.0028	-1.6	4.49	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
18131	dirMS_041712_NAR_120mM_minus.10624.10624.3	3	6.54	1	2.46E+05		(R)YLAEFA	(R)Y L/A|E F A/T G N D R K(E)		111.73	462.2338	1384.686	0.0013	0.9	6.07	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
18132	dirMS_041712_NAR_30mM_minus2.10882.10882.2	2	6.54	0	4.03E+05		(R)NGDFLP	(R)N/G D/F L/P T|R(L)		112.6	460.2363	919.463	0.0021	2.3	5.84	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
18133	dirMS_041712_NAR_30mM_minus2.5879.5879.2	2	6.54	0	5.74E+04		(R)LAEAEE	(R)L/A|E A/E E/T A R(T)		86.62	495.2478	989.49	-0.0015	-1.5	4.25	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
18134	dirMS_041712_NAR_50mM_minus2.11683.11683.3	3	6.54	0	1.16E+05		(R)VTCPNH	(R)V/T C/P N H/P D A I|L/V/E D|Y R(A)	C:Carbamidomethylation	134.83	633.641	1898.907	0.0019	1	4.54	25558.6	9.3	HUMAN	B1APE1	General transcription factor IIB (Fragment)
18135	dirMS_041712_NAR_50mM_minus2.14444.14444.3	3	6.54	1	8.33E+04	S395s	(K)LDKTVV	(K)L/D K/T/V V V A D F G L s/R(L)	s:N-acetylglucosamine (S)	149.87	574.9724	1519.848	203.0548	-14.3	5.96	72275.7	6.8	HUMAN	B5MC51	LIM domain kinase 2
18136	dirMS_041712_NAR_50mM_minus2.17918.17918.3	3	6.54	1	2.31E+05		(K)LALFQA	(K)L/A/L/F Q A/I G K E/V V D R(A)		170.53	520.3043	1558.895	0.0032	2	6.07	266161	5.68	HUMAN	E9PPU0	Epiplakin
18137	dirMS_041712_NAR_50mM_minus2.18154.18154.3	3	6.54	1	7.45E+05		(R)KAIIIFVP	(R)K A I\I I F\V/P V P Q L K(S)		173.47	489.3206	1465.95	-0.0032	-2.2	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
18138	dirMS_041712_NAR_50mM_minus2.6741.6741.3	3	6.54	1	8.76E+04	M22m M2	(K)LAEQAE	(K)L A|E/Q/A E R Y D D m A A/C m\K(S)	C:Carbamidomethylation m:Oxid	104.8	645.2741	1901.819	31.9887	-0.6	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
18139	dirMS_041712_NAR_50mM_minus2.8855.8855.3	3	6.54	1	1.13E+04	S654s	(K)LTsRSA	(K)L T/s R/S/A A/Q D L D R(M)	s:N-acetylglucosamine (S)	119.4	512.5962	1332.687	203.0874	5.2	5.96	134495.2	5.86	HUMAN	B1APN9	Liprin-alpha-4
18140	dirMS_041712_NAR_60mM_minus.15759.15759.3	3	6.54	1	4.82E+05	M81m	(K)EVNKFQ	(K)E V/N K F Q m A/Y/S N/L L R(A)	m:Oxidized methionine	146.92	576.9619	1712.879	15.9923	-1.5	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
18141	dirMS_041712_NAR_120mM_plus.10460.10460.3	3	6.54	1	8.30E+05		(R)LKYENE	(R)L K Y E N E/V/A/L R(Q)		107.93	412.2295	1234.679	-0.0051	-4.1	6.14	59054.3	5.14	HUMAN	P13645	Keratin, type I cytoskeletal 10
18142	dirMS_041712_NAR_120mM_plus.16160.16160.3	3	6.54	1	1.91E+05		(R)KSEIEY	(R)K S E I E|Y/Y/A M L A K(T)		138.35	482.5826	1445.735	-0.0012	-0.9	6.14	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
18143	dirMS_041712_NAR_20mM_plus.8593.8593.2	2	6.54	0	6.29E+04		(R)LDAEPR	(R)L D\A E|P R|P P P T/Q E\A\A(-)		129.63	746.3743	1491.744	-0.0025	-1.7	4.14	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
18144	dirMS_041712_NAR_30mM_plus2.11936.11936.2	2	6.54	0	7.33E+04		(R)GCTATL	(R)G C|T/A/T/L/G N F\A|K(A)	C:Carbamidomethylation	116.62	570.2807	1139.551	0.0028	2.4	8.75	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
18145	dirMS_041712_NAR_30mM_plus2.12191.12191.2	2	6.54	0	3.33E+05	S718s	(K)GLGGA	(K)G L G/G A/G G G s S/P S K(S)	s:N-acetylglucosamine (S)	116.67	617.791	1031.512	203.0631	-13.2	8.75	382015.9	5.85	HUMAN	Q5T011	Protein SZT2
18146	dirMS_041712_NAR_40mM_plus2.10639.10639.3	3	6.54	1	3.62E+05		(R)DGKLVS	(R)D G K/L V S\E/S|S D V/L/P K(-)		128.45	491.9315	1473.78	0.0004	0.3	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
18147	dirMS_041712_NAR_40mM_plus2.13428.13428.3	3	6.54	0	2.57E+05		(R)LSAMLV	(R)L S/A M L V P\V/T/P/E V\K P K(R)		145.75	536.9848	1608.939	0.0005	0.3	8.59	31524.1	4.5	HUMAN	P82970	High mobility group nucleosome-binding domain-containing protein 5
18148	dirMS_041712_NAR_50mM_plus2.12652.12652.3	3	6.54	1	1.23E+05	M1m	(-)mPARTN	(-)m/P A|R T N N F N/V E T L K(G)	m:Oxidized methionine	134	550.9462	1634.832	15.9921	-1.7	8.5	42541.6	5.84	HUMAN	F5H1N8	Glycogen [starch] synthase, muscle
18149	dirMS_041712_NAR_50mM_plus2.9013.9013.3	3	6.54	1	2.23E+05	M28m	(K)LAEQAE	(K)L/A|E Q A E R Y\D D M A A A/m K(A)	m:Oxidized methionine	114.55	610.2777	1812.825	15.9931	-1	4.32	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
18150	dirMS_041712_NAR_60mM_plus.17416.17416.3	3	6.54	1	1.01E+04		(R)IINEPTA	(R)I I/N E/P T A A A I A/Y G/L D K K(V)		146.77	596.6649	1787.99	-0.01	-5.6	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
18151	dirMS_041712_NAR_120mM_minus.16542.16542.3	3	6.53	1	1.67E+04	M3109m S	(K)GDmDV	(K)G D m D V s L|P/K V/E G D m K(V)	m:Oxidized methionine s:N-a	144.07	619.2763	1620.761	235.0536	-8.4	4.23	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
18152	dirMS_041712_NAR_120mM_minus.19510.19510.3	3	6.53	1	1.71E+05		(K)RSIQFV	(K)R S I Q\F\V/D/W/C/P T G F K(V)	C:Carbamidomethylation	161.58	580.9561	1740.853	0.0011	0.6	8.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
18153	dirMS_041712_NAR_120mM_minus.19836.19836.3	3	6.53	1	1.36E+05		(K)GTKHLS	(K)G T K H/L|S/P Y A T L T V G D S S H K(T)		163.2	667.0203	1999.024	0.022	11	8.51	123367.7	5.57	HUMAN	Q9BSJ8	Extended synaptotagmin-1
18154	dirMS_041712_NAR_20mM_minus.10791.10791.3	3	6.53	0	1.40E+05		(K)VNQIGS	(K)V N Q I G S V/T/E/S/I Q A/C/K(L)	C:Carbamidomethylation	155.38	545.2807	1633.821	0.0062	3.8	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
18155	dirMS_041712_NAR_20mM_minus.11233.11233.2	2	6.53	0	1.10E+05	M316m	(R)ISEQFTA	(R)I S/E Q|F/T/A m\F R(R)	m:Oxidized methionine	159.05	623.3005	1229.598	15.9954	0.4	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
18156	dirMS_041712_NAR_20mM_minus.14022.14022.2	2	6.53	0	8.06E+03		(R)DIIVIGN	(R)D I\I|V I|G N D I/T Y R(I)		192.12	696.3778	1391.753	-0.0046	-3.3	4.21	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
18157	dirMS_041712_NAR_30mM_minus2.10441.10441.2	2	6.53	0	8.52E+05		(K)YETELA	(K)Y/E|T E L/A M/R(Q)		111.27	506.7468	1012.477	0.0095	9.4	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18158	dirMS_041712_NAR_30mM_minus2.12071.12071.3	3	6.53	0	4.86E+05		(K)GISQEQ	(K)G I\S Q/E Q|M/Q E F R(A)		118.83	451.547	1352.626	0.0001	0.1	4.53	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
18159	dirMS_041712_NAR_30mM_minus2.6938.6938.2	2	6.53	0	8.10E+04		(R)SAEEGE	(R)S A|E/E/G E/L A/E S K(S)		92.15	575.2682	1149.527	0.0021	1.9	4.09	182819.3	4.77	HUMAN	Q9C0C2	182 kDa tankyrase-1-binding protein
18160	dirMS_041712_NAR_30mM_minus2.7120.7120.2	2	6.53	0	4.82E+05		(K)DAQGQ	(K)D A/Q/G/Q/P G L E R(A)		92.98	535.762	1070.523	-0.0058	-5.4	4.37	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
18161	dirMS_041712_NAR_30mM_minus2.8045.8045.2	2	6.53	0	1.06E+04		(R)AVINSA	(R)A V|I/N S A G/Y K(I)		96.8	461.7481	922.499	-0.0103	-11.2	8.63	84649.8	5.82	HUMAN	Q96TA1	Niban-like protein 1
18162	dirMS_041712_NAR_40mM_minus2.12805.12805.3	3	6.53	1	1.01E+04		(R)TIAQDY	(R)T I|A Q D Y G V/L K A D E G I S F R(G)		159.55	661.6812	1983.018	0.0109	5.5	4.56	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
18163	dirMS_041712_NAR_50mM_minus2.12445.12445.3	3	6.53	1	2.16E+05	M2709m	(K)ISmPDI	(K)I/S/m/P D I/D/L N L K G P K(V)	m:Oxidized methionine	139.38	519.6148	1540.84	15.9895	-3.5	5.96	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
18164	dirMS_041712_NAR_50mM_minus2.15514.15514.3	3	6.53	0	1.56E+05		(K)ICDQW	(K)I/C/D\Q W D A\L/G S L/T H S R(R)	C:Carbamidomethylation	156.4	586.9489	1758.823	0.0094	5.3	5.21	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
18165	dirMS_041712_NAR_60mM_minus.19538.19538.3	3	6.53	1	9.88E+04		(R)VISGVL	(R)V I|S/G V L Q/L G N I V F K K(E)		175.05	539.0023	1614.994	-0.0018	-1.1	10	227783.5	5.5	HUMAN	P35579	Myosin-9
18166	dirMS_041712_NAR_60mM_minus.7880.7880.3	3	6.53	1	4.85E+05		(R)YLAEVA	(R)Y L/A E V A/T G E K R(A)		104.22	412.8902	1236.658	-0.0022	-1.8	6.14	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
18167	dirMS_041712_NAR_60mM_minus.8059.8059.3	3	6.53	0	1.29E+05		(K)EAYPDH	(K)E A/Y/P D H T Q F E K(N)		105.03	455.5427	1364.612	0.0018	1.3	4.65	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1
18168	dirMS_041712_NAR_120mM_plus.23818.23818.4	4	6.53	2	1.48E+05	M21m	(R)IAIYELLF	(R)I A I/Y/E\L L F K E G V m V A K K(D)	m:Oxidized methionine	178.9	492.7854	1952.129	15.9909	-2.1	8.43	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
18169	dirMS_041712_NAR_20mM_plus.11461.11461.2	2	6.53	0	2.39E+05		(K)LITPAVV	(K)L I|T|P/A/V V S E R(L)		151.05	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
18170	dirMS_041712_NAR_20mM_plus.11560.11642.2	2	6.53	0	2.12E+04		(R)TIAQDY	(R)T I|A Q/D/Y G V L\K(A)		152.38	554.3056	1107.604	-0.0005	-0.5	5.5	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
18171	dirMS_041712_NAR_20mM_plus.15421.15421.3	3	6.53	0	5.72E+05		(K)VGINYQ	(K)V G I N Y Q|P P T/V|V|P G G D L A/K(V)		178.95	608.9991	1824.985	-0.0027	-1.5	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
18172	dirMS_041712_NAR_20mM_plus.17895.17895.2	2	6.53	0	1.37E+05		(R)LFDQAF	(R)L F|D/Q/A/F/G L P R(L)		195.33	582.3166	1163.621	0.0052	4.4	5.84	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
18173	dirMS_041712_NAR_20mM_plus.8661.8661.2	2	6.53	0	1.04E+05		(K)EQVANS	(K)E Q\V/A/N/S/A F V E R(C)		130.52	625.3102	1249.617	-0.004	-3.2	4.53	17664	8.77	HUMAN	H0Y6E4	Heat shock protein HSP 90-beta (Fragment)
18174	dirMS_041712_NAR_20mM_plus.9929.9929.2	2	6.53	0	1.80E+05		(K)QTLSAA	(K)Q T L S A A/A/V F N D R(L)		138.83	646.8319	1292.659	-0.0028	-2.2	5.84	378709.3	6.48	HUMAN	H3BLU6	E3 ubiquitin-protein ligase RNF213
18175	dirMS_041712_NAR_30mM_plus2.13934.13934.2	2	6.53	2	4.69E+05		(K)SSGGEG	(K)S\S G/G E G V K D\R K(G)		125.63	560.2878	1119.575	-0.007	-6.2	8.31	41734	6.51	HUMAN	A9R9N7	HLA class I histocompatibility antigen, A-68 alpha chain
18176	dirMS_041712_NAR_40mM_plus2.12298.12298.3	3	6.53	0	3.63E+04		(R)VLTEDE	(R)V L|T/E/D E/M G H P E I G D A I A R(L)		138.75	651.6493	1952.938	-0.0049	-2.5	4.17	40874	5.06	HUMAN	E9PCI9	Farnesyl pyrophosphate synthase
18177	dirMS_041712_NAR_40mM_plus2.8784.8784.2	2	6.53	0	9.52E+04		(K)TCAELV	(K)T/C/A/E L V/R(E)	C:Carbamidomethylation	114.37	424.7133	848.429	-0.0101	-12	5.66	26953.5	5.88	HUMAN	B1AQP4	Nitrilase 1
18178	dirMS_041712_NAR_50mM_plus2.10851.10851.3	3	6.53	1	2.69E+05		(K)NVDILK	(K)N V/D/I L/K/D/P E/T V K(Q)		124.72	457.5906	1370.753	0.0047	3.4	4.56	124524.8	5.71	HUMAN	O14980	Exportin-1
18179	dirMS_041712_NAR_60mM_plus.14123.14123.3	3	6.53	1	8.99E+05		(K)TTVKDL	(K)T/T\V K D L S E/L/G/S V/R(T)		130.22	468.9268	1404.769	-0.0034	-2.4	5.74	533778	5.74	HUMAN	Q15149	Plectin
18180	dirMS_041712_NAR_60mM_plus.16311.16311.3	3	6.53	1	3.36E+06		(R)MSMKE	(R)M S M K E V D E Q|M/L/N V Q/N K(N)		141.48	641.9696	1923.897	-0.003	-1.6	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
18181	dirMS_041712_NAR_60mM_plus.5786.5786.3	3	6.53	1	1.33E+04		(R)GTAAE	(R)G T A A E M V/A V K/L D K(K)		89.08	444.917	1332.719	0.0173	13	6.07	65402.5	5.57	HUMAN	B7Z4U7	Sec1 family domain containing 1, isoform CRA_b
18182	dirMS_041712_NAR_20mM_minus.10542.10542.2	2	6.52	0	1.83E+05		(R)TTPSYV	(R)T T/P S Y V|A F T D T E/R(L)		154.55	744.3547	1487.701	0.0009	0.6	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
18183	dirMS_041712_NAR_20mM_minus.12331.12331.2	2	6.52	0	1.59E+05		(R)AAVIGP	(R)A A/V|I/G/P D V F A K(L)		171.6	544.3103	1087.615	-0.0013	-1.2	5.88	266161	5.68	HUMAN	E9PPU0	Epiplakin
18184	dirMS_041712_NAR_30mM_minus2.13851.13851.2	2	6.52	0	2.26E+05		(K)TYSVEYL	(K)T Y|S V/E Y L/P K(V)		128.3	550.2855	1099.567	-0.0033	-3	5.66	258215.9	5.48	HUMAN	E7EN95	Filamin-B
18185	dirMS_041712_NAR_50mM_minus2.11737.11737.3	3	6.52	0	2.43E+05	M291m	(K)TGEEIFG	(K)T G/E/E/I/F/G T I G m R P N A\K(N)	m:Oxidized methionine	134.33	579.6239	1720.869	15.9885	-3.7	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
18186	dirMS_041712_NAR_50mM_minus2.13047.13047.3	3	6.52	1	7.44E+05		(K)VLAGDK	(K)V L|A/G D K N F\I/T A E E/L R(R)		142.85	559.3044	1675.901	-0.0027	-1.6	4.68	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
18187	dirMS_041712_NAR_50mM_minus2.5314.5314.3	3	6.52	0	7.53E+05	M434m M	(R)LESGmC	(R)L/E|S|G m Q/N m S I H/T K(T)	m:Oxidized methionine	87.88	503.2361	1475.698	31.9956	3.9	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
18188	dirMS_041712_NAR_50mM_minus2.9624.9624.3	3	6.52	0	1.28E+05		(K)MIVDPV	(K)M I\V/D P V/E/P H G E M K(F)		122.48	494.5757	1481.713	-0.0002	-0.1	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
18189	dirMS_041712_NAR_60mM_minus.5813.5813.3	3	6.52	1	1.01E+05		(K)QQTLEA	(K)Q Q/T/L E/A E E A/K/R(R)		88.6	434.8904	1302.665	-0.0082	-6.3	4.79	76925.9	4.46	HUMAN	A8MV58	Drebrin
18190	dirMS_041712_NAR_120mM_plus.12142.12142.3	3	6.52	0	4.54E+05		(R)SSHYDE	(R)S S H Y D E\L|L/A/A/E A/R(A)		117.27	487.9048	1461.697	0.003	2.1	4.65	26398.4	5.21	HUMAN	H7C597	Staphylococcal nuclease domain-containing protein 1 (Fragment)
18191	dirMS_041712_NAR_120mM_plus.7309.7309.3	3	6.52	1	5.17E+05		(K)SKAEAE	(K)S|K A E A E/S/L Y Q S K(Y)		91.33	447.5614	1340.669	0.0004	0.3	5.86	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
18192	dirMS_041712_NAR_20mM_plus.11973.11973.3	3	6.52	1	2.80E+04	M155m K1	(R)QNALYE	(R)Q N A L/Y E I E m R K k(L)	m:Oxidized methionine k:Ub	155.83	551.6252	1522.805	130.0564	11.2	8.5	19660.1	9.21	HUMAN	C9J9F8	Coiled-coil domain-containing protein 173 (Fragment)
18193	dirMS_041712_NAR_20mM_plus.13571.13571.2	2	6.52	0	1.66E+05	M98m	(R)TLTIVDT	(R)T L|T I V D\T/G/I G m T K(A)	m:Oxidized methionine	165.97	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
18194	dirMS_041712_NAR_20mM_plus.13862.13862.2	2	6.52	0	1.34E+05		(R)GGIVDE	(R)G G I\V/D/E G/A L L\R(A)		167.83	550.3066	1099.611	-0.0047	-4.3	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
18195	dirMS_041712_NAR_20mM_plus.16470.16470.3	3	6.52	0	6.48E+04	M137m M	(R)IIGATDS	(R)I I G A\T D S/S G E L/m/F L m K(W)	m:Oxidized methionine	185.8	582.2872	1712.86	31.9873	-1.5	4.37	19439.5	4.97	HUMAN	B5MD17	Chromobox protein homolog 1 (Fragment)
18196	dirMS_041712_NAR_20mM_plus.8813.8813.2	2	6.52	0	1.30E+05		(K)VLEEAN	(K)V L/E E A|N Q|A I/N/P K(L)		131.6	663.353	1325.706	-0.0072	-5.5	4.53	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
18197	dirMS_041712_NAR_20mM_plus.9945.9945.2	2	6.52	0	7.20E+04		(K)AIADTG	(K)A I/A/D T/G/A N V/V\V T G G K(V)		139.35	686.874	1372.743	-0.0023	-1.7	5.88	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
18198	dirMS_041712_NAR_30mM_plus2.12736.12736.2	2	6.52	0	5.39E+05		(R)CNNVLY	(R)C/N/N V|L Y I R(G)	C:Carbamidomethylation	120.77	526.2726	1051.535	0.0026	2.5	8.75	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F

18199	dirMS_041712_NAR_30mM_plus2.17270.17270.2	2	6.52	0	6.98E+04		(K)WPLYM	(K)W/P L/Y M/S T K(N)		144.88	513.2647	1025.513	0.0097	9.4	8.59	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
18200	dirMS_041712_NAR_30mM_plus2.17799.17799.2	2	6.52	0	2.65E+05		(K)YNLGLD	(K)Y N|L/G L D/L/R(T)		146.2	482.2695	963.526	0.0059	6.1	5.83	43177.5	7.2	HUMAN	B3KV55	Glutamate dehydrogenase
18201	dirMS_041712_NAR_40mM_plus2.17857.17857.3	3	6.52	1	7.73E+04	M116m	(R)ELAILLG	(R)E\L A I|L/L/G m L/D P A E K D E K(G)	m:Oxidized methionine	171.67	634.3333	1884.999	15.9867	-4.3	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
18202	dirMS_041712_NAR_40mM_plus2.5283.5283.2	2	6.52	0	4.93E+04		(R)QSSGAS	(R)Q S/S G A|S S/S S F/S S S R(A)		87.37	681.2998	1361.593	-0.0005	-0.3	9.75	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
18203	dirMS_041712_NAR_50mM_plus2.13681.13681.3	3	6.52	0	4.46E+05		(K)FLSDPQ	(K)F L/S D/P Q V/H T V L V E R(S)		140.13	547.2984	1639.88	0.0004	0.3	5.32	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
18204	dirMS_041712_NAR_50mM_plus2.16363.16363.3	3	6.52	0	5.57E+05		(R)QVVQGI	(R)Q V\V Q|G\L\L/S E T\Y/L/E A H R(I)		154.53	614.9984	1842.971	0.0098	5.3	5.4	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
18205	dirMS_041712_NAR_50mM_plus2.19266.19266.3	3	6.52	1	1.15E+05		(K)GLKVNLI	(K)G L K V N L\F|P|G L S/P S A L K(A)		169.47	547.6608	1640.973	-0.0056	-3.4	10	182819.3	4.77	HUMAN	Q9C0C2	182 kDa tankyrase-1-binding protein
18206	dirMS_041712_NAR_50mM_plus2.5854.5854.3	3	6.52	1	6.84E+04		(K)TAEAGG	(K)T/A|E/A G G\V/T G K G Q D G I G S K(A)		94.48	544.9471	1632.819	0.008	4.9	5.73	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
18207	dirMS_041712_NAR_60mM_plus.17598.17598.3	3	6.52	1	1.76E+05		(R)RTVQSLI	(R)R T V Q\S|L E|I/D/L/D S M R(N)		148.8	554.954	1662.848	-0.0005	-0.3	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18208	dirMS_041712_NAR_120mM_minus.14866.14866.4	4	6.51	2	1.74E+05		(K)ILAGDK	(K)I L/A G D K/N Y/I/T M D E L R/R(E)		135	477.7556	1908.001	-0.0002	-0.1	6.12	28932	4.94	HUMAN	H0YJW3	Alpha-actinin-1 (Fragment)
18209	dirMS_041712_NAR_120mM_minus.4445.4445.2	2	6.51	0	6.48E+05		(R)HSDGNL	(R)H/S D G/N L\C V\K(V)	C:Carbamidomethylation	73.82	515.2423	1029.478	-0.0009	-0.9	6.74	7781.8	6.82	HUMAN	E9PE20	Signal recognition particle 9 kDa protein
18210	dirMS_041712_NAR_120mM_minus.9116.9116.2	2	6.51	0	5.31E+05		(K)HFVALS	(K)H/F|V|A L/S/T N/T T K(V)		103.45	609.8267	1218.648	-0.0016	-1.3	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
18211	dirMS_041712_NAR_50mM_minus2.10475.10475.3	3	6.51	1	1.84E+04		(R)TEMEDL	(R)T E|M/E D L M/S S K D D V/G K(S)		127.38	562.2507	1684.74	-0.0029	-1.7	4.1	227783.5	5.5	HUMAN	P35579	Myosin-9
18212	dirMS_041712_NAR_50mM_minus2.16198.16198.3	3	6.51	1	4.43E+06		(R)VSFELFA	(R)V/S|F E L F A D K V/P K(T)		159.72	460.5908	1379.757	0.0009	0.7	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
18213	dirMS_041712_NAR_50mM_minus2.8633.8633.3	3	6.51	0	1.18E+05		(R)LGYAVYI	(R)L/G Y A V/Y E/T/P T A H N G A/K(N)		117.07	564.6215	1691.839	0.0112	6.6	6.75	25016.4	5.65	HUMAN	B3KR28	Toll-interacting protein
18214	dirMS_041712_NAR_60mM_minus.10884.10884.3	3	6.51	1	9.02E+04		(R)KGSSGN	(R)K G S S G N A S E\V\S V/A/C/L T/E R(I)	C:Carbamidomethylation	120.65	617.9652	1851.887	-0.0055	-3	6.14	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
18215	dirMS_041712_NAR_60mM_minus.17259.17259.3	3	6.51	1	1.14E+05		(R)VSFELFA	(R)V/S/F E L F A D K V/P K(T)		156	460.5911	1379.757	0.0018	1.3	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
18216	dirMS_041712_NAR_120mM_plus.18006.18006.3	3	6.51	1	3.63E+05		(K)YRGFTIP	(K)Y R/G F T|I|P E/A F R(G)		148.07	452.9069	1356.706	0.0003	0.2	8.75	27264.5	5.09	HUMAN	O00299	Chloride intracellular channel protein 1
18217	dirMS_041712_NAR_120mM_plus.20228.20228.3	3	6.51	0	2.78E+05		(R)INLWHL	(R)I N/L W H/L E I T D R(S)		159.48	470.5889	1409.754	-0.0014	-1	5.32	52204.6	5.82	HUMAN	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
18218	dirMS_041712_NAR_20mM_plus.17573.17573.2	2	6.51	0	5.44E+04	M215m	(K)TLNDEL	(K)T L|N D/E L E/I I|E G m K(F)	m:Oxidized methionine	193.07	760.8799	1504.756	15.9962	0.8	4	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
18219	dirMS_041712_NAR_20mM_plus.17625.17625.3	3	6.51	0	6.52E+04		(K)ITNLTQ	(K)I T/N L T\Q Q\L|E Q|A S I V K(K)		192.92	562.6523	1685.943	-0.0009	-0.5	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
18220	dirMS_041712_NAR_20mM_plus.18449.18449.2	2	6.51	0	1.77E+05		(R)NIPGITL	(R)N I/P G I/T L L N V S K(L)		198.83	634.8801	1268.757	-0.0043	-3.4	8.75	37884.5	11.27	HUMAN	H3BM89	60S ribosomal protein L4
18221	dirMS_041712_NAR_30mM_plus2.18178.18178.2	2	6.51	0	2.99E+05		(R)SQVEEEI	(R)S Q|V/E/E/E L F/S V/R(V)		149.15	661.8302	1322.659	-0.0055	-4.2	4.25	533778	5.74	HUMAN	Q15149	Plectin
18222	dirMS_041712_NAR_30mM_plus2.19163.19163.2	2	6.51	0	2.24E+05		(K)TVDNFV	(K)T V|D N/F|V/A L/A T G E K(G)		154.3	682.8539	1364.706	-0.0051	-3.7	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
18223	dirMS_041712_NAR_40mM_plus2.11217.11217.3	3	6.51	1	7.82E+04		(K)AVEEED	(K)A V/E E\E D\K M T|P\E Q L/A I K(N)		131.98	610.9764	1830.915	-0.0007	-0.4	4.25	34747.6	6.06	HUMAN	O00487	26S proteasome non-ATPase regulatory subunit 14
18224	dirMS_041712_NAR_40mM_plus2.15430.15430.3	3	6.51	0	2.03E+05		(K)GVTIIGP	(K)G V|T I/I/G/P A/T V G G I K/P G C F K(I)	C:Carbamidomethylation	156.62	624.683	1872.041	-0.0067	-3.6	10	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
18225	dirMS_041712_NAR_40mM_plus2.17047.17047.3	3	6.51	0	4.41E+05		(R)IHFPLAT	(R)I H F P L A T|Y\A/P V I S A E K(A)		167.57	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
18226	dirMS_041712_NAR_40mM_plus2.19523.19523.3	3	6.51	1	4.20E+05		(K)ALFEEV	(K)A L F/E/E V P E L L/T E A E K K(E)		181.82	615.9991	1845.984	-0.0017	-0.9	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
18227	dirMS_041712_NAR_50mM_plus2.15811.15811.3	3	6.51	1	4.44E+05		(K)EALESV	(K)E A/L/E/S V E V L I/K N/P K(L)		151.07	523.6299	1568.889	-0.0143	-9.1	4.79	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
18228	dirMS_041712_NAR_50mM_plus2.20246.20246.3	3	6.51	0	2.29E+05		(K)GHVDIL	(K)G H V D I\L A\P T|V Q/E L A A L E K(E)		174.67	635.3536	1904.049	-0.0025	-1.3	4.65	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
18229	dirMS_041712_NAR_60mM_plus.20625.20625.3	3	6.51	0	4.44E+05		(R)CRPDQL	(R)C R P D Q L\T\G\L/S L|L/P L S E K(A)	C:Carbamidomethylation	168.32	643.0146	1927.032	-0.0025	-1.3	6.07	533778	5.74	HUMAN	Q15149	Plectin
18230	dirMS_041712_NAR_60mM_plus.9603.9603.3	3	6.51	1	5.61E+05		(R)QDSAA	(R)Q D S A/A/V/G/F/D Y K E/K(L)		108.02	486.5682	1457.691	-0.0007	-0.4	4.56	61756.2	5.24	HUMAN	Q14247	Src substrate cortactin
18231	dirMS_041712_NAR_120mM_minus.5819.5819.3	3	6.5	1	6.74E+04		(R)QRQLAE	(R)Q R Q\L\A|E E/D/A/A/R(Q)		85.35	429.5525	1286.645	-0.0018	-1.4	4.68	533778	5.74	HUMAN	Q15149	Plectin
18232	dirMS_041712_NAR_20mM_minus.13481.13481.3	3	6.5	0	7.87E+05	M221m	(R)ALTVPE	(R)A L\T V P E L/T/Q/Q m F D/A/K(N)	m:Oxidized methionine	186.22	569.9577	1691.867	15.9913	-2.1	4.37	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
18233	dirMS_041712_NAR_30mM_minus2.13533.13533.2	2	6.5	0	2.30E+05		(K)FAFQAE	(K)F A|F/Q/A/E V N R(M)		127.28	541.2823	1081.543	0.0148	13.7	6	92752.5	4.76	HUMAN	P14625	Endoplasmin
18234	dirMS_041712_NAR_30mM_minus2.18321.18321.2	2	6.5	0	4.01E+05		(R)ADLIAYL	(R)A D/L/I/A Y/L K(K)		154.62	453.7668	906.529	-0.0032	-3.5	5.88	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
18235	dirMS_041712_NAR_40mM_minus2.12295.12295.3	3	6.5	1	2.92E+05		(K)DVAIKE	(K)D V A I K E P L|V/D V\V D/P K(Q)		156.1	546.3068	1636.916	-0.0098	-6	4.23	24376.8	6.08	HUMAN	E9PIX6	Protein arginine N-methyltransferase 1 (Fragment)
18236	dirMS_041712_NAR_40mM_minus2.8818.8818.3	3	6.5	0	3.87E+04		(R)LDDTVH	(R)L/D D T V/H V V I A T/P G R(I)		134.7	498.2749	1492.812	-0.0017	-1.1	5.21	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
18237	dirMS_041712_NAR_50mM_minus2.12522.12522.3	3	6.5	1	3.07E+05		(K)LYEQILA	(K)L Y/E/Q\I L\A/E N E K L K(A)		139.22	530.9592	1590.874	-0.0107	-6.7	4.79	22046.7	5.8	HUMAN	H0YIM2	Protein phosphatase 1 regulatory subunit 12A (Fragment)
18238	dirMS_041712_NAR_50mM_minus2.5830.5830.3	3	6.5	1	3.54E+04		(R)AQLGG	(R)A Q|L/G/G P E A A K S D/E T A A K(-)		95.17	548.6119	1643.824	-0.0024	-1.4	4.68	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
18239	dirMS_041712_NAR_60mM_minus.13014.13014.3	3	6.5	0	6.59E+05		(K)GIHPTII	(K)G I H\P T I\I/S/E/S F Q K(A)		132.77	486.2642	1456.78	-0.0014	-1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
18240	dirMS_041712_NAR_60mM_minus.18174.18174.3	3	6.5	1	5.46E+05		(K)IKTLFPLI	(K)I K T L F/P L/I E A K(K)		162.7	424.9345	1272.793	-0.0036	-2.9	8.59	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
18241	dirMS_041712_NAR_120mM_plus.11205.11205.4	4	6.5	1	3.46E+04		(R)IFHTVTT	(R)I F H T V/T T T D/D/P V/I R K(L)		111.6	436.4888	1742.944	-0.0102	-5.8	6.75	31956.7	9.73	HUMAN	B0QYA5	Eukaryotic translation initiation factor 3 subunit D (Fragment)
18242	dirMS_041712_NAR_20mM_plus.19249.19249.2	2	6.5	0	1.81E+05		(K)ILTFDQL	(K)I L/T/F/D Q/L A L D|S P K(G)		203.47	730.9063	1460.8	0.0058	4	4.21	14643	11.93	HUMAN	F8VUA6	60S ribosomal protein L18 (Fragment)
18243	dirMS_041712_NAR_20mM_plus.8368.8368.2	2	6.5	0	1.06E+05	M406m	(R)EYQELm	(R)E Y Q/E/L/m N V K(L)	m:Oxidized methionine	127.52	585.2801	1153.556	15.9971	1.9	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
18244	dirMS_041712_NAR_30mM_plus2.11592.11779.2	2	6.5	2	1.71E+06		(K)DKAEKSI	(K)D K/A E|K|S E Q M V K(E)		114.23	646.8322	1292.651	0.0056	4.4	6.18	62850.8	5.5	HUMAN	F6VX93	Vacuolar protein sorting-associated protein 53 homolog
18245	dirMS_041712_NAR_40mM_plus2.10017.10017.2	2	6.5	0	9.42E+04		(K)YEELQSL	(K)Y E|E/L/Q S L/A/G K(H)		123.57	569.2912	1137.579	-0.0035	-3.1	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
18246	dirMS_041712_NAR_50mM_plus2.12580.12580.3	3	6.5	0	1.02E+05		(K)TYSTSFT	(K)T Y/S T/S F\T/P M Y/H A V T K(R)		134.05	578.611	1733.82	-0.0019	-1.1	8.2	56826.6	9.16	HUMAN	P00390	Glutathione reductase, mitochondrial
18247	dirMS_041712_NAR_50mM_plus2.14337.14337.3	3	6.5	1	8.83E+05		(K)ATLPSP	(K)A T/L/P/S/P D K L P G F K(M)		143.57	457.5906	1370.768	-0.0106	-7.7	8.64	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
18248	dirMS_041712_NAR_50mM_plus2.14595.14595.3	3	6.5	0	1.06E+06		(R)ETHSAL	(R)E T H S\A L G|P|A\L|Q/A A F K(L)		144.3	514.2745	1540.812	-0.0029	-1.9	6.85	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
18249	dirMS_041712_NAR_60mM_plus.15207.15207.3	3	6.5	1	2.48E+05		(-)MKVELC	(-)M K V E L\C/S/F/S/G Y K(I)	C:Carbamidomethylation	136.28	483.5686	1448.691	0	0	8.26	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
18250	dirMS_041712_NAR_60mM_plus.17083.17083.3	3	6.5	2	3.44E+05	S440s	(K)AQTsKEI	(K)A Q/T/s K E L/S F K K(G)	s:N-acetylglucosamine (S)	146.7	490.5979	1266.705	203.0739	-3.7	9.7	73923.6	9.2	HUMAN	C9JKV9	Sorbin and SH3 domain-containing protein 2
18251	dirMS_041712_NAR_60mM_plus.18580.18580.3	3	6.5	1	1.52E+05		(R)CRVDLP	(R)C R V D\L|P/L|A V L S/K(M)	C:Carbamidomethylation	154.35	457.599	1370.782	0	0	8.75	7765.6	8.23	HUMAN	H3BSA6	dCTP pyrophosphatase 1
18252	dirMS_041712_NAR_120mM_minus.15957.15957.4	4	6.49	1	3.72E+05		(K)AGSMK	(K)A G/S M K D/P\L/L/D D/H G D F I R(M)		141.33	472.4817	1886.907	-0.0016	-0.8	4.56	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
18253	dirMS_041712_NAR_120mM_minus.6004.6004.3	3	6.49	1	5.64E+05		(K)TCEESSF	(K)T C/E/E S S/F C K R(Q)	C:Carbamidomethylation	86.8	435.1849	1303.541	-0.0004	-0.3	5.81	10576.1	11.44	HUMAN	E9PRF8	Neutral alpha-glucosidase AB
18254	dirMS_041712_NAR_20mM_minus.8882.8882.2	2	6.49	0	2.58E+05		(R)ALGQN	(R)A L\G Q/N/P T N A E V L K(V)		138.72	677.871	1354.733	0.0022	1.6	6.05	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
18255	dirMS_041712_NAR_40mM_minus2.12677.12677.3	3	6.49	0	1.65E+04		(R)IYALPD	(R)I Y/A L/P D D L\V E V/K P K(M)		158.17	533.9726	1599.899	0.004	2.5	4.56	70651.6	5.28	HUMAN	Q14651	Plastin-1
18256	dirMS_041712_NAR_40mM_minus2.6017.6017.2	2	6.49	0	2.58E+04		(K)AGFAG	(K)A G|F|A G D/D A P/R(A)		99.45	488.7279	976.448	0.0002	0.2	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
18257	dirMS_041712_NAR_50mM_minus2.16669.16669.3	3	6.49	1	2.61E+05		(R)SELELTL	(R)S/E|L/E/L/T/L G K L E Q V R(S)		163.6	538.9725	1614.906	-0.0032	-2	4.78	533778	5.74	HUMAN	Q15149	Plectin
18258	dirMS_041712_NAR_50mM_minus2.8459.8459.3	3	6.49	1	2.45E+04		(R)LGGSPF	(R)L/G G S/P F G P A G T G K/T E\S V K(A)		116.02	563.9636	1689.881	-0.0044	-2.6	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
18259	dirMS_041712_NAR_50mM_minus2.8801.8801.3	3	6.49	1	2.18E+05		(K)VCGDSD	(K)V/C/G/D/S D K G F V V/I/N Q K(G)	C:Carbamidomethylation	118.03	555.9474	1665.826	0.0012	0.7	5.93	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
18260	dirMS_041712_NAR_60mM_minus.10811.10811.3	3	6.49	0	1.64E+05		(K)TGNLGN	(K)T/G N/L/G\N V V/H I E R(F)		119.98	436.9057	1308.702	0.0007	0.5	6.41	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
18261	dirMS_041712_NAR_60mM_minus.13701.13701.3	3	6.49	0	1.25E+05		(R)YLDLHD	(R)Y/L/D L/H D/C Y L/K(Y)	C:Carbamidomethylation	135.9	447.218	1339.635	0.0043	3.2	5.21	52796.2	5.19	HUMAN	E7EUT8	Splicing factor 3A subunit 3
18262	dirMS_041712_NAR_60mM_minus.8181.8181.3	3	6.49	1	7.40E+04		(K)AALSEE	(K)A A/L/S E/E E L E/K K(S)		105.9	416.2162	1246.652	-0.0185	-14.8	4.49	176357.7	5.25	HUMAN	D3DNT2	Eukaryotic translation initiation factor 4 gamma 1
18263	dirMS_041712_NAR_20mM_plus.13427.13427.2	2	6.49	0	1.22E+05		(K)IFVGGLS	(K)I F/V G G L|S|P D/T/P E E K(I)		164.67	744.8731	1488.758	-0.0191	-12.8	4.14	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
18264	dirMS_041712_NAR_20mM_plus.13673.13673.2	2	6.49	0	7.90E+04		(R)ATLYVT	(R)A T L/Y/V/T\A/I E D R(Q)		166.4	626.3269	1251.658	-0.0114	-9.1	4.37	24376.8	6.08	HUMAN	E9PIX6	Protein arginine N-methyltransferase 1 (Fragment)
18265	dirMS_041712_NAR_20mM_plus.14728.14728.2	2	6.49	0	9.75E+04		(R)LNIFPD	(R)L N\I F P D\G/G I A R(L)		173.22	586.8315	1172.642	0.0135	11.5	5.84	43957.2	5.8	HUMAN	B4DY77	Allantoicase, isoform CRA_a
18266	dirMS_041712_NAR_20mM_plus.9627.9627.2	2	6.49	0	1.19E+05		(K)VAGQD	(K)V/A|G\Q/D/G S V/V Q F K(I)		138	617.8225	1234.643	-0.0049	-4	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
18267	dirMS_041712_NAR_20mM_plus.9913.9913.2	2	6.49	0	6.81E+04		(R)TDYNAS	(R)T D Y N A S V/S V/P/D/S S G P E R(I)		139.12	890.9015	1780.798	-0.0027	-1.5	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
18268	dirMS_041712_NAR_30mM_plus2.11436.11436.2	2	6.49	0	3.73E+05		(R)NGDFLP	(R)N/G/D|F L/P T\R(L)		113.47	460.2391	919.463	0.0077	8.4	5.84	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
18269	dirMS_041712_NAR_30mM_plus2.12629.12629.2	2	6.49	0	5.21E+05		(K)NAGVE	(K)N A/G\V/E/G S L I|V E K(I)		118.48	608.3313	1215.658	-0.0026	-2.2	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
18270	dirMS_041712_NAR_30mM_plus2.5697.5697.2	2	6.49	0	6.89E+04		(R)QLEDGD	(R)Q/L\E/D/G D/Q/P E S K(K)		83.85	623.2808	1245.559	-0.005	-4	3.91	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
18271	dirMS_041712_NAR_40mM_plus2.10242.10242.2	2	6.49	1	8.78E+05		(K)KITIADC	(K)K I T I\A D\C\G Q|L/E(-)	C:Carbamidomethylation	125.52	624.3146	1247.63	-0.0081	-6.5	4.75	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
18272	dirMS_041712_NAR_40mM_plus2.6199.6199.2	2	6.49	0	8.88E+04	M200m	(K)SFYmQR	(K)S/F/Y/m/Q R(C)	m:Oxidized methionine	95.47	424.1929	831.382	15.9967	2.2	8.46	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
18273	dirMS_041712_NAR_50mM_plus2.11849.11849.3	3	6.49	1	1.06E+05		(K)VEAQVY	(K)V/E/A Q/V Y I L S K E E/G G R(H)		130.02	559.9637	1677.881	-0.0041	-2.4	4.79	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
18274	dirMS_041712_NAR_50mM_plus2.15338.15338.3	3	6.49	1	4.95E+05		(R)AGDEIH	(R)A G D/E I H V L/K/R/D L/K(M)		148.98	498.6121	1493.843	-0.0217	-14.5	6.8	63591.7	6.3	HUMAN	A4QPA5	C-type lectin domain family 4 member F
18275	dirMS_041712_NAR_50mM_plus2.7368.7368.3	3	6.49	1	2.01E+04	M236m M	(K)NSVTPD	(K)N S/V/T/P D/M m E E m Y K/K(A)	m:Oxidized methionine	104.67	578.9161	1702.748	31.9853	-2.6	4.68	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
18276	dirMS_041712_NAR_50mM_plus2.9247.9247.3	3	6.49	0	1.91E+05		(K)TAVEHA	(K)T/A\V/E/H/A T D/E D I L A K(G)		115.42	504.9238	1512.754	0.0028	1.9	4.31	288852.1	5.33	HUMAN	E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein
18277	dirMS_041712_NAR_50mM_plus2.9435.9435.3	3	6.49	0	2.45E+05		(R)LVKPGN	(R)L V K P G N\Q N/T Q|V/T/E A W N K(V)		117.08	643.0046	1927.003	-0.004	-2.1	8.59	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
18278	dirMS_041712_NAR_50mM_plus2.9934.9934.3	3	6.49	1	1.41E+05		(R)DIKDTT	(R)D I K D T\T V/G T/L S Q/R(I)		119.55	478.5966	1433.759	0.0158	11	5.96	28354	7.11	HUMAN	B4DXI8	26S proteasome non-ATPase regulatory subunit 7
18279	dirMS_041712_NAR_60mM_plus.12150.12150.3	3	6.49	1	2.45E+05		(R)EYRDLT	(R)E Y R D L T\T A G A/V|T/Q/C Y R(D)	C:Carbamidomethylation	120.48	635.3051	1903.897	0.0041	2.1	6.17	18395.1	11.05	HUMAN	B4DM74	60S ribosomal protein L18a
18280	dirMS_041712_NAR_60mM_plus.16447.16447.3	3	6.49	0	6.27E+05		(R)ETHSAL	(R)E T H\S A L/G|P/A L/Q/A/A F K(L)		142.28	514.2744	1540.812	-0.0032	-2.1	6.85	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
18281	dirMS_041712_NAR_60mM_plus.5502.5502.3	3	6.49	0	4.17E+05	M21m	(R)SGSmDF	(R)S G\S m|D P S G A/H/P S V R(Q)	m:Oxidized methionine	86.32	467.5464	1384.627	15.9973	1.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
18282	dirMS_041712_NAR_120mM_minus.10534.10534.3	3	6.48	1	8.70E+04		(R)RGVVGF	(R)R G/V V G|P E|L/Y/G R(L)		111.63	401.559	1202.664	-0.0016	-1.3	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
18283	dirMS_041712_NAR_120mM_minus.11744.11893.4	4	6.48	2	7.86E+05		(K)QKQQE	(K)Q K Q Q E/A/A L E|L/E E L/K K(K)		118.35	446.9993	1784.975	0.0001	0.1	4.95	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
18284	dirMS_041712_NAR_20mM_minus.11853.11853.3	3	6.48	1	1.53E+05	M60m	(K)mKSLDV	(K)m K\S L/D/V N Q\D\S E L/K(F)	m:Oxidized methionine	167.6	508.2517	1506.747	15.9937	-0.8	4.56	11471	5.9	HUMAN	Q99584	Protein S100-A13
18285	dirMS_041712_NAR_20mM_minus.14572.14572.3	3	6.48	0	1.76E+04		(K)LAVEAL	(K)L A V\E A/L\S S L/D G D/L/A G R(Y)		199.98	529.6163	1586.838	-0.0041	-2.6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
18286	dirMS_041712_NAR_30mM_minus2.12567.12567.2	2	6.48	0	5.44E+05	M405m	(K)FDLmYA	(K)F/D|L/m Y/A K(R)	m:Oxidized methionine	122.48	452.2186	887.433	15.9968	2.1	5.83	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
18287	dirMS_041712_NAR_30mM_minus2.16785.16785.2	2	6.48	0	1.34E+04		(K)GAILTDT	(K)G A I|L T/D T S V K(R)		145.83	502.7828	1004.562	-0.0039	-3.9	5.84	42868.1	10.57	HUMAN	Q5NUL3	Free fatty acid receptor 4
18288	dirMS_041712_NAR_30mM_minus2.18047.18047.3	3	6.48	0	6.94E+04		(R)SSFYVN	(R)S S F Y V N/G|L/T/L G G Q K(C)		152.48	490.9238	1470.759	-0.0019	-1.3	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
18289	dirMS_041712_NAR_30mM_minus2.18417.18417.2	2	6.48	0	3.04E+04		(R)YEFGIFN	(R)Y E|F/G/I F N Q K(I)		154.53	573.2849	1145.563	-0.0001	-0.1	6	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
18290	dirMS_041712_NAR_40mM_minus2.8172.8172.3	3	6.48	0	2.30E+05	M35m	(K)AASDIA	(K)A A|S D I/A\m/T E L/P P T H P I R(L)	m:Oxidized methionine	128.52	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
18291	dirMS_041712_NAR_50mM_minus2.17430.17430.3	3	6.48	0	2.48E+05		(R)LLLDGA	(R)L/L/L D G A/P L I A I H K(A)		168.47	458.6218	1373.852	-0.0007	-0.5	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
18292	dirMS_041712_NAR_50mM_plus2.8166.8166.3	3	6.48	0	1.12E+04		(K)ASSEGG	(K)A S\S E/G G/T A/A/G/A G L D S L H K(N)		109.45	543.6023	1628.787	0.0049	3	5.32	41747.8	9.36	HUMAN	O15143	Actin-related protein 2/3 complex subunit 1B
18293	dirMS_041712_NAR_50mM_plus2.8968.8968.3	3	6.48	0	5.64E+05		(R)AALAHS	(R)A A L A H S/E E/V|T\A/S/Q V/A|A T K(T)		113.83	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
18294	dirMS_041712_NAR_60mM_plus.17160.17160.2	2	6.48	1	1.56E+05		(R)KLVAM	(R)K\L|V|A M G I P E S L R(G)		146.1	657.3751	1313.761	-0.018	-13.7	8.75	133849.8	5.28	HUMAN	J3KQ40	TBC1 domain family member 8
18295	dirMS_041712_NAR_60mM_plus.21280.21284.3	3	6.48	1	5.45E+05		(R)SKALGS	(R)S K\A L G S D H C P I T\L\Y\L|A\L(-)	C:Carbamidomethylation	175.57	620.326	1858.973	-0.0097	-5.2	6.46	5634.5	9.82	HUMAN	G3V574	DNA-(apurinic or apyrimidinic site) lyase
18296	dirMS_041712_NAR_20mM_minus.13278.13278.3	3	6.47	0	1.05E+05		(R)GVVDSE	(R)G V V\D S E D|I/P/L N L S R(E)		183	505.266	1513.786	-0.0022	-1.5	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
18297	dirMS_041712_NAR_20mM_minus.13486.13486.2	2	6.47	0	6.14E+05		(K)DAGTIA	(K)D A G/T\I/A/G L/N V/L R(I)		185.05	600.3403	1199.674	-0.0009	-0.8	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
18298	dirMS_041712_NAR_20mM_minus.7969.7969.2	2	6.47	0	4.16E+04		(K)VVTDTD	(K)V/V/T|D T D E T E L/A\R(Q)		129.38	674.8314	1348.659	-0.0035	-2.6	3.91	36396.8	5.02	HUMAN	P05198	Eukaryotic translation initiation factor 2 subunit 1
18299	dirMS_041712_NAR_30mM_minus2.16813.16813.2	2	6.47	0	2.37E+05		(K)FANPFP	(K)F A/N|P F/P A A V R(G)		146.12	545.2937	1089.584	-0.0039	-3.5	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
18300	dirMS_041712_NAR_40mM_minus2.6927.6927.2	2	6.47	0	6.99E+04	M239m	(K)EITALAP	(K)E I T\A/L|A/P S T m K(I)	m:Oxidized methionine	111.13	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
18301	dirMS_041712_NAR_50mM_minus2.15150.15150.3	3	6.47	0	2.79E+05	M118m	(R)AGKPVI	(R)A G K\P V I\C\A T/Q|M/L/E S m I K(K)	C:Carbamidomethylation m:Oxid	154.6	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
18302	dirMS_041712_NAR_50mM_minus2.15362.15362.3	3	6.47	0	4.10E+05	M118m	(R)AGKPVI	(R)A/G K\P V I C A\T|Q\M/L\E S m I K(K)	C:Carbamidomethylation m:Oxid	155.4	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
18303	dirMS_041712_NAR_60mM_minus.15021.15021.3	3	6.47	1	1.55E+05		(K)KVEEVV	(K)K V E E V|V/Y|D|L S I R(G)		143.52	483.9327	1449.795	-0.0112	-7.7	4.68	25685.9	6.4	HUMAN	E9PGT1	Translin
18304	dirMS_041712_NAR_60mM_minus.4720.4720.3	3	6.47	0	6.11E+05	M46m M4	(R)HQGVm	(R)H Q\G V\m|V/G m G Q K(D)	m:Oxidized methionine	77.87	401.8579	1171.571	31.9881	-1.4	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
18305	dirMS_041712_NAR_60mM_minus.9404.9404.3	3	6.47	1	2.35E+05		(R)ILKEEQE	(R)I/L K/E\E Q E/L/Y/Q K(E)		112.08	474.2636	1420.768	0.008	5.6	4.79	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
18306	dirMS_041712_NAR_120mM_plus.23778.23778.4	4	6.47	2	2.30E+05		(R)RGVML	(R)R\G V\M L|A/V/D/A V I A E L K K(Q)		179.72	429.0075	1713.009	-0.001	-0.6	8.59	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
18307	dirMS_041712_NAR_20mM_plus.16901.16901.2	2	6.47	0	4.02E+03		(K)NQALFP	(K)N Q/A/L/F|P A/C V/L/K(N)	C:Carbamidomethylation	188.28	630.8416	1260.677	-0.001	-0.8	8.75	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1

18308	dirMS_041712_NAR_30mM_plus2.10657.10657.2	2	6.47	0	1.48E+06		(R)GLSSGG	(R)G L\S S G/G S A G\R(N)		108.7	424.7147	848.422	0.0001	0.1	9.75	84561.9	5.87	HUMAN	Q9Y5P4-3	Isoform 3 of Collagen type IV alpha-3-binding protein
18309	dirMS_041712_NAR_30mM_plus2.23518.23518.2	2	6.47	0	1.80E+05		(R)IAIYELLF	(R)I/A|I\Y/E L L F K(E)		190.25	555.3331	1109.661	-0.0016	-1.4	6	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
18310	dirMS_041712_NAR_30mM_plus2.4145.4145.2	2	6.47	0	1.29E+06	M299m M	(K)NmmAA	(K)N m|m\A\A C/D|P/R(H)	C:Carbamidomethylation m:Oxid	69.25	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
18311	dirMS_041712_NAR_40mM_plus2.6098.6098.2	2	6.47	0	5.66E+04		(R)QAFPNT	(R)Q/A/F|P N T N R(W)		94.88	474.2383	947.469	0	0	9.75	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
18312	dirMS_041712_NAR_40mM_plus2.6710.6710.2	2	6.47	0	1.68E+04		(K)SLAAEEE	(K)S L|A|A E/E E A A R(Q)		99.53	523.7589	1046.511	-0.0008	-0.7	4.25	533778	5.74	HUMAN	Q15149	Plectin
18313	dirMS_041712_NAR_50mM_plus2.13448.13448.3	3	6.47	0	1.74E+05		(K)LGDVYV	(K)L G\D|V Y V/N/D/A F G T A H R(A)		138.82	545.6029	1634.792	0.002	1.2	5.21	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
18314	dirMS_041712_NAR_50mM_plus2.15270.15270.3	3	6.47	0	5.18E+05		(K)LHIIEVG	(K)L H I\I E V G/T|P/P T G N Q P F/P K(K)		147.45	649.0216	1945.054	-0.0039	-2	6.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
18315	dirMS_041712_NAR_60mM_plus.13680.13680.3	3	6.47	1	4.71E+05		(R)KYEMFA	(R)K\Y E M F A\Q|T\L/Q Q S R(G)		128.72	543.9389	1629.805	-0.0032	-2	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
18316	dirMS_041712_NAR_60mM_plus.16173.16173.3	3	6.47	0	5.79E+05		(R)ETHSAL	(R)E T H S A L/G|P\A|L Q A A F K(L)		141.82	514.2744	1540.812	-0.0032	-2.1	6.85	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
18317	dirMS_041712_NAR_120mM_minus.18200.18200.4	4	6.46	1	4.84E+05		(K)EMVELP	(K)E M/V/E/L/P L R H/P A L F K(A)		154.6	420.737	1679.93	-0.004	-2.4	6.86	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
18318	dirMS_041712_NAR_120mM_minus.6588.6588.2	2	6.46	1	8.80E+04		(R)KGESGQ	(R)K|G E S/G/Q S/W\P R(L)		90.35	566.2836	1131.554	0.0058	5.1	8.75	14686.6	4.13	HUMAN	B4DDC6	Prostaglandin E synthase 3
18319	dirMS_041712_NAR_30mM_minus2.14067.14067.2	2	6.46	0	3.08E+05		(K)FGVYDI	(K)F/G|V/Y/D I D N K(T)		130.42	535.762	1070.515	0.0014	1.3	4.21	27142.4	5.34	HUMAN	E5RG68	Copine-3 (Fragment)
18320	dirMS_041712_NAR_30mM_minus2.7929.7929.2	2	6.46	0	2.68E+05		(K)SLAAEEE	(K)S L|A|A/E/E E A A R(Q)		96.57	523.7597	1046.511	0.0008	0.8	4.25	533778	5.74	HUMAN	Q15149	Plectin
18321	dirMS_041712_NAR_50mM_minus2.10297.10297.3	3	6.46	0	2.45E+05	M35m	(K)AASDIA	(K)A A/S/D I A m T E L/P/P T H P I R(L)	m:Oxidized methionine	127.42	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
18322	dirMS_041712_NAR_50mM_minus2.14132.14132.3	3	6.46	1	2.68E+05		(K)KGVNLP	(K)K G V N L P G A|A\V/D L/P A V/S E K(D)		148.42	588.9987	1764.985	-0.0039	-2.2	6.07	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
18323	dirMS_041712_NAR_50mM_minus2.15519.15519.3	3	6.46	1	4.15E+05		(K)QGGLGF	(K)Q G\G L/G/P M N I|P L V S D P K R(T)		157.37	593.6566	1778.958	-0.0029	-1.6	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
18324	dirMS_041712_NAR_50mM_minus2.18043.18043.3	3	6.46	0	4.36E+05		(K)LVLIGSN	(K)L V|L/I G S N H S/L/P F/L/K(F)		171.27	513.3077	1537.91	-0.0015	-1	8.76	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
18325	dirMS_041712_NAR_50mM_minus2.7082.7082.3	3	6.46	0	2.46E+04		(R)LIQSHPE	(R)L/I|Q S H\P E\S A E/D L Q E/K(C)		107.17	575.2885	1723.85	0.0012	0.7	4.4	285798.6	5.23	HUMAN	A6NG51	Spectrin alpha chain, non-erythrocytic 1
18326	dirMS_041712_NAR_60mM_minus.14961.14961.3	3	6.46	1	7.20E+04		(K)LTEDKAI	(K)L T/E D K A D V Q/S/I/I G L Q R(F)		143.08	595.9938	1785.97	-0.0037	-2	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
18327	dirMS_041712_NAR_60mM_minus.16358.16358.3	3	6.46	0	3.81E+04		(R)NHLLPD	(R)N H L L P D\I|V|T C V/Q S S R(K)	C:Carbamidomethylation	151.35	580.3021	1738.891	0.0013	0.7	6.74	20940.9	10.04	HUMAN	Q9BSD7	Cancer-related nucleoside-triphosphatase
18328	dirMS_041712_NAR_60mM_minus.6022.6022.3	3	6.46	1	3.36E+05		(K)LEEAEK	(K)L/E/E A E K/A A D E/S E R(G)		92.1	492.8981	1476.681	-0.0015	-1	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
18329	dirMS_041712_NAR_60mM_minus.6563.6563.3	3	6.46	0	5.72E+04		(K)ELVSDAI	(K)E L V/S/D/A N Q H/V K(S)		95.22	413.8839	1239.633	0.0044	3.5	5.32	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
18330	dirMS_041712_NAR_120mM_plus.10797.10797.3	3	6.46	1	7.48E+04		(K)KYEFGES	(K)K\Y E F G/E/S D/L/R(S)		109.63	415.205	1243.595	0.0051	4.1	4.68	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
18331	dirMS_041712_NAR_20mM_plus.10246.10246.2	2	6.46	0	9.56E+04		(K)LEAEIAT	(K)L E|A E I A|T/Y R(R)		143.43	533.2797	1065.557	-0.0054	-5	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18332	dirMS_041712_NAR_20mM_plus.14546.14546.2	2	6.46	0	3.89E+04	M185m	(K)LAVNm	(K)L A V|N/m/V/P F P R(L)	m:Oxidized methionine	172.75	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
18333	dirMS_041712_NAR_20mM_plus.18672.18672.2	2	6.46	0	4.27E+04		(K)LLDAVD	(K)L L\D/A V D/T/Y|I P V P A R(D)		199.85	771.9239	1542.853	-0.0121	-7.8	4.21	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
18334	dirMS_041712_NAR_40mM_plus2.10223.10223.3	3	6.46	0	2.67E+05	N611n	(R)ASSYSS	(R)A S\S\Y S S V S S T N A/S G n W/R(T)	n:N-acetylglucosamine (N)	125.1	655.3008	1760.783	203.1044	12.8	8.79	77819.8	8.81	HUMAN	E9PGA7	FERM domain-containing protein 4B
18335	dirMS_041712_NAR_40mM_plus2.11555.11555.2	2	6.46	0	4.57E+04		(K)YYIGFR	(K)Y Y|I/G F R(Y)		134.2	409.7122	818.42	-0.0024	-3	8.59	37238.2	9.57	HUMAN	K7ELX4	Ferrochelatase, mitochondrial (Fragment)
18336	dirMS_041712_NAR_40mM_plus2.13058.13058.2	2	6.46	0	3.95E+04		(K)ALWFQ	(K)A L/W/F/Q G R(C)		142.78	439.2366	877.468	-0.002	-2.3	9.79	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
18337	dirMS_041712_NAR_40mM_plus2.14733.14733.3	3	6.46	0	2.16E+04		(K)IYGADDI	(K)I Y/G A D D I E\L/L/P E A Q H K(A)		153.4	604.6467	1811.917	0.0081	4.5	4.31	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
18338	dirMS_041712_NAR_40mM_plus2.9643.9643.2	2	6.46	0	1.27E+05		(K)FYEAFSK	(K)F/Y|E/A F S K(N)		120.15	446.2159	891.425	-0.0002	-0.2	6	20127.1	9.4	HUMAN	H0Y598	Heat shock protein HSP 90-beta (Fragment)
18339	dirMS_041712_NAR_50mM_plus2.14578.14578.3	3	6.46	1	5.40E+05		(R)QAIKELP	(R)Q A\I K E L P Q/F/A/T/G E N L/P R(V)		144.47	638.0091	1912.029	-0.0159	-8.3	6.14	58250.7	8.99	HUMAN	B4E283	Apoptosis inhibitor 5
18340	dirMS_041712_NAR_50mM_plus2.6735.6735.3	3	6.46	1	1.92E+05		(K)AIEQLKE	(K)A I|E Q/L/K E/Q A A T G K(Q)		100.15	462.9247	1386.759	0.0008	0.6	6.18	58392.6	9.36	HUMAN	B4DF96	Eukaryotic translation initiation factor 2A
18341	dirMS_041712_NAR_60mM_plus.10462.10462.3	3	6.46	0	1.57E+06		(K)VFEHDS	(K)V/F/E H D\S V E/L/N/C K(M)	C:Carbamidomethylation	111.77	492.8967	1476.679	-0.0032	-2.2	4.65	31975.7	6.55	HUMAN	P10768	S-formylglutathione hydrolase
18342	dirMS_041712_NAR_60mM_plus.10748.10748.3	3	6.46	1	2.86E+07	S303s	(R)DHHMs	(R)D H H M s G W S|Y/K R V E K(S)	s:N-acetylglucosamine (S)	114.77	654.9726	1759.833	203.0699	-4.8	8.51	51648.4	5.55	HUMAN	B7XGB9	Protein phosphatase 1M
18343	dirMS_041712_NAR_60mM_plus.19109.19109.3	3	6.46	0	1.74E+05	T454t	(R)HTGQtV	(R)H/T G/Q/t/V L L T/L M/R(R)	t:N-acetylglucosamine (T)	158.18	524.9582	1369.762	203.098	11.9	9.75	216055.5	4.9	HUMAN	B7ZMI4	MPDZ protein
18344	dirMS_041712_NAR_60mM_plus.6002.6002.3	3	6.46	0	3.94E+05	M103m	(R)mEELHN	(R)m E|E/L H|N Q E\M Q\K(R)	m:Oxidized methionine	89.95	478.2118	1416.625	15.9962	0.9	4.75	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
18345	dirMS_041712_NAR_20mM_minus.7984.7984.2	2	6.45	0	9.09E+03		(R)AAAGYP	(R)A A A\G Y|P D P/Y S R(A)		129.45	584.2733	1167.543	-0.0036	-3.1	5.88	266161	5.68	HUMAN	E9PPU0	Epiplakin
18346	dirMS_041712_NAR_30mM_minus2.10773.11244.2	2	6.45	0	2.91E+06	M209m	(R)VTDQLG	(R)V T|D Q|L G m F T H K(E)	m:Oxidized methionine	114.17	646.8327	1276.635	16.0227	21.5	6.71	41848	8.94	HUMAN	Q9BWS9-3	Isoform 3 of Chitinase domain-containing protein 1
18347	dirMS_041712_NAR_30mM_minus2.17346.17346.2	2	6.45	1	2.01E+05		(R)GHGPEP	(R)G H G P E|P D S P|F\R R(S)		148.68	676.3255	1351.65	-0.0064	-4.8	6.75	5236.9	12.22	HUMAN	H0YES3	TMF-regulated nuclear protein 1 (Fragment)
18348	dirMS_041712_NAR_50mM_minus2.15241.15241.3	3	6.45	1	4.25E+05		(K)GADFLV	(K)G A/D/F/L|V/T E V E N G G S L G S/K K(G)		155.5	636.662	1907.971	0.0005	0.3	4.68	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
18349	dirMS_041712_NAR_60mM_minus.12147.12147.3	3	6.45	1	2.54E+03	S195s	(R)IVSKSQL	(R)I V|S K S Q/L/P s E N R(E)	s:N-acetylglucosamine (S)	128.12	520.9529	1357.743	203.1007	13.7	8.75	44423	6.07	HUMAN	Q8N0S6-2	Isoform 2 of Centromere protein L
18350	dirMS_041712_NAR_60mM_minus.15497.15497.3	3	6.45	1	5.92E+05	M81m	(K)EVNKFQ	(K)E V N K/F Q m A/Y/S N/L L R(A)	m:Oxidized methionine	146.73	576.9619	1712.879	15.9923	-1.5	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
18351	dirMS_041712_NAR_20mM_plus.11865.11865.2	2	6.45	0	1.36E+05		(R)LILIESR	(R)L I|L/I/E/S R(I)		155.02	422.2674	843.53	-0.0023	-2.7	6	17222	10.53	HUMAN	P62277	40S ribosomal protein S13
18352	dirMS_041712_NAR_20mM_plus.11908.11908.2	2	6.45	0	6.22E+03		(K)YGEPGE	(K)Y G|E/P G E V F I N K(G)		155.3	626.8223	1252.621	0.0165	13.2	4.53	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
18353	dirMS_041712_NAR_20mM_plus.16764.16764.2	2	6.45	0	1.17E+05		(R)LLEAQIA	(R)L L\E A|Q/I/A T G G\I I D/P K(E)		185.97	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
18354	dirMS_041712_NAR_20mM_plus.18750.18750.3	3	6.45	0	1.15E+05		(K)VIGNQS	(K)V I G N Q\S L V N E|L A/F/T/A R(K)		200.67	577.9842	1731.939	-0.0008	-0.4	5.97	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
18355	dirMS_041712_NAR_30mM_plus2.21365.21365.2	2	6.45	0	1.48E+05		(R)VFIGNL	(R)V/F|I/G N L/N T L V V K(K)		167.32	658.8983	1316.794	-0.0043	-3.3	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
18356	dirMS_041712_NAR_30mM_plus2.7142.7142.2	2	6.45	0	2.31E+05		(R)AQVIYT	(R)A Q|V/I/Y T R(N)		91.63	425.7397	850.478	-0.006	-7.1	8.79	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
18357	dirMS_041712_NAR_30mM_plus2.8640.8640.2	2	6.45	0	2.39E+05		(K)SGTSEFL	(K)S G/T/S E F/L N/K(M)		99.58	491.7468	982.484	0.0023	2.4	5.72	92752.5	4.76	HUMAN	P14625	Endoplasmin
18358	dirMS_041712_NAR_40mM_plus2.11525.11525.3	3	6.45	0	5.67E+04		(R)LDDTVH	(R)L/D|D T V H V/V/I A T/P G R(I)		134.08	498.2739	1492.812	-0.0047	-3.1	5.21	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
18359	dirMS_041712_NAR_40mM_plus2.7789.7789.2	2	6.45	0	4.23E+04		(R)VLNTNI	(R)V L/N/T/N/I D/G R(R)		105.73	501.2719	1001.537	-0.0009	-0.9	5.81	17718.4	10.99	HUMAN	P62269	40S ribosomal protein S18
18360	dirMS_041712_NAR_50mM_plus2.10998.10998.3	3	6.45	0	5.11E+04	M397m	(R)ImDPNI	(R)I m|D|P N I V/G S E H Y D V A R(G)	m:Oxidized methionine	125.5	611.296	1815.869	16.004	5	4.54	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
18361	dirMS_041712_NAR_50mM_plus2.16654.16654.3	3	6.45	1	5.82E+05		(K)DANAKL	(K)D A\N A K L S E\L|E\A/A/L/Q R(A)		155.78	543.6256	1628.86	0.002	1.2	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
18362	dirMS_041712_NAR_50mM_plus2.20097.20097.3	3	6.45	0	3.62E+05		(R)NEVSFV	(R)N/E|V/S F V I H N L P V L A/K(M)		174.27	560.6531	1679.948	-0.0032	-1.9	6.75	35663.7	5.91	HUMAN	B4DWK0	Selenide, water dikinase 1
18363	dirMS_041712_NAR_50mM_plus2.5172.5172.3	3	6.45	0	2.68E+05	M21m	(R)SGSmDF	(R)S G S/m D P/S/G A H|P S V R(Q)	m:Oxidized methionine	86.13	467.5461	1384.627	15.9964	1	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
18364	dirMS_041712_NAR_120mM_minus.10282.10282.3	3	6.44	1	6.18E+04		(R)KEEELQ	(R)K\E E\E\L|Q/A A L A R(A)		111.02	419.8975	1257.68	-0.0018	-1.4	4.79	232239.1	5.52	HUMAN	F2Z2U8	Myosin-14
18365	dirMS_041712_NAR_120mM_minus.11499.11499.2	2	6.44	1	1.65E+05		(R)KLLASLV	(R)K|L/L A S L|V K(R)		116.72	436.3027	871.597	0.0006	0.7	10	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
18366	dirMS_041712_NAR_120mM_minus.19667.19667.3	3	6.44	1	1.50E+05		(K)GTKHLSI	(K)G T K H|L/S/P Y A T L T\V G D S\S H K(T)		163	667.0203	1999.024	0.022	11	8.51	123367.7	5.57	HUMAN	Q9BSJ8	Extended synaptotagmin-1
18367	dirMS_041712_NAR_120mM_minus.20105.20105.3	3	6.44	0	3.17E+05		(K)VHLVGI	(K)V H\L V G I|D\I/F T/G/K(K)		166.25	433.5866	1298.747	-0.0015	-1.1	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
18368	dirMS_041712_NAR_40mM_minus2.11832.11832.3	3	6.44	0	2.23E+05		(K)DAGEGL	(K)D A G E|G/L/L A V Q/I T D P E G K P K(K)		153.77	646.6785	1938.018	0.0031	1.6	4.32	283472.4	5.71	HUMAN	P21333	Filamin-A
18369	dirMS_041712_NAR_50mM_minus2.10294.10294.3	3	6.44	0	2.32E+05	M35m	(K)AASDIA	(K)A A|S D I/A\m T E L/P P T H P I R(L)	m:Oxidized methionine	127.37	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
18370	dirMS_041712_NAR_60mM_minus.12169.12169.3	3	6.44	2	3.83E+05		(K)IREEILEK	(K)I R/E E I/L E/K A R(R)		127.93	419.5851	1256.732	0.0086	6.9	6.23	152596.1	6.87	HUMAN	Q8NDW8	Tetratricopeptide repeat protein 21A
18371	dirMS_041712_NAR_120mM_plus.11644.11644.4	4	6.44	1	2.63E+05		(R)LQQLGE	(R)L Q Q L/G E/A/H/Q A E T E V L R R(E)		114.02	495.2678	1978.046	0.0029	1.5	5.5	97620.5	5.02	HUMAN	F5H4J1	Nuclear mitotic apparatus protein 1 (Fragment)
18372	dirMS_041712_NAR_20mM_plus.12048.12048.2	2	6.44	0	3.45E+04		(K)VSTAVLS	(K)V/S|T/A V/L/S I T A/K(A)		156.08	545.3252	1089.651	-0.0083	-7.6	8.72	106861.4	5.24	HUMAN	Q99460	26S proteasome non-ATPase regulatory subunit 1
18373	dirMS_041712_NAR_20mM_plus.15201.15201.2	2	6.44	0	9.21E+04		(K)GVEGLI	(K)G V\E/G L|I/D I|E N/P N R(V)		176.37	713.3667	1425.733	-0.0071	-5	4.14	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
18374	dirMS_041712_NAR_20mM_plus.17156.17156.2	2	6.44	0	8.67E+04		(R)AIVAIEN	(R)A I V A\I E/N|P A D/V S V I S S R(N)		189.1	870.9764	1740.949	-0.0035	-2	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
18375	dirMS_041712_NAR_20mM_plus.17538.17538.3	3	6.44	0	1.38E+04	M199m	(K)SmVPVC	(K)S m/V\P V Q\V/Q/L/D V/P V V K(V)	m:Oxidized methionine	192.58	551.9759	1637.93	15.9837	-6.8	5.55	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
18376	dirMS_041712_NAR_40mM_plus2.6588.6588.2	2	6.44	0	5.65E+04		(K)AGFAGD	(K)A G/F|A|G\D/D A P R(A)		98.63	488.728	976.448	0.0004	0.4	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
18377	dirMS_041712_NAR_50mM_plus2.9876.9876.3	3	6.44	1	2.02E+05		(R)AESGPD	(R)A E/S G P D L R Y E V T|S/G/G G G T S R(M)		119.13	665.9843	1995.937	0.0017	0.9	4.68	334221.3	6.44	HUMAN	P15924	Desmoplakin
18378	dirMS_041712_NAR_60mM_plus.14052.14052.3	3	6.44	0	1.79E+06		(K)GIHPTIIS	(K)G I H\P T I\I/S/E/S F Q K(A)		130.6	486.2646	1456.78	-0.0002	-0.1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
18379	dirMS_041712_NAR_60mM_plus.17304.17304.3	3	6.44	1	1.17E+05		(R)RFPGLEL	(R)R F P/G L\E\L S F P L L|A R(L)		147.37	539.3092	1615.932	-0.0188	-11.7	9.6	115861.1	8.73	HUMAN	C9J1X3	Activated CDC42 kinase 1
18380	dirMS_041712_NAR_120mM_minus.13800.13800.2	2	6.43	1	4.24E+06		(K)FASFIDK	(K)F/A|S/F/I D/K V R(F)		130.15	541.7968	1082.599	-0.013	-12	8.75	19569.8	9.88	HUMAN	F8VRG4	Keratin, type II cytoskeletal 8 (Fragment)
18381	dirMS_041712_NAR_120mM_minus.6945.6945.2	2	6.43	0	4.18E+05		(K)HNAAFC	(K)H|N/A A/F|C\Y K(L)	C:Carbamidomethylation	92.42	505.7282	1010.451	-0.0021	-2.1	8.6	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
18382	dirMS_041712_NAR_30mM_minus2.16889.16889.2	2	6.43	0	2.62E+05	M2243m	(K)mSIYQA	(K)m S|I|Y Q/A M/W/K(G)	m:Oxidized methionine	145.35	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
18383	dirMS_041712_NAR_50mM_minus2.10233.10233.3	3	6.43	0	1.60E+05		(K)LQAEAP	(K)L/Q\A E A/P/H/I V V/G T/P G/R(V)		127.05	515.6179	1544.854	-0.0152	-9.8	6.75	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
18384	dirMS_041712_NAR_50mM_minus2.16602.16602.3	3	6.43	0	8.52E+04		(R)LLLDIPL	(R)L/L L/D I/P\L Q T P H K(L)		162.45	463.2805	1387.831	-0.0038	-2.7	6.74	198852.6	5.95	HUMAN	A6NKT7	RanBP2-like and GRIP domain-containing protein 3
18385	dirMS_041712_NAR_50mM_minus2.7137.7137.3	3	6.43	1	3.00E+04		(R)GIEPTGN	(R)G I E/P T G N M V/K Q P A/K(F)		107.48	490.5972	1469.778	-0.001	-0.7	8.59	258215.9	5.48	HUMAN	E7EN95	Filamin-B
18386	dirMS_041712_NAR_60mM_minus.10635.10635.3	3	6.43	1	5.96E+05	M88m	(K)DVDEAY	(K)D V|D E A Y m N K/V/E L E\S R(L)	m:Oxidized methionine	118.37	605.2791	1797.832	15.9904	-2.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
18387	dirMS_041712_NAR_60mM_minus.16333.16333.3	3	6.43	0	1.54E+05		(R)FQSGDF	(R)F Q/S/G/D F H\V/I/N G V L R(T)		150.87	530.2846	1588.823	0.0162	10.2	6.74	104619	5.75	HUMAN	F8W904	Exportin-2
18388	dirMS_041712_NAR_20mM_plus.10201.10201.2	2	6.43	0	6.33E+04		(K)GYDVIA	(K)G Y/D/V|I/A Q A/Q S G T G K(T)		142.97	697.846	1394.691	-0.0063	-4.5	5.83	16071.1	4.8	HUMAN	B4E102	Eukaryotic initiation factor 4A-I
18389	dirMS_041712_NAR_20mM_plus.14487.14487.2	2	6.43	0	1.33E+05		(K)LVILANN	(K)L V|I|L|A N/N C|P A L/R(K)	C:Carbamidomethylation	171.57	677.3851	1353.767	-0.0042	-3.1	9.75	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
18390	dirMS_041712_NAR_20mM_plus.15175.15175.2	2	6.43	0	6.89E+04		(K)DVLSVAI	(K)D V/L|S/V\A/F/S S D N R(Q)		175.98	655.3293	1309.638	0.0131	10	4.21	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
18391	dirMS_041712_NAR_20mM_plus.16035.16035.3	3	6.43	0	2.45E+04		(R)ALPAVQ	(R)A L/P A V Q Q N N\L/D/E D L I R(K)		181.95	603.6541	1808.95	-0.0024	-1.3	4.03	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
18392	dirMS_041712_NAR_20mM_plus.18181.18181.2	2	6.43	0	1.02E+05		(R)AILVDLE	(R)A I L\V|D\L\E|P G T M D S V R(S)		196.63	808.419	1615.836	-0.0053	-3.3	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
18393	dirMS_041712_NAR_30mM_plus2.19431.19431.2	2	6.43	0	3.48E+05		(-)MDELQL	(-)M/D E/L|Q/L/F R(G)		156.53	526.2726	1051.524	0.0138	13.2	4.37	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
18394	dirMS_041712_NAR_50mM_plus2.12179.12179.3	3	6.43	1	2.18E+05		(R)LLIVSTT	(R)L L|I/V/S T T/P Y S E K D/T K(Q)		131.88	565.645	1694.921	-0.0006	-0.4	6.07	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
18395	dirMS_041712_NAR_50mM_plus2.12886.12886.3	3	6.43	0	5.97E+05		(R)FDAERP	(R)F/D/A E R P V/D C\S V|I|V V N K(Q)	C:Carbamidomethylation	135.82	616.6476	1847.932	-0.0038	-2	4.56	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
18396	dirMS_041712_NAR_50mM_plus2.13649.13649.3	3	6.43	0	1.38E+06		(K)STTSDIP	(K)S T|T/S D/I/P H M L N Q V E/S K(V)		140.25	596.2908	1786.864	-0.0061	-3.4	5.3	11532.2	6.34	HUMAN	H0YNA1	Protein FAM98B (Fragment)
18397	dirMS_041712_NAR_50mM_plus2.13650.13650.3	3	6.43	0	1.38E+06		(K)STTSDIP	(K)S T|T/S/D I P H M L N/Q V E S K(V)		140.25	596.2908	1786.864	-0.0061	-3.4	5.3	11532.2	6.34	HUMAN	H0YNA1	Protein FAM98B (Fragment)
18398	dirMS_041712_NAR_50mM_plus2.5864.5864.3	3	6.43	0	3.28E+05		(K)TVEAEA	(K)T V|E/A E/A A H/G T\V T R(H)		94.9	447.8962	1341.676	-0.0017	-1.2	5.37	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
18399	dirMS_041712_NAR_60mM_plus.15276.15276.3	3	6.43	0	2.00E+05		(K)HQTLQ	(K)H Q T L Q\G V/A|F/P I S/R(E)		136.2	485.2663	1453.791	-0.0067	-4.6	9.75	33635.5	6.01	HUMAN	F8VS81	Twinfilin-1 (Fragment)
18400	dirMS_041712_NAR_60mM_plus.20524.20524.3	3	6.43	0	4.28E+05		(R)CRPDQL	(R)C R P D Q L T/G L/S|L/L/P L S E K(A)	C:Carbamidomethylation	168.28	643.0146	1927.032	-0.0025	-1.3	6.07	533778	5.74	HUMAN	Q15149	Plectin
18401	dirMS_041712_NAR_120mM_minus.19959.19959.3	3	6.42	0	7.83E+04		(R)INLWHL	(R)I/N\L W H/L/E I T D/R(S)		165.22	470.5897	1409.754	0.001	0.7	5.32	52204.6	5.82	HUMAN	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
18402	dirMS_041712_NAR_120mM_minus.9545.9545.3	3	6.42	0	3.43E+05		(-)MPLYEGI	(-)M P/L Y E G|L G S G\G/E K(T)		106.45	446.5565	1337.641	0.0144	10.7	4.53	20869.1	9.77	HUMAN	F6S9Y6	Actin-related protein 10
18403	dirMS_041712_NAR_20mM_minus.10312.10312.2	2	6.42	0	2.40E+04		(R)AQAALA	(R)A Q|A\A\L/A/V/N I/S A A R(G)		152.12	628.3558	1255.712	-0.0074	-5.9	9.79	58479.6	6.23	HUMAN	P40227	T-complex protein 1 subunit zeta
18404	dirMS_041712_NAR_20mM_minus.11570.11570.2	2	6.42	0	1.39E+05	M98m	(R)TLTIVDT	(R)T L|T I V/D/T G\I/G m\T K(A)	m:Oxidized methionine	163.17	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
18405	dirMS_041712_NAR_20mM_minus.14058.14058.3	3	6.42	0	5.51E+05		(K)SYELPD	(K)S Y E L/P/D G Q V I/T I/G N E R(F)		193.73	597.6345	1790.892	-0.003	-1.7	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
18406	dirMS_041712_NAR_40mM_minus2.7818.7818.3	3	6.42	0	8.08E+04		(K)TGVAVN	(K)T/G V/A/V\N K/P A E F T V D A K(H)		124.68	549.6354	1646.875	0.0168	10.2	5.73	283472.4	5.71	HUMAN	P21333	Filamin-A
18407	dirMS_041712_NAR_50mM_minus2.11826.11826.3	3	6.42	1	3.50E+05		(K)AVLFCLS	(K)A V|L F/C L S E D K/K(N)	C:Carbamidomethylation	136	437.2326	1309.682	0.0012	0.9	6.11	22956	8.8	HUMAN	E9PK25	Cofilin-1
18408	dirMS_041712_NAR_50mM_minus2.17645.17645.3	3	6.42	0	2.46E+05		(R)LLLDGAI	(R)L L\L/D G A|P L I A I H/K(A)		168.57	458.6218	1373.852	-0.0007	-0.5	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
18409	dirMS_041712_NAR_50mM_minus2.18022.18022.3	3	6.42	1	1.52E+05		(R)GDLGIEI	(R)G D L/G I/E I/P A/E K V F L A Q K(M)		172.1	610.0112	1828.022	-0.0024	-1.3	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
18410	dirMS_041712_NAR_50mM_minus2.5323.5323.3	3	6.42	0	8.24E+05		(K)TATPQQ	(K)T A/T/P Q\Q A Q E/V H E K(L)		88.02	489.5768	1466.723	-0.0075	-5.1	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
18411	dirMS_041712_NAR_60mM_minus.7996.7996.3	3	6.42	1	1.75E+05		(K)EASKQA	(K)E A/S K Q\A D V/N/L/V N A K(L)		104.2	496.2639	1486.786	-0.0089	-6	6.17	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
18412	dirMS_041712_NAR_120mM_plus.22420.22420.4	4	6.42	2	3.40E+05		(R)TKIDPSA	(R)T K I D P S/A\L/V/Q K L/E/L D/V R(S)		171.28	482.0309	1925.107	-0.0048	-2.5	5.79	22331.4	11.18	HUMAN	C9JJU7	Protein FAM207A (Fragment)
18413	dirMS_041712_NAR_120mM_plus.4123.4123.3	3	6.42	1	1.49E+07	M310m	(R)TKTEISE	(R)T\K T E\I|S/E m/N/R(N)	m:Oxidized methionine	69.7	408.8687	1208.594	15.9976	2.2	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
18414	dirMS_041712_NAR_20mM_plus.16866.16866.2	2	6.42	0	2.06E+05		(R)IVLLDSS	(R)I V|L|L/D S S L\E Y K(K)		187.32	640.36	1279.714	-0.0017	-1.3	4.37	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
18415	dirMS_041712_NAR_20mM_plus.19312.19312.2	2	6.42	1	1.40E+05	K1159k	(K)STKPYKN	(K)S T/K/P Y K N G Q L S k(V)	k:Ubiquitin-K	204.48	732.889	1350.738	114.0331	-6.7	10	164378.2	9.31	HUMAN	E7EPB6	Cystic fibrosis transmembrane conductance regulator (Fragment)
18416	dirMS_041712_NAR_30mM_plus2.16721.16721.2	2	6.42	0	3.78E+05		(R)LWDLTT	(R)L W|D|L/T/T/G T T T R(R)		140.4	632.8304	1264.653	0.0003	0.3	5.84	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)

18417	dirMS_041712_NAR_30mM_plus2.20784.20784.2	2	6.42	0	1.08E+05		(R)YLTVAA	(R)Y L|T/V/A A V F R(G)		162.65	520.2996	1039.593	-0.0016	-1.5	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
18418	dirMS_041712_NAR_30mM_plus2.22203.22203.2	2	6.42	0	3.50E+05		(R)VGNLGL	(R)V G N L/G L|A T S F F|N/E R(N)		172.75	762.8926	1524.781	-0.0026	-1.7	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
18419	dirMS_041712_NAR_30mM_plus2.4676.4676.2	2	6.42	0	4.63E+05		(R)MGQT	(R)M/G|Q/T/M E R(I)		75.37	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
18420	dirMS_041712_NAR_30mM_plus2.6344.6344.2	2	6.42	0	8.62E+04		(K)EVYPEA	(K)E V/Y/P E A R(K)		87.3	432.2218	863.426	0.0106	12.2	4.53	17921.1	9.84	HUMAN	H7BZW6	Histone deacetylase complex subunit SAP18 (Fragment)
18421	dirMS_041712_NAR_40mM_plus2.10625.10625.2	2	6.42	0	7.56E+04		(R)LSESQLS	(R)L/S/E/S Q\L/S F R(R)		127.93	533.7789	1066.553	-0.0022	-2.1	6	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
18422	dirMS_041712_NAR_60mM_plus.15167.15167.3	3	6.42	0	4.82E+04		(K)HIGLVYS	(K)H I\G L V Y S/G\M/G/P D/Y R(V)		135.85	522.2648	1564.758	0.0222	14.2	6.74	26012.2	6.92	HUMAN	P25787	Proteasome subunit alpha type-2
18423	dirMS_041712_NAR_60mM_plus.16255.16255.3	3	6.42	1	3.69E+05		(-)MKLNISF	(-)M/K L N I S F/P/A T G/C Q K(L)	C:Carbamidomethylation	142.85	532.2733	1594.808	-0.0026	-1.7	10	10471.9	5.4	HUMAN	A2A3R7	40S ribosomal protein S6
18424	dirMS_041712_NAR_30mM_minus2.16310.16310.2	2	6.41	0	1.14E+05		(R)GLGLDD	(R)G L|G\L/D D A L/E/P R(Q)		142.1	578.299	1155.6	-0.0097	-8.4	4.03	51326.8	5.49	HUMAN	Q9Y230	RuvB-like 2
18425	dirMS_041712_NAR_30mM_minus2.17784.17784.2	2	6.41	0	3.97E+05		(R)EQLAIA	(R)E Q/L/A/I/A E F A R(S)		150.33	574.3084	1147.611	-0.0011	-0.9	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
18426	dirMS_041712_NAR_30mM_minus2.6069.6069.2	2	6.41	0	1.32E+05		(K)MAGAM	(K)M/A/G A|M/S T T/A K(T)		87.38	484.7299	968.454	-0.0014	-1.5	8.5	23963.2	8.9	HUMAN	Q9UQN3	Charged multivesicular body protein 2b
18427	dirMS_041712_NAR_40mM_minus2.8167.8167.3	3	6.41	0	1.68E+05		(R)LLEAQA	(R)L L|E/A/Q/A C T G G I I H P T T G Q K(L)	C:Carbamidomethylation	128.68	665.6822	1995.033	-0.0007	-0.4	6.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
18428	dirMS_041712_NAR_40mM_minus2.9165.9165.3	3	6.41	1	9.47E+04		(K)LAEIGA	(K)L A/E|I/G/A/P I Q G N R E E L V E R(L)		136.07	665.3586	1994.066	-0.0053	-2.6	4.49	38572.2	6.31	HUMAN	E9PJ04	Splicing factor 3B subunit 2 (Fragment)
18429	dirMS_041712_NAR_60mM_minus.12244.12244.3	3	6.41	0	8.91E+04		(R)LFFQPH	(R)L/F|F Q/P H Q A G L S K(V)		128.12	458.2502	1372.737	-0.0011	-0.8	8.76	8684.1	9.22	HUMAN	C9J0F6	Ubiquitin-like modifier-activating enzyme 5 (Fragment)
18430	dirMS_041712_NAR_60mM_minus.13373.13373.3	3	6.41	1	4.84E+05		(K)TKEVYEL	(K)T K E V Y E\L|L|D S/P/G K(V)		134.45	493.5966	1478.774	0.0015	1	4.68	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
18431	dirMS_041712_NAR_60mM_minus.16351.16351.3	3	6.41	1	1.27E+05	M84m	(K)ETmQSL	(K)E T m Q/S L/N/D/R L A/S Y L D R(V)	m:Oxidized methionine	150.62	643.3097	1911.923	15.9916	-1.7	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18432	dirMS_041712_NAR_120mM_plus.18951.18951.4	4	6.41	1	5.99E+05	K150k	(K)DKAIAG	(K)D K\A I/A G\T V k V Q N L A F/E K(T)	k:Ubiquitin-K	153.18	487.2719	1832.028	114.0381	-2.5	8.5	33094	5.86	HUMAN	Q86XI6	Protein phosphatase 1 regulatory subunit 3B
18433	dirMS_041712_NAR_120mM_plus.6240.6240.3	3	6.41	1	5.04E+05		(K)LENSHF	(K)L E N S|H F E/N G R G K(S)		86.7	463.2395	1387.671	0.0326	23.5	6.76	89971.8	7.08	HUMAN	Q14563	Semaphorin-3A
18434	dirMS_041712_NAR_20mM_plus.18061.18061.2	2	6.41	0	1.77E+05	S99s	(R)VDGLAF	(R)V D G L A F|V N E/D/I V A s K(G)	s:N-acetylglucosamine (S)	195.32	890.4414	1576.822	203.0538	-14.4	4.03	27007.4	5.06	HUMAN	H7C5N7	Leucine-rich repeat and WD repeat-containing protein 1 (Fragment)
18435	dirMS_041712_NAR_20mM_plus.18119.18119.2	2	6.41	0	7.46E+04		(R)LSVLGAI	(R)L S V\L/G A|I|T/S V Q Q R(L)		196.23	686.3953	1371.795	-0.0121	-8.8	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
18436	dirMS_041712_NAR_30mM_plus2.16743.16743.2	2	6.41	0	2.01E+05		(K)SIELFYK	(K)S I|E L F/Y/K(F)		140.65	450.2484	899.487	0.0022	2.5	5.72	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
18437	dirMS_041712_NAR_30mM_plus2.18976.18976.2	2	6.41	0	3.36E+05		(R)LTAEDLF	(R)L T|A|E/D L F E A/R(I)		153.13	582.796	1164.59	-0.0048	-4.1	4.14	533778	5.74	HUMAN	Q15149	Plectin
18438	dirMS_041712_NAR_30mM_plus2.21035.21035.2	2	6.41	0	2.54E+05		(K)VFSIGPV	(K)V/F/S I/G/P V F R(A)		164.63	511.2941	1021.583	-0.002	-2	9.72	57534.6	6.11	HUMAN	P14868	Aspartate--tRNA ligase, cytoplasmic
18439	dirMS_041712_NAR_30mM_plus2.6101.6101.2	2	6.41	0	9.08E+04		(K)VTEGGE	(K)V T|E/G G E/P Y R(L)		86.25	504.2397	1007.479	-0.0071	-7.1	4.53	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
18440	dirMS_041712_NAR_30mM_plus2.6534.6534.2	2	6.41	0	1.90E+05		(K)TLNAGA	(K)T L|N\A/G A/Y S K(V)		88.92	462.7408	924.479	-0.0042	-4.5	8.26	30197.4	7.91	HUMAN	E9PMG2	Palmitoyl-protein thioesterase 1 (Fragment)
18441	dirMS_041712_NAR_40mM_plus2.7240.7240.2	2	6.41	0	2.25E+04		(K)YICENQ	(K)Y I|C E N Q D S I/S/S K(L)	C:Carbamidomethylation	102.3	722.3232	1443.642	-0.0029	-2	4.37	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
18442	dirMS_041712_NAR_50mM_plus2.13000.13000.3	3	6.41	0	4.41E+05		(K)QVLNQ	(K)Q V/L/N/Q D L/T/F Q H I/K(I)		136.67	528.6227	1583.854	-0.0005	-0.3	6.74	26601.2	7.98	HUMAN	Q5VWZ2	Lysophospholipase-like protein 1
18443	dirMS_041712_NAR_50mM_plus2.21640.21640.3	3	6.41	0	1.12E+05		(R)GLAPVQ	(R)G L/A/P/V Q A Y L H I P D I I K(V)		184.93	583.336	1748.011	-0.0171	-9.8	6.74	58266.4	9.46	HUMAN	B4DN00	Pyruvate carboxylase, mitochondrial
18444	dirMS_041712_NAR_50mM_plus2.22114.22114.3	3	6.41	1	5.62E+05		(K)AGFLDL	(K)A/G F L D/L K D\F L/P K(E)		188.95	455.2587	1363.762	-0.0005	-0.3	6	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
18445	dirMS_041712_NAR_60mM_plus.9789.9789.3	3	6.41	1	1.29E+06		(K)EAALST	(K)E A/A L/S T/A/L/S E K R(T)		109.78	425.898	1275.69	-0.0109	-8.5	6.24	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
18446	dirMS_041712_NAR_120mM_minus.15909.15909.4	4	6.4	1	3.80E+05		(R)ALEHFT	(R)A/L E H F T D L/Y/D/I K R(A)		140.33	405.9646	1620.838	-0.0015	-0.9	5.38	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
18447	dirMS_041712_NAR_30mM_minus2.11418.11418.2	2	6.4	0	1.57E+05		(K)SIDTGM	(K)S I/D/T/G M G\L E R(L)		116.67	539.7654	1078.52	0.0038	3.5	4.37	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
18448	dirMS_041712_NAR_40mM_minus2.8184.8184.3	3	6.4	1	4.65E+04		(R)DVVICP	(R)D V/V I/C/P D A S L/E D A K K(E)	C:Carbamidomethylation	128.47	553.9467	1659.826	-0.0003	-0.2	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
18449	dirMS_041712_NAR_50mM_minus2.10038.10038.3	3	6.4	0	5.69E+05	M147m	(K)LQmEA	(K)L Q|m E A P H|I/I V/G T P G R(V)	m:Oxidized methionine	125.55	545.6267	1618.873	15.9922	-1.7	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
18450	dirMS_041712_NAR_50mM_minus2.12694.12694.3	3	6.4	1	4.48E+05	M100m	(K)QGGLG	(K)Q G G L\G/P m N\I/P L V/S D/P K R(T)	m:Oxidized methionine	140.35	598.988	1778.958	15.9913	-2	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
18451	dirMS_041712_NAR_50mM_minus2.7325.7325.3	3	6.4	1	7.81E+04	M1510m	(R)TEMEDL	(R)T\E/M/E/D L m S S K D D V G K(S)	m:Oxidized methionine	108.5	567.5829	1684.74	15.9937	-0.7	4.1	227783.5	5.5	HUMAN	P35579	Myosin-9
18452	dirMS_041712_NAR_60mM_minus.7203.7203.3	3	6.4	1	1.75E+05		(K)AADIDQ	(K)A A|D I/D Q E V K E R(A)		99.07	425.2172	1273.638	-0.0012	-1	4.32	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
18453	dirMS_041712_NAR_20mM_plus.11784.11784.2	2	6.4	0	1.43E+05		(R)AQAALA	(R)A Q|A|A L A\V N/I S/A A R(G)		154.02	628.3565	1255.712	-0.006	-4.8	9.79	58479.6	6.23	HUMAN	P40227	T-complex protein 1 subunit zeta
18454	dirMS_041712_NAR_20mM_plus.15897.15897.2	2	6.4	0	4.98E+03		(R)SSFYVN	(R)S S F Y|V/N/G L T\L G G Q K(C)		180.83	735.8818	1470.759	-0.0024	-1.6	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
18455	dirMS_041712_NAR_20mM_plus.16698.16698.3	3	6.4	0	6.48E+04	M137m M	(R)IIGATDS	(R)I I G\A T D S S G/E|L/m|F L m/K(W)	m:Oxidized methionine	185.8	582.2872	1712.86	31.9873	-1.5	4.37	19439.5	4.97	HUMAN	B5MD17	Chromobox protein homolog 1 (Fragment)
18456	dirMS_041712_NAR_20mM_plus.18335.18335.2	2	6.4	0	5.62E+04		(K)LFIGGLN	(K)L F|I G G L/N V|Q/T S E S G L R(G)		197.5	845.9573	1690.912	-0.0049	-2.9	6	31011.2	9.5	HUMAN	Q13151	Heterogeneous nuclear ribonucleoprotein A0
18457	dirMS_041712_NAR_30mM_plus2.11206.11206.2	2	6.4	0	1.69E+05		(R)LTWHSC	(R)L T W H S C\P E D\E\A|Q(-)	C:Carbamidomethylation	112.4	736.8094	1472.611	0.0005	0.3	4.13	20982.2	5.23	HUMAN	Q13185	Chromobox protein homolog 3
18458	dirMS_041712_NAR_30mM_plus2.11912.11912.2	2	6.4	0	3.47E+05		(K)ATAVM	(K)A T/A V/M/P D/G Q F K(D)		115.62	582.796	1164.572	0.013	11.1	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
18459	dirMS_041712_NAR_30mM_plus2.13259.13259.2	2	6.4	0	1.82E+06		(R)EYQELM	(R)E Y/Q/E/L/M N V K(L)		122.03	577.2809	1153.556	-0.0013	-1.1	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
18460	dirMS_041712_NAR_30mM_plus2.20445.20526.2	2	6.4	0	1.86E+05		(K)LGLENA	(K)L/G|L|E|N A E|A L I R(L)		161.08	599.8397	1198.679	-0.0069	-5.7	4.53	61411.3	8.74	HUMAN	P10155	60 kDa SS-A/Ro ribonucleoprotein
18461	dirMS_041712_NAR_30mM_plus2.21081.21081.2	2	6.4	0	1.70E+05		(R)QTLMW	(R)Q T/L/M W/S/A T W P K(E)		165.3	674.8389	1348.672	-0.0013	-1	8.75	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
18462	dirMS_041712_NAR_30mM_plus2.4851.4851.2	2	6.4	0	2.36E+05		(R)MDDYC	(R)M/D/D Y/C/R(R)	C:Carbamidomethylation	76.63	430.1579	859.307	0.0012	1.4	4.21	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
18463	dirMS_041712_NAR_40mM_plus2.17885.17885.3	3	6.4	0	9.50E+04		(R)IAPVHID	(R)I/A|P/V H I D T E S\I/S A L I K(Q)		171.7	569.6601	1706.969	-0.003	-1.7	5.32	165919.5	8.96	HUMAN	Q9NTI5	Sister chromatid cohesion protein PDS5 homolog B
18464	dirMS_041712_NAR_40mM_plus2.18221.18221.3	3	6.4	0	1.68E+05		(K)DNHLLG	(K)D N H\L L G|T\F D L T|G|I|P P A P R(G)		173.7	645.3466	1934.013	0.0122	6.3	5.21	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
18465	dirMS_041712_NAR_50mM_plus2.18798.18798.3	3	6.4	0	4.20E+05		(R)AGLGSG	(R)A G/L/G/S/G L/S L S G L/V H P E L S R(S)		167.15	617.3412	1850.013	-0.004	-2.2	6.79	73325.2	9.19	HUMAN	F5H2A9	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial
18466	dirMS_041712_NAR_50mM_plus2.7357.7357.3	3	6.4	1	1.89E+05		(R)DSFDGR	(R)D S/F/D/G R G P/P G\P E S Q S/R(A)		103.88	563.592	1688.762	-0.0009	-0.5	4.56	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
18467	dirMS_041712_NAR_50mM_plus2.8239.8239.3	3	6.4	1	9.96E+04		(R)IVEQDT	(R)I/V/E Q D/T M/P/P K G V/R(H)		110.22	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
18468	dirMS_041712_NAR_60mM_plus.11719.11719.2	2	6.4	0	1.31E+06		(R)FAQHGT	(R)F A Q/H/G T/F E\Y E/Y S Q R(W)		118.65	881.8928	1762.782	-0.0037	-2.1	5.4	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
18469	dirMS_041712_NAR_60mM_plus.8317.8317.3	3	6.4	0	6.64E+05		(R)QYDISD	(R)Q Y/D I/S/D/P Q/R P R(L)		101.42	458.8968	1374.676	-0.0002	-0.1	5.96	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
18470	dirMS_041712_NAR_120mM_minus.20219.20219.4	4	6.39	0	4.94E+05		(K)LAFPSPF	(K)L A\F P S/P F G H/L/S E/G F S H S R(W)		166.28	493.9968	1972.966	-0.0011	-0.5	6.92	16196.2	9.92	HUMAN	C9JRJ8	Sequestosome-1 (Fragment)
18471	dirMS_041712_NAR_120mM_minus.5434.5493.3	3	6.39	1	3.50E+04	M58m	(K)VTEQHR	(K)V T E Q H/R/Q m G K(G)	m:Oxidized methionine	82.9	410.5394	1213.611	15.993	-1.5	8.73	20680.1	8.86	HUMAN	C9JMY1	Insulin-like growth factor-binding protein 2
18472	dirMS_041712_NAR_20mM_minus.13310.13310.2	2	6.39	0	9.81E+05	M73m	(R)AILVDLE	(R)A I\L\V/D/L|E/P G T m D S V R(S)	m:Oxidized methionine	182.88	816.4184	1615.836	15.9935	-0.8	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
18473	dirMS_041712_NAR_30mM_minus2.7270.7270.2	2	6.39	0	2.63E+05		(R)FGPDGT	(R)F/G|P/D/G T G R(K)		94.45	403.6977	806.379	0.009	11.1	5.84	26931.3	6.81	HUMAN	B7Z8L8	A-kinase anchor protein 8
18474	dirMS_041712_NAR_40mM_minus2.6837.6837.3	3	6.39	0	1.29E+05	M44m M4	(K)SGTGIA	(K)S/G T/G I/A/A m S V m R P\E Q I m K(S)	m:Oxidized methionine	110.45	652.3173	1906.955	47.9826	-1.1	8.46	8797.3	9.3	HUMAN	H3BR50	V-type proton ATPase 16 kDa proteolipid subunit
18475	dirMS_041712_NAR_50mM_minus2.16515.16515.3	3	6.39	0	9.06E+04		(R)LLLDIPL	(R)L L/L D I/P L/Q T/P H K(L)		162.37	463.2805	1387.831	-0.0038	-2.7	6.74	198852.6	5.95	HUMAN	A6NKT7	RanBP2-like and GRIP domain-containing protein 3
18476	dirMS_041712_NAR_50mM_minus2.6149.6149.3	3	6.39	1	3.19E+04		(R)AGGEEL	(R)A/G\G E/E L D E G/V/A K/D\N A K(I)		97.85	534.9253	1602.761	0.0008	0.5	4.18	89879.1	4.58	HUMAN	Q32MZ4	Leucine-rich repeat flightless-interacting protein 1
18477	dirMS_041712_NAR_60mM_minus.15173.15173.3	3	6.39	1	2.01E+05		(R)LYSILGT	(R)L Y S/I L G/T T L K/D E G K(L)		144.85	513.2854	1537.847	-0.0056	-3.6	6.07	66876.9	6.17	HUMAN	O75083	WD repeat-containing protein 1
18478	dirMS_041712_NAR_60mM_minus.8500.8500.3	3	6.39	1	1.02E+05		(K)ELKSPD	(K)E L\K S\P D/E/G F E G K(S)		107.42	445.8849	1335.643	-0.0025	-1.9	4.41	84557.3	6.5	HUMAN	Q04609	Glutamate carboxypeptidase 2
18479	dirMS_041712_NAR_120mM_plus.10467.10467.3	3	6.39	0	6.96E+05		(R)AHSSM	(R)A H S S M\V/G\V/N|L P Q K(A)		108.2	456.5762	1367.71	0.0041	3	8.8	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
18480	dirMS_041712_NAR_120mM_plus.16501.16501.4	4	6.39	0	2.10E+05		(K)EVVHTV	(K)E V V/H T/V/S L H E I D\V I/N S R(T)		139.6	487.5113	1947.029	-0.006	-3.1	5.27	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
18481	dirMS_041712_NAR_120mM_plus.5503.5503.2	2	6.39	1	5.63E+05		(R)QREME	(R)Q R/E M/E|E|Q/M R(R)		82	618.7759	1236.546	-0.0014	-1.2	4.79	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
18482	dirMS_041712_NAR_20mM_plus.13710.13710.2	2	6.39	0	1.30E+05		(R)SLPALT	(R)S L/P/A L T N I I K(I)		166.82	535.3381	1069.662	0.0074	6.9	8.47	15666.5	6.09	HUMAN	F8W0A0	Phenylalanine-4-hydroxylase (Fragment)
18483	dirMS_041712_NAR_20mM_plus.16176.16176.2	2	6.39	0	6.61E+04		(R)LLDAQL	(R)L L D\A Q L/A|T G G I/V/D P R(L)		183.85	769.9362	1538.854	0.0114	7.4	4.21	533778	5.74	HUMAN	Q15149	Plectin
18484	dirMS_041712_NAR_20mM_plus.9562.9562.2	2	6.39	0	4.68E+05		(R)ISVYYNE	(R)I S V/Y/Y/N E/A T G/G/K(Y)		138.13	651.3211	1301.637	-0.0023	-1.8	6	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
18485	dirMS_041712_NAR_30mM_plus2.12271.12271.3	3	6.39	0	2.56E+06		(R)AQIFAN	(R)A Q\I F A N T/V/D/N A R(I)		116.83	440.5613	1319.67	-0.0009	-0.7	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18486	dirMS_041712_NAR_40mM_plus2.11321.11321.3	3	6.39	0	2.83E+04		(K)AGVSIS	(K)A G/V|S I/S V V H/G N L S/E E A\A K(Q)		132.63	589.9796	1767.924	0.0007	0.4	5.4	50949.8	9.28	HUMAN	P36551	Coproporphyrinogen-III oxidase, mitochondrial
18487	dirMS_041712_NAR_40mM_plus2.12561.12561.2	2	6.39	0	2.54E+04		(K)ICSWNV	(K)I/C|S W N/V D/G L R(A)	C:Carbamidomethylation	140.23	610.297	1219.589	-0.0021	-1.7	5.84	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
18488	dirMS_041712_NAR_40mM_plus2.6463.6463.2	2	6.39	0	1.35E+05		(K)SLESINS	(K)S L|E/S/I N S R(L)		96.88	453.2358	905.469	-0.0044	-4.8	5.72	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
18489	dirMS_041712_NAR_60mM_plus.10069.10069.3	3	6.39	0	4.64E+05		(K)TVSSHE	(K)T V/S/S H/E/V F L Q R(L)		110.63	434.9004	1302.68	0.0066	5	6.41	26418.4	5.43	HUMAN	Q5QPE4	Sorting nexin 5 (Fragment)
18490	dirMS_041712_NAR_60mM_plus.10481.10481.3	3	6.39	1	1.61E+06		(R)TNAENE	(R)T|N|A E N E\F/V T I K K(D)		112.27	465.2512	1393.732	0.0069	4.9	5.81	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
18491	dirMS_041712_NAR_60mM_plus.10766.10766.3	3	6.39	1	3.21E+04		(R)LRQLAE	(R)L R\Q L A E E\D\L/A/Q/Q R(A)		112.7	523.9486	1569.834	-0.0031	-2	4.68	533778	5.74	HUMAN	Q15149	Plectin
18492	dirMS_041712_NAR_60mM_plus.18844.18844.3	3	6.39	1	3.96E+06		(R)VSFELFA	(R)V/S\F/E L F/A D K V/P K(T)		155.83	460.5914	1379.757	0.0027	2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
18493	dirMS_041712_NAR_60mM_plus.19016.19016.3	3	6.39	1	3.50E+04		(K)SELVAM	(K)S E|L V/A M L/E E/E E L/R K(A)		158.07	559.288	1675.857	-0.0077	-4.6	4.32	18679.2	5.61	HUMAN	B4DWW1	ADP-ribosylation factor-like protein 1
18494	dirMS_041712_NAR_60mM_plus.20651.20651.3	3	6.39	0	7.27E+05		(R)LGFHLP	(R)L G\F H L P L E\V/A/Y/Q R(G)		168.62	514.9568	1542.843	0.0131	8.5	6.75	533778	5.74	HUMAN	Q15149	Plectin
18495	dirMS_041712_NAR_60mM_plus.8918.8918.3	3	6.39	0	2.35E+04		(K)IMQQET	(K)I/M/Q Q E T\S V P T L K(Q)		103.52	458.9149	1374.73	0.0004	0.3	6	76176.8	8.74	HUMAN	Q7Z417	Nuclear fragile X mental retardation-interacting protein 2
18496	dirMS_041712_NAR_30mM_minus2.8568.8568.2	2	6.38	0	6.30E+05		(R)QAEVEL	(R)Q A/E/V/E L/A/S R(V)		100.77	501.7573	1002.521	-0.0141	-14.1	4.53	533778	5.74	HUMAN	Q15149	Plectin
18497	dirMS_041712_NAR_50mM_minus2.12823.12823.3	3	6.38	0	1.53E+05		(K)ASLASLP	(K)A S L/A/S L/P/P L H V A K(L)		141.37	435.2622	1303.773	-0.0012	-0.9	8.8	141626	5.5	HUMAN	A8MY36	Dynactin subunit 1
18498	dirMS_041712_NAR_50mM_minus2.16292.16292.3	3	6.38	0	8.84E+04		(R)AVTPLR	(R)A V/T/P L R P G E L L F R(S)		160.63	490.2883	1468.863	-0.0131	-8.9	9.64	21357.6	9.92	HUMAN	B0QZ88	SET and MYND domain containing 3
18499	dirMS_041712_NAR_60mM_minus.14785.14785.3	3	6.38	1	4.01E+05		(R)IKIGDPL	(R)I K\I G D P L|L/E/D/T R(M)		142.48	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
18500	dirMS_041712_NAR_60mM_minus.7492.7492.3	3	6.38	1	5.70E+04		(K)TEADAE	(K)T E/A/D A E K/T F/E E K(Q)		101.08	466.5515	1397.643	-0.0031	-2.2	4.25	32503.1	5.29	HUMAN	H7BY16	Nucleolin (Fragment)
18501	dirMS_041712_NAR_60mM_minus.8103.8103.3	3	6.38	1	1.20E+05		(K)FAAKGE	(K)F A/A/K G E G Q L/G/P/A E/R(A)		105.55	477.5852	1430.739	0.0024	1.7	6.14	96306.4	6.41	HUMAN	P13639	Elongation factor 2
18502	dirMS_041712_NAR_60mM_minus.8180.8180.3	3	6.38	1	1.32E+05		(R)KQSTDE	(R)K Q S\T\D E\E|V/T/S L A K(S)		105.82	479.2451	1435.728	-0.0067	-4.7	4.68	12611.4	8.8	HUMAN	E5RIS7	Transcription elongation factor A protein 1
18503	dirMS_041712_NAR_60mM_minus.9739.9739.3	3	6.38	1	4.56E+04		(K)TAVCDI	(K)T A|V|C D I|P P R G L/K(M)	C:Carbamidomethylation	112.72	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
18504	dirMS_041712_NAR_120mM_plus.10668.10668.3	3	6.38	0	1.23E+06		(R)GLHQSI	(R)G L H Q S/I/E/E F R(A)		109.27	405.8796	1215.612	0.0126	10.4	5.4	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
18505	dirMS_041712_NAR_120mM_plus.9138.9138.3	3	6.38	1	7.08E+05		(K)EFFNGK	(K)E F/F N/G K/E/P S R(G)		101.52	404.2038	1210.585	0.0117	9.7	6.24	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
18506	dirMS_041712_NAR_20mM_plus.11272.11272.2	2	6.38	0	1.45E+05		(R)YALYDA	(R)Y A|L/Y/D A T Y E T K(E)		150.35	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
18507	dirMS_041712_NAR_20mM_plus.12287.12287.2	2	6.38	0	4.61E+04		(K)VALSSE	(K)V A\L/S/S\E/T E V A\L A R(D)		157.62	673.3693	1345.732	-0.0008	-0.6	4.53	246695.2	5.91	HUMAN	E7EVA0	Microtubule-associated protein
18508	dirMS_041712_NAR_20mM_plus.13409.13643.2	2	6.38	0	4.91E+05	M148m	(R)DLTDYL	(R)D L|T\D/Y L m K(I)	m:Oxidized methionine	164.78	507.7439	998.486	15.9942	-0.7	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
18509	dirMS_041712_NAR_20mM_plus.14486.14486.3	3	6.38	0	1.37E+05		(R)LQEAGIL	(R)L Q E A G I\L|S/A E E/L Q R(L)		171.65	519.6131	1556.828	-0.0031	-2	4.25	533778	5.74	HUMAN	Q15149	Plectin
18510	dirMS_041712_NAR_20mM_plus.14640.14640.2	2	6.38	0	1.41E+05		(R)IMNTFS	(R)I M N/T/F/S V/V P S\P K(V)		173.45	660.3527	1319.703	-0.0047	-3.5	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
18511	dirMS_041712_NAR_20mM_plus.14872.14872.2	2	6.38	0	1.98E+05	M179m M	(K)mFVLDE	(K)m F/V/L/D E A D E m L S R(G)	m:Oxidized methionine	173.6	794.3555	1555.713	31.9906	0.5	3.91	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
18512	dirMS_041712_NAR_20mM_plus.16053.16053.2	2	6.38	0	1.14E+05		(R)GLFIIDG	(R)G L/F/I I/D G/K(G)		182.03	431.7544	862.503	-0.0018	-2	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
18513	dirMS_041712_NAR_20mM_plus.17480.17480.2	2	6.38	0	3.36E+04		(R)YLTVAA	(R)Y L/T V/A A|V F R(G)		192.65	520.3009	1039.593	0.001	1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
18514	dirMS_041712_NAR_40mM_plus2.10615.10615.3	3	6.38	0	1.85E+05		(K)VGSLDN	(K)V/G/S\L/D N V G H\L P A G G A V K(I)		128.15	530.9567	1590.86	-0.0043	-2.7	6.71	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
18515	dirMS_041712_NAR_60mM_plus.10205.10205.2	2	6.38	0	2.03E+06		(K)GIVEFS	(K)G I|V/E/F/S G K/P A A\R(K)		111.3	616.3425	1231.679	-0.0016	-1.3	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
18516	dirMS_041712_NAR_60mM_plus.11816.11816.2	2	6.38	0	3.70E+05		(K)TGNLGN	(K)T G/N\L/G/N V V/H\I|E/R(F)		119.1	654.8542	1308.702	-0.0008	-0.6	6.41	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
18517	dirMS_041712_NAR_60mM_plus.12758.12758.3	3	6.38	1	9.60E+05	M230m	(R)mSMKE	(R)m\S M K E V D\E/Q\M/L/N/V\Q N K(N)	m:Oxidized methionine	123.5	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
18518	dirMS_041712_NAR_60mM_plus.8928.8928.3	3	6.38	0	1.59E+06		(K)EFHLNE	(K)E F H L N\E/S/G D/P/S/S K(S)		105.52	482.8882	1446.65	0.0005	0.3	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
18519	dirMS_041712_NAR_120mM_minus.4467.4467.2	2	6.37	0	2.59E+06	M46m M4	(R)HQGVm	(R)H Q|G\V\m V/G m G Q|K(D)	m:Oxidized methionine	73.72	602.2834	1171.571	31.9885	-1.1	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
18520	dirMS_041712_NAR_120mM_minus.6203.6203.3	3	6.37	1	1.20E+05		(K)AQQELE	(K)A Q/Q/E/L E/E Q T R R(A)		87.68	463.2365	1387.692	0.0025	1.8	4.79	67933	6.08	HUMAN	P26038	Moesin
18521	dirMS_041712_NAR_20mM_minus.10500.10500.2	2	6.37	0	1.02E+04	M234m	(K)mVVESA	(K)m V/V|E/S A/Y E V/I K(L)	m:Oxidized methionine	153.32	642.3318	1267.66	15.9961	0.9	4.53	36923.1	5.71	HUMAN	P07195	L-lactate dehydrogenase B chain
18522	dirMS_041712_NAR_20mM_minus.13050.13050.2	2	6.37	0	3.72E+05	M35m	(K)NDIAINE	(K)N D I A|I|N E L m K(R)	m:Oxidized methionine	181.62	588.7948	1160.598	15.9843	-9	4.37	28354	7.11	HUMAN	B4DXI8	26S proteasome non-ATPase regulatory subunit 7
18523	dirMS_041712_NAR_30mM_minus2.18324.18324.2	2	6.37	0	4.28E+05		(R)QAQEYE	(R)Q A/Q E/Y E|A/L L/N I/K(V)		154.63	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18524	dirMS_041712_NAR_30mM_minus2.6337.6337.2	2	6.37	0	1.60E+05		(K)STASAQ	(K)S T A/S A Q/N|K(E)		88.68	403.7074	806.4	0.0073	9	8.47	85247.9	5.64	HUMAN	H7BZJ7	Fanconi anemia group D2 protein (Fragment)
18525	dirMS_041712_NAR_40mM_minus2.13205.13205.2	2	6.37	0	9.83E+04		(K)SYELPD	(K)S Y E\L|P D G Q V I/T I G|N E R(F)		161.53	895.9483	1790.892	-0.0026	-1.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F

18526	dirMS_041712_NAR_40mM_minus2.7803.7803.3	3	6.37	0	8.23E+04		(K)TGVAVN	(K)T G V/A\V/N K P A E F T V D/A K(H)		124.67	549.6354	1646.875	0.0168	10.2	5.73	283472.4	5.71	HUMAN	P21333	Filamin-A
18527	dirMS_041712_NAR_50mM_minus2.16536.16536.3	3	6.37	1	1.87E+04		(R)EVQLEEI	(R)E V/Q L/E/E/L E A A R D L V/S K(E)		161.82	610.3273	1828.965	0.0023	1.2	4.25	45984.6	6.24	HUMAN	B4E1G6	Galactokinase
18528	dirMS_041712_NAR_60mM_minus.12657.12657.3	3	6.37	1	2.52E+05		(R)EMDRET	(R)E M D R E T/L/I/D/V A R(T)		129.8	483.2454	1447.721	0.0007	0.5	4.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
18529	dirMS_041712_NAR_120mM_plus.16538.16538.4	4	6.37	1	1.02E+06		(R)YAEIVHL	(R)Y/A E I V H/L/T L P D G T K R(S)		139.17	428.9885	1712.933	-0.0008	-0.5	6.75	21230	6.36	HUMAN	H0YC04	V-type proton ATPase subunit B, brain isoform (Fragment)
18530	dirMS_041712_NAR_120mM_plus.5715.5715.4	4	6.37	2	4.78E+05		(R)KTGQAP	(R)K\T G Q A/P/G/Y S/Y T A A N K N K(G)		83.5	450.4826	1798.908	0.0003	0.2	9.83	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
18531	dirMS_041712_NAR_20mM_plus.11664.11664.2	2	6.37	0	1.16E+05	M402m	(R)mAFGAT	(R)m A/F G/A/T L D/V K(T)	m:Oxidized methionine	152.93	534.7743	1052.545	15.9968	1.8	5.59	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
18532	dirMS_041712_NAR_20mM_plus.13815.13815.2	2	6.37	0	2.44E+05	M98m	(R)TLTIVDT	(R)T L|T/I|V D T G I G m T K(A)	m:Oxidized methionine	167.3	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
18533	dirMS_041712_NAR_20mM_plus.8169.8169.2	2	6.37	0	7.99E+04	M237m	(R)YVmTTT	(R)Y/V/m/T/T T T L\E R(T)	m:Oxidized methionine	126.28	615.8042	1214.609	15.9926	-1.9	6	31604.9	6.88	HUMAN	G3V4T5	Eukaryotic translation initiation factor 2 subunit 1 (Fragment)
18534	dirMS_041712_NAR_20mM_plus.8822.8822.2	2	6.37	0	1.30E+05		(K)VLEEAN	(K)V L\E\E/A|N Q|A\I/N/P K(L)		131.6	663.353	1325.706	-0.0072	-5.5	4.53	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
18535	dirMS_041712_NAR_30mM_plus2.10464.10464.2	2	6.37	0	1.04E+06		(K)DVNQQI	(K)D V|N/Q/Q E F V\R(A)		107.5	567.7813	1134.554	0.0015	1.3	4.37	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
18536	dirMS_041712_NAR_30mM_plus2.15951.15951.2	2	6.37	0	1.89E+05		(K)AMTGVE	(K)A M|T/G/V/E Q W/P/Y R(A)		136.52	669.317	1337.631	-0.004	-3	6.04	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
18537	dirMS_041712_NAR_30mM_plus2.21598.21598.2	2	6.37	0	3.32E+05		(R)NSYLEVL	(R)N S/Y/L/E V L/L/K(L)		168.03	539.8092	1078.614	-0.0032	-2.9	6	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
18538	dirMS_041712_NAR_30mM_plus2.5442.5442.2	2	6.37	0	1.84E+05		(R)TDTGEP	(R)T D|T/G/E P M G R(G)		82.82	482.2128	963.42	-0.0017	-1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
18539	dirMS_041712_NAR_40mM_plus2.11933.11933.2	2	6.37	0	3.87E+04		(R)QITVND	(R)Q I|T V N D/L/P V/G R(S)		136.42	606.3387	1211.674	-0.0041	-3.4	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
18540	dirMS_041712_NAR_40mM_plus2.5461.5461.2	2	6.37	0	2.74E+04		(K)TYGQST	(K)T Y|G/Q|S T Y S R(Q)		88.83	531.7462	1062.485	0.0001	0.1	8.25	14693.3	4.69	HUMAN	C9JLS9	26S protease regulatory subunit 7 (Fragment)
18541	dirMS_041712_NAR_50mM_plus2.10526.10526.3	3	6.37	0	2.58E+04		(R)AIGSASE	(R)A I/G S A S/E/G A Q S S L/Q E V Y H K(S)		122.58	654.657	1961.956	0.0001	0.1	5.4	20148.5	4.65	HUMAN	B4E2V4	Proteasome (Prosome, macropain) subunit, alpha type, 5, isoform CRA_c
18542	dirMS_041712_NAR_50mM_plus2.11897.11897.3	3	6.37	1	4.38E+05	M327m	(R)VAGGPC	(R)V/A|G G P Q m I/Q/L S L D/G K/R(L)	m:Oxidized methionine	131	562.6377	1669.905	15.9931	-1	8.72	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
18543	dirMS_041712_NAR_50mM_plus2.14121.14121.3	3	6.37	0	2.29E+05	T101t	(K)LADFGV	(K)L A D F G V S A/Q I T A t I A K(R)	t:Phosphorylated T	143.72	562.6227	1605.885	79.9689	1.5	5.84	93117	8.93	HUMAN	F5H5A3	Mitogen-activated protein kinase kinase kinase kinase
18544	dirMS_041712_NAR_50mM_plus2.15444.15444.3	3	6.37	1	9.72E+05		(R)KVPGVT	(R)K\V\P G V T A\I E\L/D E D T/G T F R(I)		149.82	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
18545	dirMS_041712_NAR_60mM_plus.11405.11405.3	3	6.37	0	4.60E+06		(R)GSAVHC	(R)G S|A V/H Q\L S E E/L R(C)		116.45	442.5666	1325.681	0.0044	3.4	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
18546	dirMS_041712_NAR_60mM_plus.18539.18539.3	3	6.37	0	1.84E+05		(K)DHGLEV	(K)D H G L\E\V|L/G L V R(V)		153.82	403.2318	1207.679	0.0015	1.2	5.32	17732.8	5.85	HUMAN	F5GYJ1	U8 snoRNA-decapping enzyme
18547	dirMS_041712_NAR_120mM_minus.10406.10406.3	3	6.36	1	5.43E+05	M142m	(K)VKEGMI	(K)V K E G M N I|V/E/A m E R(F)	m:Oxidized methionine	110.18	507.9186	1505.745	15.9962	0.8	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
18548	dirMS_041712_NAR_120mM_minus.9798.9798.3	3	6.36	1	2.01E+05		(R)SRSGEG	(R)S R S G\E\G E\V|S/G L M R(K)		108.07	455.559	1364.659	0.0038	2.8	5.87	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
18549	dirMS_041712_NAR_20mM_minus.7122.7122.2	2	6.36	0	3.11E+05	M33m	(R)IDEmPE	(R)I/D/E m/P E A A V K(S)	m:Oxidized methionine	118.67	559.7733	1102.545	15.9944	-0.4	4.14	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
18550	dirMS_041712_NAR_30mM_minus2.11911.11911.2	2	6.36	0	9.21E+05		(K)EVDEQM	(K)E V/D E Q|M L\N/V/Q/N/K(N)		117.53	723.8476	1446.689	-0.0014	-1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
18551	dirMS_041712_NAR_40mM_minus2.6988.6988.2	2	6.36	0	5.85E+05		(R)GYSFTTT	(R)G Y|S F/T T/T A E/R(E)		111.95	566.7661	1132.527	-0.002	-1.8	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
18552	dirMS_041712_NAR_50mM_minus2.15094.15094.3	3	6.36	1	1.33E+05		(K)VSEQGL	(K)V/S/E Q G L I E I L K K(V)		154.37	452.9385	1356.81	-0.0087	-6.4	6.11	12899.6	6.59	HUMAN	K7EL31	Programmed cell death protein 5
18553	dirMS_041712_NAR_50mM_minus2.5706.5706.3	3	6.36	0	2.41E+05		(K)ATCAPQ	(K)A T/C/A/P Q H/G A/P G P G P A\D A S K(V)	C:Carbamidomethylation	93.82	597.279	1789.829	-0.0062	-3.4	6.79	83264.1	6.04	HUMAN	E9PHF0	Filamin-A
18554	dirMS_041712_NAR_60mM_minus.10202.10202.3	3	6.36	0	8.26E+04		(R)EIVHIQA	(R)E/I V H I Q A/G Q/C/G\N Q I/G A/K(F)	C:Carbamidomethylation	116.48	608.3099	1822.923	-0.0077	-4.2	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
18555	dirMS_041712_NAR_60mM_minus.14140.14140.3	3	6.36	0	2.02E+05		(K)IVNFLLQ	(K)I V N F/L/L Q H S A/K(V)		138.23	423.9167	1269.731	0.0042	3.3	8.76	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
18556	dirMS_041712_NAR_60mM_minus.14761.14761.3	3	6.36	1	3.99E+05		(R)IKIGDPL	(R)I K\I G D P L|L E/D|T R(M)		142.4	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
18557	dirMS_041712_NAR_60mM_minus.9794.9794.2	2	6.36	1	1.76E+05		(K)IKIIAPPE	(K)I K|I/I/A P P E R(K)		114.68	518.8289	1036.651	-0.0008	-0.8	8.75	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
18558	dirMS_041712_NAR_20mM_plus.12340.12483.2	2	6.36	0	1.78E+05		(K)TIIFVETK	(K)T I|I/F V E T K(R)		158.87	475.7818	950.556	0.0006	0.6	5.66	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
18559	dirMS_041712_NAR_20mM_plus.16006.16006.2	2	6.36	0	1.13E+05		(R)GTPLISP	(R)G T/P/L/I\S P L/I K(W)		181.32	519.8306	1038.656	-0.0018	-1.8	8.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
18560	dirMS_041712_NAR_20mM_plus.16683.16683.3	3	6.36	0	8.96E+04	S639s M64	(R)WLIsAA	(R)W L I s A/A m D C S/I R(T)	C:Carbamidomethylation s:N-ace	185.8	547.9201	1422.687	219.0589	-9.4	5.84	106347.2	7.44	HUMAN	Q8NI36	WD repeat-containing protein 36
18561	dirMS_041712_NAR_20mM_plus.16821.16821.2	2	6.36	0	1.39E+05		(K)TVDNFV	(K)T V D|N F/V/A/L A T G E K(G)		186.67	682.8565	1364.706	0.0001	0.1	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
18562	dirMS_041712_NAR_20mM_plus.17461.17461.2	2	6.36	0	3.09E+03		(K)EGSIEIDI	(K)E G S/I\E|I D/I|P V P K(Y)		192.22	648.852	1296.705	-0.0078	-6	4.14	66923.1	6.88	HUMAN	E9PG35	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (Fragment)
18563	dirMS_041712_NAR_30mM_plus2.4085.4085.2	2	6.36	0	9.29E+05	M299m M	(K)NmmAA	(K)N m|m\A/A C D|P R(H)	C:Carbamidomethylation m:Oxid	68.4	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
18564	dirMS_041712_NAR_30mM_plus2.9122.9575.2	2	6.36	0	5.65E+05		(R)VAQLLEI	(R)V/A|Q/L L/E R(W)		102.67	414.7506	828.494	0.0001	0.2	5.97	533778	5.74	HUMAN	Q15149	Plectin
18565	dirMS_041712_NAR_30mM_plus2.9201.9201.2	2	6.36	0	3.96E+05		(K)ATFDAIS	(K)A T|F/D A/I S K(T)		101.98	426.7266	852.446	-0.0002	-0.3	5.88	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
18566	dirMS_041712_NAR_40mM_plus2.17836.17836.3	3	6.36	0	1.42E+05		(R)DIKPQN	(R)D I\K P Q N\L\L/L/D/P D T A V L K(L)		170.92	631.6874	1893.069	-0.0215	-11.4	4.43	47257	9.38	HUMAN	P49841	Glycogen synthase kinase-3 beta
18567	dirMS_041712_NAR_40mM_plus2.7965.7965.2	2	6.36	0	1.28E+05		(K)ASLENSL	(K)A S|L/E/N S/L R(E)		106.85	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18568	dirMS_041712_NAR_50mM_plus2.16337.16337.3	3	6.36	0	4.52E+05		(K)QLLGEH	(K)Q L/L/G E H L/T/A I L Q K(G)		153.9	488.6224	1463.858	-0.0054	-3.7	6.75	103381.4	8.47	HUMAN	K4DI93	Cullin 4B, isoform CRA_e
18569	dirMS_041712_NAR_60mM_plus.12117.12117.3	3	6.36	1	3.37E+06	M200m S2	(K)GPmsAV	(K)G P|m s A V Y I|E K|F V R(R)	m:Oxidized methionine s:N-a	120.78	572.64	1496.793	219.1125	22.2	8.59	111896.2	6.12	HUMAN	Q6PKC3	Thioredoxin domain-containing protein 11
18570	dirMS_041712_NAR_60mM_plus.7507.7510.3	3	6.36	1	9.64E+05		(R)YLAEVA	(R)Y L/A E V/A\A G D D K K(G)		97.83	427.2226	1279.653	0.0004	0.3	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
18571	dirMS_041712_NAR_120mM_minus.5424.5424.2	2	6.35	1	1.34E+05		(K)MKGDY	(K)M/K|G/D|Y Y R(Y)		82.75	466.7187	932.429	0.0007	0.7	8.25	18789.1	6.77	HUMAN	A2IDB2	14-3-3 protein eta (Fragment)
18572	dirMS_041712_NAR_120mM_minus.5608.5608.3	3	6.35	1	7.06E+04		(R)RSSTSSE	(R)R S S T S\S/E|P T P T V K(T)		84.2	459.5703	1376.702	-0.0053	-3.8	8.75	120522.3	5.57	HUMAN	F5H1H6	Cytospin-A
18573	dirMS_041712_NAR_20mM_minus.8591.8625.2	2	6.35	0	1.03E+05	M23m	(K)LYLADP	(K)L/Y|L/A/D P m K(A)	m:Oxidized methionine	135.8	483.7514	950.502	15.994	-1	5.83	7781.8	6.82	HUMAN	E9PE20	Signal recognition particle 9 kDa protein
18574	dirMS_041712_NAR_30mM_minus2.12093.12093.2	2	6.35	0	4.11E+04		(K)QALSGF	(K)Q A|L/S/G F/G Y R(L)		119.07	499.7499	998.505	-0.0129	-12.9	8.75	21925.1	5.16	HUMAN	O75340	Programmed cell death protein 6
18575	dirMS_041712_NAR_30mM_minus2.13059.13059.2	2	6.35	0	2.81E+05		(K)LSELEPG	(K)L S E|L\E|P G T G D/L/R(F)		124.52	643.8325	1286.659	-0.0009	-0.7	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
18576	dirMS_041712_NAR_30mM_minus2.13770.13770.2	2	6.35	0	4.11E+05		(K)TIVMGA	(K)T I|V/M/G A/S F R(N)		128.62	491.2611	981.519	-0.0037	-3.8	9.41	35556.4	9.3	HUMAN	F2Z393	Transaldolase
18577	dirMS_041712_NAR_30mM_minus2.7635.7635.2	2	6.35	0	8.48E+05		(R)FSNISAA	(R)F/S/N/I/S/A/A K(A)		95.77	419.2279	837.447	0.002	2.4	8.75	55232.1	8.4	HUMAN	F5H5W3	T-complex protein 1 subunit delta
18578	dirMS_041712_NAR_40mM_minus2.16115.16115.3	3	6.35	1	6.49E+05		(R)ELAILLG	(R)E L/A I/L/L G M L/D/P A E K D/E K(G)		189.63	629.0034	1884.999	-0.003	-1.6	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
18579	dirMS_041712_NAR_50mM_minus2.14826.14826.3	3	6.35	0	3.91E+04		(K)IAILTCPF	(K)I/A\I\L T C/P F E/P P K/P K(T)	C:Carbamidomethylation	152.75	537.6375	1610.898	0.0005	0.3	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
18580	dirMS_041712_NAR_60mM_minus.10676.10676.3	3	6.35	1	5.79E+04		(R)LAEVEA	(R)L/A|E|V/E A A L E K Q R(Q)		119.55	452.9148	1356.748	-0.0183	-13.5	4.79	533778	5.74	HUMAN	Q15149	Plectin
18581	dirMS_041712_NAR_60mM_minus.14892.14892.3	3	6.35	1	3.75E+05		(R)IKIGDPL	(R)I K I G D P\L|L\E D/T R(M)		142.8	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
18582	dirMS_041712_NAR_60mM_minus.5341.5341.3	3	6.35	0	1.58E+04		(K)TATPQQ	(K)T A\T|P Q Q A/Q E V/H E K(L)		85.48	489.5763	1466.723	-0.009	-6.2	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
18583	dirMS_041712_NAR_60mM_minus.8157.8157.3	3	6.35	0	1.91E+05		(R)QYDISDI	(R)Q Y/D/I/S/D/P Q/R P R(L)		105.63	458.8971	1374.676	0.0007	0.5	5.96	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
18584	dirMS_041712_NAR_120mM_plus.6791.6791.3	3	6.35	1	1.94E+05		(R)VIEDRDS	(R)V/I/E D/R D S/Q L R(S)		89.42	410.8828	1230.644	-0.0098	-8	4.56	94000.1	5.5	HUMAN	Q8N1F7	Nuclear pore complex protein Nup93
18585	dirMS_041712_NAR_20mM_plus.15840.15840.3	3	6.35	0	8.77E+03		(R)SSFYVN	(R)S S\F Y V N\G L T/L/G G/Q K(C)		179.37	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
18586	dirMS_041712_NAR_20mM_plus.9058.9058.2	2	6.35	0	4.41E+05	M161m	(K)LLIEmEC	(K)L L|I|E/m/E Q R(L)	m:Oxidized methionine	132.85	524.278	1031.555	15.9933	-1.5	4.53	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
18587	dirMS_041712_NAR_30mM_plus2.11579.11579.3	3	6.35	0	4.36E+05		(K)QTLSAA	(K)Q T L S A A A/V F N D/R(L)		114.23	431.5568	1292.659	-0.0035	-2.7	5.84	378709.3	6.48	HUMAN	H3BLU6	E3 ubiquitin-protein ligase RNF213
18588	dirMS_041712_NAR_30mM_plus2.12382.12382.2	2	6.35	0	2.06E+04		(R)LGPGM	(R)L G/P G/M/A D I C K(N)	C:Carbamidomethylation	118.68	531.266	1061.512	0.0129	12.2	5.84	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
18589	dirMS_041712_NAR_30mM_plus2.18550.18550.3	3	6.35	0	4.97E+05		(R)SSFYVN	(R)S S F Y V N\G\L T/L/G G Q K(C)		150.95	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
18590	dirMS_041712_NAR_50mM_plus2.10010.10010.3	3	6.35	0	3.83E+04		(K)INEKPQ	(K)I N|E K/P Q V\I/A/D Y E S\G R(A)		120.07	573.6314	1718.871	0.0089	5.2	4.68	16368.4	9.95	HUMAN	O60869	Endothelial differentiation-related factor 1
18591	dirMS_041712_NAR_50mM_plus2.10754.10754.3	3	6.35	1	2.12E+05		(K)AQALRD	(K)A Q|A L R\D N S T M/G Y M M/A K(K)		123.72	596.6125	1787.824	-0.0008	-0.4	8.63	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
18592	dirMS_041712_NAR_50mM_plus2.14855.14855.3	3	6.35	0	6.51E+05		(K)SPAPPLL	(K)S P|A|P/P L/L H V A A L G Q/K(Q)		145.78	500.2911	1498.874	-0.0153	-10.2	8.49	17549.1	10.39	HUMAN	E5RFJ3	DBIRD complex subunit KIAA1967 (Fragment)
18593	dirMS_041712_NAR_50mM_plus2.19830.19830.2	2	6.35	1	3.80E+05		(R)KAIIIFVP	(R)K\A I/I/I|F V\P V/P Q L K(S)		173.13	733.4779	1465.95	-0.002	-1.3	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
18594	dirMS_041712_NAR_60mM_plus.13761.13761.3	3	6.35	1	4.71E+05		(R)KYEMFA	(R)K Y E M F\A Q/T\L/Q/Q S R(G)		128.72	543.9389	1629.805	-0.0032	-2	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
18595	dirMS_041712_NAR_60mM_plus.16934.16934.3	3	6.35	1	2.49E+05		(K)IKAIPQL	(K)I K A/I|P Q|L Q/G/Y L R(S)		145.63	467.2842	1399.842	-0.0039	-2.8	9.99	25891.4	10.67	HUMAN	F8W181	60S ribosomal protein L6 (Fragment)
18596	dirMS_041712_NAR_60mM_plus.18609.18609.3	3	6.35	1	1.43E+05		(R)CRVDLP	(R)C R V D L|P\L A\V L/S K(M)	C:Carbamidomethylation	154.47	457.599	1370.782	0	0	8.75	7765.6	8.23	HUMAN	H3BSA6	dCTP pyrophosphatase 1
18597	dirMS_041712_NAR_60mM_plus.6867.6867.3	3	6.35	1	2.54E+05		(K)SKAEAES	(K)S K A E A\E/S L/Y Q S K(Y)		94.27	447.5613	1340.669	0.0001	0.1	5.86	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
18598	dirMS_041712_NAR_120mM_minus.13775.13775.3	3	6.34	1	1.12E+05		(R)KYEMFA	(R)K Y E M F\A\Q|T/L/Q/Q/S R(G)		129.37	543.9428	1629.805	0.0085	5.2	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
18599	dirMS_041712_NAR_120mM_minus.20207.20207.3	3	6.34	0	1.72E+05	M195m	(R)LHFFmP	(R)L H F F m\P/G/F/A|P L T S R(G)	m:Oxidized methionine	165.67	546.2809	1620.835	15.9926	-1.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
18600	dirMS_041712_NAR_120mM_minus.8245.8245.3	3	6.34	0	3.55E+05		(R)AAHSEG	(R)A A H S E G N T\T/A/G/L/D/M R(E)		99.15	510.9036	1530.697	-0.0003	-0.2	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
18601	dirMS_041712_NAR_50mM_minus2.14947.14947.3	3	6.34	0	2.35E+05		(K)IYGADDI	(K)I Y/G A D D I E/L\L/P E A Q H K(A)		152.93	604.6516	1811.917	0.0228	12.6	4.31	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
18602	dirMS_041712_NAR_50mM_minus2.5326.5326.3	3	6.34	0	8.24E+05		(K)TATPQQ	(K)T A|T/P Q Q/A Q E/V H E K(L)		88.02	489.5768	1466.723	-0.0075	-5.1	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
18603	dirMS_041712_NAR_50mM_minus2.6759.6759.3	3	6.34	1	2.55E+04		(K)LAQYEPI	(K)L A/Q/Y E/P P Q E E K R A E(-)		104.98	563.2743	1687.829	-0.0202	-12	4.69	11966.5	5.71	HUMAN	Q99417	C-Myc-binding protein
18604	dirMS_041712_NAR_60mM_minus.11316.11316.3	3	6.34	1	1.43E+05		(R)DGKLVS	(R)D G K L\V S E|S/S/D V L/P/K(-)		123.12	491.927	1473.78	-0.0131	-8.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
18605	dirMS_041712_NAR_120mM_plus.11055.11055.3	3	6.34	1	4.75E+05		(K)GFVEFA	(K)G F/V|E/F/A A K P P A R K(A)		110.72	473.2689	1417.795	-0.0029	-2	9.99	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
18606	dirMS_041712_NAR_120mM_plus.4447.4447.3	3	6.34	1	2.93E+05		(R)AAEEED	(R)A A E/E/E D/E A/D|P K R(Q)		72.37	453.8721	1359.602	-0.0005	-0.4	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
18607	dirMS_041712_NAR_120mM_plus.9069.9069.3	3	6.34	0	1.08E+06		(K)HTGPNS	(K)H T G P N S P/D T A/N/D/G F V/R(L)		100.23	562.26	1684.767	-0.0019	-1.2	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
18608	dirMS_041712_NAR_20mM_plus.14587.14587.2	2	6.34	0	1.62E+05		(K)LVILANN	(K)L V|I L/A N/N C|P\A L R(K)	C:Carbamidomethylation	172.32	677.3851	1353.767	-0.0042	-3.1	9.75	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
18609	dirMS_041712_NAR_20mM_plus.17101.17101.2	2	6.34	0	2.36E+05		(K)LFLVQLC	(K)L/F|L|V/Q L Q E K(A)		189.58	559.3342	1117.662	-0.0004	-0.4	6	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
18610	dirMS_041712_NAR_20mM_plus.18386.18386.2	2	6.34	0	1.65E+04		(K)LLDEVFF	(K)L L/D E|V/F F S E K(I)		198.18	613.8195	1226.63	0.0014	1.1	4.14	20360.1	6.3	HUMAN	H0YKT8	Proteasome subunit beta type (Fragment)
18611	dirMS_041712_NAR_20mM_plus.18954.18954.2	2	6.34	0	1.30E+05	M76m	(R)FLILPDm	(R)F L|I\L/P D m L K(N)	m:Oxidized methionine	201.23	553.3192	1089.638	15.9935	-1.3	5.84	13462.5	9.47	HUMAN	B4DJP7	Small nuclear ribonucleoprotein Sm D3
18612	dirMS_041712_NAR_30mM_plus2.15563.15563.2	2	6.34	0	5.65E+05		(R)QPTPPFI	(R)Q P/T/P/P F/F/G R(D)		133.77	523.7794	1046.542	0.0097	9.3	9.75	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
18613	dirMS_041712_NAR_30mM_plus2.21931.21931.2	2	6.34	0	1.56E+05		(R)QSSFALL	(R)Q S/S F/A/L L/G D L T K(A)		170.63	640.3472	1279.689	-0.0021	-1.7	5.84	46579.3	4.96	HUMAN	E5RI07	Transportin-1
18614	dirMS_041712_NAR_40mM_plus2.7809.7809.2	2	6.34	0	4.23E+04		(R)VLNTNID	(R)V L/N/T N|I D/G R(R)		105.73	501.2719	1001.537	-0.0009	-0.9	5.81	17718.4	10.99	HUMAN	P62269	40S ribosomal protein S18
18615	dirMS_041712_NAR_50mM_plus2.10652.10652.3	3	6.34	1	2.12E+05		(K)AQALRD	(K)A Q|A\L R D/N S T/M/G Y M/M A K(K)		123.72	596.6125	1787.824	-0.0008	-0.4	8.63	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
18616	dirMS_041712_NAR_50mM_plus2.13776.13776.3	3	6.34	1	4.77E+05		(R)SILKIDD	(R)S I/L K/I/D D\V/V N T R(-)		140.45	458.2605	1372.78	-0.0125	-9.1	5.68	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
18617	dirMS_041712_NAR_60mM_plus.15800.15800.3	3	6.34	0	2.34E+04		(K)ASDAFH	(K)A/S/D/A F\H/F F Q/S G Q A K(V)		138.38	514.2479	1540.718	0.0112	7.3	6.79	140989.8	6.01	HUMAN	K7EIG1	Protein CLUH
18618	dirMS_041712_NAR_60mM_plus.8643.8643.3	3	6.34	1	4.16E+05		(K)QGIETPE	(K)Q G\I/E/T/P E D Q/N D L R K(M)		102.63	548.2719	1642.803	-0.002	-1.2	4.32	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
18619	dirMS_041712_NAR_120mM_minus.10007.10007.2	2	6.33	1	1.62E+05		(R)KNGFVV	(R)K|N G F V V\L/K(G)		108.88	452.7844	904.562	0.0001	0.1	10	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
18620	dirMS_041712_NAR_120mM_minus.7563.7563.3	3	6.33	1	2.23E+05		(R)KTGQAP	(R)K\T G Q\A\P G Y/S/Y T A A/N K(N)		95.17	519.5935	1556.77	-0.0044	-2.8	9.53	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
18621	dirMS_041712_NAR_120mM_minus.7748.7748.3	3	6.33	1	1.14E+05		(R)RGGPNY	(R)R G G\P/N Y/Q|E/G L/R(V)		96.75	416.2146	1246.629	0.0005	0.4	8.75	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
18622	dirMS_041712_NAR_30mM_minus2.10768.10768.2	2	6.33	0	3.74E+05		(K)WLNENA	(K)W/L/N/E\N A V E/K(V)		112.13	551.7778	1102.553	-0.0044	-4	4.53	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
18623	dirMS_041712_NAR_30mM_minus2.7573.7573.2	2	6.33	0	1.75E+05		(K)YTQSNS	(K)Y/T|Q/S\N/S V C Y/A K(N)	C:Carbamidomethylation	95.73	660.7969	1320.589	-0.0024	-1.8	8.5	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
18624	dirMS_041712_NAR_30mM_minus2.9148.9148.2	2	6.33	0	1.77E+05		(R)LGEYED	(R)L G E/Y/E/D/V S R(V)		102.92	534.2599	1067.5	0.0121	11.4	4.14	23811.2	6.78	HUMAN	A8MVD5	Tubulin-folding cofactor B
18625	dirMS_041712_NAR_50mM_minus2.5744.5744.3	3	6.33	1	9.21E+04		(K)LEEAEKA	(K)L/E/E A E K A/A D E S E/R(G)		94.08	492.8982	1476.681	-0.0012	-0.8	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
18626	dirMS_041712_NAR_60mM_minus.11854.11854.3	3	6.33	1	1.25E+05		(K)ESNGPV	(K)E S N G/P V K V W/G S/I K(G)		126.37	467.5875	1400.753	-0.0053	-3.8	8.69	16163.7	5.7	HUMAN	P00441	Superoxide dismutase [Cu-Zn]
18627	dirMS_041712_NAR_60mM_minus.14493.14493.3	3	6.33	1	2.51E+05		(R)VEVERD	(R)V/E/V E R D N L/A/E D I M/R(L)		140.03	563.6139	1688.827	-0.0001	0	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
18628	dirMS_041712_NAR_60mM_minus.15506.15506.3	3	6.33	1	4.44E+05		(R)LLDAQL	(R)L L/D A|Q/L A T G G L V C P A R/R(L)	C:Carbamidomethylation	146.1	604.3344	1810.996	-0.007	-3.8	9.6	266161	5.68	HUMAN	E9PPU0	Epiplakin
18629	dirMS_041712_NAR_60mM_minus.17019.17019.3	3	6.33	0	1.00E+05		(R)LLANQQ	(R)L L/A/N/Q Q V/F H I S C F/R(C)	C:Carbamidomethylation	154.67	578.3012	1732.895	-0.0061	-3.5	9.75	67446.5	5.63	HUMAN	F8VQE1	LIM domain and actin-binding protein 1
18630	dirMS_041712_NAR_60mM_minus.17294.17294.3	3	6.33	0	9.52E+04		(R)GFGHIG	(R)G F G H I G I A\V|P D V/Y/S A C K(R)	C:Carbamidomethylation	156.02	597.6347	1790.889	0.0001	0.1	6.74	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
18631	dirMS_041712_NAR_120mM_plus.10764.10764.2	2	6.33	1	2.27E+06		(R)LASYLDF	(R)L A/S|Y L D/R V R(S)		109.83	546.8117	1092.616	0.0001	0.1	8.75	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18632	dirMS_041712_NAR_120mM_plus.6073.6073.4	4	6.33	2	3.23E+05		(R)KTGQAP	(R)K\T G Q A|P G/Y/S Y/T/A A N K N K(G)		84.42	450.4826	1798.908	0.0003	0.2	9.83	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
18633	dirMS_041712_NAR_20mM_plus.14112.14112.2	2	6.33	0	7.05E+04	M313m	(R)TVQSLEI	(R)T V/Q S/L/E|I D L D S m R(N)	m:Oxidized methionine	169.18	761.8738	1506.747	15.9935	-0.9	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18634	dirMS_041712_NAR_20mM_plus.7753.7753.2	2	6.33	0	8.55E+04		(K)AQAAAF	(K)A/Q\A\A\A/P A S V P A Q A P K(R)		123.6	689.3745	1377.748	-0.0068	-4.9	8.8	17808.8	11.77	HUMAN	P47914	60S ribosomal protein L29

18635	dirMS_041712_NAR_30mM_plus2.8515.8515.2	2	6.33	0	4.53E+05		(K)LAAIGE	(K)L A/A/I/G E A T R(L)		97.67	451.2545	901.51	-0.0084	-9.4	6	533778	5.74	HUMAN	Q15149	Plectin
18636	dirMS_041712_NAR_30mM_plus2.8729.8729.2	2	6.33	0	6.82E+05		(R)SMPTSG	(R)S M/P T/S G A L D R(V)		99.5	517.751	1034.494	0.0012	1.2	5.55	61733.3	6.3	HUMAN	P36871	Phosphoglucomutase-1
18637	dirMS_041712_NAR_40mM_plus2.7062.7062.2	2	6.33	0	4.77E+04		(K)SNVSDA	(K)S N\V/S|D\A V/A Q S T R(I)		101.65	617.803	1234.602	-0.0035	-2.8	5.55	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
18638	dirMS_041712_NAR_50mM_plus2.10615.10615.2	2	6.33	1	1.53E+06		(R)DGKLVS	(R)D G/K/L\V|S/E S S D\V/L|P K(-)		122.85	737.3925	1473.78	-0.0018	-1.2	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
18639	dirMS_041712_NAR_50mM_plus2.18002.18002.3	3	6.33	0	2.49E+05		(R)VTMLFL	(R)V T|M/L/F\L G/L H N V R(Q)		162.78	467.267	1399.788	-0.0014	-1	9.73	21721.5	5.37	HUMAN	H7BZ35	Aspartate--tRNA ligase, cytoplasmic (Fragment)
18640	dirMS_041712_NAR_50mM_plus2.20729.20729.3	3	6.33	0	2.04E+06		(R)AGKPVI	(R)A G K\P V I C\A T Q/M/L|E/S M I/K(K)	C:Carbamidomethylation	178.68	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
18641	dirMS_041712_NAR_50mM_plus2.21685.21685.3	3	6.33	1	1.36E+04		(K)LTFLYLA	(K)L T/F\L/Y/L A N D/V I Q N S K R(K)		184.45	632.3436	1895.039	-0.0223	-11.8	8.59	12758.1	9.69	HUMAN	E9PIQ9	Regulation of nuclear pre-mRNA domain-containing protein 1B
18642	dirMS_041712_NAR_60mM_plus.12676.12676.3	3	6.33	0	5.66E+05		(K)GSYSLS	(K)G S\Y/S L S H V\Y T P N/D|V R(M)		123.05	565.6098	1694.813	0.0016	0.9	6.74	63566.6	6.3	HUMAN	P07686	Beta-hexosaminidase subunit beta
18643	dirMS_041712_NAR_120mM_minus.14632.14632.4	4	6.32	1	1.80E+05		(K)GLDPAR	(K)G L\D P A R V N V P V/I/G G H A/G K(T)		133.78	440	1756.982	-0.0035	-2	8.76	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
18644	dirMS_041712_NAR_20mM_minus.7647.7647.2	2	6.32	0	2.24E+05		(K)TVPVEA	(K)T V|P V|E A V T S K(T)		125.37	515.7883	1030.578	-0.0086	-8.3	5.66	35720	5.34	HUMAN	B4E358	Src substrate cortactin
18645	dirMS_041712_NAR_20mM_minus.9196.9196.3	3	6.32	0	3.43E+05		(R)AQIFAN	(R)A Q I F A N T/V/D N/A R(I)		142.32	440.5612	1319.67	-0.0012	-0.9	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18646	dirMS_041712_NAR_30mM_minus2.12029.12029.2	2	6.32	0	2.65E+05		(R)IFYDMK	(R)I/F/Y D/M K(V)		119.18	408.702	816.396	0.0007	0.8	5.83	15739.2	9.3	HUMAN	F6RFD5	Destrin
18647	dirMS_041712_NAR_50mM_minus2.11228.11228.3	3	6.32	1	1.21E+05		(R)TVSKVD	(R)T/V/S K/V D D\F L/A N E A K(G)		132.27	512.9329	1536.79	-0.0063	-4.1	4.55	52385	7.18	HUMAN	B4DQJ8	6-phosphogluconate dehydrogenase, decarboxylating
18648	dirMS_041712_NAR_50mM_minus2.12581.12581.3	3	6.32	0	1.06E+06	M114m M:	(R)AGKPVI	(R)A G K\P V I/C A\T Q|m/L E S m I K(K)	C:Carbamidomethylation m:Oxid	139.83	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
18649	dirMS_041712_NAR_50mM_minus2.15467.15467.3	3	6.32	1	2.25E+04		(K)CEFQDA	(K)C E/F Q D A/Y V/L L S E/K K(I)	C:Carbamidomethylation	156.05	577.2917	1729.847	0.014	8.1	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
18650	dirMS_041712_NAR_60mM_minus.10579.10606.3	3	6.32	1	6.53E+05		(K)TAVCDI	(K)T A|V/C D|I/P P R G L K(M)	C:Carbamidomethylation	118.72	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
18651	dirMS_041712_NAR_60mM_minus.13736.13736.3	3	6.32	1	3.15E+04		(R)VFDKDG	(R)V F D K D G N G Y\I/S|A/A E L R(H)		136.6	585.6277	1754.871	-0.0022	-1.3	4.56	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
18652	dirMS_041712_NAR_60mM_minus.6333.6333.3	3	6.32	1	7.12E+04		(R)ATEGM	(R)A T\E/G M V/V A D K N/C S K(I)	C:Carbamidomethylation	94.05	503.9042	1509.704	-0.0055	-3.7	6.11	15607.8	9.99	HUMAN	B4E0P1	Proteasome (Prosome, macropain) subunit, beta type, 7, isoform CRA_b
18653	dirMS_041712_NAR_60mM_minus.9878.9878.3	3	6.32	0	9.07E+04	S17s M19n	(R)LsAmPH	(R)L s A m P H/I/D N D V K(L)	s:N-acetylglucosamine (S) m:	114.9	520.2566	1339.668	219.0878	8.7	5.21	9979.5	10.2	HUMAN	H0YKK3	GMP reductase 2
18654	dirMS_041712_NAR_120mM_plus.13465.13465.4	4	6.32	1	1.27E+06		(K)DKFNEC	(K)D K F N E/C/G H V L Y A D/I K(M)	C:Carbamidomethylation	123.87	452.9713	1808.864	-0.0002	-0.1	5.38	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
18655	dirMS_041712_NAR_50mM_plus2.10726.10726.3	3	6.32	1	8.49E+05		(R)DISTNK	(R)D I/S T N K/V/E Q\I/P Y G E R(I)		124.08	583.6304	1748.881	-0.0047	-2.7	4.68	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
18656	dirMS_041712_NAR_50mM_plus2.12787.12787.3	3	6.32	0	4.95E+05		(R)IMDPNI	(R)I/M/D/P N/I V G/S E H/Y D/V A R(G)		134.63	605.9694	1815.869	0.0242	13.3	4.54	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
18657	dirMS_041712_NAR_50mM_plus2.15587.15587.3	3	6.32	1	1.01E+06		(R)KVPGVT	(R)K\V P G V T A\I E L/D E/D/T/G T F R(I)		149.87	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
18658	dirMS_041712_NAR_50mM_plus2.7206.7206.3	3	6.32	1	7.50E+04		(K)DISTNYY	(K)D I/S T N Y/Y A S/Q/K K(T)		103.52	473.2382	1417.696	0.0043	3	8.43	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
18659	dirMS_041712_NAR_60mM_plus.15250.15250.3	3	6.32	0	8.13E+04		(K)HIGLVYS	(K)H I G L V Y\S G\M/G/P D/Y/R(V)		136.28	522.2648	1564.758	0.0222	14.2	6.74	26012.2	6.92	HUMAN	P25787	Proteasome subunit alpha type-2
18660	dirMS_041712_NAR_60mM_plus.18720.18720.3	3	6.32	1	3.96E+06		(R)VSFELFA	(R)V/S/F E L F A D K V/P K(T)		155.83	460.5914	1379.757	0.0027	2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
18661	dirMS_041712_NAR_60mM_plus.7361.7361.3	3	6.32	0	1.34E+05		(K)ALLQTHI	(K)A L/L Q/T H/P E A Q R(A)		95.23	421.8971	1263.68	-0.0037	-2.9	6.79	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
18662	dirMS_041712_NAR_120mM_minus.16027.16027.4	4	6.31	2	4.07E+05		(K)KQGGLG	(K)K Q G\G L G P M\N I|P L/V S D P K R(T)		141.73	477.5179	1907.053	-0.0034	-1.8	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
18663	dirMS_041712_NAR_120mM_minus.21396.21396.3	3	6.31	0	8.12E+05		(R)LHFFMP	(R)L H\F F M\P\G\F|A/P\L T S R(G)		182.17	540.9497	1620.835	-0.001	-0.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
18664	dirMS_041712_NAR_30mM_minus2.16602.16602.2	2	6.31	0	2.13E+05		(K)MIFVGI	(K)M/I|F/V G\I/K(K)		144.4	404.2383	807.48	-0.0104	-12.9	8.5	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
18665	dirMS_041712_NAR_30mM_minus2.18350.18350.2	2	6.31	0	1.00E+05		(K)SCDFLSS	(K)S C/D F L/S/S\F R(D)	C:Carbamidomethylation	153.87	559.7501	1118.494	-0.0006	-0.5	5.55	42963.5	5.19	HUMAN	P35237	Serpin B6
18666	dirMS_041712_NAR_30mM_minus2.8652.8652.2	2	6.31	0	2.50E+05		(K)LITYGSD	(K)L I|T/Y/G S D R(T)		101.38	462.7452	924.479	0.0046	5	5.83	15838.9	7.03	HUMAN	H0Y5U0	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
18667	dirMS_041712_NAR_40mM_minus2.11447.11447.3	3	6.31	0	4.66E+04		(R)VAPDEH	(R)V A/P D E H P I L/L T E A/P L N/P K(I)		151.97	652.0263	1954.064	-0.0001	0	4.65	42344.8	5.39	HUMAN	Q562R1	Beta-actin-like protein 2
18668	dirMS_041712_NAR_50mM_minus2.10418.10418.3	3	6.31	0	7.23E+04		(R)LTSPIVS	(R)L/T|S/P I V S T H L D/T R(N)		127.37	480.6	1439.785	0.0002	0.1	6.74	58760.2	5.26	HUMAN	Q6ZTN6	Ankyrin repeat domain-containing protein 13D
18669	dirMS_041712_NAR_50mM_minus2.12455.12455.3	3	6.31	0	9.57E+05	M114m M:	(R)AGKPVI	(R)A G K|P V\I\C\A\T\Q m/L E/S m I|K(K)	C:Carbamidomethylation m:Oxid	139.72	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
18670	dirMS_041712_NAR_50mM_minus2.14655.14655.3	3	6.31	0	4.34E+04		(R)IQALEAE	(R)I/Q/A/L E A E L Q/A V S H S K(T)		151.28	541.9562	1623.87	-0.016	-9.9	5.4	167865.2	5.34	HUMAN	Q08378	Golgin subfamily A member 3
18671	dirMS_041712_NAR_50mM_minus2.7042.7042.3	3	6.31	0	1.74E+05		(R)SAEEEA	(R)S A|E E E A A D L/P T K P/T K(I)		106.92	529.6012	1586.791	-0.0018	-1.1	4.41	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
18672	dirMS_041712_NAR_50mM_minus2.7854.7854.3	3	6.31	1	5.68E+04		(R)LGAAPE	(R)L G A\A|P E E/E S A/Y V A G E K R(Q)		111.32	592.9614	1776.876	-0.0066	-3.7	4.5	30276.7	5	HUMAN	F2Z2K0	NSFL1 cofactor p47
18673	dirMS_041712_NAR_60mM_minus.10850.10850.3	3	6.31	1	5.44E+05	M239m	(R)MSMKE	(R)M S M K E V\D E|Q\m/L/N/V Q N K(N)	m:Oxidized methionine	119.9	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
18674	dirMS_041712_NAR_60mM_minus.19961.19961.3	3	6.31	1	8.17E+05		(R)LIALLEVI	(R)L I/A\L/L/E V L/S Q K R(M)		182.02	461.6287	1382.873	-0.0014	-1	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
18675	dirMS_041712_NAR_20mM_plus.12439.12439.2	2	6.31	0	1.76E+05		(K)TIIFVETK	(K)T I|I/F V E T/K(R)		158.85	475.7818	950.556	0.0006	0.6	5.66	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
18676	dirMS_041712_NAR_20mM_plus.17997.17997.2	2	6.31	0	1.53E+05		(R)TVQSLEI	(R)T V/Q S/L/E|I D\L/D S M R(N)		195.12	753.8776	1506.747	0.0011	0.7	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18677	dirMS_041712_NAR_20mM_plus.9684.9684.2	2	6.31	0	1.20E+05		(K)VAGQD	(K)V A G Q|D/G S/V/V Q F K(I)		138.13	617.8225	1234.643	-0.0049	-4	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
18678	dirMS_041712_NAR_40mM_plus2.6469.6469.2	2	6.31	0	1.44E+05		(K)FENLCK	(K)F/E|N/L/C\K(I)	C:Carbamidomethylation	97.68	405.6971	810.381	0.0055	6.8	6	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
18679	dirMS_041712_NAR_50mM_plus2.13966.13966.3	3	6.31	0	1.21E+06		(K)DLAGCI	(K)D L/A/G C I H/G L S N V K(L)	C:Carbamidomethylation	140.62	461.9061	1383.705	-0.0012	-0.8	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
18680	dirMS_041712_NAR_50mM_plus2.19726.19726.3	3	6.31	0	2.60E+05		(R)DFNHIN	(R)D F/N H I N V|E/L|S/L L G K(K)		171.83	533.6223	1598.854	-0.0013	-0.8	5.32	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
18681	dirMS_041712_NAR_50mM_plus2.21393.21393.3	3	6.31	0	8.95E+04		(K)GAEILEV	(K)G A\E/I L E V L/H S L P A V R(Q)		183.4	535.3092	1603.917	-0.0036	-2.2	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
18682	dirMS_041712_NAR_50mM_plus2.7710.7710.3	3	6.31	1	1.36E+05		(R)LGTPELS	(R)L/G/T/P E L/S T A E R K(E)		106.72	434.5738	1301.706	0.0009	0.7	6.14	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
18683	dirMS_041712_NAR_60mM_plus.10041.10041.3	3	6.31	1	9.62E+05		(K)TAVCDI	(K)T A/V/C D I/P P R G L K(M)	C:Carbamidomethylation	110.35	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
18684	dirMS_041712_NAR_60mM_plus.12192.12210.3	3	6.31	1	1.09E+06		(K)AVPREEI	(K)A V|P R E E L F V/T/S K(L)		120.68	459.257	1375.758	-0.0015	-1.1	6.19	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
18685	dirMS_041712_NAR_120mM_minus.17663.17663.3	3	6.3	1	4.53E+05		(R)KVNNAD	(R)K V N N A D D\F|P/N L/F R(Q)		150.25	517.2634	1549.776	-0.0001	-0.1	5.96	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
18686	dirMS_041712_NAR_120mM_minus.19064.19064.4	4	6.3	1	1.74E+05		(R)SLRDLTF	(R)S L R D\L\T/P E/H/L/P L L R(N)		158.88	415.7434	1659.954	-0.0023	-1.4	6.47	38779.2	5.93	HUMAN	Q96C86	m7GpppX diphosphatase
18687	dirMS_041712_NAR_120mM_minus.7049.7049.2	2	6.3	0	4.18E+05		(K)HNAAFC	(K)H/N|A\A/F\C\Y/K(L)	C:Carbamidomethylation	92.42	505.7282	1010.451	-0.0021	-2.1	8.6	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
18688	dirMS_041712_NAR_30mM_minus2.16626.16626.2	2	6.3	0	9.48E+04		(R)GLVGIEF	(R)G L|V/G/I E F K(E)		144.22	431.7497	862.503	-0.0112	-12.9	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
18689	dirMS_041712_NAR_40mM_minus2.14536.14536.3	3	6.3	0	2.23E+05	K102k	(R)DLKPQN	(R)D L\K/P Q N\L\L|I/N E L\G A I/k(L)	k:Ubiquitin-K	169.7	631.6945	1779.037	114.0315	-6	6.07	24556.2	7.95	HUMAN	K7EJ83	Cyclin-dependent kinase 3 (Fragment)
18690	dirMS_041712_NAR_40mM_minus2.7858.7858.3	3	6.3	0	1.94E+05	N611n	(R)ASSYSS	(R)A S\S Y S S V S S T N A S G n W R(T)	n:N-acetylglucosamine (N)	125.23	655.3013	1760.783	203.1059	13.5	8.79	77819.8	8.81	HUMAN	E9PGA7	FERM domain-containing protein 4B
18691	dirMS_041712_NAR_50mM_minus2.10906.10906.3	3	6.3	0	1.79E+05	M35m	(K)AASDIA	(K)A A|S|D I/A m T E L/P P T H P I R(L)	m:Oxidized methionine	130.27	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
18692	dirMS_041712_NAR_50mM_minus2.11245.11245.3	3	6.3	0	1.65E+05		(K)VEADIP	(K)V E/A D I/P G/H/G Q E V L I\R(L)		132.63	544.9596	1632.87	-0.0061	-3.8	4.65	16045.3	7.14	HUMAN	B0QYF8	Myoglobin (Fragment)
18693	dirMS_041712_NAR_50mM_minus2.17908.17908.3	3	6.3	1	1.42E+04		(K)GVPTGF	(K)G V|P/T G F I L P I R D/I R(A)		171.02	518.6444	1553.916	0.0024	1.6	9.6	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
18694	dirMS_041712_NAR_50mM_minus2.8406.8406.3	3	6.3	1	8.27E+04	M61m	(K)NQVAm	(K)N Q|V|A m/N P T N T\V/F D A K/R(L)	m:Oxidized methionine	114.92	607.968	1805.896	15.9932	-1	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
18695	dirMS_041712_NAR_20mM_plus.11653.11653.2	2	6.3	0	1.15E+05	M402m	(R)mAFGA	(R)m A/F/G A/T L D/V/K(T)	m:Oxidized methionine	152.87	534.7743	1052.545	15.9968	1.8	5.59	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
18696	dirMS_041712_NAR_20mM_plus.14652.14652.2	2	6.3	0	8.06E+04		(K)NLYIISV	(K)N L/Y|I/I/S V K(G)		173.1	475.2896	949.572	0.0002	0.2	8.59	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
18697	dirMS_041712_NAR_20mM_plus.15935.15935.2	2	6.3	1	1.35E+05		(K)EALVSQ	(K)E A/L/V S Q\L/S/R G K(Q)		181.18	594.3403	1187.674	-0.0009	-0.8	8.85	224067.5	5.64	HUMAN	Q9UKX2	Myosin-2
18698	dirMS_041712_NAR_20mM_plus.17458.17458.2	2	6.3	0	1.06E+05		(R)FLAVGL	(R)F L/A|V/G/L V\D N T V R(I)		191.72	652.3664	1303.737	-0.0113	-8.7	5.84	136658.9	5.13	HUMAN	Q15393	Splicing factor 3B subunit 3
18699	dirMS_041712_NAR_30mM_plus2.8178.8178.2	2	6.3	0	6.17E+05		(R)STFSTN	(R)S T|F/S/T N Y R(S)		96.22	488.2306	975.453	0.0009	0.9	8.46	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18700	dirMS_041712_NAR_30mM_plus2.8199.8199.2	2	6.3	0	6.17E+05		(R)STFSTN	(R)S/T|F/S/T N Y R(S)		96.22	488.2306	975.453	0.0009	0.9	8.46	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18701	dirMS_041712_NAR_50mM_plus2.10812.10812.3	3	6.3	1	2.12E+05		(K)AQALRD	(K)A Q|A L R D N S T M/G Y M M A K(K)		123.72	596.6125	1787.824	-0.0008	-0.4	8.63	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
18702	dirMS_041712_NAR_50mM_plus2.14330.14330.3	3	6.3	0	3.47E+05		(K)LLGHEVI	(K)L/L/G H E V E D V I/I K(C)		143.48	455.5975	1364.778	-0.0004	-0.3	4.65	125655.3	6.18	HUMAN	Q92900	Regulator of nonsense transcripts 1
18703	dirMS_041712_NAR_50mM_plus2.18153.18153.3	3	6.3	0	2.99E+05		(R)VFITDDF	(R)V F/I T D D F H/D/M M/P K(Y)		164.45	532.581	1595.723	0.0052	3.2	4.41	92752.5	4.76	HUMAN	P14625	Endoplasmin
18704	dirMS_041712_NAR_50mM_plus2.8126.8126.3	3	6.3	0	1.12E+04		(K)ASSEGG	(K)A S/S/E\G/G T A A G A G L/D S\L H K(N)		109.45	543.6023	1628.787	0.0049	3	5.32	41747.8	9.36	HUMAN	O15143	Actin-related protein 2/3 complex subunit 1B
18705	dirMS_041712_NAR_50mM_plus2.9162.9162.3	3	6.3	0	1.91E+05		(K)TAVEHA	(K)T A|V/E/H A T D E D I L/A K(G)		115.42	504.9238	1512.754	0.0028	1.9	4.31	288852.1	5.33	HUMAN	E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein
18706	dirMS_041712_NAR_60mM_plus.20422.20422.3	3	6.3	1	3.02E+05		(R)AQFEGI	(R)A Q/F/E/G I/V T D L I R R(T)		167.4	506.6178	1517.843	-0.0046	-3	6.12	18505.2	10.14	HUMAN	H0YBG6	Stress-70 protein, mitochondrial (Fragment)
18707	dirMS_041712_NAR_120mM_minus.15850.15850.4	4	6.29	1	1.70E+06		(K)QLEAID	(K)Q L E A/I/D Q/L/H/L E Y A K R(A)		140.95	457.499	1826.976	-0.0018	-1	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
18708	dirMS_041712_NAR_120mM_minus.18852.18852.4	4	6.29	1	4.07E+05		(R)HATALEI	(R)H A T A L E|E L/S E/Q/L E Q A K R(F)		158.18	489.0065	1953.004	0.0006	0.3	4.91	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
18709	dirMS_041712_NAR_30mM_minus2.11445.11445.2	2	6.29	0	2.19E+05		(K)ATAVM	(K)A T\A V/M|P D G Q F K(D)		115.47	582.7922	1164.572	0.0054	4.6	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
18710	dirMS_041712_NAR_30mM_minus2.7500.7551.2	2	6.29	0	8.48E+05		(R)FSNISAA	(R)F/S|N/I/S A/A K(A)		95.77	419.2279	837.447	0.002	2.4	8.75	55232.1	8.4	HUMAN	F5H5W3	T-complex protein 1 subunit delta
18711	dirMS_041712_NAR_40mM_minus2.11286.11286.3	3	6.29	0	3.56E+05		(R)TIQVEN	(R)T I|Q\V E N\S H L I|L/T G A G/A L N K(V)		150.33	660.3663	1979.092	-0.0077	-3.9	6.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
18712	dirMS_041712_NAR_50mM_minus2.10875.10875.3	3	6.29	0	1.55E+05		(R)LLELGPK	(R)L L/E/L/G P K P E V A Q Q T R(K)		130.13	560.3182	1678.949	-0.0086	-5.1	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
18713	dirMS_041712_NAR_50mM_minus2.13768.13768.3	3	6.29	0	3.00E+04		(K)TGEEIFG	(K)T\G E\E I/F/G T I G M R P N A/K(N)		146.93	574.2947	1720.869	0.0009	0.5	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
18714	dirMS_041712_NAR_60mM_minus.14283.14283.3	3	6.29	0	4.39E+05	M84m	(K)YPIEHGI	(K)Y/P/I E H G I I|T/N/W D D m E K(I)	m:Oxidized methionine	139.23	659.6373	1960.911	15.9864	-4.3	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
18715	dirMS_041712_NAR_60mM_minus.16002.16002.3	3	6.29	1	3.45E+05		(K)LKLSILYF	(K)L K L S I\L Y/P A T T G/R(N)		149.93	478.2883	1432.852	-0.0019	-1.3	9.99	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
18716	dirMS_041712_NAR_60mM_minus.6212.6212.3	3	6.29	1	2.67E+05		(K)ETEGDV	(K)E T E/G D/V T/S V K D/A/K(I)		92.65	460.2267	1378.67	-0.0041	-3	4.32	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
18717	dirMS_041712_NAR_120mM_plus.17404.17404.3	3	6.29	2	7.61E+05		(R)NLKASLE	(R)N/L/K/A/S L/E/N S L R E V E A R(Y)		143.88	610.332	1828.988	-0.0061	-3.3	6.23	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18718	dirMS_041712_NAR_120mM_plus.6958.6958.3	3	6.29	0	4.69E+05		(K)SQFSDKI	(K)S Q/F/S/D K/P V Q/D R(G)		89.9	436.2209	1306.639	0.0095	7.3	5.68	13194	9.99	HUMAN	E9PI70	Chitinase domain-containing protein 1 (Fragment)
18719	dirMS_041712_NAR_20mM_plus.12036.12036.2	2	6.29	0	3.29E+03	M402m	(R)AFPmPG	(R)A F/P m/P G F D E/H(-)	m:Oxidized methionine	156.07	582.2437	1147.488	15.9924	-2.1	4.35	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
18720	dirMS_041712_NAR_20mM_plus.16850.16850.3	3	6.29	0	3.41E+05		(K)VQIAVA	(K)V Q\I A V A|N\A|Q/E L/L/Q R(M)		187.43	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
18721	dirMS_041712_NAR_20mM_plus.8006.8006.2	2	6.29	0	1.23E+05		(K)YIDQEEL	(K)Y/I/D/Q/E E L/N K(T)		124.7	576.2845	1151.558	0.0038	3.3	4.14	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
18722	dirMS_041712_NAR_40mM_plus2.5708.5708.2	2	6.29	0	1.12E+05		(R)FSSSSGY	(R)F S\S/S S/G/Y/G G/G S S R(V)		90.98	618.2686	1235.529	0.0012	1	8.75	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
18723	dirMS_041712_NAR_50mM_plus2.8966.8966.3	3	6.29	0	5.64E+05		(R)AALAHS	(R)A A L A H S/E E\V T/A/S/Q V\A A T K(T)		113.83	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
18724	dirMS_041712_NAR_60mM_plus.16511.16511.3	3	6.29	0	6.81E+05		(R)IAHPGS	(R)I A|H/P G/S T S/P S A P/W R(D)		142.77	488.5776	1463.739	-0.0207	-14.2	9.75	58853.5	7.77	HUMAN	Q8IXS2-2	Isoform 2 of Coiled-coil domain-containing protein 65
18725	dirMS_041712_NAR_120mM_minus.7462.7462.3	3	6.28	1	6.99E+03		(R)FRTEAA	(R)F R T E A\A|A\A/A/P/Q/R(S)		93.93	430.2279	1288.676	-0.0065	-5.1	9.6	34930.3	9.73	HUMAN	C9JFK9	BAG family molecular chaperone regulator 3 (Fragment)
18726	dirMS_041712_NAR_20mM_minus.12132.12132.3	3	6.28	0	2.19E+05	M73m	(R)AVLVDLI	(R)A V L\V/D L E/P/G T m/D S V/R(S)	m:Oxidized methionine	171.1	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
18727	dirMS_041712_NAR_30mM_minus2.15700.15700.2	2	6.28	0	3.55E+05		(K)EGALDL	(K)E/G/A L/D/L/S/G L R(A)		138.78	515.7847	1030.553	0.0094	9.1	4.37	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
18728	dirMS_041712_NAR_30mM_minus2.19237.19237.2	2	6.28	0	5.07E+05		(K)LALFQAI	(K)L A|L/F/Q A/I/G K(E)		158.9	480.7964	960.588	-0.0022	-2.2	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
18729	dirMS_041712_NAR_40mM_minus2.11150.11150.3	3	6.28	0	3.97E+05		(R)DAGEGL	(R)D A|G E/G L L A|V Q I T/D Q E G K/P K(R)		148.28	657.0157	1969.024	0.0089	4.5	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
18730	dirMS_041712_NAR_40mM_minus2.12133.12133.3	3	6.28	1	9.22E+04		(K)IIVDELK	(K)I/I|V\D E L K/Q\E V/I S T S S K(A)		154.43	597.0023	1788.995	-0.003	-1.7	4.68	30149.5	5.96	HUMAN	D6RAC2	Guanine nucleotide-binding protein subunit beta-2-like 1
18731	dirMS_041712_NAR_40mM_minus2.12875.12875.3	3	6.28	0	3.35E+05		(R)DVQIGD	(R)D V\Q|I/G D I V/T V G E C R P L S K(T)	C:Carbamidomethylation	159.67	662.684	1986.033	0.005	2.5	4.56	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
18732	dirMS_041712_NAR_40mM_minus2.14483.14483.3	3	6.28	0	1.74E+04		(K)SLCIPFKI	(K)S L C\I/P F K/P L C E L Q/P G A K(C)	C:Carbamidomethylation	170.4	653.3446	1958.024	-0.0046	-2.3	8.31	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
18733	dirMS_041712_NAR_50mM_minus2.12564.12564.3	3	6.28	1	2.25E+05	M2709m	(K)ISmPDI	(K)I/S/m|P D I\D L N L K G/P K(V)	m:Oxidized methionine	139.52	519.6148	1540.84	15.9895	-3.5	5.96	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
18734	dirMS_041712_NAR_50mM_minus2.17201.17287.3	3	6.28	1	4.37E+05		(K)GYPPED	(K)G Y/P/P E D I F/N/L V/G K K(V)		166.97	526.2832	1576.837	-0.0019	-1.2	6.07	40763.2	6.29	HUMAN	Q9NR45	Sialic acid synthase
18735	dirMS_041712_NAR_50mM_minus2.17841.17841.3	3	6.28	0	3.04E+05		(K)HNQLPL	(K)H N Q L P\L\V\I\E/F\T E Q T A/P K(I)		170.02	655.6843	1965.044	-0.0057	-2.9	5.4	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
18736	dirMS_041712_NAR_50mM_minus2.7105.7105.3	3	6.28	0	1.43E+05		(K)ISSDLDG	(K)I S/S D/L/D G H P V/P K(Q)		106.93	422.2224	1264.653	-0.0005	-0.4	5.21	63448.4	7.29	HUMAN	B4E022	Transketolase
18737	dirMS_041712_NAR_60mM_minus.11868.11868.3	3	6.28	1	1.98E+05		(R)MLFKDD	(R)M/L/F/K D D Y P/S S/P P K(C)		125.62	508.9172	1524.74	-0.0032	-2.1	5.71	20685.4	9.18	HUMAN	B0QYN7	SUMO-conjugating enzyme UBC9
18738	dirMS_041712_NAR_60mM_minus.15425.15425.3	3	6.28	0	1.81E+05		(K)LKPQYLE	(K)L K\P Q Y\L/E E\L/P G Q L K(Q)		146.05	552.6501	1655.937	-0.0009	-0.6	6.14	27015.5	5.37	HUMAN	P21266	Glutathione S-transferase Mu 3
18739	dirMS_041712_NAR_60mM_minus.17131.17131.3	3	6.28	0	1.31E+04	M400m	(K)LCHLLG	(K)L C/H\L L/G M\N|V/m/E F T R(A)	C:Carbamidomethylation m:Oxid	155.48	579.614	1720.833	15.9943	-0.4	6.75	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
18740	dirMS_041712_NAR_60mM_minus.7122.7122.3	3	6.28	1	2.74E+05		(R)IVDGKV	(R)I/V|D G K V/V S E T N D T K(V)		97.95	502.2642	1504.785	-0.0073	-4.8	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
18741	dirMS_041712_NAR_20mM_plus.10799.10799.2	2	6.28	0	8.05E+03		(R)LAEVEA	(R)L/A|E/V E A/A L E K(Q)		146.92	536.7941	1072.589	-0.0075	-7	4.25	533778	5.74	HUMAN	Q15149	Plectin
18742	dirMS_041712_NAR_20mM_plus.14853.14853.2	2	6.28	0	1.45E+05		(K)VLEQLT	(K)V L E Q|L|T/G\Q/T\P V F S K(A)		174.65	773.9244	1546.848	-0.006	-3.9	5.97	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
18743	dirMS_041712_NAR_20mM_plus.15720.15720.3	3	6.28	0	8.77E+03		(R)SSFYVN	(R)S S\F Y V N G/L/T/L/G G Q K(C)		179.37	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)

18744	dirMS_041712_NAR_20mM_plus.16040.16040.2	2	6.28	0	4.77E+04		(K)DAGTIA	(K)D A G T/I|A/G L\N V L R(I)		182.22	600.3422	1199.674	0.0029	2.4	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
18745	dirMS_041712_NAR_20mM_plus.18117.18117.2	2	6.28	0	9.83E+04		(R)APGSGL	(R)A/P G S/G L A L L/P L/K(I)		196.67	568.8548	1136.704	-0.0014	-1.3	8.8	266161	5.68	HUMAN	E9PPU0	Epiplakin
18746	dirMS_041712_NAR_30mM_plus2.4288.4288.2	2	6.28	0	4.48E+05	M558m	(R)mGANN	(R)m/G A/N N L/E/R(M)	m:Oxidized methionine	70.28	460.7158	904.431	15.9938	-1.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
18747	dirMS_041712_NAR_40mM_plus2.16245.16245.3	3	6.28	0	2.72E+05		(K)VAIVKP	(K)V A I\V K/P G V|P M/E I V/L N K(E)		161.6	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
18748	dirMS_041712_NAR_50mM_plus2.20269.20269.3	3	6.28	0	2.23E+05		(K)GHVDIL	(K)G H\V D I L A|P|T V Q E L A/A/L E K(E)		174.7	635.3536	1904.049	-0.0025	-1.3	4.65	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
18749	dirMS_041712_NAR_50mM_plus2.7757.7757.3	3	6.28	1	9.77E+04		(R)EFEDPR	(R)E F E D P R D A/P/P/P T R(A)		106.6	509.5779	1526.723	-0.0042	-2.8	4.32	51612.9	9.98	HUMAN	P08621	U1 small nuclear ribonucleoprotein 70 kDa
18750	dirMS_041712_NAR_50mM_plus2.7963.7963.3	3	6.28	0	6.93E+04		(K)QEYDES	(K)Q E/Y/D E/S G P S I/V/H R(K)		108.3	506.2382	1516.703	-0.0026	-1.7	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
18751	dirMS_041712_NAR_20mM_minus.12317.12317.2	2	6.27	0	1.34E+05		(K)LVSIGAE	(K)L V/S|I G A/E/E I V/D G N A K(M)		171.68	757.9044	1514.806	-0.0045	-3	4.14	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
18752	dirMS_041712_NAR_20mM_minus.13623.13623.2	2	6.27	0	2.17E+05		(K)LGGSAV	(K)L G G S A V I|S L\E G K|P L(-)		187.83	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
18753	dirMS_041712_NAR_20mM_minus.7602.7602.2	2	6.27	0	8.81E+05	M239m	(K)EVDEQ	(K)E V/D E Q\m L N|V/Q/N K(N)	m:Oxidized methionine	124.58	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
18754	dirMS_041712_NAR_50mM_minus2.15069.15069.3	3	6.27	1	2.43E+05		(K)LALDIEI	(K)L A/L/D I/E/I/A T Y R K(L)		154.08	469.2729	1405.805	-0.0008	-0.6	6.07	49564	5.84	HUMAN	E9PAX3	Glial fibrillary acidic protein
18755	dirMS_041712_NAR_50mM_minus2.8425.8425.3	3	6.27	1	8.32E+04		(K)NVSEEL	(K)N V|S E E L D R T/P P E V/S K(K)		115.85	567.289	1699.85	0.0027	1.6	4.41	136658.9	5.13	HUMAN	Q15393	Splicing factor 3B subunit 3
18756	dirMS_041712_NAR_60mM_minus.6539.6539.3	3	6.27	1	9.46E+04	M436m	(R)TPGKEA	(R)T/P|G K E A V/A m/E/S Y A K(A)	m:Oxidized methionine	95.08	499.9146	1481.73	15.9988	2.6	5.81	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
18757	dirMS_041712_NAR_120mM_plus.25680.25680.3	3	6.27	1	4.77E+05		(R)GVMLA	(R)G V/M/L/A V/D A V/I A E L K K(Q)		193.27	519.6402	1556.908	-0.002	-1.3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
18758	dirMS_041712_NAR_20mM_plus.10931.10931.2	2	6.27	0	1.25E+05		(K)LAEYVIT	(K)L A/E/Y V I T K(S)		148.32	468.7674	936.54	-0.0125	-13.4	6	236508.3	9.06	HUMAN	E7EUA9	Neuron navigator 3
18759	dirMS_041712_NAR_20mM_plus.13187.13187.2	2	6.27	0	9.22E+04		(R)VCEEIAII	(R)V C|E E I A\I\I|P S/K(K)	C:Carbamidomethylation	163.3	629.8346	1258.671	-0.0092	-7.3	4.53	21927.8	9.55	HUMAN	H0YK46	40S ribosomal protein S17 (Fragment)
18760	dirMS_041712_NAR_20mM_plus.17715.17715.2	2	6.27	0	1.56E+05		(R)SLVPAA	(R)S L\V/P A/A/E L L E S R(V)		194.3	642.8613	1284.716	-0.0005	-0.4	4.53	533778	5.74	HUMAN	Q15149	Plectin
18761	dirMS_041712_NAR_20mM_plus.18105.18105.2	2	6.27	0	3.31E+04		(R)FGFPEG	(R)F G/F|P/E|G S/V E L Y A E K(V)		196.17	786.889	1572.758	0.0127	8.1	4.25	18529.2	9.98	HUMAN	E9PL45	40S ribosomal protein S3
18762	dirMS_041712_NAR_30mM_plus2.5675.5675.2	2	6.27	0	2.22E+04		(R)QSSGAS	(R)Q S|S\G A|S/S|S S F/S S S R(A)		83.57	681.3013	1361.593	0.0025	1.9	9.75	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
18763	dirMS_041712_NAR_30mM_plus2.8553.8553.2	2	6.27	0	8.70E+05		(K)LAAAAN	(K)L A/A/A A/N C/Q V S K(V)	C:Carbamidomethylation	98.07	566.7922	1132.578	-0.0008	-0.7	8.75	94032.2	9.06	HUMAN	Q9H2F5	Enhancer of polycomb homolog 1
18764	dirMS_041712_NAR_40mM_plus2.10279.10279.2	2	6.27	0	1.32E+05		(R)QINLSNI	(R)Q\I|N/L/S|N I/R(A)		125.02	479.2747	957.548	-0.0055	-5.7	9.75	102679.8	6.75	HUMAN	Q7KZF4	Staphylococcal nuclease domain-containing protein 1
18765	dirMS_041712_NAR_50mM_plus2.19902.19946.3	3	6.27	0	8.05E+05		(K)LNEHFL	(K)L N E H F L\N\T T/D/F/L D T I/K(S)		173.27	640.9957	1920.97	0.0024	1.2	4.54	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
18766	dirMS_041712_NAR_50mM_plus2.7775.7775.3	3	6.27	1	1.36E+05		(R)LGTPELS	(R)L G/T|P E\L/S T A E R K(E)		106.72	434.5738	1301.706	0.0009	0.7	6.14	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
18767	dirMS_041712_NAR_60mM_plus.12522.12522.3	3	6.27	1	3.54E+06		(K)VKLEAEI	(K)V K|L E A E|I\A/T Y R(R)		122.98	431.5782	1292.721	-0.0008	-0.6	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18768	dirMS_041712_NAR_60mM_plus.15735.15735.3	3	6.27	0	3.40E+05		(R)VWYVSN	(R)V W|Y\V/S N I D G T/H I A K(T)		139.45	534.9464	1602.828	-0.0028	-1.8	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
18769	dirMS_041712_NAR_60mM_plus.18627.18627.3	3	6.27	1	1.44E+05		(R)CRVDLP	(R)C R V D\L|P|L A V/L S K(M)	C:Carbamidomethylation	154.48	457.599	1370.782	0	0	8.75	7765.6	8.23	HUMAN	H3BSA6	dCTP pyrophosphatase 1
18770	dirMS_041712_NAR_60mM_plus.9703.9703.3	3	6.27	0	9.53E+05		(K)GHENVE	(K)G H\E N\V\E A\A|Q/A/E Y/I/E K(F)		107.98	563.2692	1687.792	0.0008	0.5	4.48	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
18771	dirMS_041712_NAR_120mM_minus.11208.11208.3	3	6.26	1	2.09E+04		(K)KYEFGES	(K)K Y E F\G E/S D/L/R(S)		116.38	415.2091	1243.595	0.0174	14	4.68	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
18772	dirMS_041712_NAR_120mM_minus.5382.5382.3	3	6.26	1	3.38E+05		(R)NYDGKN	(R)N/Y/D/G K N N Y/P K(A)		82.78	404.8637	1212.564	0.0122	10	8.43	51084.6	5.75	HUMAN	F5H6V2	Phosphoglucomutase-2
18773	dirMS_041712_NAR_20mM_minus.13531.13531.2	2	6.26	0	4.35E+05		(K)DAGTIA	(K)D A G T|I/A G L N V L R(I)		185.3	600.3403	1199.674	-0.0009	-0.8	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
18774	dirMS_041712_NAR_30mM_minus2.11932.11932.2	2	6.26	0	3.79E+05		(K)MTISQQ	(K)M T|I/S Q/Q/E F/G R(T)		118.03	598.7911	1196.573	0.0021	1.7	5.75	21119.9	4.34	HUMAN	H0Y3Y9	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
18775	dirMS_041712_NAR_50mM_minus2.10993.10993.3	3	6.26	1	8.29E+04		(K)LIPDSIG	(K)L I|P/D S/I G K D I E K(A)		130.92	443.2546	1327.747	0.0025	1.9	4.56	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
18776	dirMS_041712_NAR_50mM_minus2.11880.11880.3	3	6.26	0	1.72E+04	M425m M	(R)VFITDDF	(R)V F/I|T D D F H D m m P K(Y)	m:Oxidized methionine	135.92	543.2416	1595.723	31.987	-1.7	4.41	92752.5	4.76	HUMAN	P14625	Endoplasmin
18777	dirMS_041712_NAR_50mM_minus2.13218.13218.3	3	6.26	1	2.73E+04		(K)VVSSSIV	(K)V V/S S S\I V/D K Y I/G E S A R(L)		142.6	570.6413	1709.907	0.0025	1.5	6.04	29938.9	6.07	HUMAN	H0YJC0	26S protease regulatory subunit 10B (Fragment)
18778	dirMS_041712_NAR_20mM_plus.15704.15704.2	2	6.26	0	1.02E+05		(K)SILFVPT	(K)S I L/F/V/P T S|A P R(G)		180	594.3403	1187.678	-0.005	-4.2	9.47	92752.5	4.76	HUMAN	P14625	Endoplasmin
18779	dirMS_041712_NAR_30mM_plus2.16033.16033.2	2	6.26	0	3.90E+05		(K)GVLFYG	(K)G V L|F|Y/G/P P/G C G K(T)	C:Carbamidomethylation	137.08	626.3175	1251.619	0.0087	6.9	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
18780	dirMS_041712_NAR_30mM_plus2.17251.17251.2	2	6.26	0	4.07E+05	M256m	(R)SLDmDS	(R)S/L|D m D S/I I|A E/V K(A)	m:Oxidized methionine	142.7	668.8384	1320.671	15.998	2.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
18781	dirMS_041712_NAR_30mM_plus2.17738.17738.2	2	6.26	0	2.19E+05		(R)YCAQDA	(R)Y C|A\Q/D A/F/F/Q V K(E)	C:Carbamidomethylation	146.07	688.8174	1376.63	-0.0028	-2.1	5.83	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
18782	dirMS_041712_NAR_30mM_plus2.8534.8534.2	2	6.26	0	9.40E+05		(R)ALANSL	(R)A L|A/N/S/L A C Q G K(Y)	C:Carbamidomethylation	98	566.7922	1132.578	-0.0008	-0.7	8.8	13951.6	9.48	HUMAN	H3BR68	Fructose-bisphosphate aldolase A (Fragment)
18783	dirMS_041712_NAR_40mM_plus2.10324.10324.2	2	6.26	0	9.40E+04		(K)IGGIGTV	(K)I/G/G\I/G T/V/P V G R(V)		125.75	513.3081	1025.61	-0.0013	-1.2	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
18784	dirMS_041712_NAR_40mM_plus2.14170.14170.3	3	6.26	0	1.13E+05		(R)LVLEVA	(R)L V|L/E V A Q H L G E/S T V/R(T)		149.35	550.9762	1650.917	-0.0033	-2	5.4	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
18785	dirMS_041712_NAR_40mM_plus2.5402.5402.2	2	6.26	0	6.51E+04		(K)MGGDI	(K)M/G G D/I|A N R(V)		88.98	417.1996	833.393	-0.0015	-1.8	5.59	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
18786	dirMS_041712_NAR_50mM_plus2.22265.22265.3	3	6.26	1	1.35E+06		(K)EGGLGP	(K)E G G L/G/P L/N I P L L A D V T R R(L)		191	631.029	1891.076	-0.0035	-1.9	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
18787	dirMS_041712_NAR_60mM_plus.14874.14874.3	3	6.26	1	1.45E+05		(R)ARICCD	(R)A R I\C\C D|L/D/V/L A/S K(K)	C:Carbamidomethylation	134.32	507.5883	1520.756	-0.0056	-3.7	6	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
18788	dirMS_041712_NAR_20mM_minus.10352.10352.2	2	6.25	0	4.57E+04	M145m	(R)VVLFEm	(R)V V|L|F/E m E/A/R(K)	m:Oxidized methionine	152.52	555.2868	1093.571	15.9953	0.3	4.53	27142.4	5.34	HUMAN	E5RG68	Copine-3 (Fragment)
18789	dirMS_041712_NAR_20mM_minus.12665.12665.3	3	6.25	0	1.85E+05	M73m	(R)AVLVDL	(R)A V/L\V D\L E/P G/T|m D/S V R(S)	m:Oxidized methionine	174.95	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
18790	dirMS_041712_NAR_30mM_minus2.5565.5565.2	2	6.25	0	9.01E+04		(K)DSYVGD	(K)D S Y|V/G D/E A Q S K(R)		84.13	599.7632	1198.522	-0.0031	-2.6	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
18791	dirMS_041712_NAR_30mM_minus2.8749.8749.2	2	6.25	0	1.78E+05		(K)EANEIL	(K)E A|N/E/I/L Q/R(S)		102.45	486.7596	972.511	0.001	1.1	4.53	64718.1	6.56	HUMAN	A4D0Z6	Inosine-5'-monophosphate dehydrogenase
18792	dirMS_041712_NAR_50mM_minus2.10926.10926.3	3	6.25	0	1.01E+05		(R)FVPQE	(R)F V/P Q E M/G V/H/T V S V/K(Y)		130.78	519.9402	1557.809	-0.0033	-2.1	6.75	258215.9	5.48	HUMAN	E7EN95	Filamin-B
18793	dirMS_041712_NAR_50mM_minus2.11282.11282.3	3	6.25	0	2.24E+05		(K)QADLYIS	(K)Q A D L/Y/I/S E/G L/H/P R(I)		132.08	500.2598	1498.765	0	0	5.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
18794	dirMS_041712_NAR_50mM_minus2.7342.7342.3	3	6.25	0	1.36E+04		(K)ASSEGG	(K)A S S/E G G\T A A G A G L D/S L H/K(N)		108.88	543.5973	1628.787	-0.0101	-6.2	5.32	41747.8	9.36	HUMAN	O15143	Actin-related protein 2/3 complex subunit 1B
18795	dirMS_041712_NAR_60mM_minus.6791.6791.3	3	6.25	1	5.76E+04	M372m M	(R)LQDEIQ	(R)L/Q/D E/I Q/N m K E E m A R(H)	m:Oxidized methionine	96.48	589.6068	1734.815	31.9909	0.6	4.41	49709.6	5.19	HUMAN	B0YJC4	Vimentin
18796	dirMS_041712_NAR_120mM_plus.12504.12504.4	4	6.25	0	1.03E+06		(R)EQHLA	(R)E Q H L A Q L/Q Q/L/Q/Q M H Q K(Q)		118.27	497.7567	1988.013	-0.0081	-4.1	7.01	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
18797	dirMS_041712_NAR_20mM_plus.10210.10210.2	2	6.25	0	6.33E+04		(K)GYDVIA	(K)G Y D\V/I/A\Q|A Q S G T G K(T)		142.97	697.846	1394.691	-0.0063	-4.5	5.83	16071.1	4.8	HUMAN	B4E102	Eukaryotic initiation factor 4A-I
18798	dirMS_041712_NAR_20mM_plus.15787.15787.2	2	6.25	0	4.98E+03		(R)SSFYVN	(R)S S F/Y|V N/G L T\L G G Q/K(C)		180.83	735.8818	1470.759	-0.0024	-1.6	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
18799	dirMS_041712_NAR_20mM_plus.8095.8095.2	2	6.25	0	1.63E+04		(K)TAVCDI	(K)T A/V/C/D|I/P\P R(G)	C:Carbamidomethylation	124.18	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
18800	dirMS_041712_NAR_30mM_plus2.20180.20180.2	2	6.25	0	3.58E+04		(R)TLMNLG	(R)T L|M/N L/G G L A/V/A R(D)		159.42	608.3434	1215.688	-0.0083	-6.8	9.41	22562.2	8.8	HUMAN	P37802	Transgelin-2
18801	dirMS_041712_NAR_30mM_plus2.21595.21595.2	2	6.25	0	9.29E+03		(K)TFLLAG	(K)T F/L/L A G|D|A/Q A E G K(D)		167.27	660.8437	1320.679	0.0007	0.5	4.37	417596.9	8.88	HUMAN	H3BS19	Zinc finger protein 469
18802	dirMS_041712_NAR_40mM_plus2.10457.10457.2	2	6.25	1	2.20E+04		(K)KITIADC	(K)K\I\T I A\D\C\G Q|L|E(-)	C:Carbamidomethylation	126.42	624.3146	1247.63	-0.0081	-6.5	4.75	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
18803	dirMS_041712_NAR_50mM_plus2.13817.13817.3	3	6.25	1	4.72E+05		(R)SILKIDD	(R)S I L K/I D D\V/V/N T R(-)		140.55	458.2605	1372.78	-0.0125	-9.1	5.68	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
18804	dirMS_041712_NAR_60mM_plus.11731.11731.3	3	6.25	0	2.77E+05		(K)VAKPVV	(K)V A K P V V E|M/D/G/D/E M T R(I)		118.25	559.6022	1676.798	-0.0062	-3.7	4.32	35557.8	9.19	HUMAN	H0YL11	Isocitrate dehydrogenase [NADP], mitochondrial
18805	dirMS_041712_NAR_60mM_plus.5692.5692.3	3	6.25	0	1.90E+06	M21m	(R)SGSmD	(R)S G S/m D\P/S G A/H/P S V R(Q)	m:Oxidized methionine	87.5	467.5464	1384.627	15.9973	1.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
18806	dirMS_041712_NAR_120mM_minus.12866.12866.3	3	6.24	0	2.36E+05		(K)TFTAWC	(K)T F/T\A W/C/N S/H L R(K)	C:Carbamidomethylation	123.65	464.8871	1392.648	-0.001	-0.7	9.44	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
18807	dirMS_041712_NAR_20mM_minus.11087.11087.2	2	6.24	0	2.13E+05		(K)LSELEAA	(K)L S E|L/E A/A/L Q/R(A)		159.25	565.3134	1129.621	-0.0016	-1.5	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
18808	dirMS_041712_NAR_30mM_minus2.19103.19103.2	2	6.24	0	4.66E+04		(R)YLTVAA	(R)Y L/T V A A\V F R(G)		159.13	520.2998	1039.593	-0.0012	-1.1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
18809	dirMS_041712_NAR_40mM_minus2.14386.14386.3	3	6.24	2	2.00E+05	S46s	(K)LEsTRTT	(K)L E|s T R/T T V R T G|L D L K(A)	s:N-acetylglucosamine (S)	169.45	631.6945	1689.949	203.1196	21.2	8.75	15919.3	9.57	HUMAN	C9J3I4	Protein-tyrosine sulfotransferase 1 (Fragment)
18810	dirMS_041712_NAR_40mM_minus2.8175.8175.3	3	6.24	1	4.65E+04		(R)DVVICP	(R)D V|V\I C P/D A S L E D A K K(E)	C:Carbamidomethylation	128.47	553.9467	1659.826	-0.0003	-0.2	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
18811	dirMS_041712_NAR_50mM_minus2.13095.13095.3	3	6.24	1	4.46E+03		(R)VEVERD	(R)V E|V E R D N\L/A E D I M/R(L)		141.97	563.613	1688.827	-0.0028	-1.6	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
18812	dirMS_041712_NAR_50mM_minus2.17318.17318.3	3	6.24	0	1.23E+05		(K)VHLVGI	(K)V H L\V G I/D/I F/T/G K(K)		167.63	433.5856	1298.747	-0.0045	-3.4	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
18813	dirMS_041712_NAR_60mM_minus.18604.18604.3	3	6.24	1	3.27E+04		(R)VYEFLD	(R)V Y E/F L/D/K L D V V R(S)		165.28	499.2763	1495.815	-0.0012	-0.8	4.56	41296.9	9.52	HUMAN	B4DT72	26S proteasome non-ATPase regulatory subunit 3
18814	dirMS_041712_NAR_60mM_minus.8771.8771.3	3	6.24	0	2.65E+05	S126s	(K)IAVsLNY	(K)I A/V s L/N/Y F K(I)	s:N-acetylglucosamine (S)	108.92	419.8951	1054.593	203.0776	-1.4	8.59	16194.4	9.92	HUMAN	E7EVQ5	Collagen triple helix repeat-containing protein 1
18815	dirMS_041712_NAR_20mM_plus.15923.15923.2	2	6.24	0	3.47E+05	M81m	(K)SFYPEEV	(K)S F/Y/P/E E V/S S m V L T K(M)	m:Oxidized methionine	180.75	816.8988	1616.788	16.0027	4.8	4.53	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
18816	dirMS_041712_NAR_20mM_plus.19218.19218.2	2	6.24	0	8.08E+04		(R)ASVILA	(R)A S V I/L/A/G L G F/T P K(M)		204.25	637.3763	1273.751	-0.0061	-4.8	8.8	80142.6	5.95	HUMAN	Q9NUQ8	ATP-binding cassette sub-family F member 3
18817	dirMS_041712_NAR_20mM_plus.7454.7454.2	2	6.24	0	1.59E+05		(K)VLTPTQ	(K)V/L/T/P/T Q V K(N)		120.83	443.2734	885.54	-0.0009	-1	8.72	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
18818	dirMS_041712_NAR_30mM_plus2.13069.13069.2	2	6.24	0	6.45E+05		(R)GVVGPE	(R)G V\V/G|P E/L Y G R(L)		122.37	523.7794	1046.563	-0.0114	-10.9	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
18819	dirMS_041712_NAR_30mM_plus2.19471.19471.2	2	6.24	0	1.78E+05		(K)CALDFF	(K)C/A/L/D F/F R(Q)	C:Carbamidomethylation	155.82	464.7242	928.434	0.0066	7.1	5.84	15387.4	6.92	HUMAN	F5H7V7	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8
18820	dirMS_041712_NAR_40mM_plus2.15718.15718.3	3	6.24	1	5.12E+04		(R)IILPPEKE	(R)I I/L/P/P E K E\L A M/P G E D L K(F)		158.48	631.6874	1893.04	0.0075	4	4.41	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
18821	dirMS_041712_NAR_40mM_plus2.6866.6866.2	2	6.24	0	7.56E+04		(R)TALLGG	(R)T A|L/L/G|G G Q R(R)		99.97	436.7494	872.495	-0.0033	-3.8	9.41	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
18822	dirMS_041712_NAR_40mM_plus2.8231.8231.2	2	6.24	0	1.97E+05		(R)AVVIVD	(R)A V|V I/V/D/D R(G)		108.32	443.7528	886.499	-0.0009	-1.1	4.21	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
18823	dirMS_041712_NAR_50mM_plus2.10321.10321.3	3	6.24	1	5.90E+05		(K)YGEPGE	(K)Y/G E/P G/E V/F I N K G K(G)		121.75	479.9177	1437.737	0.0013	0.9	6.14	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
18824	dirMS_041712_NAR_60mM_plus.20205.20205.3	3	6.24	1	4.80E+04		(K)LLEPVLL	(K)L L E/P V L L|L G K E R(F)		165.78	460.6254	1379.862	-0.0004	-0.3	6.14	16559.1	10.36	HUMAN	P62249	40S ribosomal protein S16
18825	dirMS_041712_NAR_60mM_plus.6866.6866.2	2	6.24	0	2.45E+05		(R)MEELHN	(R)M E|E/L\H|N Q\E M\Q\K(R)		94.28	708.8155	1416.625	-0.0009	-0.6	4.75	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
18826	dirMS_041712_NAR_60mM_plus.8703.8703.3	3	6.24	1	5.70E+05		(R)SSGGSY	(R)S S|G G S Y R D S Y/D/S/Y/A/T H N E(-)		104.62	665.9403	1995.795	0.0112	5.6	4.81	18647.7	9.51	HUMAN	Q14011	Cold-inducible RNA-binding protein
18827	dirMS_041712_NAR_120mM_minus.6529.6529.3	3	6.23	1	8.83E+05		(R)TEERAE	(R)T/E/E R A/E|L/A E S R(C)		89.17	430.8806	1290.628	-0.0012	-0.9	4.49	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
18828	dirMS_041712_NAR_20mM_minus.11694.11694.2	2	6.23	0	4.13E+05		(R)GALQNI	(R)G/A L/Q N|I/I\P A S T G A A K(A)		165.08	706.3976	1411.79	-0.0024	-1.7	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
18829	dirMS_041712_NAR_20mM_minus.12532.12532.2	2	6.23	0	6.59E+04		(K)LLGELL	(K)L L/G E L\L Q/D/N\A K(L)		173.45	607.3406	1213.679	-0.0048	-3.9	4.37	35556.4	9.3	HUMAN	F2Z393	Transaldolase
18830	dirMS_041712_NAR_30mM_minus2.5022.5022.2	2	6.23	0	3.29E+05		(R)TDTGEP	(R)T D|T|G E\P M G R(G)		81.02	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
18831	dirMS_041712_NAR_40mM_minus2.15735.15735.3	3	6.23	1	3.01E+05		(R)LGSAIQ	(R)L G/S A I Q K I/I/T I\P A A L Q Q V/K(N)		183.05	664.7423	1992.222	-0.0092	-4.6	10	265720.8	6.08	HUMAN	E7ETS8	DNA polymerase
18832	dirMS_041712_NAR_50mM_minus2.10290.10290.3	3	6.23	0	1.66E+05		(K)LQAEAP	(K)L Q|A E A P H/I/V V/G T/P G R(V)		127.08	515.6179	1544.854	-0.0152	-9.8	6.75	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
18833	dirMS_041712_NAR_50mM_minus2.13262.13262.3	3	6.23	0	1.14E+05		(K)SLLGDS	(K)S L|L/G D S\A/P T L H L N\K(G)		143.43	489.2711	1465.801	-0.0022	-1.5	6.46	56697.4	9.15	HUMAN	B8ZZY2	Arf-GAP domain and FG repeat-containing protein 1
18834	dirMS_041712_NAR_60mM_minus.11405.11429.3	3	6.23	1	9.32E+04		(R)EIAQDF	(R)E I|A/Q D F K T D/L R(F)		123.83	445.9007	1335.69	-0.0028	-2.1	4.56	14166.5	11.62	HUMAN	B4DEB1	Histone H3
18835	dirMS_041712_NAR_120mM_plus.8564.8564.3	3	6.23	0	8.62E+05		(K)QHTFVE	(K)Q H T F V/E/T E/S V/R(Y)		97.78	444.8857	1332.654	-0.0117	-8.8	5.4	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
18836	dirMS_041712_NAR_20mM_plus.11423.11423.2	2	6.23	0	2.40E+05		(K)VGLQVV	(K)V/G\L/Q/V V A V/K(A)		151.27	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
18837	dirMS_041712_NAR_20mM_plus.15784.15784.2	2	6.23	0	2.73E+05		(K)VGINYQ	(K)V G I N Y Q/P P T\V\V/P G G D L A K(V)		179.2	912.9952	1824.985	-0.0023	-1.3	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
18838	dirMS_041712_NAR_20mM_plus.17024.17024.3	3	6.23	0	2.28E+05		(K)VQIAVA	(K)V Q\I A V A N/A\Q E/L/L Q/R(M)		188.18	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
18839	dirMS_041712_NAR_30mM_plus2.19368.19384.2	2	6.23	0	2.30E+04		(K)NQALFP	(K)N Q|A/L/F/P A C V\L K(N)	C:Carbamidomethylation	155.17	630.8399	1260.677	-0.0044	-3.5	8.75	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
18840	dirMS_041712_NAR_30mM_plus2.6324.6324.2	2	6.23	0	4.35E+04		(K)NQCTQ	(K)N/Q/C T/Q V V\Q/E R(E)	C:Carbamidomethylation	87.68	631.3039	1261.595	0.0052	4.1	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
18841	dirMS_041712_NAR_40mM_plus2.7332.7332.2	2	6.23	0	1.54E+05		(R)SGYFDE	(R)S G/Y/F D/E/R(Y)		103.57	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
18842	dirMS_041712_NAR_50mM_plus2.11525.11525.3	3	6.23	1	6.51E+05		(R)DVVICP	(R)D V|V/I C/P D A S L E D A K K(E)	C:Carbamidomethylation	127.98	553.9467	1659.826	-0.0003	-0.2	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
18843	dirMS_041712_NAR_50mM_plus2.17145.17145.3	3	6.23	1	4.36E+05		(K)ISMPDI	(K)I/S/M/P D I/D/L N L K/G P K(V)		157.45	514.2847	1540.84	-0.0008	-0.5	5.96	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
18844	dirMS_041712_NAR_60mM_plus.15978.15978.3	3	6.23	0	2.82E+05		(K)NFDLRP	(K)N\F/D/L/R P G V I V R(-)		140.07	429.248	1285.738	-0.0081	-6.3	9.6	33192.3	6.77	HUMAN	B4DN45	S-adenosylmethionine synthase
18845	dirMS_041712_NAR_60mM_plus.17405.17405.3	3	6.23	1	7.09E+05		(R)LKDLEA	(R)L K D L E|A|L/L|N S K(E)		147.93	415.2483	1243.726	0.0047	3.8	6.07	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
18846	dirMS_041712_NAR_60mM_plus.8761.8761.3	3	6.23	0	1.10E+06		(K)VDNDEN	(K)V/D N/D/E N E/H Q/L/S L R(T)		102.95	523.5814	1568.73	-0.0003	-0.2	4.31	6862.5	4.32	HUMAN	E5RGW4	Nucleophosmin (Fragment)
18847	dirMS_041712_NAR_60mM_plus.9409.9409.2	2	6.23	0	1.27E+06		(K)STAGDT	(K)S T A/G D T|H\L\G/G E/D\F/D\N/R(M)		107.4	846.3654	1691.726	-0.0021	-1.2	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
18848	dirMS_041712_NAR_60mM_plus.9545.9545.3	3	6.23	0	7.11E+05		(K)VQQAEL	(K)V Q|Q A E L/H/T\G S L P R(I)		107.58	479.2585	1435.765	-0.0043	-3	6.72	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
18849	dirMS_041712_NAR_20mM_minus.14531.14531.3	3	6.22	0	5.23E+03		(K)VVVQVL	(K)V V V Q V\L/A E E/P E A V L K(G)		199.73	541.6469	1622.936	-0.0102	-6.3	4.26	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
18850	dirMS_041712_NAR_30mM_minus2.11462.11462.2	2	6.22	0	1.36E+05		(K)CGDLVF	(K)C/G\D L/V F/A/K(M)	C:Carbamidomethylation	115.57	455.2306	909.45	0.0041	4.5	5.84	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
18851	dirMS_041712_NAR_30mM_minus2.14447.14447.2	2	6.22	0	7.41E+05		(R)GLLEDV	(R)G L/L/E/D/V Q E/G R(T)		131.22	558.2882	1115.569	0	0	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
18852	dirMS_041712_NAR_30mM_minus2.5408.5408.2	2	6.22	0	1.70E+05		(K)YIDENQ	(K)Y I/D E N/Q D R(Y)		83.65	526.7389	1052.464	0.0062	5.9	4.03	6412.4	9.52	HUMAN	J3KSS4	Cytosolic non-specific dipeptidase (Fragment)

18853	dirMS_041712_NAR_30mM_minus2.5798.5798.3	3	6.22	0	7.94E+04		(R)NQGGY(	(R)N Q\G G Y G G S S S S/S/S/Y/G S G R(R)		85.28	565.5709	1694.7	-0.0019	-1.1	8.59	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
18854	dirMS_041712_NAR_30mM_minus2.6846.6846.2	2	6.22	0	2.48E+04		(R)FYAGGS	(R)F Y/A/G G S E/R(S)		91.48	443.7069	886.405	0.0012	1.3	6	30276.7	5	HUMAN	F2Z2K0	NSFL1 cofactor p47
18855	dirMS_041712_NAR_50mM_minus2.11031.11031.3	3	6.22	1	3.92E+05		(R)VVDLM/	(R)V/V|D\L M/A\H M A S K/E(-)		131.4	444.2213	1330.649	0	0	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
18856	dirMS_041712_NAR_50mM_minus2.17200.17200.3	3	6.22	0	1.66E+05	M195m	(R)LHFFmP	(R)L H\F F m\P G\F/A|P/L T S R(G)	m:Oxidized methionine	165.48	546.2872	1620.835	16.0115	10.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
18857	dirMS_041712_NAR_60mM_minus.11175.11175.3	3	6.22	1	2.49E+06		(R)MQKEIT	(R)M Q K\E I T/A|L/A/P S T M/K(I)		123.18	516.9421	1548.812	-0.0007	-0.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
18858	dirMS_041712_NAR_60mM_minus.11748.11748.3	3	6.22	1	1.98E+05		(R)MLFKDD	(R)M L\F K/D D Y/P/S/S/P P K(C)		125.62	508.9172	1524.74	-0.0032	-2.1	5.71	20685.4	9.18	HUMAN	B0QYN7	SUMO-conjugating enzyme UBC9
18859	dirMS_041712_NAR_60mM_minus.12051.12051.3	3	6.22	0	1.88E+05		(K)QQHVIE	(K)Q Q H V/I E/T L I/G/K(K)		126.9	422.5787	1265.721	0.0003	0.3	6.75	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
18860	dirMS_041712_NAR_60mM_minus.8682.8682.3	3	6.22	0	1.05E+05		(K)NCPHIV\	(K)N C|P H I\V V/G T\P G R(I)	C:Carbamidomethylation	109.23	436.2271	1306.669	-0.0017	-1.3	9.75	28185.1	10.76	HUMAN	B4DIJ6	Spliceosome RNA helicase DDX39B
18861	dirMS_041712_NAR_120mM_plus.16467.16467.4	4	6.22	1	1.34E+06		(R)LLHIEELI	(R)L L/H|I E/E/L R E L Q T K(I)		139.62	406.2361	1621.927	-0.0046	-2.8	5.5	28181.7	6.19	HUMAN	Q9Y224	UPF0568 protein C14orf166
18862	dirMS_041712_NAR_120mM_plus.9905.9905.3	3	6.22	0	3.61E+05	M140m	(K)HYGPGV	(K)H Y G/P G\W\V/S m/A N A G/K(D)	m:Oxidized methionine	104.77	497.5659	1474.69	15.9936	-0.9	8.6	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
18863	dirMS_041712_NAR_20mM_plus.10465.10465.2	2	6.22	0	1.88E+05	M592m M5	(R)mGPAm	(R)m/G/P A\m|G P/A\L G A G I E R(M)	m:Oxidized methionine	144.65	730.3568	1427.713	31.993	2.1	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
18864	dirMS_041712_NAR_20mM_plus.10702.10702.2	2	6.22	0	8.63E+04		(R)FLEQQN	(R)F L E Q\Q/N Q/V\L\Q/T K(W)		146.73	738.3942	1475.785	-0.0041	-2.8	6	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
18865	dirMS_041712_NAR_20mM_plus.16595.16595.2	2	6.22	0	5.45E+04		(K)LSVLLLEI	(K)L/S/V|L L L E/K(M)		185.25	457.8002	914.592	0.001	1.1	6	55059.8	7.86	HUMAN	H0YCY6	FAD-AMP lyase (cyclizing) (Fragment)
18866	dirMS_041712_NAR_20mM_plus.17456.17456.2	2	6.22	0	2.22E+05		(K)LLYAFAE	(K)L/L\Y A|F\A E A T V/P K(V)		192.97	661.8712	1322.736	-0.0003	-0.3	6	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
18867	dirMS_041712_NAR_20mM_plus.19337.19337.2	2	6.22	0	8.40E+04		(R)ALIAGG(	(R)A L I\A/G G G A|P E I E L A L R(L)		205.1	775.9467	1550.89	-0.0039	-2.5	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
18868	dirMS_041712_NAR_30mM_plus2.5821.5821.2	2	6.22	0	3.23E+05		(R)EMEEQI	(R)E M/E/E Q/M/R(R)		84.02	476.6984	952.386	0.0032	3.4	4.25	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
18869	dirMS_041712_NAR_40mM_plus2.10275.10275.2	2	6.22	0	2.26E+04		(R)CNNVLY	(R)C N|N/V/L/Y/I R(G)	C:Carbamidomethylation	125.38	526.2705	1051.535	-0.0016	-1.5	8.75	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F
18870	dirMS_041712_NAR_40mM_plus2.10969.10969.3	3	6.22	0	9.41E+04	M35m	(K)AASDIAr	(K)A A/S\D I/A m/T E L/P/P T H P I R(L)	m:Oxidized methionine	130.8	612.652	1819.937	16.0044	5.1	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
18871	dirMS_041712_NAR_40mM_plus2.17888.17888.3	3	6.22	2	1.42E+05		(K)DAKNSR	(K)D A K N S R A\V S P/P Q A T L P L K(S)		170.92	631.6874	1893.055	-0.0076	-4	9.99	19826.3	9.34	HUMAN	Q8ND23-3	Isoform 3 of Leucine-rich repeat-containing protein 16B
18872	dirMS_041712_NAR_30mM_minus2.12802.12802.2	2	6.21	0	4.27E+05		(R)GQVVSL	(R)G Q|V|V/S L I R(M)		122.43	436.2706	871.536	-0.0021	-2.4	9.75	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
18873	dirMS_041712_NAR_30mM_minus2.19561.19561.2	2	6.21	0	2.86E+05		(R)FLIQNVL	(R)F L/I/Q N V/L/R(L)		162	501.811	1002.61	0.0052	5.2	9.75	132902.3	5.82	HUMAN	J3KR24	Isoleucine--tRNA ligase, cytoplasmic
18874	dirMS_041712_NAR_40mM_minus2.11590.11590.3	3	6.21	1	1.33E+04		(R)DLAALG	(R)D L\A|A|L/G D K V N S L/G E/T A E R(L)		151.8	620.3199	1858.95	-0.0053	-2.9	4.32	285798.6	5.23	HUMAN	A6NG51	Spectrin alpha chain, non-erythrocytic 1
18875	dirMS_041712_NAR_60mM_minus.10446.10446.3	3	6.21	1	1.03E+05		(K)TCVFEKE	(K)T C/V/F E K E N D|P S V/M R(S)	C:Carbamidomethylation	117.7	571.2615	1711.778	-0.0079	-4.6	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
18876	dirMS_041712_NAR_60mM_minus.15897.15897.3	3	6.21	0	1.65E+04		(K)LFCIPVH	(K)L/F C I/P V H G I R(S)	C:Carbamidomethylation	148.82	404.5628	1211.672	0.0021	1.7	9.75	29040.9	5.88	HUMAN	H0YBL1	Inositol monophosphatase 1 (Fragment)
18877	dirMS_041712_NAR_60mM_minus.6245.6245.3	3	6.21	1	1.45E+04		(R)VEEKEGI	(R)V E\E K E G\I|P/P Q Q Q\R(L)		93.27	513.2702	1537.797	-0.0008	-0.6	4.79	19593.1	6.86	HUMAN	E9PL57	Protein NEDD8-MDP1 (Fragment)
18878	dirMS_041712_NAR_120mM_plus.9990.9990.3	3	6.21	0	7.16E+04	M195m	(K)HVTSECI	(K)H V/T S\E\C\L/G/W m R(Q)	C:Carbamidomethylation m:Oxid	105.35	464.5454	1375.625	15.9971	1.6	6.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
18879	dirMS_041712_NAR_20mM_plus.10613.10613.3	3	6.21	0	8.07E+04		(K)TTTLSGT	(K)T T T L S G T A/P\A/A/G V V|P S R(V)		145.97	529.2872	1585.854	-0.0074	-4.6	9.41	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
18880	dirMS_041712_NAR_20mM_plus.12548.12548.2	2	6.21	0	1.42E+05		(K)DLAGSII	(K)D L|A/G S I I/G K(G)		158.77	437.2558	873.504	0.0003	0.4	5.84	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
18881	dirMS_041712_NAR_20mM_plus.13735.13735.2	2	6.21	0	1.01E+05	M273m	(K)mISDAIF	(K)m I/S D/A/I/P E L K(A)	m:Oxidized methionine	166.25	566.7967	1116.597	15.9892	-5	4.37	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
18882	dirMS_041712_NAR_20mM_plus.14915.14915.2	2	6.21	0	1.23E+05		(R)ILNVPQE	(R)I L|N\V/P Q/E L/Y E K(G)		174.48	673.3693	1345.736	-0.0049	-3.6	4.53	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
18883	dirMS_041712_NAR_20mM_plus.9337.9337.2	2	6.21	0	7.19E+04		(R)QTVAVG	(R)Q/T V/A V/G V/I K(A)		135.88	457.7856	914.567	-0.003	-3.3	8.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
18884	dirMS_041712_NAR_30mM_plus2.18656.18656.2	2	6.21	0	2.64E+05		(R)QFLTQLI	(R)Q/F/L/T\Q/L/M Q K(E)		151.38	568.8061	1136.613	-0.0083	-7.3	8.75	81733.5	5.24	HUMAN	E9PAW1	Splicing factor 3A subunit 1
18885	dirMS_041712_NAR_40mM_plus2.13874.13874.3	3	6.21	1	2.11E+04		(K)VGLQVV	(K)V G L Q/V/V A V/K A/P/G F G D N R(K)		148.4	576.3214	1726.96	-0.0102	-5.9	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
18886	dirMS_041712_NAR_40mM_plus2.15979.15979.3	3	6.21	0	1.93E+05		(R)FGVPVI/	(R)F G V/P V I A/D G G I Q N V G H I A/K(A)		161.43	631.3436	1892.039	-0.0226	-12	6.74	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
18887	dirMS_041712_NAR_40mM_plus2.17880.17880.3	3	6.21	1	7.73E+04	M116m	(R)ELAILLG	(R)E L/A/I/L/L/G m L D P A E K D E K(G)	m:Oxidized methionine	171.67	634.3333	1884.999	15.9867	-4.3	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
18888	dirMS_041712_NAR_40mM_plus2.5466.5466.2	2	6.21	0	2.17E+04		(R)IGDEDV(	(R)I/G|D E D/V/G R(V)		89.15	430.7089	860.411	-0.0003	-0.4	4.03	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
18889	dirMS_041712_NAR_40mM_plus2.5543.5543.2	2	6.21	0	2.45E+05	M299m	(K)NmMAA	(K)N m|M/A|A C D/P R(H)	C:Carbamidomethylation m:Oxid	89.2	541.2145	1065.427	15.9943	-0.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
18890	dirMS_041712_NAR_50mM_plus2.19046.19046.3	3	6.21	0	8.17E+05		(R)CRPDQL	(R)C R P D Q\L T|G L/S L/L|P L/S E K(A)	C:Carbamidomethylation	167.72	643.0148	1927.032	-0.0019	-1	6.07	533778	5.74	HUMAN	Q15149	Plectin
18891	dirMS_041712_NAR_60mM_plus.14718.14718.3	3	6.21	1	5.29E+05		(K)NKDQGT	(K)N K D Q G T Y/E/D/Y/V E G L R(V)		133.48	596.2816	1786.824	0.006	3.4	4.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
18892	dirMS_041712_NAR_60mM_plus.7544.7572.3	3	6.21	0	2.93E+05		(K)NCPHVV	(K)N\C/P/H V\V|V/G T/P G R(I)	C:Carbamidomethylation	97.75	431.5519	1292.653	-0.0117	-9	9.75	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
18893	dirMS_041712_NAR_120mM_minus.14381.14381.4	4	6.2	1	1.15E+05		(R)ETNLDSI	(R)E T N L D/S L/P/L/V/D T H S K R(T)		132.23	456.992	1824.945	0.0012	0.6	5.38	53707.8	5.06	HUMAN	P08670	Vimentin
18894	dirMS_041712_NAR_20mM_minus.7498.7498.2	2	6.2	0	1.56E+05	M21m	(K)ATAVmF	(K)A T/A V/m/P D G Q F K(D)	m:Oxidized methionine	122.67	590.7864	1164.572	15.9938	-1	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
18895	dirMS_041712_NAR_30mM_minus2.16712.16712.2	2	6.2	0	2.38E+04		(R)FFMGN(	(R)F F|M G N Q V/L/K(V)		144.32	542.2866	1083.566	0.0004	0.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
18896	dirMS_041712_NAR_30mM_minus2.18809.18809.2	2	6.2	0	1.02E+05		(K)NLIDAG\	(K)N\L|I|D/A/G V D/A L R(V)		157.15	578.811	1156.632	-0.0173	-15	4.21	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
18897	dirMS_041712_NAR_30mM_minus2.6128.6128.2	2	6.2	0	1.58E+05		(R)AQAEQ/	(R)A/Q|A/E Q A A L R(Q)		87.72	479.2592	957.511	-0.0001	-0.1	6.05	533778	5.74	HUMAN	Q15149	Plectin
18898	dirMS_041712_NAR_50mM_minus2.11284.11284.3	3	6.2	1	1.86E+05		(R)DNKQA(	(R)D N/K Q A\G V/F/E/P T I V K(V)		132.05	515.9485	1545.827	0.0038	2.5	6.07	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
18899	dirMS_041712_NAR_50mM_minus2.17612.17612.3	3	6.2	0	2.56E+05		(R)LLLDGAI	(R)L/L L/D G A|P L I A I H K(A)		168.52	458.6218	1373.852	-0.0007	-0.5	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
18900	dirMS_041712_NAR_60mM_minus.15722.15722.3	3	6.2	1	1.09E+05	M332m	(R)AKFEELI	(R)A K F E E|L N/m/D L F/R(S)	m:Oxidized methionine	147.6	510.255	1512.752	15.9989	2.6	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
18901	dirMS_041712_NAR_60mM_minus.6606.6606.3	3	6.2	0	5.20E+04		(R)ATAPQT	(R)A T/A/P Q T Q H V/S P/M R(Q)		95.48	475.2404	1423.711	-0.0044	-3.1	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
18902	dirMS_041712_NAR_120mM_plus.10597.10597.3	3	6.2	1	1.16E+05		(R)LRQLAEI	(R)L R Q L A\E\E/D|L/A Q/Q R(A)		107.4	523.949	1569.834	-0.0019	-1.2	4.68	533778	5.74	HUMAN	Q15149	Plectin
18903	dirMS_041712_NAR_120mM_plus.7302.7302.3	3	6.2	1	1.14E+06		(R)EKVPGG	(R)E K V\P G G L/Q/G/S Q D/R(G)		92.32	457.5737	1370.702	0.0043	3.1	6.17	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
18904	dirMS_041712_NAR_20mM_plus.13920.13920.2	2	6.2	0	3.96E+04		(R)LQTSSVI	(R)L Q|T S S/V/L V/S\G L\R(G)		167.4	630.3666	1259.732	-0.0059	-4.6	9.75	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
18905	dirMS_041712_NAR_20mM_plus.15445.15445.2	2	6.2	0	3.55E+03		(R)GVVDSE	(R)G V V D\S/E|D/I/P L N L S R(E)		178.08	757.3956	1513.786	-0.0017	-1.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
18906	dirMS_041712_NAR_20mM_plus.17837.17837.3	3	6.2	0	1.86E+05		(R)TVQSLEI	(R)T V\Q S L/E I/D|L D S M/R(N)		194.85	502.9236	1506.747	0.0094	6.2	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
18907	dirMS_041712_NAR_20mM_plus.8982.8982.2	2	6.2	0	2.23E+05		(R)VLTVINC	(R)V L|T V/I N Q T\Q/K(E)		132.85	572.3399	1143.673	-0.0007	-0.6	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
18908	dirMS_041712_NAR_30mM_plus2.16846.16846.2	2	6.2	0	1.67E+05		(K)EQFLDG	(K)E Q/F/L/D/G D G W T S R(W)		141.32	705.8178	1410.628	-0.0001	-0.1	4.03	28545.1	4.5	HUMAN	K7EJB9	Calreticulin (Fragment)
18909	dirMS_041712_NAR_30mM_plus2.22578.22578.3	3	6.2	0	5.00E+05		(R)ALTVPEI	(R)A L T|V/P E L\T/Q Q/V/F D A K(N)		175.77	553.9697	1659.895	-0.0007	-0.4	4.37	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
18910	dirMS_041712_NAR_40mM_plus2.19895.19895.3	3	6.2	0	4.60E+05	M166m	(K)VLDFEHI	(K)V/L/D/F E/H F\L/P m L Q T V A K(N)	m:Oxidized methionine	187.63	635.3379	1888.004	15.9954	0.3	5.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
18911	dirMS_041712_NAR_40mM_plus2.8533.8533.2	2	6.2	0	4.20E+04		(R)LTVDEA\	(R)L/T|V/D E A/V R(A)		110.7	451.7517	902.494	0.002	2.2	4.37	533778	5.74	HUMAN	Q15149	Plectin
18912	dirMS_041712_NAR_50mM_plus2.18234.18234.2	2	6.2	0	5.46E+05		(R)IHFPLAT	(R)I H|F\P L A\T Y A/P V I/S A\E K(A)		164.65	878.9842	1756.963	-0.0021	-1.2	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
18913	dirMS_041712_NAR_50mM_plus2.7486.7486.3	3	6.2	1	2.58E+05		(K)SEETLDE	(K)S E|E T L D E/G/P P K Y T/K(S)		105.8	531.9261	1593.764	-0.0005	-0.3	4.41	25233.4	9.34	HUMAN	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3
18914	dirMS_041712_NAR_60mM_plus.19497.19497.3	3	6.2	1	4.46E+04		(R)SLADIAI	(R)S L|A/D/I A R E\E A S N F R(S)		159.53	526.9346	1578.787	0.0022	1.4	4.68	20458.8	4.99	HUMAN	G3V4X5	Proteasome subunit alpha type-3
18915	dirMS_041712_NAR_60mM_plus.7046.7046.2	2	6.2	1	4.51E+05		(K)IVSGKD\	(K)I/V/S/G K D\Y N V/T A N S\K(L)		95.18	748.3906	1495.775	-0.0012	-0.8	8.5	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
18916	dirMS_041712_NAR_120mM_minus.5452.5452.3	3	6.19	0	7.84E+04		(R)TGIYSST	(R)T/G\I/Y S S/T S C H K(T)	C:Carbamidomethylation	83.18	414.1973	1240.563	0.0147	11.8	8.28	38077.6	8.9	HUMAN	P09668	Pro-cathepsin H
18917	dirMS_041712_NAR_20mM_minus.10336.10336.2	2	6.19	0	1.09E+05		(K)DVNAAL	(K)D V/N\A/A I A T/I K(T)		151.05	508.2919	1015.578	-0.0017	-1.7	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
18918	dirMS_041712_NAR_20mM_minus.14423.14423.2	2	6.19	0	9.57E+04		(R)LTGQLFI	(R)L T|G Q\L/F L/G G S I\V K(G)		198.62	666.8967	1332.789	-0.0024	-1.8	8.75	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
18919	dirMS_041712_NAR_30mM_minus2.11420.11420.2	2	6.19	0	2.19E+05		(K)ATAVMI	(K)A T/A/V|M/P D/G Q F K(D)		115.47	582.7922	1164.572	0.0054	4.6	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
18920	dirMS_041712_NAR_30mM_minus2.5563.5563.2	2	6.19	0	1.79E+05		(R)LYQAGE	(R)L/Y|Q\A G E/G R(L)		84.6	447.2217	893.448	-0.0114	-12.8	6	38089.6	6.79	HUMAN	B4DT77	Annexin
18921	dirMS_041712_NAR_30mM_minus2.7853.7853.2	2	6.19	0	4.01E+04		(K)TDEGIA\	(K)T D|E/G/I/A Y R(G)		97.15	462.7203	924.442	-0.0088	-9.5	4.37	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
18922	dirMS_041712_NAR_40mM_minus2.11721.11721.3	3	6.19	1	5.94E+04		(R)GDVVPK	(R)G D\V|V/P K D V\N A A I A T I K(T)		152.85	537.6382	1610.911	-0.0112	-6.9	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
18923	dirMS_041712_NAR_50mM_minus2.11526.11526.3	3	6.19	0	1.47E+05		(K)IVLEDGT	(K)I V|L\E D/G T L/H V/T E G S G R(Y)		133.15	561.6271	1682.871	-0.004	-2.4	4.65	62748.9	5.95	HUMAN	Q16555	Dihydropyrimidinase-related protein 2
18924	dirMS_041712_NAR_50mM_minus2.12998.12998.3	3	6.19	2	2.21E+04	M443m	(R)LAGmTP	(R)L A|G/m T P V R E E S/T A K K(L)	m:Oxidized methionine	141.27	545.287	1617.863	15.9836	-6.9	8.59	83407.1	7.85	HUMAN	Q6ZVF9	G protein-regulated inducer of neurite outgrowth 3
18925	dirMS_041712_NAR_50mM_minus2.6818.6818.3	3	6.19	0	1.58E+04		(K)VAVADV	(K)V/A V A D V/Q F G\P M R(F)		105.38	430.5621	1289.667	0.0047	3.6	5.81	30507.2	6.61	HUMAN	E9PIJ0	High affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8A
18926	dirMS_041712_NAR_60mM_minus.11954.11954.3	3	6.19	0	1.88E+05		(K)QQHVIE	(K)Q Q H V I/E/T/L/I/G K(K)		126.9	422.5787	1265.721	0.0003	0.3	6.75	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
18927	dirMS_041712_NAR_60mM_minus.14681.14681.3	3	6.19	1	2.82E+04		(R)MSMKE\	(R)M/S M K E V D E Q\M L/N V Q/N K(N)		141.58	641.9701	1923.897	-0.0015	-0.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
18928	dirMS_041712_NAR_120mM_plus.5513.5513.3	3	6.19	0	3.14E+05		(R)IIECTHC(	(R)I/I/E/C/T/H C G C R(G)	C:Carbamidomethylation	82.05	435.8546	1305.55	-0.0004	-0.3	6.75	12475.2	9.39	HUMAN	C9JCD9	Protein BUD31 homolog
18929	dirMS_041712_NAR_120mM_plus.5697.5698.4	4	6.19	2	4.56E+05		(R)KTGQAP	(R)K\T G Q A|P/G Y/S Y T/A A N K N K(G)		83.45	450.4826	1798.908	0.0003	0.2	9.83	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
18930	dirMS_041712_NAR_20mM_plus.12247.12247.2	2	6.19	0	4.61E+04		(K)VALSSET	(K)V A\L|S|S E\T/E V A L A/R(D)		157.62	673.3693	1345.732	-0.0008	-0.6	4.53	246695.2	5.91	HUMAN	E7EVA0	Microtubule-associated protein
18931	dirMS_041712_NAR_20mM_plus.14891.14891.2	2	6.19	0	1.26E+05		(R)ILNVPQE	(R)I L/N\V|P Q/E L Y E K(G)		174.45	673.3693	1345.736	-0.0049	-3.6	4.53	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
18932	dirMS_041712_NAR_20mM_plus.17916.17916.2	2	6.19	0	1.97E+05		(K)VANVSL	(K)V/A|N V/S L L/A L\Y K(G)		195.27	595.8558	1190.714	-0.01	-8.4	8.56	15978.4	10.84	HUMAN	P62266	40S ribosomal protein S23
18933	dirMS_041712_NAR_20mM_plus.18942.18942.3	3	6.19	0	1.67E+05		(K)TLETQS/	(K)T L E T Q S A\L|G|P A L Q A A F K(L)		202.33	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
18934	dirMS_041712_NAR_20mM_plus.7160.7160.2	2	6.19	0	6.83E+04		(R)VLANPG	(R)V L A N|P/G|N S Q V A/R(V)		116.42	613.3355	1225.665	-0.001	-0.8	9.72	16598.6	5.48	HUMAN	J3QR48	Importin subunit beta-1 (Fragment)
18935	dirMS_041712_NAR_20mM_plus.8211.8211.2	2	6.19	0	4.72E+03	M239m	(K)EVDEQn	(K)E V/D E/Q m L\N|V\Q N K(N)	m:Oxidized methionine	126.32	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
18936	dirMS_041712_NAR_30mM_plus2.17192.17192.2	2	6.19	0	1.48E+05		(K)WPLYM!	(K)W/P\L/Y M S T K(N)		143.55	513.2647	1025.513	0.0097	9.4	8.59	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
18937	dirMS_041712_NAR_30mM_plus2.22672.22672.2	2	6.19	1	1.92E+06	Y1461y	(K)yVPSKDI	(K)y/V P|S K D L|P Y/I/K(D)	y:Phosphorylated Y	175.48	701.8633	1322.736	79.9839	12.5	8.43	196685.9	9.01	HUMAN	G3XAE9	KIAA0423, isoform CRA_a
18938	dirMS_041712_NAR_30mM_plus2.4883.4883.2	2	6.19	0	1.97E+05		(K)NCSETQ	(K)N/C|S/E T/Q Y E/S/K(V)	C:Carbamidomethylation	76.93	623.256	1245.505	-0.0005	-0.4	4.53	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
18939	dirMS_041712_NAR_30mM_plus2.9314.9314.2	2	6.19	0	4.71E+05		(K)TAVCDIF	(K)T A V|C\D\I\P|P R(G)	C:Carbamidomethylation	101.32	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
18940	dirMS_041712_NAR_40mM_plus2.12838.12838.3	3	6.19	0	2.04E+05		(K)NLPPSG/	(K)N L/P P S G A V P V T/G\I/P P H V V K(V)		142.07	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
18941	dirMS_041712_NAR_40mM_plus2.7934.7934.2	2	6.19	0	2.91E+04		(R)MGYMD	(R)M/G|Y M D/P R(E)		106.78	435.1865	869.364	0.0013	1.5	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
18942	dirMS_041712_NAR_40mM_plus2.9012.9012.2	2	6.19	0	3.51E+04		(K)QGYVIYI	(K)Q G/Y|V I/Y/R(I)		115.2	449.7407	898.478	-0.004	-4.5	8.59	20608.6	11.48	HUMAN	E7ENU7	Ribosomal protein L15 (Fragment)
18943	dirMS_041712_NAR_50mM_plus2.20284.20284.3	3	6.19	1	3.67E+05		(R)FLDKALE	(R)F/L|D/K A L/E L N/M L/S L K(G)		174.87	545.6431	1634.919	-0.0038	-2.4	6.07	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
18944	dirMS_041712_NAR_50mM_plus2.8669.8669.3	3	6.19	1	9.99E+04		(R)SCMLTG	(R)S C|M\L/T G T P E S V Q S A K R(L)	C:Carbamidomethylation	112.52	584.6157	1751.842	-0.0089	-5.1	8.46	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
18945	dirMS_041712_NAR_60mM_plus.18900.18900.3	3	6.19	0	1.59E+05		(R)NHPGLL	(R)N H/P G L L\L|M/D T T F R(D)		156.63	505.6001	1514.778	0.0073	4.8	6.74	130372.9	6.37	HUMAN	P11498	Pyruvate carboxylase, mitochondrial
18946	dirMS_041712_NAR_60mM_plus.5629.5629.3	3	6.19	0	1.90E+06	M21m	(R)SGSmDF	(R)S G|S/m/D\P S G A H/P S V R(Q)	m:Oxidized methionine	87.5	467.5464	1384.627	15.9973	1.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
18947	dirMS_041712_NAR_120mM_minus.11789.11789.2	2	6.18	0	2.40E+05		(R)YEAEYGI	(R)Y/E A/E Y G E K(I)		118.18	494.7161	988.426	-0.0009	-0.9	4.25	356242.3	8.87	HUMAN	E9PJL5	Uncharacterized protein C12orf55
18948	dirMS_041712_NAR_20mM_minus.11517.11517.2	2	6.18	0	1.91E+05		(R)GDLGIEI	(R)G D/L/G/I|E I P A E K(V)		163.77	571.3078	1141.61	-0.0016	-1.4	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
18949	dirMS_041712_NAR_20mM_minus.12427.12427.2	2	6.18	0	9.99E+04		(K)LVSIGAE	(K)L V/S I/G A E E\I/V\D G N A K(M)		171.98	757.9044	1514.806	-0.0045	-3	4.14	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
18950	dirMS_041712_NAR_20mM_minus.14613.14613.2	2	6.18	0	2.10E+05		(K)LAVEAL!	(K)L A|V E/A L\S/S L D/G D L A G R(Y)		201.28	793.922	1586.838	-0.0017	-1.1	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
18951	dirMS_041712_NAR_20mM_minus.7006.7006.2	2	6.18	0	4.38E+05	M281m	(R)AEAESm	(R)A E\A|E/S m Y Q/I K(Y)	m:Oxidized methionine	117.82	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
18952	dirMS_041712_NAR_20mM_minus.7031.7031.2	2	6.18	0	2.16E+05	M33m	(R)IDEmPE/	(R)I/D|E\m/P E A A V K(S)	m:Oxidized methionine	118	559.7733	1102.545	15.9944	-0.4	4.14	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
18953	dirMS_041712_NAR_20mM_minus.9667.9667.2	2	6.18	0	2.50E+05	M33m	(K)VAGmD\	(K)V A G m/D V/E|L T V/E E R(N)	m:Oxidized methionine	147.53	732.355	1447.71	15.993	-1.3	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
18954	dirMS_041712_NAR_50mM_minus2.14079.14079.3	3	6.18	1	5.56E+05	M85m	(K)TVTAmD	(K)T V|T A m D/V/V Y A L K R(Q)	m:Oxidized methionine	148.35	494.9385	1466.804	15.9974	1.7	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
18955	dirMS_041712_NAR_50mM_minus2.17483.17483.3	3	6.18	0	2.59E+04		(K)VVQND/	(K)V/V Q N D A Y T A P/A L P S\S I/R(T)		169.05	601.3217	1801.944	0.0063	3.5	5.8	20395.1	8.76	HUMAN	B4DMM2	Polymerase delta-interacting protein 3
18956	dirMS_041712_NAR_60mM_minus.8483.8483.3	3	6.18	1	1.31E+04		(K)EGYADK	(K)E G Y/A/D K N\L/I/A/K(W)		107.37	407.8897	1221.647	0.0072	5.9	6.17	12475.2	9.39	HUMAN	C9JCD9	Protein BUD31 homolog
18957	dirMS_041712_NAR_20mM_plus.12286.12286.2	2	6.18	0	4.61E+04		(K)VALSSET	(K)V A|L\S/S E T E V\A L A/R(D)		157.62	673.3693	1345.732	-0.0008	-0.6	4.53	246695.2	5.91	HUMAN	E7EVA0	Microtubule-associated protein
18958	dirMS_041712_NAR_20mM_plus.13594.13594.2	2	6.18	0	5.50E+04		(K)IFVGGLS	(K)I F|V/G G L/S P D T P E E K(I)		165.28	744.8731	1488.758	-0.0191	-12.8	4.14	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
18959	dirMS_041712_NAR_20mM_plus.16744.16744.2	2	6.18	0	8.70E+04		(R)ICDDELII	(R)I/C|D/D E L/I/L I K(N)	C:Carbamidomethylation	186.78	616.3317	1231.66	-0.0041	-3.4	4.03	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
18960	dirMS_041712_NAR_20mM_plus.7907.7907.2	2	6.18	0	9.11E+04	M21m	(K)ATAVmF	(K)A T/A V/m/P D/G Q F K(D)	m:Oxidized methionine	124.52	590.7861	1164.572	15.9932	-1.5	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
18961	dirMS_041712_NAR_30mM_plus2.10954.10954.2	2	6.18	0	5.80E+05		(R)LASFYER	(R)L/A/S\F/Y E/R(A)		110.9	443.2301	885.447	0.0064	7.3	6	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A

18962	dirMS_041712_NAR_30mM_plus2.13541.13625.2	2	6.18	0	2.10E+06		(R)GLQDVL	(R)G L|Q/D/V L/R(T)		124.27	400.7369	800.462	0.004	5.1	5.84	54099	7.15	HUMAN	B4DX20	T-complex protein 1 subunit zeta-2
18963	dirMS_041712_NAR_30mM_plus2.4211.4211.2	2	6.18	0	2.92E+05	M367m M:	(R)FGSGmN	(R)F/G/S|G/m/N m G R(I)	m:Oxidized methionine	69.75	494.7017	956.408	31.9884	-1.4	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
18964	dirMS_041712_NAR_50mM_plus2.10859.10859.3	3	6.18	2	2.98E+04	N1252n	(R)InKGVRS	(R)I n/K G\V R S A E E A E R(H)	n:N-acetylglucosamine (N)	125.75	554.6155	1458.766	203.066	-8	6.23	223779.6	5.9	HUMAN	Q96PE2	Rho guanine nucleotide exchange factor 17
18965	dirMS_041712_NAR_50mM_plus2.11122.11122.3	3	6.18	1	1.17E+05		(R)EVRSTPL	(R)E V/R S T/P L T A/T P G G/R(G)		125.7	481.2661	1441.776	0.008	5.5	9.7	11754	9.51	HUMAN	H0YJL5	Vesicle transport through interaction with t-SNAREs homolog 1B (Fragment)
18966	dirMS_041712_NAR_50mM_plus2.11151.11151.3	3	6.18	2	7.08E+04		(R)LPRARTT	(R)L P R\A R T T V/D E/T K(W)		126.18	462.9247	1386.77	-0.0104	-7.5	8.75	96812.2	9.04	HUMAN	Q9P202	Whirlin
18967	dirMS_041712_NAR_50mM_plus2.11720.11720.3	3	6.18	0	6.35E+04		(K)INEKPQV	(K)I N/E K P Q V/I A D Y E S\G R(A)		129.98	573.6314	1718.871	0.0089	5.2	4.68	16368.4	9.95	HUMAN	O60869	Endothelial differentiation-related factor 1
18968	dirMS_041712_NAR_50mM_plus2.21208.21208.3	3	6.18	0	2.29E+06		(R)AGKPVIC	(R)A G K\P V I\C A/T/Q/M|L E S M I K(K)	C:Carbamidomethylation	180.58	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
18969	dirMS_041712_NAR_50mM_plus2.6428.6428.3	3	6.18	0	2.94E+05	M70m	(K)EAPPmE	(K)E A/P/P m/E K P\E V V K(T)	m:Oxidized methionine	97.75	457.2387	1353.708	15.9933	-1.2	4.79	14798.1	10.35	HUMAN	K7EJ78	40S ribosomal protein S15 (Fragment)
18970	dirMS_041712_NAR_60mM_plus.10385.10385.3	3	6.18	1	1.29E+06		(K)IFRDGEE	(K)I/F/R D G E E\A\G/A/Y/D/G P R(T)		111.65	551.593	1652.766	-0.0019	-1.1	4.32	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
18971	dirMS_041712_NAR_60mM_plus.19047.19047.3	3	6.18	0	1.62E+04	S231s M24	(R)HLEGGC	(R)H L E G G C s V P\V/A|V/H T A m K(D)	C:Carbamidomethylation s:Phosp	157.38	630.2949	1792.883	95.9869	13.6	6.92	35931.4	6.46	HUMAN	F5H345	Porphobilinogen deaminase
18972	dirMS_041712_NAR_120mM_minus.10424.10424.3	3	6.17	1	1.05E+06		(K)IFRDGEE	(K)I F R D G E E A/G A/Y D/G P R(T)		110.27	551.5928	1652.766	-0.0025	-1.5	4.32	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
18973	dirMS_041712_NAR_20mM_minus.13708.13708.2	2	6.17	0	3.42E+05		(K)LGGSAV	(K)L G G/S A V I/S L/E G K/P L(-)		188.52	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
18974	dirMS_041712_NAR_20mM_minus.8987.8987.2	2	6.17	0	2.75E+05		(R)ALGQNF	(R)A L\G/Q/N/P T N A E V L K(V)		138.82	677.871	1354.733	0.0022	1.6	6.05	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
18975	dirMS_041712_NAR_30mM_minus2.4991.4991.2	2	6.17	0	1.22E+05		(R)ENDEFC	(R)E N/D/E F/C K(M)	C:Carbamidomethylation	80.23	471.188	941.367	0.0018	1.9	4.14	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
18976	dirMS_041712_NAR_30mM_minus2.7218.7218.2	2	6.17	0	1.28E+05		(K)LYLTNSK	(K)L/Y/L T N/S K(Q)		93.52	419.7351	838.467	-0.004	-4.7	8.59	115930.4	5.36	HUMAN	B7ZKR7	AP-3 complex subunit beta-2
18977	dirMS_041712_NAR_40mM_minus2.8817.8817.3	3	6.17	0	9.11E+03		(K)TVPEELV	(K)T V/P E E L/V K/P E E L S K(Y)		134.22	533.298	1597.868	0.0111	7	4.49	27945.7	6.25	HUMAN	F5GY56	Pre-mRNA-processing factor 19 (Fragment)
18978	dirMS_041712_NAR_50mM_minus2.12653.12653.3	3	6.17	1	6.78E+05		(R)TFNTSTC	(R)T F|N T/S T G G L L/L/P S D T K R(S)		140.77	603.3247	1807.955	0.0047	2.6	8.41	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
18979	dirMS_041712_NAR_60mM_minus.17662.17662.3	3	6.17	0	1.17E+05		(R)GGHVVE	(R)G G H V V E G L\A\G E|L E/Q L R(A)		158.32	555.2959	1663.876	-0.0031	-1.8	4.75	106088.3	5.78	HUMAN	P10275	Androgen receptor
18980	dirMS_041712_NAR_60mM_minus.6438.6438.3	3	6.17	0	7.40E+04		(R)IVNTQE	(R)I V/N\T Q E/Q L/N H R(W)		94.58	451.2405	1351.708	-0.0007	-0.5	6.75	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
18981	dirMS_041712_NAR_120mM_plus.11245.11245.3	3	6.17	0	5.57E+05		(R)SIFQHIQ	(R)S/I/F Q H I/Q/S A Q S Q R(S)		112.57	510.5986	1529.782	-0.0007	-0.4	9.49	108720.9	10.17	HUMAN	Q9Y2W1	Thyroid hormone receptor-associated protein 3
18982	dirMS_041712_NAR_120mM_plus.14436.14436.2	2	6.17	0	6.00E+05		(R)HFDQFV	(R)H|F|D\Q\F W S/A A/K(T)		128.8	618.7928	1236.58	-0.0013	-1.1	6.74	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
18983	dirMS_041712_NAR_20mM_plus.11371.11371.2	2	6.17	0	1.91E+05		(R)YALYDA	(R)Y A/L|Y D/A/T Y/E T K(E)		150.8	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
18984	dirMS_041712_NAR_20mM_plus.11434.11434.2	2	6.17	0	2.11E+05		(R)YALYDA	(R)Y/A|L/Y/D A T Y E T K(E)		151.17	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
18985	dirMS_041712_NAR_30mM_plus2.19931.19931.2	2	6.17	0	1.35E+05		(R)YAFVMF	(R)Y/A|F\V M F K(T)		157.92	453.2369	905.459	0.0076	8.3	8.59	103045.5	7.1	HUMAN	B9ZVT1	RNA-binding protein 12B
18986	dirMS_041712_NAR_30mM_plus2.19997.19997.2	2	6.17	0	1.04E+04	M378m	(K)mFLNLL	(K)m F|L/N L L S P/R(T)	m:Oxidized methionine	158.6	553.8012	1090.608	15.9874	-6.8	9.5	73080.2	9.04	HUMAN	O00178	GTP-binding protein 1
18987	dirMS_041712_NAR_40mM_plus2.12590.12590.2	2	6.17	0	2.54E+04		(K)ICSWNV	(K)I C|S/W/N V/D/G L R(A)	C:Carbamidomethylation	140.23	610.297	1219.589	-0.0021	-1.7	5.84	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
18988	dirMS_041712_NAR_40mM_plus2.15377.15377.3	3	6.17	0	2.57E+05		(K)GVTIIGP	(K)G V|T I/I/G/P A T V/G G I K P G C F K(I)	C:Carbamidomethylation	156.45	624.683	1872.041	-0.0067	-3.6	10	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
18989	dirMS_041712_NAR_40mM_plus2.6075.6075.2	2	6.17	0	4.47E+04	M238m	(K)NmGLY	(K)N m/G L/Y/G E|R(V)	m:Oxidized methionine	94.68	478.2228	939.435	16.003	8.5	6	43371.1	9.64	HUMAN	E7ERW2	Aspartate aminotransferase
18990	dirMS_041712_NAR_40mM_plus2.9067.9067.2	2	6.17	0	4.81E+05		(R)GGNFGF	(R)G G\N|F|G F/G D/S R(G)		116.33	507.2256	1013.444	0.0004	0.4	5.84	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
18991	dirMS_041712_NAR_50mM_plus2.16193.16193.3	3	6.17	0	2.66E+05		(K)ACQSIYF	(K)A C|Q S I Y/P L H D V F V/R(K)	C:Carbamidomethylation	154.37	568.9562	1704.853	0.0014	0.8	6.79	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
18992	dirMS_041712_NAR_50mM_plus2.5196.5196.3	3	6.17	0	7.90E+04		(R)AEAEAG	(R)A/E/A\E A/G S P R P D/P R(E)		85.77	451.5555	1352.655	-0.0034	-2.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
18993	dirMS_041712_NAR_50mM_plus2.9530.9530.3	3	6.17	1	1.35E+05		(R)GAVIATE	(R)G A/V/I/A T E L K/N N S Y K(L)		116.82	503.2738	1507.812	-0.0046	-3.1	8.5	20123.7	9.25	HUMAN	B0QYA3	Eukaryotic translation initiation factor 3 subunit D (Fragment)
18994	dirMS_041712_NAR_50mM_plus2.9545.9545.3	3	6.17	1	1.73E+05		(R)DYQDNK	(R)D Y/Q D N/K/A D V I L/K(Y)		116.97	474.5801	1421.727	-0.0013	-0.9	4.43	16556.2	5.07	HUMAN	O14602	Eukaryotic translation initiation factor 1A, Y-chromosomal
18995	dirMS_041712_NAR_60mM_plus.14958.14958.3	3	6.17	1	2.51E+05		(R)FKTPEEA	(R)F/K/T P E E/A/A L/F K(C)		134.73	427.5681	1280.689	0.0012	1	6.14	362585.9	5.86	HUMAN	P49792	E3 SUMO-protein ligase RanBP2
18996	dirMS_041712_NAR_120mM_minus.18793.18793.4	4	6.16	1	4.31E+05		(K)FQIPPNA	(K)F Q\I/P/P N/A E L K Y E L H/L K(S)		157.12	485.7686	1940.064	-0.0114	-5.9	6.75	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
18997	dirMS_041712_NAR_30mM_minus2.17812.17812.2	2	6.16	0	1.17E+05		(R)ILELDQF	(R)I L|E|L/D Q F K(G)		150.63	503.2871	1005.562	0.0054	5.4	4.37	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
18998	dirMS_041712_NAR_40mM_minus2.9085.9085.3	3	6.16	0	1.57E+05	M26m	(R)LSAmLV	(R)L S\A m L V|P V/T/P E V K P K(R)	m:Oxidized methionine	136.37	542.315	1608.939	15.9911	-2.3	8.59	31524.1	4.5	HUMAN	P82970	High mobility group nucleosome-binding domain-containing protein 5
18999	dirMS_041712_NAR_50mM_minus2.14991.14991.3	3	6.16	1	1.47E+05		(R)LLTTIGK	(R)L/L/T/T I/G K D L D F/E K(A)		152.78	498.2798	1492.826	-0.0009	-0.6	4.56	98682.1	4.86	HUMAN	C9JF13	Eukaryotic translation initiation factor 4 gamma 1 (Fragment)
19000	dirMS_041712_NAR_50mM_minus2.5716.5716.3	3	6.16	0	2.41E+05		(K)ATCAPQ	(K)A T/C A|P Q H G\A/P G/P G/P A D A S K(V)	C:Carbamidomethylation	93.82	597.279	1789.829	-0.0062	-3.4	6.79	83264.1	6.04	HUMAN	E9PHF0	Filamin-A
19001	dirMS_041712_NAR_60mM_minus.10906.10906.3	3	6.16	1	1.26E+05		(K)KVEAQL	(K)K V E A Q\L/Q/E/L Q/V/K(F)		121.12	471.6068	1412.811	-0.0049	-3.5	6.14	227783.5	5.5	HUMAN	P35579	Myosin-9
19002	dirMS_041712_NAR_120mM_plus.18127.18127.3	3	6.16	0	4.73E+05		(R)HLLQAP	(R)H L\L/Q A/P\V D\D A Q E|I L H S R(F)		148.32	648.0088	1942.014	-0.0023	-1.2	5.21	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
19003	dirMS_041712_NAR_20mM_plus.12113.12113.2	2	6.16	0	1.20E+05		(R)IYVVDV	(R)I Y|V\V/D/V G S E/P R(A)		156.17	617.3237	1233.647	-0.0073	-5.9	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
19004	dirMS_041712_NAR_20mM_plus.12231.12231.3	3	6.16	0	2.90E+05		(K)VNQIGS	(K)V N Q\I G S\V T\E/S/I/Q/A C K(L)	C:Carbamidomethylation	157.67	545.2781	1633.821	-0.0016	-1	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
19005	dirMS_041712_NAR_30mM_plus2.15258.15258.2	2	6.16	0	3.17E+05		(K)NYLAPD	(K)N Y\L/A P D A\T A/A D K(R)		132.53	625.3004	1249.606	-0.0124	-9.9	4.21	127856.3	9.42	HUMAN	Q9UHB7	AF4/FMR2 family member 4
19006	dirMS_041712_NAR_30mM_plus2.8151.8151.2	2	6.16	0	5.70E+05		(K)LAAIGEA	(K)L/A|A|I/G E A T R(L)		97.12	451.2545	901.51	-0.0084	-9.4	6	533778	5.74	HUMAN	Q15149	Plectin
19007	dirMS_041712_NAR_40mM_plus2.8842.8842.2	2	6.16	0	3.70E+05		(K)VCADLIF	(K)V/C/A/D L I R(G)	C:Carbamidomethylation	113.32	423.7286	846.45	-0.0003	-0.3	5.81	6885.1	10.56	HUMAN	E5RJX2	40S ribosomal protein S20
19008	dirMS_041712_NAR_50mM_plus2.20216.20216.3	3	6.16	0	5.21E+05		(R)QARPTY	(R)Q/A R P T Y A/T\A|M/L Q/S L L K(-)		174.58	597.9962	1791.979	-0.0045	-2.5	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
19009	dirMS_041712_NAR_50mM_plus2.7591.7591.3	3	6.16	0	2.12E+05		(R)SAEEEA	(R)S A E E E A A/D L/P/T K P T K(I)		105.3	529.5984	1586.791	-0.0102	-6.4	4.41	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
19010	dirMS_041712_NAR_50mM_plus2.8086.8086.3	3	6.16	1	2.94E+04		(K)ELQAAG	(K)E L/Q/A A G K/S/P E D L E R(L)		109.3	514.9321	1542.776	0.0059	3.8	4.41	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
19011	dirMS_041712_NAR_60mM_plus.16254.16254.3	3	6.16	0	4.53E+05		(K)YYITIIDA	(K)Y Y/I T I|I/D/A/P G H R(D)		141.52	473.5847	1418.743	-0.0031	-2.2	6.74	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
19012	dirMS_041712_NAR_60mM_plus.7187.7187.3	3	6.16	1	4.31E+05		(K)VVSETN	(K)V V|S E/T/N/D T K V L R(H)		95.93	454.2511	1360.743	-0.0043	-3.2	6.04	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
19013	dirMS_041712_NAR_120mM_minus.13746.13746.4	4	6.15	1	3.13E+05	K111k	(R)EHGAVP	(R)E H G A V/P L N/E A T R/A/S G D D k(S)	k:Ubiquitin-K	128.95	495.992	1866.894	114.0521	4.6	4.75	22033.3	6.21	HUMAN	E5RJ36	UBX domain-containing protein 2B
19014	dirMS_041712_NAR_120mM_minus.17271.17271.4	4	6.15	2	6.24E+05		(R)KVESLQI	(R)K\V E S L Q|E E I/A/F/L K K(L)		148.93	416.2415	1661.947	-0.0031	-1.9	6.23	49709.6	5.19	HUMAN	B0YJC4	Vimentin
19015	dirMS_041712_NAR_30mM_minus2.17917.17917.2	2	6.15	0	6.87E+04		(R)SSFYVN	(R)S S/F|Y|V/N/G L T\L G G Q K(C)		152.23	735.8825	1470.759	-0.001	-0.7	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
19016	dirMS_041712_NAR_30mM_minus2.6501.6501.2	2	6.15	0	2.34E+05		(R)QQYESV	(R)Q Q/Y/E/S V A A/K(N)		89.95	512.2534	1023.511	-0.011	-10.8	6	49709.6	5.19	HUMAN	B0YJC4	Vimentin
19017	dirMS_041712_NAR_30mM_minus2.9319.9319.2	2	6.15	0	6.79E+04		(R)CSEQVQ	(R)C S/E|Q/V/Q/D F|T K(C)	C:Carbamidomethylation	105.07	621.2773	1241.547	0.0006	0.5	4.37	13533.5	9.82	HUMAN	H7C3D8	COX assembly mitochondrial protein homolog (Fragment)
19018	dirMS_041712_NAR_40mM_minus2.8902.8902.3	3	6.15	0	7.64E+04	M237m	(R)LSSPCIm	(R)L/S/S/P/C I/m V V N H D A S S\I P R(L)	C:Carbamidomethylation m:Oxid	135.02	666.9949	1982.979	15.9915	-1.7	6.74	87267.9	6.33	HUMAN	Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase
19019	dirMS_041712_NAR_50mM_minus2.16243.16243.3	3	6.15	0	1.46E+05		(K)LDPHLVI	(K)L D|P H/L V\L\D\Q L R(C)		160.2	440.2533	1318.748	-0.0024	-1.8	5.21	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
19020	dirMS_041712_NAR_20mM_plus.17691.17691.2	2	6.15	0	8.43E+04		(R)GDGPICI	(R)G/D/G\P/I|C\L|V L/A P T R(E)	C:Carbamidomethylation	193.15	684.8681	1368.73	-0.0015	-1.1	5.84	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
19021	dirMS_041712_NAR_30mM_plus2.15900.15901.3	3	6.15	0	1.86E+05		(R)LDDDDE	(R)L D D D D E G V/P S/S/A L/R(E)		135.83	496.8957	1488.681	-0.0087	-5.9	3.71	33760.3	7.84	HUMAN	Q00535	Cyclin-dependent kinase 5
19022	dirMS_041712_NAR_30mM_plus2.15928.15928.2	2	6.15	0	1.85E+04		(K)TDTVLIL	(K)T D/T V/L/I/L/C R(K)	C:Carbamidomethylation	135.78	545.7923	1090.593	-0.0152	-13.9	5.5	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
19023	dirMS_041712_NAR_30mM_plus2.18696.18696.2	2	6.15	0	3.03E+05		(R)ESLEALL	(R)E S L/E/A L/L Q/R(A)		151.97	529.8026	1058.584	0.0139	13.1	4.53	107721.8	8.85	HUMAN	O94906	Pre-mRNA-processing factor 6
19024	dirMS_041712_NAR_30mM_plus2.6919.6919.2	2	6.15	0	1.02E+05	M357m	(K)AELDDTI	(K)A E|L/D/D T P m/R(G)	m:Oxidized methionine	90.5	532.2416	1047.478	15.9984	3.3	4.03	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
19025	dirMS_041712_NAR_40mM_plus2.12520.12520.3	3	6.15	0	1.29E+05	M114m M:	(R)AGKPVIC	(R)A G K\P V I C A\T/Q m/L\E S m I/K(K)	C:Carbamidomethylation m:Oxid	139.77	637.0002	1876.969	32.0167	14.1	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
19026	dirMS_041712_NAR_40mM_plus2.19488.19488.3	3	6.15	0	1.01E+04		(K)GAEILEV	(K)G A E/I/L/E V L/H S/L/P A V R(Q)		182.63	535.3088	1603.917	-0.0048	-3	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
19027	dirMS_041712_NAR_40mM_plus2.19647.19647.3	3	6.15	1	1.67E+05		(K)LGFAGL	(K)L/G\F|A/G L V Q E I S F/G T T K D K(M)		183.78	637.673	1911.022	-0.0178	-9.3	6.07	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
19028	dirMS_041712_NAR_50mM_plus2.19738.19738.3	3	6.15	0	7.25E+04		(K)ALESPER	(K)A L|E/S/P E/R P F L A I L\G G A/K(V)		172.62	590.3344	1768.996	-0.0069	-3.9	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
19029	dirMS_041712_NAR_50mM_plus2.20824.20824.3	3	6.15	1	2.60E+05		(R)NLQNLL	(R)N L|Q/N L/L/I/L T A I K A D/R(T)		178.05	566.0067	1696.012	-0.006	-3.6	8.75	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
19030	dirMS_041712_NAR_50mM_plus2.21823.21823.3	3	6.15	1	1.26E+05		(K)TENPLIL	(K)T E/N/P L I\L I D E/V D K\I G R(G)		185.57	609.0045	1825.007	-0.0076	-4.2	4.32	86039.3	5.74	HUMAN	F5GZ27	Lon protease homolog
19031	dirMS_041712_NAR_60mM_plus.12719.12719.3	3	6.15	1	5.25E+05		(K)ESNGPV	(K)E/S N|G/P V\K V W/G S I K(G)		124.25	467.5853	1400.753	-0.0119	-8.5	8.69	16163.7	5.7	HUMAN	P00441	Superoxide dismutase [Cu-Zn]
19032	dirMS_041712_NAR_60mM_plus.15789.15789.3	3	6.15	1	8.97E+05		(R)MSMKE	(R)M S M K E\V D\E Q|M/L/N\V Q/N K(N)		139.68	641.9696	1923.897	-0.003	-1.6	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
19033	dirMS_041712_NAR_20mM_minus.13406.13406.2	2	6.14	1	2.74E+05	K714k	(R)QAPKQ	(R)Q A/P K|Q G A V G P k(V)	k:Ubiquitin-K	185.52	597.8271	1080.616	114.0309	-10.1	10	81130.7	8.82	HUMAN	H0YL36	Disintegrin and metalloproteinase domain-containing protein 8
19034	dirMS_041712_NAR_20mM_minus.8536.8536.2	2	6.14	0	1.29E+04		(R)YEIEETE	(R)Y E|I/E/E T E T V T K(S)		134.38	671.3246	1341.642	-0.0001	-0.1	4.09	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
19035	dirMS_041712_NAR_30mM_minus2.10649.10649.2	2	6.14	0	2.32E+05		(K)AGFAGD	(K)A G F|A|G D Q/I/P K(Y)		111.9	502.2645	1003.521	0.001	1	5.88	16745.9	5.33	HUMAN	G5E9Q5	ARP1 actin-related protein 1 homolog B, centractin beta (Yeast), isoform CRA_c
19036	dirMS_041712_NAR_30mM_minus2.7009.7009.2	2	6.14	0	1.47E+05		(K)ISTVVSS	(K)I/S|T/V V/S/S K(E)		92.48	410.7405	820.477	-0.0037	-4.6	8.75	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
19037	dirMS_041712_NAR_40mM_minus2.11245.11245.3	3	6.14	0	2.05E+04		(K)VALLLLD	(K)V A\L|L L L D Q G A S/P H/A A A K(N)		150	558.9882	1674.954	-0.0037	-2.2	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
19038	dirMS_041712_NAR_50mM_minus2.11283.11283.3	3	6.14	1	1.86E+05		(R)DNKQA	(R)D N/K Q A\G\V F/E/P T I V/K(V)		132.05	515.9485	1545.827	0.0038	2.5	6.07	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
19039	dirMS_041712_NAR_50mM_minus2.17572.17572.3	3	6.14	1	3.42E+05		(R)LKLPSIPI	(R)L K L P S I/P\L\V/P V S A Q K(R)		169.62	530.669	1589.999	-0.0064	-4.1	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
19040	dirMS_041712_NAR_60mM_minus.15095.15095.3	3	6.14	0	2.01E+05		(R)IYIPLPEF	(R)I Y\I|P L/P E P/H A R(A)		143.9	435.9153	1305.731	0	0	6.75	49472.3	6.75	HUMAN	O75351	Vacuolar protein sorting-associated protein 4B
19041	dirMS_041712_NAR_60mM_minus.15643.15643.3	3	6.14	1	3.16E+05		(R)GFPTIYF	(R)G F/P T/I/Y F S P A N K K(L)		147.15	490.5972	1469.779	-0.0017	-1.1	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
19042	dirMS_041712_NAR_60mM_minus.6308.6308.3	3	6.14	1	4.66E+04		(R)LTQEPES	(R)L/T/Q E/P E S I/R K(W)		93.75	400.8938	1200.658	0.0086	7.1	6.14	8409.9	4.52	HUMAN	H0Y9Q6	Clathrin light chain B (Fragment)
19043	dirMS_041712_NAR_60mM_minus.7276.7276.3	3	6.14	1	5.43E+05	M136m M:	(K)VKEGmN	(K)V K E G m N\I|V/E/A m E R(F)	m:Oxidized methionine	100.18	513.25	1505.745	31.9904	0.4	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
19044	dirMS_041712_NAR_60mM_minus.7572.7572.3	3	6.14	1	1.62E+05	Y40y T47t	(K)TSTQEyA	(K)T S|T/Q/E/y A A K I I N t K(K)	y:Phosphorylated Y t:Phosph	102.03	576.5915	1567.833	159.9273	-3.1	8.17	21044.3	9.93	HUMAN	B4DVQ3	Calcium/calmodulin-dependent protein kinase type II subunit gamma
19045	dirMS_041712_NAR_120mM_plus.18253.18253.4	4	6.14	1	6.50E+05		(R)ILEFFGLI	(R)I L\E/F/F/G L K K E E C/P A V R(L)	C:Carbamidomethylation	148.63	484.7638	1936.036	-0.0027	-1.4	6.23	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
19046	dirMS_041712_NAR_20mM_plus.12212.12212.3	3	6.14	0	2.90E+05		(K)VNQIGS	(K)V N Q\I G S\V/T E/S/I/Q A C K(L)	C:Carbamidomethylation	157.67	545.2781	1633.821	-0.0016	-1	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
19047	dirMS_041712_NAR_20mM_plus.18860.18860.3	3	6.14	0	1.08E+05		(K)VIGNQS	(K)V I\G N Q\S L/V N E\L A/F T A R(K)		200.78	577.9842	1731.939	-0.0008	-0.4	5.97	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
19048	dirMS_041712_NAR_20mM_plus.9643.9643.2	2	6.14	0	1.18E+05		(K)VAGQD	(K)V A|G Q|D G S V V/Q/F K(I)		138.05	617.8225	1234.643	-0.0049	-4	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
19049	dirMS_041712_NAR_40mM_plus2.17548.17548.3	3	6.14	0	1.65E+05		(R)VYAILTH	(R)V/Y/A I L T H G I|F S G/P A I S R(I)		169.45	601.3376	1801.996	0.0023	1.3	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
19050	dirMS_041712_NAR_50mM_plus2.18464.18464.3	3	6.14	0	4.00E+05		(R)AVSILPL	(R)A V|S I L P L/L/G\H/G V P R(L)		165.85	476.9615	1428.869	0.0014	1	9.8	66841.7	7.74	HUMAN	F5H721	WW domain-binding protein 11
19051	dirMS_041712_NAR_50mM_plus2.19588.19588.3	3	6.14	0	6.42E+04		(K)ISSIQSIV	(K)I S\S I/Q/S/I/V/P A L E I A N A H R(K)		171.5	640.3623	1919.071	0.0015	0.8	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
19052	dirMS_041712_NAR_50mM_plus2.7825.7825.3	3	6.14	1	3.33E+04	M250m	(K)TTDmAF	(K)T/T/D m A/P S K E/T E M A L A K(D)	m:Oxidized methionine	108.25	580.6104	1723.824	15.9925	-1.4	4.68	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
19053	dirMS_041712_NAR_60mM_plus.16643.16643.3	3	6.14	1	1.69E+05		(K)LIESAEEI	(K)L I/E S/A/E E L I R D/G R(Y)		143.87	500.9392	1500.802	0.0014	0.9	4.41	58035.5	5.83	HUMAN	Q13217	DnaJ homolog subfamily C member 3
19054	dirMS_041712_NAR_60mM_plus.22049.22049.3	3	6.14	1	3.08E+05		(R)LKLLLPW	(R)L K\L L\L P/W/L E A/R(I)		187.7	451.286	1351.846	-0.0026	-1.9	8.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
19055	dirMS_041712_NAR_120mM_minus.16708.16708.3	3	6.13	0	3.53E+05		(K)HLEINPD	(K)H/L\E I N P D/H/S\I I E T L R(Q)		146.38	596.3176	1786.945	-0.0064	-3.6	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
19056	dirMS_041712_NAR_120mM_minus.7254.7254.3	3	6.13	1	2.89E+05		(R)TKTEISEI	(R)T K T E\I S|E/M/N/R(N)		93.63	403.5363	1208.594	0.0004	0.3	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
19057	dirMS_041712_NAR_20mM_minus.11787.11787.2	2	6.13	0	8.32E+04		(R)GGIVDE	(R)G G I|V/D|E G A/L L R(A)		166.5	550.3071	1099.611	-0.0037	-3.3	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
19058	dirMS_041712_NAR_20mM_minus.13551.13551.2	2	6.13	0	1.04E+05		(K)FIIPNVV	(K)F/I|I/P N V V K(Y)		186.28	465.294	929.582	-0.0011	-1.2	8.75	17529.3	9.3	HUMAN	F5GXY2	L-lactate dehydrogenase A chain (Fragment)
19059	dirMS_041712_NAR_20mM_minus.7296.7296.2	2	6.13	0	3.99E+04		(K)AVTEQG	(K)A V/T E Q/G A/E L|S N E E R(N)		120.98	766.8612	1532.719	-0.0036	-2.3	4.09	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
19060	dirMS_041712_NAR_20mM_minus.7645.7645.2	2	6.13	0	7.13E+05	M1m	(-)mAAAAN	(-)m A A A/A M A A A A\G G G A G A\A R(S)	m:Oxidized methionine	125.03	731.843	1446.694	15.9847	-7	9.5	39288.4	4.95	HUMAN	Q9NX46	Poly(ADP-ribose) glycohydrolase ARH3
19061	dirMS_041712_NAR_30mM_minus2.19030.19030.2	2	6.13	0	1.95E+05		(K)IISNLFL	(K)I I/S N/L/F L/G R(A)		157.63	516.8122	1032.62	-0.0029	-2.8	9.75	234333.2	6.01	HUMAN	J3KNX9	Unconventional myosin-XVIIIa
19062	dirMS_041712_NAR_30mM_minus2.7062.7062.2	2	6.13	0	3.54E+04		(K)ETEGDV	(K)E T/E G D V/T S V K(D)		92.93	532.7579	1064.511	-0.0021	-2	4.14	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
19063	dirMS_041712_NAR_50mM_minus2.15530.15530.3	3	6.13	0	2.72E+05	M118m	(R)AGKPVIC	(R)A G K\P V I|C\A T Q/M/L E/S m I K(K)	C:Carbamidomethylation m:Oxid	155.9	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
19064	dirMS_041712_NAR_60mM_minus.16819.16819.3	3	6.13	0	1.78E+05		(R)LLIHQSL	(R)L L/I/H Q S L|A/G G I I G V K(G)		153.38	506.9823	1518.937	-0.0043	-2.8	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
19065	dirMS_041712_NAR_60mM_minus.5082.5082.3	3	6.13	1	5.32E+04		(K)CDSSPD	(K)C D\S S/P D/S A/E D V R/K(V)	C:Carbamidomethylation	83.13	489.2127	1465.622	0.0012	0.8	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
19066	dirMS_041712_NAR_120mM_plus.19159.19159.3	3	6.13	1	6.13E+05		(R)HGVQEL	(R)H/G V Q E L E\I\E L/Q/S Q L S K/K(A)		153.85	656.0237	1966.06	-0.0038	-2	5.5	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
19067	dirMS_041712_NAR_120mM_plus.5842.5842.4	4	6.13	2	5.86E+05		(R)KTGQAP	(R)K T G Q\A P/G/Y S Y T/A A N K/N K(G)		83.75	450.4826	1798.908	0.0003	0.2	9.83	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
19068	dirMS_041712_NAR_120mM_plus.8130.8130.2	2	6.13	0	4.29E+05		(K)AGEVFIH	(K)A/G\E/V/F/I/H\K(D)		96.3	450.7531	900.494	0.0051	5.7	6.79	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
19069	dirMS_041712_NAR_20mM_plus.9401.9401.2	2	6.13	0	8.67E+04		(R)ALEESNY	(R)A L E|E/S N Y E/L E|G K(I)		136.38	691.3246	1381.648	-0.0062	-4.5	4.09	59054.3	5.14	HUMAN	P13645	Keratin, type I cytoskeletal 10
19070	dirMS_041712_NAR_30mM_plus2.12508.12508.2	2	6.13	1	6.84E+05		(R)DTVKIPK	(R)D/T/V K I/P K(K)		117.78	400.7516	800.488	0.0083	10.4	8.59	36728.3	5.6	HUMAN	A8MTV8	Epsin-2

19071	dirMS_041712_NAR_40mM_plus2.5727.5727.2	2	6.13	0	1.12E+05		(R)FSSSSGY	(R)F/S S S S/G Y/G/G G/S S R(V)		90.98	618.2686	1235.529	0.0012	1	8.75	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
19072	dirMS_041712_NAR_40mM_plus2.7376.7376.2	2	6.13	0	2.20E+05		(R)AQYDEL	(R)A Q|Y/D E/L A R(K)		102.77	483.2372	965.469	-0.0016	-1.6	4.37	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
19073	dirMS_041712_NAR_50mM_plus2.15497.15497.3	3	6.13	1	9.99E+05		(R)KVPGVT	(R)K\V/P G V T A\I E|L/D E/D\T G T F R(I)		149.85	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
19074	dirMS_041712_NAR_50mM_plus2.18753.18753.3	3	6.13	0	3.83E+05		(R)IHFPLAT	(R)I H\F P L A T Y A|P/V/I S A E K(A)		166.62	586.3252	1756.963	-0.0022	-1.2	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
19075	dirMS_041712_NAR_50mM_plus2.20376.20376.3	3	6.13	1	5.29E+04		(K)VKIPEGT	(K)V K|I P E G T I/L/T/M/D M L T V K(V)		176.68	630.3524	1889.049	-0.006	-3.2	6.04	40763.2	6.29	HUMAN	Q9NR45	Sialic acid synthase
19076	dirMS_041712_NAR_50mM_plus2.21516.21516.3	3	6.13	0	8.95E+04		(K)GAEILEV	(K)G A\E/I/L/E V/L\H\S L P/A V R(Q)		183.4	535.3092	1603.917	-0.0036	-2.2	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
19077	dirMS_041712_NAR_50mM_plus2.21727.21727.3	3	6.13	1	1.20E+05		(K)ESLCQA	(K)E S L/C/Q/A A L/G L/I L K E K(A)	C:Carbamidomethylation	185.33	558.3196	1672.93	0.014	8.4	6.24	66923.1	6.88	HUMAN	E9PG35	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (Fragment)
19078	dirMS_041712_NAR_50mM_plus2.9810.9810.3	3	6.13	1	2.54E+05		(K)TTDMAF	(K)T T/D/M/A/P S K E T E M A L/A K(D)		119.22	575.2802	1723.824	0.0019	1.1	4.68	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
19079	dirMS_041712_NAR_60mM_plus.11812.11812.2	2	6.13	1	2.66E+05		(K)TLQEVT	(K)T L/Q/E/V/T E M/D S V K R(Y)		118.98	768.3889	1535.773	-0.0029	-1.9	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
19080	dirMS_041712_NAR_60mM_plus.6471.6471.3	3	6.13	0	2.36E+05		(R)STSHTS	(R)S T/S H T S D F/N|P N S G\S D/Q R(V)		92.47	612.9373	1836.774	0.023	12.5	5.19	117082.9	9.07	HUMAN	F8VQP2	Ataxin-2
19081	dirMS_041712_NAR_60mM_plus.7631.7631.3	3	6.13	1	2.34E+05	T211t	(K)SGSEKN	(K)S G S/E K N t G R P|P/G E/A A E E A K(K)	t:Phosphorylated T	97.9	665.6355	1914.915	79.9768	5.2	4.94	60319	9.62	HUMAN	Q9UBI9	Headcase protein homolog
19082	dirMS_041712_NAR_120mM_minus.20465.20465.3	3	6.12	1	3.46E+05		(R)LDLAGR	(R)L/D\L/A/G R D L/T D Y L M K(I)		169.02	541.9508	1623.841	-0.0032	-2	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
19083	dirMS_041712_NAR_20mM_minus.12069.12069.2	2	6.12	0	7.89E+05	M313m	(R)TVQSLE	(R)T V/Q|S L/E/I\D\L|D S m R(N)	m:Oxidized methionine	170.33	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
19084	dirMS_041712_NAR_20mM_minus.9635.9635.2	2	6.12	0	3.29E+05		(K)IGGIGTV	(K)I G|G I|G T/V/P V G R(V)		147.45	513.3075	1025.61	-0.0025	-2.4	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
19085	dirMS_041712_NAR_30mM_minus2.4894.4894.2	2	6.12	0	2.34E+05		(R)SQIYGSF	(R)S Q|I/Y/G S R(Q)		79.27	405.7052	810.41	-0.0073	-9	8.46	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
19086	dirMS_041712_NAR_50mM_minus2.16204.16204.3	3	6.12	0	1.46E+05		(K)LDPHLV	(K)L D/P/H/L V L D/Q L R(C)		160.2	440.2533	1318.748	-0.0024	-1.8	5.21	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
19087	dirMS_041712_NAR_50mM_minus2.16494.16494.3	3	6.12	1	1.87E+04		(R)EVQLEE	(R)E V Q/L/E/E/L E/A A R D L V S K(E)		161.82	610.3273	1828.965	0.0023	1.2	4.25	45984.6	6.24	HUMAN	B4E1G6	Galactokinase
19088	dirMS_041712_NAR_60mM_minus.10711.10711.3	3	6.12	0	1.86E+05		(K)TGNLGN	(K)T G|N L/G N V/V H I E R(F)		120.02	436.9057	1308.702	0.0007	0.5	6.41	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
19089	dirMS_041712_NAR_60mM_minus.12675.12675.3	3	6.12	0	1.53E+05		(K)LAQAN	(K)L/A Q A N/G W/G V/M\V S H R(S)		130.08	509.2631	1525.769	0.0055	3.6	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
19090	dirMS_041712_NAR_60mM_minus.4668.4668.3	3	6.12	1	1.35E+06		(R)AAEEED	(R)A/A/E E E D E A D/P K R(Q)		78.07	453.872	1359.602	-0.0008	-0.6	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
19091	dirMS_041712_NAR_20mM_plus.10577.10577.2	2	6.12	0	4.60E+04		(R)SGYLLP	(R)S G Y|L|L/P D/T K(A)		145.88	497.2665	993.525	0.0006	0.6	5.55	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
19092	dirMS_041712_NAR_20mM_plus.14668.14668.2	2	6.12	0	3.89E+04	M185m	(K)LAVNm	(K)L A/V/N/m V/P\F/P R(L)	m:Oxidized methionine	172.75	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
19093	dirMS_041712_NAR_20mM_plus.15218.15218.2	2	6.12	0	6.46E+04		(K)TLLENT	(K)T\L/L E\N T A I/T I/G R(L)		175.9	651.3693	1301.742	-0.011	-8.5	5.66	46579.3	4.96	HUMAN	E5RI07	Transportin-1
19094	dirMS_041712_NAR_20mM_plus.17521.17521.3	3	6.12	0	2.26E+05	M90m	(R)LFVGNL	(R)L F V G N L|P P D I/T E E/E m/R(K)	m:Oxidized methionine	192.57	625.9762	1859.921	15.9933	-0.9	4	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
19095	dirMS_041712_NAR_20mM_plus.18074.18074.2	2	6.12	0	1.00E+05		(K)VDFPQD	(K)V D/F/P Q D|Q L T A L/T G R(I)		195.75	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
19096	dirMS_041712_NAR_20mM_plus.8098.8098.2	2	6.12	0	5.37E+04		(K)SVTEQG	(K)S V/T E/Q G A|E L/S N E E\R(N)		124.97	774.8589	1548.714	-0.0031	-2	4.09	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
19097	dirMS_041712_NAR_30mM_plus2.4758.4758.2	2	6.12	0	3.00E+05		(R)MDDYC	(R)M/D/D/Y/C R(R)	C:Carbamidomethylation	75.98	430.1579	859.307	0.0012	1.4	4.21	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
19098	dirMS_041712_NAR_40mM_plus2.13434.13434.3	3	6.12	0	2.64E+05		(K)NLPPSG	(K)N L/P P S\G A V P V T G I/P/P H V V K(V)		145.08	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
19099	dirMS_041712_NAR_40mM_plus2.16095.16095.3	3	6.12	0	2.04E+04		(R)ALSTPYI	(R)A L/S|T\P Y I/H/S L A P I V V E K(L)		161.45	613.3524	1838.042	0.0004	0.2	6.79	12597.4	8.27	HUMAN	H7C2X3	HEAT repeat-containing protein 5B (Fragment)
19100	dirMS_041712_NAR_50mM_plus2.7398.7398.3	3	6.12	1	3.36E+05	M2747m	(K)TLQEVT	(K)T/L|Q/E V/T E m D/S V K/R(Y)	m:Oxidized methionine	105.03	517.9284	1535.773	15.9973	1.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
19101	dirMS_041712_NAR_60mM_plus.15363.15363.3	3	6.12	1	5.50E+05		(R)MTGSEF	(R)M/T|G/S E F D F E E/M K R(K)		136.32	536.2355	1606.688	0.0043	2.7	4.41	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
19102	dirMS_041712_NAR_60mM_plus.4585.4585.3	3	6.12	1	4.63E+05	M54m	(K)SLDEmE	(K)S L|D E m E/K/Q Q/R(E)	m:Oxidized methionine	76.27	427.2032	1263.6	15.9953	0.3	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
19103	dirMS_041712_NAR_120mM_minus.14842.14842.4	4	6.11	2	1.49E+05		(K)LLVGVD	(K)L L V/G V/D E K L N P E D/I K K(H)		134.98	453.2625	1810.032	-0.0039	-2.1	4.79	121749.9	6.97	HUMAN	P53396	ATP-citrate synthase
19104	dirMS_041712_NAR_120mM_minus.15271.15271.4	4	6.11	1	2.25E+05		(K)THLPGF	(K)T H L\P G F V E Q/A E/A/L K/A K(G)		137.72	435.4914	1738.949	-0.0049	-2.8	6.42	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
19105	dirMS_041712_NAR_120mM_minus.4375.4375.3	3	6.11	0	9.11E+04		(K)NSSVNE	(K)N/S/S V N/E G S/T Y H K(S)		72.72	441.5368	1322.597	-0.0013	-1	6.75	76931.3	5.22	HUMAN	F8VZN8	Protein phosphatase 1 regulatory subunit 12A (Fragment)
19106	dirMS_041712_NAR_30mM_minus2.5265.5265.2	2	6.11	0	6.04E+05		(R)TDTGEP	(R)T D|T\G E/P M G R(G)		82.4	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
19107	dirMS_041712_NAR_40mM_minus2.14253.14253.3	3	6.11	0	2.67E+05		(R)DVCTEL	(R)D V|C/T E L L/P L I K/P Q G R(V)	C:Carbamidomethylation	168.93	580.3211	1738.952	-0.0033	-1.9	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
19108	dirMS_041712_NAR_60mM_minus.10034.10034.3	3	6.11	0	2.95E+04		(R)ISNRPA	(R)I S N\R P A/F/M|P/S E/G K(M)		115.67	478.5785	1433.721	0.0004	0.3	8.75	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
19109	dirMS_041712_NAR_60mM_minus.10871.10871.3	3	6.11	1	2.74E+05		(R)QSVEAD	(R)Q S/V/E/A/D/I N G\L R R(V)		120.7	453.2461	1357.718	0.0055	4	6.07	19213.2	4.66	HUMAN	K7EMD9	Keratin, type I cytoskeletal 13 (Fragment)
19110	dirMS_041712_NAR_60mM_minus.11740.11740.3	3	6.11	0	5.03E+04		(R)TFIAIKP	(R)T F|I/A I/K/P D G V Q R(G)		125.38	448.9208	1344.763	-0.0156	-11.6	8.41	6640.6	8.25	HUMAN	C9K028	Nucleoside diphosphate kinase A (Fragment)
19111	dirMS_041712_NAR_120mM_plus.8425.8425.4	4	6.11	1	6.92E+05		(K)AGGAA	(K)A G G A A\V V I/T E/P E/H T K E R(V)		97.57	441.9865	1764.924	0.0003	0.2	5.5	56825.2	9.49	HUMAN	Q9P258	Protein RCC2
19112	dirMS_041712_NAR_20mM_plus.10355.10355.2	2	6.11	0	1.88E+05	M592m M	(R)mGPAm	(R)m G/P A/m|G\P A L G A G I/E R(M)	m:Oxidized methionine	144.65	730.3568	1427.713	31.993	2.1	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
19113	dirMS_041712_NAR_30mM_plus2.12522.12522.2	2	6.11	0	4.46E+05		(R)QGVDA	(R)Q G V/D/A/D I/N G L R(Q)		118.15	579.2997	1157.591	0.0012	1	4.21	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
19114	dirMS_041712_NAR_30mM_plus2.18424.18424.2	2	6.11	0	1.98E+05		(R)AMLDQ	(R)A M|L/D/Q L M G/T S R(D)		150.42	611.8	1222.592	0.0009	0.7	5.88	5509.4	10.84	HUMAN	F8WB41	Putative RNA-binding protein Luc7-like 2
19115	dirMS_041712_NAR_30mM_plus2.4256.4256.2	2	6.11	0	9.01E+05	M299m M	(K)NmmAA	(K)N m\m/A|A C D|P/R(H)	C:Carbamidomethylation m:Oxid	69.92	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
19116	dirMS_041712_NAR_30mM_plus2.8066.8200.2	2	6.11	0	6.28E+05		(R)STFSTN	(R)S T|F/S/T N Y R(S)		95.67	488.2306	975.453	0.0009	0.9	8.46	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
19117	dirMS_041712_NAR_40mM_plus2.13704.13704.3	3	6.11	0	1.41E+05		(K)NLPPSG	(K)N L/P P S\G A V/P V/T G I/P P H V V/K(V)		146.62	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
19118	dirMS_041712_NAR_40mM_plus2.15895.15895.3	3	6.11	1	1.33E+05		(K)LFTAESL	(K)L F|T/A/E S L/I G L K N P/E K(S)		160.13	553.9799	1659.932	-0.0065	-3.9	6.14	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
19119	dirMS_041712_NAR_50mM_plus2.16174.16174.3	3	6.11	1	1.44E+06		(K)VTADVI	(K)V/T/A D V/I N A A E/K/L Q V V G R(A)		152.22	595.0057	1783.007	-0.0047	-2.6	6.04	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
19120	dirMS_041712_NAR_50mM_plus2.17441.17441.3	3	6.11	0	1.02E+05		(K)GEMMD	(K)G E/M/M D L Q/H G S L F L R(T)		159.92	545.2677	1633.783	0.006	3.7	5.32	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
19121	dirMS_041712_NAR_50mM_plus2.7617.7617.3	3	6.11	0	8.32E+04		(R)AGAISA	(R)A G A|I/S\A S G P E/L Q G A G H S K(L)		105.93	546.6129	1637.824	0	0	6.79	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
19122	dirMS_041712_NAR_50mM_plus2.9603.9603.3	3	6.11	0	7.71E+05		(R)DNIQGI	(R)D N\I Q G I T/K/P/A I R(R)		117.22	442.5902	1325.754	0.0025	1.9	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
19123	dirMS_041712_NAR_60mM_plus.10421.10421.3	3	6.11	1	8.41E+05		(R)LKNTLT	(R)L K N T L T\Q/T/T/E/N L R(R)		112.28	511.2871	1531.844	0.0029	1.9	8.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
19124	dirMS_041712_NAR_60mM_plus.13909.13909.3	3	6.11	1	9.19E+05		(K)TTVKDL	(K)T T/V K D L S/E|L/G S V/R(T)		129.45	468.9268	1404.769	-0.0034	-2.4	5.74	533778	5.74	HUMAN	Q15149	Plectin
19125	dirMS_041712_NAR_60mM_plus.7511.7511.3	3	6.11	0	7.47E+05		(R)ALLTNV	(R)A L|L T N V S S/V/A L\G S/R(R)		97.88	463.2618	1387.79	-0.0195	-14.1	9.79	314220.6	6.46	HUMAN	Q7Z7M0	Multiple epidermal growth factor-like domains protein 8
19126	dirMS_041712_NAR_120mM_minus.8179.8179.4	4	6.1	2	2.31E+06		(K)KGAVAE	(K)K G A\V\A E/D/G D E L R T E\P E A K(K)		99.28	479.4901	1914.94	-0.0018	-0.9	4.36	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
19127	dirMS_041712_NAR_20mM_minus.13119.13119.2	2	6.1	0	2.27E+05		(R)GNPTVE	(R)G N|P T V|E V D L F T S K(G)		183.1	703.8605	1406.716	-0.0025	-1.8	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
19128	dirMS_041712_NAR_20mM_minus.8045.8045.2	2	6.1	0	6.12E+03		(R)AAAGYP	(R)A A A/G Y|P D/P Y S/R(A)		129.75	584.2733	1167.543	-0.0036	-3.1	5.88	266161	5.68	HUMAN	E9PPU0	Epiplakin
19129	dirMS_041712_NAR_30mM_minus2.18915.18915.2	2	6.1	0	1.91E+05		(K)CFSVLG	(K)C F/S|V|L/G F/C K(S)	C:Carbamidomethylation	157.42	559.2673	1117.517	0.0104	9.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
19130	dirMS_041712_NAR_30mM_minus2.19354.19354.2	2	6.1	0	2.43E+05		(R)FEELNA	(R)F E|E|L/N A/D L F R(G)		160.83	627.3141	1253.616	0.0048	3.9	4.14	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
19131	dirMS_041712_NAR_30mM_minus2.5998.5998.2	2	6.1	0	2.31E+04		(K)TGEITAS	(K)T G\E I/T A/S S N/K(S)		87.58	504.2543	1007.5	0.0009	0.9	5.66	14992.9	9.56	HUMAN	I3L4U9	Nuclear protein localization protein 4 homolog
19132	dirMS_041712_NAR_40mM_minus2.8331.8331.3	3	6.1	0	3.89E+03		(R)LLELGPK	(R)L/L/E\L/G\P K P E V/A Q Q T R(K)		129.42	560.3204	1678.949	-0.002	-1.2	6.14	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
19133	dirMS_041712_NAR_50mM_minus2.12101.12101.3	3	6.1	1	1.96E+05		(R)LATALQ	(R)L A/T/A L Q K/L/E E\A E K(A)		137.05	481.9385	1443.805	-0.0044	-3	4.79	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
19134	dirMS_041712_NAR_50mM_minus2.14719.14719.3	3	6.1	0	2.37E+04	M202m	(K)ILGSGIS	(K)I L|G/S G I S S\S S V L/H G m/V F K(K)	m:Oxidized methionine	151.75	612.3248	1818.978	15.9816	-7.2	8.76	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
19135	dirMS_041712_NAR_50mM_minus2.15812.15812.3	3	6.1	1	8.21E+04		(K)DANAKL	(K)D A N A K L\S E/L E/A/A/L Q/R(A)		158.97	543.6248	1628.86	-0.0004	-0.2	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
19136	dirMS_041712_NAR_20mM_plus.16550.16550.2	2	6.1	0	2.56E+04		(R)LIDFLEC	(R)L I/D|F L E\C G K(T)	C:Carbamidomethylation	185.57	547.7827	1094.555	0.0031	2.8	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
19137	dirMS_041712_NAR_30mM_plus2.16701.16701.2	2	6.1	0	3.82E+05		(R)LWDLTT	(R)L W|D/L/T/T G T T T R(R)		140.33	632.8304	1264.653	0.0003	0.3	5.84	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
19138	dirMS_041712_NAR_30mM_plus2.19138.19138.2	2	6.1	0	2.16E+05	S225s	(R)NsLLGLE	(R)N/s L L G L/E/K(T)	s:N-acetylglucosamine (S)	152.88	538.7881	873.504	203.0649	-13.4	6	25813.1	5.54	HUMAN	C9JQT8	Butyrophilin subfamily 3 member A3 (Fragment)
19139	dirMS_041712_NAR_30mM_plus2.19155.19155.2	2	6.1	0	3.59E+04		(K)DAGTIA	(K)D A\G T/I/A G L/N/V L R(I)		153.85	600.3411	1199.674	0.0007	0.6	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
19140	dirMS_041712_NAR_30mM_plus2.21865.21865.3	3	6.1	0	1.77E+05		(K)GLVQAL	(K)G L V Q|A L G L/S/N/F N/S R(Q)		169.48	492.6036	1475.796	-0.0003	-0.2	9.75	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
19141	dirMS_041712_NAR_40mM_plus2.12546.12546.2	2	6.1	0	2.54E+04		(K)ICSWNV	(K)I C|S W N\V/D G L/R(A)	C:Carbamidomethylation	140.23	610.297	1219.589	-0.0021	-1.7	5.84	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
19142	dirMS_041712_NAR_50mM_plus2.12056.12056.3	3	6.1	1	3.63E+05		(K)IGRIEDV	(K)I G R I/E D V T|P I/P S D/S T R(R)		130.32	585.9784	1755.924	-0.0029	-1.7	4.56	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
19143	dirMS_041712_NAR_50mM_plus2.6376.6376.3	3	6.1	1	2.84E+05		(R)TVGERL	(R)T\V G/E R L Q D/T H S W\K(S)		98.27	519.6023	1556.782	0.0108	6.9	6.42	25912.4	7.09	HUMAN	E7EVC1	Tektin-4
19144	dirMS_041712_NAR_50mM_plus2.8209.8209.3	3	6.1	0	5.15E+05		(R)LEPKPQ	(R)L E/P K P Q/P/P|V/A E/A T P R(S)		110.33	543.9631	1629.896	-0.0211	-13	6.14	14468.1	6.76	HUMAN	K7EJ51	Septin-9 (Fragment)
19145	dirMS_041712_NAR_50mM_plus2.8884.8884.3	3	6.1	0	3.97E+05		(R)ATQQQ	(R)A T Q Q Q H D F|T L/T/Q/T A D|G R(S)		113.55	639.9699	1917.905	-0.0098	-5.1	5.21	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
19146	dirMS_041712_NAR_60mM_plus.16555.16555.3	3	6.1	1	6.26E+05		(K)AAVEW	(K)A A|V/E/W F D G K D F Q G S K(L)		143.05	562.2762	1684.797	0.0175	10.4	4.56	65213.5	9.57	HUMAN	B0QYK0	Ewing sarcoma breakpoint region 1
19147	dirMS_041712_NAR_60mM_plus.16920.16920.3	3	6.1	1	6.33E+06		(K)LKVPEW	(K)L K V/P E/W/V D/T V K(L)		145.72	438.5872	1313.746	0.0007	0.5	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
19148	dirMS_041712_NAR_120mM_minus.20154.20154.4	4	6.09	2	6.50E+03		(R)TLAEIAK	(R)T L|A E I A K V E\L/D N M/P/L R G K(Q)		165.87	500.2804	1998.105	-0.0055	-2.7	5.85	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
19149	dirMS_041712_NAR_20mM_minus.12026.12026.2	2	6.09	0	1.94E+05	M185m	(K)LAVNm	(K)L/A/V|N m V/P F/P R(L)	m:Oxidized methionine	170.02	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
19150	dirMS_041712_NAR_20mM_minus.7639.7639.2	2	6.09	0	2.24E+05		(K)TVPVEA	(K)T V/P/V E A V T S K(T)		125.3	515.7883	1030.578	-0.0086	-8.3	5.66	35720	5.34	HUMAN	B4E358	Src substrate cortactin
19151	dirMS_041712_NAR_30mM_minus2.13061.13061.2	2	6.09	0	5.04E+05		(K)LQQFFN	(K)L Q/Q/F/F N E/R(I)		125.17	541.2823	1081.543	0.0148	13.7	6	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
19152	dirMS_041712_NAR_30mM_minus2.17362.17362.2	2	6.09	0	2.79E+05		(K)FEDENF	(K)F E|D E N F\I L/K(H)		148.07	577.7894	1154.573	-0.0013	-1.1	4.14	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
19153	dirMS_041712_NAR_30mM_minus2.17490.17490.2	2	6.09	0	1.61E+05		(K)FEDENF	(K)F/E/D E\N\F I/L K(H)		148.93	577.7894	1154.573	-0.0013	-1.1	4.14	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
19154	dirMS_041712_NAR_30mM_minus2.5848.5848.2	2	6.09	0	1.32E+05		(K)TSEVNC	(K)T S/E/V/N C Y/R(C)	C:Carbamidomethylation	86.63	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
19155	dirMS_041712_NAR_30mM_minus2.7244.7244.2	2	6.09	0	3.99E+05	T6t	(-)MASSPt	(-)M A|S S/P/t K(G)	t:N-acetylglucosamine (T)	94.48	462.7203	721.355	203.0784	-1	8.5	151965	6.27	HUMAN	J3KQA9	Microtubule-associated tumor suppressor candidate 2
19156	dirMS_041712_NAR_40mM_minus2.11026.11026.3	3	6.09	1	1.14E+05	M362m	(R)EGSVmL	(R)E G S V/m/L Q/V D/V/D T V K G/G L K(L)	m:Oxidized methionine	147.85	630.9989	1874.989	15.993	-1	4.56	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
19157	dirMS_041712_NAR_50mM_minus2.12567.12567.3	3	6.09	0	3.06E+05		(K)AASDIA	(K)A A S/D I|A M T E L/P P T H|P I R(L)		139.55	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
19158	dirMS_041712_NAR_50mM_minus2.13725.13725.3	3	6.09	1	2.15E+05		(R)SEGVVA	(R)S E/G V V A V L/L T K K(S)		146.3	415.255	1243.762	-0.0116	-9.3	8.31	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
19159	dirMS_041712_NAR_50mM_minus2.6110.6110.3	3	6.09	1	5.69E+04	T501t	(K)AAARDV	(K)A A|A/R D V t/L E N R(L)	t:N-acetylglucosamine (T)	97.78	473.5826	1215.644	203.0892	6.9	6.12	59289.7	6.05	HUMAN	P49591	Serine--tRNA ligase, cytoplasmic
19160	dirMS_041712_NAR_60mM_minus.10979.10979.3	3	6.09	0	2.63E+05		(R)ALPESL	(R)A L/P E/S L/G Q H/A L R(S)		121.32	431.2376	1291.712	-0.0135	-10.4	6.79	31463.6	5.53	HUMAN	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1
19161	dirMS_041712_NAR_60mM_minus.14629.14629.3	3	6.09	0	4.16E+05		(K)AVGHPF	(K)A V/G H/P F V I/Q|L/G R(I)		141.9	431.9182	1293.743	-0.0026	-2	9.8	124524.8	5.71	HUMAN	O14980	Exportin-1
19162	dirMS_041712_NAR_60mM_minus.17710.17710.3	3	6.09	0	5.23E+05	M3139m	(K)DELVmE	(K)D E L V m/E|I L/S D L L K(R)	m:Oxidized methionine	159.68	511.9372	1517.813	15.9839	-7.2	3.91	404166.4	6.52	HUMAN	Q0VDD8	Dynein heavy chain 14, axonemal
19163	dirMS_041712_NAR_60mM_minus.18137.18137.3	3	6.09	1	1.65E+05		(R)IRVESLL	(R)I R V E S\L\L\V/T/A I S K(A)		162.5	476.9628	1428.878	-0.0046	-3.2	8.75	91730	7.16	HUMAN	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15
19164	dirMS_041712_NAR_60mM_minus.18407.18407.3	3	6.09	1	1.13E+04	S166s	(R)ATVIGsF	(R)A T V I G s\F|K/L/W/P T K(I)	s:N-acetylglucosamine (S)	163.17	550.9705	1447.831	203.0662	-8	10	71027.8	5.65	HUMAN	Q9C093-4	Isoform 4 of Sperm flagellar protein 2
19165	dirMS_041712_NAR_120mM_plus.18802.18802.3	3	6.09	2	4.37E+05		(R)KIEEIKD	(R)K|I E E I K D\F\L/L T/A R(R)		151.93	525.9746	1575.911	-0.0012	-0.8	6.18	2559	9.99	HUMAN	J3KSP2	60S ribosomal protein L38 (Fragment)
19166	dirMS_041712_NAR_20mM_plus.15085.15085.2	2	6.09	0	1.18E+05	S517s	(K)ISSQLPE	(K)I S|S Q\L/P E s D I L E K(Q)	s:Phosphorylated S	175.32	769.873	1458.769	79.9701	2.5	4.14	252894	5.62	HUMAN	F5H090	Protein unc-13 homolog C
19167	dirMS_041712_NAR_20mM_plus.16004.16004.2	2	6.09	0	3.37E+05		(R)GNPTVE	(R)G N/P T V/E V/D L\F T S/K(G)		180.87	703.861	1406.716	-0.0015	-1	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
19168	dirMS_041712_NAR_20mM_plus.18691.18691.2	2	6.09	0	5.48E+04	S3142s	(R)TVLVSs	(R)T V\L|V|S\s/G L R(E)	s:N-acetylglucosamine (S)	199.73	567.8286	931.557	203.0928	11.8	9.41	523482.6	5.17	HUMAN	Q07954	Prolow-density lipoprotein receptor-related protein 1
19169	dirMS_041712_NAR_20mM_plus.7535.7535.2	2	6.09	0	2.30E+04		(R)TVGIVGI	(R)T/V|G\I/V\G N Q/P/K(V)		121	506.7922	1012.579	-0.0014	-1.4	8.41	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
19170	dirMS_041712_NAR_30mM_plus2.14389.14389.2	2	6.09	0	3.73E+05		(R)GIFTSEI	(R)G I|F/T/S E I G T K(Q)		129	526.7806	1052.562	-0.0083	-7.9	6	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
19171	dirMS_041712_NAR_30mM_plus2.7402.7402.2	2	6.09	0	1.49E+05		(R)VTDALN	(R)V T|D/A/L\N/A T R(A)		93.77	480.759	960.511	-0.0002	-0.2	5.81	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
19172	dirMS_041712_NAR_40mM_plus2.15281.15281.3	3	6.09	0	1.14E+05		(R)IETMLGI	(R)I E/T M L G/D V/A/V/A V H P K(D)		156.3	527.286	1579.851	-0.0078	-4.9	5.32	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
19173	dirMS_041712_NAR_50mM_plus2.17081.17081.3	3	6.09	0	2.91E+05		(R)VSSISPG	(R)V/S/S I/S P G S A T L L S S V G R(L)		157.58	539.9622	1617.881	-0.0086	-5.3	9.72	9358.5	10.35	HUMAN	G3V2L5	Ubiquinone biosynthesis monooxygenase COQ6
19174	dirMS_041712_NAR_50mM_plus2.6679.6679.3	3	6.09	0	5.53E+04		(K)NSYHFS	(K)N S/Y H F S\A G F/G S P I E D K(S)		100.02	585.9333	1755.797	-0.0119	-6.8	5.32	67497.7	7.15	HUMAN	B4DXS3	Armadillo repeat-containing protein 3
19175	dirMS_041712_NAR_20mM_minus.10349.10349.2	2	6.08	0	9.30E+04		(R)NTGIICT	(R)N T\G/I|I/C T/I G/P A S R(S)	C:Carbamidomethylation	152.63	680.3561	1359.705	0	0	9.75	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
19176	dirMS_041712_NAR_30mM_minus2.10067.10067.2	2	6.08	0	1.30E+06		(R)ANFENL	(R)A N|F/E N L A/K(E)		109	453.7335	906.468	-0.0082	-9.1	6.05	35720	5.34	HUMAN	B4E358	Src substrate cortactin
19177	dirMS_041712_NAR_50mM_minus2.11308.11308.3	3	6.08	0	1.66E+04		(R)VVVLM	(R)V V|V/L/M/G S/T S D L G H C E K(I)	C:Carbamidomethylation	132.28	577.9535	1731.84	0.0055	3.2	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
19178	dirMS_041712_NAR_50mM_minus2.14610.14610.3	3	6.08	1	2.30E+05		(R)GFPTIYF	(R)G F/P T I Y/F S P A N K K(L)		150.7	490.5972	1469.779	-0.0017	-1.1	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
19179	dirMS_041712_NAR_50mM_minus2.5977.5977.3	3	6.08	0	3.55E+04		(R)ATAPQT	(R)A T/A/P Q/T Q H\V S P M/R(Q)		96.35	475.244	1423.711	0.0064	4.5	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta

19180	dirMS_041712_NAR_50mM_minus2.8321.8321.3	3	6.08	1	8.27E+04	M61m	(K)NQVAm	(K)N Q|V/A\m N/P T N T\V/F D A K R(L)	m:Oxidized methionine	114.92	607.968	1805.896	15.9932	-1	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
19181	dirMS_041712_NAR_50mM_minus2.9670.9670.3	3	6.08	1	1.76E+04		(K)GLESTTL	(K)G L/E S|T T L/A\D K D G E I Y C K(G)	C:Carbamidomethylation	122.82	633.9748	1899.9	0.0094	5	4.32	16685.6	9.7	HUMAN	E9PND2	Cysteine and glycine-rich protein 1 (Fragment)
19182	dirMS_041712_NAR_60mM_minus.12766.12766.3	3	6.08	0	4.82E+05		(K)GIHPTIIS	(K)G I H P T I\I|S/E/S F/Q K(A)		131.1	486.2642	1456.78	-0.0014	-1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
19183	dirMS_041712_NAR_120mM_plus.20912.20912.4	4	6.08	0	2.55E+05		(K)ALEHAF	(K)A L/E H A F Q L/E/H I/M D/L T R(L)		163.23	481.7493	1923.975	0.0008	0.4	5.27	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
19184	dirMS_041712_NAR_120mM_plus.5684.5684.3	3	6.08	1	2.24E+04		(R)TEERAE	(R)T/E/E R A\E\L/A E/S/R(C)		82.85	430.8806	1290.628	-0.0012	-0.9	4.49	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
19185	dirMS_041712_NAR_120mM_plus.6005.6005.2	2	6.08	1	2.29E+06		(K)IREEYPD	(K)I R/E/E\Y/P D/R(I)		84.93	539.2694	1077.532	-0.0008	-0.8	4.68	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
19186	dirMS_041712_NAR_120mM_plus.6015.6015.3	3	6.08	0	7.67E+04		(R)IAAGAG	(R)I/A/A G A G D G T L E T K(R)		84.85	401.882	1203.622	0.0099	8.2	4.37	149030.1	11.3	HUMAN	A8K8P3	Protein SFI1 homolog
19187	dirMS_041712_NAR_120mM_plus.6756.6756.2	2	6.08	0	9.17E+04		(K)EMQPTH	(K)E\M Q/P T H/P I R(L)		88.62	554.7822	1108.557	0.0003	0.3	6.85	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
19188	dirMS_041712_NAR_20mM_plus.14221.14221.3	3	6.08	1	7.33E+05	M87m M9	(K)LYKSmT	(K)L Y K S m T/L/L N/T m D R(I)	m:Oxidized methionine	170.93	539.9421	1585.808	32.0041	8.8	8.59	51131.7	6.69	HUMAN	B4DP47	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial
19189	dirMS_041712_NAR_20mM_plus.17551.17551.3	3	6.08	0	6.85E+04		(K)LAAVDA	(K)L A\A V D A T\V N/Q/V L/A S R(Y)		192.37	509.9542	1527.849	-0.0009	-0.6	5.84	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
19190	dirMS_041712_NAR_20mM_plus.18089.18089.2	2	6.08	0	2.29E+05		(R)ILVATNL	(R)I L/V|A/T N L/F G R(G)		195.22	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
19191	dirMS_041712_NAR_20mM_plus.19081.19081.2	2	6.08	0	2.04E+05		(R)VCTLAII	(R)V C T\L/A\I|I\D P G D S D I I R(S)	C:Carbamidomethylation	202.77	879.4578	1757.91	-0.0019	-1.1	3.93	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
19192	dirMS_041712_NAR_30mM_plus2.13909.13909.2	2	6.08	0	1.06E+05		(R)LNLNNT	(R)L N|L/N\N T V L/S K(R)		127.27	558.323	1115.642	-0.0032	-2.8	8.75	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
19193	dirMS_041712_NAR_30mM_plus2.20588.20628.2	2	6.08	0	1.17E+05		(K)SVVTSIF	(K)S V|V|T/S I\F G V K(N)		162.78	518.799	1036.604	-0.013	-12.5	8.47	132902.3	5.82	HUMAN	J3KR24	Isoleucine--tRNA ligase, cytoplasmic
19194	dirMS_041712_NAR_30mM_plus2.22286.22286.2	2	6.08	0	1.60E+05		(K)GLSSLLC	(K)G L/S/S L/L/C N F T K(S)	C:Carbamidomethylation	171.92	620.3199	1239.64	-0.0077	-6.2	8.75	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
19195	dirMS_041712_NAR_40mM_plus2.12134.12134.3	3	6.08	1	9.36E+04		(K)SARSSSF	(K)S A R S S/S F T S/G/E R(E)		137.35	424.5414	1271.598	0.0122	9.6	9.32	63323	6.06	HUMAN	P0C1S8	Wee1-like protein kinase 2
19196	dirMS_041712_NAR_40mM_plus2.9607.9607.2	2	6.08	0	1.27E+05		(K)FYEAFSK	(K)F/Y/E/A F S K(N)		120.15	446.2159	891.425	-0.0002	-0.2	6	20127.1	9.4	HUMAN	H0Y598	Heat shock protein HSP 90-beta (Fragment)
19197	dirMS_041712_NAR_50mM_plus2.11842.11842.3	3	6.08	1	4.35E+05		(K)QIDLSTV	(K)Q I D L S/T V/D/L K K(L)		130.47	420.5781	1259.72	-0.0008	-0.6	5.96	21156.2	9.41	HUMAN	P55145	Mesencephalic astrocyte-derived neurotrophic factor
19198	dirMS_041712_NAR_50mM_plus2.16322.16322.3	3	6.08	1	1.92E+05		(K)YAVLYQ	(K)Y A|V|L\Y Q/P L F D K R(F)		152.63	504.9436	1512.821	-0.0047	-3.1	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
19199	dirMS_041712_NAR_50mM_plus2.20714.20714.3	3	6.08	0	1.77E+06		(R)AGKPVIC	(R)A G|K\P V I C\A\T/Q/M L E S M I/K(K)	C:Carbamidomethylation	178.58	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
19200	dirMS_041712_NAR_50mM_plus2.8940.8940.3	3	6.08	0	8.15E+04	K327k	(R)THIEEKP	(R)T/H I E E K P Y/k(C)	k:Ubiquitin-K	114.35	420.2237	1144.6	114.0568	11.1	6.42	47720.4	10.06	HUMAN	H0Y5S2	Uncharacterized protein
19201	dirMS_041712_NAR_50mM_plus2.9087.9087.3	3	6.08	0	1.50E+05		(R)NDIASH	(R)N D/I/A S H P P V/E/G S Y\A P R(R)		114.92	570.6114	1709.824	-0.0045	-2.6	5.32	26398.4	5.21	HUMAN	H7C597	Staphylococcal nuclease domain-containing protein 1 (Fragment)
19202	dirMS_041712_NAR_50mM_plus2.9201.9201.3	3	6.08	1	3.70E+05		(R)IITEGFE	(R)I/I/T E/G F/E A/A K E K(A)		115.27	445.9079	1335.716	-0.0063	-4.7	4.79	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
19203	dirMS_041712_NAR_60mM_plus.18183.18183.3	3	6.08	0	1.72E+05		(R)VSLDVN	(R)V/S|L/D\V N H F A\P D E L T V K(T)		152.12	595.3095	1783.922	-0.0085	-4.8	4.54	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
19204	dirMS_041712_NAR_60mM_plus.5032.5032.3	3	6.08	1	3.95E+05		(R)AAEDDE	(R)A A|E/D/D/E D D D/V/D T K K(Q)		83.53	522.5529	1565.645	-0.0008	-0.5	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
19205	dirMS_041712_NAR_120mM_minus.19337.19337.3	3	6.07	1	1.46E+05		(K)YNQLLRI	(K)Y/N/Q/L L/R I E E E/L G S K(A)		160.73	564.6367	1691.896	-0.0007	-0.4	4.79	47510.4	7.04	HUMAN	P06733	Alpha-enolase
19206	dirMS_041712_NAR_20mM_minus.8430.8430.2	2	6.07	0	1.06E+05		(R)GYSFTT	(R)G Y|S/F/T|T T A E R(E)		133.38	566.771	1132.527	0.0078	6.9	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
19207	dirMS_041712_NAR_30mM_minus2.11654.11678.2	2	6.07	0	5.23E+05		(R)ENLSAA	(R)E N/L/S/A A/F S R(Q)		117.53	497.7529	994.495	0.0033	3.3	6.1	69497.2	5.22	HUMAN	J3KQG6	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A
19208	dirMS_041712_NAR_30mM_minus2.16187.16291.2	2	6.07	0	1.09E+05		(K)FGVIFA	(K)F/G\V|I/F/A/G A Q K(N)		141.95	519.2901	1037.578	-0.0049	-4.7	8.75	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
19209	dirMS_041712_NAR_30mM_minus2.6516.6516.2	2	6.07	0	1.01E+05		(K)VLENAE	(K)V/L/E|N/A E/G A R(T)		89.65	479.7505	958.495	-0.0015	-1.6	4.53	6809.6	9.69	HUMAN	D6RA73	Stress-70 protein, mitochondrial (Fragment)
19210	dirMS_041712_NAR_40mM_minus2.14357.14357.3	3	6.07	1	1.82E+05		(K)GNAGGI	(K)G N|A|G/G/I Q P D L L I S L T/A P K K(S)		169.37	631.6945	1893.08	-0.0114	-6	8.59	32016.3	7.83	HUMAN	Q8NCW5	NAD(P)H-hydrate epimerase
19211	dirMS_041712_NAR_50mM_minus2.12484.12484.3	3	6.07	0	6.09E+04		(K)LGDVYV	(K)L/G/D\V/Y V N\D A/F G T A/H R(A)		139.22	545.6023	1634.792	0.0002	0.1	5.21	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
19212	dirMS_041712_NAR_50mM_minus2.13411.13411.3	3	6.07	0	3.28E+05		(K)LQMEA	(K)L Q|M E A P H I/I V/G T P G R(V)		144.97	540.2947	1618.873	-0.0038	-2.4	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
19213	dirMS_041712_NAR_50mM_minus2.14500.14500.3	3	6.07	1	2.57E+05		(R)GFPTIYF	(R)G F/P T I Y F S/P/A N K K(L)		150.55	490.5972	1469.779	-0.0017	-1.1	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
19214	dirMS_041712_NAR_50mM_minus2.9649.9649.3	3	6.07	1	6.32E+04		(K)EVLPALE	(K)E V\L/P A L|E N N K E Q I Q K(I)		123.05	584.9856	1752.949	-0.0068	-3.9	4.79	16704.6	6.2	HUMAN	Q9UHV9	Prefoldin subunit 2
19215	dirMS_041712_NAR_60mM_minus.19442.19442.3	3	6.07	0	3.67E+05		(K)HSQFIG	(K)H S Q F I G\Y|P/I/T L/Y L E K(E)		173.4	603.6548	1808.958	-0.0083	-4.6	6.75	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
19216	dirMS_041712_NAR_20mM_plus.6024.6024.3	3	6.07	0	1.02E+06	M295m M	(R)mGQmA	(R)m G Q m A m\G\G|A|m/G/I N N R(G)	m:Oxidized methionine	100.27	534.8861	1538.67	63.9743	-3.4	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
19217	dirMS_041712_NAR_30mM_plus2.10512.10512.2	2	6.07	0	2.12E+05		(R)TEEGPT	(R)T E|E|G/P T L/S Y G R(D)		108.83	605.2924	1209.575	0.0029	2.4	4.53	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
19218	dirMS_041712_NAR_30mM_plus2.7799.7799.2	2	6.07	0	4.68E+05	M441m	(R)MGLVm	(R)M/G L|V/m D R(M)	m:Oxidized methionine	94.68	419.2004	821.401	15.9927	-2.6	5.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
19219	dirMS_041712_NAR_50mM_plus2.11528.11528.3	3	6.07	0	3.55E+05		(K)SNMGH	(K)S/N|M/G H/P E|P A/S G L A A L A K(V)		128.5	550.9462	1650.827	-0.0028	-1.7	6.47	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
19220	dirMS_041712_NAR_50mM_plus2.13818.13818.3	3	6.07	0	3.03E+05		(K)TSLESHT	(K)T S/L E S H T V L A P L T L\K(T)		140.87	537.3129	1609.916	0.0082	5.1	6.41	309114.3	7.58	HUMAN	J3KNV1	Zinc finger protein 292
19221	dirMS_041712_NAR_50mM_plus2.21476.21476.3	3	6.07	1	8.45E+05		(R)LGSAIQK	(R)L G/S A I Q K I I T I P A/A L Q Q V/K(N)		184.23	664.7439	1992.222	-0.0044	-2.2	10	265720.8	6.08	HUMAN	E7ETS8	DNA polymerase
19222	dirMS_041712_NAR_120mM_minus.20655.20655.4	4	6.06	0	2.20E+05		(R)VYADGII	(R)V Y A D G I/F/D/L F H S G H A R(A)		170.8	451.9763	1804.877	0.0068	3.8	5.97	37652.7	7.85	HUMAN	B4E322	Choline-phosphate cytidylyltransferase A
19223	dirMS_041712_NAR_20mM_minus.10688.10688.3	3	6.06	0	9.33E+03	M380m	(K)SPFEVQ	(K)S P/F E V/Q\V G|P/E A/G m Q K(V)	m:Oxidized methionine	154.82	540.5959	1603.778	15.9947	-0.1	4.53	258215.9	5.48	HUMAN	E7EN95	Filamin-B
19224	dirMS_041712_NAR_20mM_minus.7151.7151.2	2	6.06	0	1.29E+05		(K)VTLTSEE	(K)V T|L/T/S E/E E A R(L)		119.62	567.785	1134.564	-0.001	-0.9	4.25	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
19225	dirMS_041712_NAR_20mM_minus.9678.9678.2	2	6.06	0	1.25E+05		(R)AGTGVD	(R)A G/T G V/D/N\V/D L\E A A/T R(K)		146.78	744.8662	1488.729	-0.0038	-2.5	4.03	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
19226	dirMS_041712_NAR_30mM_minus2.15453.15453.2	2	6.06	0	1.23E+04		(K)LCDFGF	(K)L C/D/F/G/F A R(A)	C:Carbamidomethylation	137.12	493.2343	985.456	0.0053	5.4	5.84	143554.7	5.57	HUMAN	A8MU99	Serine/threonine-protein kinase 36
19227	dirMS_041712_NAR_30mM_minus2.7560.7560.2	2	6.06	0	1.19E+05		(R)GGGEQE	(R)G G/G E Q E|T Q/E/L/A/S/K(R)		95.42	667.3161	1333.623	0.0019	1.4	4.25	33411.4	5.35	HUMAN	Q96QR8	Transcriptional activator protein Pur-beta
19228	dirMS_041712_NAR_40mM_minus2.12114.12114.3	3	6.06	0	1.48E+05		(K)AAPEAS	(K)A A/P E A S S P P A S P L Q H L L/P G K(A)		154.52	656.6876	1968.055	-0.0067	-3.4	6.79	84649.8	5.82	HUMAN	Q96TA1	Niban-like protein 1
19229	dirMS_041712_NAR_40mM_minus2.8060.8060.2	2	6.06	0	7.00E+04		(R)IVLQIDN	(R)I/V|L Q/I D N A R(L)		128.1	521.3059	1041.605	-0.0006	-0.6	5.84	20842.9	5.32	HUMAN	C9JM50	Keratin, type I cytoskeletal 19 (Fragment)
19230	dirMS_041712_NAR_50mM_minus2.10669.10669.3	3	6.06	1	7.44E+03		(K)VAVVAG	(K)V A\V|V/A/G Y G D V/G K G C A Q A L R(G)	C:Carbamidomethylation	129.78	630.9952	1890.985	-0.0144	-7.6	8.56	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
19231	dirMS_041712_NAR_50mM_minus2.16493.16493.3	3	6.06	0	8.79E+04		(K)VSHLLGI	(K)V S H L\L G I\N|V/T/D F T R(G)		162.08	524.6237	1571.854	0.0025	1.6	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
19232	dirMS_041712_NAR_50mM_minus2.17369.17369.3	3	6.06	0	5.77E+03		(K)LHDNLII	(K)L H D N L|I I|S/D L/E N T V K(K)		167.5	575.3118	1723.922	-0.0016	-1	4.54	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
19233	dirMS_041712_NAR_50mM_minus2.4959.4959.3	3	6.06	1	2.84E+05	M137m	(R)mQNDT	(R)m Q N D/T A/E N E T T E\K E E K(S)	m:Oxidized methionine	83	638.2738	1896.813	15.9941	-0.4	4.14	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
19234	dirMS_041712_NAR_60mM_minus.13407.13407.3	3	6.06	1	3.11E+05		(R)KFNALF	(R)K F N A L/F\A\Q/G/N/Y S E A A K(V)		135.12	586.9642	1758.881	-0.0029	-1.7	8.5	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
19235	dirMS_041712_NAR_60mM_minus.6394.6394.3	3	6.06	1	2.41E+04		(R)VEEKEGI	(R)V E/E K E G\I|P/P Q Q\Q R(L)		95.33	513.2702	1537.797	-0.0008	-0.6	4.79	19593.1	6.86	HUMAN	E9PL57	Protein NEDD8-MDP1 (Fragment)
19236	dirMS_041712_NAR_60mM_minus.8001.8001.3	3	6.06	1	3.76E+05	M230m M	(R)mSmKE	(R)m S m K E V D/E Q/m\L/N V Q N\K(N)	m:Oxidized methionine	103.85	657.9647	1923.897	47.9823	-1.3	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
19237	dirMS_041712_NAR_120mM_plus.10263.10263.3	3	6.06	0	1.10E+05		(R)IHDPQL	(R)I H D\P Q|L|L T E/R(A)		106.9	407.8899	1221.659	-0.0035	-2.8	5.32	21721.5	5.37	HUMAN	H7BZ35	Aspartate--tRNA ligase, cytoplasmic (Fragment)
19238	dirMS_041712_NAR_120mM_plus.9481.9481.4	4	6.06	0	4.92E+04		(K)TGTITTF	(K)T G\T I/T/T F E/H A H N M/R(V)		102.92	404.6969	1615.765	0.0012	0.8	6.61	96306.4	6.41	HUMAN	P13639	Elongation factor 2
19239	dirMS_041712_NAR_20mM_plus.12726.12726.2	2	6.06	0	2.75E+04		(K)YDGIILP	(K)Y D/G I I\L|P G K(-)		160.08	488.2764	975.551	-0.0054	-5.6	5.83	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
19240	dirMS_041712_NAR_30mM_plus2.11117.11160.2	2	6.06	0	6.42E+05		(K)VSDFGL	(K)V S/D F G L A/K(A)		111.17	418.7281	836.451	-0.0023	-2.8	5.81	56910.3	9.38	HUMAN	K7EQY5	Megakaryocyte-associated tyrosine kinase, isoform CRA_a
19241	dirMS_041712_NAR_30mM_plus2.21213.21213.2	2	6.06	0	5.80E+03		(K)SCSLLSL	(K)S C|S L/L/S L/A/T I/K(V)	C:Carbamidomethylation	164.47	596.8315	1192.661	-0.0049	-4.1	8.47	84619.4	5.7	HUMAN	Q6UWE0	E3 ubiquitin-protein ligase LRSAM1
19242	dirMS_041712_NAR_30mM_plus2.7141.7141.2	2	6.06	0	2.31E+05		(R)AQVIYT	(R)A Q|V|I Y T/R(N)		91.63	425.7397	850.478	-0.006	-7.1	8.79	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
19243	dirMS_041712_NAR_40mM_plus2.11121.11121.3	3	6.06	1	7.28E+04		(K)AVEEED	(K)A V/E|E/E D K M T/P E Q L A I K(N)		131.85	610.9764	1830.915	-0.0007	-0.4	4.25	34747.6	6.06	HUMAN	O00487	26S proteasome non-ATPase regulatory subunit 14
19244	dirMS_041712_NAR_40mM_plus2.8477.8477.2	2	6.06	0	1.52E+04		(R)LLEQGIR	(R)L L/E/Q/G I R(V)		110.73	414.7481	828.494	-0.0049	-5.9	6	125112.3	6.65	HUMAN	P28340	DNA polymerase delta catalytic subunit
19245	dirMS_041712_NAR_50mM_plus2.7301.7301.3	3	6.06	0	1.68E+05		(R)SGSSQE	(R)S G/S/S/Q E L D V K/P S A S P Q E R(S)		103.85	634.6443	1901.92	-0.0016	-0.8	4.68	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
19246	dirMS_041712_NAR_60mM_plus.12244.12244.3	3	6.06	0	9.17E+05		(K)TKPYIQV	(K)T K/P/Y I Q V/D/I/G G G Q T K(T)		121.42	535.6249	1604.864	-0.0041	-2.6	8.17	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
19247	dirMS_041712_NAR_60mM_plus.13083.13083.2	2	6.06	2	6.28E+05		(K)STGVED	(K)S T G|V E D\T E E R G K R(E)		125.17	732.3483	1463.709	-0.0192	-13.1	4.87	126770.3	5.57	HUMAN	Q5T0N1	Tetratricopeptide repeat protein 18
19248	dirMS_041712_NAR_60mM_plus.16827.16827.3	3	6.06	1	5.02E+05		(K)AKLEQLF	(K)A K L E Q\L|F/Q/D\E V A K(A)		144.33	506.9426	1518.816	-0.003	-2	4.68	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
19249	dirMS_041712_NAR_60mM_plus.20697.20697.3	3	6.06	1	2.81E+05		(R)KVESLW	(R)K V\E S L|W/P/I F R(I)		169.62	425.5789	1274.726	-0.0034	-2.7	8.75	14138.1	9.89	HUMAN	C9JNV2	Protein BUD31 homolog
19250	dirMS_041712_NAR_120mM_minus.19028.19028.3	3	6.05	1	1.44E+05		(R)HATALE	(R)H A/T/A L E E L/S E Q/L E/Q A K R(F)		158.6	651.6718	1953.004	-0.0027	-1.4	4.91	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
19251	dirMS_041712_NAR_30mM_minus2.5509.5509.2	2	6.05	0	1.73E+05		(R)LYQAGE	(R)L/Y|Q/A G E G R(L)		84.55	447.2217	893.448	-0.0114	-12.8	6	38089.6	6.79	HUMAN	B4DT77	Annexin
19252	dirMS_041712_NAR_30mM_minus2.9735.9735.2	2	6.05	0	1.92E+05		(R)LGYTPV	(R)L/G/Y|T/P V C R(A)	C:Carbamidomethylation	107.18	483.2423	965.487	-0.01	-10.3	8.75	25847.9	6.33	HUMAN	Q15102	Platelet-activating factor acetylhydrolase IB subunit gamma
19253	dirMS_041712_NAR_40mM_minus2.14661.14661.3	3	6.05	0	1.67E+05	M159m	(R)SVAAIH	(R)S V/A\A I H P S/L E\I P m L I P K(E)	m:Oxidized methionine	171.32	611.3477	1816.04	15.9884	-3.5	6.47	31606.3	6.72	HUMAN	B4E329	Phosphoribosyl pyrophosphate synthase-associated protein 2
19254	dirMS_041712_NAR_50mM_minus2.10849.10849.3	3	6.05	1	4.90E+04		(R)DYSGQG	(R)D Y|S/G Q G V V/K L D V Q P K(C)		129.88	544.9596	1632.859	0.0051	3.1	5.96	66876.9	6.17	HUMAN	O75083	WD repeat-containing protein 1
19255	dirMS_041712_NAR_50mM_minus2.7733.7733.3	3	6.05	1	1.66E+04	M26m	(K)LAEQAE	(K)L A/E Q A E R Y D/D\M/A A C m K(S)	C:Carbamidomethylation m:Oxid	111.05	639.9511	1901.819	16.0197	12.9	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
19256	dirMS_041712_NAR_60mM_minus.11809.11809.3	3	6.05	0	3.08E+04		(K)SQIHDIV	(K)S Q\I H D I V\L|V/G G S T/R(I)		125.93	494.6084	1481.807	0.0036	2.4	6.46	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
19257	dirMS_041712_NAR_60mM_minus.16416.16416.3	3	6.05	1	9.56E+04		(R)SKGIYQS	(R)S K G I Y Q S L|E\G A/V\Q A/G Q\L K(V)		151.67	626.3417	1877.013	-0.0022	-1.1	8.22	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
19258	dirMS_041712_NAR_60mM_minus.8860.8860.3	3	6.05	1	1.20E+05		(R)SRAEAES	(R)S R A E|A\E\S\M/Y Q I K(Y)		109.07	471.5706	1412.684	0.0134	9.5	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
19259	dirMS_041712_NAR_120mM_plus.8888.8888.3	3	6.05	0	5.44E+05		(R)RPELEDS	(R)R P\E\L\E|D|S T L R(Y)		99.18	405.8796	1215.633	-0.0085	-7	4.68	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
19260	dirMS_041712_NAR_20mM_plus.11206.11206.2	2	6.05	0	2.01E+05		(K)LITPAVV	(K)L I|T/P A V/V S E R(L)		149.97	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
19261	dirMS_041712_NAR_20mM_plus.14892.14892.2	2	6.05	0	1.26E+05		(R)LLDAQLS	(R)L L D A Q\L S\T/G G I V D/P S K(S)		174.67	807.4389	1613.874	-0.004	-2.5	4.21	533778	5.74	HUMAN	Q15149	Plectin
19262	dirMS_041712_NAR_20mM_plus.18457.18457.2	2	6.05	0	7.03E+04		(R)VVVLGL	(R)V V/V/L G L L P R(G)		198.77	483.3247	965.651	-0.0085	-8.8	9.72	25847.9	6.33	HUMAN	Q15102	Platelet-activating factor acetylhydrolase IB subunit gamma
19263	dirMS_041712_NAR_20mM_plus.7344.7344.2	2	6.05	0	2.35E+04	M33m	(R)IDEmPE	(R)I/D|E/m/P E/A A V K(S)	m:Oxidized methionine	118.63	559.7742	1102.545	15.9962	1.2	4.14	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
19264	dirMS_041712_NAR_20mM_plus.9137.9137.2	2	6.05	0	3.16E+04	M239m	(K)EITALAP	(K)E I\T/A/L|A/P S T m K(I)	m:Oxidized methionine	133.95	589.309	1161.618	15.9923	-2.2	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
19265	dirMS_041712_NAR_20mM_plus.9550.9550.2	2	6.05	0	7.65E+04		(K)TVSPALI	(K)T V|S/P A/L I S R(F)		136.75	472.2851	943.557	0.0058	6.2	9.41	50425	5.53	HUMAN	H0YH27	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
19266	dirMS_041712_NAR_30mM_plus2.21566.21620.2	2	6.05	1	2.37E+05		(K)ARFPAF	(K)A R\F P A\F\E|L(-)		168.6	475.7563	950.509	-0.0041	-4.3	6.05	46024	8.31	HUMAN	O43813	LanC-like protein 1
19267	dirMS_041712_NAR_30mM_plus2.22094.22094.2	2	6.05	0	1.56E+05		(R)QSSFAL	(R)Q S/S/F/A/L L/G D L T K(A)		170.63	640.3472	1279.689	-0.0021	-1.7	5.84	46579.3	4.96	HUMAN	E5RI07	Transportin-1
19268	dirMS_041712_NAR_40mM_plus2.7949.7949.2	2	6.05	0	1.38E+05		(K)FCLDNG	(K)F/C|L D/N/G A K(S)	C:Carbamidomethylation	106.82	462.7191	924.424	0.0065	7.1	5.84	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
19269	dirMS_041712_NAR_50mM_plus2.11080.11080.3	3	6.05	1	2.67E+04		(R)SAAETV	(R)S/A|A/E T V/T/K G/G I M L P E K(S)		125.88	544.624	1631.867	-0.0098	-6	5.86	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
19270	dirMS_041712_NAR_60mM_plus.11117.11117.2	2	6.05	0	2.12E+06		(K)GIVEFAS	(K)G I|V E|F\A/S K/P A A R(K)		116.18	623.3504	1245.695	-0.0015	-1.2	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
19271	dirMS_041712_NAR_20mM_minus.8482.8482.2	2	6.04	0	7.57E+04		(R)IIYGGSV	(R)I I/Y G/G|S V T/G A T C K(E)	C:Carbamidomethylation	134.28	663.8403	1326.672	0.0011	0.8	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
19272	dirMS_041712_NAR_20mM_minus.8817.8817.2	2	6.04	0	1.75E+05		(K)IVVVTA	(K)I V|V|V/T A G V R(Q)		137.98	457.2947	913.583	-0.0008	-0.9	9.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
19273	dirMS_041712_NAR_30mM_minus2.16034.16034.2	2	6.04	0	1.02E+05		(R)LVQAFQ	(R)L V/Q|A F Q F T D K(H)		140.57	598.8155	1196.631	-0.0073	-6.1	5.84	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
19274	dirMS_041712_NAR_50mM_minus2.12626.12626.3	3	6.04	1	4.45E+05	M100m	(K)QGGLG	(K)Q G G L G P m N I|P L/V S D/P K R(T)	m:Oxidized methionine	140.28	598.988	1778.958	15.9913	-2	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
19275	dirMS_041712_NAR_50mM_minus2.17628.17628.3	3	6.04	0	2.52E+05		(R)LLLDGA	(R)L L/L D G A/P/L I A I H/K(A)		168.53	458.6218	1373.852	-0.0007	-0.5	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
19276	dirMS_041712_NAR_50mM_minus2.9326.9326.3	3	6.04	1	1.36E+05		(R)QEEELQ	(R)Q E/E E L/Q A/K D E E L L K(V)		121.4	567.9554	1701.854	-0.0025	-1.5	4.14	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
19277	dirMS_041712_NAR_60mM_minus.14601.14601.3	3	6.04	1	1.52E+05	M392m	(R)LRLQmE	(R)L R L Q m/E V/N/D I K(K)	m:Oxidized methionine	141.55	458.9168	1358.746	15.9898	-3.7	6.07	44348.3	9.14	HUMAN	B7Z6E8	SH3 domain-containing kinase-binding protein 1
19278	dirMS_041712_NAR_60mM_minus.18398.18398.3	3	6.04	0	6.27E+04		(K)YAPLHL	(K)Y A/P L H L V/P L I E R(L)		163.77	474.2805	1420.831	-0.0041	-2.9	6.75	147553.6	6.73	HUMAN	E7EVF4	Cytoplasmic FMR1-interacting protein 2
19279	dirMS_041712_NAR_60mM_minus.18428.18428.3	3	6.04	1	5.29E+03		(R)EFTRLEI	(R)E F T R L E I\C|N L/T/P D A/L/K(S)	C:Carbamidomethylation	164.07	640.6658	1919.989	-0.0067	-3.5	4.68	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
19280	dirMS_041712_NAR_60mM_minus.9760.9760.3	3	6.04	1	2.83E+05		(R)TNAENE	(R)T/N|A E/N E F\V T I K K(D)		114.3	465.2487	1393.732	-0.0006	-0.4	5.81	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
19281	dirMS_041712_NAR_120mM_plus.11783.11783.3	3	6.04	0	4.18E+05		(R)IDYIAGE	(R)I D Y I A G E/C P V A A S R(A)	C:Carbamidomethylation	114.27	507.918	1521.737	0.0028	1.9	4.37	16787.1	5.47	HUMAN	H3BQZ9	Adenine phosphoribosyltransferase
19282	dirMS_041712_NAR_120mM_plus.4134.4134.3	3	6.04	1	1.56E+07	M310m	(R)TKTEISE	(R)T K\T E|I/S/E/m N R(N)	m:Oxidized methionine	69.73	408.8687	1208.594	15.9976	2.2	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
19283	dirMS_041712_NAR_120mM_plus.6235.6235.3	3	6.04	0	7.54E+05		(K)QRPQAT	(K)Q R P Q\A|T/A|E Q I/R(L)		86.02	433.2367	1297.697	-0.0016	-1.2	9.6	113668.7	6.2	HUMAN	F8W726	Ubiquitin-associated protein 2-like
19284	dirMS_041712_NAR_20mM_plus.10612.10612.2	2	6.04	0	4.60E+04		(R)SGYLLPD	(R)S G Y|L|L|P D T\K(A)		145.88	497.2665	993.525	0.0006	0.6	5.55	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
19285	dirMS_041712_NAR_20mM_plus.10845.10845.2	2	6.04	0	1.15E+04	M142m	(R)VVNVSS	(R)V V|N|V|S S I m S V/R(A)	m:Oxidized methionine	147.33	603.8291	1190.656	15.9948	-0.1	9.72	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
19286	dirMS_041712_NAR_20mM_plus.17816.17816.2	2	6.04	0	8.58E+04		(K)VDFPQD	(K)V/D/F/P Q D\Q|L/T A L\T G R(I)		194.7	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
19287	dirMS_041712_NAR_20mM_plus.9780.9780.2	2	6.04	2	2.43E+05		(K)DKAEKS	(K)D K A E/K/S E Q M/V K(E)		138.55	646.8319	1292.651	0.005	3.9	6.18	62850.8	5.5	HUMAN	F6VX93	Vacuolar protein sorting-associated protein 53 homolog
19288	dirMS_041712_NAR_40mM_plus2.18748.18748.3	3	6.04	0	6.65E+04		(R)QGTPLI	(R)Q G T/P L/I/A/F S L L/P H E Q K(R)		175.4	593.6623	1778.98	-0.0076	-4.3	6.75	6068.8	5.09	HUMAN	I3L4E8	Pre-rRNA-processing protein TSR1 homolog (Fragment)

19289	dirMS_041712_NAR_40mM_plus2.7689.7689.2	2	6.04	0	1.48E+05		(R)SGYFDEI	(R)S/G Y/F D E R(Y)		104.58	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
19290	dirMS_041712_NAR_50mM_plus2.10651.10651.3	3	6.04	1	2.12E+05		(K)AQALRD	(K)A Q|A|L R D N S T/M/G Y M M A K(K)		123.72	596.6125	1787.824	-0.0008	-0.4	8.63	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
19291	dirMS_041712_NAR_50mM_plus2.14981.14981.3	3	6.04	0	6.35E+05		(K)QGPLHG	(K)Q G/P L H G M L/I|N\T/P Y V T K(D)		146.43	590.3171	1768.941	-0.0047	-2.7	8.6	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
19292	dirMS_041712_NAR_50mM_plus2.15128.15128.3	3	6.04	0	2.43E+04		(K)VALLLLD	(K)V A|L\L L/L/D Q/G A S P H A A A K(N)		147.53	558.9877	1674.954	-0.0052	-3.1	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
19293	dirMS_041712_NAR_50mM_plus2.15346.15346.3	3	6.04	1	8.13E+05		(R)GFPTIYF	(R)G F/P T I/Y F S P A N K K(L)		148.83	490.5973	1469.779	-0.0014	-0.9	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
19294	dirMS_041712_NAR_50mM_plus2.16846.16846.3	3	6.04	0	7.60E+05		(R)QYYTLLN	(R)Q Y Y/T/L\L N Q/A/P D\M L H R(K)		156.9	621.6447	1862.922	-0.0022	-1.2	6.74	4335.1	9.82	HUMAN	E5RH00	Ras GTPase-activating protein-binding protein 1
19295	dirMS_041712_NAR_50mM_plus2.7766.7766.3	3	6.04	1	2.07E+04	M250m	(K)TTDmAF	(K)T/T|D/m A P S K/E T E M A/L A K(D)	m:Oxidized methionine	108.12	580.6104	1723.824	15.9925	-1.4	4.68	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
19296	dirMS_041712_NAR_60mM_plus.9989.9989.3	3	6.04	1	1.28E+05		(K)DSQICEL	(K)D S/Q|I/C E L K/Y D K(Q)	C:Carbamidomethylation	109.98	466.8941	1398.657	0.0108	7.7	4.56	21156.2	9.41	HUMAN	P55145	Mesencephalic astrocyte-derived neurotrophic factor
19297	dirMS_041712_NAR_120mM_minus.13981.13981.4	4	6.03	1	1.60E+06		(K)ASIHEAV	(K)A/S\I/H E\A W/T/D G K E A M L K(H)		129.98	447.476	1786.879	0.0029	1.6	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
19298	dirMS_041712_NAR_120mM_minus.7338.7338.3	3	6.03	1	1.49E+06		(R)CREMDE	(R)C R E\M/D|E/Q I/R(L)	C:Carbamidomethylation	93.97	412.8591	1236.546	0.0168	13.6	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
19299	dirMS_041712_NAR_20mM_minus.11195.11195.2	2	6.03	0	7.78E+04		(R)DFTPVC	(R)D F/T/P/V C T T E/L G R(A)	C:Carbamidomethylation	159.45	698.3303	1395.657	-0.004	-2.8	4.37	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
19300	dirMS_041712_NAR_20mM_minus.13784.13784.2	2	6.03	0	2.47E+04	M882m	(K)NLEISID	(K)N L|E/I/S I D T L m|A K(I)	m:Oxidized methionine	189.73	682.3615	1347.719	15.9969	1.5	4.37	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
19301	dirMS_041712_NAR_30mM_minus2.13267.13267.2	2	6.03	0	5.77E+05		(K)ELSDIAL	(K)E L\S/D/I/A/L/R(I)		125.28	458.753	916.51	-0.0111	-12.1	4.37	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
19302	dirMS_041712_NAR_30mM_minus2.15212.15212.2	2	6.03	0	7.26E+05	M2249m	(K)MSIYQA	(K)M/S|I/Y Q A m\W K(G)	m:Oxidized methionine	135.75	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
19303	dirMS_041712_NAR_40mM_minus2.11016.11016.3	3	6.03	0	8.43E+04		(K)MLDAED	(K)M/L/D A E D I V N T A R\P D E K(A)		148.55	606.297	1816.875	0.0019	1	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
19304	dirMS_041712_NAR_50mM_minus2.15031.15031.3	3	6.03	0	1.44E+05		(K)IHYLDTT	(K)I H Y\L D T\T T/L/I/E/P V S R(S)		153.37	586.6522	1757.943	-0.0012	-0.7	5.32	25731.5	7.15	HUMAN	I3L297	Adapter molecule crk
19305	dirMS_041712_NAR_50mM_minus2.8641.8641.3	3	6.03	1	9.59E+04		(K)ALDLDSS	(K)A L|D\L D/S S C K E A A/D G Y/Q R(C)	C:Carbamidomethylation	117.47	633.6221	1898.855	-0.0031	-1.7	4.23	60404.6	6.4	HUMAN	F5H0T1	Stress-induced-phosphoprotein 1
19306	dirMS_041712_NAR_120mM_plus.12085.12085.4	4	6.03	2	3.39E+05		(K)VTQLDLI	(K)V T Q L|D L/D/G P K/E L S R R(E)		116.73	432.4918	1726.945	0.0007	0.4	6.09	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
19307	dirMS_041712_NAR_20mM_plus.12200.12200.3	3	6.03	0	4.51E+04		(K)LQAFSA	(K)L Q\A F S A A/I/E/S C N\K(A)	C:Carbamidomethylation	156.72	480.2359	1438.699	-0.0063	-4.4	6	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
19308	dirMS_041712_NAR_20mM_plus.7901.7901.3	3	6.03	0	1.18E+05		(K)VEIIAND	(K)V E\I\I\A N D Q/G/N/R(T)		124.5	410.2139	1228.628	-0.0009	-0.7	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
19309	dirMS_041712_NAR_30mM_plus2.11585.11585.3	3	6.03	0	3.53E+05		(R)GGGGNI	(R)G G\G G\N/F G|P G/P/G S N F R(G)		114.45	459.8807	1377.629	-0.0019	-1.4	9.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
19310	dirMS_041712_NAR_30mM_plus2.20127.20127.2	2	6.03	0	1.14E+05		(K)TNVALM	(K)T N\V|A/L|M C M L R(E)	C:Carbamidomethylation	159.43	604.8021	1208.595	0.0021	1.7	9.41	71929.1	5.1	HUMAN	C9JAQ9	U5 small nuclear ribonucleoprotein 200 kDa helicase
19311	dirMS_041712_NAR_50mM_plus2.17434.17434.3	3	6.03	1	1.45E+05		(R)SMSVEK	(R)S M/S/V E K I D I S|P V L L Q K(G)		159.95	596.3359	1786.998	-0.0052	-2.9	5.79	81410.7	5.8	HUMAN	B3KTC7	Double-strand break repair protein MRE11A
19312	dirMS_041712_NAR_50mM_plus2.22242.22242.3	3	6.03	0	1.01E+06		(R)GGHPPA	(R)G G H\P P A I Q\S L/I|N L|L/A D/N R(Y)		191.13	629.3448	1886.024	-0.0044	-2.3	6.74	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
19313	dirMS_041712_NAR_50mM_plus2.8300.8300.3	3	6.03	0	2.70E+05		(K)STAGDT	(K)S/T/A/G D/T H L G G E D F D/N R(M)		109.7	564.5793	1691.726	-0.0022	-1.3	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
19314	dirMS_041712_NAR_60mM_plus.18275.18275.3	3	6.03	0	1.74E+05		(K)DHGLEV	(K)D H G L\E\V|L/G L V/R(V)		153.35	403.2318	1207.679	0.0015	1.2	5.32	17732.8	5.85	HUMAN	F5GYJ1	U8 snoRNA-decapping enzyme
19315	dirMS_041712_NAR_60mM_plus.7717.7717.2	2	6.03	1	7.47E+05		(R)VITEEEK	(R)V/I|T E E E K/N F K(A)		97.92	618.8282	1236.647	0.0021	1.7	4.79	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
19316	dirMS_041712_NAR_120mM_minus.20101.20101.4	4	6.02	0	4.08E+05		(K)LAFPSPF	(K)L A|F P S/P F G H/L S E G F S H S R(W)		166.07	493.9968	1972.966	-0.0011	-0.5	6.92	16196.2	9.92	HUMAN	C9JRJ8	Sequestosome-1 (Fragment)
19317	dirMS_041712_NAR_20mM_minus.7847.7847.2	2	6.02	0	7.81E+04	M406m	(R)EYQELm	(R)E Y/Q/E L/m/N V/K(L)	m:Oxidized methionine	128.13	585.2788	1153.556	15.9945	-0.3	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
19318	dirMS_041712_NAR_20mM_minus.9326.9326.2	2	6.02	0	2.79E+05		(R)AQIFAN	(R)A Q|I/F/A/N T V D N A R(I)		142.32	660.3388	1319.67	0.0001	0.1	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
19319	dirMS_041712_NAR_30mM_minus2.16144.16144.2	2	6.02	0	1.14E+05		(R)GLGLDD	(R)G L/G/L/D D/A L E/P R(Q)		142.1	578.299	1155.6	-0.0097	-8.4	4.03	51326.8	5.49	HUMAN	Q9Y230	RuvB-like 2
19320	dirMS_041712_NAR_30mM_minus2.19124.19124.2	2	6.02	1	2.15E+05		(K)SKLEFSI	(K)S K L E F S I\Y|P A|P(-)		158.93	626.334	1251.662	-0.0012	-1	5.72	21962.5	5.85	HUMAN	C9JJQ8	Tubulin alpha-4A chain (Fragment)
19321	dirMS_041712_NAR_50mM_minus2.15111.15111.3	3	6.02	1	1.33E+05		(K)VSEQGL	(K)V/S|E/Q G L I E I L/K K(V)		154.37	452.9385	1356.81	-0.0087	-6.4	6.11	12899.6	6.59	HUMAN	K7EL31	Programmed cell death protein 5
19322	dirMS_041712_NAR_60mM_minus.10490.10490.3	3	6.02	1	1.32E+05		(R)SATKVT	(R)S A T K\V T A D|V|I/N A A E/K(L)		118.67	506.6084	1517.817	-0.0063	-4.2	5.79	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
19323	dirMS_041712_NAR_60mM_minus.19177.19177.3	3	6.02	0	1.08E+05		(K)HLLQAP	(K)H L L Q A P L\D D A\Q|E/I/L Q A R(F)		169.73	644.347	1931.035	-0.0081	-4.2	4.54	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
19324	dirMS_041712_NAR_60mM_minus.19260.19260.3	3	6.02	0	3.35E+05		(K)HGATVL	(K)H G A T\V L|T/A/L G G I L K(K)		170.82	450.939	1350.81	-0.0079	-5.9	8.76	8125.3	9.3	HUMAN	B0QYF7	Myoglobin (Fragment)
19325	dirMS_041712_NAR_120mM_plus.3649.3649.3	3	6.02	1	3.15E+06	M139m	(R)QREmEE	(R)Q/R E m E E/Q M/R(R)	m:Oxidized methionine	60.8	418.1852	1236.546	15.9951	0.1	4.79	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
19326	dirMS_041712_NAR_20mM_plus.11405.11405.2	2	6.02	0	2.31E+05		(K)VGLQVV	(K)V/G L/Q|V V A V K(A)		151.18	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
19327	dirMS_041712_NAR_20mM_plus.19071.19071.3	3	6.02	0	2.48E+05		(R)VCTLAII	(R)V C T\L\A I I/D/P G D/S D\I I R(S)	C:Carbamidomethylation	202.7	586.641	1757.91	-0.0018	-1	3.93	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
19328	dirMS_041712_NAR_30mM_plus2.5444.5444.3	3	6.02	0	1.09E+05		(K)SAAQAA	(K)S A\A\Q A A A Q/T N S N A A G K(Q)		82.75	487.575	1460.709	0.0016	1.1	8.47	45021.6	8.74	HUMAN	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein
19329	dirMS_041712_NAR_40mM_plus2.13884.13884.3	3	6.02	0	2.23E+05		(K)VALLLLD	(K)V A L\L L/L D Q/G A/S P H/A A A K(N)		148.13	558.9886	1674.954	-0.0025	-1.5	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
19330	dirMS_041712_NAR_40mM_plus2.7525.7525.2	2	6.02	0	1.30E+05		(R)YSPDELF	(R)Y/S/P D/E L R(Y)		104.95	440.2172	879.421	0.0065	7.3	4.37	57076.9	6.23	HUMAN	Q8WUB8	PHD finger protein 10
19331	dirMS_041712_NAR_50mM_plus2.12200.12200.3	3	6.02	1	3.05E+05		(K)NQVALN	(K)N Q\V/A/L N/P Q N/T V/F D A/K R(L)		131.65	605.6528	1814.951	-0.0069	-3.8	8.75	70336.2	5.48	HUMAN	P08107	Heat shock 70 kDa protein 1A/1B
19332	dirMS_041712_NAR_50mM_plus2.15452.15452.3	3	6.02	0	1.12E+06		(R)QVLIASH	(R)Q V/L/I/A S H L/P S Y E L R(H)		149.63	542.6394	1625.901	0.0027	1.6	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
19333	dirMS_041712_NAR_50mM_plus2.7505.7505.3	3	6.02	1	2.75E+05		(K)MQASIE	(K)M/Q/A/S I/E K G G S L/P K(V)		105.85	449.2397	1345.714	-0.0099	-7.3	8.35	32745.6	4.64	HUMAN	P06748	Nucleophosmin
19334	dirMS_041712_NAR_50mM_plus2.8427.8427.3	3	6.02	1	1.50E+03	M26m	(K)LAEQAE	(K)L/A|E Q/A E R Y D\D M A T C m K(A)	C:Carbamidomethylation m:Oxid	111.25	649.9476	1931.83	15.9987	1.9	4.32	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
19335	dirMS_041712_NAR_60mM_plus.17236.17236.3	3	6.02	1	4.54E+06		(K)LKVPEW	(K)L K V P E|W\V/D\T V/K(L)		146.12	438.5872	1313.746	0.0007	0.5	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
19336	dirMS_041712_NAR_60mM_plus.17904.17904.3	3	6.02	1	1.97E+05		(R)GMLRED	(R)G M/L R E D\S/M/M/E/Y L K(I)		150.62	534.9153	1602.732	-0.0011	-0.7	4.68	71218.8	6.3	HUMAN	A7YIJ8	Radixin
19337	dirMS_041712_NAR_120mM_minus.18808.18808.3	3	6.01	1	1.46E+05		(R)HATALEI	(R)H A/T A L E E\L\S/E Q/L/E Q A K R(F)		158.03	651.6718	1953.004	-0.0027	-1.4	4.91	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
19338	dirMS_041712_NAR_120mM_minus.7500.7500.3	3	6.01	1	3.20E+04	M482m	(R)SRSGEG	(R)S R/S G E\G\E|V|S/G L m R(K)	m:Oxidized methionine	95.13	460.8891	1364.659	15.9941	-0.6	5.87	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
19339	dirMS_041712_NAR_20mM_minus.10806.10806.2	2	6.01	0	6.51E+04		(K)VNQIGS	(K)V/N\Q I|G S V T/E/S I Q A C K(L)	C:Carbamidomethylation	155.47	817.4099	1633.821	-0.0089	-5.4	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
19340	dirMS_041712_NAR_20mM_minus.14673.14673.2	2	6.01	0	1.27E+05		(R)IITLAGP	(R)I I/T\L/A|G/P T N A I F K(A)		202.08	679.9047	1358.804	-0.0021	-1.5	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
19341	dirMS_041712_NAR_30mM_minus2.15200.15200.2	2	6.01	0	7.18E+05	M2249m	(K)MSIYQA	(K)M S|I|Y Q/A m W K(G)	m:Oxidized methionine	135.72	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
19342	dirMS_041712_NAR_40mM_minus2.11523.11523.3	3	6.01	0	1.37E+05		(K)VALLLLD	(K)V A L L|L L D Q/G A/S P\H A A A K(N)		150.92	558.9882	1674.954	-0.0037	-2.2	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
19343	dirMS_041712_NAR_40mM_minus2.13614.13614.3	3	6.01	1	3.98E+05		(R)VTFSGLF	(R)V T/F/S/G L R D T V/T P G E L L K(A)		164.73	611.6742	1833.012	-0.0036	-2	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
19344	dirMS_041712_NAR_40mM_minus2.8519.8519.3	3	6.01	0	2.42E+05	T1179t	(R)EATIAVN	(R)E A/T I|A V N I L D D t V/P E K(E)	t:N-acetylglucosamine (T)	132.33	644.3329	1727.906	203.078	-0.7	3.91	177306.9	4.37	HUMAN	H0Y8U6	G-protein-coupled receptor 98 (Fragment)
19345	dirMS_041712_NAR_50mM_minus2.7610.7610.3	3	6.01	0	1.15E+03	M44m M4	(K)SGTGIA	(K)S G T G|I|A/A m S V m R/P/E Q I m K(S)	m:Oxidized methionine	111.57	652.3177	1906.955	47.9838	-0.5	8.46	8797.3	9.3	HUMAN	H3BR50	V-type proton ATPase 16 kDa proteolipid subunit
19346	dirMS_041712_NAR_60mM_minus.14490.14490.3	3	6.01	0	1.24E+05		(K)QQGVLA	(K)Q Q/G/V/L A L R P Y L Q K(Q)		140.52	505.2973	1513.885	-0.0076	-5	9.99	62841.3	5.15	HUMAN	B3KVK7	Methionine--tRNA ligase, cytoplasmic
19347	dirMS_041712_NAR_60mM_minus.6883.6883.3	3	6.01	1	5.61E+05	M286m M	(R)VVDLmA	(R)V/V|D L m\A H m A S K E(-)	m:Oxidized methionine	96.77	454.8843	1330.649	31.989	-0.6	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
19348	dirMS_041712_NAR_120mM_plus.10790.10790.3	3	6.01	0	1.21E+06	T888t	(K)NVtLEED	(K)N V t L/E|E D/G T/R(A)	t:N-acetylglucosamine (T)	109.52	446.2171	1133.543	203.0934	10.5	4.14	154927.4	5.54	HUMAN	I3L100	Neuralized-like protein 4 (Fragment)
19349	dirMS_041712_NAR_120mM_plus.5525.5525.4	4	6.01	1	1.35E+06	T194t	(R)AELSLKS	(R)A E L S L K S/V/P G D/G A/t\K(A)	t:N-acetylglucosamine (T)	82.03	419.7217	1472.795	203.0695	-5.9	6.11	85072.5	8.17	HUMAN	I3L2K5	Zinc finger CCCH domain-containing protein 7A (Fragment)
19350	dirMS_041712_NAR_20mM_plus.13094.13094.2	2	6.01	0	4.13E+03	M107m	(K)LYmVLIT	(K)L/Y m/V|L/I/T T K(N)	m:Oxidized methionine	162.38	549.3156	1081.633	15.9913	-3.3	8.59	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
19351	dirMS_041712_NAR_20mM_plus.13602.13602.2	2	6.01	0	1.37E+05	M273m	(K)mISDAIP	(K)m I|S D/A I|P E L K(A)	m:Oxidized methionine	165.7	566.7967	1116.597	15.9892	-5	4.37	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
19352	dirMS_041712_NAR_20mM_plus.14046.14046.3	3	6.01	0	3.05E+04		(R)LEQGQA	(R)L E Q G Q A I|D/D L\M/P A Q K(-)		168.3	552.9426	1656.826	-0.0129	-7.8	4.03	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
19353	dirMS_041712_NAR_20mM_plus.16699.16699.2	2	6.01	0	2.56E+04		(R)LIDFLEC	(R)L I/D F/L|E C/G K(T)	C:Carbamidomethylation	185.57	547.7734	1094.555	-0.0155	-14.2	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
19354	dirMS_041712_NAR_20mM_plus.17248.17248.3	3	6.01	0	1.27E+05		(R)AVLVDLI	(R)A V L V\D L E/P G T/M/D S/V R(S)		189.67	534.6105	1601.82	-0.0034	-2.1	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
19355	dirMS_041712_NAR_20mM_plus.19265.19265.2	2	6.01	0	1.70E+04		(R)ALIAGG	(R)A L I|A\G|G/G A/P E I E\L A L R(L)		203.82	775.9467	1550.89	-0.0039	-2.5	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
19356	dirMS_041712_NAR_30mM_plus2.11541.11541.2	2	6.01	0	1.30E+05		(K)ESYSALN	(K)E/S/Y/S A/L M R(E)		113.65	478.7283	956.451	-0.0013	-1.3	6.1	533778	5.74	HUMAN	Q15149	Plectin
19357	dirMS_041712_NAR_30mM_plus2.16933.16933.2	2	6.01	0	3.62E+05		(K)GCSFLPD	(K)G C\S F/L|P D/P Y Q K(Q)	C:Carbamidomethylation	141.08	656.306	1311.604	0.0009	0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
19358	dirMS_041712_NAR_30mM_plus2.19680.19680.2	2	6.01	0	2.35E+05		(K)APDFVF	(K)A/P\D/F/V\F Y/A\P R(L)		156.72	591.8008	1182.594	0.0001	0.1	5.88	71218.8	6.3	HUMAN	A7YIJ8	Radixin
19359	dirMS_041712_NAR_30mM_plus2.22285.22285.2	2	6.01	0	2.06E+05		(K)NSSYFVE	(K)N S\S/Y F/V/E/W I/P N\N V K(V)		171.92	848.9189	1696.833	-0.0024	-1.4	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
19360	dirMS_041712_NAR_50mM_plus2.15356.15356.3	3	6.01	1	4.75E+05		(K)TVGVEP.	(K)T V|G\V/E/P A A D G K G V V V V I K(R)		148.25	580.0056	1738.011	-0.0087	-5	5.73	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
19361	dirMS_041712_NAR_50mM_plus2.18886.18886.3	3	6.01	0	7.09E+04	S193s	(R)SSPKPQ	(R)S S P/K P\Q V s|F L H A Q K(S)	s:N-acetylglucosamine (S)	166.85	586.3252	1553.843	203.1176	21.8	10	50090.9	5.99	HUMAN	A6NKC9	SH2 domain-containing protein 7
19362	dirMS_041712_NAR_50mM_plus2.6509.6509.3	3	6.01	1	3.43E+04	S340s	(K)AEKIAsC	(K)A E/K I/A s Q M I T E G R(M)	s:N-acetylglucosamine (S)	98.62	546.2803	1433.742	203.0847	3.2	6.19	48125	5.99	HUMAN	D6RAX7	COP9 signalosome complex subunit 4
19363	dirMS_041712_NAR_60mM_plus.20842.20842.3	3	6.01	1	1.88E+05		(R)LKVPPAI	(R)L K\V/P P A I/N/Q F/T Q A L/D R(Q)		170.07	604.3409	1811.017	-0.0092	-5.1	8.75	30166.2	10.79	HUMAN	P62424	60S ribosomal protein L7a
19364	dirMS_041712_NAR_60mM_plus.8061.8061.3	3	6.01	1	4.12E+05		(R)ISGGND	(R)I S|G G N|D K Q G\F/P M/K(Q)		101.2	460.2297	1378.678	-0.0038	-2.8	8.59	25082	11.29	HUMAN	A2A3R5	40S ribosomal protein S6
19365	dirMS_041712_NAR_120mM_minus.17073.17073.3	3	6	1	7.58E+04		(R)IRGETLG	(R)I R G E T L/G I|I/G L G R(V)		148.32	452.2751	1354.816	-0.0058	-4.3	9.6	20631.5	6.98	HUMAN	D6RAX2	C-terminal-binding protein 1 (Fragment)
19366	dirMS_041712_NAR_20mM_minus.10507.10507.2	2	6	0	1.02E+04	M234m	(K)mVVESA	(K)m V|V|E S A Y E V\I K(L)	m:Oxidized methionine	153.32	642.3318	1267.66	15.9961	0.9	4.53	36923.1	5.71	HUMAN	P07195	L-lactate dehydrogenase B chain
19367	dirMS_041712_NAR_30mM_minus2.12117.12117.2	2	6	0	2.32E+05		(K)STLTDSL	(K)S T|L/T/D S|L V/C K(A)	C:Carbamidomethylation	119.4	562.2838	1123.566	-0.006	-5.4	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
19368	dirMS_041712_NAR_30mM_minus2.12416.12416.2	2	6	0	1.54E+05		(K)IGVTVLS	(K)I/G/V/T/V L S R(I)		120.92	422.7649	844.525	-0.0026	-3	9.75	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
19369	dirMS_041712_NAR_30mM_minus2.17381.17381.2	2	6	0	1.11E+04		(R)EQLAIAE	(R)E Q L/A|I/A E F A R(S)		148.28	574.3084	1147.611	-0.0011	-0.9	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
19370	dirMS_041712_NAR_30mM_minus2.18938.18938.2	2	6	0	6.91E+05		(K)LAVNM	(K)L A|V|N M/V/P F P R(L)		158.72	572.3143	1143.634	-0.013	-11.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
19371	dirMS_041712_NAR_50mM_minus2.10802.10802.3	3	6	1	2.51E+05		(K)NQVAM	(K)N\Q|V|A|M N P T\N T V F D A K R(L)		129.32	602.6379	1805.896	0.0029	1.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
19372	dirMS_041712_NAR_50mM_minus2.14482.14482.3	3	6	1	2.62E+05		(R)GFPTIYF	(R)G F/P/T I Y/F S/P A N K K(L)		150.53	490.5972	1469.779	-0.0017	-1.1	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
19373	dirMS_041712_NAR_50mM_minus2.7672.7672.3	3	6	1	3.49E+04	M198m	(R)VFDKEG	(R)V F D K E G N G T/V/m/G/A E/I R(H)	m:Oxidized methionine	110.87	580.2847	1722.848	15.9916	-1.9	4.68	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
19374	dirMS_041712_NAR_50mM_minus2.8002.8002.3	3	6	1	1.21E+05		(K)TAVCDIF	(K)T A/V C D/I/P P R G L K(M)	C:Carbamidomethylation	112.2	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
19375	dirMS_041712_NAR_60mM_minus.14906.14906.3	3	6	1	5.50E+05		(K)TDKTLVI	(K)T/D K T L\V|L/L M G K(E)		142.67	406.9088	1218.713	-0.0008	-0.6	8.26	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
19376	dirMS_041712_NAR_120mM_plus.14010.14010.4	4	6	1	9.40E+05		(K)AGKFPSI	(K)A G\K\F P S/L/L T H N E N M V A K(V)		126.23	464.9972	1856.969	-0.0018	-0.9	8.64	25002	10.06	HUMAN	P62906	60S ribosomal protein L10a
19377	dirMS_041712_NAR_120mM_plus.8313.8367.3	3	6	1	4.60E+05		(K)DKDAYS	(K)D K D A\Y S/S/F/G S/R(S)		97.1	411.5235	1232.554	0.0017	1.4	5.96	15031.5	6.72	HUMAN	B4DLA0	ATP-dependent RNA helicase DDX3X
19378	dirMS_041712_NAR_120mM_plus.9772.9772.3	3	6	2	3.06E+05		(R)TGLIKGS	(R)T G/L|I K G S G T\A/E V/E L K K(G)		104.5	544.3167	1630.937	-0.0019	-1.1	8.17	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
19379	dirMS_041712_NAR_20mM_plus.13423.13423.2	2	6	0	1.40E+05	M273m	(K)mISDAIP	(K)m I/S/D A I/P E/L K(A)	m:Oxidized methionine	165.03	566.7967	1116.597	15.9892	-5	4.37	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
19380	dirMS_041712_NAR_30mM_plus2.15606.15606.2	2	6	0	7.13E+05		(R)YPVNSV	(R)Y/P/V|N S V N\I L K(A)		134.47	573.8278	1146.652	-0.0034	-3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
19381	dirMS_041712_NAR_30mM_plus2.15952.15952.2	2	6	0	1.89E+05		(K)AMTGVE	(K)A/M/T/G V\E\Q|W/P Y|R(A)		136.52	669.317	1337.631	-0.004	-3	6.04	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
19382	dirMS_041712_NAR_30mM_plus2.17410.17410.2	2	6	0	3.11E+04		(K)FANPFP	(K)F A\N/P F/P/A/A V R(G)		144.33	545.2953	1089.584	-0.0007	-0.6	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
19383	dirMS_041712_NAR_30mM_plus2.5423.5423.2	2	6	0	4.44E+05		(K)VSSFEEK	(K)V/S|S F E/E/K(M)		81.83	413.203	825.399	-0.0002	-0.2	4.53	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
19384	dirMS_041712_NAR_30mM_plus2.6942.6942.2	2	6	0	7.56E+04		(R)EQALAV	(R)E Q|A/L A/V S R(N)		90.78	437.2414	873.479	-0.0033	-3.8	6.1	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
19385	dirMS_041712_NAR_40mM_plus2.13915.13915.3	3	6	1	2.11E+04		(K)VGLQVV	(K)V/G L\Q|V/V A/V K A/P/G F G D N R(K)		148.4	576.3214	1726.96	-0.0102	-5.9	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
19386	dirMS_041712_NAR_50mM_plus2.17037.17056.3	3	6	0	3.15E+05		(K)TIVEMEI	(K)T I|V/E/M E N S G L V\H/M L K(N)		157.53	567.6319	1700.871	0.0102	6	5.37	89499.2	8.96	HUMAN	Q13618	Cullin-3
19387	dirMS_041712_NAR_50mM_plus2.18802.18802.3	3	6	0	4.51E+04		(R)MPVIKP	(R)M/P/V I/K P D I A|N W E L S V K(L)		167.02	614.0109	1840.004	0.0144	7.8	5.82	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
19388	dirMS_041712_NAR_50mM_plus2.20712.20712.3	3	6	1	1.70E+05		(R)VNSKFD	(R)V N|S K F D T\I|Y Q/I/L L/K(K)		177.62	561.3209	1681.952	-0.0042	-2.5	8.47	72626.7	9.13	HUMAN	Q14258	E3 ubiquitin/ISG15 ligase TRIM25
19389	dirMS_041712_NAR_50mM_plus2.9621.9621.3	3	6	0	7.48E+05		(K)YIQQTKI	(K)Y/I|Q/Q T K/P L T L E R(T)		117.08	497.2822	1489.837	-0.0053	-3.5	8.59	26283.8	8.96	HUMAN	O43809	Cleavage and polyadenylation specificity factor subunit 5
19390	dirMS_041712_NAR_60mM_plus.15737.15737.3	3	6	1	1.98E+05		(R)DLEEKLE	(R)D L/E E/K L/E/T L/R(L)		138.4	415.8936	1245.669	-0.0023	-1.8	4.41	141626	5.5	HUMAN	A8MY36	Dynactin subunit 1
19391	dirMS_041712_NAR_60mM_plus.19911.19911.2	2	6	1	4.41E+04		(K)SLLGKD	(K)S/L/L/G/K D/V L F/L K(D)		163.9	616.885	1232.761	0.0014	1.2	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
19392	dirMS_041712_NAR_60mM_plus.8904.8904.3	3	6	1	7.11E+05		(R)QLQLAQ	(R)Q L/Q/L A/Q E/A A Q K R(L)		104.87	461.9268	1383.77	-0.0044	-3.2	8.75	533778	5.74	HUMAN	Q15149	Plectin
19393	dirMS_041712_NAR_120mM_minus.5123.5123.3	3	5.99	1	1.03E+06	M194m	(R)CREmDE	(R)C R E m D|E Q/I/R(L)	C:Carbamidomethylation m:Oxid	80.33	418.1844	1236.546	15.9927	-1.8	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
19394	dirMS_041712_NAR_20mM_minus.9996.9996.2	2	5.99	0	8.95E+04	M196m	(K)DAGTIA	(K)D A G T/I/A|G L N V m R(I)	m:Oxidized methionine	149.48	617.3216	1217.631	16.0052	8.4	5.84	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
19395	dirMS_041712_NAR_30mM_minus2.9153.9153.2	2	5.99	0	1.73E+05		(R)LAGMTF	(R)L A/G/M T/P V/R(E)		104.18	422.7411	844.471	0.004	4.7	9.75	83407.1	7.85	HUMAN	Q6ZVF9	G protein-regulated inducer of neurite outgrowth 3
19396	dirMS_041712_NAR_50mM_minus2.15384.15384.3	3	5.99	0	3.99E+05	M118m	(R)AGKPVI	(R)A G K\P V I C A T\Q|M L/E/S m I/K(K)	C:Carbamidomethylation m:Oxid	155.45	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
19397	dirMS_041712_NAR_50mM_minus2.15913.15913.3	3	5.99	1	3.87E+05		(K)QGGLGF	(K)Q G/G L G P M N I/P L/V/S D\P K R(T)		157.72	593.6566	1778.958	-0.0029	-1.6	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1

19398	dirMS_041712_NAR_50mM_minus2.8847.8847.3	3	5.99	1	2.18E+05		(K)VCGDSD	(K)V/C|G D S D K G F V V/I/N Q K(G)	C:Carbamidomethylation	118.03	555.9474	1665.826	0.0012	0.7	5.93	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
19399	dirMS_041712_NAR_60mM_minus.15080.15080.2	2	5.99	0	4.01E+05		(R)EHALLA	(R)E/H/A|L/L/A/Y T L G V K(Q)		144.6	657.873	1314.742	-0.0029	-2.2	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
19400	dirMS_041712_NAR_60mM_minus.19153.19153.3	3	5.99	1	8.25E+05		(R)LDLAGR	(R)L D|L/A G R D L T D Y/L M/K(I)		168.87	541.9507	1623.841	-0.0035	-2.2	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
19401	dirMS_041712_NAR_60mM_minus.8470.8470.3	3	5.99	0	1.76E+04		(R)NTFDHP	(R)N T F/D H/P Y/P T T K(L)		107.17	440.8799	1320.622	0.0033	2.5	6.74	19714	5.38	HUMAN	E9PCY4	DDB1- and CUL4-associated factor 7
19402	dirMS_041712_NAR_120mM_plus.5950.5950.3	3	5.99	1	3.93E+05		(R)LNGTLRI	(R)L/N/G T L R E D/D/N R(I)		83.53	434.8849	1302.64	0.0005	0.4	4.56	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
19403	dirMS_041712_NAR_120mM_plus.7304.7304.2	2	5.99	1	4.77E+05		(K)SLDEME	(K)S/L\D E|M/E K/Q/Q R(E)		91.18	632.3059	1263.6	0.0047	3.8	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
19404	dirMS_041712_NAR_20mM_plus.12121.12121.2	2	5.99	0	3.44E+04		(K)LQAFSA	(K)L Q|A F S A A I/E/S C/N K(A)	C:Carbamidomethylation	156.63	719.8475	1438.699	-0.0118	-8.2	6	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
19405	dirMS_041712_NAR_20mM_plus.15785.15785.2	2	5.99	0	1.22E+05		(K)SILFVPT	(K)S I|L|F V/P T S/A P R(G)		180.58	594.3403	1187.678	-0.005	-4.2	9.47	92752.5	4.76	HUMAN	P14625	Endoplasmin
19406	dirMS_041712_NAR_30mM_plus2.16632.16632.2	2	5.99	0	3.67E+05		(K)QLQEMI	(K)Q L/Q/E M\L G L/S K(V)		140.15	573.8112	1146.619	-0.0036	-3.1	6	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
19407	dirMS_041712_NAR_30mM_plus2.22444.22444.2	2	5.99	0	3.49E+05		(R)VGNLGL	(R)V G N L/G L/A/T\S F F N E\R(N)		172.9	762.8926	1524.781	-0.0026	-1.7	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
19408	dirMS_041712_NAR_40mM_plus2.20030.20030.3	3	5.99	1	5.79E+05		(K)EGGLGP	(K)E G G L|G/P L N I/P L L A D V T R R(L)		189.78	631.0288	1891.076	-0.0041	-2.2	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
19409	dirMS_041712_NAR_40mM_plus2.9515.9515.3	3	5.99	0	2.64E+04		(K)ASQEPSI	(K)A S Q E/P/S P K P G/T E V I/P A A/P R(K)		119.18	644.6779	1932.018	0.0006	0.3	6.19	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
19410	dirMS_041712_NAR_50mM_plus2.11502.11502.3	3	5.99	0	3.42E+05		(K)YTVQDE	(K)Y/T/V Q/D/E S H S E/W V S C V R(F)	C:Carbamidomethylation	127.98	661.2946	1981.871	-0.0016	-0.8	4.65	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
19411	dirMS_041712_NAR_50mM_plus2.14077.14077.3	3	5.99	1	5.08E+05	T106t	(R)APLGPLI	(R)A P L G P L N\P S Y/K/S/S/P t R(N)	t:N-acetylglucosamine (T)	142.7	629.9955	1684.902	203.0703	-4.8	9.99	68204.5	8.18	HUMAN	F5GYC2	MAP7 domain-containing protein 2
19412	dirMS_041712_NAR_50mM_plus2.19981.19981.3	3	5.99	0	1.09E+05		(R)LLHLPLS	(R)L L H\L\P\L/S L/T A/L K(L)		173.43	440.2862	1318.846	-0.0016	-1.2	8.76	59982.4	4.94	HUMAN	Q9BTT6	Leucine-rich repeat-containing protein 1
19413	dirMS_041712_NAR_50mM_plus2.9562.9562.3	3	5.99	1	1.58E+05		(R)LGGSPF	(R)L/G G/S/P F/G P A G T G K T E S V K(A)		117.22	563.9657	1689.881	0.0019	1.1	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
19414	dirMS_041712_NAR_50mM_plus2.9968.9968.3	3	5.99	1	2.46E+06		(K)ATAVVD	(K)A T/A/V/V/D G A F K E V/K(L)		120.07	445.5822	1334.731	0.0006	0.5	6.11	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
19415	dirMS_041712_NAR_60mM_plus.11312.11312.2	2	5.99	0	7.77E+05		(R)TICSHV	(R)T/I/C/S/H V Q\N M\I K(G)	C:Carbamidomethylation	116.95	665.8295	1330.661	-0.0089	-6.7	8.44	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
19416	dirMS_041712_NAR_60mM_plus.7451.7451.3	3	5.99	0	8.79E+05		(R)AAHSEG	(R)A A H S E G N T/T|A/G L D/M R(E)		96.75	510.9035	1530.697	-0.0006	-0.4	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
19417	dirMS_041712_NAR_120mM_minus.13377.13377.3	3	5.98	2	2.61E+05	M32m S34	(R)KFPGSKI	(R)K F/P G S K L A/E m F s S L A/K(A)	m:Oxidized methionine s:N-	126.68	654.0058	1740.935	219.0675	-3.4	9.7	26358.9	6.92	HUMAN	B2R9R8	BTB/POZ domain-containing protein KCTD14
19418	dirMS_041712_NAR_120mM_minus.5155.5155.3	3	5.98	1	1.60E+05		(R)LKQSAEI	(R)L K Q S A E E|Q/A/Q/A/R(A)		80.68	453.5713	1358.702	-0.0029	-2.1	6.14	533778	5.74	HUMAN	Q15149	Plectin
19419	dirMS_041712_NAR_30mM_minus2.10977.10977.2	2	5.98	0	5.82E+05		(K)VAGQD	(K)V/A|G Q|D/G S V V Q|F K(I)		113.8	617.824	1234.643	-0.0019	-1.5	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
19420	dirMS_041712_NAR_30mM_minus2.6214.6214.2	2	5.98	0	9.56E+04		(K)VLCAAQ	(K)V L|C/A A Q/E R(S)	C:Carbamidomethylation	88.05	473.7466	946.477	0.0084	8.9	5.97	66457	6.51	HUMAN	A8MT19	Putative rhophilin-2-like protein RHPN2P1
19421	dirMS_041712_NAR_50mM_minus2.10800.10800.3	3	5.98	1	2.51E+05		(K)NQVAM	(K)N Q|V/A/M N/P\T/N T V F D A K R(L)		129.32	602.6379	1805.896	0.0029	1.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
19422	dirMS_041712_NAR_50mM_minus2.11273.11273.3	3	5.98	1	1.26E+05		(R)TVSKVD	(R)T/V/S K V D D\F/L/A N E A K(G)		132.38	512.9329	1536.79	-0.0063	-4.1	4.55	52385	7.18	HUMAN	B4DQJ8	6-phosphogluconate dehydrogenase, decarboxylating
19423	dirMS_041712_NAR_50mM_minus2.12824.12824.3	3	5.98	2	1.80E+04		(R)FMHIIK	(R)F/M H I I K A Q P F K\D/R(C)		141.4	544.2947	1630.889	-0.0191	-11.7	9.99	20395	6.05	HUMAN	H0YC48	E3 ubiquitin-protein ligase HACE1 (Fragment)
19424	dirMS_041712_NAR_50mM_minus2.6708.6708.3	3	5.98	1	8.76E+04	M22m M2	(K)LAEQAE	(K)L A\E/Q/A/E R Y\D D m A/A C m K(S)	C:Carbamidomethylation m:Oxid	104.8	645.2741	1901.819	31.9887	-0.6	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
19425	dirMS_041712_NAR_50mM_minus2.8484.8484.3	3	5.98	0	8.44E+04	S1354s M1	(R)NVYAsV	(R)N V/Y A s V V E D m/I L K(A)	s:N-acetylglucosamine (S) m:	116.07	567.289	1480.772	219.0809	3.9	4.37	151691.8	9.36	HUMAN	Q9ULM3	YEATS domain-containing protein 2
19426	dirMS_041712_NAR_50mM_minus2.9430.9430.3	3	5.98	1	1.31E+05	M15m	(K)mLVSGA	(K)m L/V/S G A G/D/I K L T K(D)	m:Oxidized methionine	121.65	450.2541	1332.756	15.9922	-2	8.35	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
19427	dirMS_041712_NAR_60mM_minus.4645.4645.3	3	5.98	0	6.11E+05	M46m M4	(R)HQGVm	(R)H Q\G V\m|V G m/G Q K(D)	m:Oxidized methionine	77.87	401.8579	1171.571	31.9881	-1.4	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
19428	dirMS_041712_NAR_60mM_minus.6693.6693.3	3	5.98	0	4.43E+04	M437m	(R)LESGMC	(R)L E/S G M Q N m S I/H/T/K(T)	m:Oxidized methionine	96.18	497.9023	1475.698	15.9942	-0.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
19429	dirMS_041712_NAR_120mM_plus.16327.16327.3	3	5.98	1	6.86E+05		(K)STFVLDE	(K)S T/F V/L\D E F K R(K)		138.87	414.5556	1241.652	-0.0002	-0.2	5.79	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
19430	dirMS_041712_NAR_120mM_plus.18944.18944.4	4	5.98	1	1.34E+06		(K)FQIPPN	(K)F Q\I/P/P N/A E L K Y E L H L/K(S)		152.58	485.7703	1940.064	-0.0046	-2.4	6.75	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
19431	dirMS_041712_NAR_120mM_plus.5299.5299.2	2	5.98	0	1.84E+05		(K)YLPHSA	(K)Y L/P/H S A G R(Y)		81.33	450.7388	900.469	0.0017	1.9	8.75	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
19432	dirMS_041712_NAR_20mM_plus.15007.15007.2	2	5.98	0	2.17E+05		(K)GLAITFV	(K)G L A I/T|F/V/S\D E N/D A K(I)		175.3	740.3693	1479.733	-0.0012	-0.8	4.03	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
19433	dirMS_041712_NAR_20mM_plus.18380.18380.3	3	5.98	0	7.34E+04		(K)ITSEALL	(K)I T S E A L\L/V T/Q/Q L/V K(A)		198.23	514.9762	1542.91	0.0039	2.5	6	50425	5.53	HUMAN	H0YH27	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
19434	dirMS_041712_NAR_20mM_plus.7049.7049.3	3	5.98	0	1.33E+05	M295m M	(R)mGQmA	(R)m G Q m A\m\G G|A|M/G I N N R(G)	m:Oxidized methionine	115.02	529.5557	1538.67	47.9831	-1.1	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
19435	dirMS_041712_NAR_20mM_plus.7850.7850.2	2	5.98	0	5.08E+03		(K)TAVCDIF	(K)T/A|V/C/D I/P\P R(G)	C:Carbamidomethylation	123.92	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
19436	dirMS_041712_NAR_20mM_plus.9538.9538.2	2	5.98	0	5.58E+05		(K)TIAPALV	(K)T I|A/P A L V S K(K)		136.25	450.2814	899.556	-0.0005	-0.6	8.41	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
19437	dirMS_041712_NAR_30mM_plus2.11362.11362.2	2	5.98	0	4.07E+05		(K)TTDGYLI	(K)T T|D/G Y L L|R(L)		112.72	469.75	938.494	-0.0014	-1.5	5.5	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
19438	dirMS_041712_NAR_30mM_plus2.4849.4849.2	2	5.98	0	8.06E+05		(R)MGQTM	(R)M/G Q/T M E/R(I)		76.98	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
19439	dirMS_041712_NAR_30mM_plus2.5835.5835.2	2	5.98	0	4.13E+05		(K)GSSNSY	(K)G S|S N S/Y A I/K(K)		84.45	463.7311	926.458	-0.0029	-3.1	8.59	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
19440	dirMS_041712_NAR_40mM_plus2.14495.14495.3	3	5.98	1	1.37E+05		(K)IMASSPI	(K)I M/A/S S/P D M D L A T V/S A L R\K(M)		151.5	635.9975	1905.977	0.0007	0.4	5.96	36208.1	7.21	HUMAN	B4DMU0	Pyrroline-5-carboxylate reductase
19441	dirMS_041712_NAR_40mM_plus2.19120.19120.3	3	5.98	1	3.16E+05		(R)GGPNIIT	(R)G G/P/N I|I/T L A D I V K D P V S R(T)		178.95	622.3522	1865.049	-0.007	-3.8	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
19442	dirMS_041712_NAR_40mM_plus2.6524.6524.2	2	5.98	1	3.01E+04	T5349t	(K)GDYRtG	(K)G D|Y/R t G/K(R)	t:N-acetylglucosamine (T)	97.77	500.2303	796.395	203.0585	-20.9	8.59	638399.7	5.46	HUMAN	Q9NU22	Midasin
19443	dirMS_041712_NAR_50mM_plus2.17965.17965.3	3	5.98	1	2.23E+05		(K)LVGQSII	(K)L V/G Q S\I/I A Y L Q K K(G)		161.88	487.6312	1460.883	-0.0045	-3.1	9.7	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
19444	dirMS_041712_NAR_60mM_plus.11566.11566.3	3	5.98	1	8.44E+05	M406m	(R)QLREYQ	(R)Q L R E Y\Q|E/L m N V K(L)	m:Oxidized methionine	116.7	522.9381	1550.8	16.0002	3.4	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
19445	dirMS_041712_NAR_60mM_plus.14979.14979.3	3	5.98	1	3.21E+05		(R)NLDVQL	(R)N L|D/V Q L/L/D T K R(Q)		134.67	438.9179	1314.738	0.0016	1.2	5.96	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
19446	dirMS_041712_NAR_60mM_plus.8706.8706.3	3	5.98	1	2.41E+05		(K)EFFNGKI	(K)E F/F N/G/K/E P S R(G)		104.93	404.2017	1210.585	0.0054	4.5	6.24	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
19447	dirMS_041712_NAR_30mM_minus2.5470.5470.2	2	5.97	0	9.90E+04		(K)DSYVGD	(K)D S|Y/V/G D E A Q S K(R)		83.88	599.7632	1198.522	-0.0031	-2.6	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
19448	dirMS_041712_NAR_30mM_minus2.6206.6206.2	2	5.97	0	5.52E+04		(R)SAENPP	(R)S A|E\N/P/P S G S V R(K)		87.88	550.7684	1100.533	-0.0036	-3.2	5.72	32364.3	9.76	HUMAN	Q15014	Mortality factor 4-like protein 2
19449	dirMS_041712_NAR_40mM_minus2.9379.9379.3	3	5.97	0	9.99E+04		(K)AASDIA	(K)A A S D I|A M T/E L/P P T H P I R(L)		138.25	607.3174	1819.937	0.0006	0.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
19450	dirMS_041712_NAR_50mM_minus2.17539.17539.3	3	5.97	1	2.66E+05		(R)LKLPSIPI	(R)L K L P S I|P\L V/P V S A Q K(R)		169.5	530.669	1589.999	-0.0064	-4.1	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
19451	dirMS_041712_NAR_50mM_minus2.9891.9891.3	3	5.97	0	1.78E+05		(K)TSEVDL	(K)T/S|E V D L A K/P L V K(F)		123.43	433.9205	1299.752	-0.0049	-3.8	5.73	17178.3	5.63	HUMAN	C9IZF9	Programmed cell death 6-interacting protein (Fragment)
19452	dirMS_041712_NAR_60mM_minus.7729.7729.3	3	5.97	1	5.55E+05		(R)YLAEVA	(R)Y L/A E V/A/A/G D D K K(G)		102.08	427.222	1279.653	-0.0014	-1.1	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
19453	dirMS_041712_NAR_120mM_plus.15298.15298.4	4	5.97	2	7.99E+05		(R)AGEVER	(R)A G|E/V E R D L D K/A/D S M I/R(L)		133.18	451.9773	1804.886	0.0016	0.9	4.44	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
19454	dirMS_041712_NAR_120mM_plus.23636.23636.3	3	5.97	0	6.85E+05		(R)LHFFMP	(R)L H F F M P G|F|A/P|L T S R(G)		179	540.9492	1620.835	-0.0025	-1.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
19455	dirMS_041712_NAR_20mM_plus.14688.14688.3	3	5.97	0	1.02E+05		(R)LQEAGIL	(R)L Q\E A G I|L S A E/E/L Q R(L)		172.43	519.6131	1556.828	-0.0031	-2	4.25	533778	5.74	HUMAN	Q15149	Plectin
19456	dirMS_041712_NAR_20mM_plus.6496.6496.2	2	5.97	0	2.02E+05	M216m	(R)DLmAC	(R)D L\m|A C/A Q/T\G S G K(T)	C:Carbamidomethylation m:Oxid	107.72	627.776	1238.55	15.9943	-0.5	5.84	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
19457	dirMS_041712_NAR_30mM_plus2.16394.16609.2	2	5.97	0	3.38E+05		(K)ALWFQ	(K)A L/W/F/Q G R(C)		139.33	439.2414	877.468	0.0076	8.7	9.79	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
19458	dirMS_041712_NAR_30mM_plus2.17303.17303.3	3	5.97	0	1.05E+06		(R)ASLEAAI	(R)A S L E A A I/A/D/A/E/Q R(G)		144.12	448.8963	1344.675	-0.001	-0.8	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
19459	dirMS_041712_NAR_30mM_plus2.6427.6427.2	2	5.97	0	1.59E+05		(R)AVVISG	(R)A V|V/I/S G A G K(M)		87.78	401.2461	801.483	0.002	2.6	8.8	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
19460	dirMS_041712_NAR_30mM_plus2.7148.7148.2	2	5.97	0	1.37E+05		(R)TTTGSYI	(R)T T|T/G S/Y I/A N/R(V)		91.82	542.274	1083.543	-0.0022	-2	8.41	10799.8	5.07	HUMAN	I3L3X7	Proteasome subunit beta type-6 (Fragment)
19461	dirMS_041712_NAR_30mM_plus2.8745.8745.2	2	5.97	0	4.16E+05		(R)VQMEEL	(R)V/Q|M/E\E L\S K(L)		99.43	482.2452	963.482	0.0016	1.6	4.53	533778	5.74	HUMAN	Q15149	Plectin
19462	dirMS_041712_NAR_40mM_plus2.16028.16028.3	3	5.97	1	8.50E+04	M340m	(R)ALGTEVI	(R)A L/G T E\V I Q L F/P E K G N m G K(I)	m:Oxidized methionine	160.77	650.0097	1932.026	15.9886	-3.2	6.18	67184.7	9.24	HUMAN	O95831	Apoptosis-inducing factor 1, mitochondrial
19463	dirMS_041712_NAR_40mM_plus2.18951.18951.3	3	5.97	1	1.10E+05		(K)NLGIPIIT	(K)N L/G|I/P I I T V L G D S K N N V R(A)		177.98	641.701	1923.102	-0.0137	-7.1	8.75	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
19464	dirMS_041712_NAR_40mM_plus2.5512.5512.2	2	5.97	0	1.50E+05		(R)GSNGAF	(R)G S|N/G A|F Y K(A)		89.17	422.2033	843.399	-0.0002	-0.3	8.59	66105.7	7.3	HUMAN	A8MQB8	Fragile X mental retardation protein 1
19465	dirMS_041712_NAR_50mM_plus2.12505.12505.3	3	5.97	0	1.98E+05		(R)VNAIEH	(R)V/N/A I E/H/V/I\I P R(I)		133.77	420.9182	1260.742	-0.0022	-1.8	6.72	21920.7	5.63	HUMAN	G3V2S6	V-type proton ATPase subunit D
19466	dirMS_041712_NAR_50mM_plus2.16222.16222.3	3	5.97	1	1.89E+04		(K)DVLFLKI	(K)D V/L|F/L K D C V G P E/V E K(A)	C:Carbamidomethylation	153.1	583.3027	1747.893	0	0	4.32	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
19467	dirMS_041712_NAR_50mM_plus2.7351.7351.3	3	5.97	1	1.63E+05		(R)TESTPIT	(R)T E|S/T/P I/T A V\K Q/P E K(V)		104.68	510.2769	1528.822	-0.0056	-3.6	5.81	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
19468	dirMS_041712_NAR_60mM_plus.18950.18950.3	3	5.97	1	2.62E+05		(K)YGKLEV	(K)Y/G K L E\V\A\N L/L/L Q/K(S)		156.68	496.9628	1488.878	-0.0046	-3.1	8.5	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
19469	dirMS_041712_NAR_60mM_plus.21517.21517.3	3	5.97	0	1.09E+05		(R)LHFFMP	(R)L H F F M\P/G\F|A|P\L T/S R(G)		179.2	540.9492	1620.835	-0.0025	-1.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
19470	dirMS_041712_NAR_60mM_plus.8812.8812.3	3	5.97	1	8.04E+05		(R)QLQLAQ	(R)Q L|Q/L\A Q/E A A Q K/R(L)		104.95	461.9268	1383.77	-0.0044	-3.2	8.75	533778	5.74	HUMAN	Q15149	Plectin
19471	dirMS_041712_NAR_120mM_minus.17851.17851.3	3	5.96	0	1.45E+05		(R)HLLQAP	(R)H L|L Q A/P\V/D D A Q E/I L H/S R(F)		152.37	648.0089	1942.014	-0.002	-1	5.21	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
19472	dirMS_041712_NAR_120mM_minus.19914.19914.3	3	5.96	1	1.47E+05		(R)RFDEILE	(R)R F D E\I L E\A/S\D/G/I/M/V A R(G)		164.65	607.9762	1821.916	-0.0023	-1.3	4.32	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
19473	dirMS_041712_NAR_120mM_minus.7321.7321.3	3	5.96	0	4.15E+05		(K)NNRPSE	(K)N/N/R P S E/G/P/L/Q T R(L)		94.1	456.9036	1368.698	-0.0016	-1.2	9.6	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
19474	dirMS_041712_NAR_20mM_minus.8370.8370.2	2	5.96	2	1.48E+05	S924s	(K)ITKsDKK	(K)I/T|K|s D K K(I)	s:Phosphorylated S	133.13	450.2308	819.493	79.9609	-6.1	9.7	119198.5	8.65	HUMAN	A2A2Z9	Ankyrin repeat domain-containing protein 18B
19475	dirMS_041712_NAR_20mM_minus.9478.9478.3	3	5.96	0	1.18E+04	M175m	(R)LEQGQA	(R)L E Q G Q A\I/D D L m/P A Q K(-)	m:Oxidized methionine	144.5	558.2794	1656.826	15.9975	1.5	4.03	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
19476	dirMS_041712_NAR_20mM_minus.9787.9787.2	2	5.96	0	3.36E+05		(K)IGGIGTV	(K)I/G/G\I/G T V/P V G R(V)		147.47	513.3075	1025.61	-0.0025	-2.4	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
19477	dirMS_041712_NAR_30mM_minus2.13936.13936.2	2	5.96	0	2.86E+05		(R)IYVVDV	(R)I Y|V/V\D V G/S E/P R(A)		129.47	617.3267	1233.647	-0.0013	-1	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
19478	dirMS_041712_NAR_30mM_minus2.6005.6005.2	2	5.96	0	1.25E+05		(R)AQAEQ	(R)A Q|A/E/Q A A L/R(Q)		87.07	479.2592	957.511	-0.0001	-0.1	6.05	533778	5.74	HUMAN	Q15149	Plectin
19479	dirMS_041712_NAR_40mM_minus2.13950.13950.3	3	5.96	0	3.46E+05		(R)LLEVLSG	(R)L L|E|V\L S G E I/L P K P T/K(G)		166.62	546.333	1636.988	-0.0039	-2.4	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
19480	dirMS_041712_NAR_50mM_minus2.13428.13428.3	3	5.96	0	1.81E+05		(R)DLQANV	(R)D L/Q/A/N V E H/L/V Q K(M)		144.12	465.2561	1393.743	0.0103	7.4	5.32	94165.2	8.68	HUMAN	J3KNX3	6-phosphofructokinase
19481	dirMS_041712_NAR_50mM_minus2.13812.13812.3	3	5.96	0	3.00E+04		(K)TGEEIFG	(K)T|G E|E I/F/G T I/G M R/P N A K(N)		146.93	574.2947	1720.869	0.0009	0.5	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
19482	dirMS_041712_NAR_50mM_minus2.6678.6678.3	3	5.96	1	2.52E+05		(R)ASVDTK	(R)A S|V D T K E A E/G A|P Q V E A G K(R)		104.8	596.2904	1786.882	-0.0251	-14	4.41	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
19483	dirMS_041712_NAR_60mM_minus.11531.11531.3	3	5.96	1	1.59E+05		(K)EIADYLA	(K)E I/A/D Y/L A/A/G K D/E R(A)		124.38	484.2432	1450.717	-0.0022	-1.5	4.32	41736.1	5.41	HUMAN	A8KAH5	IST1 homolog
19484	dirMS_041712_NAR_60mM_minus.12482.12482.3	3	5.96	2	9.65E+05		(K)KGAVTG	(K)K G A/V T G G E/E A K L K(K)		129.85	429.9125	1287.727	-0.0037	-2.9	8.5	212309.6	8.42	HUMAN	O14647	Chromodomain-helicase-DNA-binding protein 2
19485	dirMS_041712_NAR_60mM_minus.9290.9290.3	3	5.96	1	4.82E+04	T310t	(K)LVKNNA	(K)L V/K N N A S T S Y D V/t A K(S)	t:N-acetylglucosamine (T)	111.38	605.316	1610.838	203.095	8.6	8.5	46637.5	10.69	HUMAN	Q92901	60S ribosomal protein L3-like
19486	dirMS_041712_NAR_120mM_plus.10230.10230.3	3	5.96	0	1.24E+05		(R)IHDPQLI	(R)I H D P Q\L|L T E/R(A)		106.38	407.8899	1221.659	-0.0035	-2.8	5.32	21721.5	5.37	HUMAN	H7BZ35	Aspartate--tRNA ligase, cytoplasmic (Fragment)
19487	dirMS_041712_NAR_20mM_plus.13444.13545.2	2	5.96	0	1.64E+05	M273m	(K)mISDAIF	(K)m I|S/D/A\I/P E L K(A)	m:Oxidized methionine	165.33	566.7967	1116.597	15.9892	-5	4.37	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
19488	dirMS_041712_NAR_20mM_plus.14396.14396.2	2	5.96	0	1.59E+04		(K)TVFGVEI	(K)T V/F G|V/E P\D L T R(E)		171.18	617.3237	1233.647	-0.0073	-5.9	4.37	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
19489	dirMS_041712_NAR_20mM_plus.19121.19121.2	2	5.96	0	2.26E+05		(K)ILTFDQL	(K)I L|T|F D Q L A L D\S P K(G)		203.22	730.9063	1460.8	0.0058	4	4.21	14643	11.93	HUMAN	F8VUA6	60S ribosomal protein L18 (Fragment)
19490	dirMS_041712_NAR_30mM_plus2.14351.14351.2	2	5.96	0	2.16E+05		(K)ASEGPA	(K)A/S E/G/P A\F/F/P G R(C)		127.95	568.2831	1135.553	0.0058	5.1	6.05	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
19491	dirMS_041712_NAR_50mM_plus2.10894.10894.3	3	5.96	1	8.08E+05		(R)DISTNK	(R)D I/S T N/K V E Q\I|P Y G E R(I)		124.13	583.6304	1748.881	-0.0047	-2.7	4.68	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
19492	dirMS_041712_NAR_50mM_plus2.19407.19407.3	3	5.96	1	7.41E+05		(R)GDLGIEI	(R)G D L|G\I/E/I/P A E K V F L A Q K(M)		171.42	610.0104	1828.022	-0.0048	-2.6	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
19493	dirMS_041712_NAR_50mM_plus2.7084.7084.3	3	5.96	1	3.62E+04	M22m M2	(K)LAEQAE	(K)L A/E/Q/A E R Y D D m A A C m K(S)	C:Carbamidomethylation m:Oxid	102.98	645.2763	1901.819	31.9953	2.8	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
19494	dirMS_041712_NAR_50mM_plus2.7334.7334.3	3	5.96	0	1.68E+05		(R)SGSSQEI	(R)S G S\S/Q E L D V K/P S A S P Q E R(S)		103.85	634.6443	1901.92	-0.0016	-0.8	4.68	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
19495	dirMS_041712_NAR_60mM_plus.15837.15837.3	3	5.96	0	2.03E+05		(K)NFDLRP	(K)N/F|D/L R/P G V I V R(-)		140.08	429.248	1285.738	-0.0081	-6.3	9.6	33192.3	6.77	HUMAN	B4DN45	S-adenosylmethionine synthase
19496	dirMS_041712_NAR_60mM_plus.19012.19012.3	3	5.96	0	1.64E+05		(R)NHPGLL	(R)N H/P G L L\L|M/D/T T F R(D)		156.78	505.6001	1514.778	0.0073	4.8	6.74	130372.9	6.37	HUMAN	P11498	Pyruvate carboxylase, mitochondrial
19497	dirMS_041712_NAR_120mM_minus.20831.20831.4	4	5.95	1	5.83E+05		(R)SLHDAL	(R)S L H D A L C\V|L A Q/T V K D/S R(T)	C:Carbamidomethylation	173.1	479.0049	1912.991	0.0068	3.6	6.47	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
19498	dirMS_041712_NAR_120mM_minus.5499.5499.3	3	5.95	0	2.91E+05	M46m M4	(R)HQGVm	(R)H Q G\V\m/V/G m G Q K(D)	m:Oxidized methionine	83.3	401.8604	1171.571	31.9956	4.8	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
19499	dirMS_041712_NAR_120mM_minus.8722.8722.4	4	5.95	0	2.22E+05		(K)LLETTDR	(K)L L/E T T D R P D G H/Q/N N/L R(S)		101.72	470.4908	1878.942	-0.0003	-0.2	5.38	82375.7	4.6	HUMAN	B7ZAV6	Importin subunit beta-1
19500	dirMS_041712_NAR_20mM_minus.7708.7708.2	2	5.95	0	2.00E+05		(K)TVPVEA	(K)T V/P V/E/A V T S K(T)		125.98	515.7883	1030.578	-0.0086	-8.3	5.66	35720	5.34	HUMAN	B4E358	Src substrate cortactin
19501	dirMS_041712_NAR_20mM_minus.8197.8197.2	2	5.95	0	1.41E+05		(K)DVGSLA	(K)D V|G S L/A\S V\Q R(Y)		131.98	516.2772	1031.548	-0.0009	-0.8	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin
19502	dirMS_041712_NAR_20mM_minus.8981.8981.2	2	5.95	0	2.76E+05		(R)ALGQNF	(R)A L/G Q/N|P/T N A E V L K(V)		138.8	677.871	1354.733	0.0022	1.6	6.05	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
19503	dirMS_041712_NAR_40mM_minus2.14136.14136.3	3	5.95	0	6.82E+05		(R)IHFPLAT	(R)I H F\P L A T Y A|P/V I S A E K(A)		167.8	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
19504	dirMS_041712_NAR_50mM_minus2.11028.11028.3	3	5.95	1	3.85E+04	M72m	(R)TEmENE	(R)T\E/m|E N\E F\V L/I K K(D)	m:Oxidized methionine	131.15	499.5937	1480.772	15.995	0	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
19505	dirMS_041712_NAR_50mM_minus2.14593.14593.3	3	5.95	0	2.41E+04		(R)QADPG	(R)Q/A D\P G A Q V C A A/A/P A I G T G R(I)	C:Carbamidomethylation	151.1	604.3145	1810.887	0.0425	23.5	5.84	56068.5	10.41	HUMAN	P15863	Paired box protein Pax-1
19506	dirMS_041712_NAR_50mM_minus2.7762.7762.3	3	5.95	0	3.55E+04		(R)VILGSEA	(R)V I|L/G/S E A A Q Q H P E E V R(G)		111.43	588.3055	1762.908	-0.0063	-3.6	4.75	19458.5	4.89	HUMAN	E9PKK8	Dipeptidyl peptidase 3 (Fragment)

19507	dirMS_041712_NAR_50mM_minus2.7862.7862.3	3	5.95	1	1.46E+05		(K)TAVCDI	(K)T A|V C/D I/P P R G L/K(M)	C:Carbamidomethylation	111.9	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
19508	dirMS_041712_NAR_50mM_minus2.9905.9905.3	3	5.95	0	4.14E+05	M147m	(K)LQmEA	(K)L Q|m E/A P H I/I V G T P G R(V)	m:Oxidized methionine	124.98	545.6267	1618.873	15.9922	-1.7	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
19509	dirMS_041712_NAR_60mM_minus.15148.15148.3	3	5.95	0	1.63E+05		(R)YQEALH	(R)Y Q/E|A L/H/L G S Q L L R(E)		144.62	509.9455	1527.828	-0.0059	-3.8	6.75	47748.2	6.08	HUMAN	O00231	26S proteasome non-ATPase regulatory subunit 11
19510	dirMS_041712_NAR_60mM_minus.6307.6307.2	2	5.95	1	1.72E+05		(K)IIAPPERI	(K)I I/A/P\P E R K(Y)		94	462.287	923.567	-0.0006	-0.6	8.75	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
19511	dirMS_041712_NAR_120mM_plus.16795.16866.4	4	5.95	1	8.64E+05	M219m	(K)EmVELP	(K)E m V E L/P L R H/P A L/F/K(A)	m:Oxidized methionine	141.48	424.7366	1679.93	15.9944	-0.3	6.86	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
19512	dirMS_041712_NAR_20mM_plus.11920.11920.2	2	5.95	0	1.09E+05		(R)IYVVDV	(R)I Y|V/V/D V/G/S E P R(A)		156.05	617.3237	1233.647	-0.0073	-5.9	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
19513	dirMS_041712_NAR_20mM_plus.16976.16976.3	3	5.95	0	2.28E+05		(R)AIVAIEN	(R)A I\V A I E N\P A/D V S|V/I/S S R(N)		188.85	580.9864	1740.949	-0.0044	-2.5	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
19514	dirMS_041712_NAR_20mM_plus.17927.17927.3	3	5.95	0	1.97E+05		(R)TVQSLEI	(R)T V\Q S L E I/D|L D/S/M R(N)		194.98	502.9236	1506.747	0.0094	6.2	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
19515	dirMS_041712_NAR_20mM_plus.7495.7495.2	2	5.95	0	2.37E+05		(K)VTLTSEE	(K)V T L/T/S E/E E A R(L)		119.93	567.7865	1134.564	0.002	1.8	4.25	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
19516	dirMS_041712_NAR_30mM_plus2.17168.17168.2	2	5.95	0	1.48E+05		(K)WPLYM	(K)W/P|L/Y M S T K(N)		143.55	513.2647	1025.513	0.0097	9.4	8.59	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
19517	dirMS_041712_NAR_30mM_plus2.19739.19739.2	2	5.95	0	3.62E+05		(R)AITGASL	(R)A I|T/G A/S L A D I/M A/K(R)		156.77	631.3424	1261.682	-0.0045	-3.6	5.88	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
19518	dirMS_041712_NAR_30mM_plus2.19826.19826.2	2	5.95	0	3.08E+05		(K)LFLVQL	(K)L F|L|V/Q L Q E K(A)		157.52	559.3295	1117.662	-0.0098	-8.8	6	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
19519	dirMS_041712_NAR_30mM_plus2.8665.8665.2	2	5.95	0	4.70E+05		(R)GNLGA	(R)G N|L G A/G|N/G N L Q/G P/R(H)		99.42	662.8376	1324.672	-0.0037	-2.8	9.75	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
19520	dirMS_041712_NAR_40mM_plus2.5388.5388.2	2	5.95	0	6.82E+04		(K)EQWEE	(K)E Q/W E/E R(I)		88.42	438.6982	876.385	0.0045	5.1	4.25	71218.8	6.3	HUMAN	A7YIJ8	Radixin
19521	dirMS_041712_NAR_40mM_plus2.9729.9729.2	2	5.95	0	1.72E+05		(K)ELNYFA	(K)E/L/N/Y/F/A K(A)		121.12	442.7291	884.451	-0.0003	-0.4	6.1	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
19522	dirMS_041712_NAR_50mM_plus2.15232.15451.3	3	5.95	0	1.12E+06		(R)QVLIASH	(R)Q V/L I/A S H L/P S Y E L R(H)		149.63	542.6394	1625.901	0.0027	1.6	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
19523	dirMS_041712_NAR_120mM_minus.13740.13740.4	4	5.94	2	8.32E+05	M100m	(K)KQGGL	(K)K\Q G G L G|P m\N I/P/L V/S D P K/R(T)	m:Oxidized methionine	128.55	481.5173	1907.053	15.9942	-0.3	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
19524	dirMS_041712_NAR_120mM_minus.19286.19286.3	3	5.94	1	1.46E+05		(K)YNQLLRI	(K)Y/N/Q/L L R I E E E L G/S K(A)		160.73	564.6367	1691.896	-0.0007	-0.4	4.79	47510.4	7.04	HUMAN	P06733	Alpha-enolase
19525	dirMS_041712_NAR_20mM_minus.10734.10734.3	3	5.94	0	9.03E+04	M1m M3m	(-)mQmAD.	(-)m Q m|A D A A T I A T M N K(A)	m:Oxidized methionine	155.27	510.2283	1496.691	31.9798	-6.6	5.59	51921.7	9.69	HUMAN	Q9NSD7	Relaxin-3 receptor 1
19526	dirMS_041712_NAR_30mM_minus2.4990.4990.2	2	5.94	1	9.48E+05	S666s	(K)SQKVFsE	(K)S Q/K/V F s E/K(L)	s:Phosphorylated S	80.12	516.7465	952.51	79.9759	9.3	8.31	87498	6.43	HUMAN	C9J266	E3 ubiquitin-protein ligase RNF123
19527	dirMS_041712_NAR_30mM_minus2.7741.7741.2	2	5.94	0	1.40E+05		(K)GPSSVEI	(K)G/P|S/S V E D|I K(A)		96.57	466.2393	931.473	-0.0018	-1.9	4.37	32745.6	4.64	HUMAN	P06748	Nucleophosmin
19528	dirMS_041712_NAR_40mM_minus2.12245.12245.3	3	5.94	1	1.79E+04		(K)VVEEAP	(K)V/V/E/E A/P S I F L D A E T R R(A)		155.72	611.3244	1831.955	0.0038	2.1	4.41	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
19529	dirMS_041712_NAR_40mM_minus2.8237.8237.3	3	5.94	0	2.47E+05	M35m	(K)AASDIA	(K)A A S/D I/A m T E L/P P/T H/P\I R(L)	m:Oxidized methionine	128.65	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
19530	dirMS_041712_NAR_50mM_minus2.10405.10405.3	3	5.94	1	1.53E+05	M546m	(K)QmADT	(K)Q m A/D/T G\K L/N T L/L Q R(A)	m:Oxidized methionine	127.25	535.6231	1588.848	16.0072	7.7	8.75	91324.5	5.75	HUMAN	Q00839	Heterogeneous nuclear ribonucleoprotein U
19531	dirMS_041712_NAR_50mM_minus2.14147.14147.3	3	5.94	1	2.32E+05		(R)IIEFVPT	(R)I I/E/F V P T K T P Y\D/P R(W)		148.53	559.3044	1675.905	-0.0067	-4	6.07	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
19532	dirMS_041712_NAR_60mM_minus.11303.11303.3	3	5.94	1	8.17E+05		(K)LMIARG.	(K)L M|I A R G A/I E E/R(T)		122.1	420.2346	1258.694	-0.0044	-3.5	6.14	216055.5	4.9	HUMAN	B7ZMI4	MPDZ protein
19533	dirMS_041712_NAR_120mM_plus.20019.20019.4	4	5.94	1	3.88E+05		(K)DISTLEP	(K)D I|S T/L E/P L K K L E C L K(S)	C:Carbamidomethylation	158.17	447.5057	1786.998	0.0027	1.5	6.18	18070.1	3.52	HUMAN	Q5T6W8	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member B (Fragment)
19534	dirMS_041712_NAR_120mM_plus.7932.7932.3	3	5.94	0	1.29E+05	M437m	(R)LESGMC	(R)L E|S G/M Q N m/S I/H T K(T)	m:Oxidized methionine	95.35	497.9025	1475.698	15.9948	-0.1	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
19535	dirMS_041712_NAR_20mM_plus.8829.8829.2	2	5.94	0	2.37E+05		(R)VPPPPPI	(R)V/P/P|P P P I A/R(A)		130.68	472.2851	943.572	-0.0094	-10	9.72	32085.2	8.93	HUMAN	B4DY08	Heterogeneous nuclear ribonucleoproteins C1/C2
19536	dirMS_041712_NAR_20mM_plus.9323.9323.2	2	5.94	0	7.19E+04		(R)QTVAV	(R)Q T\V/A/V/G V I/K(A)		135.88	457.7856	914.567	-0.003	-3.3	8.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
19537	dirMS_041712_NAR_30mM_plus2.20469.20469.2	2	5.94	0	9.51E+04		(K)TENLLG	(K)T E/N L|L/G/S Y F/P K(K)		161.23	634.8311	1268.652	0.0028	2.2	5.66	28772.3	6.28	HUMAN	A6NJG9	Proteasome activator complex subunit 1
19538	dirMS_041712_NAR_30mM_plus2.8146.8172.3	3	5.94	0	4.74E+05		(K)SNVSDA	(K)S/N V S D A\V/A/Q/S/T/R(I)		96.35	412.2004	1234.602	-0.0156	-12.6	5.55	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
19539	dirMS_041712_NAR_40mM_plus2.13330.13330.2	2	5.94	0	8.98E+04		(K)FFVGGN	(K)F F/V/G/G N W K(M)		144.42	477.7448	954.483	-0.0009	-0.9	8.75	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
19540	dirMS_041712_NAR_40mM_plus2.5830.5830.2	2	5.94	1	1.68E+05		(R)SKQAEE	(R)S K\Q\A E E\E|F(-)		92.1	484.2219	967.437	-0.0002	-0.2	4.25	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
19541	dirMS_041712_NAR_50mM_plus2.14169.14169.3	3	5.94	1	2.31E+06		(R)LDAESL	(R)L D/A E/S L V K L/S/V D/R(V)		143.27	482.2828	1444.801	0.0333	23	4.56	351590.8	5.81	HUMAN	P42858	Huntingtin
19542	dirMS_041712_NAR_50mM_plus2.16384.16384.3	3	5.94	1	7.13E+04		(R)WFQQK	(R)W F\Q Q K Y D/G/I I/L/P G/K(-)		154.48	564.9788	1692.911	0.011	6.5	8.5	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
19543	dirMS_041712_NAR_50mM_plus2.18503.18503.3	3	5.94	0	3.58E+05		(R)LLLDGA	(R)L L L D G A/P L I A I H K(A)		165.82	458.622	1373.852	-0.0001	0	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
19544	dirMS_041712_NAR_60mM_plus.15698.15698.3	3	5.94	1	2.14E+05		(R)DLEEKLE	(R)D L|E E K/L/E/T L/R(L)		138.32	415.8936	1245.669	-0.0023	-1.8	4.41	141626	5.5	HUMAN	A8MY36	Dynactin subunit 1
19545	dirMS_041712_NAR_60mM_plus.16760.16760.3	3	5.94	1	8.72E+05		(R)STNKGT.	(R)S T N K G T A Y\T F|F|T/P G N L K(Q)		144.73	616.3117	1846.933	-0.0128	-7	9.7	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
19546	dirMS_041712_NAR_120mM_minus.13720.13720.4	4	5.93	2	8.32E+05	M100m	(K)KQGGL	(K)K\Q G G L G\P m\N\I|P L V/S D/P K R(T)	m:Oxidized methionine	128.55	481.5173	1907.053	15.9942	-0.3	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
19547	dirMS_041712_NAR_120mM_minus.16084.16084.3	3	5.93	1	2.26E+05		(K)STFVLDE	(K)S T/F V/L D/E F K R(K)		141.13	414.5544	1241.652	-0.0038	-3.1	5.79	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
19548	dirMS_041712_NAR_30mM_minus2.13500.13500.2	2	5.93	0	1.35E+05	M357m	(R)FFmGN	(R)F/F/m/G N/Q V\L/K(V)	m:Oxidized methionine	128	550.2855	1083.566	15.9982	3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
19549	dirMS_041712_NAR_50mM_minus2.13341.13341.3	3	5.93	0	2.51E+05		(K)VTHAVV	(K)V T H A V V T V/P A/Y|F N D A Q R(Q)		143.22	629.9954	1887.971	0.0005	0.3	6.71	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
19550	dirMS_041712_NAR_60mM_minus.10589.10589.3	3	5.93	1	1.42E+05		(R)SATKVT	(R)S A T K V\T A D V|I/N/A\A E/K(L)		118.78	506.6084	1517.817	-0.0063	-4.2	5.79	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
19551	dirMS_041712_NAR_60mM_minus.14326.14326.3	3	5.93	1	2.57E+05		(R)VEVERD	(R)V E|V/E\R D N L A E/D I M R(L)		139.95	563.6139	1688.827	-0.0001	0	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
19552	dirMS_041712_NAR_60mM_minus.16076.16076.3	3	5.93	0	2.32E+05		(R)FDASFF	(R)F/D A S F F/G V H/P K(Q)		149.48	417.8768	1251.616	0.0002	0.1	6.74	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
19553	dirMS_041712_NAR_60mM_minus.16206.16206.3	3	5.93	1	1.61E+05	M84m	(K)ETmQSL	(K)E T/m/Q/S L N D R L A/S Y L D R(V)	m:Oxidized methionine	150.3	643.3097	1911.923	15.9916	-1.7	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
19554	dirMS_041712_NAR_60mM_minus.19378.19378.3	3	5.93	1	1.89E+05		(R)KAIIIFVP	(R)K\A I I I F\V|P/V P Q L K(S)		172.82	489.3209	1465.95	-0.0023	-1.6	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
19555	dirMS_041712_NAR_60mM_minus.6821.6821.3	3	5.93	1	1.33E+05		(R)LCAGAS	(R)L/C\A/G A S/E D I R E K(L)	C:Carbamidomethylation	97.07	450.2225	1348.652	0.0004	0.3	4.68	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
19556	dirMS_041712_NAR_60mM_minus.7587.7587.3	3	5.93	1	1.06E+05	M195m	(R)GSNmDI	(R)G/S/N m/D/F R E/P T E E E/R(A)	m:Oxidized methionine	102.05	571.578	1696.723	15.9963	0.8	4.25	27441.6	6.68	HUMAN	Q15056	Eukaryotic translation initiation factor 4H
19557	dirMS_041712_NAR_120mM_plus.4898.4898.2	2	5.93	0	1.76E+05		(R)HAYGD	(R)H/A/Y/G D Q Y R(A)		77.43	505.2275	1009.449	-0.0009	-0.9	6.74	17833.3	8.73	HUMAN	C9J4N6	Isocitrate dehydrogenase [NADP] cytoplasmic (Fragment)
19558	dirMS_041712_NAR_20mM_plus.10182.10182.2	2	5.93	0	2.01E+05		(K)LSDGVA	(K)L/S|D/G V A V/L K(V)		143.02	451.2712	901.535	-0.0002	-0.2	5.84	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
19559	dirMS_041712_NAR_20mM_plus.13640.13640.2	2	5.93	0	2.77E+05		(R)GDLGIEI	(R)G D L|G|I/E I/P A E K(V)		166.72	571.3075	1141.61	-0.0022	-1.9	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
19560	dirMS_041712_NAR_20mM_plus.14733.14733.3	3	5.93	0	5.44E+04	M174m	(K)AmGAA	(K)A\m G A A Q V\V|V/T D L/S A T R(L)	m:Oxidized methionine	173.1	535.9457	1589.832	15.991	-2.5	5.88	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
19561	dirMS_041712_NAR_20mM_plus.9535.9535.2	2	5.93	0	7.42E+04		(R)DTLYEA	(R)D T/L/Y E A V R(E)		137.03	483.7515	966.489	0.0066	6.9	4.37	25002	10.06	HUMAN	P62906	60S ribosomal protein L10a
19562	dirMS_041712_NAR_30mM_plus2.10408.10408.2	2	5.93	0	1.89E+04		(K)SMSTEG	(K)S M|S\T E/G/L M\K(F)		108.35	492.2338	983.454	0.0067	6.8	5.72	50659.2	7.87	HUMAN	B4DJV2	Citrate synthase
19563	dirMS_041712_NAR_30mM_plus2.14042.14042.2	2	5.93	0	7.71E+05		(R)LAGLFNI	(R)L/A/G\L/F/N E Q/R(K)		126.13	524.279	1047.558	-0.0074	-7.1	6	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
19564	dirMS_041712_NAR_30mM_plus2.21172.21172.2	2	5.93	0	4.91E+05		(K)STLINTLI	(K)S T|L|I/N T/L F K(S)		166.58	518.799	1036.604	-0.013	-12.5	8.47	18010.4	9.42	HUMAN	K7EIE4	Septin-9 (Fragment)
19565	dirMS_041712_NAR_40mM_plus2.12608.12608.2	2	5.93	0	2.09E+05		(R)YIEIFK(S	(R)Y/I/E I/F K(S)		140.37	406.7302	812.455	-0.0021	-2.6	6	24249.1	6.99	HUMAN	D6RBM0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
19566	dirMS_041712_NAR_40mM_plus2.7652.7652.2	2	5.93	0	6.28E+04		(R)AQYDEL	(R)A Q|Y/D E L/A R(K)		105.2	483.2372	965.469	-0.0016	-1.6	4.37	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
19567	dirMS_041712_NAR_50mM_plus2.13571.13571.3	3	5.93	0	1.13E+06		(K)AASDIA	(K)A A S D\I|A M T E/L/P P T H P I R(L)		139.33	607.3177	1819.937	0.0015	0.8	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
19568	dirMS_041712_NAR_50mM_plus2.14363.14363.3	3	5.93	1	1.80E+05		(K)TITLEVEI	(K)T I/T/L/E V/E/P S D T I E N V K A K(I)		143.57	663.0232	1987.059	-0.0043	-2.2	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
19569	dirMS_041712_NAR_50mM_plus2.9271.9271.3	3	5.93	0	1.75E+04		(R)GPPPTD	(R)G P|P/P T D P Y G R P P P Y D/R(G)		115.38	594.6247	1781.861	-0.001	-0.6	5.96	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
19570	dirMS_041712_NAR_60mM_plus.5731.5731.3	3	5.93	0	1.87E+05		(R)STFETE	(R)S T/F E/T/E H A G Q R(D)		88.4	421.5294	1262.576	-0.0024	-1.9	5.38	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
19571	dirMS_041712_NAR_30mM_minus2.16787.16787.2	2	5.92	0	3.32E+05		(K)FFVGGN	(K)F/F/V/G G N/W/K(M)		144.1	477.745	954.483	-0.0005	-0.5	8.75	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
19572	dirMS_041712_NAR_40mM_minus2.11614.11614.3	3	5.92	0	1.06E+05		(K)VALLLLD	(K)V/A L/L L|L D Q G A S P H A A A K(N)		151.37	558.9882	1674.954	-0.0037	-2.2	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
19573	dirMS_041712_NAR_40mM_minus2.9536.9536.3	3	5.92	1	2.93E+04		(R)LSEDYG	(R)L/S E D Y G V L K T D/E G I/A Y R(G)		138.48	643.6603	1928.96	0.0063	3.3	4.32	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
19574	dirMS_041712_NAR_50mM_minus2.6929.6929.3	3	5.92	1	2.51E+04		(K)SFPDKA	(K)S F|P D K A P V N G T E Q/T Q K(T)		105.8	582.9583	1746.866	-0.0054	-3.1	5.79	197797.8	6.21	HUMAN	G3V1L9	Tight junction protein 1 (Zona occludens 1), isoform CRA_a
19575	dirMS_041712_NAR_50mM_minus2.6971.6971.3	3	5.92	1	1.70E+04		(K)QGIETPE	(K)Q G/I E T/P E\D/Q/N/D L R K(M)		106.13	548.2723	1642.803	-0.0008	-0.5	4.32	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
19576	dirMS_041712_NAR_120mM_plus.13618.13618.3	3	5.92	0	1.10E+06		(K)THINIVV	(K)T\H|I N I V/V/I G H V D/S G K(S)		124.08	530.2975	1588.881	-0.0026	-1.6	6.61	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
19577	dirMS_041712_NAR_120mM_plus.16530.16530.4	4	5.92	1	1.19E+06		(R)LLHIEEL	(R)L/L H/I/E/E L R E L Q T K(I)		139.85	406.2361	1621.927	-0.0046	-2.8	5.5	28181.7	6.19	HUMAN	Q9Y224	UPF0568 protein C14orf166
19578	dirMS_041712_NAR_120mM_plus.4789.4789.3	3	5.92	0	4.66E+03	M77m M7	(R)LTNSM	(R)L T/N S M/m m H G R(N)	m:Oxidized methionine	77.6	403.8446	1177.527	31.9918	1.6	9.75	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
19579	dirMS_041712_NAR_120mM_plus.5810.5810.2	2	5.92	0	8.84E+04	T809t	(R)VITWTtE	(R)V/I T W/T t/E P K(S)	t:Phosphorylated T	83.47	577.7866	1074.583	79.9829	14.4	5.97	139660.6	8.89	HUMAN	E3W994	CLIP-associating protein 2
19580	dirMS_041712_NAR_120mM_plus.5997.5997.3	3	5.92	1	7.67E+04		(R)LAADVG	(R)L/A\A\D/V G K/S G T/E R(E)		84.85	401.882	1203.633	-0.0013	-1.1	6.07	17421.8	9.94	HUMAN	I7HJJ0	ADP/ATP translocase 3 (Fragment)
19581	dirMS_041712_NAR_20mM_plus.7800.7800.2	2	5.92	0	2.03E+05		(R)ALANSL	(R)A L\A|N/S L A C Q/G K(Y)	C:Carbamidomethylation	123.82	566.7967	1132.578	0.0082	7.2	8.8	13951.6	9.48	HUMAN	H3BR68	Fructose-bisphosphate aldolase A (Fragment)
19582	dirMS_041712_NAR_20mM_plus.7962.7962.2	2	5.92	0	2.04E+05		(R)FGQGG	(R)F G Q G/G A/G/P V|G G Q G P R(G)		125.17	671.3361	1341.666	-0.0009	-0.7	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
19583	dirMS_041712_NAR_30mM_plus2.10204.10204.2	2	5.92	0	6.28E+05		(R)SPSTLLP	(R)S/P|S T L/L/P K(K)		107.67	421.7559	842.498	0.0063	7.5	8.47	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
19584	dirMS_041712_NAR_30mM_plus2.17569.17569.2	2	5.92	0	1.64E+05		(R)ASLEAAI	(R)A S L E/A/A/I/A/D A E Q\R(G)		145.03	672.8406	1344.675	-0.0015	-1.1	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
19585	dirMS_041712_NAR_40mM_plus2.16125.16242.3	3	5.92	1	2.16E+05		(K)LGVQVV	(K)L G V/Q\V/V/I T D/P E K L D Q I R(Q)		161.78	641.701	1923.091	-0.0025	-1.3	4.56	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
19586	dirMS_041712_NAR_50mM_plus2.15287.15287.3	3	5.92	0	2.34E+05		(R)LASTLV	(R)L A/S T L V H/L\G E Y Q A A/V/D G A R(K)		148.03	657.6802	1971.029	-0.0034	-1.7	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
19587	dirMS_041712_NAR_50mM_plus2.16377.16377.3	3	5.92	0	4.08E+05		(K)QLLGEH	(K)Q L L/G E/H L/T/A I L Q K(G)		154.05	488.6224	1463.858	-0.0054	-3.7	6.75	103381.4	8.47	HUMAN	K4DI93	Cullin 4B, isoform CRA_e
19588	dirMS_041712_NAR_60mM_plus.6323.6323.3	3	5.92	1	2.90E+05		(R)GSCSTE	(R)G S/C/S T/E V E K E T Q E K(M)	C:Carbamidomethylation	91.15	537.9088	1611.717	-0.0048	-3	4.49	13871.4	9.22	HUMAN	O75348	V-type proton ATPase subunit G 1
19589	dirMS_041712_NAR_60mM_plus.8512.8512.3	3	5.92	0	2.66E+05		(R)QVQHIL	(R)Q V Q H I\L/A|S A/S/P S G R(A)		102.67	484.259	1450.776	-0.0137	-9.4	9.75	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
19590	dirMS_041712_NAR_60mM_plus.9978.9978.3	3	5.92	1	2.31E+05		(K)KVTQLD	(K)K V T Q\L D/L/D|G/P K(E)		110.08	405.2308	1213.679	-0.0008	-0.7	5.96	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
19591	dirMS_041712_NAR_120mM_minus.5328.5328.2	2	5.91	0	5.03E+04	M83m	(K)EmQPT	(K)E m Q/P T/H P/I/R(L)	m:Oxidized methionine	82.42	562.7865	1108.557	16.0089	12.5	6.85	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
19592	dirMS_041712_NAR_30mM_minus2.17954.17954.2	2	5.91	0	1.04E+05		(R)LNLWIS	(R)L/N|L/W/I S R(T)		152.17	451.2694	901.525	0.0061	6.8	9.75	58791	9.93	HUMAN	E9PDI4	Ladinin-1
19593	dirMS_041712_NAR_30mM_minus2.20081.20081.2	2	5.91	0	8.03E+04		(K)SLNILTA	(K)S L/N|I/L/T A F Q K(K)		169.83	567.8283	1134.652	-0.0024	-2.1	8.47	18172.6	7.77	HUMAN	F8VY02	Endoplasmic reticulum resident protein 29
19594	dirMS_041712_NAR_50mM_minus2.7485.7485.3	3	5.91	0	5.53E+04		(R)EVEEEP	(R)E V E E/E/P G I/H S L K(H)		109.63	456.2354	1366.685	0.0068	4.9	4.48	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
19595	dirMS_041712_NAR_60mM_minus.15375.15375.3	3	5.91	1	4.32E+05		(K)YQLDKD	(K)Y/Q/L D K D G V/V L F/K(K)		146.23	475.5992	1424.778	0.0047	3.3	5.96	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
19596	dirMS_041712_NAR_120mM_plus.14603.14603.4	4	5.91	2	9.63E+05		(R)YLYTLVI	(R)Y L/Y\T\L V/I/T D K E K A E K(L)		130.57	454.2533	1813.995	-0.0032	-1.8	6.18	7621.9	10.1	HUMAN	J3KT73	60S ribosomal protein L38
19597	dirMS_041712_NAR_120mM_plus.18350.18350.4	4	5.91	0	4.29E+05		(R)QALHSLI	(R)Q A L H/S L/E L H/Y Q A/F L R(D)		149.4	457.2493	1825.971	0.0046	2.5	6.92	533778	5.74	HUMAN	Q15149	Plectin
19598	dirMS_041712_NAR_120mM_plus.18629.18629.4	4	5.91	1	1.57E+06		(K)FQIPPN	(K)F Q\I/P/P N A E L K/Y E L H L K(S)		150.52	485.7703	1940.064	-0.0046	-2.4	6.75	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
19599	dirMS_041712_NAR_120mM_plus.21326.21326.4	4	5.91	2	2.00E+06		(R)TLAEIAK	(R)T L|A/E I/A K V E L D N M/P L R G K(Q)		164.42	500.2814	1998.105	-0.0015	-0.7	5.85	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
19600	dirMS_041712_NAR_120mM_plus.9228.9228.3	3	5.91	1	1.62E+05		(K)LNRYNY	(K)L/N/R Y|N/Y|I E G T K(M)		102.02	457.5737	1370.706	0.0003	0.2	8.5	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
19601	dirMS_041712_NAR_20mM_plus.17603.17603.3	3	5.91	0	6.52E+04		(K)ITNLTQ	(K)I T N L T Q Q L|E Q A/S I/V K(K)		192.92	562.6523	1685.943	-0.0009	-0.5	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
19602	dirMS_041712_NAR_20mM_plus.8116.8116.2	2	5.91	0	1.11E+05		(R)VIGSGC	(R)V/I/G/S G C N L\D S A R(F)	C:Carbamidomethylation	125.07	624.7989	1248.6	-0.0096	-7.7	5.81	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
19603	dirMS_041712_NAR_30mM_plus2.20309.20309.2	2	5.91	0	4.80E+05		(R)ILVATNL	(R)I L|V|A/T N L F G R(G)		161.48	552.331	1103.657	-0.0024	-2.2	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
19604	dirMS_041712_NAR_30mM_plus2.21080.21080.2	2	5.91	0	2.20E+04		(R)EMVLEII	(R)E M V/L/E/I/I/R(E)		163.55	501.7877	1002.565	0.0029	2.9	4.53	61981.6	8.97	HUMAN	Q96I24	Far upstream element-binding protein 3
19605	dirMS_041712_NAR_40mM_plus2.7046.7046.2	2	5.91	0	4.77E+04		(K)SNVSDA	(K)S N|V/S D|A V\A Q S T R(I)		101.65	617.803	1234.602	-0.0035	-2.8	5.55	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
19606	dirMS_041712_NAR_50mM_plus2.17355.17355.3	3	5.91	0	2.43E+04		(K)TAMLLA	(K)T A|M|L/L/A L Q R P E L V|E R(L)		159	580.6633	1739.984	-0.0083	-4.8	5.81	34746.4	9.67	HUMAN	Q8NFV4	Alpha/beta hydrolase domain-containing protein 11
19607	dirMS_041712_NAR_50mM_plus2.6172.6172.3	3	5.91	0	1.38E+05	S89s	(R)EsSIPGA	(R)E s/S I/P G A G L G V/W A K(R)	s:Phosphorylated S	97.28	484.5721	1371.727	79.9751	6	6.1	140198.5	5.85	HUMAN	D3YTA5	PR domain zinc finger protein 16
19608	dirMS_041712_NAR_60mM_plus.17207.17207.3	3	5.91	1	2.15E+05		(K)YMACCL	(K)Y/M|A C/C L L Y R G D V V P K(E)	C:Carbamidomethylation	145.85	615.6325	1844.886	-0.0026	-1.4	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
19609	dirMS_041712_NAR_60mM_plus.5650.5650.3	3	5.91	0	1.90E+06	M21m	(R)SGSmD	(R)S G/S m/D P S G A/H/P S V R(Q)	m:Oxidized methionine	87.5	467.5464	1384.627	15.9973	1.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
19610	dirMS_041712_NAR_60mM_plus.8297.8378.3	3	5.91	1	7.22E+05		(R)DSFDGR	(R)D S|F/D/G R G P P/G/P E S Q S R(A)		101.7	563.5923	1688.762	0	0	4.56	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
19611	dirMS_041712_NAR_20mM_minus.14670.14670.2	2	5.9	0	8.83E+04		(R)IITLTGP	(R)I I/T/L/T/G P T N A I/F K(A)		201.33	694.9107	1388.815	-0.0007	-0.5	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
19612	dirMS_041712_NAR_30mM_minus2.18697.18697.2	2	5.9	0	2.71E+05		(K)YPQLLP	(K)Y/P|Q L L/P G I R(G)		156.02	528.816	1056.62	0.0047	4.4	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
19613	dirMS_041712_NAR_50mM_minus2.13450.13450.3	3	5.9	0	1.78E+05		(R)DLQANV	(R)D L/Q/A N V\E/H L V Q\K(M)		144.13	465.2561	1393.743	0.0103	7.4	5.32	94165.2	8.68	HUMAN	J3KNX3	6-phosphofructokinase
19614	dirMS_041712_NAR_60mM_minus.14346.14346.3	3	5.9	1	2.61E+05		(R)VEVERD	(R)V/E|V E R D N\L/A E/D/I M R(L)		139.97	563.6139	1688.827	-0.0001	0	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
19615	dirMS_041712_NAR_120mM_plus.19114.19114.4	4	5.9	1	1.18E+06		(K)FQIPPN	(K)F Q\I|P/P N/A E/L K Y E L H L K(S)		153.42	485.7703	1940.064	-0.0046	-2.4	6.75	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4

<table>
<tr><td>19616</td><td>dirMS_041712_NAR_120mM_plus.7686.7686.2</td><td>2</td><td>5.9</td><td>1</td><td>1.19E+06</td><td></td><td>(R)AQYDEL</td><td>(R)A Q|Y|D/E L A R K(N)</td><td></td><td>93.32</td><td>547.2874</td><td>1093.564</td><td>0.0039</td><td>3.5</td><td>6.11</td><td>43773.3</td><td>5.26</td><td>HUMAN</td><td>F8VZY9</td><td>Keratin, type I cytoskeletal 18</td></tr>
<tr><td>19617</td><td>dirMS_041712_NAR_20mM_plus.13707.13707.2</td><td>2</td><td>5.9</td><td>0</td><td>9.59E+04</td><td></td><td>(K)HSFALV</td><td>(K)H S F A\L|V S L G|F F K(N)</td><td></td><td>166.3</td><td>676.8783</td><td>1352.736</td><td>0.0132</td><td>9.8</td><td>8.76</td><td>146341.9</td><td>6.04</td><td>HUMAN</td><td>P14616</td><td>Insulin receptor-related protein</td></tr>
<tr><td>19618</td><td>dirMS_041712_NAR_20mM_plus.6670.6670.3</td><td>3</td><td>5.9</td><td>0</td><td>4.40E+04</td><td>M266m</td><td>(R)TQPmT</td><td>(R)T Q P m T\A/Q/A A S Y R(A)</td><td>m:Oxidized methionine</td><td>110.62</td><td>447.5458</td><td>1324.631</td><td>15.9914</td><td>-2.6</td><td>8.41</td><td>69661.6</td><td>9.75</td><td>HUMAN</td><td>Q96PK6</td><td>RNA-binding protein 14</td></tr>
<tr><td>19619</td><td>dirMS_041712_NAR_20mM_plus.9012.9012.2</td><td>2</td><td>5.9</td><td>0</td><td>4.59E+03</td><td>M1901m</td><td>(R)AEmEVL</td><td>(R)A E m/E/V L|L/A/S K(A)</td><td>m:Oxidized methionine</td><td>133.03</td><td>553.7889</td><td>1090.581</td><td>15.9893</td><td>-5.1</td><td>4.53</td><td>533778</td><td>5.74</td><td>HUMAN</td><td>Q15149</td><td>Plectin</td></tr>
<tr><td>19620</td><td>dirMS_041712_NAR_30mM_plus2.20199.20199.2</td><td>2</td><td>5.9</td><td>0</td><td>7.73E+05</td><td></td><td>(K)MSIYQA</td><td>(K)M S/I|Y/Q A M W K(G)</td><td></td><td>158.92</td><td>579.2783</td><td>1157.548</td><td>0.0011</td><td>1</td><td>8.34</td><td>266161</td><td>5.68</td><td>HUMAN</td><td>E9PPU0</td><td>Epiplakin</td></tr>
<tr><td>19621</td><td>dirMS_041712_NAR_30mM_plus2.20845.20845.2</td><td>2</td><td>5.9</td><td>0</td><td>2.74E+05</td><td></td><td>(K)FIIPQIVK</td><td>(K)F I/I/P Q\I V\K(Y)</td><td></td><td>164.3</td><td>479.3092</td><td>957.613</td><td>-0.002</td><td>-2.1</td><td>8.75</td><td>25445.8</td><td>5.52</td><td>HUMAN</td><td>A8MW50</td><td>L-lactate dehydrogenase (Fragment)</td></tr>
<tr><td>19622</td><td>dirMS_041712_NAR_30mM_plus2.8117.8117.2</td><td>2</td><td>5.9</td><td>0</td><td>2.73E+05</td><td></td><td>(K)EIAENAL</td><td>(K)E I/A E N A/L/G K(H)</td><td></td><td>96.92</td><td>472.755</td><td>944.505</td><td>-0.002</td><td>-2.1</td><td>4.53</td><td>36982.9</td><td>6.37</td><td>HUMAN</td><td>P31942</td><td>Heterogeneous nuclear ribonucleoprotein H3</td></tr>
<tr><td>19623</td><td>dirMS_041712_NAR_40mM_plus2.19038.19038.3</td><td>3</td><td>5.9</td><td>0</td><td>1.41E+05</td><td></td><td>(R)ETSSDV</td><td>(R)E T/S S/D V A|L/A/S H I L T A L R(E)</td><td></td><td>178.65</td><td>595.3161</td><td>1783.955</td><td>-0.0211</td><td>-11.8</td><td>5.32</td><td>36920.6</td><td>4.68</td><td>HUMAN</td><td>O00273</td><td>DNA fragmentation factor subunit alpha</td></tr>
<tr><td>19624</td><td>dirMS_041712_NAR_60mM_plus.18849.18849.3</td><td>3</td><td>5.9</td><td>1</td><td>2.18E+05</td><td></td><td>(R)TKEEALE</td><td>(R)T\K E E A L E\L|I|N/G Y I Q K(I)</td><td></td><td>155.85</td><td>583.6498</td><td>1748.943</td><td>-0.008</td><td>-4.6</td><td>4.78</td><td>16245.7</td><td>9.47</td><td>HUMAN</td><td>K7EMU7</td><td>Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1</td></tr>
<tr><td>19625</td><td>dirMS_041712_NAR_60mM_plus.19381.19381.3</td><td>3</td><td>5.9</td><td>0</td><td>6.33E+05</td><td></td><td>(K)VSHLLGI</td><td>(K)V S H L L\G I N|V/T/D/F/T R(G)</td><td></td><td>159.7</td><td>524.6233</td><td>1571.854</td><td>0.0013</td><td>0.8</td><td>6.71</td><td>227783.5</td><td>5.5</td><td>HUMAN</td><td>P35579</td><td>Myosin-9</td></tr>
<tr><td>19626</td><td>dirMS_041712_NAR_120mM_minus.8183.8183.3</td><td>3</td><td>5.89</td><td>0</td><td>3.55E+05</td><td></td><td>(R)AAHSEG</td><td>(R)A A H\S E G N\T\T/A/G L D/M R(E)</td><td></td><td>99.15</td><td>510.9036</td><td>1530.697</td><td>-0.0003</td><td>-0.2</td><td>5.32</td><td>57829.5</td><td>6.01</td><td>HUMAN</td><td>P78371</td><td>T-complex protein 1 subunit beta</td></tr>
<tr><td>19627</td><td>dirMS_041712_NAR_20mM_minus.11820.11820.2</td><td>2</td><td>5.89</td><td>0</td><td>8.32E+04</td><td></td><td>(R)GGIVDE</td><td>(R)G G I/V|D E G/A L L R(A)</td><td></td><td>166.5</td><td>550.3071</td><td>1099.611</td><td>-0.0037</td><td>-3.3</td><td>4.37</td><td>57391.2</td><td>6.29</td><td>HUMAN</td><td>O43175</td><td>D-3-phosphoglycerate dehydrogenase</td></tr>
<tr><td>19628</td><td>dirMS_041712_NAR_30mM_minus2.10964.10964.2</td><td>2</td><td>5.89</td><td>0</td><td>5.48E+04</td><td></td><td>(K)MLVIEQ</td><td>(K)M L|V/I/E Q C K(N)</td><td>C:Carbamidomethylation</td><td>114.78</td><td>510.7635</td><td>1020.522</td><td>-0.0019</td><td>-1.9</td><td>5.75</td><td>49982</td><td>5.86</td><td>HUMAN</td><td>B4DYD8</td><td>T-complex protein 1 subunit epsilon</td></tr>
<tr><td>19629</td><td>dirMS_041712_NAR_30mM_minus2.13497.13522.2</td><td>2</td><td>5.89</td><td>0</td><td>1.94E+05</td><td></td><td>(K)ITLDNAY</td><td>(K)I/T|L|D/N A Y M E K(C)</td><td></td><td>126.87</td><td>599.2902</td><td>1197.582</td><td>-0.0089</td><td>-7.4</td><td>4.37</td><td>30947.9</td><td>6.47</td><td>HUMAN</td><td>H3BQ34</td><td>Pyruvate kinase</td></tr>
<tr><td>19630</td><td>dirMS_041712_NAR_30mM_minus2.18545.18545.2</td><td>2</td><td>5.89</td><td>0</td><td>4.15E+04</td><td></td><td>(R)GIFPVLC</td><td>(R)G I|F|P/V/L/C K(D)</td><td>C:Carbamidomethylation</td><td>155.43</td><td>467.2718</td><td>933.523</td><td>0.0137</td><td>14.7</td><td>8.75</td><td>53557.7</td><td>6.39</td><td>HUMAN</td><td>H3BTN5</td><td>Pyruvate kinase (Fragment)</td></tr>
<tr><td>19631</td><td>dirMS_041712_NAR_30mM_minus2.6895.6947.2</td><td>2</td><td>5.89</td><td>0</td><td>1.96E+05</td><td>M128m</td><td>(R)QIPQAT</td><td>(R)Q\I|P Q/A T A S m K(D)</td><td>m:Oxidized methionine</td><td>92.07</td><td>545.7794</td><td>1074.561</td><td>15.9903</td><td>-4.2</td><td>8.75</td><td>57391.2</td><td>6.29</td><td>HUMAN</td><td>O43175</td><td>D-3-phosphoglycerate dehydrogenase</td></tr>
<tr><td>19632</td><td>dirMS_041712_NAR_50mM_minus2.15260.15260.3</td><td>3</td><td>5.89</td><td>0</td><td>3.85E+05</td><td>M118m</td><td>(R)AGKPVI</td><td>(R)A G K\P V I C\A/T Q/M/L/E S m I K(K)</td><td>C:Carbamidomethylation m:Oxid</td><td>155.1</td><td>631.6612</td><td>1876.969</td><td>15.9997</td><td>2.5</td><td>8.64</td><td>18466.1</td><td>5.78</td><td>HUMAN</td><td>H3BSU3</td><td>Pyruvate kinase (Fragment)</td></tr>
<tr><td>19633</td><td>dirMS_041712_NAR_60mM_minus.15704.15704.3</td><td>3</td><td>5.89</td><td>0</td><td>3.38E+05</td><td></td><td>(R)IYSHSLLI</td><td>(R)I/Y S H S L\L|P V L R(S)</td><td></td><td>148</td><td>433.2572</td><td>1297.763</td><td>-0.0056</td><td>-4.3</td><td>8.75</td><td>60871.9</td><td>6.3</td><td>HUMAN</td><td>B4DJ93</td><td>Phosphoribosylformylglycinamidine cyclo-ligase</td></tr>
<tr><td>19634</td><td>dirMS_041712_NAR_60mM_minus.18453.18453.3</td><td>3</td><td>5.89</td><td>1</td><td>8.06E+03</td><td></td><td>(R)RSLEQN</td><td>(R)R S L\E Q N I/Q/L/P A/A L L S R(F)</td><td></td><td>164.4</td><td>603.6759</td><td>1809.034</td><td>-0.021</td><td>-11.6</td><td>9.6</td><td>81934.1</td><td>6.08</td><td>HUMAN</td><td>P33993</td><td>DNA replication licensing factor MCM7</td></tr>
<tr><td>19635</td><td>dirMS_041712_NAR_60mM_minus.9846.9846.3</td><td>3</td><td>5.89</td><td>1</td><td>2.35E+05</td><td>M145m</td><td>(K)IDKTDY</td><td>(K)I/D K T D Y m|V|G\S Y G P R(A)</td><td>m:Oxidized methionine</td><td>115.05</td><td>539.9245</td><td>1601.763</td><td>15.9961</td><td>0.8</td><td>5.96</td><td>21671</td><td>5.37</td><td>HUMAN</td><td>J3KTF8</td><td>Rho GDP-dissociation inhibitor 1 (Fragment)</td></tr>
<tr><td>19636</td><td>dirMS_041712_NAR_120mM_plus.16262.16403.4</td><td>4</td><td>5.89</td><td>1</td><td>1.30E+06</td><td></td><td>(R)YAEIVHL</td><td>(R)Y A E/I/V H L T L/P D/G T K R(S)</td><td></td><td>138.97</td><td>428.9885</td><td>1712.933</td><td>-0.0008</td><td>-0.5</td><td>6.75</td><td>21230</td><td>6.36</td><td>HUMAN</td><td>H0YC04</td><td>V-type proton ATPase subunit B, brain isoform (Fragment)</td></tr>
<tr><td>19637</td><td>dirMS_041712_NAR_120mM_plus.7549.7549.3</td><td>3</td><td>5.89</td><td>1</td><td>3.18E+05</td><td></td><td>(R)EVQQGE</td><td>(R)E V/Q/Q/G/E E F E R/R(I)</td><td></td><td>92.65</td><td>469.5586</td><td>1406.666</td><td>-0.0046</td><td>-3.3</td><td>4.49</td><td>15567.5</td><td>8.13</td><td>HUMAN</td><td>H0Y4J6</td><td>Adenylate kinase isoenzyme 1 (Fragment)</td></tr>
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<tr><td>19639</td><td>dirMS_041712_NAR_20mM_plus.6738.6738.3</td><td>3</td><td>5.89</td><td>0</td><td>1.25E+05</td><td>M136m</td><td>(R)LVAGEm</td><td>(R)L V A G E m G Q N E|P D Q G/G Q R(G)</td><td>m:Oxidized methionine</td><td>111.45</td><td>601.2753</td><td>1785.818</td><td>15.9929</td><td>-1.1</td><td>4.14</td><td>17508.7</td><td>8.03</td><td>HUMAN</td><td>Q5H928</td><td>3-hydroxyacyl-CoA dehydrogenase type-2</td></tr>
<tr><td>19640</td><td>dirMS_041712_NAR_30mM_plus2.12356.12356.2</td><td>2</td><td>5.89</td><td>0</td><td>5.00E+05</td><td></td><td>(R)QGVDAI</td><td>(R)Q G|V|D/A D I/N G L R(Q)</td><td></td><td>118</td><td>579.2997</td><td>1157.591</td><td>0.0012</td><td>1</td><td>4.21</td><td>39641.8</td><td>4.93</td><td>HUMAN</td><td>K7EQQ3</td><td>Keratin, type I cytoskeletal 9</td></tr>
<tr><td>19641</td><td>dirMS_041712_NAR_30mM_plus2.16385.16385.2</td><td>2</td><td>5.89</td><td>0</td><td>4.49E+05</td><td></td><td>(R)ALVEVL</td><td>(R)A L/V|E V L G A E R(F)</td><td></td><td>138.85</td><td>528.8005</td><td>1056.605</td><td>-0.0111</td><td>-10.5</td><td>4.53</td><td>29052</td><td>10.78</td><td>HUMAN</td><td>Q8TAY7</td><td>Protein FAM110D</td></tr>
<tr><td>19642</td><td>dirMS_041712_NAR_30mM_plus2.19179.19179.2</td><td>2</td><td>5.89</td><td>0</td><td>2.35E+05</td><td></td><td>(K)TVDNFV</td><td>(K)T V/D N F V/A L A T/G E K(G)</td><td></td><td>154.42</td><td>682.8539</td><td>1364.706</td><td>-0.0051</td><td>-3.7</td><td>4.37</td><td>23799.1</td><td>9.48</td><td>HUMAN</td><td>P23284</td><td>Peptidyl-prolyl cis-trans isomerase B</td></tr>
<tr><td>19643</td><td>dirMS_041712_NAR_30mM_plus2.6185.6185.3</td><td>3</td><td>5.89</td><td>0</td><td>1.08E+05</td><td>M38m</td><td>(R)SPPPGm</td><td>(R)S P|P P G m/G L/N Q N R(G)</td><td>m:Oxidized methionine</td><td>86.57</td><td>428.5431</td><td>1267.621</td><td>15.9936</td><td>-1.1</td><td>9.47</td><td>76262.2</td><td>9.53</td><td>HUMAN</td><td>P23246</td><td>Splicing factor, proline- and glutamine-rich</td></tr>
<tr><td>19644</td><td>dirMS_041712_NAR_50mM_plus2.10827.10827.3</td><td>3</td><td>5.89</td><td>1</td><td>4.28E+05</td><td></td><td>(K)NQLTSN</td><td>(K)N Q/L/T/S N P E/N T V/F D A K/R(L)</td><td></td><td>124.88</td><td>611.9758</td><td>1833.909</td><td>0.0039</td><td>2.1</td><td>6.07</td><td>72445.7</td><td>5.07</td><td>HUMAN</td><td>P11021</td><td>78 kDa glucose-regulated protein</td></tr>
<tr><td>19645</td><td>dirMS_041712_NAR_50mM_plus2.8981.8981.3</td><td>3</td><td>5.89</td><td>1</td><td>1.46E+05</td><td></td><td>(K)TTSPPE</td><td>(K)T T/S/P/P E V S G Y S Y E K T E/R(S)</td><td></td><td>113.83</td><td>644.3093</td><td>1930.903</td><td>0.0105</td><td>5.4</td><td>4.78</td><td>271827.6</td><td>4.73</td><td>HUMAN</td><td>P46821</td><td>Microtubule-associated protein 1B</td></tr>
<tr><td>19646</td><td>dirMS_041712_NAR_60mM_plus.14775.14775.3</td><td>3</td><td>5.89</td><td>1</td><td>2.55E+05</td><td>M75m</td><td>(K)KCDEYIP</td><td>(K)K C D/E Y/I P G T T S L G m S V F(-)</td><td>C:Carbamidomethylation m:Oxid</td><td>133.78</td><td>640.9681</td><td>1904.877</td><td>16.0129</td><td>9.4</td><td>4.37</td><td>8945.7</td><td>4.69</td><td>HUMAN</td><td>F8VX12</td><td>Sodium-coupled neutral amino acid transporter 1 (Fragment)</td></tr>
<tr><td>19647</td><td>dirMS_041712_NAR_60mM_plus.17175.17175.3</td><td>3</td><td>5.89</td><td>1</td><td>3.99E+05</td><td></td><td>(R)GFPTIYF</td><td>(R)G F/P/T I Y F S/P A N K K(L)</td><td></td><td>146.97</td><td>490.5979</td><td>1469.779</td><td>0.0004</td><td>0.3</td><td>9.7</td><td>55361.8</td><td>6.42</td><td>HUMAN</td><td>G5EA52</td><td>Protein disulfide isomerase family A, member 3, isoform CRA_b</td></tr>
<tr><td>19648</td><td>dirMS_041712_NAR_60mM_plus.5417.5417.3</td><td>3</td><td>5.89</td><td>1</td><td>7.94E+04</td><td></td><td>(K)VSQGVE</td><td>(K)V S\Q/G/V/E D G P D/T K R(A)</td><td></td><td>85.7</td><td>463.233</td><td>1387.681</td><td>0.0032</td><td>2.3</td><td>4.56</td><td>33726</td><td>7.84</td><td>HUMAN</td><td>B3KNJ4</td><td>SUMO-1 activating enzyme subunit 1, isoform CRA_a</td></tr>
<tr><td>19649</td><td>dirMS_041712_NAR_60mM_plus.8733.8733.3</td><td>3</td><td>5.89</td><td>1</td><td>1.55E+06</td><td></td><td>(K)GGIMLP</td><td>(K)G G|I/M L/P E K S/Q G/K(V)</td><td></td><td>103.6</td><td>415.5607</td><td>1244.667</td><td>0.0008</td><td>0.7</td><td>8.59</td><td>10803.5</td><td>9.82</td><td>HUMAN</td><td>B8ZZL8</td><td>10 kDa heat shock protein, mitochondrial</td></tr>
<tr><td>19650</td><td>dirMS_041712_NAR_120mM_minus.8267.8267.3</td><td>3</td><td>5.88</td><td>0</td><td>3.55E+05</td><td></td><td>(R)AAHSEG</td><td>(R)A A H S E G N T T|A|G L/D M R(E)</td><td></td><td>99.15</td><td>510.9036</td><td>1530.697</td><td>-0.0003</td><td>-0.2</td><td>5.32</td><td>57829.5</td><td>6.01</td><td>HUMAN</td><td>P78371</td><td>T-complex protein 1 subunit beta</td></tr>
<tr><td>19651</td><td>dirMS_041712_NAR_20mM_minus.13177.13177.2</td><td>2</td><td>5.88</td><td>0</td><td>1.40E+05</td><td></td><td>(K)VGINYQ</td><td>(K)V G I/N Y Q|P P T V V P/G G D L A K(V)</td><td></td><td>183.15</td><td>912.9938</td><td>1824.985</td><td>-0.0051</td><td>-2.8</td><td>5.8</td><td>49012.3</td><td>4.9</td><td>HUMAN</td><td>A8MUB1</td><td>Tubulin alpha-4A chain</td></tr>
<tr><td>19652</td><td>dirMS_041712_NAR_50mM_minus2.7585.7585.3</td><td>3</td><td>5.88</td><td>1</td><td>1.66E+04</td><td>M26m</td><td>(K)LAEQAE</td><td>(K)L/A E Q/A E R Y D/D M A/A C m K(S)</td><td>C:Carbamidomethylation m:Oxid</td><td>111.05</td><td>639.9402</td><td>1901.819</td><td>15.987</td><td>-4.1</td><td>4.32</td><td>5919.6</td><td>4.73</td><td>HUMAN</td><td>E5RGE1</td><td>14-3-3 protein zeta/delta (Fragment)</td></tr>
<tr><td>19653</td><td>dirMS_041712_NAR_50mM_minus2.7768.7768.3</td><td>3</td><td>5.88</td><td>0</td><td>1.88E+04</td><td></td><td>(R)AALAHS</td><td>(R)A A L A\H S E E\V\T|A/S Q V/A A\T K(T)</td><td></td><td>112.55</td><td>595.3104</td><td>1783.919</td><td>-0.0018</td><td>-1</td><td>5.4</td><td>23903</td><td>4.94</td><td>HUMAN</td><td>H0YDN1</td><td>Plectin (Fragment)</td></tr>
<tr><td>19654</td><td>dirMS_041712_NAR_50mM_minus2.8612.8612.3</td><td>3</td><td>5.88</td><td>1</td><td>1.42E+05</td><td></td><td>(K)TAVCDIF</td><td>(K)T/A V C/D I/P P R G L K(M)</td><td>C:Carbamidomethylation</td><td>116.92</td><td>442.9126</td><td>1326.72</td><td>0.0034</td><td>2.6</td><td>8.41</td><td>50199.4</td><td>4.75</td><td>HUMAN</td><td>A6NNZ2</td><td>Tubulin beta-8 chain-like protein LOC260334</td></tr>
<tr><td>19655</td><td>dirMS_041712_NAR_60mM_minus.10839.10839.3</td><td>3</td><td>5.88</td><td>0</td><td>5.81E+04</td><td></td><td>(R)LYQTDP</td><td>(R)L Y/Q/T D|P S G T Y H A W K(A)</td><td></td><td>120.13</td><td>556.2675</td><td>1666.786</td><td>0.0019</td><td>1.2</td><td>6.74</td><td>21330</td><td>9.14</td><td>HUMAN</td><td>H0Y586</td><td>Proteasome subunit alpha type-7 (Fragment)</td></tr>
<tr><td>19656</td><td>dirMS_041712_NAR_120mM_plus.14440.14440.4</td><td>4</td><td>5.88</td><td>2</td><td>2.01E+05</td><td></td><td>(K)IKQLLKD</td><td>(K)I K Q\L/L K D K P E H V G V K(V)</td><td></td><td>129.38</td><td>433.768</td><td>1732.048</td><td>0.0022</td><td>1.3</td><td>9.53</td><td>19516.1</td><td>10.48</td><td>HUMAN</td><td>B4DJI5</td><td>HESB like domain containing 2, isoform CRA_b</td></tr>
<tr><td>19657</td><td>dirMS_041712_NAR_20mM_plus.18610.18610.2</td><td>2</td><td>5.88</td><td>0</td><td>2.98E+05</td><td></td><td>(K)TAVETA</td><td>(K)T A|V/E/T A V/L|L L R(I)</td><td></td><td>199.82</td><td>593.3625</td><td>1185.72</td><td>-0.0024</td><td>-2</td><td>5.66</td><td>56186.7</td><td>5.47</td><td>HUMAN</td><td>B4DUR8</td><td>T-complex protein 1 subunit gamma</td></tr>
<tr><td>19658</td><td>dirMS_041712_NAR_30mM_plus2.20081.20081.3</td><td>3</td><td>5.88</td><td>0</td><td>4.45E+05</td><td></td><td>(K)SYELPDC</td><td>(K)S Y E L/P D G Q/V I/T I G N E R(F)</td><td></td><td>159.7</td><td>597.6334</td><td>1790.892</td><td>-0.0063</td><td>-3.5</td><td>4.14</td><td>123097.1</td><td>5.83</td><td>HUMAN</td><td>A5A3E0</td><td>POTE ankyrin domain family member F</td></tr>
<tr><td>19659</td><td>dirMS_041712_NAR_30mM_plus2.21684.21684.3</td><td>3</td><td>5.88</td><td>0</td><td>1.81E+05</td><td></td><td>(K)GLVQAL</td><td>(K)G L/V Q A L\G L/S/N F/N S R(Q)</td><td></td><td>169.43</td><td>492.6036</td><td>1475.796</td><td>-0.0003</td><td>-0.2</td><td>9.75</td><td>36914.7</td><td>6.33</td><td>HUMAN</td><td>P14550</td><td>Alcohol dehydrogenase [NADP(+)]</td></tr>
<tr><td>19660</td><td>dirMS_041712_NAR_40mM_plus2.12252.12252.3</td><td>3</td><td>5.88</td><td>0</td><td>1.60E+05</td><td></td><td>(K)QLTEED</td><td>(K)Q L/T E/E D G V H S V/I E E N\I K(C)</td><td></td><td>138.73</td><td>647.3228</td><td>1939.961</td><td>-0.0069</td><td>-3.5</td><td>4.25</td><td>54427.4</td><td>5.96</td><td>HUMAN</td><td>K4DID9</td><td>Acetyl-CoA carboxylase 1</td></tr>
<tr><td>19661</td><td>dirMS_041712_NAR_50mM_plus2.18588.18588.3</td><td>3</td><td>5.88</td><td>1</td><td>3.49E+05</td><td></td><td>(R)GDSVIV</td><td>(R)G D/S V/I/V V L R N P L I/A G K(-)</td><td></td><td>165.37</td><td>550.9999</td><td>1650.99</td><td>-0.005</td><td>-3</td><td>8.75</td><td>6144.3</td><td>10.23</td><td>HUMAN</td><td>K7EJB5</td><td>Small nuclear ribonucleoprotein Sm D2</td></tr>
<tr><td>19662</td><td>dirMS_041712_NAR_50mM_plus2.5571.5571.3</td><td>3</td><td>5.88</td><td>1</td><td>9.44E+04</td><td></td><td>(R)AVGPTA</td><td>(R)A/V/G P T A E A D K/S A A E/K(R)</td><td></td><td>90.18</td><td>482.2464</td><td>1444.728</td><td>-0.0032</td><td>-2.2</td><td>4.68</td><td>24814.3</td><td>6.22</td><td>HUMAN</td><td>D6REL4</td><td>Protein Red (Fragment)</td></tr>
<tr><td>19663</td><td>dirMS_041712_NAR_50mM_plus2.6123.6123.3</td><td>3</td><td>5.88</td><td>0</td><td>6.16E+04</td><td></td><td>(R)VHTGER</td><td>(R)V/H T/G E/R P/F S C Q A C G R(S)</td><td>C:Carbamidomethylation</td><td>96.33</td><td>587.9271</td><td>1761.791</td><td>-0.024</td><td>-13.6</td><td>9.57</td><td>71660.7</td><td>10.89</td><td>HUMAN</td><td>H0YFS6</td><td>Zinc finger and SCAN domain-containing protein 10</td></tr>
<tr><td>19664</td><td>dirMS_041712_NAR_60mM_plus.10010.10010.3</td><td>3</td><td>5.88</td><td>1</td><td>1.28E+05</td><td></td><td>(K)DSQICEL</td><td>(K)D/S\Q/I/C/E L K Y D/K(Q)</td><td>C:Carbamidomethylation</td><td>109.98</td><td>466.8941</td><td>1398.657</td><td>0.0108</td><td>7.7</td><td>4.56</td><td>21156.2</td><td>9.41</td><td>HUMAN</td><td>P55145</td><td>Mesencephalic astrocyte-derived neurotrophic factor</td></tr>
<tr><td>19665</td><td>dirMS_041712_NAR_60mM_plus.15284.15284.3</td><td>3</td><td>5.88</td><td>0</td><td>2.64E+06</td><td></td><td>(R)LIDLHSP</td><td>(R)L I\D/L H/S/P S E I V K(Q)</td><td></td><td>137.42</td><td>450.9323</td><td>1350.763</td><td>0.0196</td><td>14.5</td><td>5.32</td><td>7304.3</td><td>9.39</td><td>HUMAN</td><td>G3XAN0</td><td>40S ribosomal protein S20</td></tr>
<tr><td>19666</td><td>dirMS_041712_NAR_60mM_plus.16096.16096.3</td><td>3</td><td>5.88</td><td>0</td><td>2.18E+05</td><td></td><td>(R)AVAIDLF</td><td>(R)A V/A/I/D L/P G L G H S K(E)</td><td></td><td>141.27</td><td>426.5775</td><td>1277.721</td><td>-0.0033</td><td>-2.6</td><td>6.79</td><td>19983.6</td><td>8.14</td><td>HUMAN</td><td>B4DQI4</td><td>Alpha/beta hydrolase domain-containing protein 14B</td></tr>
<tr><td>19667</td><td>dirMS_041712_NAR_60mM_plus.20532.20532.3</td><td>3</td><td>5.88</td><td>1</td><td>3.32E+03</td><td></td><td>(R)LKLPSIPI</td><td>(R)L K L P S I P\L/V/P V S A Q K(R)</td><td></td><td>167.77</td><td>530.6713</td><td>1589.999</td><td>0.0005</td><td>0.3</td><td>10</td><td>34958.1</td><td>9.42</td><td>HUMAN</td><td>Q15785</td><td>Mitochondrial import receptor subunit TOM34</td></tr>
<tr><td>19668</td><td>dirMS_041712_NAR_60mM_plus.20945.20945.3</td><td>3</td><td>5.88</td><td>0</td><td>3.66E+05</td><td></td><td>(R)SLHDAL</td><td>(R)S L H D A L/C\V|L/A/Q T V K(D)</td><td>C:Carbamidomethylation</td><td>171.72</td><td>518.9516</td><td>1554.831</td><td>0.0094</td><td>6.1</td><td>6.46</td><td>57204.9</td><td>6.01</td><td>HUMAN</td><td>F5GWF6</td><td>T-complex protein 1 subunit beta</td></tr>
<tr><td>19669</td><td>dirMS_041712_NAR_60mM_plus.8270.8270.3</td><td>3</td><td>5.88</td><td>1</td><td>6.35E+05</td><td></td><td>(K)AAYEAEI</td><td>(K)A A/Y/E A\E L/G D A R/K(T)</td><td></td><td>101.13</td><td>431.8884</td><td>1293.643</td><td>0.0073</td><td>5.6</td><td>4.68</td><td>74423.5</td><td>6.57</td><td>HUMAN</td><td>P02545</td><td>Prelamin-A/C</td></tr>
<tr><td>19670</td><td>dirMS_041712_NAR_120mM_minus.4947.4947.3</td><td>3</td><td>5.87</td><td>1</td><td>6.21E+05</td><td></td><td>(R)AAEEED</td><td>(R)A A/E E/E D E A/D/P K R(Q)</td><td></td><td>79.23</td><td>453.8716</td><td>1359.602</td><td>-0.002</td><td>-1.5</td><td>4.08</td><td>11529.7</td><td>4.14</td><td>HUMAN</td><td>P20962</td><td>Parathymosin</td></tr>
<tr><td>19671</td><td>dirMS_041712_NAR_20mM_minus.10475.10475.2</td><td>2</td><td>5.87</td><td>0</td><td>1.02E+04</td><td>M234m</td><td>(K)mVVESA</td><td>(K)m V/V\E/S/A/Y E V I K(L)</td><td>m:Oxidized methionine</td><td>153.32</td><td>642.3318</td><td>1267.66</td><td>15.9961</td><td>0.9</td><td>4.53</td><td>36923.1</td><td>5.71</td><td>HUMAN</td><td>P07195</td><td>L-lactate dehydrogenase B chain</td></tr>
<tr><td>19672</td><td>dirMS_041712_NAR_20mM_minus.10701.10701.3</td><td>3</td><td>5.87</td><td>0</td><td>1.40E+05</td><td></td><td>(K)VNQIGS</td><td>(K)V N Q I G S V/T/E/S I Q A/C K(L)</td><td>C:Carbamidomethylation</td><td>155.38</td><td>545.2807</td><td>1633.821</td><td>0.0062</td><td>3.8</td><td>5.97</td><td>47328.4</td><td>7.76</td><td>HUMAN</td><td>P13929</td><td>Beta-enolase</td></tr>
<tr><td>19673</td><td>dirMS_041712_NAR_20mM_minus.14485.14485.3</td><td>3</td><td>5.87</td><td>0</td><td>2.19E+05</td><td></td><td>(K)LAAELSA</td><td>(K)L A A\E\L\S A T L/E/Q A/A/A T A R(V)</td><td></td><td>198.9</td><td>562.9713</td><td>1686.902</td><td>-0.0027</td><td>-1.6</td><td>4.53</td><td>558007.1</td><td>5.44</td><td>HUMAN</td><td>P58107</td><td>Epiplakin</td></tr>
<tr><td>19674</td><td>dirMS_041712_NAR_20mM_minus.14723.14723.2</td><td>2</td><td>5.87</td><td>0</td><td>1.65E+05</td><td></td><td>(K)TAVETA</td><td>(K)T A V/E/T A/V L\L L R(I)</td><td></td><td>201.43</td><td>593.3613</td><td>1185.72</td><td>-0.0048</td><td>-4.1</td><td>5.66</td><td>56186.7</td><td>5.47</td><td>HUMAN</td><td>B4DUR8</td><td>T-complex protein 1 subunit gamma</td></tr>
<tr><td>19675</td><td>dirMS_041712_NAR_30mM_minus2.10455.10455.2</td><td>2</td><td>5.87</td><td>0</td><td>9.33E+05</td><td></td><td>(K)GSDFDC</td><td>(K)G S|D|F|D C E L/R(L)</td><td>C:Carbamidomethylation</td><td>111.28</td><td>549.7307</td><td>1098.452</td><td>0.0021</td><td>1.9</td><td>4.03</td><td>51260.6</td><td>5.39</td><td>HUMAN</td><td>P61978</td><td>Heterogeneous nuclear ribonucleoprotein K</td></tr>
<tr><td>19676</td><td>dirMS_041712_NAR_30mM_minus2.11447.11447.2</td><td>2</td><td>5.87</td><td>0</td><td>1.21E+05</td><td>M39m</td><td>(K)mFLYAD</td><td>(K)m F\L|Y/A D/N E D R(A)</td><td>m:Oxidized methionine</td><td>115.58</td><td>645.2795</td><td>1273.552</td><td>16</td><td>3.9</td><td>4.03</td><td>24724.1</td><td>5.17</td><td>HUMAN</td><td>E7ETQ7</td><td>Vacuolar protein sorting-associated protein VTA1 homolog</td></tr>
<tr><td>19677</td><td>dirMS_041712_NAR_50mM_minus2.17589.17589.3</td><td>3</td><td>5.87</td><td>1</td><td>1.25E+05</td><td></td><td>(K)NAAGAL</td><td>(K)N/A|A/G A/L D L L\K E L K(N)</td><td></td><td>168.67</td><td>452.601</td><td>1355.789</td><td>-0.0008</td><td>-0.6</td><td>6.07</td><td>13786.8</td><td>9.33</td><td>HUMAN</td><td>B7Z4S1</td><td>Transcription elongation factor A protein 1</td></tr>
<tr><td>19678</td><td>dirMS_041712_NAR_60mM_minus.11148.11148.3</td><td>3</td><td>5.87</td><td>1</td><td>7.95E+05</td><td></td><td>(K)MKEIAE</td><td>(K)M K E I A/E/A Y/L/G K(T)</td><td></td><td>122.48</td><td>418.226</td><td>1252.661</td><td>0.0029</td><td>2.3</td><td>5.9</td><td>17973</td><td>5.16</td><td>HUMAN</td><td>E9PI65</td><td>Heat shock cognate 71 kDa protein (Fragment)</td></tr>
<tr><td>19679</td><td>dirMS_041712_NAR_60mM_minus.12268.12268.2</td><td>2</td><td>5.87</td><td>1</td><td>5.02E+04</td><td></td><td>(K)FASFIDK</td><td>(K)F/A|S/F/I D/K/V R(F)</td><td></td><td>128.23</td><td>541.8015</td><td>1082.599</td><td>-0.0036</td><td>-3.3</td><td>8.75</td><td>19569.8</td><td>9.88</td><td>HUMAN</td><td>F8VRG4</td><td>Keratin, type II cytoskeletal 8 (Fragment)</td></tr>
<tr><td>19680</td><td>dirMS_041712_NAR_60mM_minus.16666.16666.3</td><td>3</td><td>5.87</td><td>0</td><td>1.75E+05</td><td></td><td>(R)LLIHQSL</td><td>(R)L/L I H Q S L|A/G G I/I G V K(G)</td><td></td><td>153.37</td><td>506.9823</td><td>1518.937</td><td>-0.0043</td><td>-2.8</td><td>8.76</td><td>51260.6</td><td>5.39</td><td>HUMAN</td><td>P61978</td><td>Heterogeneous nuclear ribonucleoprotein K</td></tr>
<tr><td>19681</td><td>dirMS_041712_NAR_60mM_minus.16781.16781.3</td><td>3</td><td>5.87</td><td>1</td><td>2.02E+05</td><td></td><td>(K)MFGIDR</td><td>(K)M/F/G I/D R D A I/A Q/A V R(G)</td><td></td><td>154.35</td><td>521.6047</td><td>1562.811</td><td>-0.0112</td><td>-7.2</td><td>5.71</td><td>63448.4</td><td>7.29</td><td>HUMAN</td><td>B4E022</td><td>Transketolase</td></tr>
<tr><td>19682</td><td>dirMS_041712_NAR_60mM_minus.19726.19726.3</td><td>3</td><td>5.87</td><td>1</td><td>4.18E+06</td><td></td><td>(R)LRLCTTL</td><td>(R)L R/L C T/T L Y/Q A P E R(A)</td><td>C:Carbamidomethylation</td><td>179.17</td><td>540.9491</td><td>1620.853</td><td>-0.0199</td><td>-12.3</td><td>8.75</td><td>175246</td><td>8.76</td><td>HUMAN</td><td>J3QTL0</td><td>Tetratricopeptide repeat protein 40</td></tr>
<tr><td>19683</td><td>dirMS_041712_NAR_60mM_minus.9894.9894.3</td><td>3</td><td>5.87</td><td>1</td><td>2.88E+05</td><td></td><td>(R)KLDPGSI</td><td>(R)K L D\P G S|E\E|T Q/T/L V R(E)</td><td></td><td>114.75</td><td>524.9451</td><td>1572.823</td><td>-0.002</td><td>-1.3</td><td>4.68</td><td>56491.1</td><td>7.78</td><td>HUMAN</td><td>B4DTG2</td><td>Elongation factor 1-gamma</td></tr>
<tr><td>19684</td><td>dirMS_041712_NAR_20mM_plus.13731.13731.2</td><td>2</td><td>5.87</td><td>0</td><td>7.95E+04</td><td>M177m</td><td>(R)FAQPGS</td><td>(R)F A Q/P/G S F E\Y E Y A m R(W)</td><td>m:Oxidized methionine</td><td>166.68</td><td>856.3717</td><td>1695.747</td><td>15.989</td><td>-3.5</td><td>4.53</td><td>29678.2</td><td>9.57</td><td>HUMAN</td><td>C9JYS8</td><td>Non-POU domain-containing octamer-binding protein (Fragment)</td></tr>
<tr><td>19685</td><td>dirMS_041712_NAR_20mM_plus.13812.13812.2</td><td>2</td><td>5.87</td><td>0</td><td>1.19E+05</td><td></td><td>(R)LVVPAT</td><td>(R)L V|V|P A T Q C G S L I/G K(G)</td><td>C:Carbamidomethylation</td><td>167.23</td><td>721.9033</td><td>1442.804</td><td>-0.0042</td><td>-2.9</td><td>8.75</td><td>38010.7</td><td>6.67</td><td>HUMAN</td><td>Q15365</td><td>Poly(rC)-binding protein 1</td></tr>
<tr><td>19686</td><td>dirMS_041712_NAR_20mM_plus.15976.15976.2</td><td>2</td><td>5.87</td><td>1</td><td>1.80E+05</td><td></td><td>(K)LPSNVVI</td><td>(K)L P S N V/V K E S A/R(A)</td><td></td><td>182.12</td><td>600.3422</td><td>1199.674</td><td>0.0029</td><td>2.4</td><td>8.75</td><td>165343.3</td><td>5.97</td><td>HUMAN</td><td>P20742</td><td>Pregnancy zone protein</td></tr>
<tr><td>19687</td><td>dirMS_041712_NAR_20mM_plus.5776.5776.2</td><td>2</td><td>5.87</td><td>0</td><td>3.09E+05</td><td>M625m M</td><td>(R)DNSTm</td><td>(R)D N\S/T/m G Y/m A A K(K)</td><td>m:Oxidized methionine</td><td>96.52</td><td>610.749</td><td>1188.502</td><td>31.9884</td><td>-1.2</td><td>5.83</td><td>85057.6</td><td>4.94</td><td>HUMAN</td><td>P07900</td><td>Heat shock protein HSP 90-alpha</td></tr>
<tr><td>19688</td><td>dirMS_041712_NAR_20mM_plus.9584.9584.2</td><td>2</td><td>5.87</td><td>0</td><td>1.40E+05</td><td></td><td>(R)GTGIVS</td><td>(R)G T G I|V|S A P V/P K(K)</td><td></td><td>136.95</td><td>513.3057</td><td>1025.599</td><td>0.0052</td><td>5</td><td>8.75</td><td>21898</td><td>11.33</td><td>HUMAN</td><td>E9PM36</td><td>40S ribosomal protein S2</td></tr>
<tr><td>19689</td><td>dirMS_041712_NAR_30mM_plus2.20785.20785.2</td><td>2</td><td>5.87</td><td>0</td><td>2.20E+05</td><td></td><td>(K)GGIVGN</td><td>(K)G G I|V/G M T/L/P I A R(D)</td><td></td><td>162.68</td><td>592.8453</td><td>1184.682</td><td>0.0013</td><td>1.1</td><td>9.75</td><td>27150.8</td><td>7.95</td><td>HUMAN</td><td>Q99714</td><td>3-hydroxyacyl-CoA dehydrogenase type-2</td></tr>
<tr><td>19690</td><td>dirMS_041712_NAR_30mM_plus2.22295.22295.2</td><td>2</td><td>5.87</td><td>0</td><td>3.79E+05</td><td></td><td>(R)VGNLGL</td><td>(R)V G N\L/G L/A/T S F/F N E R(N)</td><td></td><td>172.8</td><td>762.8926</td><td>1524.781</td><td>-0.0026</td><td>-1.7</td><td>5.97</td><td>73641.5</td><td>6.74</td><td>HUMAN</td><td>O00571</td><td>ATP-dependent RNA helicase DDX3X</td></tr>
<tr><td>19691</td><td>dirMS_041712_NAR_30mM_plus2.7081.7081.2</td><td>2</td><td>5.87</td><td>0</td><td>2.85E+05</td><td></td><td>(R)STLEPVE</td><td>(R)S/T|L/E/P\V E K(A)</td><td></td><td>92.18</td><td>451.7509</td><td>902.483</td><td>0.0116</td><td>12.8</td><td>4.53</td><td>25598.3</td><td>6.45</td><td>HUMAN</td><td>E7EP11</td><td>Heat shock 70 kDa protein 1A/1B</td></tr>
<tr><td>19692</td><td>dirMS_041712_NAR_40mM_plus2.17164.17164.3</td><td>3</td><td>5.87</td><td>0</td><td>6.64E+04</td><td></td><td>(R)IHFPLAT</td><td>(R)I H F P L A T|Y/A/P V I/S A E K(A)</td><td></td><td>166.77</td><td>586.3246</td><td>1756.963</td><td>-0.004</td><td>-2.3</td><td>6.75</td><td>49012.3</td><td>4.9</td><td>HUMAN</td><td>A8MUB1</td><td>Tubulin alpha-4A chain</td></tr>
<tr><td>19693</td><td>dirMS_041712_NAR_50mM_plus2.10509.10509.3</td><td>3</td><td>5.87</td><td>1</td><td>2.20E+07</td><td></td><td>(R)DGKLVS</td><td>(R)D G K L V\S E/S S D V L/P K(-)</td><td></td><td>122.83</td><td>491.9313</td><td>1473.78</td><td>-0.0002</td><td>-0.1</td><td>4.56</td><td>56607.4</td><td>5.37</td><td>HUMAN</td><td>F8VXB4</td><td>Keratin, type II cytoskeletal 8</td></tr>
<tr><td>19694</td><td>dirMS_041712_NAR_50mM_plus2.11050.11050.3</td><td>3</td><td>5.87</td><td>0</td><td>9.38E+04</td><td>M10m</td><td>(-)MVHKPS</td><td>(-)M V/H K P/S G Q I m/A V K(R)</td><td>m:Oxidized methionine</td><td>125.57</td><td>481.2661</td><td>1425.771</td><td>16.0133</td><td>12.7</td><td>10</td><td>18603.3</td><td>6.84</td><td>HUMAN</td><td>J3KTI6</td><td>Dual-specificity mitogen-activated protein kinase kinase 4 (Fragment)</td></tr>
<tr><td>19695</td><td>dirMS_041712_NAR_50mM_plus2.19004.19004.3</td><td>3</td><td>5.87</td><td>0</td><td>5.47E+05</td><td></td><td>(R)GFGFITF</td><td>(R)G F/G/F/I/T F/T N P E H A S V A M R(A)</td><td></td><td>168.65</td><td>661.3258</td><td>1981.959</td><td>0.004</td><td>2</td><td>6.75</td><td>17170.1</td><td>8.86</td><td>HUMAN</td><td>P98179</td><td>Putative RNA-binding protein 3</td></tr>
<tr><td>19696</td><td>dirMS_041712_NAR_50mM_plus2.8197.8197.3</td><td>3</td><td>5.87</td><td>0</td><td>5.03E+04</td><td></td><td>(R)AGAGM</td><td>(R)A G\A/G M/I/T Q H|S S N A S/P I N R(I)</td><td></td><td>109.93</td><td>604.631</td><td>1811.882</td><td>-0.0033</td><td>-1.8</td><td>9.8</td><td>71179.6</td><td>10.41</td><td>HUMAN</td><td>A8K5V8</td><td>SAFB-like transcription modulator</td></tr>
<tr><td>19697</td><td>dirMS_041712_NAR_60mM_plus.8929.8929.3</td><td>3</td><td>5.87</td><td>0</td><td>1.59E+06</td><td></td><td>(K)EFHLNES</td><td>(K)E F H L\N E/S/G/D/P S S/K(S)</td><td></td><td>105.52</td><td>482.8882</td><td>1446.65</td><td>0.0005</td><td>0.3</td><td>4.65</td><td>30992.3</td><td>4.14</td><td>HUMAN</td><td>B2REB8</td><td>Protein SET</td></tr>
<tr><td>19698</td><td>dirMS_041712_NAR_60mM_plus.9728.9728.3</td><td>3</td><td>5.87</td><td>0</td><td>9.53E+05</td><td></td><td>(K)GHENVE</td><td>(K)G H E\N V E\A|A/Q|A/E Y I E K(F)</td><td></td><td>107.98</td><td>563.2692</td><td>1687.792</td><td>0.0008</td><td>0.5</td><td>4.48</td><td>61363</td><td>8.73</td><td>HUMAN</td><td>C9JQS9</td><td>Propionyl-CoA carboxylase beta chain, mitochondrial</td></tr>
<tr><td>19699</td><td>dirMS_041712_NAR_120mM_minus.11309.11309.3</td><td>3</td><td>5.86</td><td>0</td><td>2.93E+05</td><td></td><td>(K)SAKPTKI</td><td>(K)S A K P T K P A A/S D\L|P V\P A E G V R(N)</td><td></td><td>115.03</td><td>664.3662</td><td>1991.092</td><td>-0.008</td><td>-4</td><td>8.31</td><td>54214.9</td><td>5.66</td><td>HUMAN</td><td>C9J813</td><td>Caldesmon (Fragment)</td></tr>
<tr><td>19700</td><td>dirMS_041712_NAR_120mM_minus.13420.13420.4</td><td>4</td><td>5.86</td><td>1</td><td>9.79E+05</td><td></td><td>(K)SVHSSVI</td><td>(K)S V H S S\V/P\L L N S K D/P I D R(I)</td><td></td><td>127.5</td><td>466.7525</td><td>1863.992</td><td>-0.0041</td><td>-2.2</td><td>6.47</td><td>54427.4</td><td>5.96</td><td>HUMAN</td><td>K4DID9</td><td>Acetyl-CoA carboxylase 1</td></tr>
<tr><td>19701</td><td>dirMS_041712_NAR_20mM_minus.14678.14678.3</td><td>3</td><td>5.86</td><td>0</td><td>7.26E+04</td><td></td><td>(K)IYVDDGI</td><td>(K)I Y V D D G L/I/S L/Q/V K(Q)</td><td></td><td>201.57</td><td>488.2771</td><td>1462.815</td><td>0.0016</td><td>1.1</td><td>4.21</td><td>30947.9</td><td>6.47</td><td>HUMAN</td><td>H3BQ34</td><td>Pyruvate kinase</td></tr>
<tr><td>19702</td><td>dirMS_041712_NAR_50mM_minus2.10205.10205.3</td><td>3</td><td>5.86</td><td>0</td><td>1.60E+05</td><td>M392m</td><td>(K)EmNPAL</td><td>(K)E m/N/P A/L G\I D C L/H K(G)</td><td>C:Carbamidomethylation m:Oxid</td><td>125.95</td><td>505.2416</td><td>1497.719</td><td>15.9914</td><td>-2.3</td><td>5.32</td><td>49982</td><td>5.86</td><td>HUMAN</td><td>B4DYD8</td><td>T-complex protein 1 subunit epsilon</td></tr>
<tr><td>19703</td><td>dirMS_041712_NAR_50mM_minus2.18027.18027.3</td><td>3</td><td>5.86</td><td>0</td><td>2.72E+05</td><td></td><td>(K)ISSIQSIV</td><td>(K)I S S I/Q/S/I/V/P\A L E I A/N A H R(K)</td><td></td><td>171.43</td><td>640.361</td><td>1919.071</td><td>-0.0024</td><td>-1.3</td><td>6.75</td><td>61224.7</td><td>5.7</td><td>HUMAN</td><td>P10809</td><td>60 kDa heat shock protein, mitochondrial</td></tr>
<tr><td>19704</td><td>dirMS_041712_NAR_60mM_minus.16085.16085.3</td><td>3</td><td>5.86</td><td>1</td><td>2.33E+05</td><td></td><td>(R)LELGLGF</td><td>(R)L E\L/G\L G R E R P A K(A)</td><td></td><td>150.3</td><td>446.9287</td><td>1338.785</td><td>-0.0137</td><td>-10.2</td><td>8.75</td><td>56025.3</td><td>10.24</td><td>HUMAN</td><td>G5E9N1</td><td>MON1 homolog A (Yeast), isoform CRA_a</td></tr>
<tr><td>19705</td><td>dirMS_041712_NAR_20mM_plus.10701.10701.2</td><td>2</td><td>5.86</td><td>0</td><td>8.63E+04</td><td></td><td>(R)FLEQQN</td><td>(R)F L|E|Q/Q N Q V/L Q T K(W)</td><td></td><td>146.73</td><td>738.3942</td><td>1475.785</td><td>-0.0041</td><td>-2.8</td><td>6</td><td>66208.7</td><td>8.32</td><td>HUMAN</td><td>P04264</td><td>Keratin, type II cytoskeletal 1</td></tr>
<tr><td>19706</td><td>dirMS_041712_NAR_20mM_plus.12420.12420.3</td><td>3</td><td>5.86</td><td>0</td><td>3.15E+04</td><td></td><td>(K)IISNASC</td><td>(K)I I S N\A\S C T T/N C L/A/P/L A K(V)</td><td>C:Carbamidomethylation</td><td>157.65</td><td>611.9768</td><td>1833.92</td><td>-0.0039</td><td>-2.1</td><td>8.75</td><td>31718.5</td><td>7.17</td><td>HUMAN</td><td>E7EUT4</td><td>Glyceraldehyde-3-phosphate dehydrogenase</td></tr>
<tr><td>19707</td><td>dirMS_041712_NAR_20mM_plus.18519.18519.3</td><td>3</td><td>5.86</td><td>1</td><td>2.25E+05</td><td>M767m</td><td>(K)LKSQDT</td><td>(K)L K S Q D/T V L\m/N L Y K(R)</td><td>m:Oxidized methionine</td><td>198.97</td><td>523.617</td><td>1552.84</td><td>15.9961</td><td>0.8</td><td>8.5</td><td>92207.8</td><td>6.99</td><td>HUMAN</td><td>Q2NL82</td><td>Pre-rRNA-processing protein TSR1 homolog</td></tr>
<tr><td>19708</td><td>dirMS_041712_NAR_20mM_plus.19120.19120.2</td><td>2</td><td>5.86</td><td>0</td><td>2.70E+04</td><td></td><td>(R)STGEAF</td><td>(R)S T G E\A\F|V/Q F/A S Q E I\A/E K(A)</td><td></td><td>203.23</td><td>921.4477</td><td>1841.892</td><td>-0.0035</td><td>-1.9</td><td>4.25</td><td>24249.1</td><td>6.99</td><td>HUMAN</td><td>D6RBM0</td><td>Heterogeneous nuclear ribonucleoprotein H (Fragment)</td></tr>
<tr><td>19709</td><td>dirMS_041712_NAR_20mM_plus.7744.7744.2</td><td>2</td><td>5.86</td><td>0</td><td>4.28E+04</td><td></td><td>(K)AVTEQG</td><td>(K)A V T E/Q/G A/E L/S N E E R(N)</td><td></td><td>122.93</td><td>766.8616</td><td>1532.719</td><td>-0.0028</td><td>-1.8</td><td>4.09</td><td>17219.2</td><td>5.69</td><td>HUMAN</td><td>E9PG15</td><td>14-3-3 protein theta (Fragment)</td></tr>
<tr><td>19710</td><td>dirMS_041712_NAR_30mM_plus2.16709.16709.2</td><td>2</td><td>5.86</td><td>0</td><td>2.06E+05</td><td></td><td>(R)LAIMMN</td><td>(R)L/A/I/M M M K(K)</td><td></td><td>140.58</td><td>419.2286</td><td>837.439</td><td>0.0104</td><td>12.4</td><td>8.75</td><td>51805.7</td><td>5.16</td><td>HUMAN</td><td>B3KXD6</td><td>Pescadillo homolog</td></tr>
<tr><td>19711</td><td>dirMS_041712_NAR_40mM_plus2.12114.12114.3</td><td>3</td><td>5.86</td><td>1</td><td>2.85E+04</td><td></td><td>(R)CGFQDC</td><td>(R)C G/F/Q D D V A Y G K T K(I)</td><td>C:Carbamidomethylation</td><td>137.1</td><td>496.895</td><td>1488.679</td><td>-0.0083</td><td>-5.6</td><td>5.96</td><td>111972.3</td><td>9.59</td><td>HUMAN</td><td>J3QRN6</td><td>Unconventional myosin-Id</td></tr>
<tr><td>19712</td><td>dirMS_041712_NAR_40mM_plus2.7972.7972.2</td><td>2</td><td>5.86</td><td>0</td><td>1.36E+05</td><td></td><td>(R)ELNITAA</td><td>(R)E L/N/I/T/A A K(E)</td><td></td><td>106.93</td><td>430.2474</td><td>859.488</td><td>-0.0008</td><td>-1</td><td>6.1</td><td>21311.5</td><td>10.28</td><td>HUMAN</td><td>B5MCP9</td><td>40S ribosomal protein S7</td></tr>
<tr><td>19713</td><td>dirMS_041712_NAR_50mM_plus2.10240.10240.3</td><td>3</td><td>5.86</td><td>1</td><td>1.28E+05</td><td></td><td>(K)ATAVVD</td><td>(K)A T/A/V/V/D G A F K E V K(L)</td><td></td><td>121.17</td><td>445.5822</td><td>1334.731</td><td>0.0006</td><td>0.5</td><td>6.11</td><td>15252.2</td><td>5.82</td><td>HUMAN</td><td>A6NIW5</td><td>Peroxiredoxin 2, isoform CRA_a</td></tr>
<tr><td>19714</td><td>dirMS_041712_NAR_50mM_plus2.12853.12853.3</td><td>3</td><td>5.86</td><td>0</td><td>3.30E+05</td><td></td><td>(K)EMNPAI</td><td>(K)E M N/P/A L/G|I D C L H K(G)</td><td>C:Carbamidomethylation</td><td>135.38</td><td>499.9106</td><td>1497.719</td><td>-0.0016</td><td>-1.1</td><td>5.32</td><td>49982</td><td>5.86</td><td>HUMAN</td><td>B4DYD8</td><td>T-complex protein 1 subunit epsilon</td></tr>
<tr><td>19715</td><td>dirMS_041712_NAR_50mM_plus2.13675.13675.3</td><td>3</td><td>5.86</td><td>0</td><td>4.30E+05</td><td></td><td>(K)SLATGGI</td><td>(K)S L|A|T/G G N V S Q A L A L V/G E K(A)</td><td></td><td>139.88</td><td>572.3145</td><td>1714.933</td><td>-0.0044</td><td>-2.6</td><td>5.72</td><td>163852.7</td><td>5.43</td><td>HUMAN</td><td>C9JJN9</td><td>Vacuolar protein sorting-associated protein 8 homolog</td></tr>
<tr><td>19716</td><td>dirMS_041712_NAR_50mM_plus2.8930.8930.3</td><td>3</td><td>5.86</td><td>1</td><td>2.37E+04</td><td></td><td>(R)GGSDDS</td><td>(R)G G/S D D S S K D/P I/D/V N Y\E K(L)</td><td></td><td>114.08</td><td>609.2765</td><td>1825.809</td><td>0.0063</td><td>3.5</td><td>4.03</td><td>113880.5</td><td>9.18</td><td>HUMAN</td><td>P09874</td><td>Poly [ADP-ribose] polymerase 1</td></tr>
<tr><td>19717</td><td>dirMS_041712_NAR_60mM_plus.10288.10288.3</td><td>3</td><td>5.86</td><td>1</td><td>5.26E+05</td><td></td><td>(R)LQEKED</td><td>(R)L Q\E\K E D L/Q/E/L/N D R(L)</td><td></td><td>111.75</td><td>543.9389</td><td>1629.808</td><td>-0.0057</td><td>-3.5</td><td>4.18</td><td>74423.5</td><td>6.57</td><td>HUMAN</td><td>P02545</td><td>Prelamin-A/C</td></tr>
<tr><td>19718</td><td>dirMS_041712_NAR_60mM_plus.15993.15993.3</td><td>3</td><td>5.86</td><td>1</td><td>4.35E+05</td><td></td><td>(R)IKIGDPL</td><td>(R)I/K I G D P L/L/E D/T R(M)</td><td></td><td>141.32</td><td>457.2595</td><td>1369.769</td><td>-0.0046</td><td>-3.4</td><td>4.56</td><td>47309.6</td><td>5.42</td><td>HUMAN</td><td>B4DXY7</td><td>4-trimethylaminobutyraldehyde dehydrogenase</td></tr>
<tr><td>19719</td><td>dirMS_041712_NAR_120mM_minus.6482.6482.3</td><td>3</td><td>5.85</td><td>1</td><td>2.87E+05</td><td></td><td>(R)LNGTLRI</td><td>(R)L/N/G/T L R E D D/N R(I)</td><td></td><td>90.15</td><td>434.8858</td><td>1302.64</td><td>0.0032</td><td>2.4</td><td>4.56</td><td>46648.4</td><td>9.67</td><td>HUMAN</td><td>B4DX42</td><td>Splicing factor 1</td></tr>
<tr><td>19720</td><td>dirMS_041712_NAR_20mM_minus.7528.7528.2</td><td>2</td><td>5.85</td><td>0</td><td>6.66E+05</td><td>M239m</td><td>(K)EVDEQ</td><td>(K)E V/D E/Q m L/N V Q\N K(N)</td><td>m:Oxidized methionine</td><td>123.67</td><td>731.843</td><td>1446.689</td><td>15.9894</td><td>-3.8</td><td>4.14</td><td>40069.4</td><td>4.83</td><td>HUMAN</td><td>E7EWR1</td><td>Tubulin beta chain</td></tr>
<tr><td>19721</td><td>dirMS_041712_NAR_30mM_minus2.5281.5281.2</td><td>2</td><td>5.85</td><td>0</td><td>1.85E+05</td><td></td><td>(R)SNAEDT</td><td>(R)S N|A/E/D T L/R(S)</td><td></td><td>82.72</td><td>453.2209</td><td>905.432</td><td>0.0022</td><td>2.5</td><td>4.37</td><td>533778</td><td>5.74</td><td>HUMAN</td><td>Q15149</td><td>Plectin</td></tr>
<tr><td>19722</td><td>dirMS_041712_NAR_30mM_minus2.5942.5942.2</td><td>2</td><td>5.85</td><td>0</td><td>1.98E+05</td><td></td><td>(K)TSEVNC</td><td>(K)T S|E/V/N C Y/R(C)</td><td>C:Carbamidomethylation</td><td>86.7</td><td>514.726</td><td>1028.447</td><td>-0.0018</td><td>-1.8</td><td>5.66</td><td>18946.7</td><td>9.13</td><td>HUMAN</td><td>B4DP17</td><td>Cellular nucleic acid-binding protein</td></tr>
<tr><td>19723</td><td>dirMS_041712_NAR_50mM_minus2.16263.16263.3</td><td>3</td><td>5.85</td><td>0</td><td>1.99E+05</td><td></td><td>(R)DEPIHILI</td><td>(R)D E/P I H/I L/N V A I/K(T)</td><td></td><td>160.45</td><td>454.5974</td><td>1361.779</td><td>-0.0011</td><td>-0.8</td><td>5.32</td><td>267260.7</td><td>5.95</td><td>HUMAN</td><td>Q13085</td><td>Acetyl-CoA carboxylase 1</td></tr>
<tr><td>19724</td><td>dirMS_041712_NAR_60mM_minus.10648.10648.3</td><td>3</td><td>5.85</td><td>0</td><td>1.14E+05</td><td></td><td>(R)FTQDTQ</td><td>(R)F T|Q D T Q/P H Y I Y S/P R(E)</td><td></td><td>119.57</td><td>584.9474</td><td>1752.834</td><td>-0.0064</td><td>-3.6</td><td>6.74</td><td>535136.6</td><td>6.01</td><td>HUMAN</td><td>Q14204</td><td>Cytoplasmic dynein 1 heavy chain 1</td></tr>
</table>

19725	dirMS_041712_NAR_60mM_minus.10730.10730.3	3	5.85	0	1.89E+05		(K)TGNLGN	(K)T/G N L/G N/V/V/H I E R(F)		120.03	436.9057	1308.702	0.0007	0.5	6.41	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
19726	dirMS_041712_NAR_60mM_minus.11841.11841.3	3	5.85	1	4.61E+05	M230m	(R)mSMKE	(R)m S M K E V D E\Q|M|L N V/Q N K(N)	m:Oxidized methionine	125.58	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
19727	dirMS_041712_NAR_60mM_minus.11894.11894.3	3	5.85	0	3.73E+04	M23m	(K)QmVIDV	(K)Q m V I D/V L/H/P G/K(A)	m:Oxidized methionine	126.5	418.226	1236.677	15.9865	-6.7	6.74	32886.5	10.63	HUMAN	E7EPK6	40S ribosomal protein S24
19728	dirMS_041712_NAR_60mM_minus.16396.16396.3	3	5.85	0	1.35E+04		(R)FQSGDF	(R)F/Q/S G D F H/V/I/N G V L R(T)		151.5	530.2846	1588.823	0.0162	10.2	6.74	104619	5.75	HUMAN	F8W904	Exportin-2
19729	dirMS_041712_NAR_60mM_minus.6312.6312.3	3	5.85	1	6.98E+04		(R)ATEGM	(R)A/T|E/G M V V A D K N C S K(I)	C:Carbamidomethylation	94.03	503.9042	1509.704	-0.0055	-3.7	6.11	15607.8	9.99	HUMAN	B4E0P1	Proteasome (Prosome, macropain) subunit, beta type, 7, isoform CRA_b
19730	dirMS_041712_NAR_120mM_plus.8153.8153.3	3	5.85	0	2.72E+05		(K)HEQNID	(K)H E\Q N\I|D\C/G G G Y V K(L)	C:Carbamidomethylation	96.22	492.8886	1476.654	-0.0024	-1.6	5.32	48311.8	4.29	HUMAN	P27797	Calreticulin
19731	dirMS_041712_NAR_20mM_plus.13590.13590.2	2	5.85	0	1.67E+05		(R)TETIRPA	(R)T E T I R/P A S V/Y T K(R)		166.05	683.3671	1365.737	-0.0103	-7.6	8.26	74289.2	8.73	HUMAN	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial
19732	dirMS_041712_NAR_20mM_plus.15755.15755.3	3	5.85	0	8.77E+03		(R)SSFYVN	(R)S S\F\Y V N G L/T L/G G Q K(C)		179.37	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
19733	dirMS_041712_NAR_30mM_plus2.22590.22590.3	3	5.85	0	5.00E+05		(R)ALTVPEL	(R)A L T\V/P E L T Q Q V F D/A K(N)		175.77	553.9697	1659.895	-0.0007	-0.4	4.37	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
19734	dirMS_041712_NAR_30mM_plus2.5222.5222.2	2	5.85	0	1.98E+05		(R)LLGWG	(R)L/L/G W G G G R(A)		80.72	408.2308	815.452	0.0021	2.5	9.75	70579.2	10.03	HUMAN	Q96MC4	Protein LOC100653515
19735	dirMS_041712_NAR_40mM_plus2.4570.4570.2	2	5.85	0	2.03E+05		(R)YYGGGS	(R)Y Y/G/G G S E/G G R(A)		76.08	501.7171	1002.428	-0.0006	-0.6	6	64759.2	8.88	HUMAN	P14866	Heterogeneous nuclear ribonucleoprotein L
19736	dirMS_041712_NAR_50mM_plus2.12578.12578.3	3	5.85	1	1.91E+05		(R)LIEDGR	(R)L/I/E/D/G R G C E V\I\Q E I K(S)	C:Carbamidomethylation	134.07	586.971	1758.906	-0.007	-4	4.41	22452.9	9.82	HUMAN	H0Y9N5	60 kDa SS-A/Ro ribonucleoprotein (Fragment)
19737	dirMS_041712_NAR_50mM_plus2.12766.12766.3	3	5.85	0	5.03E+05		(R)IMDPNI	(R)I M/D/P N I V/G S E H Y/D/V A R(G)		134.62	605.9694	1815.869	0.0242	13.3	4.54	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
19738	dirMS_041712_NAR_60mM_plus.10577.10577.3	3	5.85	0	1.17E+04		(R)CGAALA	(R)C/G|A A L/A/G H\Q L\I/R(G)	C:Carbamidomethylation	113.38	422.8929	1266.674	-0.0094	-7.4	9.75	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
19739	dirMS_041712_NAR_60mM_plus.20866.20866.3	3	5.85	1	1.40E+05		(K)TFVNITP	(K)T F/V/N I/T P/A E V G V L\V G K D R(S)		170.55	639.0248	1915.065	-0.0049	-2.6	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
19740	dirMS_041712_NAR_120mM_minus.14651.14651.4	4	5.84	1	1.24E+05	M251m	(K)FSHEEIA	(K)F S H/E E\I/A m/A/T V/T A/L R R(T)	m:Oxidized methionine	133.6	462.7415	1831.948	15.9958	0.5	6.76	39795.8	9.08	HUMAN	H3BQN4	Fructose-bisphosphate aldolase
19741	dirMS_041712_NAR_20mM_minus.11637.11637.3	3	5.84	0	2.64E+05		(R)GALQNI	(R)G A L Q N\I I/P/A/S T G A A K(A)		164.75	471.2674	1411.79	-0.0027	-1.9	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
19742	dirMS_041712_NAR_20mM_minus.12308.12308.2	2	5.84	0	1.67E+05		(R)AAVIGPI	(R)A A/V|I|G/P D V F A K(L)		171.53	544.3103	1087.615	-0.0013	-1.2	5.88	266161	5.68	HUMAN	E9PPU0	Epiplakin
19743	dirMS_041712_NAR_30mM_minus2.7414.7414.2	2	5.84	0	6.48E+04	S441s T445	(R)ASGGTsI	(R)A/S|G G T s E F I t\G K(D)	s:Phosphorylated S t:Phosph	94.7	657.7477	1154.569	159.9193	-10.1	6.05	87229.4	6.13	HUMAN	O00534	von Willebrand factor A domain-containing protein 5A
19744	dirMS_041712_NAR_40mM_minus2.16105.16105.3	3	5.84	1	6.69E+05		(R)ELAILLG	(R)E L\A I/L L/G M L D/P A E K D E K(G)		189.58	629.0034	1884.999	-0.003	-1.6	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
19745	dirMS_041712_NAR_50mM_minus2.17703.17703.3	3	5.84	0	4.17E+05	M203m	(R)DTGIFLD	(R)D T|G I F L/D L m H L/K(K)	m:Oxidized methionine	170.32	473.5826	1402.74	15.9933	-1.1	5.21	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
19746	dirMS_041712_NAR_50mM_minus2.8286.8286.3	3	5.84	1	1.14E+05		(K)LTSDDVI	(K)L T S D D V K/E Q I/Y/K(L)		115.72	480.252	1438.742	-0.001	-0.7	4.56	12573.5	10.39	HUMAN	E9PS50	40S ribosomal protein S13 (Fragment)
19747	dirMS_041712_NAR_60mM_minus.15726.15726.3	3	5.84	0	3.64E+05		(R)IYSHSLLI	(R)I Y/S/H S\L|L P V L R(S)		148.07	433.2572	1297.763	-0.0056	-4.3	8.75	60871.9	6.3	HUMAN	B4DJ93	Phosphoribosylformylglycinamidine cyclo-ligase
19748	dirMS_041712_NAR_60mM_minus.18244.18244.3	3	5.84	0	9.48E+04		(R)NSVSNF	(R)N S/V/S N F L H/S L E\R(G)		162.5	468.2409	1402.707	0.0008	0.6	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
19749	dirMS_041712_NAR_60mM_minus.7033.7033.3	3	5.84	1	2.68E+05		(R)VKVEPA	(R)V K\V E P A\V|D T S/R(I)		97.45	400.8938	1200.658	0.0086	7.1	6.04	258215.9	5.48	HUMAN	E7EN95	Filamin-B
19750	dirMS_041712_NAR_20mM_plus.12406.12406.3	3	5.84	0	5.11E+04		(K)VNQIGS	(K)V N Q I G S\V/T E/S I/Q A C K(L)	C:Carbamidomethylation	159.02	545.2781	1633.821	-0.0016	-1	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
19751	dirMS_041712_NAR_20mM_plus.13058.13058.2	2	5.84	0	3.89E+04		(K)ISIPEEE	(K)I S|I/P E E E V P/R(V)		162.18	584.808	1168.621	-0.0121	-10.4	4.25	16905.1	4.27	HUMAN	F8VR36	Natural resistance-associated macrophage protein 2 (Fragment)
19752	dirMS_041712_NAR_20mM_plus.14244.14244.2	2	5.84	0	1.45E+05		(R)AALQELI	(R)A/A L/Q E\L/L/S K(G)		169.47	486.789	972.572	-0.0017	-1.7	6.05	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
19753	dirMS_041712_NAR_20mM_plus.18321.18321.2	2	5.84	0	1.22E+05		(R)GVVQEL	(R)G V/V Q/E/L Q Q A I/S K(L)		198.05	650.3656	1299.727	-0.0028	-2.1	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
19754	dirMS_041712_NAR_20mM_plus.18703.18703.3	3	5.84	0	5.55E+04		(K)LLDAVD	(K)L L D\A V/D\T Y I/P V P A R(D)		199.83	514.9547	1542.853	-0.0031	-2	4.21	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
19755	dirMS_041712_NAR_30mM_plus2.6621.6636.2	2	5.84	0	2.29E+05		(K)ALDEME	(K)A/L|D/E/M E/K(Q)		89.3	418.1994	835.387	0.0049	5.9	4.14	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
19756	dirMS_041712_NAR_40mM_plus2.12095.12095.3	3	5.84	1	6.59E+04		(K)TSLVATF	(K)T S/L V/A T/P G I/D K L T/E K(S)		137.73	524.9653	1572.884	-0.003	-1.9	5.73	89370.5	5.69	HUMAN	Q8IV36	Protein HID1
19757	dirMS_041712_NAR_40mM_plus2.14335.14335.3	3	5.84	1	1.81E+05		(K)IMASSPI	(K)I M|A S/S/P D M D L A/T V S A L R K(M)		151.15	635.9975	1905.977	0.0007	0.4	5.96	36208.1	7.21	HUMAN	B4DMU0	Pyrroline-5-carboxylate reductase
19758	dirMS_041712_NAR_40mM_plus2.8905.8905.2	2	5.84	0	1.05E+05		(K)FYVGDG	(K)F/Y/V G D G/Y K(F)		115.03	474.7301	948.446	0.0068	7.1	5.83	97297	5.75	HUMAN	Q9HBG4	V-type proton ATPase 116 kDa subunit a isoform 4
19759	dirMS_041712_NAR_40mM_plus2.9791.9791.3	3	5.84	0	2.43E+05		(R)AAEDPV	(R)A A E/D|P V A A A P R P L P A G G R(L)		121.12	572.6438	1715.919	-0.0019	-1.1	6.12	73966.7	10.21	HUMAN	B3KWK6	Alpha-L-iduronidase
19760	dirMS_041712_NAR_50mM_plus2.10695.10695.3	3	5.84	1	1.94E+05	M250m	(K)EAVTGN	(K)E A/V/T G\N G I G/G K m K(I)	m:Oxidized methionine	123.17	426.5574	1261.657	16.0007	4.6	8.69	61708.7	9.56	HUMAN	O00257	E3 SUMO-protein ligase CBX4
19761	dirMS_041712_NAR_50mM_plus2.10750.10750.3	3	5.84	1	5.26E+05		(R)VAVEEV	(R)V A/V/E E V/D E E/G K F V R(L)		124.4	535.9422	1605.812	0.0002	0.1	4.25	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
19762	dirMS_041712_NAR_50mM_plus2.17281.17298.3	3	5.84	0	1.24E+05		(R)FGVPVI	(R)F G\V|P V/I A D G G I Q N V G H\I A/K(A)		159.7	631.3464	1892.039	-0.0142	-7.5	6.74	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
19763	dirMS_041712_NAR_50mM_plus2.7532.7532.3	3	5.84	1	3.25E+05		(R)IVEQDTI	(R)I V/E/Q/D T M P P K G V R(H)		105.45	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
19764	dirMS_041712_NAR_120mM_minus.17879.17879.3	3	5.83	1	1.54E+05		(R)AGKLDP	(R)A G K\L D|P H L/V L D/Q L R(C)		151.7	525.6385	1574.901	-0.0004	-0.2	6.79	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
19765	dirMS_041712_NAR_120mM_minus.19360.19360.3	3	5.83	1	3.72E+05		(K)NLRDIDE	(K)N\L\R D\I\D\E\V/S/S L L R(T)		161.42	510.614	1529.828	-0.0007	-0.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
19766	dirMS_041712_NAR_120mM_minus.9311.9311.4	4	5.83	0	1.92E+04		(R)SLEPMA	(R)S L E P M/A G Q L S/N S V A T K(L)		104.98	408.9616	1632.826	-0.0016	-1	5.72	153084.9	5.55	HUMAN	Q6P2E9	Enhancer of mRNA-decapping protein 4
19767	dirMS_041712_NAR_120mM_minus.9748.9748.2	2	5.83	1	9.73E+05		(R)SRAEAE	(R)S R/A E A E\S M\Y\Q|I K(Y)		107.27	706.8447	1412.684	-0.0017	-1.2	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
19768	dirMS_041712_NAR_20mM_minus.12666.12666.2	2	5.83	0	1.62E+05	M185m	(K)LAVNm	(K)L/A/V/N m V|P F/P R(L)	m:Oxidized methionine	175.1	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
19769	dirMS_041712_NAR_20mM_minus.13582.13582.2	2	5.83	0	1.43E+05		(R)QAQEYE	(R)Q/A Q E/Y|E A L L/N I K(V)		186.85	710.3754	1419.748	-0.0043	-3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
19770	dirMS_041712_NAR_20mM_minus.8794.8794.2	2	5.83	1	1.62E+05	T531t	(K)EVKSQtE	(K)E V K S/Q|t/E L/R(K)	t:N-acetylglucosamine (T)	137.6	646.8321	1089.59	203.0671	-9.5	6.24	85569.5	9.1	HUMAN	B1ALB4	Protein SMG7 (Fragment)
19771	dirMS_041712_NAR_30mM_minus2.12681.12681.2	2	5.83	0	2.32E+05		(R)CGYFDE	(R)C G|Y|F/D E E/M/N R(I)	C:Carbamidomethylation	122.93	660.7538	1320.498	0.002	1.5	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
19772	dirMS_041712_NAR_50mM_minus2.10540.10540.3	3	5.83	1	2.76E+05		(K)NQVAM	(K)N Q|V/A|M N P T/N T V F D A K R(L)		128.5	602.6379	1805.896	0.0029	1.6	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
19773	dirMS_041712_NAR_50mM_minus2.16388.16388.3	3	5.83	0	5.32E+04		(K)TTIENIQ	(K)T T|I/E/N/I Q L/P H/T L L S R(F)		161.2	579.326	1735.97	-0.0067	-3.8	6.41	95792.4	6.36	HUMAN	J3KPV4	DNA replication licensing factor MCM4
19774	dirMS_041712_NAR_50mM_minus2.5844.5844.3	3	5.83	1	4.33E+04		(R)AIEAAP	(R)A I|E A A/P Q E/P E/Q K R(S)		95.43	489.5922	1466.76	0.0023	1.5	4.79	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
19775	dirMS_041712_NAR_60mM_minus.14111.14111.3	3	5.83	1	3.30E+05		(R)QATKDA	(R)Q A/T/K D A G T I/A|G L/N V L R(I)		138.87	543.3073	1627.913	-0.0052	-3.2	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
19776	dirMS_041712_NAR_60mM_minus.17853.17853.3	3	5.83	1	1.80E+04		(R)KQSHPE	(R)K Q S/H P E I I/S Y L|E K(V)		160.52	524.623	1571.843	0.0117	7.4	6.75	28088.3	10.79	HUMAN	F8VP71	LETM1 domain-containing protein 1
19777	dirMS_041712_NAR_60mM_minus.7628.7628.3	3	5.83	1	5.65E+05		(R)YLAEVA	(R)Y/L|A E V/A A G D D K K(G)		102.07	427.222	1279.653	-0.0014	-1.1	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
19778	dirMS_041712_NAR_120mM_plus.6814.6814.3	3	5.83	1	1.84E+05		(K)ALDEME	(K)A/L/D E\M E/K Q/Q/R(E)		88.82	416.5394	1247.605	-0.0012	-1	4.68	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
19779	dirMS_041712_NAR_20mM_plus.16386.16386.3	3	5.83	0	4.95E+04		(R)LGGIPV	(R)L G G\I P V G V|V A V/E/T R(T)		184.27	456.2733	1366.805	0.0001	0.1	6	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
19780	dirMS_041712_NAR_20mM_plus.16635.16635.3	3	5.83	0	6.89E+04		(R)AAFTAFI	(R)A A/F T A F E\E A Q/L/P/R(L)		186.25	484.2492	1450.733	0.0005	0.4	4.53	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
19781	dirMS_041712_NAR_20mM_plus.7829.7829.3	3	5.83	0	1.06E+05		(K)AQAAAF	(K)A Q A A\A P\A|S V/P A Q A P K(R)		123.6	459.9204	1377.748	-0.0018	-1.3	8.8	17808.8	11.77	HUMAN	P47914	60S ribosomal protein L29
19782	dirMS_041712_NAR_20mM_plus.7926.7926.2	2	5.83	0	5.51E+04		(K)SVTEQG	(K)S V/T E\Q/G A E L/S N E E R(N)		124.85	774.8589	1548.714	-0.0031	-2	4.09	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
19783	dirMS_041712_NAR_20mM_plus.9199.9199.2	2	5.83	0	7.21E+04		(R)VQDIFT	(R)V\Q/D/I\F T/A G/K(L)		134.52	489.7674	978.525	0.0021	2.1	5.81	48966.7	7.79	HUMAN	B4DKT4	Large neutral amino acids transporter small subunit 2
19784	dirMS_041712_NAR_20mM_plus.9934.9934.2	2	5.83	0	1.32E+05		(K)GEATVSI	(K)G E\A T/V/S/F D/D|P P S A K(A)		140.17	710.8324	1420.659	-0.0015	-1.1	4.03	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
19785	dirMS_041712_NAR_30mM_plus2.10171.10171.2	2	5.83	0	2.10E+05		(R)LNQDQL	(R)L/N/Q/D/Q/L D A V/S K(Y)		107.3	615.819	1230.632	-0.0017	-1.4	4.21	20235.4	6.77	HUMAN	E9PLA9	Caprin-1 (Fragment)
19786	dirMS_041712_NAR_30mM_plus2.6423.6423.2	2	5.83	0	2.80E+05		(R)SPDNPM	(R)S/P\D|N|P/M/N Q R(A)		88.45	529.7357	1058.468	-0.0042	-4	5.55	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
19787	dirMS_041712_NAR_50mM_plus2.14868.14868.3	3	5.83	0	1.17E+06		(R)EHALLA	(R)E H A L\L A|Y/T/L G V K(Q)		145.75	438.9176	1314.742	-0.0034	-2.6	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
19788	dirMS_041712_NAR_50mM_plus2.15150.15150.3	3	5.83	0	2.43E+04		(K)VALLLLD	(K)V A\L\L/L L/D Q/G A/S P H A A A K(N)		147.53	558.9877	1674.954	-0.0052	-3.1	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
19789	dirMS_041712_NAR_50mM_plus2.19258.19258.3	3	5.83	0	8.39E+05		(R)DFNHIN	(R)D F N H I|N V/E|L S/L\L/G K(K)		170.08	533.6223	1598.854	-0.0013	-0.8	5.32	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
19790	dirMS_041712_NAR_50mM_plus2.8329.8329.3	3	5.83	0	2.33E+05		(K)VQQAEL	(K)V Q/Q/A E L/H T/G S L P R(I)		110.33	479.2607	1435.765	0.0023	1.6	6.72	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
19791	dirMS_041712_NAR_60mM_plus.13225.13225.3	3	5.83	1	3.46E+06		(R)VVDLMA	(R)V V|D/L M A H/M A S K/E(-)		126.57	444.2219	1330.649	0.0018	1.3	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
19792	dirMS_041712_NAR_60mM_plus.17915.17915.3	3	5.83	0	2.66E+05		(R)LLIHQSL	(R)L L I H Q\S/L|A/G G I I/G V K(G)		150.48	506.9815	1518.937	-0.0067	-4.4	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
19793	dirMS_041712_NAR_60mM_plus.8531.8531.3	3	5.83	0	6.38E+05		(K)EHDPVG	(K)E H D P V\G Q/M/V/N N/P K(I)		102.25	488.9052	1464.69	0.0111	7.6	5.32	86098.8	5.31	HUMAN	B4DUC5	Exportin-2
19794	dirMS_041712_NAR_30mM_minus2.14971.14971.2	2	5.82	0	3.59E+05		(R)LCFEGLF	(R)L/C|F/E/G L R(S)	C:Carbamidomethylation	134.43	447.7317	894.45	0.0059	6.6	6	533778	5.74	HUMAN	Q15149	Plectin
19795	dirMS_041712_NAR_30mM_minus2.16679.16679.2	2	5.82	0	2.95E+05		(K)MIFVGIK	(K)M/I/F/V/G/I K(K)		144.85	404.2383	807.48	-0.0104	-12.9	8.5	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
19796	dirMS_041712_NAR_60mM_minus.12993.12993.3	3	5.82	1	8.67E+05		(K)AVLFCLS	(K)A V/L F/C/L S E D/K K(N)	C:Carbamidomethylation	131.82	437.2334	1309.682	0.0036	2.7	6.11	22956	8.8	HUMAN	E9PK25	Cofilin-1
19797	dirMS_041712_NAR_60mM_minus.16837.16837.3	3	5.82	1	2.46E+05		(R)KGFSEGI	(R)K G F S E G\L\W\E|I/E/N N/P|T V K(A)		153.75	649.9986	1947.981	0.0002	0.1	4.79	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
19798	dirMS_041712_NAR_60mM_minus.17941.17941.3	3	5.82	1	2.67E+05		(K)LEALKDL	(K)L E A L K D|L A/S L/S R(D)		161.63	439.2618	1315.758	0.0129	9.8	6.07	18679.9	4.7	HUMAN	C9IZR8	Engulfment and cell motility protein 1 (Fragment)
19799	dirMS_041712_NAR_60mM_minus.19288.19288.3	3	5.82	0	1.48E+05		(K)HQQLLG	(K)H/Q Q L L G E\V|L/T/Q/L S S R(F)		171.07	570.3156	1708.934	-0.0018	-1.1	6.75	90361.5	8.49	HUMAN	Q13616	Cullin-1
19800	dirMS_041712_NAR_60mM_minus.7799.7799.3	3	5.82	0	1.10E+05		(K)LFQECCI	(K)L/F Q/E C C P H S/T D R(V)	C:Carbamidomethylation	103.25	517.2229	1549.652	0.0019	1.2	5.32	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
19801	dirMS_041712_NAR_120mM_plus.12373.12373.3	3	5.82	0	1.28E+06		(R)HVFGES	(R)H V F G\E/S D E\L/I/G Q/K(V)		118.87	486.9124	1458.722	0.0003	0.2	4.65	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
19802	dirMS_041712_NAR_30mM_plus2.10290.10290.2	2	5.82	0	4.36E+05		(R)GVNVSA	(R)G V/N\V/S A L S/R(D)		106.68	451.7509	902.505	-0.0109	-12.1	9.75	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
19803	dirMS_041712_NAR_30mM_plus2.16160.16160.2	2	5.82	0	1.77E+05		(R)VEVTEFE	(R)V E|V/T|E F E D I K(S)		137.82	604.8021	1208.604	-0.0076	-6.3	4	30992.3	4.14	HUMAN	B2REB8	Protein SET
19804	dirMS_041712_NAR_30mM_plus2.19664.19664.2	2	5.82	0	6.15E+05		(R)LIDFLEC	(R)L I/D/F L E C G K(T)	C:Carbamidomethylation	155.77	547.7808	1094.555	-0.0007	-0.7	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
19805	dirMS_041712_NAR_30mM_plus2.22033.22033.2	2	5.82	0	2.42E+05		(R)AFITNIP	(R)A F|I|T\N I/P F D V K(W)		171.38	632.8481	1264.694	-0.0047	-3.7	5.88	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
19806	dirMS_041712_NAR_30mM_plus2.23472.23472.2	2	5.82	0	6.82E+05		(R)IAIYELLF	(R)I/A|I/Y/E L L/F K(E)		190.72	555.3331	1109.661	-0.0016	-1.4	6	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
19807	dirMS_041712_NAR_40mM_plus2.12022.12022.2	2	5.82	0	2.48E+05		(K)LSELEAA	(K)L S E|L/E A\A/L Q R(A)		136.62	565.3103	1129.621	-0.0078	-6.9	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
19808	dirMS_041712_NAR_40mM_plus2.19543.19543.3	3	5.82	1	1.06E+06	M169m	(R)KLLMTW	(R)K/L/L M T W/A L E V A V/V m K(K)	m:Oxidized methionine	183.65	583.3378	1731.99	16.0089	8	8.59	79849.3	7.14	HUMAN	Q5BKU6	Putative uncharacterized protein LOC641298
19809	dirMS_041712_NAR_40mM_plus2.6240.6240.2	2	5.82	0	1.81E+05		(K)TEISEMN	(K)T E/I/S E M N R(N)		96.18	490.2292	979.451	-0.0002	-0.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
19810	dirMS_041712_NAR_50mM_plus2.11345.11345.3	3	5.82	0	2.13E+05		(K)NAQLNI	(K)N A Q|L N I E\L E/A A H/H(-)		127	487.2488	1459.729	0.003	2.1	5.23	13452	8.89	HUMAN	F5H246	Protein NAMPTL
19811	dirMS_041712_NAR_50mM_plus2.16729.16729.3	3	5.82	1	1.39E+07		(R)VSFELFA	(R)V S F E/L/F A D K V P K(T)		156.65	460.5906	1379.757	0.0003	0.2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
19812	dirMS_041712_NAR_50mM_plus2.9337.9337.3	3	5.82	0	5.61E+04		(K)GSLTEGA	(K)G S\L/T|E/G A/L/A H S G N P V S K(G)		116.12	542.2792	1624.829	-0.0059	-3.6	6.75	110902.8	6.09	HUMAN	D6RD46	LIM and calponin homology domains-containing protein 1
19813	dirMS_041712_NAR_60mM_plus.13253.13253.3	3	5.82	1	2.80E+04		(K)AAAGKA	(K)A A|A G K/A E L\E/L E/L G R(I)		126.13	476.5985	1427.785	-0.0043	-3	4.79	533778	5.74	HUMAN	Q15149	Plectin
19814	dirMS_041712_NAR_60mM_plus.20865.20865.3	3	5.82	1	1.95E+05		(K)LIQLMEE	(K)L I/Q L M/E E/I M/A E K E N K(T)		170.08	606.9819	1818.934	-0.0028	-1.6	4.49	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
19815	dirMS_041712_NAR_60mM_plus.9017.9017.3	3	5.82	1	3.36E+05		(K)SEETLDE	(K)S E|E/T/L D E/G P P K Y T K(S)		105.07	531.9256	1593.764	-0.002	-1.3	4.41	25233.4	9.34	HUMAN	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3
19816	dirMS_041712_NAR_120mM_minus.10959.10959.3	3	5.81	1	2.36E+05		(R)TNEKVE	(R)T N|E K V E L\Q/E L N D R(F)		114.1	529.9368	1587.797	-0.0014	-0.9	4.41	49709.6	5.19	HUMAN	B0YJC4	Vimentin
19817	dirMS_041712_NAR_120mM_minus.6608.6608.3	3	5.81	1	1.32E+05		(K)AMKEYE	(K)A/M/K E Y E/E E/E/R(K)		90.45	438.5284	1313.568	0.0028	2.2	4.32	11829.2	4.96	HUMAN	K7EIU0	Hsp90 co-chaperone Cdc37 (Fragment)
19818	dirMS_041712_NAR_120mM_minus.8982.8982.3	3	5.81	1	2.10E+05		(-)MAPASA	(-)M A P A S/A S G E/D L/R K(L)		102.12	444.8897	1332.658	-0.0031	-2.3	5.82	97863.5	6.11	HUMAN	Q8NDZ2	SUMO-interacting motif-containing protein 1
19819	dirMS_041712_NAR_20mM_minus.11781.11781.2	2	5.81	0	1.10E+05	M98m	(R)TLTIVDT	(R)T L\T/I V/D/T G\I/G m T K(A)	m:Oxidized methionine	166.9	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
19820	dirMS_041712_NAR_20mM_minus.12524.12524.2	2	5.81	0	6.64E+04		(K)LLGELLQ	(K)L/L/G\E\L/L/Q D N A K(L)		173.45	607.3406	1213.679	-0.0048	-3.9	4.37	35556.4	9.3	HUMAN	F2Z393	Transaldolase
19821	dirMS_041712_NAR_20mM_minus.13133.13133.2	2	5.81	0	3.16E+05	M35m	(K)NDIAINE	(K)N D I\A|I|N E L m K(R)	m:Oxidized methionine	181.93	588.7948	1160.598	15.9843	-9	4.37	28354	7.11	HUMAN	B4DXI8	26S proteasome non-ATPase regulatory subunit 7
19822	dirMS_041712_NAR_20mM_minus.13645.13645.2	2	5.81	0	1.38E+05		(K)DIYALISD	(K)D I\Y/A/L I/S D Q K(H)		186.93	583.3076	1165.61	-0.002	-1.7	4.21	266161	5.68	HUMAN	E9PPU0	Epiplakin
19823	dirMS_041712_NAR_30mM_minus2.16686.16686.2	2	5.81	0	2.38E+04		(R)FFMGN	(R)F F|M/G N Q V L\K(V)		144.32	542.2866	1083.566	0.0004	0.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
19824	dirMS_041712_NAR_30mM_minus2.19010.19010.2	2	5.81	0	2.02E+05		(K)IISNLFLG	(K)I I/S N/L F/L G R(A)		157.62	516.8122	1032.62	-0.0029	-2.8	9.75	234333.2	6.01	HUMAN	J3KNX9	Unconventional myosin-XVIIIa
19825	dirMS_041712_NAR_30mM_minus2.6778.6778.2	2	5.81	0	3.67E+05		(K)VLEEEEC	(K)V/L/E/E E E|Q R(R)		90.42	516.2552	1031.5	0.0027	2.7	4.09	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
19826	dirMS_041712_NAR_50mM_minus2.13862.13862.3	3	5.81	1	3.29E+04		(R)ELISNAS	(R)E L I/S/N/A S/D\A L D\K I R(L)		146.95	515.6179	1544.828	0.0113	7.3	4.56	5582.4	4.81	HUMAN	F8W026	Endoplasmin (Fragment)
19827	dirMS_041712_NAR_50mM_minus2.14344.14344.3	3	5.81	1	8.33E+04		(R)LSQELEY	(R)L/S Q/E\L E/Y L T E D V/K\R(L)		149.87	574.9724	1722.891	0.0118	6.8	4.41	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
19828	dirMS_041712_NAR_60mM_minus.17663.17663.3	3	5.81	1	3.15E+05		(K)YGKLEV	(K)Y G K L E V A|N/L/L/L Q K(S)		159.28	496.9631	1488.878	-0.0037	-2.5	8.5	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
19829	dirMS_041712_NAR_60mM_minus.7336.7336.3	3	5.81	1	2.13E+05		(K)IPTKENV	(K)I P/T/K E N V Y E/A K(S)		100.52	431.2376	1291.689	0.009	7	6.14	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
19830	dirMS_041712_NAR_60mM_minus.8491.8491.3	3	5.81	0	1.38E+04		(R)SAEEEA	(R)S A|E E E/A A D L/P/T K/P T K(I)		107.37	529.6002	1586.791	-0.0048	-3	4.41	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
19831	dirMS_041712_NAR_20mM_plus.12592.12592.3	3	5.81	0	6.37E+04		(K)AINQQT	(K)A I N Q Q T G A F/V/E/I S R(Q)		159.7	511.9382	1533.802	-0.0019	-1.3	6.05	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
19832	dirMS_041712_NAR_20mM_plus.17888.17888.2	2	5.81	0	1.65E+05		(R)TVQSLEI	(R)T V|Q S\L/E|I D L D S M R(N)		194.92	753.8776	1506.747	0.0011	0.7	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
19833	dirMS_041712_NAR_30mM_plus2.11493.11730.2	2	5.81	0	9.40E+05		(K)YGDGIQ	(K)Y/G|D|G/I/Q L T R(S)		114.05	511.766	1022.527	-0.0018	-1.8	5.83	334221.3	6.44	HUMAN	P15924	Desmoplakin

19834	dirMS_041712_NAR_30mM_plus2.18566.18566.3	3	5.81	0	4.97E+05		(R)SSFYVN(	(R)S S\F Y V N G\L/T/L/G G Q K(C)		150.95	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
19835	dirMS_041712_NAR_30mM_plus2.21106.21106.2	2	5.81	0	3.77E+04		(R)EMVLEII	(R)E M/V/L/E/I I R(E)		164.45	501.7877	1002.565	0.0029	2.9	4.53	61981.6	8.97	HUMAN	Q96I24	Far upstream element-binding protein 3
19836	dirMS_041712_NAR_30mM_plus2.9079.9079.2	2	5.81	0	2.58E+05		(R)ACTELGI	(R)A/C|T/E L G I/R(T)	C:Carbamidomethylation	101.07	460.2391	919.467	0.0043	4.7	6.05	58266.4	9.46	HUMAN	B4DN00	Pyruvate carboxylase, mitochondrial
19837	dirMS_041712_NAR_30mM_plus2.9986.9986.2	2	5.81	0	2.55E+05		(R)ELVDQD	(R)E/L V/D Q D V Q P A R(Y)		105.78	635.3292	1269.643	0.0078	6.1	4.03	91388.8	5.78	HUMAN	Q8NFZ4	Neuroligin-2
19838	dirMS_041712_NAR_40mM_plus2.8215.8215.2	2	5.81	0	2.68E+03		(K)LNCSPD:	(K)L N/C|S/P D S F R(C)	C:Carbamidomethylation	109.17	548.2538	1095.489	0.0116	10.5	5.84	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
19839	dirMS_041712_NAR_50mM_plus2.19852.19852.3	3	5.81	0	5.26E+04		(K)GLCLLEC	(K)G L/C L L/E Q I D S F K/P P Q R(S)	C:Carbamidomethylation	172.9	634.3344	1900.995	-0.0063	-3.3	6.07	45536.8	9.03	HUMAN	B7Z1K2	HBS1-like protein
19840	dirMS_041712_NAR_50mM_plus2.9561.9561.3	3	5.81	0	2.45E+05		(R)LVKPGN	(R)L V K/P G N Q N T Q/V/T E A W N K(V)		117.08	643.0046	1927.003	-0.004	-2.1	8.59	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
19841	dirMS_041712_NAR_60mM_plus.19186.19186.3	3	5.81	0	1.30E+05		(K)SLLKPFC	(K)S L L K/P F C A A/L/L K(H)	C:Carbamidomethylation	158.03	454.2724	1360.802	0.0005	0.4	10	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
19842	dirMS_041712_NAR_60mM_plus.19299.19299.3	3	5.81	1	5.22E+05		(R)TRIEGLL	(R)T R I E G L|L A/A/F/P/K(L)		159.48	439.262	1315.773	-0.0018	-1.4	8.41	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
19843	dirMS_041712_NAR_60mM_plus.21135.21135.3	3	5.81	1	3.16E+04		(K)LKEAELL	(K)L K E A E L L|E|P/L/M/P A I R(A)		173.85	574.9975	1722.982	-0.0043	-2.5	4.79	56164.6	6.01	HUMAN	E9PP73	Coatomer subunit beta (Fragment)
19844	dirMS_041712_NAR_120mM_minus.10372.10372.3	3	5.8	1	4.00E+04	M118m	(R)LSFDKD/	(R)L S/F D K/D\A m/V A/R(A)	m:Oxidized methionine	109.95	423.5471	1252.635	15.9913	-2.8	5.96	35556.4	9.3	HUMAN	F2Z393	Transaldolase
19845	dirMS_041712_NAR_20mM_minus.14511.14511.2	2	5.8	0	2.97E+04		(R)LSVEEA\	(R)L S V E E/A\V A/A/G V/V/G G E I Q E K(L)		199.53	942.996	1884.991	-0.0066	-3.5	4.09	266161	5.68	HUMAN	E9PPU0	Epiplakin
19846	dirMS_041712_NAR_20mM_minus.7542.7542.3	3	5.8	0	8.44E+05	M239m	(K)EVDEQn	(K)E V D E Q/m/L/N V/Q N K(N)	m:Oxidized methionine	123.83	488.2327	1446.689	15.9942	-0.5	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
19847	dirMS_041712_NAR_20mM_minus.9674.9674.2	2	5.8	0	1.26E+05		(R)AGTGVD	(R)A G/T G V|D N/V/D L E/A A T R(K)		146.77	744.8662	1488.729	-0.0038	-2.5	4.03	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
19848	dirMS_041712_NAR_30mM_minus2.11339.11339.2	2	5.8	0	1.40E+05		(R)AATSPA	(R)A A\T S/P/A\L F N R(C)		115.4	524.2789	1047.558	-0.0076	-7.3	9.79	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
19849	dirMS_041712_NAR_30mM_minus2.17990.17990.2	2	5.8	1	5.45E+04		(K)IPRTLQT	(K)I P/R T/L Q T A P E K(E)		152.37	627.3629	1253.721	-0.0027	-2.1	8.75	93078.6	9.36	HUMAN	A6NJZ9	Nucleolar complex protein 3 homolog
19850	dirMS_041712_NAR_30mM_minus2.6472.6472.2	2	5.8	0	1.91E+04		(K)EVEEDE\	(K)E V/E/E/D E/Y K(A)		89.48	520.7257	1040.442	0.0023	2.2	3.91	92752.5	4.76	HUMAN	P14625	Endoplasmin
19851	dirMS_041712_NAR_30mM_minus2.9716.9759.2	2	5.8	0	4.35E+05		(K)TTIFTDA	(K)T T|I F/T/D/A K(E)		107.35	448.7371	896.472	-0.0055	-6.1	5.5	18139.1	5.71	HUMAN	B7WPD3	Transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B), isoform CRA_a
19852	dirMS_041712_NAR_40mM_minus2.12631.12631.3	3	5.8	1	1.55E+04		(K)ALLQDK	(K)A L L Q D K D V\I/A|I N Q D P L/G K(Q)		157.85	651.0317	1951.086	-0.0053	-2.7	4.43	49507.6	5.35	HUMAN	P06280	Alpha-galactosidase A
19853	dirMS_041712_NAR_50mM_minus2.13362.13362.3	3	5.8	1	1.89E+05	M26m	(K)GAEEME	(K)G A|E|E/M/E T V I/P V D/V m R R(A)	m:Oxidized methionine	143.85	616.6435	1831.904	16.0119	9.2	4.41	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
19854	dirMS_041712_NAR_60mM_minus.8595.8595.3	3	5.8	0	9.13E+04		(R)ISVYYNE	(R)I S V Y Y/N E/A S S H K(Y)		107.72	466.5604	1397.67	-0.0029	-2.1	6.75	18402.2	5.06	HUMAN	G3V2N6	HCG1983504, isoform CRA_d
19855	dirMS_041712_NAR_120mM_plus.18000.18000.3	3	5.8	0	4.73E+05		(R)HLLQAP'	(R)H L L Q/A\P V D/D A/Q E/I/L H S R(F)		148.32	648.0088	1942.014	-0.0023	-1.2	5.21	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
19856	dirMS_041712_NAR_20mM_plus.15441.15441.2	2	5.8	0	7.27E+04		(R)AVLNPL(	(R)A V/L|N/P L C Q V D Y R(A)	C:Carbamidomethylation	178.62	724.3735	1447.736	0.0035	2.4	5.88	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
19857	dirMS_041712_NAR_30mM_plus2.16809.16809.2	2	5.8	0	3.06E+05		(K)SNQQLV	(K)S N/Q Q/L/V/D I|I E K(V)		141.15	643.8504	1286.695	-0.0015	-1.2	4.37	22568.6	6.35	HUMAN	B3KQ25	Proteasome activator complex subunit 3
19858	dirMS_041712_NAR_30mM_plus2.18677.18677.2	2	5.8	0	2.71E+05		(R)QFLTQLI	(R)Q\F/L/T/Q/L M/Q K(E)		151.42	568.8061	1136.613	-0.0083	-7.3	8.75	81733.5	5.24	HUMAN	E9PAW1	Splicing factor 3A subunit 1
19859	dirMS_041712_NAR_30mM_plus2.19741.19741.2	2	5.8	0	3.55E+05		(K)SNNVEN	(K)S N|N\V/E/M D\W/V L K(H)		156.9	667.8205	1334.641	-0.0072	-5.4	4.37	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
19860	dirMS_041712_NAR_30mM_plus2.20190.20190.2	2	5.8	0	1.53E+05		(K)IVILGDN	(K)I V|I L G D/N W/K(Q)		159.97	529.3028	1057.604	-0.0057	-5.4	5.84	41803.7	9.36	HUMAN	B3KSF0	SEC14-like 4 (S. cerevisiae), isoform CRA_b
19861	dirMS_041712_NAR_30mM_plus2.20508.20508.2	2	5.8	0	2.80E+04		(K)LAVNM\	(K)L A|V/N M|V|P F P R(L)		161	572.32	1143.634	-0.0016	-1.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
19862	dirMS_041712_NAR_30mM_plus2.9497.9497.2	2	5.8	0	7.10E+05		(K)LIEVDDE	(K)L I|E/V D D/E R(K)		104.63	494.7532	988.495	0.0046	4.6	3.91	10471.9	5.4	HUMAN	A2A3R7	40S ribosomal protein S6
19863	dirMS_041712_NAR_40mM_plus2.6546.6546.2	2	5.8	0	1.18E+05		(K)YCQVIR(	(K)Y/C|Q/V I/R(V)	C:Carbamidomethylation	98.15	419.7152	838.424	-0.0009	-1	8.75	31471	10.11	HUMAN	B5MCW2	60S ribosomal protein L3 (Fragment)
19864	dirMS_041712_NAR_40mM_plus2.7754.7754.2	2	5.8	0	4.23E+04		(R)VLNTNIL	(R)V/L/N T N I D/G R(R)		105.73	501.2719	1001.537	-0.0009	-0.9	5.81	17718.4	10.99	HUMAN	P62269	40S ribosomal protein S18
19865	dirMS_041712_NAR_50mM_plus2.20182.20182.3	3	5.8	1	1.14E+05		(R)FLIPVLN	(R)F L|I/P/V L N G L E K K(E)		174.58	457.6182	1370.841	-0.0006	-0.4	8.59	142001.7	5.82	HUMAN	Q92797	Symplekin
19866	dirMS_041712_NAR_50mM_plus2.20603.20603.3	3	5.8	1	2.42E+05		(R)GGPNIIT	(R)G G P/N I/I/T L A D/I V K D/P V S R(T)		177	622.3526	1865.049	-0.0058	-3.1	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
19867	dirMS_041712_NAR_60mM_plus.10542.10542.2	2	5.8	1	1.63E+06		(R)VKYETEL	(R)V/K|Y/E/T E/L/A M R(Q)		113.12	620.326	1239.64	0.0045	3.7	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
19868	dirMS_041712_NAR_60mM_plus.17163.17163.3	3	5.8	1	2.91E+05		(R)ASLISAV	(R)A/S/L I/S A V S D K/L R(W)		146.83	420.5832	1259.732	0.0033	2.6	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
19869	dirMS_041712_NAR_60mM_plus.20962.20962.3	3	5.8	0	3.86E+05		(R)SLHDAL(	(R)S L H D A L/C/V|L A Q/T V K(D)	C:Carbamidomethylation	171.88	518.9516	1554.831	0.0094	6.1	6.46	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
19870	dirMS_041712_NAR_120mM_minus.13731.13731.3	3	5.79	0	4.19E+04		(R)CPGESSI	(R)C/P/G E S S H\I C D F\I R(K)	C:Carbamidomethylation	129.23	526.5672	1577.684	0.0035	2.2	5.32	30197.4	7.91	HUMAN	E9PMG2	Palmitoyl-protein thioesterase 1 (Fragment)
19871	dirMS_041712_NAR_120mM_minus.16684.16684.4	4	5.79	0	6.80E+05		(K)HLEINPD	(K)H L\E\I\N/P D H S I I/E/T L R(Q)		146.28	447.4904	1786.945	-0.0049	-2.7	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
19872	dirMS_041712_NAR_120mM_minus.8221.8221.2	2	5.79	0	4.37E+05		(R)HQGVM	(R)H Q|G/V M V/G M/G Q/K(D)		99.03	586.2907	1171.571	0.0031	2.6	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
19873	dirMS_041712_NAR_30mM_minus2.11084.11084.2	2	5.79	0	4.49E+05		(R)GYSFTTT	(R)G Y|S/F/T/T/T A E R(E)		114.07	566.7699	1132.527	0.0056	4.9	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
19874	dirMS_041712_NAR_30mM_minus2.18167.18167.2	2	5.79	0	2.92E+04		(R)LINLVGE	(R)L I/N\L/V/G E S L R(L)		153.3	557.3333	1113.663	-0.0033	-3	6	119157.2	5.4	HUMAN	B0UX83	HLA-B associated transcript 3
19875	dirMS_041712_NAR_30mM_minus2.6204.6204.2	2	5.79	0	5.52E+04		(R)SAENPP:	(R)S A|E N/P|P S G S V R(K)		87.88	550.7684	1100.533	-0.0036	-3.2	5.72	32364.3	9.76	HUMAN	Q15014	Mortality factor 4-like protein 2
19876	dirMS_041712_NAR_50mM_minus2.16666.16666.3	3	5.79	0	1.27E+05		(K)VSHLLGI	(K)V S H L L\G I N V|T/D F T/R(G)		162.28	524.6237	1571.854	0.0025	1.6	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
19877	dirMS_041712_NAR_60mM_minus.18694.18694.3	3	5.79	1	9.51E+04		(R)VYEFLDI	(R)V Y E/F L D/K L D|V V R(S)		165.37	499.2763	1495.815	-0.0012	-0.8	4.56	41296.9	9.52	HUMAN	B4DT72	26S proteasome non-ATPase regulatory subunit 3
19878	dirMS_041712_NAR_60mM_minus.6297.6297.3	3	5.79	1	1.03E+04		(R)TKTEISEI	(R)T K T/E I/S|E/M N R(N)		93.73	403.5374	1208.594	0.0037	3	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
19879	dirMS_041712_NAR_60mM_minus.9687.9687.3	3	5.79	1	2.83E+05		(R)SPTMAC	(R)S P T M/A G G L F A V S/K K(Y)		114.3	465.2487	1393.751	-0.0193	-13.8	10	67035.7	7.32	HUMAN	F8VUJ3	Protein POC1B-GALNT4
19880	dirMS_041712_NAR_120mM_plus.10689.10689.3	3	5.79	1	1.21E+06		(R)EKLEME	(R)E\K\L E M\E|M E/A A/R(H)		109.52	446.2171	1336.623	0.0132	9.9	4.49	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)
19881	dirMS_041712_NAR_120mM_plus.14254.14254.3	3	5.79	1	2.66E+04	M313m	(R)RTVQSLI	(R)R T V Q S L/E|I/D/L/D S m R(N)	m:Oxidized methionine	127.45	560.2841	1662.848	15.9898	-3	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
19882	dirMS_041712_NAR_120mM_plus.7985.7985.2	2	5.79	0	1.42E+06		(R)HQGVM	(R)H/Q/G V M\V/G M G Q/K(D)		96.13	586.2888	1171.571	-0.0007	-0.6	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
19883	dirMS_041712_NAR_120mM_plus.9205.9205.3	3	5.79	2	3.66E+05	M49m	(R)TIEKFEK	(R)T I/E K/F E K E A A/E m G K(G)	m:Oxidized methionine	101.48	542.94	1610.809	15.996	0.7	4.94	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
19884	dirMS_041712_NAR_20mM_plus.16908.16908.2	2	5.79	0	1.75E+05		(K)LGGSAV	(K)L G G S A V|I S L E/G K|P L(-)		187.1	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
19885	dirMS_041712_NAR_20mM_plus.8678.8678.2	2	5.79	0	1.06E+05		(K)EQVANS	(K)E Q|V|A/N S\A F/V E R(C)		130.53	625.3102	1249.617	-0.004	-3.2	4.53	17664	8.77	HUMAN	H0Y6E4	Heat shock protein HSP 90-beta (Fragment)
19886	dirMS_041712_NAR_30mM_plus2.12184.12208.2	2	5.79	0	2.80E+05		(R)LAVYIDF	(R)L/A|V/Y I D R(V)		116.78	425.239	849.483	-0.0122	-14.3	5.83	74423.5	6.57	HUMAN	P02545	Prelamin-A/C
19887	dirMS_041712_NAR_40mM_plus2.14485.14485.3	3	5.79	0	2.80E+05		(K)IAILTCPF	(K)I/A I|L/T/C/P F E P P K P K(T)	C:Carbamidomethylation	153.25	537.6381	1610.898	0.0023	1.4	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
19888	dirMS_041712_NAR_40mM_plus2.6085.6085.2	2	5.79	0	1.78E+04		(R)NGYDYC	(R)N G Y|D|Y/G/Q|C R(L)	C:Carbamidomethylation	94.57	566.7355	1132.448	0.0161	14.2	5.83	25655.9	8.94	HUMAN	Q13242	Serine/arginine-rich splicing factor 9
19889	dirMS_041712_NAR_50mM_plus2.14326.14326.3	3	5.79	0	4.78E+05	S6s	(-)MVHKPs	(-)M V/H K/P s G/Q I\M/A V K(R)	s:N-acetylglucosamine (S)	143.6	543.6256	1425.771	203.0918	7.6	10	18603.3	6.84	HUMAN	J3KTI6	Dual-specificity mitogen-activated protein kinase kinase 4 (Fragment)
19890	dirMS_041712_NAR_50mM_plus2.19928.19928.3	3	5.79	0	3.74E+05		(K)NGGLGH	(K)N G\G L G H M/N\I|A|L/L/S D L T K(Q)		173.03	585.311	1753.927	-0.0081	-4.6	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
19891	dirMS_041712_NAR_60mM_plus.13127.13127.3	3	5.79	1	5.76E+05		(R)VVNGKV	(R)V/V/N G K/V/E Y F L K(W)		124.92	432.5826	1295.736	-0.0026	-2	8.47	11857.8	9.63	HUMAN	B8ZZ43	Chromobox homolog 3 (HP1 gamma homolog, Drosophila), isoform CRA_b
19892	dirMS_041712_NAR_60mM_plus.15866.15866.3	3	5.79	1	2.94E+04		(R)VEVERD	(R)V/E|V/E R D N L/A E\D/I M R(L)		139.05	563.613	1688.827	-0.0028	-1.6	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
19893	dirMS_041712_NAR_120mM_minus.11010.11010.3	3	5.78	1	5.95E+05		(R)RFDDAV	(R)R F D D A\V|V/Q/S D/M K(H)		114.73	470.8939	1410.668	-0.001	-0.7	4.43	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
19894	dirMS_041712_NAR_120mM_minus.17507.17507.4	4	5.78	2	3.09E+05		(R)NLKASLE	(R)N L K/A S L E/N S/L R E V E\A/R(Y)		150.33	458.0011	1828.988	-0.005	-2.7	6.23	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
19895	dirMS_041712_NAR_120mM_minus.17561.17561.4	4	5.78	2	1.63E+06		(R)GYSFTTT	(R)G Y S F/T/T T A E R E I V R D/I K(E)		150.62	497.2619	1986.029	-0.0033	-1.7	6.18	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
19896	dirMS_041712_NAR_120mM_minus.18918.18918.4	4	5.78	1	1.87E+05		(R)SLRDLTF	(R)S L R D\L\T/P E/H L/P\L L R(N)		158.72	415.7434	1659.954	-0.0023	-1.4	6.47	38779.2	5.93	HUMAN	Q96C86	m7GpppX diphosphatase
19897	dirMS_041712_NAR_120mM_minus.19462.19462.3	3	5.78	0	7.14E+05		(R)NSVSNF	(R)N\S/V\S/N/F L/H/S L E/R(G)		162.22	468.2346	1402.707	-0.0181	-12.9	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
19898	dirMS_041712_NAR_120mM_minus.6546.6546.2	2	5.78	0	5.54E+04		(K)LGIHEDS	(K)L G I/H/E/D\S Q N/R(K)		89.67	584.7891	1168.571	0.0004	0.3	5.32	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
19899	dirMS_041712_NAR_120mM_minus.7343.7343.2	2	5.78	1	9.63E+04		(R)LSVDYGI	(R)L/S|V/D Y G K K(S)		94.15	455.2555	909.504	-0.0003	-0.3	8.5	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
19900	dirMS_041712_NAR_30mM_minus2.12473.12473.2	2	5.78	0	1.25E+05		(K)IGVTVLS	(K)I/G|V/T/V L S R(I)		121.35	422.7649	844.525	-0.0026	-3	9.75	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
19901	dirMS_041712_NAR_30mM_minus2.14276.14276.2	2	5.78	0	3.51E+05		(R)VIDVGSE	(R)V I/D|V/G S E W/R(T)		130.73	530.7694	1060.542	-0.0107	-10.1	4.37	25558.6	9.3	HUMAN	B1APE1	General transcription factor IIB (Fragment)
19902	dirMS_041712_NAR_50mM_minus2.10052.10052.3	3	5.78	1	9.65E+04		(R)VFDKEG	(R)V F D K E G|N G T/V|M G A E I R(H)		125.6	574.9529	1722.848	-0.0038	-2.2	4.68	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
19903	dirMS_041712_NAR_50mM_minus2.16199.16199.3	3	5.78	1	4.43E+06		(R)VSFELFA	(R)V S/F/E L/F A D K V/P/K(T)		159.72	460.5908	1379.757	0.0009	0.7	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
19904	dirMS_041712_NAR_60mM_minus.14492.14492.3	3	5.78	0	1.24E+05		(K)QQGVLA	(K)Q\Q/G V/L A/L R P/Y L Q K(Q)		140.52	505.2973	1513.885	-0.0076	-5	9.99	62841.3	5.15	HUMAN	B3KVK7	Methionine--tRNA ligase, cytoplasmic
19905	dirMS_041712_NAR_120mM_plus.7169.7169.2	2	5.78	2	6.21E+05		(R)QFGKLH	(R)Q/F/G K/L/H T D/K K(Q)		91.1	601.3295	1201.669	-0.0171	-14.2	9.7	83881.6	9.35	HUMAN	Q13823	Nucleolar GTP-binding protein 2
19906	dirMS_041712_NAR_20mM_plus.13878.13878.2	2	5.78	0	3.21E+04	M178m	(K)GGIVGm	(K)G G I|V/G m/T L P I/A R(D)	m:Oxidized methionine	167.35	600.8402	1184.682	15.9911	-3.1	9.75	27150.8	7.95	HUMAN	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2
19907	dirMS_041712_NAR_20mM_plus.7305.7305.2	2	5.78	0	3.29E+05	M281m	(R)AEAESm	(R)A E|A|E/S/m Y Q I K(Y)	m:Oxidized methionine	118.6	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
19908	dirMS_041712_NAR_30mM_plus2.15217.15217.2	2	5.78	0	1.49E+05		(K)AFQNVF	(K)A F/Q/N|V/F A/P R(N)		132.4	525.2819	1049.553	0.0038	3.7	9.79	60786.2	8.94	HUMAN	B4DYH8	N-acetylglucosamine-6-sulfatase
19909	dirMS_041712_NAR_30mM_plus2.16824.16824.2	2	5.78	0	3.49E+05		(K)QLQEMI	(K)Q\L/Q E/M/L/G L/S K(V)		140.92	573.8112	1146.619	-0.0036	-3.1	6	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
19910	dirMS_041712_NAR_30mM_plus2.19394.19394.2	2	5.78	0	1.18E+05		(K)VQIAVA	(K)V Q\I/A/V/A\N A/Q E\L L/Q R(M)		155.67	776.9425	1552.881	-0.0028	-1.8	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
19911	dirMS_041712_NAR_30mM_plus2.21397.21397.2	2	5.78	0	8.05E+04		(R)SPVTFLS	(R)S P\V/T/F L S D/L R(S)		167.13	567.8152	1134.615	0.0078	6.9	5.55	269273.3	6.66	HUMAN	A5YKK6	CCR4-NOT transcription complex subunit 1
19912	dirMS_041712_NAR_120mM_minus.17481.17481.4	4	5.77	1	5.43E+05		(R)GFGHIG	(R)G F G H I\G I A\V/P/D/V Y S A C K R(F)	C:Carbamidomethylation	150.4	487.502	1946.991	-0.0044	-2.2	8.6	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
19913	dirMS_041712_NAR_120mM_minus.19987.19987.3	3	5.77	0	7.83E+04		(R)INLWHL	(R)I/N L/W H/L E I T D R(S)		165.22	470.5897	1409.754	0.001	0.7	5.32	52204.6	5.82	HUMAN	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
19914	dirMS_041712_NAR_120mM_minus.9139.9139.2	2	5.77	0	5.02E+05		(K)HFVALST	(K)H F|V|A\L S T N/T T K(V)		103.5	609.8267	1218.648	-0.0016	-1.3	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
19915	dirMS_041712_NAR_20mM_minus.12108.12108.2	2	5.77	0	9.65E+04		(K)LVSIGAE	(K)L V/S\I/G/A E/E I V D G N\A K(M)		170.62	757.9044	1514.806	-0.0045	-3	4.14	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
19916	dirMS_041712_NAR_20mM_minus.12171.12171.3	3	5.77	0	2.80E+05	M73m	(R)AVLVDLI	(R)A V L V D L E/P/G T m/D/S V R(S)	m:Oxidized methionine	171.27	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
19917	dirMS_041712_NAR_30mM_minus2.18906.18906.2	2	5.77	0	1.32E+04		(R)NTWLYC	(R)N T|W/L/Y Q A L/R(E)		157.48	582.8109	1164.616	-0.0015	-1.3	8.75	49457.5	6.47	HUMAN	P56545	C-terminal-binding protein 2
19918	dirMS_041712_NAR_40mM_minus2.16071.16071.3	3	5.77	1	7.20E+05		(R)ELAILLG	(R)E L|A I/L L G M L/D P A E K D E K(G)		189.48	629.0034	1884.999	-0.003	-1.6	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
19919	dirMS_041712_NAR_50mM_minus2.15591.15591.3	3	5.77	0	1.99E+05		(R)QVVQGI	(R)Q V/V/Q/G\L\L/S E T Y/L/E A H R(I)		156.78	614.9953	1842.971	0.0005	0.3	5.4	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
19920	dirMS_041712_NAR_50mM_minus2.7313.7313.3	3	5.77	1	8.39E+04		(K)ELQAAG	(K)E L/Q|A|A G K S P E D/L E R(L)		108.02	514.9262	1542.776	-0.0118	-7.6	4.41	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
19921	dirMS_041712_NAR_60mM_minus.14551.14551.3	3	5.77	0	1.43E+05		(K)NFDLRP(	(K)N/F/D/L R/P G V I V R(-)		141.03	429.2503	1285.738	-0.0012	-0.9	9.6	33192.3	6.77	HUMAN	B4DN45	S-adenosylmethionine synthase
19922	dirMS_041712_NAR_20mM_plus.10352.10352.2	2	5.77	0	8.32E+04		(K)AVYTQD	(K)A V|Y|T Q/D C/P L/A A A K(A)	C:Carbamidomethylation	144.03	704.3502	1407.694	-0.0006	-0.4	5.88	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
19923	dirMS_041712_NAR_20mM_plus.14348.14348.3	3	5.77	0	3.00E+04	M61m	(R)IIPGFmC	(R)I I/P G F m C Q G G D F T/R(H)	C:Carbamidomethylation m:Oxid	170.67	538.9176	1598.745	15.9929	-1.3	5.84	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
19924	dirMS_041712_NAR_20mM_plus.15099.15099.2	2	5.77	1	1.61E+05	N88n	(R)nFAEPCI	(R)n F A/E|P/C E D S R R(S)	C:Carbamidomethylation n:N-ac	176.2	792.3469	1380.596	203.0904	7	4.68	12980.5	9.75	HUMAN	C9JXY5	Sentan
19925	dirMS_041712_NAR_20mM_plus.15273.15273.3	3	5.77	0	2.04E+05	M73m	(R)AILVDLE	(R)A I\L V D\L E/P/G T/m D/S V R(S)	m:Oxidized methionine	177.03	544.6139	1615.836	15.9912	-2.3	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
19926	dirMS_041712_NAR_20mM_plus.17157.17157.2	2	5.77	0	8.67E+04		(R)AIVAIEN	(R)A I V\A\I/E/N/P A D V/S V/I\S S R(N)		189.1	870.9764	1740.949	-0.0035	-2	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
19927	dirMS_041712_NAR_20mM_plus.9874.9874.2	2	5.77	0	6.91E+04		(R)ALGQNF	(R)A L G Q|N/P/T N A/E V L K(V)		140.02	677.8702	1354.733	0.0006	0.5	6.05	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
19928	dirMS_041712_NAR_30mM_plus2.14226.14226.2	2	5.77	0	5.73E+05		(K)CCSGAII'	(K)C C|S\G A/I\I V L/T K(S)	C:Carbamidomethylation	128.2	611.3189	1221.633	-0.0025	-2	8.75	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
19929	dirMS_041712_NAR_30mM_plus2.15274.15274.2	2	5.77	0	3.09E+05		(R)GGYIGST	(R)G G Y|I/G\S/T Y/F E/R(C)		132.57	625.3004	1249.585	0.0087	7	6	21184.9	7.82	HUMAN	P61081	NEDD8-conjugating enzyme Ubc12
19930	dirMS_041712_NAR_30mM_plus2.22011.22011.2	2	5.77	0	1.03E+05		(K)NFYFLEI	(K)N F|Y|F/L E M N T R(L)		170.5	667.8205	1334.62	0.0139	10.4	6	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
19931	dirMS_041712_NAR_30mM_plus2.5393.5393.3	3	5.77	0	6.70E+04		(R)GGSGGS	(R)G/G S G G S Y G G G G S G G G/Y/G\G G S\G/S R(G)		82.82	597.9128	1791.728	-0.0039	-2.2	8.59	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
19932	dirMS_041712_NAR_30mM_plus2.6938.6938.2	2	5.77	0	4.50E+05		(K)CNLCYR(	(K)C N|L/C Y R(V)	C:Carbamidomethylation	91.5	443.1849	885.371	-0.008	-9.1	8.75	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
19933	dirMS_041712_NAR_50mM_plus2.10511.10511.3	3	5.77	0	5.29E+04		(R)LQAQQI	(R)L Q/A Q Q D\A V/N I V/C H S K(T)	C:Carbamidomethylation	123.17	570.9571	1710.859	-0.0024	-1.4	6.74	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
19934	dirMS_041712_NAR_50mM_plus2.12000.12000.3	3	5.77	1	4.88E+05	M327m	(R)VAGGPC	(R)V/A|G/G P Q m I/Q/L S L D G K R(L)	m:Oxidized methionine	131.12	562.6377	1669.905	15.9931	-1	8.72	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
19935	dirMS_041712_NAR_60mM_plus.10392.10392.3	3	5.77	0	9.73E+05		(R)KPLLESG	(R)K\P L\L\E/S G T L/G T K(G)		112.1	415.2483	1243.726	0.0047	3.8	8.59	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
19936	dirMS_041712_NAR_20mM_minus.10357.10357.3	3	5.76	0	3.83E+03	M4040m	(R)SQVmDI	(R)S Q\V m D E A/T/A L/Q L R(E)	m:Oxidized methionine	152.85	493.2546	1461.737	16.0126	12	4.37	533778	5.74	HUMAN	Q15149	Plectin
19937	dirMS_041712_NAR_20mM_minus.9930.9930.2	2	5.76	0	9.65E+04	M196m	(K)DAGTIA(	(K)D A/G/T I|A/G/L N V m R(I)	m:Oxidized methionine	149.37	617.3216	1217.631	16.0052	8.4	5.84	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
19938	dirMS_041712_NAR_30mM_minus2.14018.14018.2	2	5.76	0	2.85E+05		(K)CDFPIM	(K)C D|F|P I/M K(F)	C:Carbamidomethylation	129.62	455.7144	910.416	0.0054	5.9	5.84	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
19939	dirMS_041712_NAR_30mM_minus2.16062.16114.2	2	5.76	0	5.21E+05		(R)DFFLAN/	(R)D F|F|L\A|N A S R(A)		141.95	520.763	1040.516	0.0028	2.6	5.84	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
19940	dirMS_041712_NAR_30mM_minus2.17868.17868.2	2	5.76	0	2.20E+05		(K)EGMNIV	(K)E G\M N I|V E/A M E/R(F)		152.3	639.7955	1278.582	0.002	1.6	4.25	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
19941	dirMS_041712_NAR_40mM_minus2.13536.13536.3	3	5.76	0	3.00E+04		(K)YVDTPF(	(K)Y V/D\T|P F G K P S D A L I L G K(I)		163.33	607.6637	1820.979	-0.0027	-1.5	5.96	33699.1	7.18	HUMAN	B4DUC8	S-methyl-5'-thioadenosine phosphorylase
19942	dirMS_041712_NAR_50mM_minus2.12631.12631.3	3	5.76	1	1.14E+06	M320m	(K)YmACCL	(K)Y m|A\C C L L Y R/G D V V/P K(E)	C:Carbamidomethylation m:Oxid	140.9	620.9644	1844.886	15.9931	-1	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3

19943	dirMS_041712_NAR_50mM_minus2.8640.8640.3	3	5.76	1	8.70E+04		(R)LLDEEEA	(R)L/L\D/E E E A T/D N D L R A/K(F)		117.43	577.9535	1731.84	0.0064	3.7	4.02	96649	6.13	HUMAN	Q8WUM4	Programmed cell death 6-interacting protein
19944	dirMS_041712_NAR_60mM_minus.16710.16710.3	3	5.76	1	2.87E+05		(R)LKLPAV\	(R)L K L/P A V/V/T/A D/L R(L)		153.82	432.6056	1295.805	-0.0023	-1.8	8.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
19945	dirMS_041712_NAR_120mM_plus.16372.16372.4	4	5.76	2	1.47E+06		(K)SIYGERF	(K)S I/Y G E/R F P D E N F K/L K(H)		138.47	461.4898	1842.939	-0.0011	-0.6	5.9	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
19946	dirMS_041712_NAR_20mM_plus.14195.14195.3	3	5.76	0	7.24E+03		(R)VPTANV	(R)V P T A N V\S V\V/D/L/T C R(L)	C:Carbamidomethylation	169.75	510.9348	1530.795	-0.0046	-3	5.81	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
19947	dirMS_041712_NAR_20mM_plus.16931.16931.2	2	5.76	0	1.07E+05		(R)ELLIIGG\	(R)E L|L\I/I/G/G V A A R(D)		187.43	556.3437	1111.683	-0.0032	-2.9	6.1	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
19948	dirMS_041712_NAR_20mM_plus.18130.18130.3	3	5.76	0	1.71E+05		(R)LSVLGAI	(R)L S V L G A I/T/S/V Q/Q R(L)		196.13	457.9354	1371.795	-0.0038	-2.8	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
19949	dirMS_041712_NAR_30mM_plus2.12152.12152.2	2	5.76	0	1.44E+06		(K)GIYAVGI	(K)G I/Y|A|V/G D V C G K(A)	C:Carbamidomethylation	117.63	569.7798	1138.556	-0.0038	-3.3	5.83	56826.6	9.16	HUMAN	P00390	Glutathione reductase, mitochondrial
19950	dirMS_041712_NAR_30mM_plus2.16792.16792.2	2	5.76	1	2.81E+05		(K)AVESLR/	(K)A V/E S/L R A I S(-)		141.23	473.2687	945.536	-0.0062	-6.6	6.05	16786.7	4.97	HUMAN	C9J9C1	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform (Fragment)
19951	dirMS_041712_NAR_30mM_plus2.18382.18382.2	2	5.76	0	3.76E+05		(R)SQVEEEI	(R)S Q|V/E|E E L F S V R(V)		149.5	661.8302	1322.659	-0.0055	-4.2	4.25	533778	5.74	HUMAN	Q15149	Plectin
19952	dirMS_041712_NAR_30mM_plus2.19790.19790.2	2	5.76	0	1.51E+05		(R)YAFVMF	(R)Y/A|F V M/F K(T)		157.65	453.2369	905.459	0.0076	8.3	8.59	103045.5	7.1	HUMAN	B9ZVT1	RNA-binding protein 12B
19953	dirMS_041712_NAR_30mM_plus2.9567.9567.2	2	5.76	0	2.09E+05		(R)LAAVDV	(R)L/A|A|V/D V S A R(A)		103.52	451.2545	901.51	-0.0084	-9.4	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin
19954	dirMS_041712_NAR_50mM_plus2.11464.11464.3	3	5.76	1	2.61E+05		(K)CATITPD	(K)C A|T/I/T/P D E A R V E E F K(L)	C:Carbamidomethylation	127.75	589.2842	1765.843	-0.0045	-2.5	4.41	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
19955	dirMS_041712_NAR_50mM_plus2.12724.12724.3	3	5.76	0	4.57E+05		(K)YYVTIID/	(K)Y/Y\V T I I/D/A/P/G H R(D)		135.28	468.9142	1404.727	0.001	0.7	6.74	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
19956	dirMS_041712_NAR_50mM_plus2.18316.18316.3	3	5.76	1	1.43E+06		(R)ELIKVLEI	(R)E L I K V L\E E A N|Q|A I N|P K(L)		164.18	603.6741	1809.012	-0.0039	-2.2	4.79	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
19957	dirMS_041712_NAR_50mM_plus2.7727.7727.3	3	5.76	1	1.77E+05		(R)IVEQDTI	(R)I V/E Q/D T/M/P P K G V R(H)		106.13	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
19958	dirMS_041712_NAR_60mM_plus.19245.19245.3	3	5.76	0	4.07E+05		(K)TEASLV\	(K)T E/A/S L V|W F T/P P R(T)		159.25	468.5804	1403.732	-0.0051	-3.7	5.66	55537.7	9.13	HUMAN	Q9UHN1	DNA polymerase subunit gamma-2, mitochondrial
19959	dirMS_041712_NAR_60mM_plus.5707.5707.3	3	5.76	0	5.51E+04		(K)CLACES/	(K)C/L|A/C E S A K/P G T K(S)	C:Carbamidomethylation	88.02	441.2128	1321.624	0	0	8.59	158989.2	9.5	HUMAN	F6QR24	Nuclear pore complex protein Nup153
19960	dirMS_041712_NAR_60mM_plus.8299.8299.3	3	5.76	0	6.94E+05		(R)QYDISDI	(R)Q Y/D/I/S D/P Q/R P R(L)		101.32	458.8968	1374.676	-0.0002	-0.1	5.96	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
19961	dirMS_041712_NAR_20mM_minus.7121.7121.2	2	5.75	0	1.64E+05		(R)AAQVA(	(R)A A Q/V/A/Q D E E I A R(L)		118.83	650.8255	1300.649	-0.0054	-4.2	4.14	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
19962	dirMS_041712_NAR_30mM_minus2.12823.12823.2	2	5.75	0	5.13E+05		(R)VNFAMI	(R)V N|F/A/M N/V G K(A)		124.1	490.2513	979.503	-0.0076	-7.8	8.72	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
19963	dirMS_041712_NAR_30mM_minus2.17384.17384.2	2	5.75	0	2.60E+05		(R)NGGQIL	(R)N G\G Q|I|L I/A\D L R(G)		148.73	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
19964	dirMS_041712_NAR_30mM_minus2.17569.17569.2	2	5.75	1	2.16E+05	M799m	(K)DLLmND	(K)D L|L m/N D R L P G K(K)	m:Oxidized methionine	149.7	644.3426	1271.678	16.0003	4.2	5.96	165919.5	8.96	HUMAN	Q9NTI5	Sister chromatid cohesion protein PDS5 homolog B
19965	dirMS_041712_NAR_40mM_minus2.8164.8164.3	3	5.75	0	2.24E+05	M35m	(K)AASDIAr	(K)A A/S D\I|A m T E|L/P P T H P I R(L)	m:Oxidized methionine	128.48	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
19966	dirMS_041712_NAR_50mM_minus2.16454.16454.3	3	5.75	1	6.62E+04	M590m S5	(K)LLSmAY	(K)L L S m A Y s/A V\G\K L/S\S/R(M)	m:Oxidized methionine s:N-a	162.95	601.3217	1582.862	219.0884	7.8	9.99	225629.8	9.3	HUMAN	J3KN16	Protein KIAA0368
19967	dirMS_041712_NAR_50mM_minus2.9984.9984.3	3	5.75	1	1.18E+05		(R)VGEPVA	(R)V/G/E/P V/A L S E E E R L K(L)		124.97	519.2824	1555.833	0	0	4.49	8516.9	5.1	HUMAN	E9PIL8	Splicing factor 3B subunit 2 (Fragment)
19968	dirMS_041712_NAR_60mM_minus.10443.10443.3	3	5.75	0	2.01E+05		(R)LSNLAL\	(R)L S/N L A/L/V K P E\K(T)		118.57	404.5829	1211.736	-0.0017	-1.4	8.59	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
19969	dirMS_041712_NAR_60mM_minus.10691.10691.3	3	5.75	1	1.05E+06		(K)TAVCDIF	(K)T A/V/C D I/P/P R G L K(M)	C:Carbamidomethylation	118.65	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
19970	dirMS_041712_NAR_60mM_minus.11414.11414.3	3	5.75	0	6.67E+04		(K)TSEVDL/	(K)T\S\E/V D L/A/K P L V K(F)		123.52	433.9193	1299.752	-0.0085	-6.5	5.73	17178.3	5.63	HUMAN	C9IZF9	Programmed cell death 6-interacting protein (Fragment)
19971	dirMS_041712_NAR_60mM_minus.14381.14381.3	3	5.75	1	1.19E+05		(R)KLVILEG	(R)K L V I/L E/G E L|E R(A)		139.82	433.5934	1298.768	-0.0022	-1.7	4.79	12073.4	4.67	HUMAN	K7EMU5	Tropomyosin alpha-4 chain (Fragment)
19972	dirMS_041712_NAR_120mM_plus.7401.7401.3	3	5.75	1	1.80E+06	M281m	(R)SRAEAE!	(R)S R A\E\A\E|S|m/Y Q I K(Y)	m:Oxidized methionine	92.92	476.8977	1412.684	15.9947	-0.1	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
19973	dirMS_041712_NAR_20mM_plus.10021.10074.2	2	5.75	0	6.11E+05		(K)LVSESSD	(K)L V|S E S S D V/L P K(-)		141.47	587.3192	1173.636	-0.005	-4.3	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
19974	dirMS_041712_NAR_20mM_plus.14180.14180.3	3	5.75	0	7.24E+03		(R)VPTANV	(R)V P T A N V S\V V/D/L/T/C R(L)	C:Carbamidomethylation	169.75	510.9348	1530.795	-0.0046	-3	5.81	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
19975	dirMS_041712_NAR_20mM_plus.16950.16950.3	3	5.75	0	3.00E+05		(K)VQIAVA	(K)V Q\I A\V A N A|Q/E/L/L Q/R(M)		187.88	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
19976	dirMS_041712_NAR_20mM_plus.17719.17719.3	3	5.75	0	1.72E+05	M90m	(R)LFVGNLI	(R)L F V G N L/P/P D I/T E/E E m R(K)	m:Oxidized methionine	193.38	625.9762	1859.921	15.9933	-0.9	4	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
19977	dirMS_041712_NAR_20mM_plus.18316.18316.2	2	5.75	0	5.11E+04		(K)FIIPQIVK	(K)F I|I/P Q I V K(Y)		197.13	479.3081	957.613	-0.0042	-4.4	8.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
19978	dirMS_041712_NAR_30mM_plus2.4569.4569.2	2	5.75	0	3.58E+05		(R)SYTSGP(	(R)S Y T/S/G/P G S/R(I)		73.72	456.2155	911.422	0.002	2.2	8.46	19288.4	10.19	HUMAN	F8VQY3	Keratin, type II cytoskeletal 8 (Fragment)
19979	dirMS_041712_NAR_30mM_plus2.5975.5975.2	2	5.75	0	3.57E+04		(R)VGPNAF	(R)V/G/P N/A|P E/E K(K)		85.55	470.7391	940.473	-0.0025	-2.7	4.53	66105.7	7.3	HUMAN	A8MQB8	Fragile X mental retardation protein 1
19980	dirMS_041712_NAR_50mM_plus2.11811.11811.3	3	5.75	0	3.17E+04		(K)SNMGH	(K)S N/M/G\H P E\P A S/G L A A L A K(V)		130.23	550.9462	1650.827	-0.0028	-1.7	6.47	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
19981	dirMS_041712_NAR_50mM_plus2.22065.22065.3	3	5.75	1	5.90E+05		(K)AGFLDLI	(K)A/G|F L D/L K D\F L/P K(E)		188.88	455.2587	1363.762	-0.0005	-0.3	6	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
19982	dirMS_041712_NAR_50mM_plus2.7378.7378.3	3	5.75	1	1.18E+05		(K)AAIAQLI	(K)A A/I/A Q L N G K E/V K(G)		104.82	414.5758	1241.721	-0.0084	-6.7	8.64	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
19983	dirMS_041712_NAR_60mM_plus.14720.14720.3	3	5.75	1	5.21E+05		(K)NKDQGT	(K)N K D Q G T Y\E/D\Y/V/E/G L R(V)		133.53	596.2816	1786.824	0.006	3.4	4.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
19984	dirMS_041712_NAR_60mM_plus.15979.15979.3	3	5.75	0	2.82E+05		(K)NFDLRP(	(K)N F/D/L/R P G V I/V/R(-)		140.07	429.248	1285.738	-0.0081	-6.3	9.6	33192.3	6.77	HUMAN	B4DN45	S-adenosylmethionine synthase
19985	dirMS_041712_NAR_120mM_minus.12340.12340.3	3	5.74	1	3.47E+05		(K)LFNLSKE	(K)L F/N/L S K E D D/V R(Q)		121.27	445.9006	1335.69	-0.0031	-2.3	4.56	25082	11.29	HUMAN	A2A3R5	40S ribosomal protein S6
19986	dirMS_041712_NAR_120mM_minus.6073.6073.3	3	5.74	1	5.64E+05		(K)TCEESSF	(K)T/C E E|S/S/F/C K R(Q)	C:Carbamidomethylation	86.8	435.1849	1303.541	-0.0004	-0.3	5.81	10576.1	11.44	HUMAN	E9PRF8	Neutral alpha-glucosidase AB
19987	dirMS_041712_NAR_120mM_minus.6756.6756.2	2	5.74	1	1.62E+05		(K)VQVEYK	(K)V Q|V/E/Y K/G E\T\K(S)		91.35	590.8128	1180.621	-0.0025	-2.1	6.11	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
19988	dirMS_041712_NAR_120mM_minus.9477.9477.3	3	5.74	0	8.41E+05		(K)SPQYCQ	(K)S P Q\Y/C/Q|V I/H R(L)	C:Carbamidomethylation	106.35	429.8855	1287.626	0.0157	12.2	8.49	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
19989	dirMS_041712_NAR_20mM_minus.13052.13052.2	2	5.74	0	9.72E+05	M73m	(R)AILVDLE	(R)A I L|V D\L|E/P G T/m D S V R(S)	m:Oxidized methionine	182.58	816.4184	1615.836	15.9935	-0.8	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
19990	dirMS_041712_NAR_30mM_minus2.15842.15842.2	2	5.74	0	4.68E+04		(R)INEILSN/	(R)I N|E|I|L S N/A L K(R)		139.15	557.8242	1114.647	-0.0055	-5	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
19991	dirMS_041712_NAR_30mM_minus2.19099.19099.2	2	5.74	1	2.15E+05		(K)SKLEFSI\	(K)S K L E F S/I\Y|P\A|P(-)		158.93	626.334	1251.662	-0.0012	-1	5.72	21962.5	5.85	HUMAN	C9JJQ8	Tubulin alpha-4A chain (Fragment)
19992	dirMS_041712_NAR_50mM_minus2.17161.17161.3	3	5.74	0	7.69E+03		(K)ALSAIAD	(K)A/L S/A|I A D L L/T N E H E R(V)		165.92	551.6261	1652.86	0.0035	2.1	4.65	105417.2	6.41	HUMAN	C9JZR2	Catenin delta-1
19993	dirMS_041712_NAR_50mM_minus2.6682.6682.3	3	5.74	1	2.17E+04	M678m	(R)QNSSSG	(R)Q N|S/S S G S P R m E I\C S G S N K(T)	C:Carbamidomethylation m:Oxid	104.62	647.9543	1925.844	16.0043	4.9	8.75	169445	9.13	HUMAN	Q15648	Mediator of RNA polymerase II transcription subunit 1
19994	dirMS_041712_NAR_120mM_plus.7373.7373.3	3	5.74	1	7.86E+05		(R)KTGQAP	(R)K\T G Q A\P G Y|S|Y/T A/A N K(N)		91.62	519.5943	1556.77	-0.002	-1.3	9.53	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
19995	dirMS_041712_NAR_120mM_plus.7489.7489.2	2	5.74	0	1.77E+05		(R)LYVHEA\	(R)L/Y/V/H E A V K(A)		93.27	479.7757	958.536	0.0085	8.8	6.75	533778	5.74	HUMAN	Q15149	Plectin
19996	dirMS_041712_NAR_20mM_plus.16798.16798.2	2	5.74	0	1.01E+05		(K)VLTPELY	(K)V L/T|P/E L Y A/E L R(A)		187.45	652.3664	1303.726	-0.0001	-0.1	4.53	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
19997	dirMS_041712_NAR_20mM_plus.8010.8010.3	3	5.74	0	4.57E+05	M239m	(K)EVDEQn	(K)E V/D E/Q m\L/N V/Q N K(N)	m:Oxidized methionine	125.12	488.2328	1446.689	15.9945	-0.3	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
19998	dirMS_041712_NAR_30mM_plus2.17015.17015.2	2	5.74	0	2.20E+05		(R)GLGLDD	(R)G L|G\L/D D/A/L|E P R(Q)		142.2	578.3042	1155.6	0.0007	0.6	4.03	51326.8	5.49	HUMAN	Q9Y230	RuvB-like 2
19999	dirMS_041712_NAR_30mM_plus2.19857.19857.2	2	5.74	0	1.52E+05		(K)SNSVEM	(K)S N\S/V/E/M D W/V L K(H)		157.77	654.3191	1307.63	0.0009	0.7	4.37	49548	5.89	HUMAN	P55795	Heterogeneous nuclear ribonucleoprotein H2
20000	dirMS_041712_NAR_30mM_plus2.4421.4421.2	2	5.74	0	3.69E+05		(R)SYTSGP(	(R)S Y|T/S/G P G S R(I)		72.6	456.2155	911.422	0.002	2.2	8.46	19288.4	10.19	HUMAN	F8VQY3	Keratin, type II cytoskeletal 8 (Fragment)
20001	dirMS_041712_NAR_50mM_plus2.15592.15592.3	3	5.74	1	9.15E+05		(K)EAFSLFD	(K)E A/F S/L/F/D/K D/G D G T I T T K(E)		149.95	615.6348	1844.891	-0.0014	-0.8	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
20002	dirMS_041712_NAR_50mM_plus2.8599.8599.3	3	5.74	0	5.20E+04		(K)EQIVPKF	(K)E Q|I/V/P K/P E E E V A Q K(K)		112.15	541.9524	1623.859	-0.0162	-10	4.49	17265	10.31	HUMAN	B4E3C2	60S ribosomal protein L17
20003	dirMS_041712_NAR_120mM_minus.10303.10303.4	4	5.73	2	2.05E+05		(K)QLQEED	(K)Q|L\Q/E|E D L K A Q A Q/L Q K R(Y)		110.22	482.2659	1926.04	0.0015	0.8	6.18	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
20004	dirMS_041712_NAR_120mM_minus.6024.6024.3	3	5.73	1	5.64E+05		(K)TCEESSF	(K)T|C/E E S S F/C K/R(Q)	C:Carbamidomethylation	86.8	435.1849	1303.541	-0.0004	-0.3	5.81	10576.1	11.44	HUMAN	E9PRF8	Neutral alpha-glucosidase AB
20005	dirMS_041712_NAR_120mM_minus.8022.8022.3	3	5.73	0	9.40E+04		(R)SCYDLS(	(R)S C|Y/D L S/C H/A R(A)	C:Carbamidomethylation	97.97	423.5114	1268.515	0.005	3.9	6.46	83905.8	6.62	HUMAN	P41250	Glycine--tRNA ligase
20006	dirMS_041712_NAR_20mM_minus.11691.11691.2	2	5.73	0	4.23E+05		(R)GALQNI	(R)G A L Q/N|I/I\P A S T G A A/K(A)		165.05	706.3976	1411.79	-0.0024	-1.7	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
20007	dirMS_041712_NAR_30mM_minus2.12361.12361.2	2	5.73	0	3.29E+05		(K)NIILGGV	(K)N/I|I|L G G/V/K(A)		121.02	407.263	813.519	-0.0005	-0.7	8.75	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
20008	dirMS_041712_NAR_30mM_minus2.16442.16442.2	2	5.73	0	2.53E+05		(R)ASLEAAI	(R)A S L|E/A/A/I/A D A E Q R(G)		143.58	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
20009	dirMS_041712_NAR_50mM_minus2.11485.11485.3	3	5.73	0	9.30E+04		(R)DLQSNV	(R)D L Q/S N V E H L T E/K(M)		133.7	471.5727	1412.702	0.0019	1.4	4.65	23167	8.94	HUMAN	B1APP8	6-phosphofructokinase type C
20010	dirMS_041712_NAR_20mM_plus.8076.8076.2	2	5.73	0	1.05E+05		(K)VTEDTS!	(K)V T/E/D T S S\V/L R(S)		126.02	553.7889	1106.569	0.0017	1.6	4.37	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
20011	dirMS_041712_NAR_30mM_plus2.12961.13151.2	2	5.73	0	6.42E+05		(K)NQAVNI	(K)N/Q|A/V/N F L/R(M)		121.7	481.2676	961.521	0.0065	6.8	9.75	22166.1	7.91	HUMAN	Q7LBR1	Charged multivesicular body protein 1b
20012	dirMS_041712_NAR_30mM_plus2.14498.14498.3	3	5.73	0	1.03E+04		(K)VNQIGS'	(K)V N Q\I G S\V/T/E/S/I Q/A C K(L)	C:Carbamidomethylation	127.72	545.28	1633.821	0.0041	2.5	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
20013	dirMS_041712_NAR_30mM_plus2.20724.20724.2	2	5.73	1	2.44E+05	S189s	(K)TKLLVsD	(K)T K/L L/V s D K(S)	s:N-acetylglucosamine (S)	162.95	553.831	903.551	203.1038	22	8.26	54496.9	9.31	HUMAN	Q6P461	Acyl-coenzyme A synthetase ACSM6, mitochondrial
20014	dirMS_041712_NAR_30mM_plus2.20872.20872.2	2	5.73	0	2.51E+05		(R)ASLSLW	(R)A S L/S/L/W/Q A M E K(G)		163.15	632.3231	1263.64	-0.0013	-1	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
20015	dirMS_041712_NAR_30mM_plus2.20983.20983.2	2	5.73	0	2.99E+04		(R)QTLMW	(R)Q T L M\W|S A T W P K(E)		164.97	674.8389	1348.672	-0.0013	-1	8.75	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
20016	dirMS_041712_NAR_30mM_plus2.21170.21170.2	2	5.73	0	2.85E+05		(R)FDAMPF	(R)F/D|A\M/P F T L/R(A)		166.32	549.276	1097.545	-0.0001	-0.1	5.84	42088	5.39	HUMAN	F8VTY8	Proliferation-associated protein 2G4
20017	dirMS_041712_NAR_30mM_plus2.21735.21735.2	2	5.73	0	1.77E+05		(K)ALELNM	(K)A/L/E\L N M L/S/L K(G)		169.52	566.3204	1131.644	-0.0107	-9.4	6.05	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
20018	dirMS_041712_NAR_50mM_plus2.10460.10460.3	3	5.73	0	1.42E+05		(R)ILSKPIE\	(R)I L/S K P I E\V/Q/V/G G R(S)		122.35	465.9487	1395.832	-0.0003	-0.2	8.75	117873.5	9.45	HUMAN	Q7L014	Probable ATP-dependent RNA helicase DDX46
20019	dirMS_041712_NAR_50mM_plus2.10775.10775.3	3	5.73	0	1.17E+04		(K)AVMEQ!	(K)A V M E/Q S G/A W V Q L S Q/K(-)		125.62	554.6155	1661.832	0.0004	0.2	6.05	18670.2	9.84	HUMAN	F8VWX1	RNA-binding protein Nova-1 (Fragment)
20020	dirMS_041712_NAR_50mM_plus2.10934.10934.3	3	5.73	0	2.31E+05		(K)TKPYIQ\	(K)T K P Y\I Q V/D\I/G/G G Q T K(T)		125.32	535.6231	1604.864	-0.0095	-5.9	8.17	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
20021	dirMS_041712_NAR_50mM_plus2.11935.11935.3	3	5.73	1	3.08E+05		(K)VEAQVY	(K)V E|A Q V/Y I/L S K E E G G R(H)		130.6	559.9637	1677.881	-0.0041	-2.4	4.79	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
20022	dirMS_041712_NAR_50mM_plus2.20878.20878.3	3	5.73	1	4.35E+04		(R)ITSEAED	(R)I T/S E A E D L V/A N/F F/P K K(L)		178	603.6541	1808.943	0.0049	2.7	4.68	14931.6	5.53	HUMAN	B7Z8D3	Proteasome activator complex subunit 3
20023	dirMS_041712_NAR_60mM_plus.6584.6584.3	3	5.73	0	2.19E+05		(R)CPPGVV	(R)C P/P G V\V|P A C H N S/K(D)	C:Carbamidomethylation	92.8	474.8947	1422.662	0.0079	5.5	8.76	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
20024	dirMS_041712_NAR_60mM_plus.9544.9544.3	3	5.73	2	7.11E+05		(R)CEAAFKI	(R)C/E A A F K L K E I\A/R(R)	C:Carbamidomethylation	107.58	479.2585	1435.773	-0.0116	-8.1	8.59	292339.6	6.05	HUMAN	Q9HCK8	Chromodomain-helicase-DNA-binding protein 8
20025	dirMS_041712_NAR_120mM_minus.7704.7704.3	3	5.72	0	3.74E+05		(R)AFHNEA	(R)A F H N E\A\Q V|N/P E R(K)		96.65	471.229	1411.671	0.0011	0.8	5.4	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
20026	dirMS_041712_NAR_120mM_minus.8732.8732.3	3	5.72	1	1.37E+05		(R)LRDTEEI	(R)L R D T\E|E/M/L/S K(K)		102.05	407.877	1221.614	0.0021	1.7	4.68	24949.7	4.76	HUMAN	Q9H444	Charged multivesicular body protein 4b
20027	dirMS_041712_NAR_20mM_minus.7069.7069.2	2	5.72	0	2.40E+05	M33m	(R)IDEmPE/	(R)I/D|E m|P E A A V/K(S)	m:Oxidized methionine	118.12	559.7733	1102.545	15.9944	-0.4	4.14	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
20028	dirMS_041712_NAR_20mM_minus.9373.9373.2	2	5.72	0	1.40E+05		(K)VLQATV	(K)V L/Q A T V V/A V/G S/G S K(G)		143.35	658.3754	1315.758	-0.0145	-11	8.72	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
20029	dirMS_041712_NAR_30mM_minus2.13039.13039.2	2	5.72	1	2.68E+05	T620t	(K)DTRLLtF	(K)D/T R/L L t F K(A)	t:N-acetylglucosamine (T)	124.45	598.8338	993.573	203.0876	6.8	8.75	80959.4	9.31	HUMAN	E7EPX9	EGF-like module-containing mucin-like hormone receptor-like 1
20030	dirMS_041712_NAR_50mM_minus2.14050.14050.3	3	5.72	0	6.70E+04		(R)EALAEA/	(R)E A|L/A/E/A/A L E S P R P A L V R(S)		148.12	598.3345	1792.992	-0.0026	-1.5	4.79	22148.2	5.87	HUMAN	B3KY21	Na(+)/H(+) exchange regulatory cofactor NHE-RF1
20031	dirMS_041712_NAR_120mM_plus.10125.10125.4	4	5.72	0	1.57E+06		(K)NLPLAD(	(K)N L/P/L/A D Q/G S S H H I T\V/K(I)		106.5	429.9809	1716.903	-0.001	-0.6	6.92	334221.3	6.44	HUMAN	P15924	Desmoplakin
20032	dirMS_041712_NAR_120mM_plus.8612.8612.3	3	5.72	0	1.28E+06		(R)RPELED!	(R)R P E L E|D/S\T/L/R(Y)		98.25	405.8796	1215.633	-0.0085	-7	4.68	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
20033	dirMS_041712_NAR_120mM_plus.8748.8748.3	3	5.72	1	8.93E+04		(R)RGVTIKF	(R)R G V T I K P T V/D/D|D(-)		99.28	439.2268	1315.685	-0.0194	-14.7	4.68	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
20034	dirMS_041712_NAR_120mM_plus.8902.8902.3	3	5.72	0	2.25E+06		(K)HTGPNS	(K)H T\G P N S\P D\T A/N/D G F/V R(L)		99.48	562.26	1684.767	-0.0019	-1.2	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
20035	dirMS_041712_NAR_20mM_plus.11610.11610.2	2	5.72	0	1.44E+04	M94m	(K)mLLYTE\	(K)m L|L|Y/T E V T\R(Y)	m:Oxidized methionine	152.37	571.3075	1125.597	16.0105	13.6	5.75	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
20036	dirMS_041712_NAR_20mM_plus.13822.13822.2	2	5.72	0	4.19E+04		(K)IVLTNPV	(K)I V|L T N/P V C T E V G E K(I)	C:Carbamidomethylation	167.07	779.9082	1558.815	-0.0054	-3.5	4.53	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
20037	dirMS_041712_NAR_20mM_plus.16364.16364.2	2	5.72	0	4.87E+04		(R)SNLGSV'	(R)S N\L/G/S V V L/Q L K(K)		184.22	579.3448	1157.689	-0.0065	-5.6	8.47	91730	7.16	HUMAN	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15
20038	dirMS_041712_NAR_20mM_plus.16608.16608.3	3	5.72	0	6.48E+04	M137m M	(R)IIGATDS	(R)I I\G A T D S S G E L/m/F\L m K(W)	m:Oxidized methionine	185.8	582.2872	1712.86	31.9873	-1.5	4.37	19439.5	4.97	HUMAN	B5MD17	Chromobox protein homolog 1 (Fragment)
20039	dirMS_041712_NAR_20mM_plus.17509.17509.2	2	5.72	0	3.36E+04		(R)YLTVAA\	(R)Y L|T|V A A\V F R(G)		192.65	520.3009	1039.593	0.001	1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
20040	dirMS_041712_NAR_20mM_plus.6452.6452.2	2	5.72	0	2.02E+05	M216m	(R)DLmAC/	(R)D L m|A C A Q/T/G S G K(T)	C:Carbamidomethylation m:Oxid	107.72	627.776	1238.55	15.9943	-0.5	5.84	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
20041	dirMS_041712_NAR_30mM_plus2.13675.13717.2	2	5.72	1	5.97E+05		(K)QYSGKF	(K)Q Y/S/G K/F/F(-)		124.78	438.7176	876.425	0.0029	3.3	8.59	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
20042	dirMS_041712_NAR_30mM_plus2.19895.19895.2	2	5.72	0	1.51E+05		(K)SNSVEM	(K)S N/S/V/E|M D W V\L K(H)		157.87	654.3191	1307.63	0.0009	0.7	4.37	49548	5.89	HUMAN	P55795	Heterogeneous nuclear ribonucleoprotein H2
20043	dirMS_041712_NAR_40mM_plus2.8875.8875.2	2	5.72	0	1.19E+05		(R)GYSFTTT	(R)G Y/S/F/T T T\A E R(E)		114.9	566.7672	1132.527	0.0002	0.2	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
20044	dirMS_041712_NAR_50mM_plus2.13965.13965.3	3	5.72	0	1.21E+06		(K)DLAGCII	(K)D L/A G\C/I/H/G L S N V K(L)	C:Carbamidomethylation	140.62	461.9061	1383.705	-0.0012	-0.8	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
20045	dirMS_041712_NAR_60mM_plus.15376.15376.3	3	5.72	1	5.97E+05		(R)FVNVVP	(R)F V\N\V/V/P T F G K K(K)		137.58	412.5761	1235.715	-0.0009	-0.7	10	10904.6	11.56	HUMAN	E9PR30	40S ribosomal protein S30
20046	dirMS_041712_NAR_60mM_plus.6272.6272.3	3	5.72	1	1.49E+05		(K)VGGTSD	(K)V/G/G T/S/D V/E V N E K K(D)		91.77	454.5636	1361.691	-0.0145	-10.6	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
20047	dirMS_041712_NAR_60mM_plus.8551.8551.3	3	5.72	0	2.66E+05		(K)LQETFPI	(K)L Q E T F P/I T S D A T K(L)		102.67	484.259	1450.742	0.02	13.8	4.37	59603	6.13	HUMAN	E9PDB0	Uncharacterized protein
20048	dirMS_041712_NAR_60mM_plus.9290.9290.3	3	5.72	1	1.49E+06		(R)SRAEAE!	(R)S R A E\A E/S M/Y Q I K(Y)		105.95	471.5691	1412.684	0.0089	6.3	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
20049	dirMS_041712_NAR_120mM_minus.12084.12084.2	2	5.71	1	3.39E+05		(K)MKEIAE/	(K)M K|E/I/A E A Y/L/G K(T)		119.63	626.8305	1252.661	-0.0069	-5.5	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
20050	dirMS_041712_NAR_30mM_minus2.14854.14854.2	2	5.71	0	2.52E+05		(R)YLIEIAK(	(R)Y/L/I E I/A K(N)		134.45	425.2556	849.508	-0.0041	-4.8	6	41736.1	5.41	HUMAN	A8KAH5	IST1 homolog
20051	dirMS_041712_NAR_50mM_minus2.12547.12547.3	3	5.71	1	2.27E+05	M4131m	(K)ISmPEVI	(K)I/S m/P E V D/L N L K G P/K(M)	m:Oxidized methionine	139.5	519.6148	1540.84	15.9895	-3.5	6.07	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK

20052	dirMS_041712_NAR_60mM_minus.9303.9303.3	3	5.71	0	9.34E+04		(K)GHENVE	(K)G H E N V E\A\A/Q/A/E Y I E K(F)		111.78	563.2673	1687.792	-0.0049	-2.9	4.48	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
20053	dirMS_041712_NAR_120mM_plus.10382.10382.4	4	5.71	2	8.70E+05		(K)MQASIE	(K)M Q\A S/I E/K G G S L P K V E A K(F)		106.83	443.9944	1772.958	-0.0017	-1	8.25	32745.6	4.64	HUMAN	P06748	Nucleophosmin
20054	dirMS_041712_NAR_120mM_plus.13023.13023.4	4	5.71	1	1.55E+06		(K)GVIVDKI	(K)G V/I/V D/K D/F S H P Q M P/K(K)		121.9	425.2229	1697.868	0.0018	1.1	6.75	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
20055	dirMS_041712_NAR_20mM_plus.10762.10762.2	2	5.71	0	4.28E+04		(K)NVTELN	(K)N V|T E/L\N/E/P/L S N E E R(N)		146.48	822.3937	1643.787	-0.007	-4.3	4.09	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
20056	dirMS_041712_NAR_20mM_plus.15008.15008.3	3	5.71	0	1.09E+05		(K)VLEQLT	(K)V L E Q L\T G Q/T|P V/F S K(A)		174.63	516.2866	1546.848	-0.0023	-1.5	5.97	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
20057	dirMS_041712_NAR_30mM_plus2.15989.15989.2	2	5.71	0	6.10E+05		(R)GALQNI	(R)G A L/Q\N I|I P A S T G\A A K(A)		137.35	706.3979	1411.79	-0.0018	-1.3	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
20058	dirMS_041712_NAR_30mM_plus2.18487.18487.2	2	5.71	0	2.76E+05		(R)TEMDW	(R)T/E|M D W/V L K(H)		149.6	511.2577	1021.502	0.0058	5.7	4.37	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
20059	dirMS_041712_NAR_30mM_plus2.19953.19953.2	2	5.71	0	4.29E+04		(R)ISEQFTA	(R)I/S\E Q/F/T A M F/R(R)		158.45	615.3024	1229.598	-0.0008	-0.6	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
20060	dirMS_041712_NAR_30mM_plus2.21179.21179.2	2	5.71	0	3.26E+05		(R)GVVQEL	(R)G V/V|Q E/L Q/Q/A\I/S K(L)		165.78	650.3632	1299.727	-0.0076	-5.8	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
20061	dirMS_041712_NAR_40mM_plus2.5490.5490.2	2	5.71	0	1.50E+05		(R)GSNGAF	(R)G S|N/G/A/F/Y/K(A)		89.17	422.2033	843.399	-0.0002	-0.3	8.59	66105.7	7.3	HUMAN	A8MQB8	Fragile X mental retardation protein 1
20062	dirMS_041712_NAR_50mM_plus2.6486.6486.3	3	5.71	1	3.41E+04		(K)IIVGDAT	(K)I I|V/G D A/T/E K D A S K(K)		98.78	449.5766	1346.716	-0.0009	-0.7	4.56	45188.9	5.76	HUMAN	Q96I25	Splicing factor 45
20063	dirMS_041712_NAR_60mM_plus.15168.15168.3	3	5.71	0	4.82E+04		(K)HIGLVYS	(K)H I G L V Y S G\M/G|P D/Y R(V)		135.85	522.2648	1564.758	0.0222	14.2	6.74	26012.2	6.92	HUMAN	P25787	Proteasome subunit alpha type-2
20064	dirMS_041712_NAR_60mM_plus.18543.18543.3	3	5.71	1	2.05E+05	T1242t	(K)TRLDNG	(K)T/R L D N G V T/G F I/P t K(F)	t:N-acetylglucosamine (T)	154.48	574.6347	1518.828	203.0621	-10	8.41	200324.3	4.81	HUMAN	Q7KZ85	Transcription elongation factor SPT6
20065	dirMS_041712_NAR_60mM_plus.19449.19449.3	3	5.71	0	6.28E+05		(K)VSHLLGI	(K)V S H L L G I/N|V/T/D/F T R(G)		159.88	524.6233	1571.854	0.0013	0.8	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
20066	dirMS_041712_NAR_60mM_plus.20333.20333.3	3	5.71	0	1.38E+04		(R)FTARPL	(R)F T|A/R P L V/E T\I F E R(G)		166.62	526.9566	1578.864	-0.0086	-5.5	6.14	78432.3	6.17	HUMAN	E9PB70	Kinesin-like protein KIF2A
20067	dirMS_041712_NAR_20mM_minus.8274.8274.2	2	5.7	0	1.25E+05		(K)VTADVI	(K)V T|A/D/V I N A A E K(L)		132.47	565.8065	1130.605	0.0005	0.5	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
20068	dirMS_041712_NAR_30mM_minus2.13964.13964.2	2	5.7	0	1.71E+04	M770m	(K)FAEFDQ	(K)F/A|E|F/D Q I m K(S)	m:Oxidized methionine	129.45	572.7726	1128.539	15.9985	3.1	4.37	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
20069	dirMS_041712_NAR_30mM_minus2.15727.15727.2	2	5.7	1	5.34E+04	K64k	(R)TTTGSYI	(R)T T/T/G/S Y I A N R V T D k(L)	k:Ubiquitin-K	139.08	820.9034	1526.781	114.0186	-14.8	8.25	10799.8	5.07	HUMAN	I3L3X7	Proteasome subunit beta type-6 (Fragment)
20070	dirMS_041712_NAR_30mM_minus2.15737.15737.2	2	5.7	0	9.59E+04		(R)GSTDNL	(R)G S T D/N/L/M/D D I E R(A)		138.8	683.3009	1365.595	-0.0006	-0.4	3.84	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
20071	dirMS_041712_NAR_30mM_minus2.16354.16354.3	3	5.7	1	7.41E+04		(K)AVQYEE	(K)A V Q Y E|E/K N P C R(T)	C:Carbamidomethylation	142.5	465.216	1393.653	-0.0194	-13.9	6.19	33651.7	6.11	HUMAN	O75558	Syntaxin-11
20072	dirMS_041712_NAR_50mM_minus2.12787.12787.3	3	5.7	0	2.63E+05		(K)AASDIA	(K)A A\S D/I/A M T E L/P P T/H/P I R(L)		140.78	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
20073	dirMS_041712_NAR_50mM_minus2.17844.17844.3	3	5.7	1	1.00E+05		(K)ITQDIFQ	(K)I/T/Q D I F Q Q L/L K R(G)		169.87	501.6277	1502.869	-0.0004	-0.3	8.75	72796.9	6.75	HUMAN	A6NC17	Methionine--tRNA ligase, cytoplasmic
20074	dirMS_041712_NAR_120mM_plus.14665.14665.3	3	5.7	1	9.62E+05		(K)LDKSQI	(K)L D K/S Q I H D\I\V|L V G G S T R(I)		130.48	613.3369	1838.013	-0.0169	-9.2	6.75	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
20075	dirMS_041712_NAR_20mM_plus.14505.14505.3	3	5.7	0	1.27E+05		(R)ASLEAAI	(R)A S L\E/A\A I/A D/A E Q R(G)		171.88	448.8957	1344.675	-0.0028	-2.1	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
20076	dirMS_041712_NAR_20mM_plus.7388.7388.2	2	5.7	0	2.86E+05		(K)TGQAP	(K)T G Q|A|P G Y S Y T A A/N K(N)		119.52	714.8394	1428.675	-0.0039	-2.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
20077	dirMS_041712_NAR_20mM_plus.7863.7863.2	2	5.7	0	5.08E+03		(K)TAVCDI	(K)T A/V|C D/I/P|P R(G)	C:Carbamidomethylation	123.92	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
20078	dirMS_041712_NAR_30mM_plus2.21087.21087.2	2	5.7	0	1.97E+05		(R)FDAMP	(R)F D\A/M/P F/T L/R(A)		166.15	549.276	1097.545	-0.0001	-0.1	5.84	42088	5.39	HUMAN	F8VTY8	Proliferation-associated protein 2G4
20079	dirMS_041712_NAR_30mM_plus2.4469.4469.2	2	5.7	0	3.00E+05		(K)EDAAN	(K)E D/A/A/N/N/Y A/R(G)		72.8	512.2281	1023.449	-0.0001	-0.1	4.37	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
20080	dirMS_041712_NAR_30mM_plus2.5710.5710.2	2	5.7	0	4.13E+05		(K)GSSNSY	(K)G S|S/N/S/Y A I/K(K)		84.45	463.7311	926.458	-0.0029	-3.1	8.59	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
20081	dirMS_041712_NAR_30mM_plus2.8666.8666.2	2	5.7	0	4.70E+05		(R)GNLGA	(R)G N|L G\A/G/N G N L/Q/G P R(H)		99.42	662.8376	1324.672	-0.0037	-2.8	9.75	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
20082	dirMS_041712_NAR_30mM_plus2.9554.9554.2	2	5.7	0	8.52E+04		(K)VCNPIIT	(K)V/C|N/P I I|T K(L)	C:Carbamidomethylation	104.22	472.7711	944.523	0.0116	12.2	8.72	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
20083	dirMS_041712_NAR_40mM_plus2.12541.12541.3	3	5.7	0	1.29E+05	M114m M	(R)AGKPVI	(R)A G K\P V\I\C|A T Q/m\L E/S m I K(K)	C:Carbamidomethylation m:Oxid	139.77	637.0002	1876.969	32.0167	14.1	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
20084	dirMS_041712_NAR_40mM_plus2.12634.12634.3	3	5.7	0	3.25E+05		(K)AASDIA	(K)A A S D I/A M T E L/P P T H P I R(L)		140.5	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
20085	dirMS_041712_NAR_40mM_plus2.15903.15903.3	3	5.7	0	6.94E+03		(R)DLKPSN	(R)D L K P S N L\L|I/N T T C D L K(I)	C:Carbamidomethylation	159.45	615.6661	1844.979	0.0051	2.8	5.96	30925	5.63	HUMAN	B3KR49	Mitogen-activated protein kinase 3
20086	dirMS_041712_NAR_50mM_plus2.16142.16142.3	3	5.7	0	1.05E+06		(R)LSFQHD	(R)L S F Q/H D|P E T S V/L/V L R(K)		152.42	580.9801	1740.928	-0.0022	-1.2	5.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
20087	dirMS_041712_NAR_60mM_plus.17943.17943.3	3	5.7	1	1.63E+05		(R)MKIDPE	(R)M K I D|P E A F/I T R(H)		150.6	440.9074	1320.698	0.0096	7.3	5.82	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
20088	dirMS_041712_NAR_60mM_plus.18479.18479.3	3	5.7	1	6.96E+05		(K)EVNKFQ	(K)E V|N K F Q M A/Y/S/N L L R(A)		153.1	571.6293	1712.879	-0.0055	-3.2	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
20089	dirMS_041712_NAR_120mM_minus.15651.15651.3	3	5.69	1	2.83E+05		(R)MSMKE	(R)M/S M K E V D E\Q M L/N/V Q/N K(N)		139.38	641.9706	1923.897	0	0	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
20090	dirMS_041712_NAR_120mM_minus.8039.8039.3	3	5.69	0	2.04E+05	Y763y	(K)IHVFyID	(K)I H V F y|I D/Y G/N R(E)	y:Phosphorylated Y	97.95	492.8901	1396.701	79.9549	-7.7	6.74	102679.8	6.75	HUMAN	Q7KZF4	Staphylococcal nuclease domain-containing protein 1
20091	dirMS_041712_NAR_20mM_minus.9177.9177.3	3	5.69	0	6.36E+03		(R)AQIFAN	(R)A Q I F\A N T/V/D/N/A R(I)		141.6	440.5612	1319.67	-0.0012	-0.9	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
20092	dirMS_041712_NAR_40mM_minus2.12563.12563.3	3	5.69	1	4.81E+04		(K)ALLQDK	(K)A L\L Q D K D V\I A|I/N/Q/D P L G K(Q)		157.28	651.0317	1951.086	-0.0053	-2.7	4.43	49507.6	5.35	HUMAN	P06280	Alpha-galactosidase A
20093	dirMS_041712_NAR_40mM_minus2.14608.14608.3	3	5.69	1	1.01E+06		(K)TFVNITP	(K)T F\V/N/I/T/P A E V G V L V G K D R(S)		171.55	639.0252	1915.065	-0.0037	-1.9	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
20094	dirMS_041712_NAR_50mM_minus2.6235.6235.3	3	5.69	0	2.41E+05	M434m	(R)LESGmC	(R)L E|S G m/Q N M S I H/T K(T)	m:Oxidized methionine	98.83	497.9018	1475.698	15.9927	-1.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
20095	dirMS_041712_NAR_60mM_minus.11574.11574.3	3	5.69	1	1.59E+05		(K)EIADYLA	(K)E I/A/D/Y/L/A A G K D/E R(A)		124.38	484.2432	1450.717	-0.0022	-1.5	4.32	41736.1	5.41	HUMAN	A8KAH5	IST1 homolog
20096	dirMS_041712_NAR_60mM_minus.15962.15962.3	3	5.69	1	3.51E+05		(K)KANLQI	(K)K A\N L Q I D Q\I/N/T/D/L N L E R(S)		148.15	666.6911	1998.061	-0.0027	-1.3	4.56	227783.5	5.5	HUMAN	P35579	Myosin-9
20097	dirMS_041712_NAR_60mM_minus.18022.18022.3	3	5.69	0	3.59E+03		(R)GGYVLH	(R)G G Y V/L H I/G T I Y/G D/L/K(V)		161.65	535.9574	1605.863	-0.0059	-3.7	6.74	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
20098	dirMS_041712_NAR_60mM_minus.18055.18055.3	3	5.69	0	2.53E+05		(R)VLDPFTI	(R)V/L/D/P F T I/K/P L D R(K)		161.35	471.9394	1413.81	-0.0064	-4.5	5.93	63448.4	7.29	HUMAN	B4E022	Transketolase
20099	dirMS_041712_NAR_120mM_plus.11920.11920.4	4	5.69	2	6.06E+04	M72m	(K)LDELLG	(K)L D E L L G K D/H/T Q\V A G m R L(-)	m:Oxidized methionine	114.37	478.7604	1896.001	16.019	12.6	5.38	8678.8	6.07	HUMAN	E5RH51	Protein SMIM12
20100	dirMS_041712_NAR_20mM_plus.12823.12823.2	2	5.69	0	3.14E+05	M316m	(R)ISEQFTA	(R)I/S/E Q\F/T/A m F R(R)	m:Oxidized methionine	161.38	623.3012	1229.598	15.9968	1.5	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
20101	dirMS_041712_NAR_20mM_plus.8053.8053.2	2	5.69	0	1.28E+05		(R)VIGSGC	(R)V I|G S G/C N/L D S A R(F)	C:Carbamidomethylation	124.95	624.7989	1248.6	-0.0096	-7.7	5.81	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
20102	dirMS_041712_NAR_20mM_plus.8191.8191.2	2	5.69	0	1.06E+05		(K)VTEDTS	(K)V/T/E/D T S/S/V L R(S)		126.02	553.7889	1106.569	0.0017	1.6	4.37	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
20103	dirMS_041712_NAR_50mM_plus2.16326.16433.3	3	5.69	1	1.86E+05		(R)FFVADT	(R)F/F|V/A D T A N E A L E A A K R(L)		154.23	584.9601	1752.892	-0.0258	-14.7	4.68	41666	7.73	HUMAN	E9PDQ8	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial
20104	dirMS_041712_NAR_50mM_plus2.19330.19330.3	3	5.69	0	1.75E+05		(R)LHPVILA	(R)L H\P V I L/A\S I/V D S Y E R(R)		169.85	571.3163	1711.938	-0.0034	-2	5.32	39260.1	5.25	HUMAN	B3KSH1	Eukaryotic translation initiation factor 3 subunit F
20105	dirMS_041712_NAR_60mM_plus.11630.11630.3	3	5.69	1	2.93E+06		(K)KAEAGA	(K)K A E A G A G S\A|T/E/F Q/F R(G)		118.23	523.9277	1569.766	0.003	1.9	6.14	18897.4	10.15	HUMAN	P46783	40S ribosomal protein S10
20106	dirMS_041712_NAR_60mM_plus.16468.16468.3	3	5.69	0	2.62E+05		(R)HSVGM	(R)H S V G\M A\V/L/G Q L A R(R)		142.87	446.9171	1338.731	0.0057	4.2	9.75	20278.4	11.86	HUMAN	C9J7Z1	Probable peptidyl-tRNA hydrolase
20107	dirMS_041712_NAR_60mM_plus.9724.9724.3	3	5.69	1	1.35E+06		(K)CAADLG	(K)C/A/A/D L G L/N/K/G Y R(M)	C:Carbamidomethylation	109.32	446.56	1337.663	0.0024	1.8	8.59	13915.8	6.43	HUMAN	P49773	Histidine triad nucleotide-binding protein 1
20108	dirMS_041712_NAR_120mM_minus.10513.10513.2	2	5.68	0	3.51E+05		(R)VHIEIGP	(R)V H|I|E I\G/P D/G R(V)		111.28	546.7932	1092.58	-0.0005	-0.5	5.32	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
20109	dirMS_041712_NAR_120mM_minus.14996.14996.3	3	5.68	1	1.11E+05		(R)RREGSH	(R)R R E G S H F W E A/K(T)		135.73	468.2346	1402.698	-0.0082	-5.9	8.75	12401	9.45	HUMAN	F2Z2E6	Leucine zipper transcription factor-like protein 1
20110	dirMS_041712_NAR_50mM_minus2.10829.10829.3	3	5.68	1	1.35E+05	K145k	(K)IVESQIN	(K)I V E S/Q/I N F H\G K k(L)	k:Ubiquitin-K	129.78	505.2683	1399.769	114.0211	-14.4	8.6	22650.4	9.12	HUMAN	E7EV40	Deleted in azoospermia-like (Fragment)
20111	dirMS_041712_NAR_50mM_minus2.13350.13350.3	3	5.68	0	2.42E+05		(K)VIQYLAY	(K)V I/Q Y L/A\Y/V A S S H K(S)		144.77	493.6043	1478.8	-0.0018	-1.2	8.48	227783.5	5.5	HUMAN	P35579	Myosin-9
20112	dirMS_041712_NAR_50mM_minus2.5968.5968.3	3	5.68	1	3.93E+04	M101m	(R)GIEPTG	(R)G I|E/P/T G N m V K Q/P A K(F)	m:Oxidized methionine	96.45	495.9271	1469.778	15.9887	-4.2	8.59	258215.9	5.48	HUMAN	E7EN95	Filamin-B
20113	dirMS_041712_NAR_120mM_plus.21201.21201.4	4	5.68	1	2.30E+05	S155s	(K)ELEALM	(K)E L E/A L/M\P s A\A G Q E K Q R(D)	s:N-acetylglucosamine (S)	164.62	491.0027	1757.885	203.1039	12.5	4.79	135026.2	8.04	HUMAN	F5H658	ATP-dependent RNA helicase DHX8
20114	dirMS_041712_NAR_120mM_plus.6436.6436.3	3	5.68	1	1.68E+04	M253m	(R)mGRGP	(R)m G R\G P G|P/L/Q E R(S)	m:Oxidized methionine	86.73	405.209	1197.616	15.9967	1.5	9.35	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
20115	dirMS_041712_NAR_120mM_plus.6727.6749.3	3	5.68	1	1.24E+05		(K)SKDTVS	(K)S K\D T|V S E/D/T I/R(L)		88.55	417.5461	1250.622	0.0015	1.2	4.56	29390.7	9.9	HUMAN	Q96E11	Ribosome-recycling factor, mitochondrial
20116	dirMS_041712_NAR_20mM_plus.11219.11219.2	2	5.68	0	2.10E+05		(K)LITPAVV	(K)L I|T|P/A V/V S E R(L)		150.02	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
20117	dirMS_041712_NAR_20mM_plus.7621.7621.2	2	5.68	0	1.57E+05		(K)IAVAAQ	(K)I A|V/A/A/Q N C Y K(V)	C:Carbamidomethylation	122.43	569.2902	1137.572	0.001	0.9	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
20118	dirMS_041712_NAR_30mM_plus2.15507.15507.2	2	5.68	0	6.19E+05		(R)QPTPPF	(R)Q P/T/P/P F F G R(D)		133.6	523.7794	1046.542	0.0097	9.3	9.75	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
20119	dirMS_041712_NAR_30mM_plus2.16740.16740.2	2	5.68	0	1.25E+05		(R)MGPAM	(R)M G/P A\M|G/P A\L\G\A G I E R(M)		140.25	714.3615	1427.713	0.0024	1.7	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
20120	dirMS_041712_NAR_30mM_plus2.22294.22294.3	3	5.68	0	5.24E+05		(R)VGNLGL	(R)V G N L G L A/T S/F/F N E\R(N)		172.8	508.9306	1524.781	-0.0033	-2.1	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
20121	dirMS_041712_NAR_40mM_plus2.15088.15088.3	3	5.68	0	2.12E+05		(R)DVQIGD	(R)D V\Q|I|G D/I V T V G E C R P L S/K(T)	C:Carbamidomethylation	156.8	662.6815	1986.033	-0.0025	-1.3	4.56	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
20122	dirMS_041712_NAR_40mM_plus2.7368.7368.2	2	5.68	0	2.20E+05		(R)AQYDEL	(R)A Q|Y/D/E L A/R(K)		102.77	483.2372	965.469	-0.0016	-1.6	4.37	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
20123	dirMS_041712_NAR_40mM_plus2.8172.8172.2	2	5.68	0	3.13E+04		(K)LIEVDDE	(K)L I/E|V D D/E R(K)		108.03	494.7521	988.495	0.0024	2.4	3.91	10471.9	5.4	HUMAN	A2A3R7	40S ribosomal protein S6
20124	dirMS_041712_NAR_50mM_plus2.10912.10912.3	3	5.68	1	2.21E+06		(R)MQKEIT	(R)M Q K E I T/A|L/A/P S T M K(I)		124.1	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
20125	dirMS_041712_NAR_50mM_plus2.12224.12224.3	3	5.68	1	1.90E+04		(R)TPSDVKI	(R)T P\S D/V K E L V/L/D/N S R(S)		131.18	524.9505	1572.823	0.0142	9	4.55	20111	4.47	HUMAN	H0YN26	Acidic leucine-rich nuclear phosphoprotein 32 family member A
20126	dirMS_041712_NAR_60mM_plus.15305.15305.3	3	5.68	0	6.26E+05	T82t M92m	(R)GWtQM	(R)G W t Q\M Q|L P E G L S m R(Q)	t:N-acetylglucosamine (T) m:	136.53	618.2833	1633.783	219.0528	-11.6	6	15938.9	6.42	HUMAN	B4DUW4	Small ubiquitin-related modifier 3
20127	dirMS_041712_NAR_20mM_minus.11398.11398.2	2	5.67	0	2.40E+04	M1m N6n	(-)mPLFPnL	(-)m P|L F/P n L\P/R(L)	m:Oxidized methionine n:N-	161.42	652.3395	1084.597	219.0745	0.2	9.5	39133.5	4.5	HUMAN	Q8TD91-2	Isoform 2 of Melanoma-associated antigen C3
20128	dirMS_041712_NAR_30mM_minus2.8416.8416.2	2	5.67	0	1.50E+05		(R)LMSAVT	(R)L/M S/A V T\A R(A)		100.42	424.7339	848.466	-0.0053	-6.3	9.75	61148.9	8.98	HUMAN	P83111	Serine beta-lactamase-like protein LACTB, mitochondrial
20129	dirMS_041712_NAR_40mM_minus2.13122.13122.3	3	5.67	1	7.25E+04		(R)VTTVTEI	(R)V/T|T V T E I/G K D V I G L/R(I)		160.8	534.3113	1600.927	-0.0075	-4.7	6.04	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
20130	dirMS_041712_NAR_40mM_minus2.16029.16029.3	3	5.67	2	5.39E+05		(K)EPGGEI	(K)E P G/G E I E E/K T/G K L E Q L K(S)		189.22	629.0034	1884.991	0.0043	2.3	4.65	160751.2	5.24	HUMAN	B7WPL9	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 1
20131	dirMS_041712_NAR_40mM_minus2.6829.6829.3	3	5.67	0	1.29E+05	M44m M4	(K)SGTGIA	(K)S G T/G I/A A m/S V m R P E Q I/m K(S)	m:Oxidized methionine	110.45	652.3173	1906.955	47.9826	-1.1	8.46	8797.3	9.3	HUMAN	H3BR50	V-type proton ATPase 16 kDa proteolipid subunit
20132	dirMS_041712_NAR_50mM_minus2.16601.16601.3	3	5.67	1	9.23E+04		(R)DSEQVA	(R)D S|E/Q V/A E L/K Q E L A T L K(S)		163.05	601.3217	1801.954	-0.0036	-2	4.41	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
20133	dirMS_041712_NAR_60mM_minus.10177.10177.3	3	5.67	0	2.56E+05		(K)HVGNQ	(K)H V G N Q Q\Y/N/V/T/Y/V V K(E)		116.78	550.2838	1648.844	-0.0073	-4.4	8.51	258215.9	5.48	HUMAN	E7EN95	Filamin-B
20134	dirMS_041712_NAR_60mM_minus.11365.11365.3	3	5.67	1	1.35E+05		(R)MGIVGF	(R)M G/I/V/G/P E F K D K(L)		123.85	407.5515	1220.634	0.0056	4.6	5.82	533778	5.74	HUMAN	Q15149	Plectin
20135	dirMS_041712_NAR_120mM_plus.10049.10049.3	3	5.67	0	1.08E+06		(R)ILRPWQ	(R)I L/R|P W\Q/S/S E T R(S)		106.02	458.2486	1372.733	-0.0019	-1.4	9.6	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
20136	dirMS_041712_NAR_120mM_plus.6463.6463.3	3	5.67	1	1.10E+05		(R)RTAQEV	(R)R T A Q\E|V/E/T Y R(R)		87.97	418.2137	1252.628	-0.0015	-1.2	6.14	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
20137	dirMS_041712_NAR_20mM_plus.10004.10004.2	2	5.67	0	1.63E+05		(K)GEATVS	(K)G E A/T/V/S/F/D D P P S A/K(A)		140.55	710.8324	1420.659	-0.0015	-1.1	4.03	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
20138	dirMS_041712_NAR_20mM_plus.12194.12194.2	2	5.67	0	1.26E+04	M320m	(K)YmACCL	(K)Y m A/C C/L/L/Y R(G)	C:Carbamidomethylation m:Oxid	157.05	633.2796	1249.553	15.9993	3.5	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
20139	dirMS_041712_NAR_20mM_plus.15321.15321.2	2	5.67	0	2.38E+04	M73m	(R)AILVDLE	(R)A I L/V D\L/E|P G T m D S V R(S)	m:Oxidized methionine	176.97	816.4181	1615.836	15.9929	-1.2	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
20140	dirMS_041712_NAR_20mM_plus.18435.18435.3	3	5.67	0	1.97E+04		(R)APVPAS	(R)A P V P A S E L|L/A/S/G/V L S R(A)		199.55	522.9655	1566.885	-0.003	-1.9	6.05	533778	5.74	HUMAN	Q15149	Plectin
20141	dirMS_041712_NAR_30mM_plus2.20898.20898.2	2	5.67	0	2.27E+05		(R)ASLSLW	(R)A S\L S/L/W\Q A/M/E K(G)		163.25	632.3231	1263.64	-0.0013	-1	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
20142	dirMS_041712_NAR_30mM_plus2.6613.6613.2	2	5.67	0	4.72E+05		(R)SPDNP	(R)S/P|D\N/P M N/Q R(A)		88.95	529.7357	1058.468	-0.0042	-4	5.55	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
20143	dirMS_041712_NAR_50mM_plus2.14619.14619.3	3	5.67	1	7.97E+05		(K)AAVEW	(K)A A/V/E/W/F D G K/D F Q G S K(L)		144.37	562.2729	1684.797	0.0076	4.5	4.56	65213.5	9.57	HUMAN	B0QYK0	Ewing sarcoma breakpoint region 1
20144	dirMS_041712_NAR_50mM_plus2.7790.7790.3	3	5.67	0	8.21E+03		(R)IEPADA	(R)I E/P A D/A H V L Q K(N)		107.3	407.5589	1220.663	-0.0012	-1	5.32	11018.4	8.89	HUMAN	B0AZT5	N-alpha-acetyltransferase 50
20145	dirMS_041712_NAR_60mM_plus.11564.11564.2	2	5.67	0	8.15E+05		(R)TICSHV	(R)T I/C/S H V\Q N M\I K(G)	C:Carbamidomethylation	117.03	665.8295	1330.661	-0.0089	-6.7	8.44	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
20146	dirMS_041712_NAR_60mM_plus.17246.17246.3	3	5.67	1	4.46E+05		(R)GPIKFN	(R)G P I/K F N V|W/D|T\A G Q E K(F)		146.8	563.9572	1689.86	-0.0024	-1.4	6.07	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
20147	dirMS_041712_NAR_60mM_plus.21432.21432.3	3	5.67	1	3.68E+05		(R)ARDDLI	(R)A R\D D L\I/T/D/L L N E/A K(Q)		177.42	529.6165	1586.838	-0.0035	-2.2	4.23	23653.1	9.28	HUMAN	C9J8H1	V-type proton ATPase subunit E 1 (Fragment)
20148	dirMS_041712_NAR_60mM_plus.6415.6415.3	3	5.67	1	9.09E+04	M193m	(K)ALSRQE	(K)A L/S R Q E m\Q|E/V/Q S S R(S)	m:Oxidized methionine	92.15	555.6058	1648.807	15.9957	0.5	6.19	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
20149	dirMS_041712_NAR_120mM_minus.10526.10527.2	2	5.66	1	2.63E+05		(R)VKYETEL	(R)V/K|Y|E/T E L A M R(Q)		111.62	620.3232	1239.64	-0.0011	-0.9	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
20150	dirMS_041712_NAR_50mM_minus2.12674.12674.3	3	5.66	1	4.53E+05	M100m	(K)QGGLGF	(K)Q G G L/G/P m N\I|P L V/S D/P K R(T)	m:Oxidized methionine	140.33	598.988	1778.958	15.9913	-2	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
20151	dirMS_041712_NAR_50mM_minus2.6625.6625.3	3	5.66	1	8.25E+04		(R)YLAEVA	(R)Y L/A E V/A A/G D\D K/K(G)		103.72	427.2223	1279.653	-0.0005	-0.4	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
20152	dirMS_041712_NAR_50mM_minus2.6725.6725.3	3	5.66	1	8.76E+04	M22m M2	(K)LAEQAE	(K)L A|E Q/A E R Y D D\m/A A C m K(S)	C:Carbamidomethylation m:Oxid	104.8	645.2741	1901.819	31.9887	-0.6	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
20153	dirMS_041712_NAR_120mM_plus.5848.5848.3	3	5.66	1	1.60E+05		(K)AMKEYE	(K)A M/K/E Y/E/E E/E R(K)		84.12	438.5281	1313.568	0.0019	1.5	4.32	11829.2	4.96	HUMAN	K7EIU0	Hsp90 co-chaperone Cdc37 (Fragment)
20154	dirMS_041712_NAR_20mM_plus.11588.11588.2	2	5.66	0	3.29E+04		(K)GGKPEP	(K)G G K P E P P A M/P Q P V/P T A(-)		152.55	787.4034	1573.804	-0.0048	-3	6	25541.5	9.92	HUMAN	E9PL09	40S ribosomal protein S3
20155	dirMS_041712_NAR_20mM_plus.14691.14691.2	2	5.66	0	9.83E+04	M1m S4s	(-)mAQsG	(-)m A/Q s G G E A R P/G P K(T)	m:Oxidized methionine s:N-	173.2	752.8674	1285.632	219.0958	14.3	8.5	55021	8.68	HUMAN	Q9BRS8	La-related protein 6
20156	dirMS_041712_NAR_20mM_plus.6990.6990.3	3	5.66	0	1.33E+05	M295m M	(R)mGQm	(R)m G Q m\A m\G G\A\M/G I/N N R(G)	m:Oxidized methionine	115.02	529.5557	1538.67	47.9831	-1.1	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
20157	dirMS_041712_NAR_20mM_plus.9328.9328.3	3	5.66	0	1.27E+05		(K)SVTNED	(K)S V\T N E D V T Q/E/E L/G G A K(T)		136	559.6039	1676.797	-0.0002	-0.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
20158	dirMS_041712_NAR_30mM_plus2.18465.18465.2	2	5.66	0	1.64E+04		(K)VVNSIL	(K)V V/N/S/I\L A F R(E)		149.52	509.8031	1018.604	-0.0055	-5.4	9.72	56564.1	6.56	HUMAN	B4DNW0	Aminoacylase-1
20159	dirMS_041712_NAR_30mM_plus2.20590.20590.2	2	5.66	0	2.46E+05		(R)FEELNA	(R)F E|E|L/N A D/L\F/R(G)		161.32	627.3106	1253.616	-0.0022	-1.7	4.14	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
20160	dirMS_041712_NAR_30mM_plus2.21285.21285.3	3	5.66	0	5.51E+05		(R)VNQAIV	(R)V N Q A I W|L|L/C T G A/R(E)	C:Carbamidomethylation	166.88	501.2717	1501.794	0.0062	4.1	9.72	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5

20161	dirMS_041712_NAR_40mM_plus2.12032.12032.3	3	5.66	1	9.18E+04	S189s	(K)TATKAYI	(K)T A/T K\A Y|P\Q s P K(T)	s:Phosphorylated S	137.3	424.5414	1191.637	79.9728	5.1	9.7	68204.5	8.18	HUMAN	F5GYC2	MAP7 domain-containing protein 2
20162	dirMS_041712_NAR_40mM_plus2.15968.15968.2	2	5.66	0	8.37E+04		(R)YLTVAA	(R)Y/L|T\V/A A V F R(G)		161.67	520.2997	1039.593	-0.0014	-1.3	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
20163	dirMS_041712_NAR_40mM_plus2.7404.7404.2	2	5.66	0	1.82E+05		(R)SGYFDEI	(R)S G|Y|F D/E R(Y)		103.75	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
20164	dirMS_041712_NAR_40mM_plus2.9592.9592.2	2	5.66	0	8.12E+04		(K)TNFFGTI	(K)T N/F/F/G/T R(D)		120.5	421.7119	842.415	0.001	1.2	9.41	24897.7	9.84	HUMAN	A8MTM1	Carbonyl reductase [NADPH] 1
20165	dirMS_041712_NAR_50mM_plus2.11633.11633.3	3	5.66	0	1.58E+05		(R)NLDIERF	(R)N L/D\I/E R/P T Y/T N L N R(L)		130.17	573.6314	1718.882	-0.0024	-1.4	6.07	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
20166	dirMS_041712_NAR_50mM_plus2.13233.13233.3	3	5.66	0	2.15E+06		(R)SCTVNIN	(R)S C/T/V/N I M/F G T P Q E H R(N)	C:Carbamidomethylation	138.4	592.9438	1776.816	0.0012	0.7	6.47	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
20167	dirMS_041712_NAR_50mM_plus2.13519.13519.3	3	5.66	0	1.11E+06	N110n M1	(R)IInYPHD	(R)I/I|n Y P H D m K P S A V/K(D)	n:N-acetylglucosamine (N) m	138.83	611.3256	1612.852	219.1107	19.9	8.5	29936.1	5.96	HUMAN	Q9NRE1	Matrix metalloproteinase-26
20168	dirMS_041712_NAR_50mM_plus2.6070.6070.3	3	5.66	0	3.37E+04		(K)CIGKPGC	(K)C\I/G K/P G G S/L D N/S E Q/K(C)	C:Carbamidomethylation	96.05	530.5884	1589.759	-0.0081	-5.1	6.07	9122.2	9.22	HUMAN	K7EIT2	Mitochondrial import inner membrane translocase subunit Tim13
20169	dirMS_041712_NAR_50mM_plus2.7013.7013.3	3	5.66	0	8.91E+04		(K)SSPSVKF	(K)S S/P S V K/P A V/D P A A A K(L)		102.5	475.5987	1424.774	0.0072	5	8.31	26321.7	6.24	HUMAN	H3BPG7	Anamorsin
20170	dirMS_041712_NAR_60mM_plus.9686.9686.3	3	5.66	1	5.14E+04		(K)IKQEILPI	(K)I K Q E\I|L/P E E R(M)		107.23	418.9051	1254.705	-0.0045	-3.6	4.79	91344.6	6.07	HUMAN	E9PGZ0	Cold shock domain-containing protein E1
20171	dirMS_041712_NAR_60mM_plus.9743.9743.3	3	5.66	0	1.33E+06		(K)LVNANG	(K)L|V N A N G E A V Y C K(F)	C:Carbamidomethylation	109.38	446.56	1337.652	0.0136	10.2	6	59983.3	6.9	HUMAN	P04040	Catalase
20172	dirMS_041712_NAR_120mM_minus.13767.13767.4	4	5.65	1	1.60E+06		(K)ASIHEA	(K)A/S|I H/E A W\T D/G K E A M L K(H)		129.97	447.476	1786.879	0.0029	1.6	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
20173	dirMS_041712_NAR_20mM_minus.14644.14644.2	2	5.65	0	2.02E+05		(K)TAVETA	(K)T A\V/E/T A\V L\L/L R(I)		201.2	593.3613	1185.72	-0.0048	-4.1	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
20174	dirMS_041712_NAR_30mM_minus2.16638.16638.2	2	5.65	0	1.61E+05		(R)NPSAAF	(R)N/P\S A/A F/F/C V A R(L)	C:Carbamidomethylation	144.1	620.3013	1239.594	0.0014	1.1	9.75	18626.5	5.64	HUMAN	B8ZZK2	Gamma-glutamylcyclotransferase
20175	dirMS_041712_NAR_30mM_minus2.18146.18146.2	2	5.65	0	2.92E+04		(R)LINLVGE	(R)L I|N L|V|G E S L/R(L)		153.3	557.3333	1113.663	-0.0033	-3	6	119157.2	5.4	HUMAN	B0UX83	HLA-B associated transcript 3
20176	dirMS_041712_NAR_30mM_minus2.4632.4632.2	2	5.65	0	7.51E+05		(K)QASEGP	(K)Q/A/S/E G P L/K(G)		76.43	415.2235	829.441	-0.0017	-2	6	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
20177	dirMS_041712_NAR_30mM_minus2.8119.8119.2	2	5.65	0	2.20E+05		(K)SFQQSSI	(K)S\F\Q/Q/S S/L S R(D)		99.18	520.2591	1039.517	-0.0058	-5.6	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
20178	dirMS_041712_NAR_30mM_minus2.8371.8371.2	2	5.65	0	4.91E+05		(K)SFQQSSI	(K)S F/Q/Q/S S L S R(D)		100.43	520.2591	1039.517	-0.0058	-5.6	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
20179	dirMS_041712_NAR_50mM_minus2.10662.10662.3	3	5.65	1	3.06E+04		(R)IAEFTTN	(R)I A|E/F T T N\L T E E E E/K S K(S)		128.63	623.6418	1868.912	-0.0015	-0.8	4.32	227783.5	5.5	HUMAN	P35579	Myosin-9
20180	dirMS_041712_NAR_50mM_minus2.6714.6714.3	3	5.65	1	8.76E+04	M22m M2	(K)LAEQAE	(K)L/A/E/Q A E R Y D D m A A C m K(S)	C:Carbamidomethylation m:Oxid	104.8	645.2741	1901.819	31.9887	-0.6	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
20181	dirMS_041712_NAR_50mM_minus2.6907.6907.3	3	5.65	1	6.78E+04		(R)TESTPIT	(R)T E|S T/P I T A V K Q P/E K(V)		105.98	510.2775	1528.822	-0.0038	-2.5	5.81	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
20182	dirMS_041712_NAR_60mM_minus.13939.13939.3	3	5.65	0	3.54E+05		(K)LHLGTT	(K)L H\L G T T Q N S\L/T/E A D/F R(E)		137.45	601.6438	1802.903	0.0137	7.6	5.32	49472.3	6.75	HUMAN	O75351	Vacuolar protein sorting-associated protein 4B
20183	dirMS_041712_NAR_60mM_minus.18916.18916.3	3	5.65	0	2.34E+05		(R)CRPDQL	(R)C R\P D\Q L T/G/L S L/L/P L S/E K(A)	C:Carbamidomethylation	167.98	643.0129	1927.032	-0.0076	-3.9	6.07	533778	5.74	HUMAN	Q15149	Plectin
20184	dirMS_041712_NAR_60mM_minus.6845.6845.3	3	5.65	1	2.18E+05		(K)IDDIRKP	(K)I/D D\I R K P G E S E/E(-)		96.37	463.2294	1387.67	0.0037	2.7	4.37	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
20185	dirMS_041712_NAR_60mM_minus.8582.8582.3	3	5.65	0	3.02E+05		(K)EFHLNES	(K)E F H\L N E/S/G/D/P S S K(S)		108.08	482.8882	1446.65	0.0005	0.3	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
20186	dirMS_041712_NAR_60mM_minus.9300.9300.3	3	5.65	0	2.51E+05		(K)QADNPH	(K)Q A D\N/P H V/A L/Y Q A R(F)		111.68	494.9197	1482.745	-0.0003	-0.2	6.74	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
20187	dirMS_041712_NAR_20mM_plus.15740.15740.2	2	5.65	0	4.98E+03		(R)SSFYVN	(R)S S F/Y/V N/G L/T\L G G Q K(C)		180.83	735.8818	1470.759	-0.0024	-1.6	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
20188	dirMS_041712_NAR_20mM_plus.7723.7723.2	2	5.65	0	4.28E+04		(K)AVTEQG	(K)A V\T E/Q/G A E L|S/N E E R(N)		122.93	766.8616	1532.719	-0.0028	-1.8	4.09	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
20189	dirMS_041712_NAR_30mM_plus2.18589.18589.2	2	5.65	0	5.13E+05		(R)GFVDDII	(R)G/F\V/D/D I|I\Q P S S T R(A)		150.37	717.8617	1434.722	-0.0062	-4.3	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
20190	dirMS_041712_NAR_30mM_plus2.20570.20570.2	2	5.65	0	2.16E+04		(K)ALAVGG	(K)A L|A\V/G G L G S I\I R(V)		161.85	563.8448	1126.694	-0.0119	-10.6	9.79	16940.9	6.15	HUMAN	Q9BPX5	Actin-related protein 2/3 complex subunit 5-like protein
20191	dirMS_041712_NAR_30mM_plus2.7078.7078.2	2	5.65	0	2.58E+05		(K)MAQFD	(K)M/A|Q/F/D A K(K)		91.35	405.6961	810.381	0.0035	4.3	5.59	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
20192	dirMS_041712_NAR_40mM_plus2.13581.13581.3	3	5.65	1	1.31E+04		(K)DMELPT	(K)D M/E|L/P/T E K E V A L V K(D)		146.4	534.6192	1601.845	-0.0024	-1.5	4.41	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
20193	dirMS_041712_NAR_40mM_plus2.14357.14357.3	3	5.65	1	1.77E+05		(K)IMASSPI	(K)I M|A S/S/P D M D L/A T V S A L R K(M)		151.22	635.9975	1905.977	0.0007	0.4	5.96	36208.1	7.21	HUMAN	B4DMU0	Pyrroline-5-carboxylate reductase
20194	dirMS_041712_NAR_40mM_plus2.15010.15010.3	3	5.65	0	2.95E+04		(K)VMLMA	(K)V M/L/M\A S/P/S M E D/L Y H K(S)		155.07	584.6129	1751.816	0.0076	4.4	5.32	76236.6	8.48	HUMAN	F5H1H2	Cell division cycle and apoptosis regulator protein 1 (Fragment)
20195	dirMS_041712_NAR_40mM_plus2.15189.15189.3	3	5.65	0	1.01E+05		(R)IETMLGI	(R)I E|T M L/G D V A|V/A V H P K(D)		156.27	527.286	1579.851	-0.0078	-4.9	5.32	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
20196	dirMS_041712_NAR_50mM_plus2.10707.10707.3	3	5.65	0	4.45E+05		(K)MIVDPV	(K)M I|V D/P V E P H G E M K(F)		123.4	494.5783	1481.713	0.0076	5.2	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
20197	dirMS_041712_NAR_50mM_plus2.11353.11353.3	3	5.65	2	1.17E+06	S37s	(K)DIRINLV	(K)D I R I N|L|V S\s/K K(I)	s:N-acetylglucosamine (S)	126.95	492.6069	1272.763	203.0427	-24.8	9.99	17255.7	9.64	HUMAN	B7Z8K6	T-cell receptor delta chain C region
20198	dirMS_041712_NAR_50mM_plus2.11952.11952.3	3	5.65	1	4.35E+05		(K)QIDLSTV	(K)Q I/D L S/T/V D/L K K(L)		130.47	420.5781	1259.72	-0.0008	-0.6	5.96	21156.2	9.41	HUMAN	P55145	Mesencephalic astrocyte-derived neurotrophic factor
20199	dirMS_041712_NAR_50mM_plus2.17362.17362.3	3	5.65	1	1.01E+06		(K)DNNGVI	(K)D N/N/G V/I G L L E/P M K K(S)		159.03	509.9448	1527.82	-0.0001	-0.1	6.07	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
20200	dirMS_041712_NAR_50mM_plus2.18126.18126.3	3	5.65	0	2.77E+05		(R)DIKPDNI	(R)D I\K P D N F|L/M/G I G R(H)		163.17	492.5943	1475.767	0.0008	0.6	5.96	27968.7	9.69	HUMAN	D6REM4	Casein kinase I isoform alpha
20201	dirMS_041712_NAR_50mM_plus2.20071.20071.3	3	5.65	0	2.09E+05		(R)NEVSFVI	(R)N E/V|S/F V I H N L P\V/L A K(M)		174.5	560.6531	1679.948	-0.0032	-1.9	6.75	35663.7	5.91	HUMAN	B4DWK0	Selenide, water dikinase 1
20202	dirMS_041712_NAR_50mM_plus2.9429.9429.3	3	5.65	0	7.71E+05		(R)DNIQGI	(R)D N|I/Q G\I/T K P A I R(R)		117.22	442.5902	1325.754	0.0025	1.9	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
20203	dirMS_041712_NAR_60mM_plus.10486.10486.3	3	5.65	0	9.97E+05		(K)YAVTTG	(K)Y/A\V/T T G D/H G I I R(T)		112.45	434.9004	1302.68	0.0066	5	6.74	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
20204	dirMS_041712_NAR_120mM_minus.13744.13744.3	3	5.64	1	1.12E+05		(R)KYEMFA	(R)K Y E M F\A Q|T/L/Q/Q S/R(G)		129.37	543.9428	1629.805	0.0085	5.2	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
20205	dirMS_041712_NAR_120mM_minus.16301.16301.3	3	5.64	2	1.19E+05		(K)KQGGLG	(K)K Q G G L G P M N\I|P/L V/S D P K R(T)		143.52	636.3552	1907.053	-0.0021	-1.1	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
20206	dirMS_041712_NAR_20mM_minus.12092.12092.2	2	5.64	0	3.57E+05	M185m	(K)LAVNm	(K)L A|V/N m V/P F P R(L)	m:Oxidized methionine	170.77	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
20207	dirMS_041712_NAR_40mM_minus2.16063.16063.3	3	5.64	1	7.07E+05		(R)ELAILLG	(R)E L A I/L/L G M L D/P A/E K D E K(G)		189.47	629.0034	1884.999	-0.003	-1.6	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
20208	dirMS_041712_NAR_50mM_minus2.16901.16901.3	3	5.64	0	2.82E+04		(K)QTVFLLE	(K)Q T|V/F\L/L E K P F S V K(A)		164.4	512.6325	1535.883	-0.0002	-0.2	8.59	60559.7	5.18	HUMAN	O60678	Protein arginine N-methyltransferase 3
20209	dirMS_041712_NAR_60mM_minus.7351.7351.3	3	5.64	0	1.07E+05	M434m	(R)LESGmC	(R)L E/S\G m/Q N M S I/H T\K(T)	m:Oxidized methionine	99.98	497.9023	1475.698	15.9942	-0.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
20210	dirMS_041712_NAR_120mM_plus.14590.14590.3	3	5.64	1	7.33E+05		(K)LDKSQIH	(K)L D K/S Q I H/D\I\V L|V\G/G S T R(I)		129.98	613.3369	1838.013	-0.0169	-9.2	6.75	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
20211	dirMS_041712_NAR_120mM_plus.18265.18266.3	3	5.64	0	6.47E+05		(R)NCWQN	(R)N/C|W/Q N Y/L D/F H R(C)	C:Carbamidomethylation	149.1	518.2327	1552.675	0.0085	5.5	6.74	12263.5	6.83	HUMAN	J3KPM8	Cytochrome c oxidase subunit 6B1
20212	dirMS_041712_NAR_120mM_plus.5509.5509.3	3	5.64	0	2.91E+05	M21m	(R)SGSmDF	(R)S G\S/m D/P S/G A H/P S V R(Q)	m:Oxidized methionine	81.98	467.5478	1384.627	16.0015	4.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
20213	dirMS_041712_NAR_20mM_plus.11287.11287.2	2	5.64	0	6.87E+04		(R)LAAQFIF	(R)L A/A|Q F I/P K(F)		150.1	444.2681	887.535	-0.006	-6.8	8.75	58250.7	8.99	HUMAN	B4E283	Apoptosis inhibitor 5
20214	dirMS_041712_NAR_20mM_plus.9381.9381.2	2	5.64	0	8.44E+04		(R)ALEESN	(R)A L\E|E/S N|Y E L E G K(I)		136.35	691.3246	1381.648	-0.0062	-4.5	4.09	59054.3	5.14	HUMAN	P13645	Keratin, type I cytoskeletal 10
20215	dirMS_041712_NAR_30mM_plus2.13201.13201.2	2	5.64	0	2.49E+05		(K)FGPALS	(K)F/G|P A L S V/K(V)		122.13	409.7432	818.477	0.0021	2.5	8.75	65918.2	9.74	HUMAN	E7EQV3	Polyadenylate-binding protein 1
20216	dirMS_041712_NAR_30mM_plus2.14367.14367.2	2	5.64	0	3.40E+05		(R)GIFTSEI	(R)G I|F T/S E I G T K(Q)		128.92	526.7806	1052.562	-0.0083	-7.9	6	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
20217	dirMS_041712_NAR_30mM_plus2.7401.7401.2	2	5.64	0	6.06E+04		(R)ANITLSG	(R)A N\I/T L/S\G/K(K)		93.87	402.2347	803.462	0	0	8.8	11656.8	12.34	HUMAN	E9PLD3	Uncharacterized protein
20218	dirMS_041712_NAR_50mM_plus2.10411.10411.3	3	5.64	0	1.39E+05		(R)LIAHAGS	(R)L I/A/H A\G S|L T N L A K(Y)		122	436.9248	1308.763	-0.0036	-2.7	8.76	24485.6	9.74	HUMAN	H0Y653	Nucleolar protein 56 (Fragment)
20219	dirMS_041712_NAR_50mM_plus2.15797.15797.3	3	5.64	0	2.06E+05		(K)YPIEHGI	(K)Y/P/I/E H G I I\T N|W D D M/E K(I)		151.1	654.3085	1960.911	0	0	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
20220	dirMS_041712_NAR_50mM_plus2.5872.5872.3	3	5.64	0	3.28E+05		(K)TVEAEA	(K)T V|E/A E A/A/H G T V T R(H)		94.9	447.8962	1341.676	-0.0017	-1.2	5.37	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
20221	dirMS_041712_NAR_50mM_plus2.9256.9256.3	3	5.64	1	3.17E+04	T194t	(K)EItVHFW	(K)E I t/V/H F W N/G K/A A\K(V)	t:Phosphorylated T	115.58	527.5905	1500.796	79.9612	-3.3	8.69	52692.4	9.25	HUMAN	Q9NQ32	Uncharacterized protein C11orf16
20222	dirMS_041712_NAR_60mM_plus.13343.13343.3	3	5.64	1	4.13E+05		(R)LDDRVY	(R)L/D D R V/Y/A/M C Q I K(S)	C:Carbamidomethylation	126.03	504.5817	1511.735	-0.0039	-2.6	5.96	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
20223	dirMS_041712_NAR_60mM_plus.18990.18990.3	3	5.64	1	2.62E+05		(K)YGKLEV	(K)Y G K L E\V|A/N L/L/L Q K(S)		156.68	496.9628	1488.878	-0.0046	-3.1	8.5	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
20224	dirMS_041712_NAR_60mM_plus.6086.6086.3	3	5.64	1	3.11E+05		(R)GSCSTE	(R)G S\C/S/T E V/E K E T Q E K(M)	C:Carbamidomethylation	91.05	537.9088	1611.717	-0.0048	-3	4.49	13871.4	9.22	HUMAN	O75348	V-type proton ATPase subunit G 1
20225	dirMS_041712_NAR_60mM_plus.7125.7125.3	3	5.64	1	5.16E+05		(K)GLVPED	(K)G L/V/P/E D D T K E K(I)		95.55	410.8799	1230.621	0.0039	3.2	4.32	81733.5	5.24	HUMAN	E9PAW1	Splicing factor 3A subunit 1
20226	dirMS_041712_NAR_60mM_plus.8915.8915.3	3	5.64	0	1.59E+06		(K)EFHLNES	(K)E F H L N E/S/G D|P S S K(S)		105.52	482.8882	1446.65	0.0005	0.3	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
20227	dirMS_041712_NAR_120mM_minus.12491.12491.4	4	5.63	2	2.74E+05		(K)DTSTTTI	(K)D\T S T T T I\R T G/K G H S/N T/E/K(-)		121.18	484.251	1933.957	0.0248	12.8	8.6	15429.2	6.79	HUMAN	B4DR92	UPF0489 protein C5orf22
20228	dirMS_041712_NAR_20mM_minus.12046.12046.2	2	5.63	0	2.31E+05	M185m	(K)LAVNm	(K)L/A V N/m/V P F P R(L)	m:Oxidized methionine	170.15	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
20229	dirMS_041712_NAR_20mM_minus.14712.14712.2	2	5.63	0	1.41E+05		(R)IITLAGP	(R)I I|T L/A|G P T N A I F/K(A)		202.18	679.9047	1358.804	-0.0021	-1.5	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
20230	dirMS_041712_NAR_30mM_minus2.11593.11593.2	2	5.63	0	1.58E+05		(R)TPCEEIL	(R)T/P|C E E I/L V/K(H)	C:Carbamidomethylation	118.02	544.7899	1088.566	0.0069	6.3	4.53	83264.1	6.04	HUMAN	E9PHF0	Filamin-A
20231	dirMS_041712_NAR_30mM_minus2.17702.17702.2	2	5.63	0	1.01E+05		(R)SQVEEEI	(R)S Q|V|E E E L/F S\V R(V)		150.75	661.8369	1322.659	0.0079	5.9	4.25	533778	5.74	HUMAN	Q15149	Plectin
20232	dirMS_041712_NAR_30mM_minus2.19272.19272.2	2	5.63	0	2.47E+05		(R)LTIAILR	(R)L T/I/A I L R(H)		159.37	400.2731	799.54	-0.0011	-1.3	9.75	87498	6.43	HUMAN	C9J266	E3 ubiquitin-protein ligase RNF123
20233	dirMS_041712_NAR_40mM_minus2.10279.10279.3	3	5.63	1	5.84E+05		(K)TITLEVEI	(K)T I|T/L/E V E/P S D T I E N V K A K(I)		144.4	663.0226	1987.059	-0.0061	-3.1	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
20234	dirMS_041712_NAR_50mM_minus2.13114.13114.3	3	5.63	1	1.64E+05		(R)NVIFQP	(R)N V/I\F Q P V A/E L K K(Q)		142.83	462.6086	1385.815	-0.0039	-2.8	8.59	23167	8.94	HUMAN	B1APP8	6-phosphofructokinase type C
20235	dirMS_041712_NAR_50mM_minus2.5952.5952.3	3	5.63	1	2.99E+04		(K)TQSVEIT	(K)T Q/S V/E/I/T K T D T E/G K(I)		96.22	512.9329	1536.775	0.009	5.8	4.68	71678	6.07	HUMAN	Q9Y5K6	CD2-associated protein
20236	dirMS_041712_NAR_120mM_plus.6434.6434.3	3	5.63	1	1.74E+04		(K)DSYVGD	(K)D S/Y/V/G D E A/Q S K R(G)		87.23	452.2133	1354.623	0.002	1.5	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
20237	dirMS_041712_NAR_20mM_plus.9327.9327.2	2	5.63	0	9.62E+03		(K)AEPVEV	(K)A E/P V E/V/V/A P R(G)		135.58	533.798	1066.589	-0.0004	-0.4	4.53	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
20238	dirMS_041712_NAR_40mM_plus2.12697.12697.2	2	5.63	0	6.04E+04		(K)NYIFLR(	(K)N Y|I/F/L R(N)		141.17	413.2357	825.462	0.0024	2.9	8.75	41595	8.51	HUMAN	P78406	mRNA export factor
20239	dirMS_041712_NAR_40mM_plus2.12858.12884.2	2	5.63	1	1.14E+05		(R)RTPDYFI	(R)R T P D\Y|F|L(-)		141.97	456.2358	911.462	0.0022	2.4	5.83	6212.9	6.77	HUMAN	H0YBN9	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform (Fragment)
20240	dirMS_041712_NAR_50mM_plus2.10799.10799.3	3	5.63	1	1.08E+05		(R)EIAQDFI	(R)E I A|Q D/F K T D/L R(F)		124.48	445.9079	1335.69	0.0188	14.1	4.56	14166.5	11.62	HUMAN	B4DEB1	Histone H3
20241	dirMS_041712_NAR_50mM_plus2.9518.9518.3	3	5.63	1	1.58E+05		(R)LGGSPF	(R)L/G|G S|P F G/P A G T G K T E S V K(A)		117.22	563.9657	1689.881	0.0019	1.1	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
20242	dirMS_041712_NAR_60mM_plus.11907.11907.2	2	5.63	1	1.06E+06		(R)FPGQLN	(R)F/P/G\Q\L/N A D/L R\K(L)		119.6	629.8482	1258.69	-0.0011	-0.9	8.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
20243	dirMS_041712_NAR_60mM_plus.14059.14059.3	3	5.63	0	1.49E+05		(K)LAQANG	(K)L A|Q|A N/G W G V M\V S H R(S)		130.15	509.2606	1525.769	-0.002	-1.3	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
20244	dirMS_041712_NAR_60mM_plus.14431.14431.3	3	5.63	0	4.57E+05		(K)NLLHSL	(K)N L|L H S/L Q/S S/G I/G S K(A)		132.03	480.9305	1440.781	-0.0036	-2.5	8.76	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
20245	dirMS_041712_NAR_60mM_plus.19397.19397.3	3	5.63	1	2.05E+05		(R)AGEAGK	(R)A/G E\A|G K L\E E/V|M Q E L R(A)		159.62	553.9525	1659.837	0.0059	3.6	4.49	54918.3	5.61	HUMAN	Q9BR76	Coronin-1B
20246	dirMS_041712_NAR_60mM_plus.7028.7068.3	3	5.63	1	5.99E+05		(R)GIPAPEE	(R)G I|P/A/P E E E R T R(Q)		95.23	418.8876	1254.644	0.0046	3.6	4.79	23092.1	6.93	HUMAN	G3V438	Activator of 90 kDa heat shock protein ATPase homolog 1 (Fragment)
20247	dirMS_041712_NAR_60mM_plus.8601.8601.3	3	5.63	1	4.16E+05		(K)QGIETPE	(K)Q/G I E/T/P E D Q N D L R K(M)		102.63	548.2719	1642.803	-0.002	-1.2	4.32	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
20248	dirMS_041712_NAR_120mM_minus.16096.16096.4	4	5.62	0	6.61E+03	T436t	(R)tQLLDLS	(R)t/Q L L D L S S L Y/Q/A V A T R(E)	t:N-acetylglucosamine (T)	141.75	496.2613	1778.965	203.0587	-10.4	5.5	51577.3	6.49	HUMAN	H0YMZ3	Semaphorin-4B (Fragment)
20249	dirMS_041712_NAR_30mM_minus2.15049.15049.2	2	5.62	1	6.03E+06		(K)INWSKQ	(K)I N W S/K/Q|Q/K(R)		134.48	516.281	1031.563	-0.0085	-8.3	10	526822	6.64	HUMAN	Q9NZJ4	Sacsin
20250	dirMS_041712_NAR_30mM_minus2.16307.16307.2	2	5.62	0	1.09E+05		(K)FGVIFAG	(K)F/G|V|I|F A G A Q K(N)		141.95	519.2901	1037.578	-0.0049	-4.7	8.75	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
20251	dirMS_041712_NAR_30mM_minus2.9071.9071.2	2	5.62	0	4.04E+05		(R)GLEVTD	(R)G L|E|V/T D D S/P K(Y)		103.98	530.7694	1060.516	0.0158	14.9	4.03	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
20252	dirMS_041712_NAR_40mM_minus2.12511.12511.3	3	5.62	0	1.12E+05		(K)GLPQTA	(K)G L/P Q T|A V C N L N/I/T L P A H K(K)	C:Carbamidomethylation	157.42	649.6858	1947.048	-0.0052	-2.7	8.76	112066.5	5.59	HUMAN	B1AQT2	Ankyrin 3, node of Ranvier (Ankyrin G)
20253	dirMS_041712_NAR_60mM_minus.10179.10179.3	3	5.62	1	2.30E+04	T15t	(K)tVNPFLP	(K)t V N P\F L/P S T P/G P/K K(A)	t:Phosphorylated T	115.8	521.6047	1482.832	79.9681	1.1	10	52605.8	6.75	HUMAN	Q7Z572	Spermatogenesis-associated protein 21
20254	dirMS_041712_NAR_120mM_plus.10235.10235.2	2	5.62	0	5.25E+05		(R)VHIEIGP	(R)V/H|I|E I\G P D/G R(V)		105.87	546.7931	1092.58	-0.0007	-0.6	5.32	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
20255	dirMS_041712_NAR_120mM_plus.17508.17508.3	3	5.62	1	8.69E+05	S56s	(K)GLDYLHS	(K)G L D Y L H/s E R/K(I)	s:N-acetylglucosamine (S)	145.62	474.2314	1217.627	203.0523	-19	6.75	39436.2	8.5	HUMAN	A8K6Z3	Serine/threonine-protein kinase 25
20256	dirMS_041712_NAR_120mM_plus.8144.8144.3	3	5.62	1	1.22E+06		(K)MVQFEE	(K)M V|Q F/E/E N G R K(E)		96.97	413.2074	1237.599	0.0083	6.7	5.9	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
20257	dirMS_041712_NAR_120mM_plus.8733.8733.3	3	5.62	1	2.74E+04		(R)TNYNDR	(R)T/N/Y N D R Y D E/I R(R)		99.25	486.8905	1458.661	-0.0038	-2.6	4.55	30166.2	10.79	HUMAN	P62424	60S ribosomal protein L7a
20258	dirMS_041712_NAR_20mM_plus.15544.15544.3	3	5.62	0	1.87E+05		(R)GVVDSE	(R)G V/V\D S E D\I/P/L N L S R(E)		179.25	505.2667	1513.786	-0.0001	-0.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
20259	dirMS_041712_NAR_20mM_plus.16725.16725.2	2	5.62	0	1.65E+05		(K)TVDNFV	(K)T V/D\N F/V/A L A T G E/K(G)		186.22	682.8565	1364.706	0.0001	0.1	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
20260	dirMS_041712_NAR_20mM_plus.19004.19004.2	2	5.62	0	3.29E+03		(R)TTNFAG	(R)T T N\F\A/G I L S Q G L/R(I)		202.27	689.3745	1377.748	-0.0068	-4.9	9.41	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
20261	dirMS_041712_NAR_20mM_plus.19256.19256.2	2	5.62	0	7.00E+03		(R)AFITNIP	(R)A F|I/T N\I/P F D V K(W)		203.68	632.8492	1264.694	-0.0025	-2	5.88	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
20262	dirMS_041712_NAR_20mM_plus.8821.8821.3	3	5.62	1	1.39E+05		(R)QQEPPG	(R)Q Q E/P P G P\A Q R/G D/G P R(D)		130.63	530.6038	1589.778	0.019	11.9	6.07	21936.7	11.52	HUMAN	H0YIG3	Keratin, type II cytoskeletal 72 (Fragment)
20263	dirMS_041712_NAR_30mM_plus2.20235.20235.2	2	5.62	0	1.82E+05		(R)FEELNAI	(R)F E|E/L/N A D L F R(G)		160.58	627.3106	1253.616	-0.0022	-1.7	4.14	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
20264	dirMS_041712_NAR_40mM_plus2.15403.15403.3	3	5.62	0	2.31E+05		(K)GVTIIGP	(K)G V T\I|I/G P A/T V G G I K P G C F K(I)	C:Carbamidomethylation	156.53	624.683	1872.041	-0.0067	-3.6	10	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
20265	dirMS_041712_NAR_50mM_plus2.15548.15548.3	3	5.62	1	5.41E+04		(R)GLNGGI	(R)G L/N|G/G I/T P L N S I S P L K K(N)		149.72	570.3327	1708.996	-0.012	-7.1	10	77923	6.41	HUMAN	B7ZLQ8	CPEB4 protein
20266	dirMS_041712_NAR_50mM_plus2.17818.17818.3	3	5.62	0	2.36E+05		(R)ILVTLLH	(R)I L/V T/L/L H T L/E R(M)		162.35	436.6064	1307.805	0.0001	0.1	6.75	45212.4	9.41	HUMAN	B7Z233	Acetyl-CoA acetyltransferase, cytosolic
20267	dirMS_041712_NAR_50mM_plus2.8087.8087.3	3	5.62	1	1.75E+04		(R)VLVNDA	(R)V L|V/N/D/A Q K\V T E G Q Q E R(L)		108.38	605.3151	1813.94	-0.0095	-5.2	4.68	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
20268	dirMS_041712_NAR_50mM_plus2.8688.8688.3	3	5.62	0	1.95E+04		(R)TVAIYSE	(R)T V/A\I Y/S/E Q D T/G Q M H R(Q)		113.87	579.2737	1735.807	-0.0003	-0.2	5.29	58266.4	9.46	HUMAN	B4DN00	Pyruvate carboxylase, mitochondrial
20269	dirMS_041712_NAR_30mM_minus2.18413.18413.2	2	5.61	0	9.87E+03		(K)LNLGTV	(K)L N\L/G/T/V/G F Y R(T)		154.28	570.3115	1139.621	-0.005	-4.4	8.75	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase

20270	dirMS_041712_NAR_30mM_minus2.19285.19285.2	2	5.61	1	1.57E+05		(K)SKLEFSI	(K)S K L E F S I/Y|P A/P(-)		159.12	626.334	1251.662	-0.0012	-1	5.72	21962.5	5.85	HUMAN	C9JJQ8	Tubulin alpha-4A chain (Fragment)
20271	dirMS_041712_NAR_40mM_minus2.10067.10067.2	2	5.61	0	1.46E+06		(R)VAPEEH	(R)V A/P E E H|P V L L/T E A\P\L N P K(A)		141.5	977.5343	1954.064	-0.0031	-1.6	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
20272	dirMS_041712_NAR_50mM_minus2.12087.12087.3	3	5.61	0	1.57E+05		(K)EMNPAL	(K)E M N/P A/L/G\I/D C L H K(G)	C:Carbamidomethylation	136.93	499.9082	1497.719	-0.0088	-5.9	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
20273	dirMS_041712_NAR_50mM_minus2.16286.16287.3	3	5.61	0	1.54E+05		(K)VVDELN	(K)V/V|D E/L/N L L H T E L A K(Q)		160.45	531.9638	1593.885	-0.0078	-4.9	4.65	16381.6	5.83	HUMAN	F8VWV2	DCC-interacting protein 13-beta (Fragment)
20274	dirMS_041712_NAR_50mM_minus2.9979.9979.3	3	5.61	0	5.70E+05	M147m	(K)LQmEAP	(K)L Q/m E A\P H\I/I V/G/T P G R(V)	m:Oxidized methionine	125.38	545.6267	1618.873	15.9922	-1.7	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
20275	dirMS_041712_NAR_60mM_minus.7989.7989.3	3	5.61	1	3.82E+05	M230m M	(R)mSmKE	(R)m S m K E\V D/E/Q|m L/N\V Q/N K(N)	m:Oxidized methionine	103.83	657.9647	1923.897	47.9823	-1.3	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
20276	dirMS_041712_NAR_20mM_plus.15908.15908.2	2	5.61	1	1.37E+05		(K)EALVSQ	(K)E A L\V S Q|L/S R G K(Q)		181.1	594.3403	1187.674	-0.0009	-0.8	8.85	224067.5	5.64	HUMAN	Q9UKX2	Myosin-2
20277	dirMS_041712_NAR_20mM_plus.6997.6997.2	2	5.61	0	4.27E+05		(R)IQEAGT	(R)I Q|E/A/G T E V V K(A)		115.35	537.2946	1073.584	-0.0018	-1.7	4.53	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
20278	dirMS_041712_NAR_30mM_plus2.13829.13829.2	2	5.61	0	1.44E+05		(K)ITFCTGI	(K)I/T|F/C/T G I/R(V)	C:Carbamidomethylation	125.48	484.2579	967.503	0.0056	5.7	9.75	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
20279	dirMS_041712_NAR_30mM_plus2.6977.6977.2	2	5.61	0	7.69E+04		(R)VSEDVY	(R)V/S|E D/V Y/R(S)		91.13	434.2164	867.421	0.0049	5.6	4.37	71312.8	8.92	HUMAN	P43155	Carnitine O-acetyltransferase
20280	dirMS_041712_NAR_50mM_plus2.15166.15166.3	3	5.61	1	6.48E+05		(R)GFPTIYF	(R)G F/P T I/Y F/S P A N K K(L)		148.47	490.5973	1469.779	-0.0014	-0.9	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
20281	dirMS_041712_NAR_50mM_plus2.17025.17025.3	3	5.61	1	1.77E+06		(R)VTTVTEI	(R)V T/T/V T E I/G K D V I/G L R(I)		156.87	534.308	1600.927	-0.0174	-10.9	6.04	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
20282	dirMS_041712_NAR_50mM_plus2.18020.18020.3	3	5.61	0	7.94E+04		(K)LILPHVD	(K)L I/L/P H/V D I Q L K(Y)		163.23	430.2706	1288.799	-0.0015	-1.2	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
20283	dirMS_041712_NAR_50mM_plus2.19831.19831.3	3	5.61	1	1.66E+05		(R)TSLLTLE	(R)T/S L/L T L E D/V K Q E/L I|K(L)		172.32	577.3359	1729.995	-0.0014	-0.8	4.68	156316.8	8.61	HUMAN	Q7Z478	ATP-dependent RNA helicase DHX29
20284	dirMS_041712_NAR_50mM_plus2.8801.8801.3	3	5.61	1	2.37E+04		(R)GGSDDS	(R)G G/S D/D S S K D|P I D V/N Y E K(L)		114.08	609.2765	1825.809	0.0063	3.5	4.03	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
20285	dirMS_041712_NAR_60mM_plus.16461.16461.3	3	5.61	0	7.52E+05		(K)MTHLPE	(K)M T H L\P E L D/T|L/S/S E R(A)		142.2	543.6023	1628.795	-0.0025	-1.5	4.65	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
20286	dirMS_041712_NAR_60mM_plus.7320.7320.3	3	5.61	1	2.03E+05		(K)KYEEIDN	(K)K Y E E I\D N\A/P E/E R(A)		96.03	498.2381	1492.691	0.0083	5.6	4.25	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
20287	dirMS_041712_NAR_60mM_plus.8111.8111.3	3	5.61	1	6.93E+05		(K)ALSRQEI	(K)A L/S R Q E M\Q/E/V/Q S S R(S)		100.48	550.2735	1648.807	-0.0012	-0.7	6.19	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
20288	dirMS_041712_NAR_120mM_minus.7277.7277.3	3	5.6	1	1.49E+06		(R)CREMDE	(R)C R\E\M|D E/Q/I/R(L)	C:Carbamidomethylation	93.97	412.8591	1236.546	0.0168	13.6	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
20289	dirMS_041712_NAR_20mM_minus.10718.10718.2	2	5.6	0	9.16E+04		(K)FLIPNAS	(K)F L\I|P N A S/Q\A E/S K(V)		154.67	652.8447	1304.685	-0.0024	-1.8	6	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
20290	dirMS_041712_NAR_30mM_minus2.12418.12418.2	2	5.6	0	5.81E+04		(R)GVVGPE	(R)G V|V/G|P E L/Y G R(L)		121.18	523.7834	1046.563	-0.0034	-3.2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
20291	dirMS_041712_NAR_30mM_minus2.18763.18763.3	3	5.6	0	4.14E+04		(R)LNALGF	(R)L N A\L/G F/S L/E Q/R(L)		156.73	416.5615	1247.674	-0.0043	-3.5	6	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
20292	dirMS_041712_NAR_30mM_minus2.20417.20417.2	2	5.6	0	3.99E+05		(R)FLTWIL	(R)F L/T/W I/L N R(Y)		175.78	531.8089	1062.61	0.001	1	9.75	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
20293	dirMS_041712_NAR_40mM_minus2.15146.15146.3	3	5.6	0	7.51E+05		(K)ALIEVLQ	(K)A L|I E|V\L Q/P L I A E H Q A R(R)		175.3	601.0146	1801.033	-0.0038	-2.1	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
20294	dirMS_041712_NAR_50mM_minus2.17312.17312.2	2	5.6	0	2.61E+05		(R)IHFPLAT	(R)I H|F|P L A/T Y\A P V I S A E K(A)		167.35	878.9837	1756.963	-0.0031	-1.8	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
20295	dirMS_041712_NAR_60mM_minus.17016.17016.3	3	5.6	1	2.75E+05	M182m	(R)GmLRED	(R)G m L/R E D A|V|L/E\Y L K(I)	m:Oxidized methionine	154.95	518.2737	1536.809	15.9975	1.7	4.68	67933	6.08	HUMAN	P26038	Moesin
20296	dirMS_041712_NAR_120mM_plus.6137.6137.3	3	5.6	1	7.70E+05		(R)TAQEVE	(R)T/A|Q/E V E/T Y R R(S)		84.7	418.2137	1252.628	-0.0015	-1.2	5.81	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
20297	dirMS_041712_NAR_20mM_plus.19227.19227.2	2	5.6	0	1.54E+05		(R)TGAIVD	(R)T G A\I|V/D V/P V/G E E L L G R(V)		204.4	812.9497	1624.891	0.0017	1	4.14	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
20298	dirMS_041712_NAR_30mM_plus2.5113.5113.2	2	5.6	0	9.98E+04		(K)SACGVC	(K)S A C|G V/C P\G/R(L)	C:Carbamidomethylation	79.63	482.2128	963.414	0.0048	5	9.47	13520.9	11.92	HUMAN	P49207	60S ribosomal protein L34
20299	dirMS_041712_NAR_40mM_plus2.7905.7905.2	2	5.6	0	1.43E+05		(K)ASLENSL	(K)A/S|L E/N S L R(E)		106.82	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
20300	dirMS_041712_NAR_40mM_plus2.9658.9658.2	2	5.6	0	1.27E+05		(K)FYEAFSK	(K)F/Y|E/A F/S K(N)		120.15	446.2159	891.425	-0.0002	-0.2	6	20127.1	9.4	HUMAN	H0Y598	Heat shock protein HSP 90-beta (Fragment)
20301	dirMS_041712_NAR_50mM_plus2.13069.13069.3	3	5.6	1	4.12E+05		(K)DMESPT	(K)D M/E/S/P T K L D V T L A K(D)		136.93	516.6001	1547.799	-0.0128	-8.3	4.56	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
20302	dirMS_041712_NAR_50mM_plus2.16814.16814.3	3	5.6	1	6.78E+06		(K)QLDDLK	(K)Q L D D L/K/V/E L/S/Q L R(V)		155.75	519.6261	1556.864	-0.0005	-0.3	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
20303	dirMS_041712_NAR_50mM_plus2.17835.17835.3	3	5.6	1	2.25E+04		(R)EVLEAL	(R)E V/L E|A/L/G E V M V S R P R E(-)		161.83	605.3151	1813.948	-0.0169	-9.3	4.69	59918.2	5.27	HUMAN	E9PC67	ATP-binding cassette sub-family F member 1
20304	dirMS_041712_NAR_50mM_plus2.8919.8919.3	3	5.6	2	1.54E+05	S706s	(K)KTDKSIL	(K)K T D/K S I L V/s\P T/G P S/R(V)	s:Phosphorylated S	114.37	555.9644	1585.891	79.9879	12.9	9.99	84825.4	9.89	HUMAN	Q14684	Ribosomal RNA processing protein 1 homolog B
20305	dirMS_041712_NAR_60mM_plus.11654.11654.3	3	5.6	1	2.78E+04		(R)GMDLQ	(R)G M/D\L Q/P/G N A L K/R(F)		119.22	433.8981	1299.684	-0.004	-3.1	8.75	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
20306	dirMS_041712_NAR_60mM_plus.13477.13477.3	3	5.6	1	6.01E+06		(R)VVDLM	(R)V V/D L M A/H M A/S K E(-)		127.27	444.2219	1330.649	0.0018	1.3	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
20307	dirMS_041712_NAR_120mM_minus.20339.20339.4	4	5.59	1	2.73E+05		(R)GIEKPPF	(R)G I E K/P P F E L/P D F I K R(T)		167.05	447.2523	1785.99	-0.0024	-1.4	6.18	98282.7	5.49	HUMAN	E9PPJ0	Splicing factor 3B subunit 2
20308	dirMS_041712_NAR_120mM_minus.5384.5384.2	2	5.59	1	1.25E+05		(R)KAYGQA	(R)K|A\Y G Q A L/A K(L)		82.73	475.2763	949.547	-0.0012	-1.3	9.7	63448.4	7.29	HUMAN	B4E022	Transketolase
20309	dirMS_041712_NAR_120mM_minus.9665.9665.3	3	5.59	1	3.36E+05		(R)ALSTGE	(R)A/L|S T/G E K G F G Y K(G)		107	419.8868	1257.647	-0.0015	-1.2	8.54	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
20310	dirMS_041712_NAR_20mM_minus.11611.11611.2	2	5.59	0	2.23E+05		(R)GDLGIEI	(R)G D L G\I|E/I/P A E\K(V)		163.93	571.3078	1141.61	-0.0016	-1.4	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
20311	dirMS_041712_NAR_20mM_minus.13663.13663.3	3	5.59	0	2.07E+05		(R)QAQEYE	(R)Q A Q E Y\E|A/L/L/N I K(V)		187.08	473.9203	1419.748	-0.0015	-1	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
20312	dirMS_041712_NAR_20mM_minus.8217.8217.2	2	5.59	0	1.44E+05		(K)DVGSLA	(K)D V|G\S/L/A/S V Q R(Y)		132.02	516.2772	1031.548	-0.0009	-0.8	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin
20313	dirMS_041712_NAR_30mM_minus2.16556.16556.2	2	5.59	0	2.80E+05		(R)ASLEAAI	(R)A S L E A/A/I/A D/A/E/Q R(G)		143.7	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
20314	dirMS_041712_NAR_30mM_minus2.16975.16975.2	2	5.59	0	1.97E+05	M2243m	(K)mSIYQA	(K)m S I|Y/Q/A M/W K(G)	m:Oxidized methionine	145.78	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
20315	dirMS_041712_NAR_50mM_minus2.14635.14635.3	3	5.59	1	1.31E+05	M405m	(K)LSKNEVI	(K)L S K/N E V L m V N\I/G S L/S T/G G R(V)	m:Oxidized methionine	151.43	664.3565	1975.064	15.9909	-2	8.75	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
20316	dirMS_041712_NAR_50mM_minus2.18196.18196.3	3	5.59	1	6.74E+05		(R)VLEALLP	(R)V/L/E/A/L L/P L K G L E E R(V)		172.47	527.3171	1579.942	-0.005	-3.2	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
20317	dirMS_041712_NAR_60mM_minus.15252.15252.3	3	5.59	0	2.18E+05		(R)YQEALH	(R)Y Q|E A L/H/L/G S Q L L\R(E)		144.63	509.9455	1527.828	-0.0059	-3.8	6.75	47748.2	6.08	HUMAN	O00231	26S proteasome non-ATPase regulatory subunit 11
20318	dirMS_041712_NAR_60mM_minus.16430.16430.3	3	5.59	1	3.17E+05		(K)LKLSILYF	(K)L K L S I\L Y|P A/T T G R(N)		151.1	478.2883	1432.852	-0.0019	-1.3	9.99	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
20319	dirMS_041712_NAR_60mM_minus.6558.6558.3	3	5.59	1	2.18E+05		(R)KTGQAP	(R)K\T G/Q A\P G\Y|S Y T/A A/N K(N)		95.27	519.5963	1556.77	0.004	2.6	9.53	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
20320	dirMS_041712_NAR_120mM_plus.5430.5430.3	3	5.59	0	2.33E+05	S336s	(R)FsPVEM	(R)F/s P/V/E M A I/R(T)	s:N-acetylglucosamine (S)	82.05	418.2137	1049.545	203.0817	1.9	6	41525.7	8.53	HUMAN	A8MYZ0	Protein FAM188B2
20321	dirMS_041712_NAR_20mM_plus.10315.10315.2	2	5.59	0	1.14E+05	M189m M	(K)SLAmEm	(K)S L|A m/E m V/L/T/G D R(I)	m:Oxidized methionine	144.07	677.8126	1322.644	31.9736	-12	4.37	31843.3	8.87	HUMAN	P30084	Enoyl-CoA hydratase, mitochondrial
20322	dirMS_041712_NAR_20mM_plus.13959.13959.3	3	5.59	0	2.35E+05	M313m	(R)TVQSLEI	(R)T V Q S L E I/D/L|D S m/R(N)	m:Oxidized methionine	168.4	508.2519	1506.747	15.9943	-0.4	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
20323	dirMS_041712_NAR_20mM_plus.14081.14081.2	2	5.59	0	2.09E+05	S461s	(K)SLSEAsV	(K)S\L|S E A s/V\A V D R(F)	s:N-acetylglucosamine (S)	168.68	668.8371	1133.58	203.0872	5.9	4.37	53403.3	9.78	HUMAN	F8WCY8	Multidrug resistance-associated protein 5
20324	dirMS_041712_NAR_30mM_plus2.16515.16515.2	2	5.59	0	3.14E+05		(R)LWDLTT	(R)L W|D\L/T/T G T T T R(R)		139.72	632.8304	1264.653	0.0003	0.3	5.84	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
20325	dirMS_041712_NAR_30mM_plus2.4482.4482.2	2	5.59	0	3.72E+05		(R)SYTSGP	(R)S Y|T/S G/P G S R(I)		73.08	456.2155	911.422	0.002	2.2	8.46	19288.4	10.19	HUMAN	F8VQY3	Keratin, type II cytoskeletal 8 (Fragment)
20326	dirMS_041712_NAR_30mM_plus2.5564.5564.2	2	5.59	0	1.90E+04		(R)YQEQGC	(R)Y Q|E/Q\G G E\A\S/P Q R(T)		83.22	675.3045	1349.608	-0.0063	-4.7	4.53	37271.3	5.01	HUMAN	B4DEM2	Drebrin-like protein
20327	dirMS_041712_NAR_30mM_plus2.7782.7782.2	2	5.59	0	3.15E+05		(R)AQIDNL	(R)A Q|I/D/N L/T R(E)		94.68	465.7534	930.5	-0.0008	-0.9	5.88	334221.3	6.44	HUMAN	P15924	Desmoplakin
20328	dirMS_041712_NAR_30mM_plus2.9495.9496.2	2	5.59	0	7.10E+05		(K)LIEVDDE	(K)L I|E/V D/D/E R(K)		104.63	494.7532	988.495	0.0046	4.6	3.91	10471.9	5.4	HUMAN	A2A3R7	40S ribosomal protein S6
20329	dirMS_041712_NAR_40mM_plus2.12198.12198.3	3	5.59	1	3.30E+03	M62m	(R)LPAAGV	(R)L P/A/A G V G D/M|V m A T V K K(G)	m:Oxidized methionine	137.97	535.2935	1587.86	16.0063	7.1	8.59	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
20330	dirMS_041712_NAR_40mM_plus2.9285.9285.2	2	5.59	0	5.48E+04		(K)TIAPALV	(K)T I|A|P A L V S K(K)		116.88	450.2765	899.556	-0.0103	-11.5	8.41	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
20331	dirMS_041712_NAR_50mM_plus2.17810.17810.3	3	5.59	0	1.46E+05		(K)SPILLGSI	(K)S P/I/L L G/S L A/H Q I Y/R(M)		161.63	523.3008	1567.896	-0.0076	-4.9	8.49	35727.7	8.87	HUMAN	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial
20332	dirMS_041712_NAR_50mM_plus2.21894.21894.3	3	5.59	0	2.98E+04		(K)GLAPDLI	(K)G L/A/P D/L/P E/D L Y H/L I K(K)		186.45	565.3101	1693.916	-0.0002	-0.1	4.54	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
20333	dirMS_041712_NAR_60mM_plus.11653.11679.3	3	5.59	1	2.78E+04		(R)GMDLQ	(R)G M|D|L Q/P G N A L K R(F)		119.22	433.8981	1299.684	-0.004	-3.1	8.75	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
20334	dirMS_041712_NAR_60mM_plus.12737.12737.3	3	5.59	0	3.02E+05		(R)ILHLLGC	(R)I L H\L L/G\Q E|G P K(T)		123.6	402.2397	1204.705	-0.0003	-0.2	6.75	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
20335	dirMS_041712_NAR_60mM_plus.6622.6622.3	3	5.59	0	7.55E+05		(K)LVDQSG	(K)L/V D\Q/S G P\P H E P K(F)		93.77	435.2257	1303.664	-0.0015	-1.2	5.32	142137.5	9.17	HUMAN	E7ENU4	Double-stranded RNA-specific adenosine deaminase
20336	dirMS_041712_NAR_120mM_minus.11705.11705.3	3	5.58	0	4.59E+05		(R)NLCHFQ	(R)N L/C H/F Q/A/L/G C/R(T)	C:Carbamidomethylation	117.9	459.2166	1375.636	-0.0005	-0.4	9.75	27594.3	8.15	HUMAN	H0Y6C3	Pyrroline-5-carboxylate reductase 3 (Fragment)
20337	dirMS_041712_NAR_120mM_minus.13284.13284.4	4	5.58	0	3.03E+05		(R)VLSAPPI	(R)V L/S A/P P/H F H F/G Q T N R(T)		126.7	427.7219	1707.871	-0.0056	-3.3	9.74	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
20338	dirMS_041712_NAR_120mM_minus.20805.20805.4	4	5.58	1	5.83E+05		(R)SLHDAL	(R)S L H D A L C\V L A Q T/V K/D/S R(T)	C:Carbamidomethylation	173.1	479.0049	1912.991	0.0068	3.6	6.47	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
20339	dirMS_041712_NAR_30mM_minus2.19360.19360.2	2	5.58	0	1.17E+05	S852s	(R)FsLNLGS	(R)F s L N L G/S I T/D/A P K(S)	s:N-acetylglucosamine (S)	160.42	783.4108	1362.726	203.088	5.5	5.84	555035.4	6.1	HUMAN	Q9Y6V0	Protein piccolo
20340	dirMS_041712_NAR_30mM_minus2.7997.7997.2	2	5.58	0	1.83E+05		(K)GSGTAE	(K)G S/G T/A/E V E/L K(K)		98.32	495.7528	990.51	-0.0119	-12	4.53	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
20341	dirMS_041712_NAR_30mM_minus2.9547.9547.2	2	5.58	0	2.45E+05		(K)ATFDAIS	(K)A/T|F/D A I S/K(T)		105.97	426.7259	852.446	-0.0016	-1.9	5.88	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
20342	dirMS_041712_NAR_50mM_minus2.11306.11306.3	3	5.58	1	1.14E+05		(K)AVAFSP	(K)A V|A/F/S P V/T E L K K(D)		132.35	430.585	1289.746	-0.0059	-4.6	8.64	85815.7	7.35	HUMAN	P17858	6-phosphofructokinase, liver type
20343	dirMS_041712_NAR_50mM_minus2.11365.11365.3	3	5.58	1	1.29E+05		(K)NQVALN	(K)N Q/V/A|L N/P Q N T/V F D A K R(L)		132.68	605.6545	1814.951	-0.0018	-1	8.75	70336.2	5.48	HUMAN	P08107	Heat shock 70 kDa protein 1A/1B
20344	dirMS_041712_NAR_50mM_minus2.14150.14150.3	3	5.58	1	1.31E+05		(R)QFVPIK	(R)Q F V/P I/K V E Q I\E/A/G T P G R(L)		148.68	623.6775	1869.023	-0.0049	-2.6	6.14	55287.2	6.08	HUMAN	B2R5P6	Thioredoxin reductase 1, cytoplasmic
20345	dirMS_041712_NAR_50mM_minus2.5873.5873.3	3	5.58	1	4.33E+04		(R)AIEAAP	(R)A I|E/A/A/P Q E P E\Q K R(S)		95.43	489.5922	1466.76	0.0023	1.5	4.79	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
20346	dirMS_041712_NAR_60mM_minus.10366.10366.3	3	5.58	0	5.97E+05		(K)AQVARP	(K)A Q|V/A R P G G D T I/F/G K(I)		117.88	472.9235	1416.759	-0.0034	-2.4	8.79	7323.5	9.4	HUMAN	D6RC06	Histidine triad nucleotide-binding protein 1
20347	dirMS_041712_NAR_60mM_minus.11276.11276.3	3	5.58	1	8.89E+05		(R)FPGQLN	(R)F/P G Q/L|N A D L R K(L)		122.05	420.2346	1258.69	-0.001	-0.8	8.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
20348	dirMS_041712_NAR_60mM_minus.11402.11402.2	2	5.58	0	1.82E+05		(R)HEIVQTI	(R)H/E|I/V Q\T L S L K(D)		123.68	584.3389	1167.673	-0.0027	-2.3	6.75	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
20349	dirMS_041712_NAR_60mM_minus.15705.15705.3	3	5.58	0	3.38E+05		(R)IYSHSLLI	(R)I Y/S H S L/L/P/V L R(S)		148	433.2572	1297.763	-0.0056	-4.3	8.75	60871.9	6.3	HUMAN	B4DJ93	Phosphoribosylformylglycinamidine cyclo-ligase
20350	dirMS_041712_NAR_60mM_minus.15723.15723.3	3	5.58	1	3.12E+05		(K)VAAIRGI	(K)V/A|A I R G E V T A\A D/L|F N S R(V)		147.35	597.3237	1789.956	0.001	0.6	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
20351	dirMS_041712_NAR_60mM_minus.5470.5470.3	3	5.58	1	1.87E+05		(R)GLPAPG	(R)G L/P/A/P G P S P A D K/K(R)		86.03	412.2311	1234.679	-0.0003	-0.2	8.59	53139.8	6.18	HUMAN	P42768	Wiskott-Aldrich syndrome protein
20352	dirMS_041712_NAR_120mM_plus.20925.20925.4	4	5.58	0	2.63E+05		(K)ALEHAF	(K)A L/E H A F\Q L E H/I/M D/L T R(L)		163.27	481.7493	1923.975	0.0008	0.4	5.27	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
20353	dirMS_041712_NAR_20mM_plus.12713.12713.2	2	5.58	0	1.07E+05		(R)LAVEAL	(R)L A|V|E/A L V/R(T)		160.57	435.7739	870.541	-0.0002	-0.2	6	65558.6	9.87	HUMAN	G3V1S7	Hyaluronan synthase 1
20354	dirMS_041712_NAR_20mM_plus.17507.17507.3	3	5.58	0	6.38E+03		(K)ITNLTQC	(K)I T N L T\Q Q|L/E Q A S/I V/K(K)		192.28	562.6523	1685.943	-0.0009	-0.5	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
20355	dirMS_041712_NAR_30mM_plus2.13830.13830.2	2	5.58	0	1.91E+05		(K)YSSNLGI	(K)Y S|S N/L/G/N\F N Y E/R(S)		125.3	732.3364	1463.655	0.0105	7.2	6	57111.4	5.72	HUMAN	Q9BZZ5-2	Isoform 2 of Apoptosis inhibitor 5
20356	dirMS_041712_NAR_30mM_plus2.16096.16096.2	2	5.58	0	1.11E+05		(R)ITQLPCL	(R)I T/Q/L P C L/K(V)	C:Carbamidomethylation	136.43	486.7894	972.555	0.0169	17.3	8.75	46798.4	10.09	HUMAN	Q8N1E6	F-box/LRR-repeat protein 14
20357	dirMS_041712_NAR_30mM_plus2.4023.4023.2	2	5.58	0	5.39E+05	M299m M	(K)NmmAA	(K)N m\m|A\A C\D|P R(H)	C:Carbamidomethylation m:Oxid	67.75	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
20358	dirMS_041712_NAR_40mM_plus2.13586.13586.3	3	5.58	0	7.35E+04		(K)LINSLYPI	(K)L I/N S L Y P P G Q E/P I P K(I)		146.3	555.9769	1665.921	-0.0049	-2.9	6	8937.1	9.16	HUMAN	H7C5N2	Transgelin-3 (Fragment)
20359	dirMS_041712_NAR_40mM_plus2.6540.6540.2	2	5.58	0	5.93E+04		(K)TDEGIA	(K)T/D|E/G I/A Y R(G)		97.82	462.7191	924.442	-0.0112	-12.1	4.37	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
20360	dirMS_041712_NAR_40mM_plus2.8406.8406.2	2	5.58	0	2.62E+05		(R)FGSGM	(R)F/G|S|G|M N M G R(I)		109.52	478.706	956.408	-0.003	-3.1	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
20361	dirMS_041712_NAR_50mM_plus2.10016.10016.2	2	5.58	1	1.45E+05		(K)ATAVVD	(K)A/T\A\V/V D\G A\F K E V K(L)		119.97	667.8687	1334.731	-0.0013	-1	6.11	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
20362	dirMS_041712_NAR_60mM_plus.13175.13175.3	3	5.58	1	3.99E+04	M2152m	(R)mALLAT	(R)m/A L L A/T/V L G R F(-)	m:Oxidized methionine	125.95	403.2318	1191.692	15.989	-4.9	9.5	238243.7	6.1	HUMAN	F8VPD4	CAD protein
20363	dirMS_041712_NAR_60mM_plus.17032.17032.3	3	5.58	1	2.25E+05		(R)ASLISAV	(R)A/S L I/S A/V/S D K L/R(W)		145.97	420.5832	1259.732	0.0033	2.6	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
20364	dirMS_041712_NAR_60mM_plus.18651.18651.3	3	5.58	0	1.58E+04		(R)GFGHIG	(R)G F G H I G I\A V|P/D V Y/S A C K(R)	C:Carbamidomethylation	154.07	597.6338	1790.889	-0.0026	-1.4	6.74	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
20365	dirMS_041712_NAR_60mM_plus.19161.19161.3	3	5.58	1	5.73E+03		(K)EVLAELE	(K)E V/L/A E/L E/A L E/R R(V)		158.1	476.5985	1427.785	-0.0043	-3	4.49	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
20366	dirMS_041712_NAR_60mM_plus.8168.8168.3	3	5.58	1	6.84E+05		(R)FEPYANI	(R)F E|P/Y/A N/P T K R(Y)		100.87	408.2176	1222.622	0.0167	13.7	8.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
20367	dirMS_041712_NAR_120mM_minus.14462.14462.3	3	5.57	1	1.43E+05	M313m	(R)RTVQSLI	(R)R T V Q\S|L\E|I D|L D S m R(N)	m:Oxidized methionine	133.25	560.2849	1662.848	15.9922	-1.6	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
20368	dirMS_041712_NAR_30mM_minus2.11049.11049.2	2	5.57	0	5.46E+05		(R)FASGGC	(R)F/A|S\G G/C D N L I/K(L)	C:Carbamidomethylation	113.6	591.2858	1181.562	0.0024	2	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
20369	dirMS_041712_NAR_30mM_minus2.6464.6464.2	2	5.57	0	1.88E+05		(R)ASFNNP	(R)A/S|F/N/N/P D R(A)		89.48	460.7171	920.422	0.0049	5.3	5.88	35061.2	4.66	HUMAN	G5E9P0	RAD23 homolog B (S. cerevisiae), isoform CRA_a
20370	dirMS_041712_NAR_30mM_minus2.8908.8908.2	2	5.57	0	1.36E+05	M328m	(K)ALmDEV	(K)A L|m/D E/V V K(A)	m:Oxidized methionine	103.57	460.7407	904.481	15.9933	-1.8	4.37	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
20371	dirMS_041712_NAR_40mM_minus2.7840.7840.3	3	5.57	1	1.59E+05		(R)DGKLVS	(R)D/G K L V\S E/S/S/D V L P K(-)		125.2	491.9311	1473.78	-0.0008	-0.5	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
20372	dirMS_041712_NAR_60mM_minus.11556.11556.3	3	5.57	1	1.59E+05		(K)EIADYLA	(K)E I A D/Y L/A A G K D E R(A)		124.38	484.2432	1450.717	-0.0022	-1.5	4.32	41736.1	5.41	HUMAN	A8KAH5	IST1 homolog
20373	dirMS_041712_NAR_60mM_minus.14115.14115.3	3	5.57	1	1.20E+05		(R)SILKIDD	(R)S I/L\K I\D D\V|V/N T R(-)		138.5	458.2637	1372.78	-0.0029	-2.1	5.68	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
20374	dirMS_041712_NAR_20mM_plus.17806.17806.3	3	5.57	0	1.79E+05		(R)TVQSLEI	(R)T V\Q/S\L E I D/L D S/M R(N)		194.8	502.9236	1506.747	0.0094	6.2	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
20375	dirMS_041712_NAR_40mM_plus2.17072.17072.3	3	5.57	0	1.24E+05		(K)LQAVEV	(K)L Q/A/V/E V V I\T H L A/P G T K(H)		166.93	559.3259	1675.974	-0.011	-6.6	6.75	16120	9.05	HUMAN	Q9Y2V2	Calcium-regulated heat stable protein 1
20376	dirMS_041712_NAR_50mM_plus2.16398.16398.3	3	5.57	1	7.13E+04		(R)WFQQK	(R)W/F Q Q/K Y D/G I I L/P G\K(-)		154.48	564.9788	1692.911	0.011	6.5	8.5	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
20377	dirMS_041712_NAR_50mM_plus2.19516.19516.3	3	5.57	0	7.75E+05		(R)DFNHIN	(R)D F\N H I N\V/E/L/S L L G K(K)		170.17	533.6223	1598.854	-0.0013	-0.8	5.32	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
20378	dirMS_041712_NAR_60mM_plus.22148.22148.3	3	5.57	0	2.57E+05	K120k	(K)IILYENP	(K)I I L/Y E N P/N F T G k(K)	k:Ubiquitin-K	190.15	508.2614	1408.747	114.0226	-13.4	6	23493.6	6.5	HUMAN	P43320	Beta-crystallin B2

20379	dirMS_041712_NAR_60mM_plus.7409.7409.3	3	5.57	1	1.93E+06		(R)SEEKISD	(R)S E|E K I/S\D/S E G F K(A)		96.8	452.5501	1355.632	0.0032	2.4	4.41	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
20380	dirMS_041712_NAR_60mM_plus.8824.8824.3	3	5.57	1	5.73E+05		(K)ELKSPDE	(K)E L/K S P/D E/G F E G K(S)		104.5	445.8862	1335.643	0.0014	1	4.41	84557.3	6.5	HUMAN	Q04609	Glutamate carboxypeptidase 2
20381	dirMS_041712_NAR_120mM_minus.11868.11889.4	4	5.56	1	1.33E+06		(K)LGLRPGI	(K)L G L R P G\I|H H S\L F G D V K K(L)		118.48	469.2701	1874.076	-0.0173	-9.3	9.99	63309.2	9.46	HUMAN	H7BXW3	Melanoma-associated antigen D2
20382	dirMS_041712_NAR_120mM_minus.12158.12158.4	4	5.56	1	1.23E+06		(K)TLTTVQ	(K)T L T T V Q/G I/A/D D Y D K K/K(L)		120.03	449.7423	1795.944	0.0038	2.1	5.71	13778.5	7.96	HUMAN	K7EM18	Eukaryotic translation initiation factor 1
20383	dirMS_041712_NAR_30mM_minus2.14371.14600.2	2	5.56	0	5.48E+05		(K)SNFAEAI	(K)S N/F A|E A L A A H/K(Y)		132.62	579.7876	1158.59	-0.0223	-19.2	6.47	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
20384	dirMS_041712_NAR_30mM_minus2.18829.18829.2	2	5.56	0	1.91E+05		(K)CFSVLGF	(K)C F/S V/L G F/C K(S)	C:Carbamidomethylation	157.42	559.2673	1117.517	0.0104	9.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
20385	dirMS_041712_NAR_30mM_minus2.6570.6570.2	2	5.56	0	9.40E+04		(K)VLENAE	(K)V L|E\N A E/G A R(T)		89.9	479.7505	958.495	-0.0015	-1.6	4.53	6809.6	9.69	HUMAN	D6RA73	Stress-70 protein, mitochondrial (Fragment)
20386	dirMS_041712_NAR_40mM_minus2.12744.12744.3	3	5.56	0	3.80E+05		(K)FTISDHP	(K)F T/I S D H/P Q P I D/P L L\K(N)		159.45	574.3124	1720.927	-0.0042	-2.4	5.21	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
20387	dirMS_041712_NAR_40mM_minus2.14607.14607.3	3	5.56	1	1.01E+06		(K)TFVNITP	(K)T F\V\N I T/P A E V G V L\V G K D R(S)		171.55	639.0252	1915.065	-0.0037	-1.9	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
20388	dirMS_041712_NAR_40mM_minus2.14946.14946.3	3	5.56	0	9.64E+05		(K)ISSIQSIV	(K)I/S S I Q S I/V/P A L/E I A N A H R(K)		172.28	640.3618	1919.071	0	0	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
20389	dirMS_041712_NAR_50mM_minus2.7171.7171.3	3	5.56	1	2.32E+04		(K)AAAAAS	(K)A A|A/A/A S A/A G P G G L V A G K E E K(K)		107.67	575.9781	1725.913	0.0068	3.9	6.18	28364.3	5.45	HUMAN	A6NIH7	Protein unc-119 homolog B
20390	dirMS_041712_NAR_50mM_minus2.7940.7940.2	2	5.56	1	1.27E+05	M239m	(R)MQKEIT	(R)M/Q\K E\I|T\A L\A|P S T m K(I)	m:Oxidized methionine	112.32	782.9062	1548.812	15.9927	-1.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
20391	dirMS_041712_NAR_50mM_minus2.8125.8125.3	3	5.56	1	1.57E+05		(K)GILAADE	(K)G I\L|A/A D E/S T G S I A K R(L)		113.93	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
20392	dirMS_041712_NAR_60mM_minus.16397.16397.3	3	5.56	0	3.81E+04		(R)NHLLPD	(R)N H\L\L P D I\V|T C/V/Q S S R(K)	C:Carbamidomethylation	151.35	580.3021	1738.891	0.0013	0.7	6.74	20940.9	10.04	HUMAN	Q9BSD7	Cancer-related nucleoside-triphosphatase
20393	dirMS_041712_NAR_120mM_plus.24038.24038.3	3	5.56	1	2.96E+05	M145m	(R)GVmLA	(R)G V/m|L/A V D A V/I A E/L K K(Q)	m:Oxidized methionine	180.07	524.9713	1556.908	15.9913	-2.3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
20394	dirMS_041712_NAR_120mM_plus.6494.6494.2	2	5.56	0	4.57E+05		(K)HQPTAII	(K)H Q|P T A I/I\A K(T)		87.75	489.7897	978.573	-0.001	-1	8.76	63448.4	7.29	HUMAN	B4E022	Transketolase
20395	dirMS_041712_NAR_20mM_plus.10610.10610.2	2	5.56	0	4.02E+04		(R)TPTAPA	(R)T/P/T A|P A V N L A G A R(T)		145.83	619.8456	1238.685	-0.0012	-1	9.41	300351.7	12.1	HUMAN	Q9UQ35	Serine/arginine repetitive matrix protein 2
20396	dirMS_041712_NAR_20mM_plus.12192.12192.2	2	5.56	0	1.59E+05		(K)DLAGSII	(K)D L/A/G S I/I/G K(G)		157.8	437.2558	873.504	0.0003	0.4	5.84	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
20397	dirMS_041712_NAR_20mM_plus.9350.9350.2	2	5.56	0	9.62E+03		(K)AEPVEV	(K)A E|P V/E V V/A/P R(G)		135.58	533.798	1066.589	-0.0004	-0.4	4.53	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
20398	dirMS_041712_NAR_30mM_plus2.11500.11500.2	2	5.56	0	3.61E+05		(R)NGDFLP	(R)N/G|D|F/L|P T|R(L)		113.78	460.2391	919.463	0.0077	8.4	5.84	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
20399	dirMS_041712_NAR_30mM_plus2.21450.21450.2	2	5.56	0	3.33E+05		(R)NSYLEVL	(R)N S|Y/L/E V L L K(L)		167.73	539.8092	1078.614	-0.0032	-2.9	6	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
20400	dirMS_041712_NAR_40mM_plus2.6433.6433.2	2	5.56	0	2.12E+05	M154m	(R)mGYMD	(R)m G/Y\M D/P/R(E)	m:Oxidized methionine	96.87	443.1854	869.364	15.9991	4.7	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
20401	dirMS_041712_NAR_40mM_plus2.6535.6535.2	2	5.56	0	6.37E+04		(R)SDYDGI	(R)S D/Y/D/G I G S R(G)		97.52	485.2217	969.427	0.0089	9.2	4.21	15031.5	6.72	HUMAN	B4DLA0	ATP-dependent RNA helicase DDX3X
20402	dirMS_041712_NAR_50mM_plus2.12397.12397.3	3	5.56	1	2.80E+05		(R)ESDVPLI	(R)E S D\V/P L/K/T E E F E V T K(T)		132.68	584.2981	1750.874	0.0052	3	4.25	18909	6.21	HUMAN	Q969H8	UPF0556 protein C19orf10
20403	dirMS_041712_NAR_50mM_plus2.13126.13126.3	3	5.56	1	2.67E+05		(K)ATEPVIA	(K)A T E/P V I A F/Y E K R(G)		137.27	475.2562	1423.758	-0.0039	-2.8	6.19	15567.5	8.13	HUMAN	H0Y4J6	Adenylate kinase isoenzyme 1 (Fragment)
20404	dirMS_041712_NAR_50mM_plus2.14108.14108.3	3	5.56	0	6.71E+05		(K)QMVID	(K)Q M V/I/D V/L H P G K(A)		142.27	412.894	1236.677	-0.0095	-7.6	6.74	32886.5	10.63	HUMAN	E7EPK6	40S ribosomal protein S24
20405	dirMS_041712_NAR_50mM_plus2.6098.6098.3	3	5.56	0	1.25E+05		(R)SGSMDI	(R)S G\S|M/D P/S G A H P S V R(Q)		96.5	462.214	1384.627	0.0001	0	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
20406	dirMS_041712_NAR_50mM_plus2.8692.8692.3	3	5.56	1	2.37E+04		(R)GGSDDS	(R)G G/S/D/D/S S K D\P I/D V N Y E K(L)		114.08	609.2765	1825.809	0.0063	3.5	4.03	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
20407	dirMS_041712_NAR_120mM_minus.10004.10004.4	4	5.55	0	3.14E+05		(K)LITQTFS	(K)L I/T Q/T F/S/H H N Q L A Q K(T)		108.88	442.2355	1765.934	-0.0142	-8.1	8.76	38299.3	5.27	HUMAN	Q9Y266	Nuclear migration protein nudC
20408	dirMS_041712_NAR_120mM_minus.11642.11642.4	4	5.55	1	4.65E+05		(K)AAQASD	(K)A A\Q|A S D L E K/I H L D/E K(S)		117.83	417.7202	1667.86	-0.0009	-0.6	4.75	37710.6	6.36	HUMAN	P37837	Transaldolase
20409	dirMS_041712_NAR_30mM_minus2.11542.11542.2	2	5.55	0	1.57E+05		(K)SIDTGM	(K)S I/D/T/G\M/G\L E R(L)		116.67	539.7654	1078.52	0.0038	3.5	4.37	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
20410	dirMS_041712_NAR_30mM_minus2.15665.15665.2	2	5.55	0	1.99E+05		(R)IGSGFDI	(R)I G|S/G F/D/N I D/I/K(S)		138.88	589.8069	1178.605	0.0013	1.1	4.21	20631.5	6.98	HUMAN	D6RAX2	C-terminal-binding protein 1 (Fragment)
20411	dirMS_041712_NAR_30mM_minus2.9907.9907.2	2	5.55	0	1.44E+05		(R)SSTETCY	(R)S S T/E/T/C Y/S A I/P K(A)	C:Carbamidomethylation	108.25	672.31	1343.615	-0.002	-1.5	5.72	258215.9	5.48	HUMAN	E7EN95	Filamin-B
20412	dirMS_041712_NAR_40mM_minus2.14238.14238.3	3	5.55	0	1.90E+04		(R)VSAAVLI	(R)V/S/A/A/V/L/P L V/H P L P E/G L R(A)		167.98	590.0205	1768.048	-0.001	-0.6	6.72	63124.2	9.53	HUMAN	E7EVU5	Nuclear receptor corepressor 1 (Fragment)
20413	dirMS_041712_NAR_40mM_minus2.7842.7842.3	3	5.55	1	1.59E+05	S76s	(K)AsLREN	(K)A s L R E N/V L/G S/P K(E)	s:N-acetylglucosamine (S)	125.2	491.9311	1270.711	203.0674	-8.1	8.79	37177.3	9.46	HUMAN	P78382	CMP-sialic acid transporter
20414	dirMS_041712_NAR_50mM_minus2.15499.15499.3	3	5.55	1	1.18E+05		(K)VEALSP	(K)V E A/L S P G D\R Q/Q I Y E K(G)		156.07	578.2997	1732.886	-0.0019	-1.1	4.68	118536.6	6.45	HUMAN	C9JSL2	Presequence protease, mitochondrial
20415	dirMS_041712_NAR_50mM_minus2.16999.16999.3	3	5.55	1	8.59E+04		(R)MIDWV	(R)M/I/D/W V S/W P L\G K N I\D K(W)		165.23	601.3217	1801.931	0.02	11.1	5.72	34114.9	6.31	HUMAN	E9PRM2	Ubiquitin carboxyl-terminal hydrolase 35 (Fragment)
20416	dirMS_041712_NAR_50mM_minus2.9532.9532.2	2	5.55	1	7.15E+05		(R)DGKLVS	(R)D/G K L\V|S E S S D V\L P|K(-)		121.97	737.3927	1473.78	-0.0014	-0.9	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
20417	dirMS_041712_NAR_60mM_minus.10128.10128.3	3	5.55	1	6.76E+04		(K)ALDLDS	(K)A L/D L D|S S C K E A/A/D/G Y Q R(C)	C:Carbamidomethylation	115.93	633.6235	1898.855	0.0011	0.6	4.23	60404.6	6.4	HUMAN	F5H0T1	Stress-induced-phosphoprotein 1
20418	dirMS_041712_NAR_60mM_minus.18572.18572.3	3	5.55	0	2.54E+05		(K)LHDNLII	(K)L H D N L\I|I/S/D/L/E N T V K(K)		165.72	575.3117	1723.922	-0.0019	-1.1	4.54	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
20419	dirMS_041712_NAR_60mM_minus.7932.7932.3	3	5.55	1	1.24E+05		(K)FEDKTV	(K)F E\D K T V A|Y T/E Q\K(M)		104.4	486.908	1458.711	-0.0017	-1.1	4.68	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
20420	dirMS_041712_NAR_120mM_plus.8662.8662.3	3	5.55	0	6.13E+05		(K)QHTFVE	(K)Q H\T F V/E|T/E S V R(Y)		98.12	444.8857	1332.654	-0.0117	-8.8	5.4	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
20421	dirMS_041712_NAR_20mM_plus.14647.14647.2	2	5.55	0	3.89E+04	M185m	(K)LAVNm	(K)L/A/V/N m V/P/F/P R(L)	m:Oxidized methionine	172.75	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
20422	dirMS_041712_NAR_20mM_plus.16320.16320.2	2	5.55	0	2.67E+04		(K)ALQFLEE	(K)A L|Q/F L/E E V K(V)		184.07	538.8009	1076.599	-0.0041	-3.8	4.53	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
20423	dirMS_041712_NAR_20mM_plus.6408.6408.2	2	5.55	0	2.42E+04		(R)SQSAAV	(R)S Q S A A/V/T|P S S T T S S T R(A)		107.12	784.3802	1567.756	-0.0027	-1.7	9.47	42437.8	4.97	HUMAN	Q16186	Proteasomal ubiquitin receptor ADRM1
20424	dirMS_041712_NAR_20mM_plus.8079.8079.2	2	5.55	0	8.95E+04		(R)AAPGAE	(R)A A/P G\A E F A|P N K(R)		125.58	536.7749	1072.542	0.0003	0.3	6.05	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
20425	dirMS_041712_NAR_30mM_plus2.18321.18321.2	2	5.55	0	1.69E+04		(R)VVNVSS	(R)V V/N\V/S S I M/S V R(A)		149.1	595.8347	1190.656	0.006	5	9.72	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
20426	dirMS_041712_NAR_30mM_plus2.19428.19428.2	2	5.55	0	2.30E+04		(K)NQALFP	(K)N Q|A\L|F/P A/C V/L K(N)	C:Carbamidomethylation	155.17	630.8399	1260.677	-0.0044	-3.5	8.75	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
20427	dirMS_041712_NAR_30mM_plus2.22112.22112.2	2	5.55	0	1.40E+05		(K)ETLLAM	(K)E/T|L/L/A/M/F K(Y)		170.98	476.7621	952.517	-0.0003	-0.3	6.1	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
20428	dirMS_041712_NAR_40mM_plus2.10250.10250.2	2	5.55	0	1.27E+05		(R)QINLSNI	(R)Q I/N/L/S N I R(A)		124.97	479.2747	957.548	-0.0055	-5.7	9.75	102679.8	6.75	HUMAN	Q7KZF4	Staphylococcal nuclease domain-containing protein 1
20429	dirMS_041712_NAR_40mM_plus2.13625.13625.3	3	5.55	0	1.89E+05		(R)LSAMLV	(R)L S\A M L V/P V/T/P E/V K P K(R)		145.9	536.9848	1608.939	0.0005	0.3	8.59	31524.1	4.5	HUMAN	P82970	High mobility group nucleosome-binding domain-containing protein 5
20430	dirMS_041712_NAR_40mM_plus2.5426.5426.2	2	5.55	0	4.44E+04		(R)SQESGY	(R)S Q|E\S/G/Y Y D R(M)		88.63	552.733	1104.459	-0.0005	-0.5	4.37	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
20431	dirMS_041712_NAR_50mM_plus2.16298.16298.3	3	5.55	0	4.80E+05		(K)QLLGEH	(K)Q L/L/G E H L T A\I/L|Q K(G)		153.73	488.6224	1463.858	-0.0054	-3.7	6.75	103381.4	8.47	HUMAN	K4DI93	Cullin 4B, isoform CRA_e
20432	dirMS_041712_NAR_50mM_plus2.18036.18036.3	3	5.55	1	1.57E+06		(R)ELIKVLEI	(R)E L I K V L E E A/N/Q\A I/N/P K(L)		163.35	603.6741	1809.012	-0.0039	-2.2	4.79	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
20433	dirMS_041712_NAR_20mM_minus.8137.8137.2	2	5.54	0	3.12E+05	M239m	(K)EITALAP	(K)E I|T/A|L/A/P S T m K(I)	m:Oxidized methionine	131.35	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
20434	dirMS_041712_NAR_20mM_minus.9860.9860.2	2	5.54	0	5.44E+03	S1890s	(K)sSEGFSL	(K)s S E/G F S/L F/V\K(I)	s:N-acetylglucosamine (S)	149.4	652.3395	1100.562	203.1095	23.1	5.72	250929.1	9.14	HUMAN	B9A011	Unconventional myosin-VIIa
20435	dirMS_041712_NAR_30mM_minus2.15327.15327.2	2	5.54	0	1.92E+05		(K)EILFYDR	(K)E I|L/F/Y D/R(I)		137.05	478.2479	955.488	0.0002	0.2	4.37	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b
20436	dirMS_041712_NAR_40mM_minus2.14197.14197.3	3	5.54	0	1.90E+04		(R)VSAAVLI	(R)V/S/A/A V/L P L V H P L P E/G L R(A)		167.98	590.0205	1768.048	-0.001	-0.6	6.72	63124.2	9.53	HUMAN	E7EVU5	Nuclear receptor corepressor 1 (Fragment)
20437	dirMS_041712_NAR_50mM_minus2.16267.16268.3	3	5.54	0	1.54E+05		(K)VVDELN	(K)V/V|D E L N L/L H T E L A K(Q)		160.45	531.9638	1593.885	-0.0078	-4.9	4.65	16381.6	5.83	HUMAN	F8VWV2	DCC-interacting protein 13-beta (Fragment)
20438	dirMS_041712_NAR_50mM_minus2.8773.8773.3	3	5.54	1	9.69E+04		(K)TAVCDIF	(K)T A|V/C D\I/P P/R G L K(M)	C:Carbamidomethylation	117.47	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
20439	dirMS_041712_NAR_60mM_minus.16700.16700.3	3	5.54	2	8.10E+04	T30t	(R)KtYVGD	(R)K t Y V/G D Q/L/Q/R T S K(K)	t:N-acetylglucosamine (T)	152.85	576.307	1523.818	203.0888	5.5	9.7	5663.5	8.38	HUMAN	H0YAS2	Ran-binding protein 17 (Fragment)
20440	dirMS_041712_NAR_120mM_plus.10553.10553.3	3	5.54	0	1.23E+06		(R)GLHQSII	(R)G L/H Q S\I/E/E/F R(A)		109.27	405.8796	1215.612	0.0126	10.4	5.4	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
20441	dirMS_041712_NAR_120mM_plus.19793.19793.4	4	5.54	2	8.91E+05	S26s	(R)GLsPGR	(R)G L\s P G/R A G R E/L V E L R(V)	s:N-acetylglucosamine (S)	156.72	454.0073	1609.913	203.0941	8.1	9.51	24141.9	11.15	HUMAN	K7EJG0	HCG27535
20442	dirMS_041712_NAR_120mM_plus.9048.9048.3	3	5.54	0	1.20E+06		(K)HTGPNS	(K)H T G\P N S\P\D T|A|N D/G F V R(L)		100.17	562.26	1684.767	-0.0019	-1.2	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
20443	dirMS_041712_NAR_20mM_plus.11562.11562.2	2	5.54	0	1.23E+05	M402m	(R)mAFGA	(R)m A/F|G A/T L D V/K(T)	m:Oxidized methionine	152.35	534.7743	1052.545	15.9968	1.8	5.59	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
20444	dirMS_041712_NAR_20mM_plus.19076.19076.2	2	5.54	0	2.04E+05		(R)VCTLAII	(R)V C|T L/A|I I/D\P G D S D I I R(S)	C:Carbamidomethylation	202.77	879.4578	1757.91	-0.0019	-1.1	3.93	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
20445	dirMS_041712_NAR_30mM_plus2.19407.19407.2	2	5.54	0	5.76E+04		(R)QAQEYE	(R)Q A Q/E/Y/E/A\L|L N I K(V)		155.35	710.3766	1419.748	-0.0019	-1.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
20446	dirMS_041712_NAR_50mM_plus2.11487.11487.3	3	5.54	0	4.19E+05		(K)GFVEFA	(K)G F|V/E F A A K/P P A R(K)		127.83	430.5716	1289.7	0.0002	0.1	8.75	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
20447	dirMS_041712_NAR_50mM_plus2.18693.18693.3	3	5.54	0	3.87E+05		(R)AVSILPL	(R)A V/S I L/P L/L/G H/G V P R(L)		165.92	476.9615	1428.869	0.0014	1	9.8	66841.7	7.74	HUMAN	F5H721	WW domain-binding protein 11
20448	dirMS_041712_NAR_60mM_plus.17503.17503.3	3	5.54	0	2.78E+04		(R)WETFDV	(R)W/E T F D V S P A V\L R(W)		148.57	473.9176	1419.727	0.0116	8.1	4.37	31686	10.02	HUMAN	H0YLW3	Bone morphogenetic protein 4 (Fragment)
20449	dirMS_041712_NAR_120mM_minus.11479.11479.3	3	5.53	0	1.12E+05		(R)NISHYEE	(R)N/I/S H Y E E Q/L V K(M)		116.78	453.9026	1359.69	0.0029	2.2	5.4	10305.6	6.94	HUMAN	H7C330	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
20450	dirMS_041712_NAR_30mM_minus2.12822.12822.2	2	5.53	0	3.00E+04		(R)GQVVSL	(R)G Q|V|V/S L I R(M)		123.58	436.2706	871.536	-0.0021	-2.4	9.75	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
20451	dirMS_041712_NAR_30mM_minus2.15364.15489.2	2	5.53	0	2.08E+05		(K)EILFYDR	(K)E I|L/F/Y D R(I)		137.32	478.2479	955.488	0.0002	0.2	4.37	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b
20452	dirMS_041712_NAR_30mM_minus2.15849.15849.3	3	5.53	0	7.22E+04		(R)TINEVEN	(R)T I\N E V E N|Q/I L T/R(D)		139.48	477.2603	1429.765	0.0018	1.3	4.53	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
20453	dirMS_041712_NAR_30mM_minus2.15895.15895.2	2	5.53	0	1.25E+05		(R)TINEVEN	(R)T I/N E|V E/N Q/I/L/T R(D)		139.6	715.3834	1429.765	-0.005	-3.5	4.53	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
20454	dirMS_041712_NAR_30mM_minus2.17537.17537.2	2	5.53	0	3.80E+04		(R)ALCYLVL	(R)A L/C|Y L V/L K(Q)	C:Carbamidomethylation	150.68	490.2854	979.564	-0.001	-1	8.63	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
20455	dirMS_041712_NAR_30mM_minus2.17934.17934.2	2	5.53	0	6.98E+04		(R)SSFYVN	(R)S S F/Y|V/N G L T\L G G Q K(C)		152.25	735.8825	1470.759	-0.001	-0.7	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
20456	dirMS_041712_NAR_40mM_minus2.13553.13553.3	3	5.53	0	2.43E+05		(R)LWADP	(R)L W A D/P G A Q A C F S R(S)	C:Carbamidomethylation	163.07	493.5654	1478.685	-0.0029	-1.9	5.84	41436.5	7.82	HUMAN	P19086	Guanine nucleotide-binding protein G(z) subunit alpha
20457	dirMS_041712_NAR_60mM_minus.18413.18413.3	3	5.53	1	5.29E+03		(R)EFTRLEI	(R)E/F T R L E\I/C N L/T/P/D A L K(S)	C:Carbamidomethylation	164.07	640.6658	1919.989	-0.0067	-3.5	4.68	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
20458	dirMS_041712_NAR_60mM_minus.8165.8165.3	3	5.53	1	8.67E+04		(K)GEFKDEI	(K)G E/F K D E E|E/T/V T T K(H)		105.5	504.913	1512.706	0.018	11.9	4.25	68315.4	6.01	HUMAN	Q14677	Clathrin interactor 1
20459	dirMS_041712_NAR_60mM_minus.9820.9820.3	3	5.53	0	7.93E+05		(-)XQEQYLE	(-)X Q|E Q Y L/E A H D R(L)		114.85	467.8879	1401.676	-0.0266	-19	4.65	18987.6	4.75	HUMAN	H0YDS9	Nuclear autoantigenic sperm protein (Fragment)
20460	dirMS_041712_NAR_120mM_plus.10683.10683.3	3	5.53	1	3.57E+05		(R)KLDPGSI	(R)K L D P G S/E E|T Q/T L/V/R(E)		108.97	524.9451	1572.823	-0.002	-1.3	4.68	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
20461	dirMS_041712_NAR_120mM_plus.12498.12498.4	4	5.53	1	1.18E+06	S57s M64	(R)LFVsWR	(R)L/F V/s W R S P T G/m D C K(L)	C:Carbamidomethylation s:N-ace	118.7	476.4703	1683.798	219.0612	-6.9	8.75	33937.8	6.34	HUMAN	A4D161	Protein FAM221A
20462	dirMS_041712_NAR_120mM_plus.15171.15171.4	4	5.53	2	7.74E+05		(K)AMGDA	(K)A/M/G D/A E/I K D G E R L P L A V/K(D)		132.67	479.0094	1913.016	-0.0003	-0.2	4.78	99900.1	5.04	HUMAN	B4DZI8	Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b
20463	dirMS_041712_NAR_120mM_plus.15187.15187.4	4	5.53	1	1.02E+06		(K)DHASIQ	(K)D H A S I Q|M/N V/A E V D K V/T G R(F)		133.15	493.25	1969.976	0.0022	1.1	5.38	9225.3	9.16	HUMAN	P63220	40S ribosomal protein S21
20464	dirMS_041712_NAR_120mM_plus.20212.20212.3	3	5.53	1	3.26E+05		(R)AKFEELN	(R)A K F E E L|N/M/D/L F R(S)		159.17	504.9201	1512.752	-0.0058	-3.8	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
20465	dirMS_041712_NAR_120mM_plus.5374.5374.2	2	5.53	0	3.43E+05	M49m	(R)HQGVM	(R)H Q|G V M V/G m G Q/K(D)	m:Oxidized methionine	81.55	594.2868	1171.571	15.9953	0.3	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
20466	dirMS_041712_NAR_20mM_plus.10760.10760.2	2	5.53	1	6.30E+04	K26k	(K)VDAGGk	(K)V D/A G G/k V K K(G)	k:Ubiquitin-K	147.08	508.292	901.547	114.0302	-12.6	9.7	8141.6	10.62	HUMAN	F8VRY1	60S ribosomal protein L6 (Fragment)
20467	dirMS_041712_NAR_20mM_plus.12114.12114.2	2	5.53	0	1.46E+04	M66m	(R)GGGVG	(R)G G G V/G/G F L|P A m/K(Q)	m:Oxidized methionine	156.62	553.7889	1090.571	15.9991	3.8	8.75	19338.9	5.33	HUMAN	E7EQS9	tRNA-splicing ligase RtcB homolog
20468	dirMS_041712_NAR_30mM_plus2.15418.15418.2	2	5.53	0	4.29E+05		(R)YNFFTG	(R)Y/N|F/F T/G C P K(A)	C:Carbamidomethylation	133.32	567.2595	1133.508	0.0033	2.9	8.59	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
20469	dirMS_041712_NAR_30mM_plus2.7486.7486.2	2	5.53	0	7.39E+05		(K)MQLDNI	(K)M/Q/L/D N P S/K(V)		93.82	466.7319	932.451	0.0059	6.4	5.59	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
20470	dirMS_041712_NAR_50mM_plus2.10332.10332.3	3	5.53	0	1.09E+05		(K)MSIAQC	(K)M S/I/A Q C T S/S/H/P I/I R(Q)	C:Carbamidomethylation	121.63	534.2701	1600.793	0.0023	1.5	9.52	18283.4	9.29	HUMAN	Q8N8C4	Coiled-coil-helix-coiled-coil-helix domain-containing protein 5
20471	dirMS_041712_NAR_50mM_plus2.15864.15864.3	3	5.53	1	3.11E+05		(R)NVEELVI	(R)N/V/E/E L\V/I V L K/K(E)		151.47	428.6017	1283.793	-0.0028	-2.2	6.14	56164.6	6.01	HUMAN	E9PP73	Coatomer subunit beta (Fragment)
20472	dirMS_041712_NAR_60mM_plus.19361.19361.3	3	5.53	0	5.02E+04		(K)VSHLLGI	(K)V S H L\L G\I|N\V/T D/F T R(G)		159.5	524.6233	1571.854	0.0013	0.8	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
20473	dirMS_041712_NAR_60mM_plus.20172.20172.3	3	5.53	0	3.65E+04		(K)HELLQPI	(K)H E L L\Q|P F/N V L/Y E K(E)		165.45	543.9625	1629.863	0.0094	5.8	5.4	42088	5.39	HUMAN	F8VTY8	Proliferation-associated protein 2G4
20474	dirMS_041712_NAR_120mM_minus.4929.4929.3	3	5.52	0	1.07E+06	M46m M4	(R)HQGVm	(R)H Q G V\m|V/G m G Q/K(D)	m:Oxidized methionine	77.55	401.8604	1171.571	31.9956	4.8	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
20475	dirMS_041712_NAR_30mM_minus2.6468.6468.2	2	5.52	0	2.34E+05		(R)QQYESV	(R)Q\Q/Y/E/S V A A/K(N)		89.95	512.2534	1023.511	-0.011	-10.8	6	49709.6	5.19	HUMAN	B0YJC4	Vimentin
20476	dirMS_041712_NAR_50mM_minus2.10006.10006.3	3	5.52	0	1.74E+05	M392m	(K)EmNPAL	(K)E m/N P A/L G/I D C L/H K(G)	C:Carbamidomethylation m:Oxid	125.58	505.2416	1497.719	15.9914	-2.3	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
20477	dirMS_041712_NAR_50mM_minus2.7983.7983.3	3	5.52	1	5.62E+04	S136s M13	(R)AKELsV	(R)A K E L\s V|m F I E T S/A K(T)	s:N-acetylglucosamine (S) m:	112.35	591.6389	1553.824	219.0778	2	6.18	22448.2	5.58	HUMAN	B7Z337	Ras-related protein Rab-6B
20478	dirMS_041712_NAR_60mM_minus.14313.14313.3	3	5.52	1	1.25E+05		(R)DLEEKLE	(R)D L/E/E K L E T L R(L)		139.63	415.8949	1245.669	0.0016	1.3	4.41	141626	5.5	HUMAN	A8MY36	Dynactin subunit 1
20479	dirMS_041712_NAR_60mM_minus.16687.16687.3	3	5.52	0	1.78E+05		(R)LLIHQSL	(R)L/L/I H Q S/L/A|G\G I I G V/K(G)		153.38	506.9823	1518.937	-0.0043	-2.8	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
20480	dirMS_041712_NAR_60mM_minus.7437.7437.3	3	5.52	1	2.56E+04	M2211m	(R)STTQELr	(R)S/T/T Q/E L/m E D D\R V K(R)	m:Oxidized methionine	101.02	523.2497	1551.732	16.0026	4.9	4.32	266161	5.68	HUMAN	E9PPU0	Epiplakin
20481	dirMS_041712_NAR_120mM_plus.5209.5209.3	3	5.52	1	2.26E+04		(R)YEREQY	(R)Y E/R E Q\Y\A D/R(A)		80.25	410.5196	1229.555	-0.0103	-8.4	4.68	37433.2	9.17	HUMAN	B0LM41	Protein RBM14-RBM4
20482	dirMS_041712_NAR_120mM_plus.9680.9680.4	4	5.52	2	3.92E+06		(R)VLTVIN	(R)V L/T V/I/N Q/T Q K E N L R K(F)		104.23	446.7653	1784.039	0.0005	0.3	9.99	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
20483	dirMS_041712_NAR_20mM_plus.11710.11710.2	2	5.52	0	1.33E+05		(R)AQAALA	(R)A Q A|A L/A V N I/S/A A R(G)		153.65	628.3565	1255.712	-0.006	-4.8	9.79	58479.6	6.23	HUMAN	P40227	T-complex protein 1 subunit zeta
20484	dirMS_041712_NAR_30mM_plus2.22136.22136.2	2	5.52	0	1.73E+05		(K)GLSSLLC	(K)G L/S\S/L/L/C N F/T K(S)	C:Carbamidomethylation	171.82	620.3199	1239.64	-0.0077	-6.2	8.75	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
20485	dirMS_041712_NAR_40mM_plus2.12596.12596.3	3	5.52	0	4.95E+03		(K)LTGDVEI	(K)L/T/G D V/E E L E\I Q E K/P A L/K(V)		140.8	638.0075	1912.027	-0.0194	-10.1	4.25	74103.6	5.35	HUMAN	G5E9W3	Cleavage and polyadenylation specific factor 3, 73kDa, isoform CRA_b
20486	dirMS_041712_NAR_50mM_plus2.18864.18864.3	3	5.52	0	2.66E+05		(K)LAKPLSS	(K)L A K P L S S L/T|P L/I M A A K(E)		167.48	552.004	1653.997	0.0003	0.2	10	24711.4	5.19	HUMAN	H7C1X3	PAK-2p34 (Fragment)
20487	dirMS_041712_NAR_50mM_plus2.7714.7714.3	3	5.52	1	9.77E+04		(R)EFEDPRI	(R)E F E D P R D A/P/P P/T R(A)		106.6	509.5779	1526.723	-0.0042	-2.8	4.32	51612.9	9.98	HUMAN	P08621	U1 small nuclear ribonucleoprotein 70 kDa

20488	dirMS_041712_NAR_60mM_plus.6108.6108.3	3	5.52	1	3.16E+05		(R)GSCSTE\	(R)G S/C/S T E V/E K E T Q E K(M)	C:Carbamidomethylation	91.05	537.9088	1611.717	-0.0048	-3	4.49	13871.4	9.22	HUMAN	O75348	V-type proton ATPase subunit G 1
20489	dirMS_041712_NAR_60mM_plus.7091.7091.3	3	5.52	0	6.23E+04		(R)TFTEMD	(R)T\F/T E/M/D S H E E K(V)		95.23	451.8597	1353.563	0.0018	1.3	4.4	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
20490	dirMS_041712_NAR_60mM_plus.9729.9729.2	2	5.52	0	1.96E+05		(R)FATHAA	(R)F A T/H/A/A/A L/S V R(N)		108.95	572.3143	1143.627	-0.0056	-4.9	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
20491	dirMS_041712_NAR_120mM_minus.8327.8327.2	2	5.51	1	2.26E+05		(K)FSEVLKR	(K)F/S/E/V L K/R(L)		99.5	439.7574	878.509	-0.0019	-2.2	8.75	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
20492	dirMS_041712_NAR_30mM_minus2.6819.6819.2	2	5.51	0	1.71E+05		(R)GCLDEE'	(R)G C|L/D E E/T S R(A)	C:Carbamidomethylation	91.75	533.7297	1066.447	0.0052	4.8	4.14	533778	5.74	HUMAN	Q15149	Plectin
20493	dirMS_041712_NAR_40mM_minus2.10345.10345.2	2	5.51	0	9.91E+05		(R)VAPEEH	(R)V A/P E E/H\P V/L/L T E A|P L\N P K(A)		143.67	977.5343	1954.064	-0.0031	-1.6	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
20494	dirMS_041712_NAR_40mM_minus2.13429.13429.3	3	5.51	1	1.96E+05		(K)LGVQVV	(K)L G\V Q/V/V/I/T D P E K L D Q I R(Q)		163.38	641.7007	1923.091	-0.0034	-1.8	4.56	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
20495	dirMS_041712_NAR_40mM_minus2.13547.13547.3	3	5.51	0	1.65E+05	K592k	(R)VDLPTW	(R)V/D/L P T W E A E T I I Q k I/K(Q)	k:Ubiquitin-K	163.3	666.6932	1884.048	114.0174	-12.8	4.68	68047.7	6.79	HUMAN	F5GXI6	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1
20496	dirMS_041712_NAR_50mM_minus2.13747.13747.3	3	5.51	0	3.00E+04		(K)TGEEIFG	(K)T G E/E I/F G T I G M/R/P N A K(N)		146.93	574.2947	1720.869	0.0009	0.5	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
20497	dirMS_041712_NAR_50mM_minus2.13940.13940.3	3	5.51	1	1.44E+05		(R)SEGVVA	(R)S E/G V V A/V L L/T K K(S)		146.85	415.255	1243.762	-0.0116	-9.3	8.31	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
20498	dirMS_041712_NAR_50mM_minus2.17523.17523.3	3	5.51	1	1.24E+05		(K)NAAGAL	(K)N A/A/G A/L D L/L K E L/K(N)		168.65	452.601	1355.789	-0.0008	-0.6	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
20499	dirMS_041712_NAR_60mM_minus.13826.13826.3	3	5.51	0	2.71E+05		(K)YGGELV	(K)Y/G G\E L\V/P H F P A R(V)		138.02	448.2371	1342.69	0.0065	4.8	6.75	258215.9	5.48	HUMAN	E7EN95	Filamin-B
20500	dirMS_041712_NAR_120mM_plus.10472.10472.3	3	5.51	1	2.28E+05		(R)LRQLAEI	(R)L R Q\L A E\E D/L A/Q/Q R(A)		107.12	523.949	1569.834	-0.0019	-1.2	4.68	533778	5.74	HUMAN	Q15149	Plectin
20501	dirMS_041712_NAR_20mM_plus.11715.11715.2	2	5.51	0	1.36E+05		(R)AQAALA	(R)A Q\A|A L/A/V N I S A A R(G)		153.7	628.3565	1255.712	-0.006	-4.8	9.79	58479.6	6.23	HUMAN	P40227	T-complex protein 1 subunit zeta
20502	dirMS_041712_NAR_20mM_plus.18265.18265.2	2	5.51	0	5.11E+04		(K)FIIPQIVK	(K)F/I|I/P Q I V K(Y)		197.13	479.3081	957.613	-0.0042	-4.4	8.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
20503	dirMS_041712_NAR_20mM_plus.18829.18829.2	2	5.51	0	1.55E+05		(R)IITLTGP1	(R)I I/T\L/T/G\P T N A|I F K(A)		200.48	694.9091	1388.815	-0.0039	-2.8	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
20504	dirMS_041712_NAR_20mM_plus.7704.7704.3	3	5.51	0	1.18E+04		(K)AVTEQG	(K)A V T E Q G A E|L/S N E/E R(N)		122.92	511.5761	1532.719	-0.005	-3.2	4.09	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
20505	dirMS_041712_NAR_30mM_plus2.10255.10255.2	2	5.51	0	5.74E+05		(K)FVIATST	(K)F/V|I/A T S T K(I)		107.58	433.7497	866.498	-0.0061	-7	8.75	25891.4	10.67	HUMAN	F8W181	60S ribosomal protein L6 (Fragment)
20506	dirMS_041712_NAR_30mM_plus2.10555.10555.2	2	5.51	0	2.76E+05		(K)NFGDQF	(K)N F|G D/Q P D/I R(C)		109.17	531.2555	1061.501	0.0027	2.5	4.21	136658.9	5.13	HUMAN	Q15393	Splicing factor 3B subunit 3
20507	dirMS_041712_NAR_30mM_plus2.16684.16684.2	2	5.51	0	3.85E+05		(K)QLQEMI	(K)Q L/Q E M/L/G L/S K(V)		140.38	573.8112	1146.619	-0.0036	-3.1	6	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
20508	dirMS_041712_NAR_30mM_plus2.21289.21289.2	2	5.51	0	1.45E+05		(R)DWVLNI	(R)D W|V/L/N\E F R(S)		167.05	539.7718	1078.532	0.0047	4.4	4.37	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
20509	dirMS_041712_NAR_30mM_plus2.22247.22247.2	2	5.51	0	2.53E+05		(R)AFITNIP	(R)A F I/T N\\|/P F/D V K(W)		171.35	632.8481	1264.694	-0.0047	-3.7	5.88	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
20510	dirMS_041712_NAR_30mM_plus2.9945.9945.2	2	5.51	0	6.65E+05		(K)NNTQVL	(K)N N|T Q/V|L/I/N\C R(N)	C:Carbamidomethylation	105.42	616.3143	1231.621	0.0001	0.1	9.75	8948	9.6	HUMAN	K7ERG4	Small nuclear ribonucleoprotein Sm D2
20511	dirMS_041712_NAR_40mM_plus2.8914.8914.2	2	5.51	0	1.05E+05		(K)FYEQFSK	(K)F/Y/E/Q F S/K(N)		115.03	474.7301	948.446	0.0068	7.1	6	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
20512	dirMS_041712_NAR_50mM_plus2.10312.10312.3	3	5.51	0	8.80E+04	M778m	(R)mLTGPV	(R)m L/T\G/P V Y/S Q S T A L T H K(Q)	m:Oxidized methionine	121.92	583.9631	1733.889	15.9857	-5.3	8.37	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
20513	dirMS_041712_NAR_20mM_minus.7258.7258.2	2	5.5	0	2.46E+04		(K)IAVAAQ	(K)I A/V\A|A Q N C Y K(V)	C:Carbamidomethylation	120.58	569.2917	1137.572	0.004	3.5	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
20514	dirMS_041712_NAR_30mM_minus2.5711.5711.2	2	5.5	0	1.64E+05		(R)LYQAGE	(R)L Y/Q A G/E/G R(L)		84.8	447.2217	893.448	-0.0114	-12.8	6	38089.6	6.79	HUMAN	B4DT77	Annexin
20515	dirMS_041712_NAR_50mM_minus2.14176.14176.3	3	5.5	0	5.78E+04		(K)LVTSIGD	(K)L/V|T/S I/G D V V N H D P V V G D R(L)		148.83	631.3336	1891.987	-0.001	-0.5	4.41	27786.2	5.93	HUMAN	H0Y4Z6	Phosphorylase (Fragment)
20516	dirMS_041712_NAR_50mM_minus2.5765.5765.3	3	5.5	1	9.21E+04		(K)LEEAEK/	(K)L E/E A/E K/A/A D E/S E R(G)		94.08	492.8982	1476.681	-0.0012	-0.8	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
20517	dirMS_041712_NAR_50mM_minus2.9008.9008.3	3	5.5	1	2.17E+04		(K)VCGDSD	(K)V/C/G\D S D K/G F\V V I N Q K(G)	C:Carbamidomethylation	119.55	555.9474	1665.826	0.0012	0.7	5.93	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
20518	dirMS_041712_NAR_60mM_minus.10886.10886.3	3	5.5	1	1.26E+05		(K)LKQSLPF	(K)L K Q S L/P/P G L A/V K(E)		121.03	417.5985	1250.783	-0.0021	-1.7	10	8274.8	10.19	HUMAN	P63173	60S ribosomal protein L38
20519	dirMS_041712_NAR_120mM_plus.15354.15354.4	4	5.5	1	1.41E+06		(R)VKPAPD	(R)V K P A/P D E T/S/F/S E A L L K R(N)		133.45	472.7599	1888.017	0.0003	0.2	6.15	43289.6	5.19	HUMAN	Q12905	Interleukin enhancer-binding factor 2
20520	dirMS_041712_NAR_120mM_plus.8633.8633.3	3	5.5	0	1.23E+06		(R)RPELEDS	(R)R P\E\L\E\D|S/T/L/R(Y)		98.33	405.8796	1215.633	-0.0085	-7	4.68	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
20521	dirMS_041712_NAR_20mM_plus.14930.14930.2	2	5.5	0	1.90E+05	M179m M:	(K)mFVLDE	(K)m F/V/L/D E A/D E\m L S R(G)	m:Oxidized methionine	173.63	794.3555	1555.713	31.9906	0.5	3.91	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
20522	dirMS_041712_NAR_20mM_plus.15660.15660.3	3	5.5	0	1.93E+04		(R)IIDVVYN	(R)I I D V V Y N/A\S N/N E L V/R(T)		179.13	573.6388	1718.907	-0.0053	-3.1	4.37	24490	10.56	HUMAN	P62241	40S ribosomal protein S8
20523	dirMS_041712_NAR_20mM_plus.16801.16801.2	2	5.5	0	3.52E+05		(K)LGGSAV	(K)L G G S A/V/I\S/L E/G/K|P L(-)		186.13	670.8917	1340.778	-0.0023	-1.7	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
20524	dirMS_041712_NAR_20mM_plus.7446.7446.2	2	5.5	0	6.35E+03		(K)ALELDSN	(K)A L/E/L/D S N/N E K(G)		119.68	566.7715	1132.548	-0.0123	-10.9	4.14	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
20525	dirMS_041712_NAR_30mM_plus2.14499.14499.3	3	5.5	0	1.03E+04		(K)VNQIGS'	(K)V N\Q\I G/S\V T/E/S I/Q A C K(L)	C:Carbamidomethylation	127.72	545.28	1633.821	0.0041	2.5	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
20526	dirMS_041712_NAR_30mM_plus2.17579.17579.3	3	5.5	0	8.25E+05		(R)ASLEAAI	(R)A S L E A A I/A/D A E/Q R(G)		144.8	448.8963	1344.675	-0.001	-0.8	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
20527	dirMS_041712_NAR_30mM_plus2.4089.4126.2	2	5.5	0	1.27E+06	M299m M:	(K)NmmAA	(K)N m\m\A/A C D|P/R(H)	C:Carbamidomethylation m:Oxid	68.87	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
20528	dirMS_041712_NAR_30mM_plus2.8161.8161.2	2	5.5	0	2.73E+05		(K)EIAENAL	(K)E I|A E/N A L G K(H)		96.92	472.755	944.505	-0.002	-2.1	4.53	36982.9	6.37	HUMAN	P31942	Heterogeneous nuclear ribonucleoprotein H3
20529	dirMS_041712_NAR_40mM_plus2.7856.7856.2	2	5.5	0	5.86E+05		(K)ASLENSL	(K)A S|L/E/N/S L R(E)		105.63	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
20530	dirMS_041712_NAR_50mM_plus2.10147.10147.3	3	5.5	0	3.78E+05		(R)MVQVH	(R)M/V|Q V/H E L S\C E G I S K(S)	C:Carbamidomethylation	121.6	539.5992	1616.777	0.006	3.7	5.38	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
20531	dirMS_041712_NAR_50mM_plus2.12274.12274.3	3	5.5	0	6.81E+04		(R)MSCFSR	(R)M S/C F S/R P S M S|P T P L D R(C)	C:Carbamidomethylation	132.48	623.6215	1868.845	0.0048	2.5	9.35	300351.7	12.1	HUMAN	Q9UQ35	Serine/arginine repetitive matrix protein 2
20532	dirMS_041712_NAR_50mM_plus2.13027.13027.3	3	5.5	0	7.93E+05		(R)VLHVSEI	(R)V L H V S E\N\P\V|P L T V/R(V)		137.38	520.6339	1559.89	-0.0033	-2.1	6.72	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
20533	dirMS_041712_NAR_50mM_plus2.13779.13779.3	3	5.5	1	5.35E+05		(K)GGELVY	(K)G G E|L/V/Y T D S E A R D V F E K(A)		141.18	638.9735	1914.908	-0.002	-1.1	4.18	533778	5.74	HUMAN	Q15149	Plectin
20534	dirMS_041712_NAR_50mM_plus2.14114.14114.3	3	5.5	1	4.28E+05		(K)TSIAIDTI	(K)T S|I/A I D/T/I/I N Q K R(F)		142.58	491.6191	1472.843	-0.0004	-0.3	8.41	48851.3	9.2	HUMAN	K7EK63	ATP synthase subunit alpha, mitochondrial
20535	dirMS_041712_NAR_50mM_plus2.14562.14562.3	3	5.5	1	5.40E+05		(R)QAIKELF	(R)Q A I\K E L P Q/F A/T/G E N L/P R(V)		144.47	638.0091	1912.029	-0.0159	-8.3	6.14	58250.7	8.99	HUMAN	B4E283	Apoptosis inhibitor 5
20536	dirMS_041712_NAR_50mM_plus2.20588.20588.3	3	5.5	1	1.67E+04		(K)SSVLENF	(K)S S/V|L/E/N F/V G R D F L P\R(G)		177.28	579.3128	1735.913	0.0113	6.5	5.79	73288.1	8.96	HUMAN	E5RHK8	Dynamin-3
20537	dirMS_041712_NAR_50mM_plus2.9226.9226.3	3	5.5	1	8.76E+05		(K)TAVCDIF	(K)T/A/V/C D/I/P/P R G L K(M)	C:Carbamidomethylation	116.07	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
20538	dirMS_041712_NAR_120mM_minus.14610.14610.3	3	5.49	1	1.65E+05	S40s	(K)LsDLDV(	(K)L s/D L D V Q K S L/R(V)	s:N-acetylglucosamine (S)	133.72	492.947	1273.711	203.1154	24.4	5.96	6723.7	5.37	HUMAN	H7BZC4	28S ribosomal protein S9, mitochondrial (Fragment)
20539	dirMS_041712_NAR_120mM_minus.20295.20295.3	3	5.49	0	3.63E+05		(K)VHLVGII	(K)V H\L V G\I\D|I|F/T/G K(K)		166.53	433.5866	1298.747	-0.0015	-1.1	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
20540	dirMS_041712_NAR_30mM_minus2.6257.6257.2	2	5.49	0	9.32E+04		(R)EAEEVYI	(R)E A E/E/V/Y R(N)		88.23	448.2136	895.416	0.0043	4.8	4.25	54793.4	10.51	HUMAN	B7Z4Q3	Putative RNA-binding protein Luc7-like 2
20541	dirMS_041712_NAR_50mM_minus2.15767.15767.3	3	5.49	0	6.86E+04		(K)LLDSSTV	(K)L L\D S S/T/V/T H L F K(I)		157.67	454.2542	1360.747	0.001	0.7	6.74	25746.2	6.77	HUMAN	B4DXJ9	Proteasome (Prosome, macropain) subunit, alpha type, 6, isoform CRA_a
20542	dirMS_041712_NAR_50mM_minus2.5983.5983.3	3	5.49	1	2.99E+04		(K)TQSVEIT	(K)T Q/S V/E/I\T K T D T E/G K(I)		96.22	512.9329	1536.775	0.009	5.8	4.68	71678	6.07	HUMAN	Q9Y5K6	CD2-associated protein
20543	dirMS_041712_NAR_60mM_minus.10697.10697.3	3	5.49	1	1.21E+05		(R)VLTVINC	(R)V L/T V I/N Q/T Q K E N L R(K)		119.27	552.6501	1655.944	-0.0081	-4.9	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
20544	dirMS_041712_NAR_20mM_plus.10936.10936.2	2	5.49	0	6.28E+04		(K)LSELEPG	(K)L S E\L/E|P G T G D L R(F)		147.43	643.8371	1286.659	0.0083	6.4	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
20545	dirMS_041712_NAR_20mM_plus.16018.16018.3	3	5.49	0	2.45E+04		(R)ALPAVQ	(R)A L/P A V Q Q N N/L D E/D L/I/R(K)		181.95	603.6541	1808.95	-0.0024	-1.3	4.03	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
20546	dirMS_041712_NAR_20mM_plus.18047.18047.3	3	5.49	0	1.71E+05		(R)LSVLGAI	(R)L S V L G A I T/S/V/Q Q R(L)		196.13	457.9354	1371.795	-0.0038	-2.8	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
20547	dirMS_041712_NAR_20mM_plus.18102.18102.2	2	5.49	0	7.40E+04		(R)LSVLGAI	(R)L S\V|L/G A I/T\S V Q/Q R(L)		196.18	686.3953	1371.795	-0.0121	-8.8	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
20548	dirMS_041712_NAR_30mM_plus2.12968.12968.2	2	5.49	0	3.84E+05		(K)NIILGGV	(K)N/I/I/L G G\V K(A)		120.6	407.2629	813.519	-0.0007	-0.9	8.75	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
20549	dirMS_041712_NAR_30mM_plus2.14895.14987.2	2	5.49	0	3.63E+05		(K)SLQMYL	(K)S L|Q/M/Y/L E R(L)		130.8	520.2659	1039.524	0.0004	0.4	5.72	32242.7	9.27	HUMAN	H3BP91	Enoyl-CoA delta isomerase 1, mitochondrial (Fragment)
20550	dirMS_041712_NAR_30mM_plus2.20871.20871.2	2	5.49	0	6.28E+05		(K)QEFLINL	(K)Q E/F/L I\N L V\K(Q)		162.82	552.331	1103.646	0.0088	8	6	72331.1	5.39	HUMAN	J3KMX3	Alpha-fetoprotein
20551	dirMS_041712_NAR_30mM_plus2.4267.4267.2	2	5.49	0	8.67E+05	M299m M:	(K)NmmAA	(K)N m|m/A\A C/D|P R(H)	C:Carbamidomethylation m:Oxid	69.95	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
20552	dirMS_041712_NAR_50mM_plus2.10727.10727.3	3	5.49	0	4.20E+05		(K)TSEVDL/	(K)T/S/E V/D L A K/P L V K(F)		123.78	433.922	1299.752	-0.0004	-0.3	5.73	17178.3	5.63	HUMAN	C9IZF9	Programmed cell death 6-interacting protein (Fragment)
20553	dirMS_041712_NAR_50mM_plus2.10764.10764.3	3	5.49	1	2.46E+06		(R)MQKEIT	(R)M Q\K\E I T\A|L\A/P S T M K(I)		124.03	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
20554	dirMS_041712_NAR_50mM_plus2.15149.15149.3	3	5.49	1	4.10E+05		(R)LSQELEY	(R)L S/Q/E L E/Y L|T E D/V K R(L)		147.4	574.9669	1722.891	-0.0047	-2.7	4.41	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
20555	dirMS_041712_NAR_50mM_plus2.21628.21628.3	3	5.49	1	2.38E+05		(K)LGFAGL\	(K)L/G F A G L/V Q E I/S F G T T K D K(M)		184.83	637.6781	1911.022	-0.0025	-1.3	6.07	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
20556	dirMS_041712_NAR_60mM_plus.18366.18366.3	3	5.49	1	1.76E+04		(K)MFIGGL'	(K)M F/I/G G L S/W D T T K K(D)		154.18	495.2592	1483.761	0.0017	1.1	8.35	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
20557	dirMS_041712_NAR_60mM_plus.7270.7270.3	3	5.49	1	4.98E+05		(K)TIIQNPT	(K)T/I\I/Q/N/P T D Q Q K K(D)		95.72	471.9324	1413.77	0.013	9.2	8.26	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
20558	dirMS_041712_NAR_120mM_minus.16067.16067.3	3	5.48	1	2.26E+05		(K)STFVLDE	(K)S T|F V/L D/E/F/K/R(K)		141.13	414.5544	1241.652	-0.0038	-3.1	5.79	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
20559	dirMS_041712_NAR_120mM_minus.7538.7538.3	3	5.48	1	2.18E+05		(K)SKAEAES	(K)S K A E A E/S/L|Y Q S K(Y)		95.33	447.558	1340.669	-0.0098	-7.3	5.86	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
20560	dirMS_041712_NAR_120mM_minus.8222.8222.3	3	5.48	2	1.08E+06		(K)KGAVAE	(K)K\G A\V/A E D/G D\E L R T E|P E/A K(K)		99.27	638.9836	1914.94	-0.0041	-2.1	4.36	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
20561	dirMS_041712_NAR_120mM_minus.8811.8811.3	3	5.48	0	7.27E+05		(R)RPELEDS	(R)R P E\L\E/D/S/T/L R(Y)		102.42	405.8796	1215.633	-0.0085	-7	4.68	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
20562	dirMS_041712_NAR_20mM_minus.7356.7356.3	3	5.48	0	8.31E+03	M13m M1!	(K)ISGGSV\	(K)I S/G G S\V V E m Q/G/D E m T/R(I)	m:Oxidized methionine	121.18	576.5901	1695.768	31.9881	-1	4.14	17833.3	8.73	HUMAN	C9J4N6	Isocitrate dehydrogenase [NADP] cytoplasmic (Fragment)
20563	dirMS_041712_NAR_20mM_minus.8231.8231.2	2	5.48	0	5.74E+03		(K)DQVANS	(K)D Q|V|A|N/S A F/V E R(L)		131.7	618.3098	1235.602	0.0108	8.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
20564	dirMS_041712_NAR_20mM_minus.8451.8451.2	2	5.48	0	3.26E+05	M239m	(K)EITALAP	(K)E I T A|L\A/P S T/m K(I)	m:Oxidized methionine	133.58	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
20565	dirMS_041712_NAR_30mM_minus2.13559.13559.2	2	5.48	0	1.80E+04		(R)TACVQG	(R)T A C V Q G G|L/H K(L)	C:Carbamidomethylation	127.03	535.762	1070.541	-0.0244	-22.8	8.44	228643.1	8.37	HUMAN	E7EQS8	Methylcytosine dioxygenase TET2
20566	dirMS_041712_NAR_30mM_minus2.16136.16136.2	2	5.48	0	2.98E+05	M185m	(K)LAVNm\	(K)L A|V/N m V/P F/P R(L)	m:Oxidized methionine	142.3	580.3178	1143.634	15.994	-0.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
20567	dirMS_041712_NAR_120mM_plus.14394.14394.4	4	5.48	1	7.87E+05	M204m S2(	(K)LAAVmF	(K)L A A V/m R Q s Q L/L/D F L S G K(Q)	m:Oxidized methionine s:Pho	127.72	494.0077	1877.031	95.9776	8.3	8.75	74166.5	9.44	HUMAN	B4DZ31	PCNA-interacting partner
20568	dirMS_041712_NAR_20mM_plus.11205.11205.2	2	5.48	0	2.01E+05		(K)LITPAVV	(K)L I|T/P/A V V|S\E R(L)		149.97	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
20569	dirMS_041712_NAR_20mM_plus.11328.11328.2	2	5.48	0	5.10E+03		(R)TSGSVYI	(R)T S|G S|V Y/I T L K(K)		150.4	534.8004	1068.594	0	0	8.26	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
20570	dirMS_041712_NAR_30mM_plus2.22057.22057.2	2	5.48	0	1.47E+05		(K)GLSSLLC	(K)G L\S\S L/L/C N F T/K(S)	C:Carbamidomethylation	171.65	620.3199	1239.64	-0.0077	-6.2	8.75	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
20571	dirMS_041712_NAR_30mM_plus2.5461.5461.2	2	5.48	0	2.27E+03		(-)MAEETQ	(-)M A/E/E/T Q H N\K(L)		82.62	544.2373	1087.484	-0.0164	-15	5.38	71842.4	7.17	HUMAN	A6NC78	Golgin subfamily A member 8I
20572	dirMS_041712_NAR_50mM_plus2.12808.12808.3	3	5.48	1	3.70E+05		(K)LAEIGAF	(K)L/A|E I/G A/P I Q G N R E E L V E R(L)		135.93	665.3593	1994.066	-0.0032	-1.6	4.49	38572.2	6.31	HUMAN	E9PJ04	Splicing factor 3B subunit 2 (Fragment)
20573	dirMS_041712_NAR_50mM_plus2.20220.20220.3	3	5.48	1	3.93E+05		(R)FLDKALE	(R)F L|D K A L E L/N M/L/S L K(G)		174.78	545.6431	1634.919	-0.0038	-2.4	6.07	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
20574	dirMS_041712_NAR_50mM_plus2.7967.7967.3	3	5.48	1	5.05E+04		(K)ELQAAG	(K)E L/Q/A A G K S/P E/D L E R(L)		108.27	514.9321	1542.776	0.0059	3.8	4.41	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
20575	dirMS_041712_NAR_120mM_minus.11454.11454.3	3	5.47	1	2.66E+05	M216m	(K)ASIHEAV	(K)A S I/H\E A W/T D/G K/E A m L/K(H)	m:Oxidized methionine	116.6	601.6303	1786.879	15.9971	1.2	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
20576	dirMS_041712_NAR_120mM_minus.13939.13939.3	3	5.47	1	5.35E+05		(K)ASIHEAV	(K)A/S I/H/E/A W T/D/G K E A M\L/K(H)		130.1	596.2973	1786.879	-0.0019	-1.1	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
20577	dirMS_041712_NAR_120mM_minus.4442.4442.3	3	5.47	0	1.32E+05		(R)QELMQ\	(R)Q E L M Q/V/H G E K(R)		73.15	400.1991	1198.589	-0.0057	-4.8	5.4	167865.2	5.34	HUMAN	Q08378	Golgin subfamily A member 3
20578	dirMS_041712_NAR_120mM_minus.8659.8659.3	3	5.47	0	5.76E+05		(R)THYSNIE	(R)T\H Y\S N\I\E\A N/E/S E E V R(Q)		102.13	593.2723	1777.799	0.0036	2	4.48	21983.3	4.68	HUMAN	K7EIV0	Calpain small subunit 1
20579	dirMS_041712_NAR_120mM_minus.8664.8664.3	3	5.47	0	6.78E+05		(R)SNTENL!	(R)S/N/T E N L/S Q/H/F/R(K)		101.78	444.8813	1332.629	0.0002	0.2	6.47	43303.4	8.7	HUMAN	F8VRN8	LIM domain and actin-binding protein 1
20580	dirMS_041712_NAR_120mM_minus.9564.9564.3	3	5.47	1	3.73E+05		(R)ALSTGEI	(R)A L|S T/G E/K/G F G Y K(G)		106.88	419.8868	1257.647	-0.0015	-1.2	8.54	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
20581	dirMS_041712_NAR_20mM_minus.13549.13549.3	3	5.47	0	1.85E+05		(R)ETTDTD'	(R)E T T D T D T A/D\Q/V I/A S F K(V)		186.35	581.2735	1741.813	-0.0067	-3.9	3.84	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
20582	dirMS_041712_NAR_30mM_minus2.13742.13771.2	2	5.47	0	4.17E+05		(K)TIVMGA	(K)T I|V|M/G A S F/R(N)		128.58	491.2611	981.519	-0.0037	-3.8	9.41	35556.4	9.3	HUMAN	F2Z393	Transaldolase
20583	dirMS_041712_NAR_30mM_minus2.5033.5033.2	2	5.47	1	7.89E+04		(R)EEVVQK	(R)E\E|V|V Q/K E Q E(-)		80.67	559.2673	1117.537	-0.0098	-8.8	4.33	27441.6	6.68	HUMAN	Q15056	Eukaryotic translation initiation factor 4H
20584	dirMS_041712_NAR_50mM_minus2.11123.11123.3	3	5.47	0	2.46E+05		(K)VTVLFA(	(K)V T V L\F/A/G Q H I/S K(S)		130.98	433.9205	1299.742	0.005	3.8	8.73	258215.9	5.48	HUMAN	E7EN95	Filamin-B
20585	dirMS_041712_NAR_50mM_minus2.9775.9775.3	3	5.47	1	5.81E+03	M227m	(R)mQKEIT.	(R)m Q K E I T/A\L/A P S/T M K(I)	m:Oxidized methionine	123.53	522.2727	1548.812	15.9911	-2.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
20586	dirMS_041712_NAR_120mM_plus.20336.20336.3	3	5.47	1	6.54E+05		(R)RFDEILE	(R)R F D E I\L E/A/S|D G/I/M/V A R(G)		160.22	607.9762	1821.916	-0.0023	-1.3	4.32	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
20587	dirMS_041712_NAR_20mM_plus.15883.15883.2	2	5.47	0	5.34E+04		(K)IGIVGLP	(K)I/G I|V/G L P N V G K(S)		180.67	533.8346	1066.662	0	0	8.75	12416	9.45	HUMAN	C9JTK6	Obg-like ATPase 1 (Fragment)
20588	dirMS_041712_NAR_20mM_plus.8468.8468.2	2	5.47	0	4.73E+04		(K)EAESSPF	(K)E A/E S S/P/F V E/R(L)		128.55	575.7771	1150.537	0.0094	8.2	4.25	92752.5	4.76	HUMAN	P14625	Endoplasmin
20589	dirMS_041712_NAR_30mM_plus2.10681.10717.2	2	5.47	0	2.09E+05		(K)ALVAYY(	(K)A L|V/A Y/Y Q K(Y)		109.27	478.2658	955.525	-0.0004	-0.4	8.54	16559.1	10.36	HUMAN	P62249	40S ribosomal protein S16
20590	dirMS_041712_NAR_30mM_plus2.5820.5820.2	2	5.47	0	3.23E+05		(R)EMEEQN	(R)E M|E/E Q/M R(R)		84.02	476.6984	952.386	0.0032	3.4	4.25	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
20591	dirMS_041712_NAR_50mM_plus2.17731.17731.3	3	5.47	0	6.14E+03		(K)NVEQSS	(K)N V/E/Q S S D L Q/D Q L N H/L L K(-)		160.73	661.0046	1980.998	0.0007	0.4	4.54	11621	6.27	HUMAN	Q96B45	UPF0693 protein C10orf32
20592	dirMS_041712_NAR_50mM_plus2.8849.8849.3	3	5.47	0	4.13E+05		(R)ATQQQI	(R)A T Q Q\Q H D F T\L/T/Q T A D/G R(S)		113.5	639.9699	1917.905	-0.0098	-5.1	5.21	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
20593	dirMS_041712_NAR_60mM_plus.11442.11442.3	3	5.47	1	8.44E+05		(K)VSRMVA	(K)V/S R M V A E S/S G/I S T S R(A)		116.7	522.9381	1566.79	0.0093	5.9	9.57	20234.8	5.04	HUMAN	B7Z8B3	Peroxisomal biogenesis factor 19
20594	dirMS_041712_NAR_60mM_plus.13255.13255.3	3	5.47	1	2.80E+04		(K)AAAGKA	(K)A/A\A/A/G K A E L|E L E/L/G R(I)		126.13	476.5985	1427.785	-0.0043	-3	4.79	533778	5.74	HUMAN	Q15149	Plectin
20595	dirMS_041712_NAR_60mM_plus.18144.18144.3	3	5.47	1	8.53E+05		(K)EVNKFQ	(K)E V N K F Q/M/A/Y/S N L L R(A)		152.62	571.6293	1712.879	-0.0055	-3.2	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
20596	dirMS_041712_NAR_60mM_plus.19649.19649.3	3	5.47	0	5.25E+04		(R)NSVSNF	(R)N S V/S N F/L H/S L E/R(G)		162.97	468.2401	1402.707	-0.0016	-1.1	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1

20597	dirMS_041712_NAR_60mM_plus.7310.7310.3	3	5.47	1	9.36E+05		(R)AVTGYK	(R)A V T G Y/K/D/P Y/S/G K(L)		96.6	429.2193	1285.642	0.0011	0.8	8.47	533778	5.74	HUMAN	Q15149	Plectin
20598	dirMS_041712_NAR_120mM_minus.12322.12322.3	3	5.46	1	5.88E+04		(K)LFNLSKE	(K)L F N/L/S K E D D/V R(Q)		120.22	445.9006	1335.69	-0.0031	-2.3	4.56	25082	11.29	HUMAN	A2A3R5	40S ribosomal protein S6
20599	dirMS_041712_NAR_120mM_minus.13721.13721.4	4	5.46	2	8.32E+05	M100m	(K)KQGGLG	(K)K\Q G G L G\P m N I/P L V S D/P K R(T)	m:Oxidized methionine	128.55	481.5173	1907.053	15.9942	-0.3	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
20600	dirMS_041712_NAR_120mM_minus.16420.16420.3	3	5.46	0	3.91E+05		(R)EHALLA	(R)E H\A\L L\A/Y/T L/G V K(Q)		144.38	438.9186	1314.742	-0.0004	-0.3	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
20601	dirMS_041712_NAR_120mM_minus.17043.17043.3	3	5.46	1	4.97E+05		(K)RISEQFT	(K)R I S E Q\F\T|A M F R(R)		147.8	462.5714	1385.699	0.0002	0.2	9.6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
20602	dirMS_041712_NAR_120mM_minus.7574.7574.4	4	5.46	1	4.21E+05		(R)RVIVPA	(R)R V I/V P A D/L P Y E\P/P R(R)		96.05	406.2323	1621.906	0.0013	0.8	6.07	18794.8	5.78	HUMAN	B4E3C5	Transcriptional regulator ERG
20603	dirMS_041712_NAR_20mM_minus.14119.14119.2	2	5.46	0	1.41E+06		(K)SYELPD	(K)S Y\E\L/P D\G Q V I/T I\G N E R(F)		194.15	895.9481	1790.892	-0.003	-1.7	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
20604	dirMS_041712_NAR_30mM_minus2.15663.15663.2	2	5.46	0	2.70E+04	M1342m	(R)ASLSLW	(R)A S L/S L/W Q/A m/E K(G)	m:Oxidized methionine	138.55	640.3185	1263.64	15.9895	-4.2	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
20605	dirMS_041712_NAR_30mM_minus2.5471.5471.2	2	5.46	0	9.90E+04		(K)DSYVGD	(K)D S\Y/V/G D E A Q S K(R)		83.88	599.7632	1198.522	-0.0031	-2.6	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
20606	dirMS_041712_NAR_30mM_minus2.9515.9630.2	2	5.46	0	3.09E+05	S27s	(K)IEVDPsK	(K)I E|V/D/P s K(H)	s:N-acetylglucosamine (S)	106.52	495.7528	787.42	203.0787	-0.7	4.37	111614	6.1	HUMAN	Q9P1Q0	Vacuolar protein sorting-associated protein 54
20607	dirMS_041712_NAR_50mM_minus2.10517.10517.3	3	5.46	0	2.90E+05	M35m	(K)AASDIA	(K)A A/S\D/I A m T E|L/P P T\H P I R(L)	m:Oxidized methionine	127.9	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
20608	dirMS_041712_NAR_50mM_minus2.14846.14846.3	3	5.46	1	6.81E+04	M84m	(K)ETmQSL	(K)E T m/Q S/L N D R L A S Y L D/R(V)	m:Oxidized methionine	152.25	643.3122	1911.923	15.9991	2.2	4.56	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
20609	dirMS_041712_NAR_50mM_minus2.9431.9431.3	3	5.46	0	6.17E+04		(R)DLSKPIG	(R)D L/S K P I/G A/L/N/P K(R)		121.75	418.2465	1252.726	-0.001	-0.8	8.59	84798.4	5.92	HUMAN	B7Z2H9	Neurobeachin
20610	dirMS_041712_NAR_60mM_minus.16580.16580.3	3	5.46	1	9.23E+04		(R)KQSLGE	(R)K Q S L G E\L|I|G T L/N A/A K(V)		152.13	514.9657	1542.885	-0.0024	-1.6	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
20611	dirMS_041712_NAR_120mM_plus.25634.25634.3	3	5.46	1	4.34E+05		(R)GVMLA	(R)G V M/L/A/V D A V/I/A E L/K K(Q)		193.17	519.6402	1556.908	-0.002	-1.3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
20612	dirMS_041712_NAR_120mM_plus.6130.6130.2	2	5.46	1	2.22E+06		(K)IREEYPD	(K)I R|E E|Y P D|R(I)		84.97	539.2694	1077.532	-0.0008	-0.8	4.68	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
20613	dirMS_041712_NAR_20mM_plus.9563.9563.2	2	5.46	0	4.68E+05		(R)ISVYYNE	(R)I/S|V/Y Y N E A/T/G G K(Y)		138.13	651.3211	1301.637	-0.0023	-1.8	6	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
20614	dirMS_041712_NAR_30mM_plus2.12565.12565.2	2	5.46	0	2.52E+05		(R)NCSSFLI	(R)N/C|S/S/F L I/K(R)	C:Carbamidomethylation	118.73	484.7469	968.487	-0.0005	-0.5	8.75	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
20615	dirMS_041712_NAR_30mM_plus2.16471.16471.3	3	5.46	0	4.35E+05		(K)LLDLVQ	(K)L L D\L\V\Q Q/S C N Y K(Q)	C:Carbamidomethylation	139.08	494.2566	1480.746	0.0088	5.9	5.83	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
20616	dirMS_041712_NAR_30mM_plus2.17150.17150.2	2	5.46	0	1.48E+05		(K)WPLYM	(K)W/P/L/Y M S T K(N)		143.55	513.2647	1025.513	0.0097	9.4	8.59	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
20617	dirMS_041712_NAR_30mM_plus2.17464.17464.2	2	5.46	0	3.19E+05		(R)LSYTQLL	(R)L S\Y T/Q/L L/R(R)		145.38	497.2902	993.573	0.0004	0.4	8.75	533778	5.74	HUMAN	Q15149	Plectin
20618	dirMS_041712_NAR_40mM_plus2.19040.19040.3	3	5.46	1	6.36E+03		(R)VISGVLC	(R)V I/S G\V\L Q/L G N I V F K K(E)		178.52	539.0014	1614.994	-0.0045	-2.8	10	227783.5	5.5	HUMAN	P35579	Myosin-9
20619	dirMS_041712_NAR_40mM_plus2.9546.9546.3	3	5.46	0	3.47E+04		(R)GGGGNI	(R)G G G G\N/F\G P/G/P G S/N F R(G)		119.3	459.8801	1377.629	-0.0037	-2.7	9.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
20620	dirMS_041712_NAR_50mM_plus2.18299.18299.3	3	5.46	0	3.57E+05		(K)MLNIHP	(K)M L/N I H/P S L L/P S F K(G)		164.5	499.6132	1496.829	-0.0043	-2.9	8.52	60871.9	6.3	HUMAN	B4DJ93	Phosphoribosylformylglycinamidine cyclo-ligase
20621	dirMS_041712_NAR_50mM_plus2.9487.9487.3	3	5.46	1	3.39E+05		(R)AGTGVD	(R)A G T/G/V\D N V/D/L E A A\T R K(G)		117.4	539.6108	1616.824	-0.006	-3.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
20622	dirMS_041712_NAR_50mM_plus2.9994.9994.3	3	5.46	0	2.40E+04	M457m M4	(R)mGPLGL	(R)m/G|P L/G/L D H m A S S I E\R(M)	m:Oxidized methionine	119.67	549.2613	1613.777	31.9919	1.3	5.3	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
20623	dirMS_041712_NAR_60mM_plus.15129.15129.3	3	5.46	1	1.67E+05		(R)GYISPYF	(R)G Y/I/S|P Y F I N\T S K G Q K(C)		134.73	568.2935	1702.88	-0.014	-8.2	9.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
20624	dirMS_041712_NAR_60mM_plus.18526.18526.3	3	5.46	1	1.18E+05		(K)MFIGGL	(K)M/F/I/G G L/S W D/T T K K(D)		154.27	495.2592	1483.761	0.0017	1.1	8.35	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
20625	dirMS_041712_NAR_60mM_plus.5026.5026.3	3	5.46	1	3.95E+05		(R)AAEDDE	(R)A A|E D D E/D D D V/D/T K K(Q)		83.53	522.5529	1565.645	-0.0008	-0.5	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
20626	dirMS_041712_NAR_60mM_plus.9482.9482.3	3	5.46	0	8.21E+04		(K)QEYDES	(K)Q E/Y D E S/G/P S I/V/H/R(K)		107.52	506.2392	1516.703	0.0004	0.3	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
20627	dirMS_041712_NAR_120mM_minus.8454.8454.3	3	5.45	0	6.90E+05		(K)YKPESEE	(K)Y K P E S\E/E L/T/A E R(I)		100.73	484.5714	1451.701	-0.0016	-1.1	4.5	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
20628	dirMS_041712_NAR_20mM_minus.11850.11850.2	2	5.45	0	1.25E+05	M98m	(R)TLTIVDT	(R)T L|T I|V/D T G I G/m/T K(A)	m:Oxidized methionine	167.03	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
20629	dirMS_041712_NAR_20mM_minus.8570.8570.2	2	5.45	0	1.04E+04		(K)TIAPALV	(K)T I|A\P A L V|S K(K)		134.53	450.2808	899.556	-0.0017	-1.9	8.41	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
20630	dirMS_041712_NAR_30mM_minus2.13874.13874.2	2	5.45	0	2.14E+05		(R)SISLYYT	(R)S I|S L/Y/Y/T/G E K(G)		128.28	580.7949	1160.583	-0.0009	-0.7	5.72	32503.1	5.29	HUMAN	H7BY16	Nucleolin (Fragment)
20631	dirMS_041712_NAR_30mM_minus2.16733.16733.2	2	5.45	0	2.26E+05		(R)FFMGN	(R)F/F|M/G N/Q V L\K(V)		145.15	542.2866	1083.566	0.0004	0.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
20632	dirMS_041712_NAR_30mM_minus2.18318.18318.3	3	5.45	0	5.00E+05		(R)QAQEYE	(R)Q A Q E Y/E/A/L/L N I K(V)		154.63	473.9196	1419.748	-0.0036	-2.5	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
20633	dirMS_041712_NAR_50mM_minus2.11654.11654.3	3	5.45	1	1.89E+04		(R)IVLANDI	(R)I V|L A/N D P D/A D R L A V A E K(Q)		134.4	603.9924	1809.97	-0.0079	-4.3	4.23	32837.5	6.16	HUMAN	B4E0G8	Phosphoglucomutase-2
20634	dirMS_041712_NAR_60mM_minus.18439.18439.3	3	5.45	0	2.38E+05		(K)SQLDIII	(K)S Q|L D I/I/I H/S\L K(K)		164.08	422.9181	1266.742	-0.0019	-1.5	6.46	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
20635	dirMS_041712_NAR_20mM_plus.11013.11013.2	2	5.45	0	6.40E+03	M94m	(R)FSmVVC	(R)F S/m/V/V/Q D G I V K(A)	m:Oxidized methionine	147.97	619.8249	1222.65	15.9925	-1.9	5.84	13010.7	9.97	HUMAN	A6NC19	Peroxiredoxin-5, mitochondrial
20636	dirMS_041712_NAR_20mM_plus.14043.14043.2	2	5.45	0	1.56E+05	M98m	(R)TLTIVDT	(R)T L T/I/V\D T/G I/G m T K(A)	m:Oxidized methionine	167.85	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
20637	dirMS_041712_NAR_20mM_plus.19219.19219.2	2	5.45	0	8.08E+04		(R)ASVILAG	(R)A S V/I\L\A/G L G F T P K(M)		204.25	637.3763	1273.751	-0.0061	-4.8	8.8	80142.6	5.95	HUMAN	Q9NUQ8	ATP-binding cassette sub-family F member 3
20638	dirMS_041712_NAR_20mM_plus.8636.8636.2	2	5.45	0	5.56E+03		(R)LTPEEIEI	(R)L T/P E/E I E R(M)		129.98	493.7649	986.515	0.0072	7.3	4.25	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
20639	dirMS_041712_NAR_30mM_plus2.11284.11284.3	3	5.45	0	3.70E+05	M304m	(R)MGQMA	(R)M G Q M A M\G G\A\m/G I/N N R(G)	m:Oxidized methionine	112.93	518.8921	1538.67	15.9923	-1.7	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
20640	dirMS_041712_NAR_30mM_plus2.19450.19450.2	2	5.45	0	1.78E+05		(K)CALDFFF	(K)C/A|L/D/F/F R(Q)	C:Carbamidomethylation	155.77	464.7242	928.434	0.0066	7.1	5.84	15387.4	6.92	HUMAN	F5H7V7	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8
20641	dirMS_041712_NAR_30mM_plus2.6961.6961.2	2	5.45	0	2.58E+05		(K)MAQFD	(K)M/A/Q/F D A/K(K)		91.35	405.6961	810.381	0.0035	4.3	5.59	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
20642	dirMS_041712_NAR_30mM_plus2.7778.7778.2	2	5.45	0	2.03E+05		(R)LEEQLGI	(R)L E/E/Q/L/G R(G)		94.75	422.7299	844.452	0.0002	0.3	4.53	202288.6	5.88	HUMAN	A9Z1Z3	Fer-1-like protein 4
20643	dirMS_041712_NAR_40mM_plus2.19427.19427.3	3	5.45	0	1.01E+04		(K)GAEILEV	(K)G A/E/I L E V/L H S L/P A V R(Q)		182.63	535.3088	1603.917	-0.0048	-3	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
20644	dirMS_041712_NAR_40mM_plus2.5842.5842.2	2	5.45	1	1.68E+05		(R)SKQAEE	(R)S K Q\A\E E\E|F(-)		92.1	484.2219	967.437	-0.0002	-0.2	4.25	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
20645	dirMS_041712_NAR_50mM_plus2.11509.11509.3	3	5.45	1	2.02E+05		(R)MVDVVI	(R)M/V|D|V V/E K E D V N E A I R(L)		128.03	582.6309	1745.874	0.0043	2.5	4.18	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
20646	dirMS_041712_NAR_50mM_plus2.15506.15506.3	3	5.45	1	6.37E+05		(R)GFPTIYF	(R)G F/P T I/Y F S/P A N K K(L)		149.13	490.5973	1469.779	-0.0014	-0.9	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
20647	dirMS_041712_NAR_50mM_plus2.18866.18866.3	3	5.45	0	2.66E+05		(K)LAKPLSS	(K)L A\K\P L S S L T/P L I M A A/K(E)		167.48	552.004	1653.997	0.0003	0.2	10	24711.4	5.19	HUMAN	H7C1X3	PAK-2p34 (Fragment)
20648	dirMS_041712_NAR_50mM_plus2.9919.9919.3	3	5.45	0	1.78E+05	M72m	(K)STTSDIP	(K)S T/T/S/D I/P H m L N Q V E S K(V)	m:Oxidized methionine	119.57	601.6245	1786.864	15.995	0	5.3	11532.2	6.34	HUMAN	H0YNA1	Protein FAM98B (Fragment)
20649	dirMS_041712_NAR_60mM_plus.18917.18917.3	3	5.45	1	1.07E+04		(K)LLVYEAL	(K)L L/V|Y E A L/E/Y/A K R(A)		156.65	489.9411	1467.821	-0.0118	-8.1	6.14	32535.6	9.19	HUMAN	B4DZW6	Regulator of microtubule dynamics protein 1
20650	dirMS_041712_NAR_60mM_plus.8129.8129.3	3	5.45	1	3.25E+05		(R)LSQIGVE	(R)L/S Q/I/G V E N T E E N R R(L)		100.75	548.9468	1644.83	-0.0041	-2.5	4.79	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
20651	dirMS_041712_NAR_60mM_plus.8156.8156.3	3	5.45	1	5.12E+04		(K)DISTNYY	(K)D I S T/N Y Y A S Q K K(T)		101.03	473.2367	1417.696	-0.0002	-0.2	8.43	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
20652	dirMS_041712_NAR_120mM_minus.7721.7721.3	3	5.44	1	3.26E+05	S633s	(R)LNEQsRI	(R)L\N/E/Q/s R/H S S I R(D)	s:Phosphorylated S	95.97	469.5586	1326.687	79.974	5.4	9.61	77630.7	8.66	HUMAN	Q9NPG1	Frizzled-3
20653	dirMS_041712_NAR_20mM_minus.9459.9459.2	2	5.44	0	2.04E+05		(R)LQAEIEG	(R)L/Q|A E/I E/G L/K(G)		145.3	500.7862	1000.567	-0.0022	-2.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
20654	dirMS_041712_NAR_20mM_minus.9675.9675.2	2	5.44	0	1.26E+05		(R)AGTGVD	(R)A G T G\V/D N/V/D L/E A A T R(K)		146.77	744.8662	1488.729	-0.0038	-2.5	4.03	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
20655	dirMS_041712_NAR_30mM_minus2.12314.12314.2	2	5.44	0	1.33E+05		(K)SIYYITGE	(K)S I/Y/Y/I T G E S K(E)		121.08	580.7949	1160.583	-0.0009	-0.7	5.72	16789.1	8.77	HUMAN	H0Y5S7	Heat shock protein HSP 90-beta (Fragment)
20656	dirMS_041712_NAR_30mM_minus2.15872.15872.2	2	5.44	0	2.59E+04		(R)ALQASA	(R)A L\Q/A/S A L/N/A/W/R(G)		139.9	600.8272	1200.648	-0.0013	-1	9.79	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
20657	dirMS_041712_NAR_30mM_minus2.17916.17916.2	2	5.44	0	5.55E+04	S6s	(-)MSMILsA	(-)M/S M I L s/A S\V/I R(V)	s:Phosphorylated S	150.52	644.3165	1207.654	79.972	4.4	9.5	11800.5	7.98	HUMAN	C9J463	Vesicle-trafficking protein SEC22a (Fragment)
20658	dirMS_041712_NAR_30mM_minus2.9516.9516.2	2	5.44	0	1.11E+05		(R)ISVYYNE	(R)I S V/Y\Y N E A T G G K(Y)		105.88	651.322	1301.637	-0.0005	-0.4	6	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
20659	dirMS_041712_NAR_50mM_minus2.17602.17602.3	3	5.44	1	5.84E+04		(R)GLFIIDD	(R)G L|F I/I D D K/G I L/R(Q)		168.88	453.9381	1359.8	0.0003	0.2	5.96	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
20660	dirMS_041712_NAR_60mM_minus.15275.15275.3	3	5.44	1	2.07E+05	T98t	(R)INIAGW	(R)I N I/A G W K/t/D/G K(W)	t:N-acetylglucosamine (T)	145.25	469.2589	1202.653	203.1093	21.3	8.59	52994.6	9.09	HUMAN	Q17RR3	Pancreatic lipase-related protein 3
20661	dirMS_041712_NAR_60mM_minus.17043.17043.3	3	5.44	1	3.04E+05		(K)ILLAELE	(K)I L|L/A E L/E Q L K G Q G K(S)		154.45	513.9734	1539.911	-0.0048	-3.1	6.14	49709.6	5.19	HUMAN	B0YJC4	Vimentin
20662	dirMS_041712_NAR_60mM_minus.4841.4841.3	3	5.44	1	1.28E+05	M75m M8	(R)mGPSG	(R)m G|P S/G G E|G m E P E R R(D)	m:Oxidized methionine	80.42	507.8846	1489.652	31.987	-1.8	4.78	23181	4.83	HUMAN	B4DGQ0	LIM and SH3 domain protein 1
20663	dirMS_041712_NAR_120mM_plus.10885.10885.3	3	5.44	0	1.18E+06		(R)GSAVHC	(R)G S/A/V/H Q/L/S E\E L R(C)		110.8	442.5657	1325.681	0.0017	1.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
20664	dirMS_041712_NAR_20mM_plus.18131.18131.2	2	5.44	0	1.31E+05	M153m	(K)VVTYGm	(K)V V T\Y/G/m/A N L L T G P K(R)	m:Oxidized methionine	196.32	740.3997	1463.793	15.9995	3.1	8.56	28454.5	6.24	HUMAN	B0AZP7	Synaptic vesicle membrane protein VAT-1 homolog
20665	dirMS_041712_NAR_20mM_plus.8895.8895.2	2	5.44	0	5.76E+04		(R)GLDVED	(R)G L/D|V E D/V K(F)		131.6	437.7292	874.452	-0.0005	-0.6	4.03	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
20666	dirMS_041712_NAR_30mM_plus2.10419.10420.2	2	5.44	0	2.95E+05		(R)SLSYSPV	(R)S L|S Y/S\P V/E R(R)		108.3	519.2668	1037.526	0.0001	0.1	5.72	9057.8	12.09	HUMAN	I3L4U6	Serine/arginine repetitive matrix protein 2 (Fragment)
20667	dirMS_041712_NAR_30mM_plus2.13910.13910.2	2	5.44	0	1.34E+05		(R)TQADLD	(R)T Q|A/D\L D/S L V R(E)		124.57	559.2986	1117.585	0.0051	4.6	4.21	24187.6	9.44	HUMAN	J3KS22	L-xylulose reductase (Fragment)
20668	dirMS_041712_NAR_30mM_plus2.16604.16604.2	2	5.44	0	2.74E+05		(K)VQQTVC	(K)V Q|Q/T V/Q D\L F/G R(A)		139.48	645.842	1290.68	-0.0034	-2.6	5.81	73964.5	5.87	HUMAN	P38646	Stress-70 protein, mitochondrial
20669	dirMS_041712_NAR_40mM_plus2.12963.12963.2	2	5.44	0	4.56E+04		(K)ALWFQ	(K)A L|W/F/Q/G R(C)		142.62	439.2366	877.468	-0.002	-2.3	9.79	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
20670	dirMS_041712_NAR_40mM_plus2.5432.5432.3	3	5.44	0	1.94E+04	S1287s	(K)MTsTTA	(K)M/T|s T T A E G A G E Q(-)	s:N-acetylglucosamine (S)	88.85	462.5329	1182.494	203.0898	7.6	3.79	145630.3	5.31	HUMAN	F8W7J9	Neurabin-1
20671	dirMS_041712_NAR_50mM_plus2.7336.7336.3	3	5.44	1	2.74E+04		(R)LAQATQ	(R)L/A/Q A T Q E R T D\L Y A/K(Q)		104.57	536.6151	1607.839	-0.008	-5	6.07	141938.5	6.77	HUMAN	Q9UQE7	Structural maintenance of chromosomes protein 3
20672	dirMS_041712_NAR_50mM_plus2.8268.8268.3	3	5.44	1	3.49E+05		(R)VAVEAK	(R)V/A/V E A/K N/P A D L/P K(L)		110.53	451.2563	1351.758	-0.0036	-2.7	6.04	96306.4	6.41	HUMAN	P13639	Elongation factor 2
20673	dirMS_041712_NAR_60mM_plus.5545.5545.3	3	5.44	0	3.12E+05	M111m	(R)MEELHN	(R)M/E|E/L H/N Q E m Q K(R)	m:Oxidized methionine	87.4	478.2118	1416.625	15.9962	0.9	4.75	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
20674	dirMS_041712_NAR_60mM_plus.7371.7371.3	3	5.44	0	9.36E+05		(R)AAHSEG	(R)A A H S E G N T\T/A/G L D/M/R(E)		96.68	510.9035	1530.697	-0.0006	-0.4	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
20675	dirMS_041712_NAR_120mM_minus.21384.21384.3	3	5.43	0	8.08E+05	T241t	(K)NLTLMA	(K)N L T/L M|A/t T S Q L P K(L)	t:N-acetylglucosamine (T)	182.17	540.9497	1417.772	203.0626	-10.3	8.75	44909.6	6.22	HUMAN	B7Z7D2	Lysosomal acid phosphatase
20676	dirMS_041712_NAR_30mM_minus2.5315.5315.2	2	5.43	0	2.01E+05		(R)SNAEDT	(R)S N|A/E/D T L R(S)		82.97	453.2209	905.432	0.0022	2.5	4.37	533778	5.74	HUMAN	Q15149	Plectin
20677	dirMS_041712_NAR_40mM_minus2.13385.13385.3	3	5.43	0	1.46E+05		(K)VAIVKP	(K)V A|I/V K P G V\P M|E I V L/N K(E)		163.22	569.6777	1707.024	-0.0052	-3	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
20678	dirMS_041712_NAR_50mM_minus2.16399.16399.3	3	5.43	1	1.60E+05		(K)VVSSVL	(K)V V/S/S V L/Q/F G N I/S F K K(E)		162	551.6488	1652.937	-0.0052	-3.1	10	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
20679	dirMS_041712_NAR_60mM_minus.11442.11442.3	3	5.43	1	2.49E+05		(K)NQLTSN	(K)N Q/L/T S N/P E N T V F\D A K R(L)		123.97	611.9739	1833.909	-0.0018	-1	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
20680	dirMS_041712_NAR_60mM_minus.14040.14040.3	3	5.43	1	2.09E+05		(R)GYSFTT	(R)G Y/S/F/T T T A E R E/I V R(D)		137.57	543.9458	1629.823	-0.0003	-0.2	6.14	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
20681	dirMS_041712_NAR_60mM_minus.18605.18605.3	3	5.43	0	2.81E+05		(K)LHDNLII	(K)L H\D N L I|I/S D L/E N T V K(K)		165.82	575.3117	1723.922	-0.0019	-1.1	4.54	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
20682	dirMS_041712_NAR_60mM_minus.18662.18662.3	3	5.43	0	1.25E+05		(R)IDILDSA	(R)I/D|I L/D/S A L L R P G R(I)		165.38	480.2832	1438.838	-0.0026	-1.8	5.96	44954.5	8.44	HUMAN	A8K3Z3	26S protease regulatory subunit 8
20683	dirMS_041712_NAR_60mM_minus.6540.6540.3	3	5.43	1	2.18E+05		(R)KTGQAP	(R)K\T G Q A|P G Y S/Y T/A/A/N/K(N)		95.27	519.5963	1556.77	0.004	2.6	9.53	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
20684	dirMS_041712_NAR_120mM_plus.4886.4886.2	2	5.43	0	1.72E+05		(R)HAYGDC	(R)H/A|Y/G D\Q Y/R(A)		77.4	505.2275	1009.449	-0.0009	-0.9	6.74	17833.3	8.73	HUMAN	C9J4N6	Isocitrate dehydrogenase [NADP] cytoplasmic (Fragment)
20685	dirMS_041712_NAR_20mM_plus.15839.15839.3	3	5.43	0	8.77E+03		(R)SSFYVN	(R)S S F Y V N G L/T/L/G\G Q K(C)		179.37	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
20686	dirMS_041712_NAR_30mM_plus2.20644.20644.2	2	5.43	0	3.47E+05		(K)GGIVGM	(K)G G I/V\G/M/T L/P I A R(D)		161.98	592.8453	1184.682	0.0013	1.1	9.75	27150.8	7.95	HUMAN	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2
20687	dirMS_041712_NAR_30mM_plus2.6494.6494.2	2	5.43	0	1.82E+05		(K)TLNAGA	(K)T L\N/A|G/A Y S K(V)		88.78	462.7408	924.479	-0.0042	-4.5	8.26	30197.4	7.91	HUMAN	E9PMG2	Palmitoyl-protein thioesterase 1 (Fragment)
20688	dirMS_041712_NAR_40mM_plus2.14051.14051.3	3	5.43	1	8.78E+04		(R)STGLELE	(R)S T|G L/E L E T/P S L V/P V K K(N)		148.73	566.6552	1697.968	-0.0173	-10.2	5.86	34828	9.96	HUMAN	F5H5K4	Serine/threonine-protein phosphatase 1 regulatory subunit 10
20689	dirMS_041712_NAR_50mM_plus2.9788.9788.3	3	5.43	1	2.02E+05		(R)AESGPD	(R)A E/S/G P D/L R Y E\V/T/S/G G G G T S R(M)		119.13	665.9843	1995.937	0.0017	0.9	4.68	334221.3	6.44	HUMAN	P15924	Desmoplakin
20690	dirMS_041712_NAR_60mM_plus.13006.13006.3	3	5.43	0	2.35E+05		(R)DAYSGG	(R)D A/Y/S|G G/A V N L Y H V R(E)		124.72	507.9187	1521.745	-0.0029	-1.9	6.74	17952.8	6.73	HUMAN	E9PAV2	Proteasome subunit beta type-5
20691	dirMS_041712_NAR_60mM_plus.8117.8117.3	3	5.43	1	3.25E+05		(R)LSQIGVE	(R)L S Q/I/G V E N T E E N R R(L)		100.75	548.9468	1644.83	-0.0041	-2.5	4.79	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
20692	dirMS_041712_NAR_20mM_minus.10484.10484.2	2	5.42	0	1.42E+05		(R)IYVVDV	(R)I Y\V/V|D/V G S E P R(A)		152.95	617.3216	1233.647	-0.0115	-9.3	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
20693	dirMS_041712_NAR_30mM_minus2.13662.13662.2	2	5.42	0	2.26E+05		(K)TYSVEYL	(K)T Y|S V/E Y L/P K(V)		128.3	550.2855	1099.567	-0.0033	-3	5.66	258215.9	5.48	HUMAN	E7EN95	Filamin-B
20694	dirMS_041712_NAR_40mM_minus2.10876.10876.3	3	5.42	0	2.00E+05		(R)DLSHIGI	(R)D L S H\I\G D A\V\V/I/S C/A K(D)	C:Carbamidomethylation	147.25	528.9384	1584.805	-0.0044	-2.8	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
20695	dirMS_041712_NAR_40mM_minus2.9982.9982.3	3	5.42	1	6.91E+05		(R)LQNPAI	(R)L Q N P/A I T G P A V P Y/S/R E F K(Q)		141.53	663.3508	1988.06	-0.0221	-11.1	8.59	74534.3	5.06	HUMAN	K7ERN1	E3 ubiquitin-protein ligase NEDD4-like (Fragment)
20696	dirMS_041712_NAR_50mM_minus2.8684.8684.3	3	5.42	0	1.18E+05		(R)LGYAVYI	(R)L G\Y A V/Y E T/P T A/H N G A K(N)		117.1	564.6215	1691.839	0.0112	6.6	6.75	25016.4	5.65	HUMAN	B3KR28	Toll-interacting protein
20697	dirMS_041712_NAR_60mM_minus.12229.12229.2	2	5.42	0	7.41E+04		(K)ESTLHLV	(K)E S/T/L/H/L V L/R(L)		127.95	534.3121	1067.621	-0.0038	-3.6	6.85	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
20698	dirMS_041712_NAR_60mM_minus.6879.6879.3	3	5.42	0	6.14E+04	T4t	(-)MAQtPD	(-)M A/Q t P/D G I S C/E/L R(G)	C:Carbamidomethylation t:N-ace	97.03	560.916	1477.677	203.0561	-13.9	4.37	149688.5	6.12	HUMAN	B8X2Z3	CARMIL2b
20699	dirMS_041712_NAR_60mM_minus.7482.7482.3	3	5.42	0	1.58E+05		(R)AAHSEG	(R)A A H S E G N/T T/A/G L D/M R(E)		101.22	510.9003	1530.697	-0.0102	-6.7	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
20700	dirMS_041712_NAR_120mM_plus.12928.12928.3	3	5.42	1	5.99E+05	M393m	(R)ISRTDSF	(R)I/S/R T/D S F S S m V/R(C)	m:Oxidized methionine	121.98	467.9029	1385.684	16.01	10.7	9.6	52462.4	7.15	HUMAN	P42331-2	Isoform 2 of Rho GTPase-activating protein 25
20701	dirMS_041712_NAR_120mM_plus.18044.18044.4	4	5.42	1	6.27E+05		(R)ILEFFGLI	(R)I L E/F/F G L K K/E E/C/P A V R(L)	C:Carbamidomethylation	148.62	484.7638	1936.036	-0.0027	-1.4	6.23	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
20702	dirMS_041712_NAR_20mM_plus.12111.12111.2	2	5.42	0	5.20E+04		(K)VVLVLA	(K)V V|L\V/L/A G R(Y)		156.4	413.778	826.551	-0.0022	-2.6	9.72	4480.4	11.2	HUMAN	K7ERY7	60S ribosomal protein L27
20703	dirMS_041712_NAR_20mM_plus.17078.17078.2	2	5.42	0	1.91E+05		(K)VQIAVA	(K)V Q|I A\V/A/N/A Q E L/L Q/R(M)		188.3	776.9419	1552.881	-0.004	-2.6	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
20704	dirMS_041712_NAR_20mM_plus.18654.18654.2	2	5.42	0	8.06E+04	M80m	(R)APLPDL	(R)A P|L|P D L/Y\P F/G T m R(G)	m:Oxidized methionine	200.33	747.3751	1477.751	15.9921	-1.9	5.88	81122.9	9.03	HUMAN	H3BLZ8	Probable ATP-dependent RNA helicase DDX17
20705	dirMS_041712_NAR_20mM_plus.19325.19325.2	2	5.42	0	1.58E+05		(R)TGAIVD	(R)T G\A\I V/D\V|P V G E E L L G R(V)		204.57	812.9497	1624.891	0.0017	1	4.14	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)

20706	dirMS_041712_NAR_30mM_plus2.18175.18175.2	2	5.42	0	1.92E+04		(R)GENLGL	(R)G E N L G/L/E F R(D)		147.07	517.7625	1034.526	-0.0088	-8.5	4.53	215817.4	6.43	HUMAN	Q9HCM2	Plexin-A4
20707	dirMS_041712_NAR_30mM_plus2.5334.5334.2	2	5.42	0	5.67E+04		(R)TDTGEP	(R)T|D|T/G E\P M G/R(G)		81.95	482.2128	963.42	-0.0017	-1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
20708	dirMS_041712_NAR_40mM_plus2.10111.10111.3	3	5.42	2	1.35E+05		(K)DQLQGE	(K)D Q/L/Q G/E H S R A I L A R S K(L)		124.5	603.6536	1808.973	-0.0263	-14.6	8.75	77031	4.9	HUMAN	Q8N3L3	Beta-taxilin
20709	dirMS_041712_NAR_40mM_plus2.8370.8370.2	2	5.42	0	2.86E+05		(R)FGSGMI	(R)F/G S|G/M N/M\G R(I)		109.45	478.706	956.408	-0.003	-3.1	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
20710	dirMS_041712_NAR_40mM_plus2.9535.9535.2	2	5.42	0	3.15E+04		(R)TSASIILF	(R)T S|A/S I I/L R(G)		119.23	430.7617	860.52	-0.0039	-4.5	9.41	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
20711	dirMS_041712_NAR_50mM_plus2.20037.20037.3	3	5.42	0	5.28E+05		(R)QARPTY	(R)Q/A R P T Y A\T\A\M\L Q S/L L/K(-)		174.55	597.9962	1791.979	-0.0045	-2.5	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
20712	dirMS_041712_NAR_60mM_plus.19046.19046.3	3	5.42	1	3.50E+04		(K)SELVAM	(K)S E L V/A M/L/E/E E E L R K(A)		158.07	559.288	1675.857	-0.0077	-4.6	4.32	18679.2	5.61	HUMAN	B4DWW1	ADP-ribosylation factor-like protein 1
20713	dirMS_041712_NAR_60mM_plus.5657.5657.3	3	5.42	1	1.53E+05	M131m	(R)QmGQP	(R)Q m/G\Q|P/C D/A/Y Q K R(L)	C:Carbamidomethylation m:Oxid	87.98	499.8898	1481.662	15.9925	-1.6	8.59	334221.3	6.44	HUMAN	P15924	Desmoplakin
20714	dirMS_041712_NAR_120mM_minus.11045.11045.3	3	5.41	1	1.83E+05		(R)NREILDE	(R)N R E I\L/D|E/S/L R(L)		114.83	415.5534	1244.659	-0.0137	-11	4.68	96649	6.13	HUMAN	Q8WUM4	Programmed cell death 6-interacting protein
20715	dirMS_041712_NAR_120mM_minus.14906.14906.3	3	5.41	1	2.69E+05		(K)KKELEEI	(K)K K E L E E\I/V/Q/P/I I/S\K(L)		135.13	551.9968	1653.978	-0.0027	-1.6	6.23	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
20716	dirMS_041712_NAR_120mM_minus.9940.9940.3	3	5.41	1	4.51E+04		(R)TFKEICA	(R)T F K/E I|C/A V/S R(I)	C:Carbamidomethylation	108.55	404.2126	1210.625	-0.0016	-1.3	8.41	25558.6	9.3	HUMAN	B1APE1	General transcription factor IIB (Fragment)
20717	dirMS_041712_NAR_20mM_minus.11255.11255.2	2	5.41	0	2.77E+05		(K)LSELEAA	(K)L S/E/L/E A/A L Q R(A)		159.52	565.3134	1129.621	-0.0016	-1.5	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
20718	dirMS_041712_NAR_20mM_minus.12393.12393.3	3	5.41	0	2.02E+03		(R)VPTANV	(R)V P T A N V S\V V/D/L/T C R(L)	C:Carbamidomethylation	171.53	510.9357	1530.795	-0.0019	-1.2	5.81	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
20719	dirMS_041712_NAR_50mM_minus2.6126.6126.2	2	5.41	0	3.56E+04		(K)AGFAGD	(K)A G F|A|G D D A P R(A)		97.78	488.7293	976.448	0.003	3.1	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
20720	dirMS_041712_NAR_60mM_minus.11277.11277.3	3	5.41	1	8.89E+05		(R)FPGQLN	(R)F/P|G Q L N/A/D L R K(L)		122.05	420.2346	1258.69	-0.001	-0.8	8.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
20721	dirMS_041712_NAR_60mM_minus.14272.14272.3	3	5.41	0	8.88E+04		(K)ALGTLVS	(K)A L/G T/L V/S H V T L R(L)		139.2	422.9181	1266.753	-0.0131	-10.3	9.8	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
20722	dirMS_041712_NAR_60mM_minus.18220.18220.3	3	5.41	0	8.73E+03		(K)EFSHIAF	(K)E/F S H I A/F/L T/I K(G)		162.55	435.9153	1305.72	0.0112	8.6	6.85	54978.6	6.16	HUMAN	P10619	Lysosomal protective protein
20723	dirMS_041712_NAR_120mM_plus.7981.7981.4	4	5.41	1	8.94E+05		(K)VLATVTI	(K)V L\A/T V/T K/P V G G D K N G G T/R(V)		95.88	443.251	1769.987	-0.0047	-2.6	9.99	12738	10.72	HUMAN	F8VWR1	60S ribosomal protein L6 (Fragment)
20724	dirMS_041712_NAR_20mM_plus.10446.10446.2	2	5.41	0	1.04E+05		(K)VQISPDS	(K)V Q|I|S|P D S G G L/P E R(S)		144.55	677.8458	1354.696	-0.0118	-8.7	4.37	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
20725	dirMS_041712_NAR_20mM_plus.11409.11409.2	2	5.41	0	2.37E+05		(K)VGLQVV	(K)V G L/Q/V/V A/V K(A)		151.22	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
20726	dirMS_041712_NAR_20mM_plus.14428.14428.2	2	5.41	0	7.72E+04	M23m	(R)SQNVm	(R)S Q/N V/m A A A S I A N I V K(S)	m:Oxidized methionine	170.52	766.9048	1516.815	15.9871	-5.1	8.47	47423	5.43	HUMAN	E7ERF2	T-complex protein 1 subunit alpha
20727	dirMS_041712_NAR_20mM_plus.8015.8015.2	2	5.41	0	4.21E+05	M239m	(K)EVDEQm	(K)E/V/D E/Q m L/N|V/Q N K(N)	m:Oxidized methionine	125.1	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
20728	dirMS_041712_NAR_20mM_plus.9153.9153.2	2	5.41	0	1.11E+05		(R)GYSFTTT	(R)G Y/S/F\T|T/T A E R(E)		133.87	566.7715	1132.527	0.0088	7.8	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
20729	dirMS_041712_NAR_30mM_plus2.15763.15763.2	2	5.41	0	4.53E+05		(K)LLYNNVS	(K)L L/Y N/N/V/S/N F G R(L)		136.07	648.8354	1296.67	-0.006	-4.6	8.75	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
20730	dirMS_041712_NAR_30mM_plus2.18565.18565.2	2	5.41	0	7.55E+05		(K)AAIDWF	(K)A A|I/D/W/F D/G K(E)		150.98	511.7539	1022.494	0.0064	6.2	4.21	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
20731	dirMS_041712_NAR_30mM_plus2.18952.18952.2	2	5.41	0	2.30E+05		(K)QIWQNI	(K)Q I/W/Q N/L G/L D D T/K(I)		152.73	715.866	1430.727	-0.0027	-1.9	4.21	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
20732	dirMS_041712_NAR_30mM_plus2.5870.5870.2	2	5.41	0	1.36E+05		(R)EAEEVYI	(R)E A/E/E V/Y/R(N)		85.32	448.2113	895.416	-0.0003	-0.3	4.25	54793.4	10.51	HUMAN	B7Z4Q3	Putative RNA-binding protein Luc7-like 2
20733	dirMS_041712_NAR_30mM_plus2.5896.5896.2	2	5.41	0	4.28E+05		(K)MIYASSI	(K)M/I|Y A S/S K(D)		85.65	400.2035	799.402	-0.0021	-2.7	8.34	22956	8.8	HUMAN	E9PK25	Cofilin-1
20734	dirMS_041712_NAR_30mM_plus2.8832.8832.2	2	5.41	0	6.93E+05		(K)IHDPEAI	(K)I H|D P/E/A K(W)		99.85	405.2125	809.415	0.0025	3.1	5.32	86952.9	5.85	HUMAN	E9PDL2	Dipeptidyl aminopeptidase-like protein 6
20735	dirMS_041712_NAR_40mM_plus2.17034.17034.3	3	5.41	1	2.26E+05		(K)VIAATNI	(K)V I/A A/T N R V D I L|D P A L L R(S)		167.6	617.3636	1850.086	-0.0096	-5.2	5.93	32827.5	5.92	HUMAN	E9PKD5	26S protease regulatory subunit 6A (Fragment)
20736	dirMS_041712_NAR_50mM_plus2.11291.11291.3	3	5.41	1	2.98E+05		(R)ETGVDLT	(R)E T/G V/D L T K D N/M/A/L Q/R(V)		127.18	564.2856	1690.843	-0.0006	-0.4	4.56	73964.5	5.87	HUMAN	P38646	Stress-70 protein, mitochondrial
20737	dirMS_041712_NAR_120mM_minus.15369.15369.3	3	5.4	1	2.03E+05	M214m	(K)GDQGAI	(K)G D Q G A m G S P G L H G G P/G A K G E K(G)	m:Oxidized methionine	138.27	641.9706	1907.903	15.9944	-0.3	6.75	49991.6	8.98	HUMAN	A6NHN0	Otolin-1
20738	dirMS_041712_NAR_30mM_minus2.14458.14458.2	2	5.4	0	2.19E+05		(K)QVSVFQ	(K)Q V/S V/F Q A M/K(K)		132.58	519.2752	1037.545	-0.0017	-1.6	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
20739	dirMS_041712_NAR_50mM_minus2.5201.5201.3	3	5.4	1	5.68E+04		(K)EEASGSS	(K)E E/A/S/G/S S V/T A E E A K K(F)		87.22	508.2436	1522.723	-0.0069	-4.5	4.49	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
20740	dirMS_041712_NAR_60mM_minus.11136.11136.3	3	5.4	1	2.22E+05	M183m	(R)VEVERD	(R)V/E|V/E R D N\L/A/E D I m R(L)	m:Oxidized methionine	122.3	568.9449	1688.827	15.9929	-1.2	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
20741	dirMS_041712_NAR_60mM_minus.12170.12196.3	3	5.4	1	2.56E+05		(R)LLGIFEQ	(R)L L|G/I F\E Q N Q D R K(H)		127.93	487.5978	1460.786	-0.0068	-4.6	6.07	20662	6	HUMAN	Q9NZJ9-2	Isoform 2 of Diphosphoinositol polyphosphate phosphohydrolase 2
20742	dirMS_041712_NAR_60mM_minus.12444.12444.4	4	5.4	0	1.81E+04		(R)NLDIERF	(R)N L D I E R P T Y T/N L N/R(L)		130.48	430.4748	1718.882	-0.0047	-2.7	6.07	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
20743	dirMS_041712_NAR_60mM_minus.5065.5065.3	3	5.4	1	3.69E+04		(K)KTGSPG	(K)K T G S\P G S/P G A|G G V/Q S T A K(K)		83.02	529.6145	1586.813	0.0157	9.9	10	45232	5.78	HUMAN	B4DZP4	Cytoplasmic dynein 1 light intermediate chain 2
20744	dirMS_041712_NAR_20mM_plus.11102.11102.2	2	5.4	0	9.72E+04	M196m	(K)DAGTIA	(K)D A G T|I|A/G/L N V m R(I)	m:Oxidized methionine	148.75	617.3237	1217.631	16.0094	11.8	5.84	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
20745	dirMS_041712_NAR_20mM_plus.13017.13017.2	2	5.4	0	2.33E+04		(K)AVDSLVI	(K)A V|D S L/V/P I G\R(G)		162.43	513.8007	1026.594	-0.0001	-0.1	5.88	48851.3	9.2	HUMAN	K7EK63	ATP synthase subunit alpha, mitochondrial
20746	dirMS_041712_NAR_20mM_plus.18811.18811.2	2	5.4	0	1.29E+05		(R)LFFLQVK	(R)L F|F/L Q V/K(E)		201.5	447.7765	894.545	0.001	1.1	8.75	71218.8	6.3	HUMAN	A7YIJ8	Radixin
20747	dirMS_041712_NAR_20mM_plus.8878.8878.2	2	5.4	0	1.04E+04		(R)DLTSWV	(R)D L T/S|W V T\E M K(A)		131.55	605.296	1209.582	0.0027	2.3	4.37	285798.6	5.23	HUMAN	A6NG51	Spectrin alpha chain, non-erythrocytic 1
20748	dirMS_041712_NAR_30mM_plus2.4819.4819.2	2	5.4	0	8.18E+05		(R)MGQTM	(R)M/G Q/T M E/R(I)		76.82	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
20749	dirMS_041712_NAR_30mM_plus2.4846.4846.2	2	5.4	0	2.40E+05		(R)MDDYCI	(R)M/D/D Y C R(R)	C:Carbamidomethylation	76.58	430.1579	859.307	0.0012	1.4	4.21	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
20750	dirMS_041712_NAR_40mM_plus2.6110.6110.2	2	5.4	0	5.66E+04		(R)QAFPNT	(R)Q A|F|P N T N R(W)		94.88	474.2383	947.469	0	0	9.75	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
20751	dirMS_041712_NAR_50mM_plus2.14919.14919.3	3	5.4	0	5.70E+05		(R)QIFHPE	(R)Q I/F/H/P E Q L I/T G K(E)		147.1	470.9293	1410.774	-0.0006	-0.4	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
20752	dirMS_041712_NAR_50mM_plus2.18044.18044.3	3	5.4	1	4.52E+05		(K)ASIAQA	(K)A S I/A/Q/A V R D G L L/P T G L G Q R(L)		162.8	641.6959	1923.077	-0.0039	-2	9.64	266161	5.68	HUMAN	E9PPU0	Epiplakin
20753	dirMS_041712_NAR_50mM_plus2.18824.18824.3	3	5.4	0	4.20E+05		(R)AGLGSG	(R)A G L/G/S/G L/S L/S/G L V/H P E\L S R(S)		167.15	617.3412	1850.013	-0.004	-2.2	6.79	73325.2	9.19	HUMAN	F5H2A9	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial
20754	dirMS_041712_NAR_50mM_plus2.7680.7680.3	3	5.4	1	6.00E+04		(K)SAEAAA	(K)S A/E\A/A A E A T/K\N M E/A G A G R(A)		106.47	578.9478	1734.807	0.0213	12.3	4.78	59288.4	7.16	HUMAN	Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)
20755	dirMS_041712_NAR_60mM_plus.15991.15991.3	3	5.4	0	2.19E+04		(K)SLTNDW	(K)S L/T N/D W/E/D H L A V/K(H)		140.35	509.919	1527.744	-0.0014	-0.9	4.53	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
20756	dirMS_041712_NAR_60mM_plus.7327.7327.3	3	5.4	0	9.36E+05		(R)AAHSEG	(R)A A H S E G N/T T/A/G L D/M R(E)		96.68	510.9035	1530.697	-0.0006	-0.4	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
20757	dirMS_041712_NAR_120mM_minus.19698.19698.4	4	5.39	0	1.69E+04		(K)IGPEGLV	(K)I G P E G L V T Q V E\N G G|V L G S R(K)		163.92	471.2583	1882.003	0.0085	4.5	4.53	62228.4	7.91	HUMAN	P30613	Pyruvate kinase isozymes R/L
20758	dirMS_041712_NAR_20mM_minus.10686.10686.2	2	5.39	0	3.43E+05		(K)DVNAAI	(K)D V|N|A/A/I/A A I/K(T)		155.83	493.287	985.568	-0.0009	-1	5.84	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
20759	dirMS_041712_NAR_30mM_minus2.5361.5361.2	2	5.39	2	3.21E+05	M78m	(K)ImRQKE	(K)I/m/R Q K E G(-)	m:Oxidized methionine	83.92	439.2266	861.461	15.9848	-11.5	8.75	9563.9	9.77	HUMAN	Q5RI53	Thrombospondin-2 (Fragment)
20760	dirMS_041712_NAR_30mM_minus2.6441.6441.2	2	5.39	0	1.91E+04		(K)EVEEDE	(K)E V/E/E/D E/Y K(A)		89.48	520.7257	1040.442	0.0023	2.2	3.91	92752.5	4.76	HUMAN	P14625	Endoplasmin
20761	dirMS_041712_NAR_30mM_minus2.7353.7353.2	2	5.39	0	3.13E+05		(R)NCAAYL	(R)N/C|A/A Y L/K(L)	C:Carbamidomethylation	94.67	420.2085	839.408	0.0017	2.1	8.59	232239.1	5.52	HUMAN	F2Z2U8	Myosin-14
20762	dirMS_041712_NAR_30mM_minus2.8491.8491.2	2	5.39	0	2.48E+05		(K)ATDFVA	(K)A T|D F|V/A D R(A)		101.3	447.7224	894.432	0.006	6.7	4.21	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
20763	dirMS_041712_NAR_50mM_minus2.12478.12478.3	3	5.39	0	9.86E+05	M114m M:	(R)AGKPVI	(R)A G K\P V I|C A T Q m/L E/S m I K(K)	C:Carbamidomethylation m:Oxid	139.75	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
20764	dirMS_041712_NAR_60mM_minus.16523.16523.3	3	5.39	0	1.27E+05	S853s	(R)SVVTETV	(R)S\V\V/T E T V/s/T Y V I R(D)	s:N-acetylglucosamine (S)	151.93	552.9674	1453.79	203.098	11.2	5.72	104321.6	9.31	HUMAN	Q5VWG9	Transcription initiation factor TFIID subunit 3
20765	dirMS_041712_NAR_60mM_minus.17751.17751.3	3	5.39	1	4.16E+05	M148m	(R)LDLAGR	(R)L/D/L/A/G R D L T D Y/L m K(I)	m:Oxidized methionine	159.32	547.2829	1623.841	15.9931	-1.1	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
20766	dirMS_041712_NAR_60mM_minus.17922.17922.3	3	5.39	0	4.81E+03	M1m	(-)mKPLVVI	(-)m K P L\V V F|V L/G/G P\G A G K(G)	m:Oxidized methionine	160.67	529.3066	1569.919	15.9867	-5.2	10	22450.2	5.44	HUMAN	P30085	UMP-CMP kinase
20767	dirMS_041712_NAR_60mM_minus.18746.18746.3	3	5.39	1	2.67E+05		(K)NAAGAL	(K)N A/A G A/L/D L L K|E L/K(N)		166.87	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
20768	dirMS_041712_NAR_120mM_plus.9412.9412.3	3	5.39	0	1.03E+06		(K)EFHLNES	(K)E F H L N E/S/G/D/P S S K(S)		102.32	482.8884	1446.65	0.0011	0.7	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
20769	dirMS_041712_NAR_20mM_plus.16777.16777.2	2	5.39	0	1.17E+05		(R)LLEAQIA	(R)L L E/A\Q I\A T G/G I I/D/P K(E)		185.97	769.9362	1538.879	-0.0137	-8.9	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
20770	dirMS_041712_NAR_20mM_plus.6942.6942.2	2	5.39	0	5.79E+04		(R)LQAEEV	(R)L Q/A/E\E V A/Q Q K(S)		114.23	572.3108	1143.6	0.0139	12.2	4.53	533778	5.74	HUMAN	Q15149	Plectin
20771	dirMS_041712_NAR_20mM_plus.7934.7934.2	2	5.39	0	1.40E+05	M316m	(R)AmGEQ	(R)A m/G/E|Q A V/A L A/R(A)	m:Oxidized methionine	123.73	566.7967	1116.583	16.0031	7.2	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
20772	dirMS_041712_NAR_20mM_plus.9988.9988.2	2	5.39	0	6.91E+04		(R)ALGQNF	(R)A L G Q\N/P T N/A E/V L K(V)		140.02	677.8702	1354.733	0.0006	0.5	6.05	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
20773	dirMS_041712_NAR_30mM_plus2.10527.10527.2	2	5.39	0	3.54E+05		(R)DPYGFG	(R)D P|Y/G\F\G|D S R(D)		108.9	507.2274	1013.432	0.0152	15	4.21	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
20774	dirMS_041712_NAR_30mM_plus2.19435.19435.2	2	5.39	0	1.33E+05		(K)IIGNLLY	(K)I I|G N/L/L Y Y R(Y)		155.5	562.8247	1124.646	-0.0041	-3.7	8.59	125076	8.92	HUMAN	H0YLE8	Ras GTPase-activating-like protein IQGAP1
20775	dirMS_041712_NAR_30mM_plus2.19455.19455.2	2	5.39	0	1.85E+04		(K)MNEFLE	(K)M/N|E/F/L|E N F\E K(N)		155.87	650.7974	1300.588	-0.0003	-0.2	4.25	28580.2	9.35	HUMAN	Q9UFN0	Protein NipSnap homolog 3A
20776	dirMS_041712_NAR_30mM_plus2.19538.19538.2	2	5.39	0	3.54E+05		(K)SNNVEN	(K)S N\N/V|E/M D/W V L|K(H)		156.47	667.8205	1334.641	-0.0072	-5.4	4.37	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
20777	dirMS_041712_NAR_30mM_plus2.20331.20331.2	2	5.39	0	1.80E+05		(K)GSFSEQ	(K)G S/F\S/E Q G/I/N E F L R(E)		161	742.362	1483.718	-0.0009	-0.6	4.53	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
20778	dirMS_041712_NAR_30mM_plus2.21061.21061.2	2	5.39	0	2.58E+05		(R)GVVQEL	(R)G V V/Q E/L\Q/Q\A I/S K(L)		165.53	650.3632	1299.727	-0.0076	-5.8	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
20779	dirMS_041712_NAR_30mM_plus2.4921.4921.2	2	5.39	0	4.78E+05	M571m	(R)mGANSI	(R)m/G/A/N/S L E/R(M)	m:Oxidized methionine	77	447.2119	877.42	15.9969	2.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
20780	dirMS_041712_NAR_30mM_plus2.6346.6346.2	2	5.39	0	1.09E+05		(K)FNYSGS	(K)F N|Y/S/G S G G R(S)		87.1	472.7087	944.422	-0.0119	-12.6	8.75	96205.6	9.06	HUMAN	G5E9M5	Interleukin enhancer binding factor 3, 90kDa, isoform CRA_b
20781	dirMS_041712_NAR_40mM_plus2.18487.18487.3	3	5.39	1	1.38E+06		(R)GDLGIEI	(R)G D L/G/I E I/P A E K V F L A Q K(M)		174.08	610.0115	1828.022	-0.0015	-0.8	4.68	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
20782	dirMS_041712_NAR_50mM_plus2.19757.19757.3	3	5.39	0	2.77E+05		(R)VCSTLLC	(R)V C|S T/L L G L E E H L N A/L D R(A)	C:Carbamidomethylation	172.07	647.3311	1939.991	-0.0118	-6.1	4.65	55059.8	7.86	HUMAN	H0YCY6	FAD-AMP lyase (cyclizing) (Fragment)
20783	dirMS_041712_NAR_50mM_plus2.9502.9502.3	3	5.39	1	3.39E+05		(R)AGTGVD	(R)A G/T/G/V/D N V D/L E A A T R K(G)		117.4	539.6108	1616.824	-0.006	-3.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
20784	dirMS_041712_NAR_60mM_plus.10920.10920.3	3	5.39	1	2.07E+05		(R)VKYETEL	(R)V K Y E T E/L/A/M/R(Q)		114.87	413.8859	1239.64	0.003	2.4	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
20785	dirMS_041712_NAR_60mM_plus.13330.13330.3	3	5.39	1	4.51E+06		(R)VVDLMA	(R)V/V/D L/M/A H M A/S K E(-)		126.87	444.2219	1330.649	0.0018	1.3	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
20786	dirMS_041712_NAR_60mM_plus.7312.7312.3	3	5.39	0	4.47E+05	M1m S7s	(-)mAESLGS	(-)m/A E S/L G s/A/E L L R(Q)	m:Oxidized methionine s:N-a	96.48	499.2424	1276.657	219.0561	-12.2	4.53	95720.1	6.64	HUMAN	Q7L576-2	Isoform 2 of Cytoplasmic FMR1-interacting protein 1
20787	dirMS_041712_NAR_20mM_minus.13536.13536.2	2	5.38	0	1.29E+05		(K)DIYALISI	(K)D I|Y\A/L/I S D Q K(H)		186.38	583.3076	1165.61	-0.002	-1.7	4.21	266161	5.68	HUMAN	E9PPU0	Epiplakin
20788	dirMS_041712_NAR_20mM_minus.7983.7983.2	2	5.38	1	2.97E+04	S12s M16n	(K)EsIETmR	(K)E s I/E T|m R T R(L)	s:N-acetylglucosamine (S) m:	129.55	671.3246	1122.557	219.0847	7.8	6.24	9692.2	9.51	HUMAN	K7EIN4	Transmembrane emp24 domain-containing protein 1
20789	dirMS_041712_NAR_30mM_minus2.16484.16484.2	2	5.38	0	1.44E+05		(R)NPSAAF	(R)N/P\S A|A/F/F/C V A R(L)	C:Carbamidomethylation	143.62	620.3013	1239.594	0.0014	1.1	9.75	18626.5	5.64	HUMAN	B8ZZK2	Gamma-glutamylcyclotransferase
20790	dirMS_041712_NAR_50mM_minus2.12467.12467.3	3	5.38	0	2.90E+05		(K)AASDIAI	(K)A A|S/D\I/A M T E L/P P T H P I R(L)		139.23	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
20791	dirMS_041712_NAR_50mM_minus2.19018.19018.3	3	5.38	1	1.33E+06		(R)KEGGLG	(R)K E G G L G P L\N\I|P/L L A/D V T/R(R)		187.5	621.6941	1863.07	-0.0021	-1.1	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
20792	dirMS_041712_NAR_60mM_minus.10303.10303.3	3	5.38	0	1.70E+05	M502m	(R)SGGmEF	(R)S/G/G m/E R P F V L A R(A)	m:Oxidized methionine	116.93	445.9007	1319.689	15.9987	2.8	9.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
20793	dirMS_041712_NAR_60mM_minus.19263.19263.3	3	5.38	0	3.35E+05		(K)HGATVL	(K)H G A T V\L/T A/L/G G I L K(K)		170.82	450.939	1350.81	-0.0079	-5.9	8.76	8125.3	9.3	HUMAN	B0QYF7	Myoglobin (Fragment)
20794	dirMS_041712_NAR_20mM_plus.10516.10516.2	2	5.38	0	2.30E+05		(K)YEELQVT	(K)Y/E/E\L/Q V T A G K(H)		145.75	569.2902	1137.579	-0.0055	-4.8	4.53	58119.8	6.75	HUMAN	Q5XKE5	Keratin, type II cytoskeletal 79
20795	dirMS_041712_NAR_20mM_plus.11928.11928.2	2	5.38	0	1.09E+05		(R)IYVVDV	(R)I Y|V V/D V/G S E/P R(A)		156.05	617.3237	1233.647	-0.0073	-5.9	4.37	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
20796	dirMS_041712_NAR_20mM_plus.16403.16403.3	3	5.38	1	2.38E+04	S98s	(K)GGPSQL	(K)G G P S Q L L/I K F A/s G N\E G/K(V)	s:N-acetylglucosamine (S)	184.35	636.0108	1702.912	203.1056	13.8	8.59	105427.9	5.9	HUMAN	H0Y8X6	E3 ubiquitin-protein ligase (Fragment)
20797	dirMS_041712_NAR_20mM_plus.18513.18513.2	2	5.38	1	1.25E+05		(K)DIGFIKLI	(K)D/I/G/F I/K/L D(-)		198.2	460.7578	920.509	-0.0004	-0.5	4.53	6904.9	11.35	HUMAN	P62273	40S ribosomal protein S29
20798	dirMS_041712_NAR_20mM_plus.8457.8457.2	2	5.38	0	2.72E+04	M254m M:	(R)LIDDmV	(R)L I|D D m/V A/Q/A m K(S)	m:Oxidized methionine	128.07	633.8075	1234.617	31.9907	0.7	4.21	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
20799	dirMS_041712_NAR_20mM_plus.9509.9509.3	3	5.38	1	4.20E+04		(R)HQKTHL	(R)H Q K T H L G/E/Q A G K(D)		136.68	445.2335	1333.697	-0.0112	-8.4	8.61	35565.7	9.45	HUMAN	Q5VV50	Zinc finger protein 691
20800	dirMS_041712_NAR_30mM_plus2.13700.13700.2	2	5.38	1	5.61E+05		(K)QYSGKF	(K)Q Y/S G K/F/F(-)		124.88	438.7176	876.425	0.0029	3.3	8.59	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
20801	dirMS_041712_NAR_50mM_plus2.12781.12781.3	3	5.38	1	6.91E+05		(K)SAPSIPK	(K)S A|P S I/P K E N F/S C/L T R(L)	C:Carbamidomethylation	135.22	569.6265	1706.853	0.0119	7	8.46	23209	6.92	HUMAN	B9A041	Malate dehydrogenase, cytoplasmic
20802	dirMS_041712_NAR_50mM_plus2.17104.17104.3	3	5.38	1	2.98E+05		(K)LSKNEVI	(K)L S K N E V L M V/N|I/G/S L/S T G G R(V)		157.18	659.0229	1975.064	-0.0099	-5	8.75	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
20803	dirMS_041712_NAR_50mM_plus2.20558.20558.3	3	5.38	1	4.37E+04		(K)GKLPIVN	(K)G K L\P I V N E D\D E\L\V|A/I I/A R(T)		177.43	655.7032	1965.102	-0.0065	-3.3	4.32	30838.7	4.9	HUMAN	E7ETK5	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
20804	dirMS_041712_NAR_50mM_plus2.6920.6920.3	3	5.38	1	8.65E+05		(K)IVADKD	(K)I V/A/D K D Y/S V T A N S K(I)		101.45	504.2628	1510.775	-0.0009	-0.6	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
20805	dirMS_041712_NAR_50mM_plus2.9704.9704.3	3	5.38	1	4.76E+05		(K)LTSDDVI	(K)L/T/S/D D/V K E/Q I Y K(L)		117.47	480.2521	1438.742	-0.0007	-0.5	4.56	12573.5	10.39	HUMAN	E9PS50	40S ribosomal protein S13 (Fragment)
20806	dirMS_041712_NAR_30mM_minus2.12514.12514.2	2	5.37	0	1.25E+05		(R)TIGISVD	(R)T I/G\I/S V D/P R(R)		121.77	479.2746	957.536	0.0056	5.8	5.5	14749.1	12.2	HUMAN	J3QSB4	60S ribosomal protein L13 (Fragment)
20807	dirMS_041712_NAR_30mM_minus2.16979.16979.2	2	5.37	0	1.40E+05		(R)TLINELV	(R)T L/I/N E L V/K(G)		146.25	465.2877	929.567	0.0015	1.6	5.66	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
20808	dirMS_041712_NAR_40mM_minus2.9363.9363.3	3	5.37	0	1.31E+05		(K)VQASLA	(K)V Q\A|S L/A A N T F/T I T G H A E T K(Q)		137.35	654.0087	1960.013	-0.0019	-1	6.72	11802.2	5.6	HUMAN	D6RDG3	Transcription factor BTF3 (Fragment)
20809	dirMS_041712_NAR_50mM_minus2.11285.11285.3	3	5.37	0	1.86E+05	T2141t	(R)tQSLSLA	(R)t Q/S L S/L|A V I P/E G K(I)	t:N-acetylglucosamine (T)	132.05	515.9485	1342.758	203.0733	-3.9	5.66	252964	5.72	HUMAN	G3V2D8	Zinc finger FYVE domain-containing protein 26
20810	dirMS_041712_NAR_50mM_minus2.12133.12133.3	3	5.37	0	9.82E+04	M240m	(K)mLDAED	(K)m L|D/A E D\I/V N T A R P D\E/K(A)	m:Oxidized methionine	137.35	611.6283	1816.875	15.9958	0.5	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
20811	dirMS_041712_NAR_50mM_minus2.13360.13360.3	3	5.37	0	3.52E+05		(R)AVAIDLF	(R)A V|A I/D L/P G L G/H S K(E)		144.57	426.5785	1277.721	-0.0003	-0.2	6.79	19983.6	8.14	HUMAN	B4DQI4	Alpha/beta hydrolase domain-containing protein 14B
20812	dirMS_041712_NAR_60mM_minus.13764.13764.3	3	5.37	1	2.11E+05		(R)MTGSEF	(R)M/T/G|S E F D F E E/M K R(K)		136.43	536.2333	1606.688	-0.0023	-1.4	4.41	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
20813	dirMS_041712_NAR_120mM_plus.7859.7859.3	3	5.37	1	1.64E+05		(R)RVLEEGS	(R)R V L\E\E/G\S V/E/A/R(T)		94.43	415.5576	1244.659	-0.0011	-0.9	4.79	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
20814	dirMS_041712_NAR_20mM_plus.13655.13655.2	2	5.37	0	8.22E+04		(R)ATLYVTA	(R)A T/L|Y/V/T A/I E D R(Q)		166.33	626.3269	1251.658	-0.0114	-9.1	4.37	24376.8	6.08	HUMAN	E9PIX6	Protein arginine N-methyltransferase 1 (Fragment)

20815	dirMS_041712_NAR_20mM_plus.16661.16661.3	3	5.37	0	2.21E+05		(K)VQIAVA	(K)V Q\I\A V A N A/Q/E L/L Q/R(M)		186.37	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
20816	dirMS_041712_NAR_20mM_plus.17139.17139.2	2	5.37	0	8.91E+04		(R)AIVAIEN	(R)A I/V\A I\E N/P/A D V S/V I S S R(N)		189.08	870.9764	1740.949	-0.0035	-2	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
20817	dirMS_041712_NAR_20mM_plus.18882.18882.2	2	5.37	0	2.53E+05		(K)LAVEALS	(K)L A\V E A\L/S/S L/D/G D L A\G R(Y)		200.58	793.9214	1586.838	-0.0029	-1.8	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
20818	dirMS_041712_NAR_20mM_plus.7091.7091.2	2	5.37	0	1.82E+05	M35m	(R)VEFmDD	(R)V/E|F\m/D D T/S R(S)	m:Oxidized methionine	115.75	558.2383	1099.473	15.9969	1.8	4.03	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
20819	dirMS_041712_NAR_20mM_plus.7990.7990.3	3	5.37	0	4.52E+05	M239m	(K)EVDEQn	(K)E V D E Q\m L N V/Q/N K(N)	m:Oxidized methionine	125.12	488.2328	1446.689	15.9945	-0.3	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
20820	dirMS_041712_NAR_30mM_plus2.12886.12886.2	2	5.37	0	3.40E+05		(R)LLVVTDI	(R)L L|V V/T/D/P R(A)		120.38	456.779	912.551	-0.0006	-0.6	5.84	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
20821	dirMS_041712_NAR_30mM_plus2.16640.16640.2	2	5.37	0	4.30E+05		(K)GCSFLPI	(K)G C\S F/L|P D/P Y\Q K(Q)	C:Carbamidomethylation	140.47	656.306	1311.604	0.0009	0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
20822	dirMS_041712_NAR_40mM_plus2.16091.16091.3	3	5.37	1	7.98E+04	M340m	(R)ALGTEVI	(R)A L/G/T E V I Q L F/P/E/K G N m G K(I)	m:Oxidized methionine	161.12	650.0097	1932.026	15.9886	-3.2	6.18	67184.7	9.24	HUMAN	O95831	Apoptosis-inducing factor 1, mitochondrial
20823	dirMS_041712_NAR_40mM_plus2.19534.19534.3	3	5.37	0	1.06E+06		(R)GLAPVQ	(R)G L\A/P V|Q A Y L H I P D I/I K(V)		183.65	583.3378	1748.011	-0.0117	-6.7	6.74	58266.4	9.46	HUMAN	B4DN00	Pyruvate carboxylase, mitochondrial
20824	dirMS_041712_NAR_40mM_plus2.5288.5288.2	2	5.37	0	8.85E+04		(K)GSSNSY	(K)G S/S/N S Y A I/K(K)		87.32	463.7315	926.458	-0.0021	-2.2	8.59	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
20825	dirMS_041712_NAR_40mM_plus2.9095.9095.2	2	5.37	0	5.54E+05		(K)SSFFSDR	(K)S S|F/F/S D\R(G)		116.22	423.1935	845.379	0.0009	1.1	5.55	15031.5	6.72	HUMAN	B4DLA0	ATP-dependent RNA helicase DDX3X
20826	dirMS_041712_NAR_50mM_plus2.17125.17125.3	3	5.37	1	4.47E+05	T129t	(K)EESTKYL	(K)E E S T K Y L|L L/t S I V/L R(I)	t:Phosphorylated T	158.28	615.664	1765.011	79.9669	0.3	6.24	81008.4	8.99	HUMAN	Q9H0V1	Transmembrane protein 168
20827	dirMS_041712_NAR_50mM_plus2.19392.19392.3	3	5.37	1	2.22E+05		(K)SGGIVIS	(K)S G G I/V/I/S P F R L E E L T N R(L)		170.32	630.0135	1888.029	-0.0027	-1.5	5.87	53461.2	6.87	HUMAN	Q16204	Coiled-coil domain-containing protein 6
20828	dirMS_041712_NAR_50mM_plus2.9161.9161.3	3	5.37	0	1.91E+05		(K)TAVEHA	(K)T A/V E/H/A T/D E\D I L A K(G)		115.42	504.9238	1512.754	0.0028	1.9	4.31	288852.1	5.33	HUMAN	E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein
20829	dirMS_041712_NAR_60mM_plus.13270.13270.3	3	5.37	0	7.61E+05	M1m	(-)mVNHFI	(-)m V N H\F|I/A E|F K(R)	m:Oxidized methionine	125.98	417.8778	1235.624	15.9947	-0.2	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
20830	dirMS_041712_NAR_60mM_plus.19459.19459.3	3	5.37	1	6.31E+03		(K)DDINRG	(K)D D I N R G\A|P/S I/T S V T\P R(G)		161.08	566.9611	1698.877	-0.0082	-4.8	5.96	46835.9	6.23	HUMAN	E7EQA9	TRAF family member-associated NF-kappa-B activator
20831	dirMS_041712_NAR_120mM_minus.9626.9626.3	3	5.36	0	4.38E+05		(K)QEYDES	(K)Q E\Y D E S/G|P S I/V H R(K)		107.47	506.2424	1516.703	0.01	6.6	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
20832	dirMS_041712_NAR_20mM_minus.11858.11858.2	2	5.36	0	1.25E+05	M98m	(R)TLTIVDT	(R)T L/T/I/V/D T G/I G m T/K(A)	m:Oxidized methionine	167.03	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
20833	dirMS_041712_NAR_20mM_minus.13051.13051.3	3	5.36	0	2.67E+04	M73m	(R)AILVDLE	(R)A I L V D L E/P G T/m D S V R(S)	m:Oxidized methionine	181.62	544.6138	1615.836	15.9909	-2.5	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
20834	dirMS_041712_NAR_40mM_minus2.11672.11672.3	3	5.36	1	4.75E+04		(R)QVFGEA	(R)Q V/F/G E A T K Q/P G I T F I A/A K(F)		152.53	636.0167	1906.043	-0.0077	-4.1	8.59	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
20835	dirMS_041712_NAR_40mM_minus2.15140.15140.3	3	5.36	0	7.46E+05		(K)ALIEVLQ	(K)A L/I|E/V/L Q/P L I A E H Q A R(R)		175.3	601.0146	1801.033	-0.0038	-2.1	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
20836	dirMS_041712_NAR_40mM_minus2.5749.5749.2	2	5.36	1	9.06E+04		(R)YSGGNY	(R)Y S/G G N/Y/R D N Y\D/N(-)		95.47	719.2874	1437.567	0.001	0.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
20837	dirMS_041712_NAR_40mM_minus2.6367.6367.2	2	5.36	0	1.62E+05		(R)AQYDEL	(R)A Q|Y/D E/L A R(K)		103.27	483.2366	965.469	-0.0028	-2.9	4.37	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
20838	dirMS_041712_NAR_40mM_minus2.7825.7825.3	3	5.36	0	7.49E+04	M47m M5	(K)SGTGIA	(K)S G T G|I/A/A/M S V m R P E Q/I/m K(S)	m:Oxidized methionine	125.22	646.9867	1906.955	31.9908	0.5	8.46	8797.3	9.3	HUMAN	H3BR50	V-type proton ATPase 16 kDa proteolipid subunit
20839	dirMS_041712_NAR_40mM_minus2.8758.8758.3	3	5.36	1	6.30E+03		(K)DVDEAY	(K)D V/D\E|A Y M N K V/E L E/S R(L)		134.07	599.947	1797.832	-0.0059	-3.3	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
20840	dirMS_041712_NAR_50mM_minus2.14845.14845.3	3	5.36	1	1.85E+05		(R)LLTTIGK	(R)L/L/T T/I/G\K D/L/D F E K(A)		152.48	498.2798	1492.826	-0.0009	-0.6	4.56	98682.1	4.86	HUMAN	C9JF13	Eukaryotic translation initiation factor 4 gamma 1 (Fragment)
20841	dirMS_041712_NAR_60mM_minus.11930.11930.3	3	5.36	0	1.51E+05		(R)DAYSGG	(R)D A/Y|S/G G A V/N L Y/H V R(E)		126.83	507.9181	1521.745	-0.0047	-3.1	6.74	17952.8	6.73	HUMAN	E9PAV2	Proteasome subunit beta type-5
20842	dirMS_041712_NAR_60mM_minus.16189.16189.3	3	5.36	1	1.19E+05		(K)AGTQIEI	(K)A G T/Q I/E N I/D E D F R D G L K(L)		149.6	640.9818	1920.93	0.0011	0.6	4.11	59872.5	4.85	HUMAN	F5GXS2	Alpha-actinin-4
20843	dirMS_041712_NAR_20mM_plus.13519.13519.2	2	5.36	0	1.03E+05		(K)IFVGGLS	(K)I F|V/G G L S\P D/T P E E/K(I)		165.33	744.8731	1488.758	-0.0191	-12.8	4.14	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
20844	dirMS_041712_NAR_30mM_plus2.12654.12654.2	2	5.36	0	9.16E+04		(R)CNNVLY	(R)C\N/N V/L/Y/I/R(G)	C:Carbamidomethylation	118.73	526.2726	1051.535	0.0026	2.5	8.75	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F
20845	dirMS_041712_NAR_30mM_plus2.13494.13494.2	2	5.36	0	1.80E+06		(K)IYFMAG	(K)I Y|F|M A G/S S/R(K)		125.02	516.2597	1031.498	0.0142	13.8	8.75	92752.5	4.76	HUMAN	P14625	Endoplasmin
20846	dirMS_041712_NAR_40mM_plus2.10980.10980.3	3	5.36	0	9.57E+04	M35m	(K)AASDIAr	(K)A A/S D\I/A/m T E/L/P P T H P I R(L)	m:Oxidized methionine	130.82	612.652	1819.937	16.0044	5.1	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
20847	dirMS_041712_NAR_40mM_plus2.17827.17827.3	3	5.36	0	1.01E+04		(K)DMTVPI	(K)D M|T\V/P I L V S K P P V F T G K(D)		171.23	610.3443	1829.024	-0.0058	-3.2	8.59	53885.5	9	HUMAN	P11182	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial
20848	dirMS_041712_NAR_40mM_plus2.6841.6841.2	2	5.36	0	1.02E+04		(K)YTCSFCC	(K)Y/T/C/S F C G/K(T)	C:Carbamidomethylation	100.23	511.7046	1022.407	-0.0051	-5	8.59	10867.7	10.82	HUMAN	A6NKH3	Putative 60S ribosomal protein L37a-like
20849	dirMS_041712_NAR_40mM_plus2.7017.7017.2	2	5.36	0	1.57E+05	M1m S4s	(-)mVFsR(R	(-)m V/F s|R(R)	m:Oxidized methionine s:N-a	100.97	429.7019	639.328	219.0682	-7.1	9.5	103463.7	5.03	HUMAN	Q9Y5I3	Protocadherin alpha-1
20850	dirMS_041712_NAR_40mM_plus2.9134.9134.2	2	5.36	0	9.69E+04		(R)LSIYEAR	(R)L/S/I/Y/E/A R(C)		116.07	426.2316	851.462	-0.0062	-7.3	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
20851	dirMS_041712_NAR_40mM_plus2.9752.9752.2	2	5.36	0	9.01E+04		(R)GYFSEEI	(R)G Y/F/S/E E M N R(V)		121.47	566.7355	1132.473	-0.0091	-8	4.53	533778	5.74	HUMAN	Q15149	Plectin
20852	dirMS_041712_NAR_50mM_plus2.14192.14192.3	3	5.36	1	7.24E+05		(R)ALPAVQ	(R)A L/P A V/Q Q N N L D E D/L I R K(L)		142.62	646.3522	1937.045	-0.003	-1.6	4.56	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
20853	dirMS_041712_NAR_50mM_plus2.8557.8557.3	3	5.36	1	2.16E+04		(R)AIDSSNI	(R)A I|D|S\S N L\K D/D\Y S T A Q R(V)		111.82	595.2868	1783.846	0.0002	0.1	4.43	46656.7	9.19	HUMAN	Q5JVF3	PCI domain-containing protein 2
20854	dirMS_041712_NAR_60mM_plus.16188.16188.3	3	5.36	1	1.12E+06		(K)TDKTLVI	(K)T D K T/L V|L/L/M/G K(E)		141.08	406.908	1218.713	-0.0032	-2.6	8.26	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
20855	dirMS_041712_NAR_60mM_plus.19169.19169.3	3	5.36	0	5.02E+04		(K)VSHLLGI	(K)V S H L L G I/N|V/T D F T R(G)		159.5	524.6233	1571.854	0.0013	0.8	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
20856	dirMS_041712_NAR_120mM_minus.11934.11934.3	3	5.35	0	2.85E+04		(K)LLEPPNF	(K)L L E P P/N F F Q/K(Y)		119.22	411.5568	1232.667	-0.0115	-9.4	6	42428.4	9.45	HUMAN	Q59G05	Poly(A) polymerase gamma (Fragment)
20857	dirMS_041712_NAR_20mM_minus.14486.14486.2	2	5.35	0	5.82E+04		(K)LAAELSA	(K)L A A E L/S/A T L/E Q A A\A T A/R(V)		198.88	843.955	1686.902	0.0006	0.4	4.53	558007.1	5.44	HUMAN	P58107	Epiplakin
20858	dirMS_041712_NAR_20mM_minus.14694.14694.2	2	5.35	0	9.62E+04		(K)IYVDDGI	(K)I Y/V/D/D G L I|S/L Q V K(Q)		201.6	731.9104	1462.815	-0.0016	-1.1	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
20859	dirMS_041712_NAR_50mM_minus2.13750.13750.3	3	5.35	1	1.28E+05		(K)NLKVTA	(K)N L K V T A\V|P/T L L K(Y)		147.07	432.9468	1296.825	0.0009	0.7	10	11462.8	5.18	HUMAN	I3L2R6	Thioredoxin domain-containing protein 17
20860	dirMS_041712_NAR_50mM_minus2.15076.15076.3	3	5.35	0	1.60E+05		(R)NSSHAG	(R)N S S H A G A F\V\I|V/T|E/E A I A K(G)		154.07	615.3184	1843.955	-0.0142	-7.7	5.4	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
20861	dirMS_041712_NAR_50mM_minus2.16387.16387.3	3	5.35	1	5.41E+04		(K)SELVAM	(K)S E|L V\A/M L E E E E L/R K(A)		161.32	559.2917	1675.857	0.0034	2	4.32	18679.2	5.61	HUMAN	B4DWW1	ADP-ribosylation factor-like protein 1
20862	dirMS_041712_NAR_50mM_minus2.17693.17693.3	3	5.35	0	1.00E+05		(K)TTLLNYI	(K)T/T/L L N Y I L/T/E Q H S K(R)		169.97	554.3024	1660.891	0.0022	1.3	6.41	42238.2	4.88	HUMAN	B4DNG9	COBW domain-containing protein 3
20863	dirMS_041712_NAR_50mM_minus2.17847.17847.3	3	5.35	1	2.28E+05	M116m	(R)ELAILLG	(R)E L|A/I L/L/G m L D P A E K D\E K(G)	m:Oxidized methionine	170.82	634.3353	1884.999	15.9927	-1.2	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
20864	dirMS_041712_NAR_60mM_minus.19315.19315.3	3	5.35	0	4.54E+05		(R)THNGES	(R)T H N G E S V S|Y|L\F S H\V|P L(-)		171.93	596.2923	1786.876	-0.0135	-7.6	5.92	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
20865	dirMS_041712_NAR_120mM_plus.4409.4409.3	3	5.35	0	6.30E+05	M76m M7	(R)LTNSmM	(R)L/T/N S m/M m H/G R(N)	m:Oxidized methionine	71.33	403.8446	1177.527	31.9918	1.6	9.75	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
20866	dirMS_041712_NAR_20mM_plus.10440.10440.2	2	5.35	0	1.19E+05	M297m M	(K)mAILQIr	(K)m A/I|L/Q/I/m K(E)	m:Oxidized methionine	144.77	490.2722	947.542	31.9955	5.8	8.5	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
20867	dirMS_041712_NAR_20mM_plus.13610.13610.2	2	5.35	0	7.03E+04		(K)ADSLLA	(K)A/D/S\L/L A V V/K(R)		165.95	458.2789	915.551	-0.0004	-0.5	5.88	103309.5	5.34	HUMAN	A0AV56	SAFB protein
20868	dirMS_041712_NAR_20mM_plus.17457.17457.3	3	5.35	0	6.85E+04		(K)LAAVDA	(K)L A\A V D A T/V\N/Q V/L A S R(Y)		192.37	509.9542	1527.849	-0.0009	-0.6	5.84	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
20869	dirMS_041712_NAR_20mM_plus.7441.7441.2	2	5.35	0	7.57E+04		(K)SNVSDA	(K)S N|V/S D/A/V A/Q S T R(I)		119.48	617.8019	1234.602	-0.0057	-4.6	5.55	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
20870	dirMS_041712_NAR_20mM_plus.7465.7465.2	2	5.35	0	1.67E+05		(K)VLTPTQ	(K)V L|T|P T Q V K(N)		120.87	443.2734	885.54	-0.0009	-1	8.72	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
20871	dirMS_041712_NAR_20mM_plus.9286.9286.2	2	5.35	0	6.25E+04		(R)SVSLTG	(R)S V|S L|T|G A\P E S V/Q K(A)		135.53	651.848	1302.69	-0.0012	-1	5.72	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
20872	dirMS_041712_NAR_30mM_plus2.6540.6540.2	2	5.35	0	1.51E+05	M514m M	(K)NEEmm	(K)N E/E m/m\E Q K(E)	m:Oxidized methionine	88.83	535.7086	1038.423	31.9869	-2.8	4.25	67721.3	5.54	HUMAN	P32456	Interferon-induced guanylate-binding protein 2
20873	dirMS_041712_NAR_40mM_plus2.13010.13010.3	3	5.35	0	2.74E+05		(K)NLPPSG	(K)N L/P\P S G A V P V T/G I/P P H/V V K(V)		143.28	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
20874	dirMS_041712_NAR_50mM_plus2.12616.12616.3	3	5.35	1	8.84E+05		(R)ELISNSSI	(R)E L/I/S/N/S S D A L D K I/R(Y)		134.15	520.9473	1560.823	0.0046	2.9	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
20875	dirMS_041712_NAR_50mM_plus2.17333.17333.3	3	5.35	0	3.44E+05		(K)DIPVVH	(K)D I|P V/V H Q L/L T R(Y)		159.57	430.9226	1290.753	0.0004	0.3	6.74	57147.5	7.81	HUMAN	P30419	Glycylpeptide N-tetradecanoyltransferase 1
20876	dirMS_041712_NAR_60mM_plus.6942.6942.2	2	5.35	0	1.84E+05	S363s	(R)EESSYsD	(R)E E/S S|Y s D I P D V K(N)	s:Phosphorylated S	94.67	724.8008	1368.617	79.9778	7.9	3.91	95109.8	8.56	HUMAN	Q8IWT6	Leucine-rich repeat-containing protein 8A
20877	dirMS_041712_NAR_120mM_minus.18773.18773.3	3	5.34	1	3.30E+05		(R)ARFEEL	(R)A R F E E L|C/S D/L F R(S)	C:Carbamidomethylation	156.88	514.9175	1542.737	0.001	0.7	4.68	25598.3	6.45	HUMAN	E7EP11	Heat shock 70 kDa protein 1A/1B
20878	dirMS_041712_NAR_30mM_minus2.19497.19508.2	2	5.34	0	2.79E+05		(R)ILVATNL	(R)I L|V|A/T\N L F G R(G)		161.98	552.3309	1103.657	-0.0026	-2.4	9.75	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
20879	dirMS_041712_NAR_30mM_minus2.8898.8898.2	2	5.34	0	2.07E+05		(K)QAEILQI	(K)Q A\E/I/L Q/E/S R(M)		102.72	537.2824	1073.559	-0.001	-1	4.53	15962.5	9.61	HUMAN	B4DT30	Tubulin-specific chaperone A
20880	dirMS_041712_NAR_50mM_minus2.13556.13556.3	3	5.34	1	2.80E+05		(K)ITDIIGKE	(K)I T/D\I/I\G K E E G I/G/P E N L R(G)		145.55	618.665	1853.997	-0.0163	-8.8	4.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
20881	dirMS_041712_NAR_50mM_minus2.7479.7479.3	3	5.34	1	4.69E+06	M227m M	(R)mQKEIT	(R)m Q/K E I T A\L/A|P S T m K(I)	m:Oxidized methionine	108.52	527.6049	1548.812	31.9877	-1.3	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
20882	dirMS_041712_NAR_60mM_minus.11170.11170.2	2	5.34	1	2.01E+05		(R)DGKLVS	(R)D/G K|L V\S E S S D|V L|P K(-)		122.23	737.3855	1473.78	-0.0158	-10.7	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
20883	dirMS_041712_NAR_60mM_minus.17639.17639.3	3	5.34	1	1.05E+05		(K)TSPVEGI	(K)T S P V E G L S G\N/P A D L E K R(R)		158.08	590.6453	1769.903	0.0185	10.5	4.68	139115.8	6.2	HUMAN	P23634	Plasma membrane calcium-transporting ATPase 4
20884	dirMS_041712_NAR_60mM_minus.8532.8532.3	3	5.34	0	4.41E+04		(R)SSTPLHS	(R)S S/T/P L H S/P S P I\R(V)		107.45	426.8957	1278.68	-0.0075	-5.9	9.49	34930.3	9.73	HUMAN	C9JFK9	BAG family molecular chaperone regulator 3 (Fragment)
20885	dirMS_041712_NAR_120mM_plus.10531.10531.4	4	5.34	2	5.94E+05	M27m	(R)GDVmD	(R)G D V m D F Y K T/L R G G/A T/V/K(V)	m:Oxidized methionine	108.02	469.2379	1857.953	15.977	-9.5	8.5	15297.8	5.01	HUMAN	D6RDA9	Glucocorticoid receptor (Fragment)
20886	dirMS_041712_NAR_20mM_plus.11289.11289.2	2	5.34	0	7.52E+04		(R)IASLEVE	(R)I A\S L/E V/E/N Q S\L R(G)		150.37	679.8662	1358.727	-0.0023	-1.7	4.53	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
20887	dirMS_041712_NAR_20mM_plus.17785.17785.2	2	5.34	0	8.14E+04		(R)TTLLPGL	(R)T/T|L\L/P G L L K(T)		193.85	478.3131	955.619	0.0003	0.3	8.41	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
20888	dirMS_041712_NAR_30mM_plus2.13213.13296.2	2	5.34	0	8.26E+05		(R)FGPGGC	(R)F/G|P/G G Q L I/K(V)		123.22	458.7641	916.525	-0.0042	-4.5	8.75	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
20889	dirMS_041712_NAR_40mM_plus2.11375.11375.2	2	5.34	0	4.95E+04	M320m	(K)YmACCL	(K)Y m|A C C L L/Y R(G)	C:Carbamidomethylation m:Oxid	133.18	633.2788	1249.553	15.9977	2.2	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
20890	dirMS_041712_NAR_50mM_plus2.13088.13088.3	3	5.34	0	5.10E+05		(K)QVLNQI	(K)Q V/L N Q D/L/T F Q H/I/K(I)		137.08	528.6227	1583.854	-0.0005	-0.3	6.74	26601.2	7.98	HUMAN	Q5VWZ2	Lysophospholipase-like protein 1
20891	dirMS_041712_NAR_50mM_plus2.21751.21751.3	3	5.34	0	2.90E+05		(K)AYNMVI	(K)A Y/N M V D I I H/S V V D/E R(E)		185.6	587.6346	1760.864	0.0257	14.6	4.54	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
20892	dirMS_041712_NAR_50mM_plus2.22203.22203.3	3	5.34	0	1.22E+06		(R)DALSDL	(R)D A|L/S D/L A/L/H F L N K(M)		191.62	486.2644	1456.78	-0.0008	-0.6	5.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
20893	dirMS_041712_NAR_50mM_plus2.9079.9079.3	3	5.34	1	2.70E+05		(K)AQALRD	(K)A/Q|A\L R D N S T/M G/Y M A A K(K)		115.12	576.611	1727.82	-0.0019	-1.1	8.63	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
20894	dirMS_041712_NAR_60mM_plus.18777.18777.3	3	5.34	1	1.11E+05		(K)LSKNEVI	(K)L S K N E V L M/V N\I|G S L/S T G G R(V)		155.83	659.0238	1975.064	-0.0072	-3.7	8.75	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
20895	dirMS_041712_NAR_60mM_plus.5637.5637.3	3	5.34	0	7.68E+04		(R)TAEHEA	(R)T A E H E A\A\Q\Q/D/L Q/S K(F)		87.8	519.2487	1555.735	-0.0031	-2	4.65	156557.7	5.52	HUMAN	Q86UP2	Kinectin
20896	dirMS_041712_NAR_120mM_minus.4977.4977.3	3	5.33	1	3.73E+05	T520t M52	(R)QDtSFm	(R)Q D t S/F/m K/K(N)	t:N-acetylglucosamine (T) m:	78.1	401.8604	984.482	219.0848	8.7	8.59	93852.6	6.3	HUMAN	H9KV44	Protein EFR3 homolog A
20897	dirMS_041712_NAR_20mM_minus.10425.10425.2	2	5.33	1	4.90E+04	S2692s	(R)LLsHINR	(R)L/L|s H I/N R D K(L)	s:N-acetylglucosamine (S)	152.72	649.8694	1095.627	203.1046	19.4	8.76	336378.7	9.73	HUMAN	Q9NR48	Histone-lysine N-methyltransferase ASH1L
20898	dirMS_041712_NAR_30mM_minus2.16364.16364.2	2	5.33	0	1.94E+05		(K)ACGNFG	(K)A/C|G N\F|G I\P C E L R(V)	C:Carbamidomethylation	142.57	697.3207	1393.635	-0.001	-0.7	6.05	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
20899	dirMS_041712_NAR_40mM_minus2.6237.6237.3	3	5.33	0	5.09E+04		(R)EATNPP	(R)E A T N/P\P V I/Q E E K P K(K)		102.47	527.2804	1579.833	-0.006	-3.8	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
20900	dirMS_041712_NAR_50mM_minus2.12545.12545.3	3	5.33	1	3.81E+05	M100m	(K)QGGLGF	(K)Q G G L|G/P m N/I|P L V S D P K R(T)	m:Oxidized methionine	140.1	598.988	1778.958	15.9913	-2	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
20901	dirMS_041712_NAR_50mM_minus2.18055.18055.3	3	5.33	2	3.85E+04	T439t	(K)LLDIKQK	(K)L L D/I/K Q K C/T/t A K(Q)	C:Carbamidomethylation t:N-ace	171.9	541.3004	1418.804	203.0831	2.3	9.7	185198.6	5.3	HUMAN	Q8TDY2	RB1-inducible coiled-coil protein 1
20902	dirMS_041712_NAR_50mM_minus2.8303.8303.3	3	5.33	1	8.27E+04	M61m	(K)NQVAm	(K)N Q|V/A m N/P T N T/V/F D A K R(L)	m:Oxidized methionine	114.92	607.968	1805.896	15.9932	-1	8.75	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
20903	dirMS_041712_NAR_60mM_minus.20094.20094.3	3	5.33	0	4.05E+05		(K)GHYTEG	(K)G H Y T E\G A E L/V|D S/V/L D V V R(K)		184.27	653.6647	1958.982	-0.0022	-1.1	4.31	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
20904	dirMS_041712_NAR_60mM_minus.5041.5041.3	3	5.33	0	2.73E+04	M152m	(K)EQmQP	(K)E Q/m Q P T/H/P I R(L)	m:Oxidized methionine	82.8	418.2075	1236.615	15.9926	-1.9	6.85	18789.1	6.77	HUMAN	A2IDB2	14-3-3 protein eta (Fragment)
20905	dirMS_041712_NAR_60mM_minus.8225.8225.3	3	5.33	1	3.12E+05		(K)TVDDVII	(K)T V/D/D V I/K E Q N R(E)		105.67	439.5636	1316.68	-0.0042	-3.2	4.55	20828.6	6.05	HUMAN	C9J0A7	Charged multivesicular body protein 2b
20906	dirMS_041712_NAR_20mM_plus.18077.18077.3	3	5.33	0	1.70E+05		(K)VDFPQD	(K)V D F P Q D Q L/T\A/L T/G R(I)		195.7	520.9379	1560.802	-0.0025	-1.6	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
20907	dirMS_041712_NAR_20mM_plus.7392.7392.2	2	5.33	0	2.65E+05	M281m	(R)AEAESm	(R)A E|A E/S m Y/Q I K(Y)	m:Oxidized methionine	118.87	593.2759	1169.551	15.9938	-0.9	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
20908	dirMS_041712_NAR_20mM_plus.7884.7884.3	3	5.33	0	1.18E+05		(K)VEIIAND	(K)V E|I\I A N/D/Q/G N R(T)		124.5	410.2139	1228.628	-0.0009	-0.7	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
20909	dirMS_041712_NAR_30mM_plus2.23533.23533.2	2	5.33	0	1.32E+06		(R)DLPLLLF	(R)D L/P/L|L L F R(T)		189.7	493.8049	986.603	-0.0008	-0.8	5.84	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
20910	dirMS_041712_NAR_40mM_plus2.14304.14304.2	2	5.33	0	1.98E+05		(K)LLCGLLA	(K)L/L|C G L L/A/E R(L)	C:Carbamidomethylation	150.18	522.7962	1044.587	-0.0019	-1.8	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
20911	dirMS_041712_NAR_40mM_plus2.7977.7977.2	2	5.33	0	2.27E+04		(K)ASLENSI	(K)A S/L/E/N\S L R(E)		107.33	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
20912	dirMS_041712_NAR_50mM_plus2.14579.14579.3	3	5.33	1	5.40E+05		(R)QAIKELP	(R)Q A I K E L/P Q F A/T/G/E N L P R(V)		144.47	638.0091	1912.029	-0.0159	-8.3	6.14	58250.7	8.99	HUMAN	B4E283	Apoptosis inhibitor 5
20913	dirMS_041712_NAR_50mM_plus2.14732.14732.3	3	5.33	1	9.00E+05		(R)LYSILGT	(R)L/Y/S I/L G T T L K D E G K(L)		145.9	513.2859	1537.847	-0.0041	-2.6	6.07	66876.9	6.17	HUMAN	O75083	WD repeat-containing protein 1
20914	dirMS_041712_NAR_50mM_plus2.9287.9287.3	3	5.33	1	1.90E+05		(R)EVLEKQI	(R)E V\L E K Q/P V/L/S Q T E/A R(D)		116.27	576.3137	1726.933	-0.0068	-4	4.79	29260.8	5.72	HUMAN	P28070	Proteasome subunit beta type-4
20915	dirMS_041712_NAR_60mM_plus.14058.14058.3	3	5.33	0	1.49E+05		(K)LAQANG	(K)L A/Q|A N/G W/G V M\V S H R(S)		130.15	509.2606	1525.769	-0.002	-1.3	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
20916	dirMS_041712_NAR_120mM_minus.15428.15428.3	3	5.32	2	9.57E+05		(R)ALKDEEI	(R)A L/K|D E E K M\E/L Q E I Q/L K(E)		137.72	649.0139	1945.031	-0.0039	-2	4.58	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
20917	dirMS_041712_NAR_120mM_minus.15929.15929.3	3	5.32	0	4.17E+05		(R)QLHDDY	(R)Q L H D D Y/F Y H D E\L(-)		140.6	532.2321	1594.681	0.0009	0.6	4.21	24852.9	4.29	HUMAN	A8MXP8	Reticulocalbin-2
20918	dirMS_041712_NAR_30mM_minus2.16536.16536.2	2	5.32	0	4.02E+05	M185m	(K)LAVNm	(K)L A|V\N m|V|P F P R(L)	m:Oxidized methionine	142.73	580.3178	1143.634	15.994	-0.8	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
20919	dirMS_041712_NAR_40mM_minus2.7973.7973.3	3	5.32	0	1.53E+05		(K)QAAASA	(K)Q A A A|S A T/Q T I A/A A Q H A A S T P K(A)		126.57	665.6822	1995.025	0.0067	3.3	8.76	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
20920	dirMS_041712_NAR_50mM_minus2.13014.13014.3	3	5.32	1	4.16E+04		(K)VLCGGD	(K)V L C G G D I\Y\V/P E D/P K L K(D)	C:Carbamidomethylation	142.45	601.6487	1802.936	-0.0042	-2.3	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
20921	dirMS_041712_NAR_50mM_minus2.14802.14802.3	3	5.32	0	3.07E+04		(K)GQYFGE	(K)G Q|Y F/G E L A L V/T/N K P R(A)		152.52	564.9709	1692.907	-0.0086	-5.1	8.59	10305.6	6.94	HUMAN	H7C330	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
20922	dirMS_041712_NAR_60mM_minus.12092.12092.3	3	5.32	0	4.46E+05		(K)VTVLFA	(K)V T V L/F A G Q H I S K(S)		127.47	433.9193	1299.742	0.0014	1.1	8.73	258215.9	5.48	HUMAN	E7EN95	Filamin-B
20923	dirMS_041712_NAR_60mM_minus.6483.6483.3	3	5.32	1	6.33E+04		(R)GTDDSP	(R)G T\D D/S P K D S Q/E\D/L\Q E/R(H)		94.48	607.2707	1819.794	0.0035	1.9	3.96	23420.8	4.74	HUMAN	Q5H9L2	Transcription elongation factor A protein-like 5

20924	dirMS_041712_NAR_20mM_plus.10656.10656.2	2	5.32	1	5.17E+04		(K)VISSLEK	(K)V/I/S S/L E K S R(D)		145.8	509.8006	1018.589	0.0048	4.7	8.72	120850.8	5.44	HUMAN	C9JKA9	Kinesin-like protein KIF15
20925	dirMS_041712_NAR_30mM_plus2.18301.18301.2	2	5.32	0	1.69E+04		(R)VVNVSS	(R)V V|N\V/S/S I/M S V R(A)		149.1	595.8347	1190.656	0.006	5	9.72	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
20926	dirMS_041712_NAR_30mM_plus2.20874.20874.2	2	5.32	0	1.27E+05	M153m	(K)VVTYGm	(K)V V T/Y/G/m/A N L L T G P K(R)	m:Oxidized methionine	163.65	740.3971	1463.793	15.9943	-0.4	8.56	28454.5	6.24	HUMAN	B0AZP7	Synaptic vesicle membrane protein VAT-1 homolog
20927	dirMS_041712_NAR_40mM_plus2.18023.18023.3	3	5.32	0	1.71E+05		(K)ISSIQSIV	(K)I S S I Q S I/V/P A L E I/A N A H R(K)		172.4	640.3668	1919.071	0.015	7.8	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
20928	dirMS_041712_NAR_60mM_plus.13310.13310.3	3	5.32	1	4.04E+06		(R)VVDLM	(R)V/V/D L/M A/H M A S K E(-)		126.73	444.2219	1330.649	0.0018	1.3	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
20929	dirMS_041712_NAR_120mM_minus.17818.17818.4	4	5.31	1	3.17E+05		(K)KTTIENI	(K)K T T I E N\I Q L/P/H\T L L S R(F)		151.6	466.7676	1864.065	-0.0165	-8.9	8.76	95792.4	6.36	HUMAN	J3KPV4	DNA replication licensing factor MCM4
20930	dirMS_041712_NAR_30mM_minus2.5510.5510.2	2	5.31	0	1.73E+05		(R)LYQAGE	(R)L/Y/Q/A/G E G R(L)		84.55	447.2217	893.448	-0.0114	-12.8	6	38089.6	6.79	HUMAN	B4DT77	Annexin
20931	dirMS_041712_NAR_50mM_minus2.7337.7337.3	3	5.31	0	7.38E+04		(K)QLAVAE	(K)Q L A V/A E G K/P P E/A P K(G)		108.58	478.9368	1434.795	0.0007	0.5	6.14	24364.9	9.64	HUMAN	H0YIP0	Methionine--tRNA ligase, cytoplasmic (Fragment)
20932	dirMS_041712_NAR_60mM_minus.12082.12082.3	3	5.31	0	8.76E+04		(K)VVDELN	(K)V/V/D E L N L L/H/T E L A(-)		127.17	489.262	1465.79	-0.0182	-12.4	4.13	7015.9	5.12	HUMAN	F8W124	DCC-interacting protein 13-beta (Fragment)
20933	dirMS_041712_NAR_60mM_minus.14119.14119.3	3	5.31	0	8.54E+04		(R)ASPSPLP	(R)A S|P\S\P L P T C L L/Q E R(K)	C:Carbamidomethylation	138.52	523.6047	1568.81	-0.0106	-6.7	6.05	13059	10.2	HUMAN	H0YNJ1	HCG2004619
20934	dirMS_041712_NAR_60mM_minus.18422.18422.3	3	5.31	0	1.13E+04		(R)HLEPAL	(R)H L E P A L A\F\Q/L/E/L/N R(M)		163.17	550.9705	1650.896	0.0007	0.4	5.4	97883.4	6.02	HUMAN	F6QQI9	Acetyl-CoA carboxylase 2
20935	dirMS_041712_NAR_60mM_minus.7090.7090.3	3	5.31	0	9.81E+04	T121t	(K)QWLMtI	(K)Q W L/M t E/A L V N(-)	t:N-acetylglucosamine (T)	98.38	469.8979	1204.603	203.0761	-2.3	4	13973.5	9.73	HUMAN	E5RIW4	Transcription initiation factor IIE subunit beta (Fragment)
20936	dirMS_041712_NAR_60mM_minus.9952.9952.3	3	5.31	1	5.63E+05	M230m M2	(R)mSmKE	(R)m S m K E V D|E Q|M/L/N/V Q N/K(N)	m:Oxidized methionine	114.97	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
20937	dirMS_041712_NAR_120mM_plus.10000.10000.3	3	5.31	1	1.08E+06		(R)QYFEEIC	(R)Q Y/F/E/E I Q R/R(F)		106.22	423.5524	1268.638	0.0044	3.5	6.14	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
20938	dirMS_041712_NAR_120mM_plus.6136.6136.3	3	5.31	1	7.70E+05		(R)TAQEVE	(R)T A|Q/E/V E T Y R R(S)		84.7	418.2137	1252.628	-0.0015	-1.2	5.81	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
20939	dirMS_041712_NAR_120mM_plus.8276.8276.4	4	5.31	2	1.47E+05		(R)ASVDTK	(R)A/S/V D T K E A E/G A/P Q/V E A G K R(L)		96.9	486.5008	1942.983	-0.0015	-0.8	4.87	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
20940	dirMS_041712_NAR_20mM_plus.15864.15864.2	2	5.31	0	1.48E+05		(K)VGINYQ	(K)V G I/N Y Q/P/P T V/V/P G G D L A K(V)		179.68	912.9952	1824.985	-0.0023	-1.3	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
20941	dirMS_041712_NAR_20mM_plus.16657.16657.3	3	5.31	0	7.34E+04		(R)AAFTAFI	(R)A A F T A F|E/E/A Q L P R(L)		186.33	484.2492	1450.733	0.0005	0.4	4.53	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
20942	dirMS_041712_NAR_20mM_plus.17961.17961.2	2	5.31	0	1.12E+05		(K)VDFPQD	(K)V D/F/P\Q D Q L T\A/L\T G R(I)		195.37	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
20943	dirMS_041712_NAR_20mM_plus.18419.18419.2	2	5.31	0	1.22E+05		(R)GVVQEL	(R)G V V|Q E\L Q\Q A I/S K(L)		198.05	650.3656	1299.727	-0.0028	-2.1	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
20944	dirMS_041712_NAR_20mM_plus.18887.18887.2	2	5.31	1	5.61E+04	Y582y	(R)LVKVTLy	(R)L/V/K V T/L|y G S Q I K(L)	y:Phosphorylated Y	201.58	714.8991	1348.82	79.9711	3.3	9.7	128647.2	6.02	HUMAN	D3DWF9	Exportin 6, isoform CRA_a
20945	dirMS_041712_NAR_20mM_plus.7835.7835.3	3	5.31	0	1.01E+04	M13m M1	(K)ISGGSV	(K)I S G G S V V E/m/Q/G D E m T R(I)	m:Oxidized methionine	123.68	576.588	1695.768	31.9818	-4.6	4.14	17833.3	8.73	HUMAN	C9J4N6	Isocitrate dehydrogenase [NADP] cytoplasmic (Fragment)
20946	dirMS_041712_NAR_20mM_plus.8864.8864.2	2	5.31	0	3.83E+04	M124m	(K)GImGED	(K)G I/m/G E/D T Y|P Y Q G K(-)	m:Oxidized methionine	131.53	737.8295	1458.657	15.9948	-0.1	4.37	15020.6	6.72	HUMAN	E9PKT6	Cathepsin H (Fragment)
20947	dirMS_041712_NAR_30mM_plus2.19542.19542.2	2	5.31	0	2.45E+05		(K)APDFVF	(K)A P/D F|V|F Y A/P R(L)		156.57	591.8008	1182.594	0.0001	0.1	5.88	71218.8	6.3	HUMAN	A7YIJ8	Radixin
20948	dirMS_041712_NAR_30mM_plus2.20462.20462.2	2	5.31	0	2.08E+05		(K)NIEDVIA	(K)N I/E D V/I A/Q/G I/G K(L)		160.5	628.8445	1256.685	-0.0028	-2.2	4.37	9098.8	4.38	HUMAN	H0YDD8	60S acidic ribosomal protein P2 (Fragment)
20949	dirMS_041712_NAR_40mM_plus2.13331.13331.2	2	5.31	0	8.98E+04		(K)FFVGGN	(K)F F|V/G G N W/K(M)		144.42	477.7448	954.483	-0.0009	-0.9	8.75	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
20950	dirMS_041712_NAR_40mM_plus2.14882.14882.3	3	5.31	2	8.78E+04	K453k	(R)RAGESG	(R)R\A/G E S G H T V A/D Y L K F k(D)	k:Ubiquitin-K	154.62	631.6626	1778.918	114.0548	6.3	8.5	62267.1	9.31	HUMAN	F8W9I9	Dual-specificity tyrosine-phosphorylation-regulated kinase 1A
20951	dirMS_041712_NAR_50mM_plus2.10173.10173.3	3	5.31	1	6.78E+04		(K)TLQEVT	(K)T L/Q E/V/T/E M D S V K/R(Y)		121.03	512.5958	1535.773	-0.0005	-0.3	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
20952	dirMS_041712_NAR_60mM_plus.11305.11305.2	2	5.31	0	7.25E+05		(R)GSAVHC	(R)G S A\V/H Q/L S E E L R(C)		116.43	663.3438	1325.681	-0.0005	-0.4	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
20953	dirMS_041712_NAR_60mM_plus.15362.15362.3	3	5.31	1	6.65E+04		(K)SKLTFSC	(K)S K L T\F S C|L/G/G S D N/F K(H)	C:Carbamidomethylation	137.6	554.2751	1660.8	0.0108	6.5	8.31	15014.9	3.9	HUMAN	B4DHP2	Prostaglandin E synthase 3
20954	dirMS_041712_NAR_60mM_plus.17054.17054.3	3	5.31	1	2.34E+05		(R)ASLISAV	(R)A/S/L I/S A/V/S D K L R(W)		146.07	420.5832	1259.732	0.0033	2.6	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
20955	dirMS_041712_NAR_60mM_plus.6400.6400.2	2	5.31	1	1.56E+06		(K)DSYVGD	(K)D S Y|V|G D/E A Q S K R(G)		91.98	677.8149	1354.623	-0.0008	-0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
20956	dirMS_041712_NAR_120mM_minus.12170.12170.3	3	5.3	1	1.54E+05		(R)LSFDKD	(R)L/S/F/D K/D A M/V A R(A)		120.35	418.2193	1252.635	0.0079	6.3	5.96	35556.4	9.3	HUMAN	F2Z393	Transaldolase
20957	dirMS_041712_NAR_120mM_minus.6922.6922.2	2	5.3	0	4.89E+05		(K)HQPTAII	(K)H/Q|P/T A I\I\A\K(T)		91.83	489.7898	978.573	-0.0008	-0.8	8.76	63448.4	7.29	HUMAN	B4E022	Transketolase
20958	dirMS_041712_NAR_20mM_minus.12877.12877.2	2	5.3	0	3.48E+05		(R)FAIQDIS	(R)F A\I/Q/D I|S V E E T S A K(E)		178.78	769.3885	1537.774	-0.0047	-3.1	4.14	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
20959	dirMS_041712_NAR_30mM_minus2.8791.8813.2	2	5.3	0	9.30E+04		(K)WLGESE	(K)W|L/G E S\E/K(L)		102.48	424.7117	848.415	0.0013	1.5	4.53	32617.4	7.2	HUMAN	I3L4J1	Uncharacterized protein (Fragment)
20960	dirMS_041712_NAR_40mM_minus2.12034.12034.3	3	5.3	0	2.84E+05		(K)DAGEGL	(K)D A/G\E/G L L A V Q I T D/P E G K P K(K)		154.05	646.6785	1938.018	0.0031	1.6	4.32	283472.4	5.71	HUMAN	P21333	Filamin-A
20961	dirMS_041712_NAR_40mM_minus2.7377.7377.3	3	5.3	0	1.00E+05		(K)ASQEPSI	(K)A S Q\E/P S/P K P G T E V I/P A A P R(K)		119.13	644.6737	1932.018	-0.012	-6.2	6.19	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
20962	dirMS_041712_NAR_50mM_minus2.13917.13917.3	3	5.3	2	1.52E+04	S316s	(K)EGLsKVK	(K)E G L/s K V/K S I/L E S/V T R(L)	s:Phosphorylated S	147.17	575.9781	1645.948	79.9714	3	8.69	38610.4	5.31	HUMAN	Q8N6G5-2	Isoform 2 of Chondroitin sulfate N-acetylgalactosaminyltransferase 2
20963	dirMS_041712_NAR_50mM_minus2.13959.13959.3	3	5.3	1	3.85E+05		(K)ITDIIGKE	(K)I T/D I I G K E E G I/G/P E N L R(G)		146.92	618.665	1853.997	-0.0163	-8.8	4.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
20964	dirMS_041712_NAR_50mM_minus2.9784.9784.3	3	5.3	0	1.51E+05		(R)ISMSEVI	(R)I S M S E V D L N/V A A/P K(V)		123.38	491.9322	1473.762	0.0203	13.8	4.37	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
20965	dirMS_041712_NAR_60mM_minus.16733.16733.3	3	5.3	1	1.67E+05		(K)VSEQGL	(K)V/S E Q/G L/I E I/L K K(V)		152.93	452.9408	1356.81	-0.0018	-1.4	6.11	12899.6	6.59	HUMAN	K7EL31	Programmed cell death protein 5
20966	dirMS_041712_NAR_60mM_minus.8613.8613.3	3	5.3	1	3.08E+05	Y455y S461	(R)APSLPAF	(R)A P S L P A P/P y A/G A/P G s P R T K(R)	y:Phosphorylated Y s:Phosph	107.23	665.636	1834.981	159.9124	-10.1	9.99	52919.9	9.85	HUMAN	Q69YU3	Ankyrin repeat domain-containing protein 34A
20967	dirMS_041712_NAR_60mM_minus.8989.8989.3	3	5.3	1	3.60E+05	M230m M2	(R)mSMKE	(R)m S M K E V D E Q|m\L N|V/Q/N K(N)	m:Oxidized methionine	110.3	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
20968	dirMS_041712_NAR_60mM_minus.9874.9874.3	3	5.3	1	9.29E+04		(K)FAQNVG	(K)F A/Q/N V G/K S L T S K(R)		114.83	427.2322	1279.7	-0.0184	-14.4	10	56911.3	8.55	HUMAN	P49802-5	Isoform 5 of Regulator of G-protein signaling 7
20969	dirMS_041712_NAR_20mM_plus.16572.16572.2	2	5.3	0	6.68E+04	M50m	(R)DSLLQD	(R)D S L L/Q/D/G E/F S m D L R(T)	m:Oxidized methionine	185.58	821.3739	1625.748	15.993	-1.2	3.84	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
20970	dirMS_041712_NAR_20mM_plus.17176.17176.2	2	5.3	0	1.09E+05		(K)FATEAAI	(K)F A/T|E A|A\I/T I L R(I)		189.05	603.3442	1205.689	-0.0077	-6.4	6	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
20971	dirMS_041712_NAR_20mM_plus.9786.9786.2	2	5.3	0	1.16E+05		(K)VAGQD	(K)V/A/G Q/D G S V/V Q F K(I)		138.38	617.8225	1234.643	-0.0049	-4	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
20972	dirMS_041712_NAR_50mM_plus2.12565.12565.3	3	5.3	1	3.79E+04		(K)DMALAT	(K)D M|A|L/A/T K T E/V A L A K(D)		135.32	487.9361	1461.798	-0.0044	-3	6.07	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
20973	dirMS_041712_NAR_50mM_plus2.14116.14116.3	3	5.3	1	7.81E+05		(R)MSMKE	(R)M S M K E V D E\Q M|L\N/V/Q N K(N)		142.88	641.9706	1923.897	0	0	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
20974	dirMS_041712_NAR_50mM_plus2.15308.15308.3	3	5.3	1	8.49E+05		(R)GFPTIYF	(R)G F/P T I Y F/S/P A N K\K(L)		148.77	490.5973	1469.779	-0.0014	-0.9	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
20975	dirMS_041712_NAR_50mM_plus2.21649.21649.3	3	5.3	0	1.01E+05		(K)THLPLAL	(K)T H L P L A\L|L|P Q/T L L D Q K(V)		183.97	601.0191	1801.058	-0.0154	-8.6	6.41	22243.5	7.91	HUMAN	E9PKR8	Sulfotransferase 1A2 (Fragment)
20976	dirMS_041712_NAR_60mM_plus.18096.18096.3	3	5.3	1	6.97E+05	T788t	(K)SLKRDPS	(K)S L K/R/D P/S A t D A\Q K(L)	t:N-acetylglucosamine (T)	151.38	540.6114	1416.744	203.0755	-2.4	8.31	580884.1	6.01	HUMAN	Q86UQ4	ATP-binding cassette sub-family A member 13
20977	dirMS_041712_NAR_60mM_plus.19514.19514.3	3	5.3	0	1.33E+05		(R)NSVSNF	(R)N S/V/S/N F L/H S L E/R(G)		161.23	468.2401	1402.707	-0.0016	-1.1	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
20978	dirMS_041712_NAR_120mM_minus.9941.9941.2	2	5.29	0	5.79E+04		(R)HVLSVLS	(R)H/V|L S V\L/S K(T)		109.37	441.7733	882.541	-0.0014	-1.6	8.76	38349.2	6.69	HUMAN	B7Z514	Glutathione synthetase
20979	dirMS_041712_NAR_20mM_minus.10328.10328.2	2	5.29	0	7.27E+04		(K)AVLSLYA	(K)A V/L/S/L/Y/A S G R(T)		152.48	518.7929	1036.579	0	0	8.79	14579.3	5.13	HUMAN	K7EM38	Actin, cytoplasmic 2, N-terminally processed (Fragment)
20980	dirMS_041712_NAR_30mM_minus2.12931.12931.2	2	5.29	0	1.49E+05		(R)YTSLMLI	(R)Y/T/S/L M L R(D)		123.27	442.2405	883.471	0.0031	3.5	8.75	66876.9	6.17	HUMAN	O75083	WD repeat-containing protein 1
20981	dirMS_041712_NAR_30mM_minus2.6713.6713.2	2	5.29	0	8.96E+04		(R)LQDTSS	(R)L Q|D T/S S Y/A/K(I)		92	506.7468	1012.495	-0.0082	-8.1	5.83	334221.3	6.44	HUMAN	P15924	Desmoplakin
20982	dirMS_041712_NAR_40mM_minus2.10927.10927.3	3	5.29	1	1.14E+05	M362m	(R)EGSVmL	(R)E G S/V\m/L Q/V/D\V D T V K G G L K(L)	m:Oxidized methionine	147.85	630.9989	1874.989	15.993	-1	4.56	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
20983	dirMS_041712_NAR_50mM_minus2.12412.12412.3	3	5.29	0	2.81E+05		(K)QLTEED	(K)Q\L|T\E/E D G V H S V/I\E E N I K(C)		138.65	647.3249	1939.961	-0.0006	-0.3	4.25	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
20984	dirMS_041712_NAR_50mM_minus2.12479.12479.3	3	5.29	0	1.00E+06	M114m M1	(R)AGKPVI	(R)A G\K\P V I|C A\T Q m L E\S m I/K(K)	C:Carbamidomethylation m:Oxid	139.77	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
20985	dirMS_041712_NAR_50mM_minus2.13811.13811.3	3	5.29	1	2.93E+05		(K)LTEDKAI	(K)L/T/E D K A D V\Q/S\I I/G|L Q R(F)		146.48	595.9939	1785.97	-0.0034	-1.9	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
20986	dirMS_041712_NAR_60mM_minus.7764.7764.3	3	5.29	1	2.86E+05		(R)VITEEEK	(R)V/I/T E/E E K N F K(A)		103.67	412.8902	1236.647	0.009	7.3	4.79	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
20987	dirMS_041712_NAR_60mM_minus.9275.9275.3	3	5.29	0	2.51E+05		(K)QADNPH	(K)Q\A D N/P H/V/A/L Y\Q A R(F)		111.68	494.9197	1482.745	-0.0003	-0.2	6.74	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
20988	dirMS_041712_NAR_20mM_plus.16235.16235.2	2	5.29	0	8.43E+04		(R)AYILNLV	(R)A Y|I/L N L V K(Q)		183.77	467.2905	933.577	-0.0031	-3.3	8.63	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
20989	dirMS_041712_NAR_40mM_plus2.18421.18421.3	3	5.29	1	2.56E+04		(R)IAEVGG	(R)I A\E V/G G V/P\Y/L L P L V N Q K K(V)		174.58	646.716	1938.142	-0.0088	-4.5	8.5	18803.3	5.55	HUMAN	E9PIP1	Ester hydrolase C11orf54 (Fragment)
20990	dirMS_041712_NAR_40mM_plus2.7628.7628.2	2	5.29	0	8.64E+03		(R)INISEGN	(R)I N/I/S\E/G N C/P E R(I)	C:Carbamidomethylation	104.55	644.7998	1288.595	-0.0027	-2.1	4.53	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
20991	dirMS_041712_NAR_50mM_plus2.12396.12396.3	3	5.29	1	2.80E+05		(R)ESDVPLK	(R)E S D V/P L K\T E E/F E V T K(T)		132.68	584.2981	1750.874	0.0052	3	4.25	18909	6.21	HUMAN	Q969H8	UPF0556 protein C19orf10
20992	dirMS_041712_NAR_50mM_plus2.20587.20587.3	3	5.29	1	2.42E+05		(K)VKIPEGT	(K)V K I P E G T\I L/T/M D M L T/V K(V)		177.1	630.3524	1889.049	-0.006	-3.2	6.04	40763.2	6.29	HUMAN	Q9NR45	Sialic acid synthase
20993	dirMS_041712_NAR_50mM_plus2.8073.8073.3	3	5.29	0	7.80E+04		(K)QEYDES	(K)Q E Y D E S/G P/S I/V/H/R(K)		109.4	506.2382	1516.703	-0.0026	-1.7	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
20994	dirMS_041712_NAR_60mM_plus.13566.13566.3	3	5.29	1	1.03E+05		(R)VIDRELY	(R)V/I/D R E L Y|Q/Q L Q/R(G)		126.43	520.952	1560.849	-0.0078	-5	6.04	533778	5.74	HUMAN	Q15149	Plectin
20995	dirMS_041712_NAR_60mM_plus.21186.21186.3	3	5.29	0	2.16E+05		(K)ALESPER	(K)A L|E S P E R P F/L A\I L G G/A K(V)		174.75	590.3367	1768.996	0	0	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
20996	dirMS_041712_NAR_120mM_minus.7332.7332.3	3	5.28	1	7.89E+05		(K)IQDKEGI	(K)I Q D K E G\I|P/P D Q Q R(L)		94.87	508.5981	1523.781	-0.0015	-1	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
20997	dirMS_041712_NAR_120mM_minus.9122.9122.3	3	5.28	1	1.48E+04		(R)VASSTLL	(R)V/A/S S T/L L D\D R/R(N)		104.6	411.5568	1232.659	-0.0035	-2.8	5.93	108806.2	4.84	HUMAN	O60763	General vesicular transport factor p115
20998	dirMS_041712_NAR_20mM_minus.13214.13214.2	2	5.28	0	1.40E+05		(K)VGINYQ	(K)V G I N/Y Q|P P T V/V|P G G D L A K(V)		183.15	912.9938	1824.985	-0.0051	-2.8	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
20999	dirMS_041712_NAR_20mM_minus.9436.9436.3	3	5.28	0	1.18E+04	M175m	(R)LEQGQA	(R)L E Q G Q A\I D/D L m P A Q K(-)	m:Oxidized methionine	144.5	558.2794	1656.826	15.9975	1.5	4.03	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
21000	dirMS_041712_NAR_40mM_minus2.15447.15447.3	3	5.28	1	1.10E+05		(R)VISGVLC	(R)V I|S G V L Q L/G N I/V F K K(E)		178.23	539.0017	1614.994	-0.0036	-2.2	10	227783.5	5.5	HUMAN	P35579	Myosin-9
21001	dirMS_041712_NAR_50mM_minus2.13700.13700.3	3	5.28	1	1.15E+05		(K)LTEDKAI	(K)L T/E D K A D V\Q/S/I I/G L Q R(F)		146.42	595.9939	1785.97	-0.0034	-1.9	4.56	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
21002	dirMS_041712_NAR_60mM_minus.4803.4803.3	3	5.28	1	7.13E+05	M137m	(R)mQNDT	(R)m Q|N/D T/A/E N/E T T E K E|E K(S)	m:Oxidized methionine	79.37	638.2735	1896.813	15.9932	-0.9	4.14	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
21003	dirMS_041712_NAR_60mM_minus.5770.5770.3	3	5.28	1	4.87E+05	M178m	(R)DmSVR	(R)D m|S V\R G M E G S L E R(E)	m:Oxidized methionine	88.53	494.9008	1466.673	16.0152	13.7	4.68	45458.9	9.26	HUMAN	Q5T427	Zinc finger protein 438
21004	dirMS_041712_NAR_60mM_minus.9740.9740.3	3	5.28	1	4.56E+04		(K)TAVCDIF	(K)T/A/V C D I/P P R G L K(M)	C:Carbamidomethylation	112.72	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
21005	dirMS_041712_NAR_20mM_plus.10147.10147.2	2	5.28	0	1.65E+05		(K)GEATVSI	(K)G E\A T V/S/F/D D P P S A K(A)		142.02	710.8324	1420.659	-0.0015	-1.1	4.03	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
21006	dirMS_041712_NAR_20mM_plus.11580.11580.2	2	5.28	0	1.25E+05	M402m	(R)mAFGA	(R)m A|F|G A T L D V K(T)	m:Oxidized methionine	152.47	534.7743	1052.545	15.9968	1.8	5.59	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
21007	dirMS_041712_NAR_20mM_plus.13680.13680.2	2	5.28	0	2.77E+05		(R)GDLGIEI	(R)G D L/G|I/E I P A E K(V)		166.72	571.3075	1141.61	-0.0022	-1.9	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
21008	dirMS_041712_NAR_30mM_plus2.14879.14879.2	2	5.28	0	6.27E+05		(R)TFEDFVI	(R)T F/E|D/F V R(I)		130.15	457.2312	913.441	0.0137	15	4.37	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
21009	dirMS_041712_NAR_30mM_plus2.4765.4765.2	2	5.28	0	7.75E+05		(R)MGQTM	(R)M/G\Q/T/M/E/R(I)		76.45	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
21010	dirMS_041712_NAR_30mM_plus2.6797.6797.2	2	5.28	0	6.44E+04		(K)LLEGEES	(K)L L/E|G E/E S R(I)		91.32	466.7379	932.468	0.0002	0.2	4.25	49709.6	5.19	HUMAN	B0YJC4	Vimentin
21011	dirMS_041712_NAR_40mM_plus2.10092.10092.3	3	5.28	0	7.56E+03		(R)TIVITSHI	(R)T I/V I T/S H P G Q I V K(H)		123.77	464.9449	1392.821	-0.0008	-0.6	8.44	27999.4	5.61	HUMAN	B7Z5C0	DnaJ homolog subfamily A member 1
21012	dirMS_041712_NAR_40mM_plus2.12239.12239.2	2	5.28	0	4.51E+04		(R)YIELLTR	(R)Y I/E/L/L T/R(S)		138.12	454.2649	907.525	-0.0022	-2.4	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
21013	dirMS_041712_NAR_40mM_plus2.13410.13410.3	3	5.28	0	8.69E+04		(R)ILSDVTH	(R)I L/S D V T H\S/A V/F G V/P A S K(S)		145.1	576.6463	1727.933	-0.0083	-4.8	6.74	74453	9.65	HUMAN	E9PG46	AP2-associated protein kinase 1
21014	dirMS_041712_NAR_40mM_plus2.13529.13529.3	3	5.28	0	2.60E+05		(R)VAPDEH	(R)V/A/P D E H\P I L/L T E A/P L N/P K(I)		145.53	652.0252	1954.064	-0.0034	-1.7	4.65	42344.8	5.39	HUMAN	Q562R1	Beta-actin-like protein 2
21015	dirMS_041712_NAR_50mM_plus2.10911.10911.3	3	5.28	1	2.21E+06		(R)MQKEIT	(R)M Q K E I T A\L/A/P/S T M/K(I)		124.1	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
21016	dirMS_041712_NAR_50mM_plus2.12034.12034.3	3	5.28	0	4.17E+05		(K)QADLYIS	(K)Q/A/D L/Y I/S E/G L/H P\R(I)		131.4	500.2606	1498.765	0.0024	1.6	5.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
21017	dirMS_041712_NAR_50mM_plus2.15208.15208.3	3	5.28	1	3.76E+05		(R)MGLAIS	(R)M/G L A I S L\V/A T E K/E K(V)		147.77	497.2822	1489.829	0.0026	1.7	5.9	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
21018	dirMS_041712_NAR_50mM_plus2.22159.22159.3	3	5.28	1	1.16E+04		(K)EGGLGP	(K)E G G L/G/P L/N I/P L L A D V T R R(L)		190.08	631.029	1891.076	-0.0035	-1.9	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
21019	dirMS_041712_NAR_50mM_plus2.9331.9331.3	3	5.28	0	1.33E+05		(K)AEITLVA	(K)A E|I T/L V A/T K/P E K(L)		116.23	433.922	1299.752	-0.0004	-0.3	6.18	98761.7	5.56	HUMAN	Q9UBF2	Coatomer subunit gamma-2
21020	dirMS_041712_NAR_60mM_plus.18674.18674.3	3	5.28	1	7.89E+03	T64t	(K)DGCRVP	(K)D G C R V P A/V/V\F T/t L R(G)	C:Carbamidomethylation t:N-ace	155.07	598.6543	1590.842	203.1063	15	9.6	11568.4	10.14	HUMAN	Q5VZ75	C-C motif chemokine 19
21021	dirMS_041712_NAR_60mM_plus.7186.7186.3	3	5.28	0	4.32E+05		(K)HSGPNS	(K)H S G P N S\A/D/S/A/N/D G F V R(L)		95.72	544.2474	1630.72	0.0072	4.4	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
21022	dirMS_041712_NAR_120mM_minus.12134.12134.3	3	5.27	1	1.14E+05		(R)LRDYEA	(R)L R D Y\E|A/G L/G L K(S)		120.18	412.2282	1234.679	-0.009	-7.3	6.07	54670.1	6.62	HUMAN	O00635	Tripartite motif-containing protein 38
21023	dirMS_041712_NAR_120mM_minus.9907.9907.3	3	5.27	1	8.35E+04		(R)RLDECE	(R)R L D E C\E/E/A/F Q/G T|K(V)	C:Carbamidomethylation	108.6	528.2437	1582.717	0	0	4.41	22568.6	6.35	HUMAN	B3KQ25	Proteasome activator complex subunit 3
21024	dirMS_041712_NAR_30mM_minus2.17253.17253.2	2	5.27	1	8.20E+04	S530s	(K)GsPERH	(K)G s/P/E R H/H K(Q)	s:N-acetylglucosamine (S)	146.93	575.7971	947.481	203.1063	23.4	8.76	68325.8	5.42	HUMAN	G8JLJ4	Phostensin
21025	dirMS_041712_NAR_30mM_minus2.19126.19126.3	3	5.27	0	1.79E+05		(K)SYELPD	(K)S Y\E\L\P D G Q V\I/T I/G N E R(F)		158.88	597.6343	1790.892	-0.0036	-2	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
21026	dirMS_041712_NAR_30mM_minus2.6167.6167.2	2	5.27	0	2.75E+05		(K)TSEVNC	(K)T/S|E/V/N C Y R(C)	C:Carbamidomethylation	87.85	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
21027	dirMS_041712_NAR_50mM_minus2.10611.10611.3	3	5.27	0	2.79E+05	M35m	(K)AASDIA	(K)A A S/D|I A\m T E L/P P T H P I R(L)	m:Oxidized methionine	128.3	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
21028	dirMS_041712_NAR_50mM_minus2.8233.8233.3	3	5.27	1	8.03E+04		(K)TAVCDIF	(K)T A|V/C D I/P/P R G L K(M)	C:Carbamidomethylation	115.22	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
21029	dirMS_041712_NAR_60mM_minus.6319.6319.3	3	5.27	1	1.97E+04	M172m	(K)ALmAAE	(K)A L/m A A E D/K Y S Q K(E)	m:Oxidized methionine	93.85	457.5567	1354.667	15.9884	-4.7	6.11	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
21030	dirMS_041712_NAR_120mM_plus.17524.17524.3	3	5.27	0	9.94E+05	K102k	(K)DIHGFEI	(K)D I H G F/E/F Q W k(E)	k:Ubiquitin-K	145.7	474.2314	1306.622	114.0581	10.7	5.32	62340.4	9.74	HUMAN	Q5VIY5	Zinc finger protein 468
21031	dirMS_041712_NAR_120mM_plus.20194.20194.4	4	5.27	1	2.83E+05		(K)STLVHSL	(K)S T/L V H S L F L/T D L Y K D R(K)		158.62	477.7626	1908.023	0.006	3.2	6.46	37862.6	5.73	HUMAN	B4DJ62	HCG2002594, isoform CRA_a
21032	dirMS_041712_NAR_120mM_plus.6132.6132.3	3	5.27	0	6.89E+05		(K)QRPQAT	(K)Q R P Q\A\T|A/E Q/I R(L)		85.9	433.2367	1297.697	-0.0016	-1.2	9.6	113668.7	6.2	HUMAN	F8W726	Ubiquitin-associated protein 2-like

21033	dirMS_041712_NAR_20mM_plus.11022.11022.2	2	5.27	0	5.17E+04		(R)GATQQI	(R)G A\T/Q/Q I/L D/E\A\E R(S)		148.35	665.8352	1330.66	0.0034	2.5	4.14	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
21034	dirMS_041712_NAR_20mM_plus.14418.14418.3	3	5.27	0	1.17E+05	M174m	(K)AmGAA	(K)A m G\A A Q V|V/V/T D L/S A T R(L)	m:Oxidized methionine	171.2	535.9457	1589.832	15.991	-2.5	5.88	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
21035	dirMS_041712_NAR_20mM_plus.18024.18024.2	2	5.27	0	7.44E+04		(R)LSVLGAI	(R)L S/V\L/G/A I/T/S V Q Q R(L)		195.93	686.3953	1371.795	-0.0121	-8.8	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
21036	dirMS_041712_NAR_40mM_plus2.8258.8258.2	2	5.27	0	1.92E+05		(R)AVVIVD	(R)A/V V I/V/D/D/R(G)		108.33	443.7528	886.499	-0.0009	-1.1	4.21	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
21037	dirMS_041712_NAR_40mM_plus2.9769.9769.2	2	5.27	0	1.73E+05		(K)ELNYFA	(K)E L/N Y/F/A/K(A)		121.18	442.7291	884.451	-0.0003	-0.4	6.1	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
21038	dirMS_041712_NAR_50mM_plus2.13279.13279.3	3	5.27	1	1.66E+05		(K)GQILMP	(K)G Q|I/L/M/P N I G Y G S N K K(T)		137.87	540.6161	1619.857	-0.0236	-14.6	9.7	15730.4	11.67	HUMAN	D3YTB1	60S ribosomal protein L32 (Fragment)
21039	dirMS_041712_NAR_50mM_plus2.13684.13684.3	3	5.27	1	1.88E+06		(R)QATKDA	(R)Q\A T K D A G T I A|G L/N V L R(I)		140	543.3085	1627.913	-0.0016	-1	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
21040	dirMS_041712_NAR_50mM_plus2.16873.16873.3	3	5.27	1	4.69E+05	T360t S361	(R)IPEQRts	(R)I P E Q R t s S/m V S E V K(T)	t:Phosphorylated T s:Phosph	156.72	589.5785	1590.816	175.9054	-12.6	6.14	47175.1	9.74	HUMAN	Q969Z4	Tumor necrosis factor receptor superfamily member 19L
21041	dirMS_041712_NAR_50mM_plus2.18465.18465.3	3	5.27	1	5.92E+05		(K)LLEPVLL	(K)L L/E P V L L/L G K E/R(F)		164.52	460.6256	1379.862	0.0002	0.1	6.14	16559.1	10.36	HUMAN	P62249	40S ribosomal protein S16
21042	dirMS_041712_NAR_50mM_plus2.22097.22097.3	3	5.27	1	5.87E+05		(K)AGFLDL	(K)A/G/F L/D L K D F L/P K(E)		188.9	455.2587	1363.762	-0.0005	-0.3	6	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
21043	dirMS_041712_NAR_60mM_plus.12133.12133.3	3	5.27	1	7.31E+06		(R)DGKLVS	(R)D G K\L V\S\E/S\S D/V\L/P K(-)		120.27	491.928	1473.78	-0.0101	-6.8	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
21044	dirMS_041712_NAR_60mM_plus.18364.18364.3	3	5.27	1	9.77E+04		(R)STVRDI	(R)S T V R D I D|P Q/N/D L T F L R(I)		153.1	630.661	1889.972	-0.0031	-1.7	4.43	16537.8	6.59	HUMAN	B1AKR6	Dynein light chain roadblock-type 1
21045	dirMS_041712_NAR_120mM_minus.10662.10662.3	3	5.26	1	8.70E+04		(R)RGVVG	(R)R G V V|G|P E|L/Y G R(L)		111.63	401.559	1202.664	-0.0016	-1.3	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
21046	dirMS_041712_NAR_120mM_minus.10723.10723.2	2	5.26	1	1.13E+06		(K)IKIIAPPE	(K)I/K/I/I/A\P P E R(K)		113.33	518.8303	1036.651	0.002	1.9	8.75	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
21047	dirMS_041712_NAR_30mM_minus2.14635.14635.2	2	5.26	0	1.81E+05		(K)WIWFE	(K)W/I/W F E/N S K(N)		133.38	555.2675	1109.542	-0.0137	-12.4	6	224627.6	6.68	HUMAN	B5MCY1	Uncharacterized protein (Fragment)
21048	dirMS_041712_NAR_60mM_minus.10426.10426.3	3	5.26	0	1.96E+05		(R)LSNLAL	(R)L/S N/L A L/V K P E K(T)		118.55	404.5829	1211.736	-0.0017	-1.4	8.59	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
21049	dirMS_041712_NAR_60mM_minus.15572.15572.3	3	5.26	1	1.09E+05	M332m	(R)AKFEEL	(R)A K F\E E\L N\m/D|L/F R(S)	m:Oxidized methionine	147.6	510.255	1512.752	15.9989	2.6	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
21050	dirMS_041712_NAR_120mM_plus.10504.10679.3	3	5.26	0	7.55E+05		(R)AHSSM	(R)A H S S M\V/G\V/N/L/P Q K(A)		108.35	456.5762	1367.71	0.0041	3	8.8	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
21051	dirMS_041712_NAR_120mM_plus.11170.11170.3	3	5.26	0	1.25E+06		(R)GSAVH	(R)G S/A V/H/Q L/S/E E/L R(C)		111.32	442.5657	1325.681	0.0017	1.3	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
21052	dirMS_041712_NAR_20mM_plus.12901.12901.2	2	5.26	0	4.79E+05	M1m N6n	(-)mPLFPn	(-)m P|L F|P n L P R(L)	m:Oxidized methionine n:N-	161.78	652.3439	1084.597	219.0833	6.9	9.5	39133.5	4.5	HUMAN	Q8TD91-2	Isoform 2 of Melanoma-associated antigen C3
21053	dirMS_041712_NAR_20mM_plus.8725.8725.3	3	5.26	0	1.41E+05	M224m	(K)GGKPEP	(K)G G K P E P P A m\P Q/P V/P/T/A(-)	m:Oxidized methionine	130.62	530.6038	1573.804	15.9926	-1.5	6	25541.5	9.92	HUMAN	E9PL09	40S ribosomal protein S3
21054	dirMS_041712_NAR_30mM_plus2.21976.21976.2	2	5.26	0	2.23E+05		(R)AFITNIP	(R)A F I/T|N I/P F D V/K(W)		171.32	632.8481	1264.694	-0.0047	-3.7	5.88	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
21055	dirMS_041712_NAR_30mM_plus2.5478.5478.2	2	5.26	0	6.24E+04		(K)QSQDEP	(K)Q S\Q/D|E/P/L R(S)		83.02	486.741	972.475	0.0002	0.2	4.37	33803.8	6.12	HUMAN	B1AKP7	TAR DNA binding protein
21056	dirMS_041712_NAR_40mM_plus2.17141.17141.3	3	5.26	0	6.64E+04		(R)IHFPLAT	(R)I H\F\P L A T Y A/P V/I S A E K(A)		166.77	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
21057	dirMS_041712_NAR_40mM_plus2.17698.17698.3	3	5.26	0	5.36E+04		(K)ASVITQ	(K)A/S|V I/T Q V F H V P L E E R(K)		170.05	575.6528	1724.933	0.0109	6.3	5.4	24511.6	6.62	HUMAN	C9J5E5	Vigilin (Fragment)
21058	dirMS_041712_NAR_50mM_plus2.11279.11279.3	3	5.26	0	5.44E+05		(R)LLEAQA	(R)L L|E A Q/A C/T G G I/I/H P T T G Q\K(L)	C:Carbamidomethylation	127.32	665.6855	1995.033	0.0092	4.6	6.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
21059	dirMS_041712_NAR_50mM_plus2.18134.18134.3	3	5.26	1	1.09E+05		(K)DLEIKIP	(K)D L E|I/K I/P/V\V V R(L)		163.5	427.6021	1280.794	-0.0019	-1.5	6.07	44183.5	5.64	HUMAN	F5GXC8	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial
21060	dirMS_041712_NAR_60mM_plus.5111.5111.3	3	5.26	1	3.95E+05		(R)AAEDDE	(R)A A|E D D\E D D D/V D T K K(Q)		83.53	522.5529	1565.645	-0.0008	-0.5	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
21061	dirMS_041712_NAR_120mM_minus.13793.13793.3	3	5.25	1	2.28E+05		(R)IHAGEKI	(R)I H\A\G E K I P/E/N A K(A)		129.02	436.2378	1306.711	-0.0125	-9.6	6.76	86619.1	10.16	HUMAN	E7EPS0	Zinc finger protein 667
21062	dirMS_041712_NAR_20mM_minus.10330.10330.2	2	5.25	0	4.57E+04	M145m	(R)VVLFEm	(R)V/V|L/F E m E A R(K)	m:Oxidized methionine	152.52	555.2868	1093.571	15.9953	0.3	4.53	27142.4	5.34	HUMAN	E5RG68	Copine-3 (Fragment)
21063	dirMS_041712_NAR_20mM_minus.11733.11733.2	2	5.25	0	3.25E+05		(R)GALQNI	(R)G A L\Q\N/I/I\P\A S T/G A A K(A)		165.33	706.3976	1411.79	-0.0024	-1.7	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
21064	dirMS_041712_NAR_20mM_minus.13061.13061.2	2	5.25	0	3.70E+05	M35m	(K)NDIAINE	(K)N D I/A|I|N E L m\K(R)	m:Oxidized methionine	181.67	588.7948	1160.598	15.9843	-9	4.37	28354	7.11	HUMAN	B4DXI8	26S proteasome non-ATPase regulatory subunit 7
21065	dirMS_041712_NAR_30mM_minus2.12259.12259.2	2	5.25	0	2.35E+04		(K)GDYPLE	(K)G D/Y/P/L E A V R(M)		119.97	510.2598	1019.516	-0.0033	-3.2	4.37	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
21066	dirMS_041712_NAR_40mM_minus2.12122.12122.3	3	5.25	0	2.87E+05		(R)LQQELD	(R)L Q|Q/E/L/D D L T V D L D H Q R(Q)		154.23	646.6596	1937.956	0.0079	4.1	4.03	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
21067	dirMS_041712_NAR_50mM_minus2.16918.16918.3	3	5.25	1	3.18E+05	S119s	(K)LATVVG	(K)L A/T V V G E/N G s V L R R(V)	s:N-acetylglucosamine (S)	165.27	558.6442	1470.839	203.0793	0	9.6	19174.7	10.16	HUMAN	E9PM67	Inner centromere protein (Fragment)
21068	dirMS_041712_NAR_50mM_minus2.9995.9995.3	3	5.25	1	1.32E+06		(R)MQKEIT	(R)M Q\K E I T A|L\A|P S T/M/K(I)		124.15	516.9426	1548.812	0.0008	0.5	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
21069	dirMS_041712_NAR_60mM_minus.19449.19449.3	3	5.25	0	3.65E+05		(K)HSQFIG	(K)H S Q F I/G\Y|P I/T L Y L E K(E)		173.42	603.6548	1808.958	-0.0083	-4.6	6.75	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
21070	dirMS_041712_NAR_120mM_plus.12253.12253.2	2	5.25	1	3.06E+05		(R)KGDIFL	(R)K/G/D\I/F\L V R(G)		117.15	474.2836	947.567	-0.0074	-7.8	8.75	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
21071	dirMS_041712_NAR_30mM_plus2.21547.21547.2	2	5.25	0	3.34E+05		(R)NSYLEV	(R)N S/Y L/E V|L/L K(L)		167.95	539.8092	1078.614	-0.0032	-2.9	6	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
21072	dirMS_041712_NAR_30mM_plus2.6662.6662.2	2	5.25	0	8.79E+03		(R)DSCPLD	(R)D S C|P L D/C K(V)	C:Carbamidomethylation	88.93	497.7072	994.397	0.0103	10.3	4.21	14431.1	10.95	HUMAN	B4E241	Serine/arginine-rich-splicing factor 3
21073	dirMS_041712_NAR_40mM_plus2.10622.10622.2	2	5.25	0	1.63E+05		(R)LGSVEA	(R)L G|S/V E A P K(T)		128.13	400.7336	800.451	0.0087	10.8	6	17167.5	5.69	HUMAN	F5GWB7	Putative ribosomal RNA methyltransferase NOP2 (Fragment)
21074	dirMS_041712_NAR_40mM_plus2.13452.13452.3	3	5.25	0	2.49E+05		(K)NLPPSG	(K)N L|P P S G\A V P V T G I/P P H V V K(V)		145.22	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
21075	dirMS_041712_NAR_40mM_plus2.7523.7523.2	2	5.25	0	1.89E+05		(R)SGYFDE	(R)S G/Y|F D/E R(Y)		104.25	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
21076	dirMS_041712_NAR_50mM_plus2.15585.15585.3	3	5.25	1	1.01E+06		(R)KVPGVT	(R)K V\P G V T A I\E\L|D/E/D|T G T F R(I)		149.87	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
21077	dirMS_041712_NAR_50mM_plus2.18449.18449.3	3	5.25	0	3.44E+05		(R)VFITDD	(R)V F|I T D/D F H D M/M P K(Y)		164.57	532.581	1595.723	0.0052	3.2	4.41	92752.5	4.76	HUMAN	P14625	Endoplasmin
21078	dirMS_041712_NAR_50mM_plus2.7947.7947.3	3	5.25	1	5.05E+04		(-)MEMGK	(-)M E/M G K/W I H/L E L R(N)		108.27	514.9321	1542.792	-0.0102	-6.6	6.51	14919.8	4.98	HUMAN	O95626	Acidic leucine-rich nuclear phosphoprotein 32 family member D
21079	dirMS_041712_NAR_60mM_plus.8239.8239.3	3	5.25	1	8.27E+05		(R)FEPYAN	(R)F/E|P/Y/A N P T K R(Y)		101.38	408.2176	1222.622	0.0167	13.7	8.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
21080	dirMS_041712_NAR_120mM_minus.11251.11251.3	3	5.24	0	1.74E+05		(R)GFCLPP	(R)G F C L/P/P/H C S R(G)	C:Carbamidomethylation	114.25	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
21081	dirMS_041712_NAR_120mM_minus.11688.11688.3	3	5.24	0	1.17E+05		(R)HQSFVL	(R)H Q\S F V\L|V/G E T G/S G K(T)		117.82	482.5826	1445.738	-0.0051	-3.5	6.75	91730	7.16	HUMAN	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15
21082	dirMS_041712_NAR_120mM_minus.4943.4943.3	3	5.24	1	6.21E+05		(R)AAEEED	(R)A A E E/E D E A/D P K/R(Q)		79.23	453.8716	1359.602	-0.002	-1.5	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
21083	dirMS_041712_NAR_50mM_minus2.13652.13652.3	3	5.24	0	3.35E+05	N153n	(K)InTGMA	(K)I n T/G M A D I/L V/V F A R(G)	n:N-acetylglucosamine (N)	146.07	574.9724	1519.83	203.0725	-4	5.84	54171.7	8.89	HUMAN	P39900	Macrophage metalloelastase
21084	dirMS_041712_NAR_50mM_minus2.8602.8602.3	3	5.24	1	4.70E+04		(R)ELRTFSL	(R)E L/R T F S L/S P D A/P R(L)		115.78	496.9372	1488.781	0.0165	11.1	6.17	98826.2	5.71	HUMAN	Q9UMF0	Intercellular adhesion molecule 5
21085	dirMS_041712_NAR_50mM_minus2.9886.9886.3	3	5.24	1	1.11E+05		(R)VGEPVA	(R)V/G E/P V A L S E E E/R L/K(L)		124.5	519.2824	1555.833	0	0	4.49	8516.9	5.1	HUMAN	E9PIL8	Splicing factor 3B subunit 2 (Fragment)
21086	dirMS_041712_NAR_60mM_minus.10815.10815.3	3	5.24	1	3.89E+05		(K)TAVCDI	(K)T A/V|C D/I P P R G L K(M)	C:Carbamidomethylation	119.88	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
21087	dirMS_041712_NAR_60mM_minus.12151.12151.3	3	5.24	1	9.57E+05		(R)VVDLM	(R)V/V|D L/M/A/H M A S K E(-)		127.78	444.2256	1330.649	0.0129	9.7	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
21088	dirMS_041712_NAR_60mM_minus.15936.15936.3	3	5.24	1	3.61E+05		(K)KANLQI	(K)K A N L Q I D\Q\I/N/T/D L/N L E R(S)		148.13	666.6911	1998.061	-0.0027	-1.3	4.56	227783.5	5.5	HUMAN	P35579	Myosin-9
21089	dirMS_041712_NAR_60mM_minus.18606.18606.3	3	5.24	0	2.81E+05		(K)LHDNLI	(K)L H D N L\I|I/S D L E N T V K(K)		165.82	575.3117	1723.922	-0.0019	-1.1	4.54	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
21090	dirMS_041712_NAR_20mM_plus.10249.10249.2	2	5.24	0	1.19E+05	M189m M	(K)SLAmE	(K)S L A/m/E m V|L/T G\D R(I)	m:Oxidized methionine	143.4	677.8247	1322.644	31.9978	5.9	4.37	31843.3	8.87	HUMAN	P30084	Enoyl-CoA hydratase, mitochondrial
21091	dirMS_041712_NAR_20mM_plus.16918.16918.2	2	5.24	0	8.84E+04		(K)TVDNFV	(K)T/V D N\F/V A/L A T/G E\K(G)		187.57	682.8565	1364.706	0.0001	0.1	4.37	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
21092	dirMS_041712_NAR_20mM_plus.8645.8645.2	2	5.24	0	5.58E+03		(K)GGELVY	(K)G G\E L|V/Y\T D S E A R(D)		129.88	648.8045	1296.607	-0.0049	-3.8	4.14	533778	5.74	HUMAN	Q15149	Plectin
21093	dirMS_041712_NAR_30mM_plus2.4564.4564.2	2	5.24	0	2.94E+05		(R)SMPEQT	(R)S M/P E/Q T G E K(-)		73.53	503.7289	1006.451	-0.0005	-0.5	4.53	12955	9.87	HUMAN	P62888	60S ribosomal protein L30
21094	dirMS_041712_NAR_50mM_plus2.7822.7822.3	3	5.24	1	9.96E+04		(K)ELQAAG	(K)E L Q|A/A G K/S/P E/D L E R(L)		106.57	514.9321	1542.776	0.0059	3.8	4.41	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
21095	dirMS_041712_NAR_50mM_plus2.8078.8078.3	3	5.24	1	1.75E+04	M306m	(K)SQQIAA	(K)S Q Q I A\A L I E/D H m/T/G K R(S)	m:Oxidized methionine	108.38	605.3151	1797.928	16.0032	4.5	6.47	124075.6	5.93	HUMAN	Q92625	Ankyrin repeat and SAM domain-containing protein 1A
21096	dirMS_041712_NAR_50mM_plus2.8887.8887.3	3	5.24	0	3.97E+05		(R)ATQQQ	(R)A T Q Q Q H D F T L\T Q/T/A/D|G R(S)		113.55	639.9699	1917.905	-0.0098	-5.1	5.21	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
21097	dirMS_041712_NAR_60mM_plus.12078.12172.3	3	5.24	1	4.54E+05	T336t	(K)tRVAVYI	(K)t/R/V A V Y I A/K(D)	t:N-acetylglucosamine (T)	120.42	408.5774	1020.62	203.0976	14.9	9.99	117999.2	5.38	HUMAN	Q9BYX4	Interferon-induced helicase C domain-containing protein 1
21098	dirMS_041712_NAR_60mM_plus.13580.13580.3	3	5.24	1	4.97E+06		(R)VVDLM	(R)V/V/D L/M A H M A S K E(-)		127.5	444.2219	1330.649	0.0018	1.3	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
21099	dirMS_041712_NAR_120mM_minus.11076.11076.3	3	5.23	0	5.83E+05		(R)GLHQSI	(R)G L H Q\S I/E/E/F/R(A)		114.27	405.8796	1215.612	0.0126	10.4	5.4	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
21100	dirMS_041712_NAR_30mM_minus2.11480.11480.2	2	5.23	0	1.36E+05		(K)CGDLVF	(K)C/G\D/L V/F/A/K(M)	C:Carbamidomethylation	115.57	455.2306	909.45	0.0041	4.5	5.84	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
21101	dirMS_041712_NAR_60mM_minus.10544.10544.3	3	5.23	0	2.08E+05		(R)LSNLAL	(R)L/S N\L A/L V K/P E K(T)		118.6	404.5829	1211.736	-0.0017	-1.4	8.59	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
21102	dirMS_041712_NAR_60mM_minus.14966.14966.3	3	5.23	1	9.08E+04		(-)MKLNISF	(-)M K L N I S F/P/A/T/G/C Q K(L)	C:Carbamidomethylation	143.78	532.2747	1594.808	0.0016	1	10	10471.9	5.4	HUMAN	A2A3R7	40S ribosomal protein S6
21103	dirMS_041712_NAR_60mM_minus.17099.17099.3	3	5.23	1	3.47E+04		(K)DREGFF	(K)D R E G F\F\T N/G/L/T L/G A K(K)		155.48	542.6145	1625.828	0.0008	0.5	6.07	9954.3	9.57	HUMAN	C9J0J7	Profilin-2
21104	dirMS_041712_NAR_60mM_minus.19268.19268.3	3	5.23	0	3.35E+05		(K)HGATVL	(K)H G A T\V\L T A|L/G G I L K(K)		170.82	450.939	1350.81	-0.0079	-5.9	8.76	8125.3	9.3	HUMAN	B0QYF7	Myoglobin (Fragment)
21105	dirMS_041712_NAR_120mM_plus.7259.7259.3	3	5.23	1	4.42E+05		(K)AQLEPV	(K)A Q/L E/P V A S/P A K K P K(V)		91.1	488.6234	1463.858	-0.0024	-1.6	9.7	533778	5.74	HUMAN	Q15149	Plectin
21106	dirMS_041712_NAR_20mM_plus.11412.11412.2	2	5.23	0	2.16E+05		(R)YALYDA	(R)Y/A|L/Y/D A T Y E T\K(E)		151.1	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
21107	dirMS_041712_NAR_30mM_plus2.14372.14372.2	2	5.23	0	1.13E+04		(R)QLLEEEL	(R)Q L/L/E E/E/L A/R(L)		128.93	550.8009	1100.595	-0.0001	-0.1	4.25	533778	5.74	HUMAN	Q15149	Plectin
21108	dirMS_041712_NAR_30mM_plus2.22727.22727.2	2	5.23	0	2.69E+05		(R)ELSDFIS	(R)E L S/D F|I/S Y L/Q/R(E)		177.22	685.8507	1370.695	-0.0009	-0.7	4.37	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
21109	dirMS_041712_NAR_40mM_plus2.6627.6627.2	2	5.23	0	5.65E+04		(K)AGFAGD	(K)A/G F/A|G D D A P R(A)		98.63	488.728	976.448	0.0004	0.4	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
21110	dirMS_041712_NAR_40mM_plus2.7416.7416.3	3	5.23	0	6.28E+03	T375t	(K)LGSHPH	(K)L G S H P H S t/Y V K(M)	t:Phosphorylated T	104.08	435.8697	1225.632	79.9622	-3.2	8.6	48109.1	5.56	HUMAN	Q96HD1-2	Isoform 2 of Cysteine-rich with EGF-like domain protein 1
21111	dirMS_041712_NAR_40mM_plus2.9974.9974.2	2	5.23	0	2.48E+05		(K)EQFAW	(K)E Q/F/A/W R(H)		122.88	418.706	836.405	-0.0002	-0.3	6.1	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
21112	dirMS_041712_NAR_50mM_plus2.11625.11625.3	3	5.23	1	2.97E+05		(K)VEAQVY	(K)V E|A/Q/V/Y/I L/S K E E G G R(H)		128.78	559.9637	1677.881	-0.0041	-2.4	4.79	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
21113	dirMS_041712_NAR_50mM_plus2.12838.12838.3	3	5.23	1	3.08E+05		(R)FFGDSA	(R)F F/G D S A A\S M A I K N|P K(A)		136.25	528.6008	1583.789	-0.0008	-0.5	8.59	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
21114	dirMS_041712_NAR_50mM_plus2.14112.14112.3	3	5.23	1	4.06E+05		(R)NVIFQP	(R)N V/I/F/Q P/V A E L K K(Q)		142.33	462.6094	1385.815	-0.0015	-1.1	8.59	23167	8.94	HUMAN	B1APP8	6-phosphofructokinase type C
21115	dirMS_041712_NAR_50mM_plus2.14291.14291.3	3	5.23	1	4.62E+05	M26m	(K)GAEEME	(K)G A|E/E|M/E T V I/P V D V m R R(A)	m:Oxidized methionine	143.47	616.6377	1831.904	15.9945	-0.2	4.41	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
21116	dirMS_041712_NAR_50mM_plus2.22304.22304.3	3	5.23	0	1.51E+06		(R)DALSDL	(R)D A|L/S/D L/A L/H/F L/N K(M)		191.8	486.2644	1456.78	-0.0008	-0.6	5.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
21117	dirMS_041712_NAR_50mM_plus2.5994.5994.3	3	5.23	1	2.40E+04		(R)GTDDSP	(R)G T/D D S P K D S Q\E/D|L/Q/E R(H)		95.62	607.2766	1819.794	0.0212	11.6	3.96	23420.8	4.74	HUMAN	Q5H9L2	Transcription elongation factor A protein-like 5
21118	dirMS_041712_NAR_60mM_plus.17452.17452.3	3	5.23	1	3.74E+05		(R)KVPGVT	(R)K\V P G V\T A I E|L/D\E\D T G T F R(I)		148.18	650.0017	1948.002	-0.0117	-6	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
21119	dirMS_041712_NAR_60mM_plus.9080.9080.3	3	5.23	0	2.06E+06		(K)NCPHIV	(K)N C/P H I/V V/G T/P G R(I)	C:Carbamidomethylation	106.13	436.2272	1306.669	-0.0014	-1.1	9.75	28185.1	10.76	HUMAN	B4DIJ6	Spliceosome RNA helicase DDX39B
21120	dirMS_041712_NAR_120mM_minus.11690.11690.3	3	5.22	0	1.09E+05		(K)TGNLGN	(K)T/G\N\L/G N/V/V/H I E\R(F)		117.88	436.9023	1308.702	-0.0095	-7.3	6.41	14478.1	9.37	HUMAN	C9JYQ9	60S ribosomal protein L22-like 1
21121	dirMS_041712_NAR_20mM_minus.12717.12717.2	2	5.22	0	1.88E+05	M179m M	(K)mFVLDE	(K)m F\V|L|D/E A\D E m L S R(G)	m:Oxidized methionine	176.6	794.3534	1555.713	31.9864	-2.1	3.91	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
21122	dirMS_041712_NAR_20mM_minus.8937.8937.2	2	5.22	0	2.78E+05		(R)ALGQN	(R)A L/G/Q|N|P T N A/E V L K(V)		138.8	677.871	1354.733	0.0022	1.6	6.05	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
21123	dirMS_041712_NAR_50mM_minus2.11428.11428.3	3	5.22	1	1.41E+05		(K)MLVSGA	(K)M/L/V/S/G A G D I K L/T K(D)		132.82	444.9227	1332.756	-0.002	-1.5	8.35	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
21124	dirMS_041712_NAR_60mM_minus.18468.18468.3	3	5.22	0	1.13E+04		(R)HLEPAL	(R)H L E/P A L A\F/Q/L E/L/N R(M)		163.17	550.9705	1650.896	0.0007	0.4	5.4	97883.4	6.02	HUMAN	F6QQI9	Acetyl-CoA carboxylase 2
21125	dirMS_041712_NAR_60mM_minus.9287.9287.3	3	5.22	0	4.15E+04		(K)FNQTYQ	(K)F/N Q T Y Q\L/A H\G T A E/E K(M)		111.53	579.614	1736.824	0.0036	2.1	5.4	74230.8	5.34	HUMAN	B1AH89	Tubulin tyrosine ligase-like family, member 12
21126	dirMS_041712_NAR_120mM_plus.18590.18590.4	4	5.22	0	4.36E+04		(R)LGWDP	(R)L G W D P K/P/G E G H/L/D A L L R(G)		150.98	469.253	1873.992	-0.0017	-0.9	5.38	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
21127	dirMS_041712_NAR_120mM_plus.4099.4099.3	3	5.22	1	6.00E+04	M54m	(K)SLDEmE	(K)S/L/D E/m E/K Q Q R(E)	m:Oxidized methionine	68.53	427.2032	1263.6	15.9953	0.3	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
21128	dirMS_041712_NAR_30mM_plus2.16034.16034.2	2	5.22	0	2.88E+05		(R)YSVDIPL	(R)Y/S|V/D I/P L D K(T)		136.3	525.2819	1049.551	0.0052	4.9	4.21	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
21129	dirMS_041712_NAR_30mM_plus2.16804.16804.2	2	5.22	0	3.48E+05		(K)QLQEM	(K)Q L|Q/E/M/L|G L S K(V)		140.83	573.8112	1146.619	-0.0036	-3.1	6	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
21130	dirMS_041712_NAR_30mM_plus2.23478.23478.2	2	5.22	0	9.81E+03		(R)IAIYELLF	(R)I A/I Y E/L L F K(E)		189.98	555.3331	1109.661	-0.0016	-1.4	6	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
21131	dirMS_041712_NAR_40mM_plus2.15978.15978.3	3	5.22	0	6.94E+03		(R)DLKPSN	(R)D L/K P S N\L\L/I/N T T C/D L K(I)	C:Carbamidomethylation	159.45	615.6661	1844.979	0.0051	2.8	5.96	30925	5.63	HUMAN	B3KR49	Mitogen-activated protein kinase 3
21132	dirMS_041712_NAR_40mM_plus2.16004.16004.3	3	5.22	1	1.23E+05		(R)MAREE	(R)M A R E E P A|P A A L/A A A G Q P G G G/R(G)		161.03	660.0113	1977.992	0.027	13.7	5.9	63912.9	6.57	HUMAN	E9PBX2	Acid-sensing ion channel 2
21133	dirMS_041712_NAR_50mM_plus2.16153.16153.3	3	5.22	1	1.50E+06		(K)VTADVI	(K)V/T|A D V/I N A A E K L Q V V/G R(A)		152.23	595.0057	1783.007	-0.0047	-2.6	6.04	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
21134	dirMS_041712_NAR_50mM_plus2.21621.21621.3	3	5.22	1	2.38E+05		(K)LGFAGL	(K)L/G F/A/G L V Q E I S F G T T K D K(M)		184.83	637.6781	1911.022	-0.0025	-1.3	6.07	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
21135	dirMS_041712_NAR_50mM_plus2.7661.7661.3	3	5.22	0	1.57E+04		(R)EQTEGE	(R)E Q/T E/G E Y/S S L E/H E/S A\R(G)		106.15	617.9371	1851.799	-0.0024	-1.3	4.32	42468.2	8.95	HUMAN	O43837	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial
21136	dirMS_041712_NAR_50mM_plus2.7674.7674.3	3	5.22	1	5.25E+04	S583s S587	(K)GLGEGs	(K)G L/G E G s K Q W s S S A P/N L G K(S)	s:Phosphorylated S	106.27	654.9486	1802.903	159.9281	-2.3	8.59	104434.3	6.56	HUMAN	Q02779	Mitogen-activated protein kinase kinase kinase 10
21137	dirMS_041712_NAR_50mM_plus2.8283.8283.3	3	5.22	0	9.05E+04		(K)QQSIAG	(K)Q Q S I/A/G S A/D/S K/P I D V S R(L)		110.42	586.971	1758.898	0.0004	0.2	5.96	34637.3	8.91	HUMAN	Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1
21138	dirMS_041712_NAR_60mM_plus.14697.14697.3	3	5.22	1	5.84E+05		(R)ELAVQI	(R)E L/A V/Q I/Y E E A R K(F)		133.5	483.5949	1448.774	-0.0042	-2.9	4.79	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
21139	dirMS_041712_NAR_60mM_plus.18016.18016.3	3	5.22	1	4.97E+04		(R)ARFEEL	(R)A R F E E\L\N A/D/L F R(G)		151.58	494.2554	1480.754	-0.0027	-1.8	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
21140	dirMS_041712_NAR_120mM_minus.13474.13474.3	3	5.21	1	2.25E+05		(R)VIDRELY	(R)V/I/D R E L\Y\Q Q/L Q/R(G)		128.15	520.955	1560.849	0.0012	0.8	6.04	533778	5.74	HUMAN	Q15149	Plectin
21141	dirMS_041712_NAR_120mM_minus.6035.6035.3	3	5.21	1	2.07E+04		(K)NVICDK	(K)N/V/I/C D/K C/E G R(G)	C:Carbamidomethylation	86.4	417.525	1250.562	-0.0012	-0.9	6.07	45609.1	6.66	HUMAN	P31689	DnaJ homolog subfamily A member 1

21142	dirMS_041712_NAR_40mM_minus2.5402.5402.2	2	5.21	0	1.03E+05		(K)DSYVGD	(K)D S Y|V/G D|E A Q S K(R)		89.65	599.7638	1198.522	-0.0019	-1.6	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
21143	dirMS_041712_NAR_40mM_minus2.9226.9226.3	3	5.21	1	5.15E+03	M331m	(R)YGSDIVF	(R)Y G/S D I/V/P F S K V D E/E Q m K(Y)	m:Oxidized methionine	136.67	663.3223	1971.937	16.0155	10.4	4.32	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
21144	dirMS_041712_NAR_50mM_minus2.9376.9376.3	3	5.21	0	1.54E+05		(R)TPVIDAI	(R)T P/V\I/D/A D K/P/V/S S Q L R(V)		121.28	542.6354	1625.886	0.0059	3.7	5.62	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
21145	dirMS_041712_NAR_60mM_minus.13488.13488.3	3	5.21	1	1.16E+05	M160m	(K)FRQDLm	(K)F R Q\D L m N|I|A/G T T L S S K(L)	m:Oxidized methionine	135.43	599.9744	1781.921	15.9872	-4.3	8.75	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
21146	dirMS_041712_NAR_60mM_minus.14332.14332.3	3	5.21	0	2.62E+05		(R)ILDPHTY	(R)I L/D/P H\T Y P L|A\P(-)		139.9	412.8902	1236.662	-0.0063	-5.1	5.08	8931.3	8.21	HUMAN	E9PCR5	Vasoactive intestinal polypeptide receptor 2
21147	dirMS_041712_NAR_60mM_minus.14356.14356.3	3	5.21	1	3.03E+04		(R)SILKIDD	(R)S I/L K I\D D\V V/N T/R(-)		139.63	458.2637	1372.78	-0.0029	-2.1	5.68	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
21148	dirMS_041712_NAR_60mM_minus.18821.18821.3	3	5.21	0	1.43E+05		(K)VAHALA	(K)V A H A L A\E\G L G|V/I/A C I/G E K(L)	C:Carbamidomethylation	166.95	603.3262	1807.974	-0.0094	-5.2	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
21149	dirMS_041712_NAR_60mM_minus.18833.18833.3	3	5.21	1	2.67E+05		(K)NAAGAL	(K)N A A/G A/L D/L L K/E/L/K(N)		166.87	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
21150	dirMS_041712_NAR_60mM_minus.7263.7263.3	3	5.21	0	4.40E+04	K306k	(R)GGSPLIL	(R)G G S P L I L G/D/P L H/k(Q)	k:Ubiquitin-K	99.28	473.258	1303.737	114.0226	-14.3	6.74	35128.2	9.07	HUMAN	Q1HG44	Dual oxidase maturation factor 2
21151	dirMS_041712_NAR_20mM_plus.17587.17587.2	2	5.21	0	8.56E+04		(R)GDGPICI	(R)G D/G|P I/C/L V L|A/P T R(E)	C:Carbamidomethylation	193.13	684.8681	1368.73	-0.0015	-1.1	5.84	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
21152	dirMS_041712_NAR_20mM_plus.8092.8092.2	2	5.21	0	1.06E+05		(K)VTEDTS	(K)V/T/E/D T/S S V L R(S)		126.02	553.7889	1106.569	0.0017	1.6	4.37	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
21153	dirMS_041712_NAR_20mM_plus.9881.9881.3	3	5.21	1	6.34E+04	M256m N2	(R)EAmLKV	(R)E A m L/K V I n/R(K)	m:Oxidized methionine n:N-	138.75	431.5577	1073.614	219.045	-22.7	8.85	51697.7	9.58	HUMAN	A8MXT2	Melanoma-associated antigen B17
21154	dirMS_041712_NAR_30mM_plus2.9681.9681.2	2	5.21	0	1.36E+06		(R)QLSSGV	(R)Q L/S/S G V/S\E I/R(H)		104.9	538.2855	1075.574	-0.0105	-9.8	6	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
21155	dirMS_041712_NAR_40mM_plus2.11581.11581.2	2	5.21	0	2.17E+05		(R)NLLSVA	(R)N/L/L/S/V A Y K(N)		134.93	454.2649	907.525	-0.0022	-2.4	8.59	18789.1	6.77	HUMAN	A2IDB2	14-3-3 protein eta (Fragment)
21156	dirMS_041712_NAR_40mM_plus2.19276.19276.3	3	5.21	0	1.75E+05		(R)LQQAQL	(R)L Q/Q\A Q L Y/P I A I F/I K/P K(S)		180.67	624.3737	1871.115	-0.0088	-4.7	9.7	94175.4	6.59	HUMAN	Q5JUW8	Discs, large homolog 3 (Neuroendocrine-dlg, Drosophila)
21157	dirMS_041712_NAR_40mM_plus2.5312.5312.2	2	5.21	0	1.31E+05		(R)DYSGYQ	(R)D Y/S/G Y Q R(D)		87.43	444.6967	888.385	0.0015	1.7	5.83	70523.3	4.94	HUMAN	G3V153	Caprin-1
21158	dirMS_041712_NAR_40mM_plus2.5381.5381.2	2	5.21	0	1.37E+05		(R)GSNGAF	(R)G S/N/G A F/Y K(A)		89.07	422.2033	843.399	-0.0002	-0.3	8.59	66105.7	7.3	HUMAN	A8MQB8	Fragile X mental retardation protein 1
21159	dirMS_041712_NAR_50mM_plus2.10426.10426.2	2	5.21	1	1.53E+06		(R)DGKLVS	(R)D/G K/L V|S E S S D V\L/P K(-)		122.85	737.3925	1473.78	-0.0018	-1.2	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
21160	dirMS_041712_NAR_50mM_plus2.13020.13020.3	3	5.21	1	4.00E+05		(K)DMESPT	(K)D M|E S/P T K L/D V T L A K(D)		136.83	516.6001	1547.799	-0.0128	-8.3	4.56	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
21161	dirMS_041712_NAR_60mM_plus.8486.8486.2	2	5.21	0	4.27E+05		(R)FACHSA	(R)F A/C/H/S A S L T V R(N)	C:Carbamidomethylation	102.73	624.8118	1248.615	0.001	0.8	9.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
21162	dirMS_041712_NAR_120mM_minus.11090.11090.3	3	5.2	0	3.10E+05		(-)XCSFGVC	(-)X C\S F G V Q/L/M G/K(W)	C:Carbamidomethylation	114.05	413.885	1239.622	0.018	14.5	8.75	30682.5	9.45	HUMAN	H0Y355	High affinity immunoglobulin gamma Fc receptor IB (Fragment)
21163	dirMS_041712_NAR_120mM_minus.6235.6235.3	3	5.2	1	8.56E+03	K756k	(K)LSHGDY	(K)L S H/G D/Y/Y R k(R)	k:Ubiquitin-K	86.52	418.2046	1138.564	114.0353	-6.1	8.5	244013.5	5.54	HUMAN	Q5TH69	Brefeldin A-inhibited guanine nucleotide-exchange protein 3
21164	dirMS_041712_NAR_120mM_minus.7430.7430.3	3	5.2	0	1.20E+05		(R)NIDEHA	(R)N I|D E/H/A N E D V/E R(M)		94.67	480.884	1440.635	0.0025	1.7	4.17	22768.7	8.94	HUMAN	P61026	Ras-related protein Rab-10
21165	dirMS_041712_NAR_30mM_minus2.11278.11278.2	2	5.2	0	2.06E+05		(K)GEIHGG	(K)G E/I H/G G S N G I Y K(G)		114.72	616.3091	1231.607	0.0043	3.5	6.75	66346.9	7.94	HUMAN	P08842	Steryl-sulfatase
21166	dirMS_041712_NAR_30mM_minus2.19041.19041.2	2	5.2	0	1.68E+05		(R)SNPSVL	(R)S N/P S/V L Q/G L L R(I)		158.58	592.3428	1183.679	-0.001	-0.9	9.47	80859.6	6.43	HUMAN	B4DPF6	E3 ubiquitin-protein ligase UBR4
21167	dirMS_041712_NAR_30mM_minus2.7989.7989.2	2	5.2	0	1.83E+05		(K)GSGTAE	(K)G S|G/T/A/E V/E L K(K)		98.32	495.7528	990.51	-0.0119	-12	4.53	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
21168	dirMS_041712_NAR_50mM_minus2.12933.12933.3	3	5.2	0	1.28E+05		(K)ITHLSTL	(K)I T H L S T L Q V/G S L/N V K(C)		141.7	537.3126	1609.927	-0.0039	-2.4	8.76	26760.1	8.93	HUMAN	H3BPK3	Hydroxyacylglutathione hydrolase, mitochondrial (Fragment)
21169	dirMS_041712_NAR_50mM_minus2.12965.12965.3	3	5.2	0	2.35E+04	T1417t	(K)VDDDLG	(K)V D D/D L G t|I E/S L E E A K(K)	t:N-acetylglucosamine (T)	141.45	612.9482	1633.78	203.0497	-16.1	3.71	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
21170	dirMS_041712_NAR_50mM_minus2.14166.14166.3	3	5.2	0	2.61E+05		(R)TIQVEN	(R)T I|Q/V E N S H L I|L T\G A/G A L N K(V)		149.02	660.367	1979.092	-0.0056	-2.8	6.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
21171	dirMS_041712_NAR_60mM_minus.16820.16820.3	3	5.2	1	2.55E+05		(R)YRVPDV	(R)Y R V P D\V L\V A/D/P P I A R(L)		154.5	560.9843	1680.943	-0.0048	-2.9	5.96	96499.9	5.43	HUMAN	F5H6X6	Neutral alpha-glucosidase AB
21172	dirMS_041712_NAR_60mM_minus.19218.19218.3	3	5.2	0	3.35E+05		(K)HGATVL	(K)H G A T V|L|T/A|L/G G I L K(K)		170.82	450.939	1350.81	-0.0079	-5.9	8.76	8125.3	9.3	HUMAN	B0QYF7	Myoglobin (Fragment)
21173	dirMS_041712_NAR_60mM_minus.6411.6411.3	3	5.2	1	1.75E+05		(K)IYEDGD	(K)I/Y E/D/G D D D/M K/R(T)		93.87	452.8686	1356.574	0.0176	13	4.03	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
21174	dirMS_041712_NAR_120mM_plus.12162.12162.3	3	5.2	0	4.94E+05		(R)SSHYDEI	(R)S S H Y D E\L\L|A/A/E A R(A)		117.35	487.9048	1461.697	0.003	2.1	4.65	26398.4	5.21	HUMAN	H7C597	Staphylococcal nuclease domain-containing protein 1 (Fragment)
21175	dirMS_041712_NAR_20mM_plus.13966.13966.2	2	5.2	0	9.54E+04	M2232m	(R)SLLVNPE	(R)S L L V/N|P E G/P/T L m/R(L)	m:Oxidized methionine	167.48	721.8852	1426.772	15.9909	-2.8	5.72	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
21176	dirMS_041712_NAR_30mM_plus2.16915.16915.3	3	5.2	0	5.02E+05	M313m	(R)TVQSLEI	(R)T V\Q\S L E I D/L/D S m/R(N)	m:Oxidized methionine	142.1	508.2535	1506.747	15.9991	2.8	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
21177	dirMS_041712_NAR_30mM_plus2.19577.19577.2	2	5.2	0	1.94E+05		(K)NFSGAE	(K)N/F|S/G A E L E/G/L V R(A)		155.72	646.3361	1291.664	0.0008	0.6	4.53	71924.9	6.25	HUMAN	B4DFA2	Vesicle-fusing ATPase
21178	dirMS_041712_NAR_30mM_plus2.21180.21180.2	2	5.2	0	1.81E+05		(R)QTLMW	(R)Q T|L/M/W/S A T W/P K(E)		165.72	674.8389	1348.672	-0.0013	-1	8.75	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
21179	dirMS_041712_NAR_30mM_plus2.22326.22326.3	3	5.2	0	5.24E+05		(R)VGNLGL	(R)V G N L G L A/T S\F/F N E R(N)		172.8	508.9306	1524.781	-0.0033	-2.1	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
21180	dirMS_041712_NAR_30mM_plus2.5861.5861.2	2	5.2	0	1.94E+05		(R)VISEYQK	(R)V/I/S E Y/Q K(L)		85.45	433.7317	866.462	-0.0057	-6.6	5.97	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
21181	dirMS_041712_NAR_30mM_plus2.8099.8099.2	2	5.2	0	3.09E+05		(R)MYSYPA	(R)M/Y|S Y/P A\R(V)		95.77	444.2085	887.408	0.0017	1.9	8.35	32085.2	8.93	HUMAN	B4DY08	Heterogeneous nuclear ribonucleoproteins C1/C2
21182	dirMS_041712_NAR_40mM_plus2.16246.16246.3	3	5.2	0	2.72E+05		(K)VAIVKPC	(K)V/A|I V K P G V\P|M E I V L/N K(E)		161.6	569.6778	1707.024	-0.0049	-2.9	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
21183	dirMS_041712_NAR_40mM_plus2.17434.17434.3	3	5.2	0	1.53E+05		(R)VYAILTH	(R)V Y/A I L T H G I/F/S G P A I S\R(I)		169.28	601.3376	1801.996	0.0023	1.3	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
21184	dirMS_041712_NAR_50mM_plus2.10580.10580.3	3	5.2	1	2.25E+04		(R)MQKEIT	(R)M Q/K E I T A/L A|P/S/T M K(I)		123	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
21185	dirMS_041712_NAR_50mM_plus2.12306.12306.3	3	5.2	1	3.20E+05		(K)LSAEKVE	(K)L/S A E K/V|E I/A T/L T R(E)		132.33	477.6113	1430.821	-0.002	-1.4	6.14	26661.1	7.81	HUMAN	H0YL69	Proteasome subunit alpha type (Fragment)
21186	dirMS_041712_NAR_50mM_plus2.14172.14172.3	3	5.2	1	1.04E+06		(K)ALQQGL	(K)A L/Q Q G L/V/G L E/L K E K(L)		142.23	509.3022	1525.895	-0.0028	-1.8	6.18	266161	5.68	HUMAN	E9PPU0	Epiplakin
21187	dirMS_041712_NAR_50mM_plus2.14191.14191.3	3	5.2	0	5.08E+05		(K)VTHAVV	(K)V T H A V V T V/P A/Y/F N D A\Q R(Q)		142.7	629.9955	1887.971	0.0008	0.4	6.71	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
21188	dirMS_041712_NAR_50mM_plus2.21333.21333.3	3	5.2	1	5.25E+05	M145m	(R)GVmLA	(R)G V\m|L A V/D A/V/I A E L K K(Q)	m:Oxidized methionine	182.27	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
21189	dirMS_041712_NAR_50mM_plus2.9812.9812.3	3	5.2	1	1.96E+05		(K)GAAPN	(K)G A\A/P/N V V/Y T Y T G K R(I)		119.35	499.5943	1496.786	-0.0173	-11.5	9.7	11682.5	3.98	HUMAN	F8W084	Cleavage and polyadenylation-specificity factor subunit 6
21190	dirMS_041712_NAR_60mM_plus.14742.14742.3	3	5.2	1	5.05E+05		(K)NKDQG	(K)N K D Q G T Y E D/Y/V/E/G L R(V)		133.62	596.2816	1786.824	0.006	3.4	4.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
21191	dirMS_041712_NAR_120mM_minus.14562.14562.4	4	5.19	1	2.55E+06		(K)LDKSQI	(K)L D K S Q I H D I V L\V/G/G S T R(I)		133.8	460.2577	1838.013	-0.0041	-2.2	6.75	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
21192	dirMS_041712_NAR_120mM_minus.9189.9189.3	3	5.19	1	2.08E+05		(R)EQAEEE	(R)E Q/A/E E E R Y F R(A)		105.05	452.8778	1356.618	0.001	0.7	4.5	12248.6	9.34	HUMAN	Q9UII2	ATPase inhibitor, mitochondrial
21193	dirMS_041712_NAR_30mM_minus2.6253.6253.2	2	5.19	0	4.16E+05		(K)YAEAVTI	(K)Y/A|E A V T R(A)		87.57	405.2098	809.415	-0.0029	-3.5	6	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
21194	dirMS_041712_NAR_50mM_minus2.16079.16079.3	3	5.19	1	1.21E+05		(R)NTISLLV	(R)N T I/S L L/V/A G L K K(E)		159.28	419.5997	1256.794	-0.0091	-7.2	10	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
21195	dirMS_041712_NAR_50mM_minus2.17862.17862.3	3	5.19	0	1.43E+05		(K)TTLLNYI	(K)T T/L/L\N Y/I/L T E Q H S K(R)		170.55	554.3024	1660.891	0.0022	1.3	6.41	42238.2	4.88	HUMAN	B4DNG9	COBW domain-containing protein 3
21196	dirMS_041712_NAR_60mM_minus.11346.11346.3	3	5.19	0	1.16E+05		(K)SFTNSFS	(K)S F/T/N S/F S L T I H/R(R)		123.13	470.5828	1409.717	0.0167	11.8	9.49	49881.2	9.85	HUMAN	Q8N988	Zinc finger protein 557
21197	dirMS_041712_NAR_60mM_minus.13168.13168.3	3	5.19	1	3.55E+05	S24s	(K)LGLPKSS	(K)L G|L/P/K S/S E s A/L K(C)	s:Phosphorylated S	132.88	437.2334	1229.71	79.9757	7.1	8.59	46004.3	9.57	HUMAN	Q14722-3	Isoform KvB1.2 of Voltage-gated potassium channel subunit beta-1
21198	dirMS_041712_NAR_60mM_minus.19230.19230.3	3	5.19	1	4.87E+04		(K)TFVNITP	(K)T\F\V/N I T P A E V/G V L V/G K D R(S)		170.42	639.0293	1915.065	0.0086	4.5	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
21199	dirMS_041712_NAR_60mM_minus.8547.8606.3	3	5.19	1	1.25E+05		(R)QLQLAC	(R)Q\L Q/L A Q/E A/A Q K R(L)		107.87	461.9241	1383.77	-0.0125	-9.1	8.75	533778	5.74	HUMAN	Q15149	Plectin
21200	dirMS_041712_NAR_120mM_plus.9693.9693.2	2	5.19	1	3.82E+05		(R)KNGFVV	(R)K|N G/F V V/L|K(G)		104.52	452.7836	904.562	-0.0015	-1.7	10	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
21201	dirMS_041712_NAR_20mM_plus.11601.11601.2	2	5.19	0	8.93E+04		(R)AQAALA	(R)A Q|A\A L|A V N I S/A A R(G)		153.17	628.3565	1255.712	-0.006	-4.8	9.79	58479.6	6.23	HUMAN	P40227	T-complex protein 1 subunit zeta
21202	dirMS_041712_NAR_20mM_plus.15896.15896.2	2	5.19	0	1.02E+04		(K)ALTLIAG	(K)A L/T\L/I|A\G S P L/K(I)		180.78	542.3395	1083.677	-0.0055	-5.1	8.8	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
21203	dirMS_041712_NAR_20mM_plus.16096.16096.2	2	5.19	0	4.77E+04		(K)DAGTIA	(K)D A\G/T\I/A/G L/N/V L R(I)		182.22	600.3422	1199.674	0.0029	2.4	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
21204	dirMS_041712_NAR_40mM_plus2.10684.10684.3	3	5.19	0	6.79E+04	M35m	(K)AASDIAr	(K)A A/S D|I/A m T E L P P T H P I R(L)	m:Oxidized methionine	128.38	612.652	1819.937	16.0044	5.1	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
21205	dirMS_041712_NAR_40mM_plus2.10998.10998.2	2	5.19	0	7.20E+03		(R)GDFCIQ	(R)G D F/C/I/Q/V/G R(-)	C:Carbamidomethylation	131.12	526.2539	1051.499	0.0016	1.5	5.84	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
21206	dirMS_041712_NAR_40mM_plus2.6567.6567.2	2	5.19	0	2.94E+04		(K)AGFAGD	(K)A G F/A/G/D D/A/P R(A)		97.9	488.728	976.448	0.0004	0.4	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
21207	dirMS_041712_NAR_50mM_plus2.11328.11328.3	3	5.19	1	1.17E+06		(K)VGDKVL	(K)V G D K V L|L/P E Y/G G T K(V)		126.95	492.6069	1475.81	-0.0043	-2.9	6.04	5189.9	4.56	HUMAN	B8ZZ54	10 kDa heat shock protein, mitochondrial
21208	dirMS_041712_NAR_50mM_plus2.18881.18881.3	3	5.19	0	2.77E+05		(K)LAKPLSS	(K)L A K P L S S\L T/P L/I/M A A K(E)		167.55	552.004	1653.997	0.0003	0.2	10	24711.4	5.19	HUMAN	H7C1X3	PAK-2p34 (Fragment)
21209	dirMS_041712_NAR_50mM_plus2.18943.18943.3	3	5.19	1	4.36E+05		(K)AAIDWF	(K)A/A/I/D W/F D G K E F S G N P I K(V)		167.18	632.3186	1894.933	0.0079	4.1	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
21210	dirMS_041712_NAR_50mM_plus2.19413.19413.3	3	5.19	0	1.72E+05		(R)LHPVILA	(R)L H P/V I L A S\I V/D S Y E R(R)		169.87	571.3163	1711.938	-0.0034	-2	5.32	39260.1	5.25	HUMAN	B3KSH1	Eukaryotic translation initiation factor 3 subunit F
21211	dirMS_041712_NAR_50mM_plus2.7837.7837.3	3	5.19	0	1.21E+05		(K)EAPPME	(K)E A|P/P/M E K/P E V V K(T)		106.95	451.9073	1353.708	-0.0009	-0.7	4.79	14798.1	10.35	HUMAN	K7EJ78	40S ribosomal protein S15 (Fragment)
21212	dirMS_041712_NAR_60mM_plus.11409.11409.2	2	5.19	0	8.24E+05		(R)TICSHVC	(R)T I|C S|H/V/Q N M\I K(G)	C:Carbamidomethylation	117.02	665.8295	1330.661	-0.0089	-6.7	8.44	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
21213	dirMS_041712_NAR_120mM_minus.10536.10536.2	2	5.18	0	1.38E+04		(R)VHIEIGP	(R)V/H/I E|I/G P D G R(V)		111.72	546.7932	1092.58	-0.0005	-0.5	5.32	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
21214	dirMS_041712_NAR_120mM_minus.17794.17794.4	4	5.18	1	3.24E+05		(K)TLPAGVI	(K)T\L\P\A G V L R/E G A V Q F L/H R(G)		151.57	466.7676	1864.055	-0.0066	-3.5	9.29	26988.7	10.68	HUMAN	Q8TF63	Dendritic cell nuclear protein 1
21215	dirMS_041712_NAR_120mM_minus.9815.9815.4	4	5.18	0	1.86E+05		(R)TSSAQV	(R)T S\S A Q V E G G V/H S/L/H S Y E K(R)		107.95	479.7393	1915.914	0.0209	10.9	5.94	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
21216	dirMS_041712_NAR_20mM_minus.10193.10193.2	2	5.18	0	2.43E+04		(R)IAAQTLI	(R)I/A|A/Q/T L|L G T A K(M)		151.42	543.825	1086.652	-0.009	-8.3	8.75	14626.5	7.07	HUMAN	B5MD87	Pyrroline-5-carboxylate reductase 3
21217	dirMS_041712_NAR_30mM_minus2.18375.18375.2	2	5.18	0	3.04E+04		(R)YEFGIFN	(R)Y E/F G\I F/N Q K(I)		154.53	573.2849	1145.563	-0.0001	-0.1	6	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
21218	dirMS_041712_NAR_30mM_minus2.8236.8236.2	2	5.18	0	4.05E+05		(K)SFQQSSI	(K)S F\Q\Q/S|S L/S R(D)		99.87	520.2591	1039.517	-0.0058	-5.6	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
21219	dirMS_041712_NAR_40mM_minus2.7885.7885.2	2	5.18	0	1.59E+05		(R)IFNSFVY	(R)I F|N S/F V Y T E K(I)		125.98	624.3175	1247.631	-0.0029	-2.4	6	144341.1	5.97	HUMAN	Q5VU97	VWFA and cache domain-containing protein 1
21220	dirMS_041712_NAR_50mM_minus2.14345.14345.3	3	5.18	1	2.52E+05		(R)GDVVPK	(R)G D V\V/P K D V\N\A A/I A/T I K(T)		150.27	537.6375	1610.911	-0.0133	-8.2	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
21221	dirMS_041712_NAR_50mM_minus2.16451.16451.3	3	5.18	0	1.75E+05	M1m	(-)mKPLVVI	(-)m K P L\V V F\V|L/G/G P G|A/G K(G)	m:Oxidized methionine	161.27	529.3077	1569.919	15.99	-3.1	10	22450.2	5.44	HUMAN	P30085	UMP-CMP kinase
21222	dirMS_041712_NAR_50mM_minus2.18208.18208.3	3	5.18	1	2.31E+05		(K)LKEAELL	(K)L K E A E L\L|E|P L\M/P A I R(A)		172.78	574.9957	1722.982	-0.0097	-5.6	4.79	56164.6	6.01	HUMAN	E9PP73	Coatomer subunit beta (Fragment)
21223	dirMS_041712_NAR_50mM_minus2.18680.18680.3	3	5.18	0	3.42E+05		(R)AGKPVI(	(R)A G K\P V I C|A T/Q|M/L E S M I K(K)	C:Carbamidomethylation	180.9	626.3309	1876.969	0.0088	4.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
21224	dirMS_041712_NAR_50mM_minus2.6906.6906.3	3	5.18	1	6.78E+04		(R)TESTPIT	(R)T E/S T/P/I\T/A V/K Q P E\K(V)		105.98	510.2775	1528.822	-0.0038	-2.5	5.81	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
21225	dirMS_041712_NAR_50mM_minus2.7311.7311.3	3	5.18	1	1.49E+05		(R)IAECSSC	(R)I A|E C S S/Q L A/E E E E K/A K(N)	C:Carbamidomethylation	108.03	607.9557	1821.853	-0.0009	-0.5	4.32	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
21226	dirMS_041712_NAR_50mM_minus2.9103.9103.3	3	5.18	1	4.63E+04	M621m	(R)mVDVVI	(R)m\V/D V|V/E K E D/V N E A I R(L)	m:Oxidized methionine	120.13	587.962	1745.874	15.9976	1.5	4.18	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
21227	dirMS_041712_NAR_120mM_plus.12814.12814.2	2	5.18	0	4.99E+05		(K)HLSVND	(K)H|L|S V/N D/L P V G R(S)		119.88	603.8321	1206.659	-0.002	-1.7	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
21228	dirMS_041712_NAR_120mM_plus.5372.5372.3	3	5.18	0	5.66E+04	M46m M4	(R)HQGVm	(R)H Q G V m|V/G/m G Q K(D)	m:Oxidized methionine	82.17	401.8588	1171.571	31.9908	0.8	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
21229	dirMS_041712_NAR_30mM_plus2.11792.11792.2	2	5.18	0	4.85E+05		(R)AMGEQ	(R)A/M/G E/Q A V/A L A/R(A)		114.22	558.7944	1116.583	-0.0015	-1.3	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
21230	dirMS_041712_NAR_30mM_plus2.14242.14242.2	2	5.18	0	5.73E+05		(K)CCSGAII	(K)C C|S/G A\I I V L T/K(S)	C:Carbamidomethylation	128.2	611.3189	1221.633	-0.0025	-2	8.75	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
21231	dirMS_041712_NAR_40mM_plus2.13371.13371.3	3	5.18	0	2.49E+05		(R)LSAMLV	(R)L S A M L/V/P V\T/P E V K P K(R)		145.73	536.9848	1608.939	0.0005	0.3	8.59	31524.1	4.5	HUMAN	P82970	High mobility group nucleosome-binding domain-containing protein 5
21232	dirMS_041712_NAR_40mM_plus2.14183.14183.3	3	5.18	1	1.19E+05		(K)IMASSPI	(K)I/M|A/S S P D/M D/L A T V S A L R K(M)		150.62	635.9975	1905.977	0.0007	0.4	5.96	36208.1	7.21	HUMAN	B4DMU0	Pyrroline-5-carboxylate reductase
21233	dirMS_041712_NAR_50mM_plus2.16849.16849.3	3	5.18	0	2.32E+05		(K)GFDILGI	(K)G F|D I L/G I/K/P V Q R(M)		156.23	448.2656	1342.784	-0.0019	-1.4	8.75	52817.9	6.2	HUMAN	F5H3T8	Arginine--tRNA ligase, cytoplasmic
21234	dirMS_041712_NAR_50mM_plus2.20393.20393.3	3	5.18	0	1.29E+05		(R)AFIDPLG	(R)A F/I/D/P L G L P D R P F Y R(H)		175.4	592.986	1776.943	0.0003	0.2	6	84557.3	6.5	HUMAN	Q04609	Glutamate carboxypeptidase 2
21235	dirMS_041712_NAR_50mM_plus2.20779.20779.3	3	5.18	0	2.02E+05		(K)HSQFIG	(K)H S Q F\I/G\Y|P I/T L F V E K(E)		178.8	593.6536	1778.948	-0.0013	-0.8	6.75	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
21236	dirMS_041712_NAR_50mM_plus2.21313.21313.3	3	5.18	1	1.80E+05		(K)ALFEEVF	(K)A L/F/E E V P E L/L T E A E K K(E)		182.43	615.9987	1845.984	-0.0029	-1.6	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
21237	dirMS_041712_NAR_50mM_plus2.6182.6182.3	3	5.18	1	1.11E+05	M286m M	(R)VVDLmA	(R)V V/D L/m A H m A S K/E(-)	m:Oxidized methionine	96.87	454.8843	1330.649	31.989	-0.6	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
21238	dirMS_041712_NAR_50mM_plus2.8991.8991.3	3	5.18	0	1.80E+05		(K)TPVEPE	(K)T\P V/E P E/V/A I H/R(I)		113.98	416.5627	1247.674	-0.0007	-0.6	5.37	5429.1	9.6	HUMAN	E5RIP1	40S ribosomal protein S20
21239	dirMS_041712_NAR_60mM_plus.14015.14015.3	3	5.18	1	1.00E+06		(K)TTVKDLS	(K)T|T\V K D L S E|L/G S V/R(T)		129.85	468.9268	1404.769	-0.0034	-2.4	5.74	533778	5.74	HUMAN	Q15149	Plectin
21240	dirMS_041712_NAR_60mM_plus.8913.8913.3	3	5.18	0	1.59E+06		(K)EFHLNES	(K)E F H L N\E S/G D/P/S S K(S)		105.52	482.8882	1446.65	0.0005	0.3	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
21241	dirMS_041712_NAR_120mM_minus.15847.15847.3	3	5.17	1	1.98E+05		(R)TSFLDD	(R)T/S/F L|D D/A/F\R K(N)		140.05	400.5402	1199.605	0.0005	0.4	5.62	21195.7	6.97	HUMAN	H0YJ21	Cytoplasmic dynein 1 heavy chain 1 (Fragment)
21242	dirMS_041712_NAR_120mM_minus.8495.8495.3	3	5.17	1	4.66E+05		(R)QREVTL	(R)Q R E\V\T|L/G Q V/A K(L)		100.85	410.2375	1228.701	-0.0029	-2.3	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
21243	dirMS_041712_NAR_30mM_minus2.11549.11549.2	2	5.17	0	1.98E+05	M39m	(K)mFLYAD	(K)m F/L|Y/A D/N E D R(A)	m:Oxidized methionine	116.02	645.2795	1273.552	16	3.9	4.03	24724.1	5.17	HUMAN	E7ETQ7	Vacuolar protein sorting-associated protein VTA1 homolog
21244	dirMS_041712_NAR_40mM_minus2.10353.10353.3	3	5.17	0	4.13E+03		(-)XTPLTLA	(-)X T/P L T L A/A Q L D D S V/E V I K(A)		145.02	642.6926	1926.079	-0.0161	-8.4	4.03	11907.3	5.92	HUMAN	H7BZP8	SH3 and multiple ankyrin repeat domains protein 2 (Fragment)
21245	dirMS_041712_NAR_40mM_minus2.15081.15081.3	3	5.17	0	1.44E+05		(K)LFLFHTS	(K)L F L F H T S L|P|I/A/E|A P G K(L)		173.92	580.9924	1740.968	-0.0057	-3.3	6.75	108105.4	6.57	HUMAN	E7EP00	Protein transport protein Sec24C
21246	dirMS_041712_NAR_50mM_minus2.14235.14235.3	3	5.17	1	1.56E+05		(K)KGVNLP	(K)K G V N L P G\A A\V/D|L/P A V S E K(D)		148.73	588.9987	1764.985	-0.0039	-2.2	6.07	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
21247	dirMS_041712_NAR_50mM_minus2.14519.14519.3	3	5.17	0	4.40E+05		(R)QVLIASH	(R)Q V|L/I/A S H L/P S Y E L R(H)		150.95	542.6354	1625.901	-0.0093	-5.7	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
21248	dirMS_041712_NAR_50mM_minus2.15474.15474.3	3	5.17	0	7.78E+04		(R)DLTPEHI	(R)D L/T P/E/H L/P L L R(N)		155.98	435.2497	1303.737	-0.0023	-1.8	5.32	38779.2	5.93	HUMAN	Q96C86	m7GpppX diphosphatase
21249	dirMS_041712_NAR_50mM_minus2.17849.17849.3	3	5.17	0	4.42E+04		(K)EAAASG	(K)E A A A S G/L P L/M V I I H K(S)		170.42	517.2991	1549.877	0.0057	3.7	6.85	19376.6	5.25	HUMAN	O95881	Thioredoxin domain-containing protein 12
21250	dirMS_041712_NAR_50mM_minus2.9935.9935.3	3	5.17	0	1.36E+05	M392m	(K)EmNPAL	(K)E m N|P A/L G/I D C L H K(G)	C:Carbamidomethylation m:Oxid	125.37	505.2416	1497.719	15.9914	-2.3	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon

21251	dirMS_041712_NAR_60mM_minus.19272.19272.3	3	5.17	0	3.35E+05		(K)HGATVL	(K)H G A\T V\L T/A/L/G G I L K(K)		170.82	450.939	1350.81	-0.0079	-5.9	8.76	8125.3	9.3	HUMAN	B0QYF7	Myoglobin (Fragment)
21252	dirMS_041712_NAR_120mM_plus.6489.6489.2	2	5.17	0	5.24E+05	M46m	(R)HQGVm	(R)H/Q|G V|m/V G M\G Q K(D)	m:Oxidized methionine	87.48	594.2868	1171.571	15.9953	0.3	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
21253	dirMS_041712_NAR_120mM_plus.9956.9956.2	2	5.17	0	5.40E+05	Y617y	(K)LDFyGG	(K)L D|F|y G G A/M A S W E K(A)	y:Phosphorylated Y	105.22	777.8095	1474.667	79.9446	-14	4.37	117469.2	6.33	HUMAN	Q9NPP4	NLR family CARD domain-containing protein 4
21254	dirMS_041712_NAR_20mM_plus.11068.11068.2	2	5.17	0	2.02E+04		(K)VQTLSN	(K)V Q|T/L/S N Q/P L L/K(S)		148.5	620.86	1240.726	-0.0132	-10.7	8.72	17549.1	10.39	HUMAN	E5RFJ3	DBIRD complex subunit KIAA1967 (Fragment)
21255	dirMS_041712_NAR_20mM_plus.14717.14717.2	2	5.17	0	1.36E+04		(R)ASLEAAI	(R)A S/L E A A/I/A|D A E|Q R(G)		173.07	672.8417	1344.675	0.0007	0.5	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
21256	dirMS_041712_NAR_20mM_plus.18184.18184.2	2	5.17	0	1.14E+04		(K)AIDLFTD	(K)A I/D\L/F T D A I K(L)		197.1	553.8073	1106.609	-0.0019	-1.7	4.21	18141.9	4.7	HUMAN	F6VDH7	Hsc70-interacting protein (Fragment)
21257	dirMS_041712_NAR_20mM_plus.8607.8607.2	2	5.17	2	1.10E+04		(K)ESPKAGI	(K)E/S/P/K/A G K S G K(S)		129.63	494.7737	988.542	-0.0021	-2.1	9.7	64633.4	6.29	HUMAN	F5GWP3	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform
21258	dirMS_041712_NAR_20mM_plus.9417.9417.2	2	5.17	0	6.69E+04		(K)TGQEIP	(K)T G Q|E/I/P V N V R(F)		135.92	556.8027	1112.606	-0.0077	-6.9	5.66	28051.5	4.98	HUMAN	J3QKT2	Cytosolic non-specific dipeptidase (Fragment)
21259	dirMS_041712_NAR_20mM_plus.9634.9634.2	2	5.17	0	1.20E+05		(K)VAGQD	(K)V/A/G Q/D G S V V\Q\F K(I)		138.03	617.8225	1234.643	-0.0049	-4	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
21260	dirMS_041712_NAR_30mM_plus2.21628.21628.2	2	5.17	0	1.34E+05		(K)EVLAELE	(K)E V/L/A/E L E/A L E R(R)		168.87	636.3523	1271.684	0.0132	10.4	4.09	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
21261	dirMS_041712_NAR_30mM_plus2.21705.21705.2	2	5.17	0	1.33E+05		(R)NSILAQ	(R)N/S I\L\A/Q V L/D Q S A R(A)		169.78	707.8889	1414.765	0.0057	4	5.84	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
21262	dirMS_041712_NAR_30mM_plus2.7548.7548.2	2	5.17	0	3.61E+05		(R)MNEAF	(R)M/N|E\A/F G D/T K(F)		93.75	506.7256	1012.44	0.0035	3.5	4.37	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
21263	dirMS_041712_NAR_40mM_plus2.12074.12074.2	2	5.17	0	9.40E+04		(R)NFDEILR	(R)N F|D/E/I L R(V)		136.52	453.7354	906.468	-0.0044	-4.9	4.37	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
21264	dirMS_041712_NAR_50mM_plus2.6111.6111.3	3	5.17	0	1.25E+05		(R)SGSMDI	(R)S G S M/D/P S G A/H/P S V/R(Q)		96.5	462.214	1384.627	0.0001	0	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
21265	dirMS_041712_NAR_60mM_plus.10316.10316.3	3	5.17	1	8.18E+05		(K)TAVCDIF	(K)T\A V/C D I/P P R G L K(M)	C:Carbamidomethylation	111.95	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
21266	dirMS_041712_NAR_120mM_minus.15999.15999.4	4	5.16	1	3.72E+05		(K)AGSMKI	(K)A G S M K D/P L/L/D D H G D F I R(M)		141.33	472.4817	1886.907	-0.0016	-0.8	4.56	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
21267	dirMS_041712_NAR_20mM_minus.9440.9440.3	3	5.16	0	1.18E+04	M175m	(R)LEQGQA	(R)L E Q G Q A\I/D D\L/m/P A Q K(-)	m:Oxidized methionine	144.5	558.2794	1656.826	15.9975	1.5	4.03	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
21268	dirMS_041712_NAR_30mM_minus2.14772.14772.2	2	5.16	0	3.15E+05		(K)FVMQEE	(K)F V|M Q\E\E/F S R(D)		133.63	586.7762	1172.541	0.0047	4	4.53	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
21269	dirMS_041712_NAR_30mM_minus2.16660.16660.2	2	5.16	0	2.41E+05		(K)NAAGAL	(K)N A|A|G A/L D L L K(E)		144.1	493.2881	985.568	0.0013	1.3	5.84	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
21270	dirMS_041712_NAR_30mM_minus2.6316.6316.2	2	5.16	0	1.62E+05		(K)MQASIE	(K)M/Q/A/S I/E/K(G)		88.65	403.7074	806.408	-0.0001	-0.2	5.75	32745.6	4.64	HUMAN	P06748	Nucleophosmin
21271	dirMS_041712_NAR_50mM_minus2.12784.12784.3	3	5.16	0	3.94E+05		(K)SLATGGI	(K)S L|A/T G G N V S Q/A/L A L V G E K(A)		140.23	572.3135	1714.933	-0.0074	-4.3	5.72	163852.7	5.43	HUMAN	C9JJN9	Vacuolar protein sorting-associated protein 8 homolog
21272	dirMS_041712_NAR_50mM_minus2.16752.16752.3	3	5.16	1	8.28E+04		(K)AAILPTS	(K)A A/I/L/P T S I F L T N K K(G)		164.08	506.3077	1516.91	-0.0012	-0.8	10	61676.9	5.5	HUMAN	B4DV00	Protein arginine N-methyltransferase 5
21273	dirMS_041712_NAR_60mM_minus.7677.7677.3	3	5.16	1	5.65E+05		(R)YLAEVA	(R)Y/L/A/E V/A/A G D D K K(G)		102.07	427.222	1279.653	-0.0014	-1.1	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
21274	dirMS_041712_NAR_120mM_plus.21391.21391.4	4	5.16	2	4.53E+05	M145m	(R)RGVmLA	(R)R G V\m L\A/V/D/A V I/A E L K K(Q)	m:Oxidized methionine	166.22	433.0059	1713.009	15.9926	-1.3	8.59	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
21275	dirMS_041712_NAR_120mM_plus.7971.7971.2	2	5.16	0	1.36E+05		(K)NVPNW	(K)N V/P/N W H R(D)		95.12	461.7364	922.464	0.0013	1.4	9.75	14844.8	5.89	HUMAN	B4DV51	GTP-binding nuclear protein Ran
21276	dirMS_041712_NAR_20mM_plus.18179.18179.2	2	5.16	0	9.83E+04		(R)APGSGL	(R)A/P|G S G L A L L|P L K(I)		196.67	568.8548	1136.704	-0.0014	-1.3	8.8	266161	5.68	HUMAN	E9PPU0	Epiplakin
21277	dirMS_041712_NAR_30mM_plus2.11480.11480.2	2	5.16	0	3.62E+05		(R)NGDFLP	(R)N G|D/F/L/P T|R(L)		113.7	460.2391	919.463	0.0077	8.4	5.84	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
21278	dirMS_041712_NAR_30mM_plus2.15987.15987.2	2	5.16	0	6.20E+05		(R)ALQALEI	(R)A L/Q/A/L/E/E L R(L)		137.1	521.7961	1042.589	-0.0042	-4	4.53	533778	5.74	HUMAN	Q15149	Plectin
21279	dirMS_041712_NAR_30mM_plus2.16659.16659.2	2	5.16	0	3.82E+05		(K)QLQEMI	(K)Q L/Q/E/M L/G L\S K(V)		140.32	573.8112	1146.619	-0.0036	-3.1	6	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
21280	dirMS_041712_NAR_30mM_plus2.17903.17903.2	2	5.16	0	1.24E+05		(R)INSANG	(R)I N/S A N/G\L E I K(S)		147.32	529.8026	1058.584	0.0139	13.1	6	40159.7	6.47	HUMAN	F5H5G1	Limbic system-associated membrane protein
21281	dirMS_041712_NAR_30mM_plus2.21876.21876.2	2	5.16	0	1.03E+05		(K)NFYFLEI	(K)N F/Y|F/L E M N T R(L)		170.5	667.8205	1334.62	0.0139	10.4	6	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
21282	dirMS_041712_NAR_30mM_plus2.8474.8474.2	2	5.16	0	7.92E+05		(K)TAVCDIF	(K)T A|V/C/D/I P\P R(G)	C:Carbamidomethylation	99.28	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
21283	dirMS_041712_NAR_40mM_plus2.7567.7567.2	2	5.16	0	5.50E+04		(R)INISEGN	(R)I N|I/S/E/G N C P E R(I)	C:Carbamidomethylation	105.02	644.7998	1288.595	-0.0027	-2.1	4.53	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
21284	dirMS_041712_NAR_50mM_plus2.21016.21016.3	3	5.16	0	4.24E+06		(R)AGKPVI	(R)A G K\P V I C A T|Q|M|L/E S M I\K(K)	C:Carbamidomethylation	179.77	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
21285	dirMS_041712_NAR_50mM_plus2.8200.8200.3	3	5.16	1	7.95E+04		(R)DTGEKL	(R)D T|G\E K L T V|A E N E A/E T K(L)		109.95	578.9478	1734.839	-0.0104	-6	4.25	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
21286	dirMS_041712_NAR_60mM_plus.17360.17360.3	3	5.16	1	6.72E+05		(R)LKDLEAI	(R)L K D/L E A|L\L N S K(E)		147.78	415.2483	1243.726	0.0047	3.8	6.07	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
21287	dirMS_041712_NAR_60mM_plus.19291.19291.3	3	5.16	0	5.02E+04		(K)VSHLLGI	(K)V S H L\L G I|N|V/T/D\F T R(G)		159.5	524.6233	1571.854	0.0013	0.8	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
21288	dirMS_041712_NAR_120mM_minus.13580.13580.3	3	5.15	0	7.83E+04		(K)LSLGTYA	(K)L S\L/G T\Y/A/S L H/G R(I)		128.13	425.5623	1274.685	-0.0128	-10.1	8.75	67446.5	5.63	HUMAN	F8VQE1	LIM domain and actin-binding protein 1
21289	dirMS_041712_NAR_120mM_minus.9432.9432.2	2	5.15	0	7.86E+05		(K)STITIVAE	(K)S T|I|T I V A E E/V S G(-)		106.33	603.3111	1205.626	-0.0111	-9.2	3.79	16755.8	5.07	HUMAN	H0YNM7	Copine-6 (Fragment)
21290	dirMS_041712_NAR_20mM_minus.11583.11583.2	2	5.15	0	8.03E+04		(R)ATLYVT	(R)A T L/Y|V/T A I E D/R(Q)		163.27	626.3282	1251.658	-0.0088	-7	4.37	24376.8	6.08	HUMAN	E9PIX6	Protein arginine N-methyltransferase 1 (Fragment)
21291	dirMS_041712_NAR_30mM_minus2.15957.15957.2	2	5.15	0	7.79E+04		(K)LGEWV	(K)L/G/E/W V|G L C K(I)	C:Carbamidomethylation	141.05	531.2806	1061.545	0.0091	8.6	6	14914.1	6.84	HUMAN	P25398	40S ribosomal protein S12
21292	dirMS_041712_NAR_30mM_minus2.20085.20085.2	2	5.15	0	8.40E+03		(R)VIFGLFG	(R)V I|F/G L F G K(T)		169.65	440.768	880.529	-0.0004	-0.4	8.72	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
21293	dirMS_041712_NAR_40mM_minus2.12718.12718.3	3	5.15	0	2.38E+04	S21s	(K)VLWGSV	(K)V/L W/G S W s V L G P W N R(F)	s:N-acetylglucosamine (S)	158.45	620.659	1656.864	203.0979	10	9.72	16871.7	5.47	HUMAN	H0Y4Y2	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D (Fragment)
21294	dirMS_041712_NAR_50mM_minus2.9617.9617.3	3	5.15	0	1.73E+05	M329m	(K)SNmGHI	(K)S N/m G H P E|P/A S G L A A L/A K(V)	m:Oxidized methionine	122.73	556.279	1650.827	15.9956	0.4	6.47	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
21295	dirMS_041712_NAR_60mM_minus.15682.15682.3	3	5.15	1	1.09E+05	M332m	(R)AKFEELI	(R)A K\F E E L N/m/D/L F/R(S)	m:Oxidized methionine	147.6	510.255	1512.752	15.9989	2.6	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
21296	dirMS_041712_NAR_120mM_plus.7228.7228.4	4	5.15	0	6.60E+05		(R)IHEGCEE	(R)I H\E\G C\E\E/P A T H/N A L/A K(I)	C:Carbamidomethylation	91.42	444.9633	1776.833	-0.002	-1.1	5.32	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
21297	dirMS_041712_NAR_30mM_plus2.12590.12590.2	2	5.15	0	5.86E+05		(R)SGYLLPI	(R)S G/Y|L L P D/T/K(A)		118.18	497.2641	993.525	-0.0042	-4.2	5.55	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
21298	dirMS_041712_NAR_30mM_plus2.6570.6570.2	2	5.15	0	4.72E+05		(R)SPDNPN	(R)S/P/D/N|P M N Q R(A)		88.83	529.7357	1058.468	-0.0042	-4	5.55	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
21299	dirMS_041712_NAR_40mM_plus2.17012.17012.3	3	5.15	0	1.26E+05		(R)LLEVLSG	(R)L L E|V\L\S/G E I\L P K P T K(G)		165.95	546.3323	1636.988	-0.006	-3.7	6.14	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
21300	dirMS_041712_NAR_40mM_plus2.19580.19580.3	3	5.15	0	3.40E+04		(K)GAEILEV	(K)G A\E/I L E V L H\S L/P A V R(Q)		183.02	535.3088	1603.917	-0.0048	-3	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
21301	dirMS_041712_NAR_40mM_plus2.7938.7938.2	2	5.15	0	2.91E+04		(R)MGYMD	(R)M/G Y/M D/P R(E)		106.78	435.1865	869.364	0.0013	1.5	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
21302	dirMS_041712_NAR_40mM_plus2.9102.9102.2	2	5.15	0	8.93E+04		(K)GSDFDC	(K)G S|D\F/D/C E L R(L)	C:Carbamidomethylation	115.47	549.7296	1098.452	-0.0001	-0.1	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
21303	dirMS_041712_NAR_50mM_plus2.10310.10310.3	3	5.15	1	3.14E+05		(K)TAVCDIF	(K)T A|V/C D I/P P R G L K(M)	C:Carbamidomethylation	121.85	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
21304	dirMS_041712_NAR_50mM_plus2.11052.11052.3	3	5.15	1	4.11E+04	M278m	(K)DmESPT	(K)D m|E/S/P T K/L D V T/L/A/K(D)	m:Oxidized methionine	125.45	521.9356	1547.799	15.9937	-0.8	4.56	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
21305	dirMS_041712_NAR_50mM_plus2.22054.22054.3	3	5.15	1	5.81E+05		(K)AGFLDLI	(K)A/G|F L/D L K D F/L/P K(E)		188.87	455.2587	1363.762	-0.0005	-0.3	6	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
21306	dirMS_041712_NAR_60mM_plus.14082.14082.3	3	5.15	1	1.18E+06	M383m	(K)DFAHmI	(K)D F A H/m/P L L K A V L K(E)	m:Oxidized methionine	130.57	500.2895	1482.85	16.0038	5.9	8.6	60633	9.35	HUMAN	Q02318	Sterol 26-hydroxylase, mitochondrial
21307	dirMS_041712_NAR_60mM_plus.16001.16001.3	3	5.15	0	2.79E+05		(K)NFDLRP	(K)N F|D|L R/P G V I V/R(-)		140.12	429.248	1285.738	-0.0081	-6.3	9.6	33192.3	6.77	HUMAN	B4DN45	S-adenosylmethionine synthase
21308	dirMS_041712_NAR_60mM_plus.5560.5560.3	3	5.15	0	7.18E+04		(K)AAGPSL	(K)A A|G P/S L/S H T S G G T Q S K(V)		87.65	495.9135	1485.729	-0.0033	-2.2	8.8	68764.6	6.96	HUMAN	P27694	Replication protein A 70 kDa DNA-binding subunit
21309	dirMS_041712_NAR_120mM_minus.19003.19003.4	4	5.14	1	3.75E+05		(R)HATALEI	(R)H A T A\L/E\E\L/S E Q L E/Q A K R(F)		158.5	489.0065	1953.004	0.0006	0.3	4.91	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
21310	dirMS_041712_NAR_120mM_minus.19846.19846.3	3	5.14	1	2.68E+05		(R)GFKDQI	(R)G F K D Q I|Y/D\I/F Q K(L)		164.43	501.2607	1501.769	-0.001	-0.7	5.96	26945.8	8.07	HUMAN	J3KSZ0	Eukaryotic initiation factor 4A-I (Fragment)
21311	dirMS_041712_NAR_120mM_minus.19988.19988.3	3	5.14	0	1.13E+05		(R)QFLFRP	(R)Q F L/F/R/P W D V/T K(L)		164.88	479.5936	1436.768	-0.0022	-1.6	8.75	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
21312	dirMS_041712_NAR_30mM_minus2.16547.16547.2	2	5.14	0	1.05E+04		(R)SSGLTA	(R)S S G L/T/A/V/W\V A R(N)		142.22	573.8112	1146.627	-0.0115	-10	9.47	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
21313	dirMS_041712_NAR_40mM_minus2.7694.7694.3	3	5.14	0	7.75E+04	M778m	(R)mLTGPV	(R)m L/T G P V Y|S Q/S/T A L T/H K(Q)	m:Oxidized methionine	123.6	583.9659	1733.889	15.9941	-0.5	8.37	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
21314	dirMS_041712_NAR_50mM_minus2.9665.9665.3	3	5.14	1	6.43E+04		(R)NINRKL	(R)N I N/R K L S A/A G M H E A L K(L)		123.07	584.9856	1752.954	-0.0115	-6.6	9.99	54466.9	9.71	HUMAN	P34969	5-hydroxytryptamine receptor 7
21315	dirMS_041712_NAR_20mM_plus.10370.10370.2	2	5.14	0	8.19E+04		(K)AVYTQD	(K)A V/Y/T Q D C P L A A|A K(A)	C:Carbamidomethylation	144.1	704.3502	1407.694	-0.0006	-0.4	5.88	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
21316	dirMS_041712_NAR_20mM_plus.12887.12887.2	2	5.14	0	3.26E+05	M316m	(R)ISEQFTA	(R)I S/E\Q/F/T A/m F R(R)	m:Oxidized methionine	161.43	623.3012	1229.598	15.9968	1.5	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
21317	dirMS_041712_NAR_20mM_plus.18752.18752.2	2	5.14	0	1.37E+05	S402s	(K)IIIQSsNK	(K)I I I Q S s|N K(Q)	s:N-acetylglucosamine (S)	201.15	553.3192	902.531	203.1006	19.2	8.75	99204.3	6.1	HUMAN	A8MTZ9	Uncharacterized protein
21318	dirMS_041712_NAR_20mM_plus.7213.7213.2	2	5.14	0	1.60E+04		(R)ITESEEV	(R)I/T/E/S E E/V V S/R(E)		117.27	574.792	1148.579	-0.0026	-2.3	4.25	74423.5	6.57	HUMAN	P02545	Prelamin-A/C
21319	dirMS_041712_NAR_30mM_plus2.19165.19165.2	2	5.14	0	9.69E+04		(R)VYSLFLD	(R)V/Y/S/L F/L D E/S R(S)		153.07	614.8154	1228.621	0.0027	2.2	4.37	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
21320	dirMS_041712_NAR_40mM_plus2.12848.12848.3	3	5.14	0	1.02E+04		(R)LSSPCIN	(R)L/S/S/P C I/M V V N H D A/S S I P R(L)	C:Carbamidomethylation	141.52	661.6617	1982.979	-0.0081	-4.1	6.74	87267.9	6.33	HUMAN	Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase
21321	dirMS_041712_NAR_40mM_plus2.12962.12962.3	3	5.14	0	3.01E+05		(K)NLPPSG	(K)N L|P P S\G A V/P V T G I/P P H V V/K(V)		142.87	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
21322	dirMS_041712_NAR_40mM_plus2.14377.14377.2	2	5.14	0	1.14E+05		(K)LLCGLLA	(K)L L/C/G L L/A E R(L)	C:Carbamidomethylation	150.63	522.7962	1044.587	-0.0019	-1.8	6	12647.2	8.07	HUMAN	P14174	Macrophage migration inhibitory factor
21323	dirMS_041712_NAR_40mM_plus2.17901.17901.3	3	5.14	1	7.73E+04	M116m	(R)ELAILLG	(R)E L A\I/L/L/G m L D/P A E K D E K(G)	m:Oxidized methionine	171.67	634.3333	1884.999	15.9867	-4.3	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
21324	dirMS_041712_NAR_50mM_plus2.10896.10896.3	3	5.14	1	2.69E+05		(K)NVDILKI	(K)N V/D/I/L/K D P E T V/K(Q)		124.72	457.5906	1370.753	0.0047	3.4	4.56	124524.8	5.71	HUMAN	O14980	Exportin-1
21325	dirMS_041712_NAR_50mM_plus2.10956.10956.3	3	5.14	0	3.32E+05	M147m	(K)LQmEAP	(K)L Q|m E A P H\I|I V/G T P\G R(V)	m:Oxidized methionine	125.17	545.6261	1618.873	15.9904	-2.8	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
21326	dirMS_041712_NAR_50mM_plus2.5966.5966.3	3	5.14	1	6.04E+04	T184t S186	(K)HGTKtV	(K)H G T K/t V/s A L G L D/P S G A R(L)	t:Phosphorylated T s:Phosph	95.17	609.6035	1666.887	159.9088	-13	8.76	43753	4.96	HUMAN	D6RIW8	WD repeat-containing protein 70
21327	dirMS_041712_NAR_50mM_plus2.9623.9623.3	3	5.14	0	7.71E+05		(R)DNIQGI	(R)D N/I Q/G I T K/P\A I R(R)		117.22	442.5902	1325.754	0.0025	1.9	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
21328	dirMS_041712_NAR_60mM_plus.8474.8474.3	3	5.14	0	2.22E+06		(K)HTGPNS	(K)H T G\P N S P D T\A/N/D G F V R(L)		102.07	562.2601	1684.767	-0.0016	-1	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
21329	dirMS_041712_NAR_120mM_minus.11536.11536.3	3	5.13	1	2.55E+05		(R)VDWQE	(R)V/D\W Q/E N D F/S K R(I)		117	475.225	1423.66	0.0004	0.3	4.56	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
21330	dirMS_041712_NAR_20mM_minus.8236.8236.2	2	5.13	0	5.74E+03		(K)DQVAN	(K)D Q|V/A N S A/F V E R(L)		131.7	618.3098	1235.602	0.0108	8.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
21331	dirMS_041712_NAR_30mM_minus2.11658.11658.2	2	5.13	0	1.06E+05		(K)AFSGYL	(K)A F/S/G/Y|L G T/D Q S K(W)		117.27	637.3079	1273.606	0.0026	2.1	5.88	25823.8	6.41	HUMAN	H7BZT7	S-formylglutathione hydrolase (Fragment)
21332	dirMS_041712_NAR_30mM_minus2.16209.16209.2	2	5.13	0	1.21E+05		(K)SSEELLS	(K)S S/E/E|L\L/S A L/Q K(K)		141.47	602.816	1204.642	-0.0172	-14.3	4.53	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
21333	dirMS_041712_NAR_30mM_minus2.16891.16891.2	2	5.13	0	3.21E+05		(K)FANPFP	(K)F A/N/P F P A A V R(G)		146.33	545.2937	1089.584	-0.0039	-3.5	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
21334	dirMS_041712_NAR_30mM_minus2.8272.8272.2	2	5.13	0	1.96E+04		(R)QLEEAEI	(R)Q L/E E/A/E/E/E A Q R(A)		99.67	666.3076	1331.607	0.0006	0.4	3.98	227783.5	5.5	HUMAN	P35579	Myosin-9
21335	dirMS_041712_NAR_50mM_minus2.11486.11486.3	3	5.13	0	2.93E+03	M677m	(R)EVNDmI	(R)E V/N D m H/H T L\L D\S S L K(L)	m:Oxidized methionine	133.25	585.6112	1738.843	15.9762	-10.7	5.21	342291.8	5.65	HUMAN	Q5TBA9	Protein furry homolog
21336	dirMS_041712_NAR_60mM_minus.13696.13696.3	3	5.13	0	2.40E+04	S277s	(K)IsRPPTS	(K)I s R P P/T/S V G H Y/K(M)	s:N-acetylglucosamine (S)	135.68	515.6165	1341.727	203.1076	18.3	9.99	44212.5	9.66	HUMAN	O60512	Beta-1,4-galactosyltransferase 3
21337	dirMS_041712_NAR_120mM_plus.9118.9118.3	3	5.13	1	7.08E+05		(K)EFFNGKI	(K)E F/F N/G K/E/P S R(G)		101.52	404.2038	1210.585	0.0117	9.7	6.24	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
21338	dirMS_041712_NAR_20mM_plus.12052.12052.2	2	5.13	0	8.55E+04		(K)TLQAQA	(K)T L/Q A Q A/P E K(S)		156.77	493.2711	985.531	0.0036	3.7	5.66	54056.1	9.99	HUMAN	P12645	Bone morphogenetic protein 3
21339	dirMS_041712_NAR_20mM_plus.15436.15436.2	2	5.13	0	2.33E+03		(R)ALDEGD	(R)A L/D/E/G D I A L/L/K(T)		177.02	579.3248	1157.641	0.0011	0.9	4.03	14693.3	4.69	HUMAN	C9JLS9	26S protease regulatory subunit 7 (Fragment)
21340	dirMS_041712_NAR_20mM_plus.15775.15775.3	3	5.13	0	6.00E+05		(K)VGINYQ	(K)V G I N Y\Q\P P T V/V/P G G D L\A K(V)		179.37	608.9991	1824.985	-0.0027	-1.5	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
21341	dirMS_041712_NAR_20mM_plus.9901.9901.2	2	5.13	0	9.64E+04		(R)VLLPTGI	(R)V L|L/P T\G N Q R(A)		140.05	499.2863	997.579	-0.0136	-13.6	9.72	99570.4	9.54	HUMAN	P53814	Smoothelin
21342	dirMS_041712_NAR_50mM_plus2.10293.10293.3	3	5.13	0	1.27E+05		(R)TITVALA	(R)T I T/V A/L A D/G G R P D N/T G R(G)		120.45	571.9661	1713.888	-0.0041	-2.4	5.63	107550.2	5.34	HUMAN	P49588	Alanine--tRNA ligase, cytoplasmic
21343	dirMS_041712_NAR_50mM_plus2.10545.10545.3	3	5.13	0	2.58E+04		(R)AIGSASE	(R)A I/G S/A S E G\A/Q S S L\Q E V Y H K(S)		122.58	654.657	1961.956	0.0001	0.1	5.4	20148.5	4.65	HUMAN	B4E2V4	Proteasome (Prosome, macropain) subunit, alpha type, 5, isoform CRA_c
21344	dirMS_041712_NAR_50mM_plus2.11751.11751.3	3	5.13	1	1.06E+05		(K)VEAQVY	(K)V/E/A Q V/Y I L/S K E E G G R(H)		130.02	559.9637	1677.881	-0.0041	-2.4	4.79	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
21345	dirMS_041712_NAR_50mM_plus2.13586.13586.3	3	5.13	0	1.12E+06		(K)AASDIAI	(K)A A S D I/A/M T E/L/P/P T H P I/R(L)		139.37	607.3177	1819.937	0.0015	0.8	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
21346	dirMS_041712_NAR_50mM_plus2.13865.13865.3	3	5.13	0	1.44E+06		(K)STTSDIP	(K)S T|T/S/D I P H M L N Q V E/S K(V)		140.33	596.2908	1786.864	-0.0061	-3.4	5.3	11532.2	6.34	HUMAN	H0YNA1	Protein FAM98B (Fragment)
21347	dirMS_041712_NAR_50mM_plus2.5949.5949.3	3	5.13	0	1.85E+04		(R)VEAKPE	(R)V E/A K/P E V Q/S Q/P P R(V)		95.3	488.9312	1464.781	-0.0015	-1	6.11	54177.2	5.41	HUMAN	Q9UN86	Ras GTPase-activating protein-binding protein 2
21348	dirMS_041712_NAR_50mM_plus2.9646.9646.3	3	5.13	0	9.82E+04		(K)YIQQTKI	(K)Y I Q Q T K/P L/T L E R(T)		118.75	497.2822	1489.837	-0.0053	-3.5	8.59	26283.8	8.96	HUMAN	O43809	Cleavage and polyadenylation specificity factor subunit 5
21349	dirMS_041712_NAR_60mM_plus.13559.13559.3	3	5.13	0	1.06E+06		(K)NVDDILI	(K)N/V/D D I L K/P P\G R(E)		127.58	408.563	1223.674	0.0002	0.2	5.96	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
21350	dirMS_041712_NAR_60mM_plus.20526.20526.3	3	5.13	1	3.08E+05		(K)ITQDIFQ	(K)I/T/Q/D I F/Q Q L L/K R(G)		167.97	501.626	1502.869	-0.0055	-3.7	8.75	72796.9	6.75	HUMAN	A6NC17	Methionine--tRNA ligase, cytoplasmic
21351	dirMS_041712_NAR_120mM_minus.17281.17281.3	3	5.12	2	1.62E+05		(R)KVESLQI	(R)K\V/E S L\Q E E I/A F L|K/K(L)		149	554.6531	1661.947	-0.0025	-1.5	6.23	49709.6	5.19	HUMAN	B0YJC4	Vimentin
21352	dirMS_041712_NAR_20mM_minus.13235.13235.3	3	5.12	0	7.44E+04		(R)GNPTVE	(R)G N P T\V E V D\L/F/T/S K(G)		183.13	469.5754	1406.716	-0.0045	-3.2	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
21353	dirMS_041712_NAR_20mM_minus.14490.14490.3	3	5.12	0	4.72E+03		(R)AAVEEG	(R)A A V E E G I|V/L/G G G C A L L R(C)	C:Carbamidomethylation	199.5	562.3053	1684.905	-0.0037	-2.2	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
21354	dirMS_041712_NAR_30mM_minus2.16698.16698.3	3	5.12	0	7.17E+05		(R)ASLEAAI	(R)A S L\E A A/I/A/D/A/E Q R(G)		144.27	448.8965	1344.675	-0.0004	-0.3	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
21355	dirMS_041712_NAR_50mM_minus2.12733.12733.3	3	5.12	0	9.95E+05	M114m M	(R)AGKPVI	(R)A G K\P V I\C A T Q/m/L E/S m I K(K)	C:Carbamidomethylation m:Oxid	139.97	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
21356	dirMS_041712_NAR_50mM_minus2.18040.18040.3	3	5.12	0	2.72E+05		(K)ISSIQSIV	(K)I S S I/Q/S/I V/P A L/E I A N A H R(K)		171.43	640.361	1919.071	-0.0024	-1.3	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
21357	dirMS_041712_NAR_60mM_minus.7875.7875.3	3	5.12	1	3.82E+05	M230m M	(R)mSmKE	(R)m S m K E V\D E Q|m\L/N V Q/N K(N)	m:Oxidized methionine	103.83	657.9647	1923.897	47.9823	-1.3	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
21358	dirMS_041712_NAR_60mM_minus.8779.8779.3	3	5.12	1	1.45E+05		(R)SRAEAE	(R)S R\A/E\A\E/S/M/Y Q/I K(Y)		108.83	471.5706	1412.684	0.0134	9.5	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
21359	dirMS_041712_NAR_120mM_plus.23656.23656.4	4	5.12	1	1.93E+05		(R)EENVKA	(R)E E N V K A D V/F H/A/Y L S/L L K(Q)		178.78	494.7707	1976.049	0.0122	6.2	5.45	50425	5.53	HUMAN	H0YH27	Cullin-associated NEDD8-dissociated protein 1 (Fragment)

21360	dirMS_041712_NAR_120mM_plus.7628.7628.3	3	5.12	0	4.43E+05		(R)SGSMDI	(R)S G/S|M/D/P S G A H P S V R(Q)		93.87	462.218	1384.627	0.0121	8.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
21361	dirMS_041712_NAR_20mM_plus.13076.13076.2	2	5.12	0	8.45E+04		(K)VTAVPTI	(K)V/T\A/V/P T L L K(Y)		161.93	471.3032	941.603	-0.0039	-4.1	8.72	11462.8	5.18	HUMAN	I3L2R6	Thioredoxin domain-containing protein 17
21362	dirMS_041712_NAR_20mM_plus.15093.15093.3	3	5.12	1	5.17E+04		(K)RWYVPI	(K)R W Y/V P P/D/Q V K(G)		175.77	429.9015	1287.684	0.0055	4.3	8.59	49361.5	9.78	HUMAN	O95081	Arf-GAP domain and FG repeat-containing protein 2
21363	dirMS_041712_NAR_20mM_plus.17772.17772.3	3	5.12	0	1.66E+05		(R)TVQSLEI	(R)T V Q S L E/I/D/L/D/S M/R(N)		194.73	502.9236	1506.747	0.0094	6.2	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
21364	dirMS_041712_NAR_20mM_plus.18444.18444.2	2	5.12	0	1.31E+05	M332m	(R)IVSQLLT	(R)I V S Q L/L/T/L/m D G\L K(Q)	m:Oxidized methionine	199.03	723.9145	1430.829	15.993	-1.3	5.84	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
21365	dirMS_041712_NAR_40mM_plus2.11129.11129.3	3	5.12	1	3.24E+05		(R)DVVICPI	(R)D/V|V I C P D/A S L/E D A K K(E)	C:Carbamidomethylation	130.9	553.9465	1659.826	-0.0009	-0.5	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
21366	dirMS_041712_NAR_40mM_plus2.5686.5686.2	2	5.12	0	1.24E+05		(R)NQGGY(	(R)N Q\G G Y/G G/S S/S S S S Y G S/G\R(R)		90.58	847.8525	1694.7	-0.0024	-1.4	8.59	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
21367	dirMS_041712_NAR_50mM_plus2.19806.19806.3	3	5.12	1	1.70E+05		(R)TSLLTLEI	(R)T S/L/L/T L/E D V K Q E L I K(L)		172.28	577.3359	1729.995	-0.0014	-0.8	4.68	156316.8	8.61	HUMAN	Q7Z478	ATP-dependent RNA helicase DHX29
21368	dirMS_041712_NAR_60mM_plus.17649.17649.3	3	5.12	1	3.22E+05		(K)EIIDPVLI	(K)E I/I/D P V/L D R I R(K)		149.82	446.9288	1338.774	-0.0021	-1.6	4.56	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
21369	dirMS_041712_NAR_120mM_minus.17908.17908.3	3	5.11	0	1.58E+05		(R)HLLQAP'	(R)H L/L Q A P V D/D\A\Q/E I/L\H S R(F)		152.58	648.0089	1942.014	-0.002	-1	5.21	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
21370	dirMS_041712_NAR_20mM_minus.11598.11598.3	3	5.11	0	2.10E+05		(R)GALQNI	(R)G A L\Q/N I\I/P A/S/T G A A K(A)		164.52	471.2674	1411.79	-0.0027	-1.9	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
21371	dirMS_041712_NAR_30mM_minus2.8262.8262.2	2	5.11	0	1.96E+04		(R)QLEEAEI	(R)Q L/E/E A/E|E/E A/Q R(A)		99.67	666.3076	1331.607	0.0006	0.4	3.98	227783.5	5.5	HUMAN	P35579	Myosin-9
21372	dirMS_041712_NAR_40mM_minus2.11637.11637.3	3	5.11	1	1.06E+05		(R)IINEPTA	(R)I I/N E/P T/A A/A I A Y G L D K K(V)		152.32	596.6671	1787.99	-0.0034	-1.9	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
21373	dirMS_041712_NAR_40mM_minus2.13295.13295.3	3	5.11	0	3.21E+05		(R)NGNQD	(R)N G N Q/D E V/L S E A F R(L)		162.28	493.5654	1478.687	-0.0054	-3.6	4.14	74049.8	9.05	HUMAN	Q9P0U3	Sentrin-specific protease 1
21374	dirMS_041712_NAR_40mM_minus2.14281.14281.3	3	5.11	0	1.90E+04		(R)VSAAVLI	(R)V S/A A V L/P/L\V H/P L P E G L R(A)		167.98	590.0205	1768.048	-0.001	-0.6	6.72	63124.2	9.53	HUMAN	E7EVU5	Nuclear receptor corepressor 1 (Fragment)
21375	dirMS_041712_NAR_50mM_minus2.10372.10372.3	3	5.11	0	7.23E+04		(R)LTSPIVS'	(R)L T/S P I V S T H L/D/T R(N)		127.37	480.6	1439.785	0.0002	0.1	6.74	58760.2	5.26	HUMAN	Q6ZTN6	Ankyrin repeat domain-containing protein 13D
21376	dirMS_041712_NAR_50mM_minus2.14461.14461.3	3	5.11	1	2.65E+05		(R)GFPTIYF	(R)G F/P T/I Y F\S P A N K K(L)		150.5	490.5972	1469.779	-0.0017	-1.1	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
21377	dirMS_041712_NAR_60mM_minus.9215.9215.3	3	5.11	1	1.13E+06	M289m	(R)VVDLM/	(R)V/V|D|L M/A H m A S K E(-)	m:Oxidized methionine	111.42	449.5563	1330.649	16.005	7.5	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
21378	dirMS_041712_NAR_120mM_plus.14452.14452.2	2	5.11	0	5.79E+05		(R)HFDQFV	(R)H/F|D/Q F\W/S A A K(T)		128.83	618.7928	1236.58	-0.0013	-1.1	6.74	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
21379	dirMS_041712_NAR_120mM_plus.7017.7017.3	3	5.11	1	1.61E+05		(R)NKQTYS	(R)N K Q T Y S/T E/P N N L K(A)		90.15	512.9261	1536.765	-0.0015	-1	8.5	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
21380	dirMS_041712_NAR_20mM_plus.10682.10682.2	2	5.11	0	4.78E+04		(K)GILAADI	(K)G I/L\A A/D E S T G S I\A K(R)		145.93	666.8531	1332.7	-0.0016	-1.2	4.37	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
21381	dirMS_041712_NAR_20mM_plus.13045.13045.3	3	5.11	0	7.64E+04	M120m	(K)VTNGAF	(K)V T N G A/F T/G/E\I/S P G m I K(D)	m:Oxidized methionine	162.3	546.6106	1621.825	15.9918	-1.9	5.97	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
21382	dirMS_041712_NAR_20mM_plus.18573.18573.3	3	5.11	0	4.28E+04	M332m	(R)IVSQLLT	(R)I V S Q L L/T/L m D G/L K(Q)	m:Oxidized methionine	199.9	482.9449	1430.829	15.9914	-2.4	5.84	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
21383	dirMS_041712_NAR_20mM_plus.8051.8051.3	3	5.11	0	4.57E+05	M239m	(K)EVDEQm	(K)E V D E Q|m\L N V/Q/N K(N)	m:Oxidized methionine	125.12	488.2328	1446.689	15.9945	-0.3	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
21384	dirMS_041712_NAR_30mM_plus2.9316.9316.2	2	5.11	0	2.19E+05		(R)LEAVLAS	(R)L/E/A V L A S R(S)		102.05	429.7522	858.504	-0.0072	-8.4	6	58866.1	7.1	HUMAN	Q9BVI4	Nucleolar complex protein 4 homolog
21385	dirMS_041712_NAR_40mM_plus2.10126.10126.3	3	5.11	0	1.35E+05	M1087m	(R)mPLPAP	(R)m P L/P A P S L S H Q/P/P P A P R(V)	m:Oxidized methionine	124.5	603.6536	1792.953	15.9936	-0.7	9.52	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
21386	dirMS_041712_NAR_40mM_plus2.15549.15549.3	3	5.11	1	1.13E+04	M132m	(R)TLAEIAK	(R)T L/A E I/A K V/E L D/N m P\L/R(G)	m:Oxidized methionine	158	610.3313	1812.989	15.9906	-2.4	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
21387	dirMS_041712_NAR_40mM_plus2.5967.5967.2	2	5.11	0	1.61E+05	M367m	(R)FGSGmI	(R)F G/S/G m N/M/G R(I)	m:Oxidized methionine	92.73	486.7054	956.408	15.9958	1	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
21388	dirMS_041712_NAR_40mM_plus2.7256.7256.2	2	5.11	0	6.89E+03		(K)QGGGG(	(K)Q G G/G G G G G S V/P G I E/R(M)		102.55	642.8175	1284.629	-0.0014	-1.1	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
21389	dirMS_041712_NAR_40mM_plus2.8050.8050.2	2	5.11	0	1.94E+04		(R)SSQSSS(	(R)S S Q/S/S S/Q Q F S/G\I G/R(S)		107.55	728.3504	1455.682	0.0113	7.7	9.47	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
21390	dirMS_041712_NAR_50mM_plus2.15001.15001.3	3	5.11	0	6.25E+05		(K)QGPLHG	(K)Q G P L\H G M L/I N/T/P Y V/T K(D)		146.47	590.3171	1768.941	-0.0047	-2.7	8.6	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
21391	dirMS_041712_NAR_50mM_plus2.6929.6929.3	3	5.11	1	8.65E+05		(K)IVADKD'	(K)I/V/A D K D Y S V/T A/N/S K(I)		101.45	504.2628	1510.775	-0.0009	-0.6	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
21392	dirMS_041712_NAR_50mM_plus2.9976.9976.3	3	5.11	0	3.50E+05		(K)VAKPVV	(K)V A\K P V V E|M/D\G D E M T R(I)		119.73	559.6043	1676.798	0.0001	0.1	4.32	35557.8	9.19	HUMAN	H0YL11	Isocitrate dehydrogenase [NADP], mitochondrial
21393	dirMS_041712_NAR_60mM_plus.21677.21677.3	3	5.11	1	6.69E+05		(K)EIIDLVLI	(K)E I/I/D L/V/L D R I R(K)		180.82	452.2733	1354.805	0.0001	0.1	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
21394	dirMS_041712_NAR_60mM_plus.6063.6063.3	3	5.11	0	4.41E+04	M14m	(K)SPEEmY	(K)S P/E E m Y I/Q Q K(V)	m:Oxidized methionine	90	423.5361	1252.588	16.0059	8.7	4.53	9170.2	5.33	HUMAN	Q9NSA3	Beta-catenin-interacting protein 1
21395	dirMS_041712_NAR_60mM_plus.6203.6203.3	3	5.11	0	3.09E+05	S1173s	(R)TSYLHSF	(R)T/S Y L H S P/F/s/T G R(S)	s:Phosphorylated S	90.12	478.2118	1352.659	79.9615	-3.4	8.44	147586.4	6.62	HUMAN	B3KV94	Jumonji, AT rich interactive domain 1B (RBP2-like), isoform CRA_a (Fragment)
21396	dirMS_041712_NAR_30mM_minus2.13816.13816.2	2	5.1	0	5.51E+05		(K)TCTFILR(	(K)T/C|T/F/I L R(G)	C:Carbamidomethylation	128.42	455.7458	910.481	0.0028	3.1	9.41	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
21397	dirMS_041712_NAR_50mM_minus2.17958.17958.3	3	5.1	1	4.40E+04		(R)GLFIIDD	(R)G L/F/I I/D/D K/G I L R(Q)		170.97	453.9381	1359.8	0.0003	0.2	5.96	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
21398	dirMS_041712_NAR_50mM_minus2.8039.8039.3	3	5.1	0	1.36E+05	M378m	(K)mIVDPV	(K)m I V D/P V E/P H G E\M K(F)	m:Oxidized methionine	113.33	499.9082	1481.713	15.9973	1.6	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
21399	dirMS_041712_NAR_60mM_minus.10595.10595.3	3	5.1	0	9.70E+04		(R)NRPPFG	(R)N R|P P F G Q G Y T\Q|P G/P G Y R(-)		118.75	631.3087	1891.92	-0.0083	-4.4	9.99	43076.8	5.01	HUMAN	G5E9V1	Protein TFG
21400	dirMS_041712_NAR_60mM_minus.11164.11164.3	3	5.1	1	7.95E+05		(K)MKEIAE/	(K)M/K E I A E|A/Y L/G/K(T)		122.48	418.226	1252.661	0.0029	2.3	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
21401	dirMS_041712_NAR_60mM_minus.7538.7539.3	3	5.1	0	6.18E+04	T494t	(R)ILPtHTEI	(R)I/L/P t H T E P R(R)	t:N-acetylglucosamine (T)	101.22	422.8919	1063.59	203.0717	-6.1	6.75	60886.4	6.26	HUMAN	Q9HBI6	Cytochrome P450 4F11
21402	dirMS_041712_NAR_120mM_plus.12264.12264.4	4	5.1	1	7.57E+05		(K)ILKDFPE	(K)I L K/D/F P E E D D P/T N W L R(C)		118.47	497.7567	1987.976	0.029	14.6	4.11	19058.6	7.89	HUMAN	B0QY04	Neutrophil cytosol factor 4 (Fragment)
21403	dirMS_041712_NAR_120mM_plus.15230.15230.4	4	5.1	1	6.04E+05		(K)KKELEEI'	(K)K K E L E E\I\V Q/P I/I/S/K(L)		133.32	414.2493	1653.978	-0.0032	-1.9	6.23	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
21404	dirMS_041712_NAR_120mM_plus.6365.6365.2	2	5.1	1	3.44E+05		(K)DSYVGD	(K)D/S/Y|V/G D E A Q S K/R(G)		86.3	677.815	1354.623	-0.0006	-0.5	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
21405	dirMS_041712_NAR_20mM_plus.19200.19200.2	2	5.1	0	1.37E+05		(R)TGAIVD'	(R)T G\A I/V|D V|P V G E E/L L G R(V)		204.23	812.9497	1624.891	0.0017	1	4.14	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
21406	dirMS_041712_NAR_20mM_plus.8561.8561.2	2	5.1	0	3.02E+05		(K)DVNQQI	(K)D V/N|Q/Q E|F/V/R(A)		129.47	567.7865	1134.554	0.0119	10.5	4.37	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
21407	dirMS_041712_NAR_50mM_plus2.10089.10089.3	3	5.1	1	2.46E+06		(K)ATAVVD	(K)A/T/A V/V/D G A F K E|V K(L)		120.07	445.5822	1334.731	0.0006	0.5	6.11	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
21408	dirMS_041712_NAR_50mM_plus2.10857.10857.3	3	5.1	0	1.82E+05		(K)GYAEVV	(K)G Y/A/E V/V/V A S E N S V H K(L)		124.73	530.2702	1588.797	-0.0005	-0.3	5.4	16170.5	4.37	HUMAN	C9J286	Cleavage and polyadenylation-specificity factor subunit 7 (Fragment)
21409	dirMS_041712_NAR_50mM_plus2.20002.20356.3	3	5.1	1	6.00E+05		(R)SKALGSI	(R)S K A L G S D H C P I T L\Y\L|A|L(-)	C:Carbamidomethylation	174.58	620.3259	1858.973	-0.01	-5.4	6.46	5634.5	9.82	HUMAN	G3V574	DNA-(apurinic or apyrimidinic site) lyase
21410	dirMS_041712_NAR_50mM_plus2.5896.5896.3	3	5.1	1	1.71E+05		(R)ATEGM\	(R)A T/E/G M V V A D K N/C S K(I)	C:Carbamidomethylation	94.28	503.9061	1509.704	0.0002	0.1	6.11	15607.8	9.99	HUMAN	B4E0P1	Proteasome (Prosome, macropain) subunit, beta type, 7, isoform CRA_b
21411	dirMS_041712_NAR_60mM_plus.12433.12433.3	3	5.1	1	3.80E+06		(K)LFNLSKE	(K)L/F/N L/S K E\D D V R(Q)		121.62	445.9046	1335.69	0.0089	6.7	4.56	25082	11.29	HUMAN	A2A3R5	40S ribosomal protein S6
21412	dirMS_041712_NAR_60mM_plus.13653.13653.3	3	5.1	0	4.98E+05		(R)IHQIEYA	(R)I H Q I E\Y A/M E A V/K(Q)		128.4	477.9163	1431.73	0.0043	3	5.4	18685.5	9.45	HUMAN	B4DEV8	Proteasome subunit alpha type
21413	dirMS_041712_NAR_60mM_plus.16170.16170.3	3	5.1	0	4.81E+05		(K)TTITMAI	(K)T T/I/T M A/H/L L\A A/R(E)		141.7	433.5839	1298.725	0.0122	9.4	9.44	37589.6	5.96	HUMAN	Q52LJ0	Protein FAM98B
21414	dirMS_041712_NAR_120mM_minus.16654.16654.3	3	5.09	0	3.56E+05		(K)HLEINPI	(K)H/L E I\N P D H|S\I I/E T L R(Q)		145.77	596.3176	1786.945	-0.0064	-3.6	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
21415	dirMS_041712_NAR_120mM_minus.19593.19593.3	3	5.09	1	1.58E+05		(K)RSIQFVI	(K)R S I/Q\F\V/D\W C P T G F/K(V)	C:Carbamidomethylation	161.68	580.9561	1740.853	0.0011	0.6	8.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
21416	dirMS_041712_NAR_20mM_plus.10599.10599.3	3	5.09	0	1.34E+04		(R)ELAEDG'	(R)E L A E D G Y/S/G V/E/V R(V)		145.72	475.2279	1423.67	-0.0008	-0.6	4	13054.7	9.59	HUMAN	E9PJH4	40S ribosomal protein S3
21417	dirMS_041712_NAR_20mM_plus.15634.15634.3	3	5.09	0	1.93E+04		(R)IIDVVYN	(R)I I D V V/Y N/A|S/N N E L\V R(T)		179.13	573.6388	1718.907	-0.0053	-3.1	4.37	24490	10.56	HUMAN	P62241	40S ribosomal protein S8
21418	dirMS_041712_NAR_20mM_plus.16701.16701.2	2	5.09	0	8.37E+04		(R)SSIAGLL	(R)S S/I/A G L/L L K(A)		186.6	451.2885	901.572	-0.002	-2.2	8.47	533778	5.74	HUMAN	Q15149	Plectin
21419	dirMS_041712_NAR_20mM_plus.18013.18013.3	3	5.09	0	1.71E+05		(R)LSVLGAI	(R)L S V L G A/I/T/S V Q Q R(L)		196.13	457.9354	1371.795	-0.0038	-2.8	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
21420	dirMS_041712_NAR_20mM_plus.6402.6402.3	3	5.09	0	5.31E+04		(R)GPQVQ(	(R)G P Q V\Q\Q P/P/P S N R(F)		107.1	435.561	1304.671	-0.0021	-1.6	9.75	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
21421	dirMS_041712_NAR_30mM_plus2.18021.18021.2	2	5.09	0	2.32E+05		(R)QITLNDI	(R)Q I/T/L/N/D L P V/G R(S)		147.83	613.3465	1225.69	-0.0042	-3.4	5.84	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
21422	dirMS_041712_NAR_30mM_plus2.5746.5746.2	2	5.09	0	6.14E+04		(R)SGPPPS!	(R)S G/P P/P S/S G M S S R(V)		84.53	573.7642	1146.521	0.0003	0.3	9.47	15125	6.83	HUMAN	A6PVI0	RNA binding motif protein 12 (Fragment)
21423	dirMS_041712_NAR_30mM_plus2.8855.8855.3	3	5.09	0	7.01E+05		(K)VEIIAND	(K)V E\I\I/A N/D Q/G N/R(T)		99.73	410.2146	1228.628	0.0012	1	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
21424	dirMS_041712_NAR_50mM_plus2.17482.17482.3	3	5.09	1	5.25E+05		(K)VKLAAV	(K)V K L A A V D A\T V/N/Q/V/L A/S/R(Y)		160.33	585.6736	1755.012	-0.0061	-3.5	8.72	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
21425	dirMS_041712_NAR_60mM_plus.10797.10797.3	3	5.09	1	1.33E+06		(R)TAAEND	(R)T A|A/E N D/F V/T L K K(D)		114.95	446.2368	1336.711	-0.0149	-11.1	5.73	65717	8.32	HUMAN	P35908	Keratin, type II cytoskeletal 2 epidermal
21426	dirMS_041712_NAR_60mM_plus.13933.13933.3	3	5.09	1	2.55E+04		(R)FASEND	(R)F A|S E/N D/L/P E W K E R(G)		129.5	540.9287	1620.765	0.0063	3.9	4.41	19157.5	10.04	HUMAN	C9JDM3	Ran-specific GTPase-activating protein (Fragment)
21427	dirMS_041712_NAR_60mM_plus.16148.16148.3	3	5.09	1	5.19E+05		(R)VTNRDII	(R)V T N R D I I\C\Q/I|A Y A R(I)	C:Carbamidomethylation	141.1	564.9631	1692.885	-0.0103	-6.1	8.71	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
21428	dirMS_041712_NAR_120mM_minus.16594.16594.4	4	5.08	0	1.50E+05		(K)HLEINPI	(K)H L E I\N/P D H S I I E/T L R(Q)		144.17	447.4904	1786.945	-0.0049	-2.7	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
21429	dirMS_041712_NAR_120mM_minus.19325.19325.3	3	5.08	1	3.72E+05		(K)NLRDIDI	(K)N L R D I D E|V/S/S L/L R(T)		161.42	510.614	1529.828	-0.0007	-0.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
21430	dirMS_041712_NAR_20mM_minus.10178.10178.2	2	5.08	0	2.43E+04		(R)IAAQTLL	(R)I/A/A Q/T L/L\G T/A K(M)		151.42	543.825	1086.652	-0.009	-8.3	8.75	14626.5	7.07	HUMAN	B5MD87	Pyrroline-5-carboxylate reductase 3
21431	dirMS_041712_NAR_20mM_minus.7525.7525.2	2	5.08	0	6.67E+05	M239m	(K)EVDEQm	(K)E V|D E/Q|m L\N V Q/N K(N)	m:Oxidized methionine	123.65	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
21432	dirMS_041712_NAR_30mM_minus2.5059.5059.2	2	5.08	1	8.34E+05	S666s	(K)SQKVFsI	(K)S Q/K/V F s E/K(L)	s:Phosphorylated S	80.27	516.7465	952.51	79.9759	9.3	8.31	87498	6.43	HUMAN	C9J266	E3 ubiquitin-protein ligase RNF123
21433	dirMS_041712_NAR_30mM_minus2.7953.7953.2	2	5.08	0	3.11E+05		(R)MNEAF(	(R)M/N\E|A/F|G D T K(F)		98.13	506.725	1012.44	0.0023	2.3	4.37	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
21434	dirMS_041712_NAR_40mM_minus2.14718.14800.3	3	5.08	0	1.19E+06		(K)ISSIQSIV	(K)I S\S I/Q S I/V/P A L E I A/N A H R(K)		172.1	640.3618	1919.071	0	0	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
21435	dirMS_041712_NAR_50mM_minus2.12086.12086.3	3	5.08	0	1.21E+05		(K)YYVTIID/	(K)Y Y V/T I/I/D/A P G H R(D)		137.07	468.9141	1404.727	0.0007	0.5	6.74	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
21436	dirMS_041712_NAR_50mM_minus2.18026.18026.3	3	5.08	0	2.72E+05		(K)ISSIQSIV	(K)I/S S I\Q S I V/P A L E\I A/N A H R(K)		171.43	640.361	1919.071	-0.0024	-1.3	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
21437	dirMS_041712_NAR_60mM_minus.17627.17627.3	3	5.08	0	1.17E+05		(R)GGHVVI	(R)G G H V V E G L|A|G E/L E/Q/L R(A)		158.32	555.2959	1663.876	-0.0031	-1.8	4.75	106088.3	5.78	HUMAN	P10275	Androgen receptor
21438	dirMS_041712_NAR_60mM_minus.6206.6206.3	3	5.08	1	2.71E+05		(K)ETEGDV	(K)E T E/G/D V/T S V K D/A K(I)		92.63	460.2267	1378.67	-0.0041	-3	4.32	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
21439	dirMS_041712_NAR_120mM_plus.7650.7650.3	3	5.08	0	3.70E+05		(R)NADHSN	(R)N A D H S M N|Y Q/Y R(-)		93.73	466.8673	1398.585	0.0018	1.3	6.74	96205.6	9.06	HUMAN	G5E9M5	Interleukin enhancer binding factor 3, 90kDa, isoform CRA_b
21440	dirMS_041712_NAR_20mM_plus.11621.11621.2	2	5.08	0	1.09E+05		(K)LITPAVV	(K)L I|T|P/A V V S E R(L)		151.6	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
21441	dirMS_041712_NAR_20mM_plus.19201.19201.2	2	5.08	0	8.88E+04		(R)ASVILAG	(R)A S V/I\L/A/G L G F/T P K(M)		203.98	637.3763	1273.751	-0.0061	-4.8	8.8	80142.6	5.95	HUMAN	Q9NUQ8	ATP-binding cassette sub-family F member 3
21442	dirMS_041712_NAR_20mM_plus.7977.7977.2	2	5.08	0	1.35E+05		(K)VEIIAND	(K)V/E|I I/A/N D Q G N R(T)		124.65	614.8177	1228.628	0.0001	0.1	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
21443	dirMS_041712_NAR_30mM_plus2.19563.19563.2	2	5.08	0	2.55E+05		(K)APDFVF'	(K)A P/D|F/V/F Y/A P R(L)		156.6	591.8008	1182.594	0.0001	0.1	5.88	71218.8	6.3	HUMAN	A7YIJ8	Radixin
21444	dirMS_041712_NAR_30mM_plus2.4844.4844.2	2	5.08	0	8.09E+05		(R)MGQTM	(R)M/G\Q/T/M E/R(I)		76.95	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
21445	dirMS_041712_NAR_40mM_plus2.5662.5662.2	2	5.08	0	1.28E+05		(K)INYTEGF	(K)I N|Y/T/E/G R(A)		90.6	426.7143	852.421	0.0003	0.4	6	16867	10.86	HUMAN	K7ELR7	Glucose-6-phosphate isomerase (Fragment)
21446	dirMS_041712_NAR_50mM_plus2.10982.10982.3	3	5.08	0	2.31E+05		(K)TKPYIQ\	(K)T K/P Y\I Q/V D I/G/G G Q T K(T)		125.32	535.6231	1604.864	-0.0095	-5.9	8.17	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
21447	dirMS_041712_NAR_50mM_plus2.16970.16970.3	3	5.08	0	7.73E+05		(R)QYYTLLI	(R)Q Y Y/T L/L N\Q/A/P D M L H R(K)		156.93	621.6447	1862.922	-0.0022	-1.2	6.74	4335.1	9.82	HUMAN	E5RH00	Ras GTPase-activating protein-binding protein 1
21448	dirMS_041712_NAR_50mM_plus2.17000.17000.3	3	5.08	1	3.71E+05		(K)LSKNEVI	(K)L S K N E V L M V N\I|G/S/L/S T G G R(V)		157	659.0229	1975.064	-0.0099	-5	8.75	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
21449	dirMS_041712_NAR_50mM_plus2.6188.6188.3	3	5.08	0	8.84E+04		(K)AGYSTD	(K)A G/Y S|T/D/E S S S S S/L H A T R(T)		97.38	585.9333	1755.778	0.0073	4.2	5.32	74564.3	5.95	HUMAN	P51116	Fragile X mental retardation syndrome-related protein 2
21450	dirMS_041712_NAR_60mM_plus.17061.17061.3	3	5.08	1	2.06E+05		(R)MRIESLS	(R)M R I E S L S S Q/L/S N/L|Q K(E)		146.28	578.6436	1733.921	-0.0052	-3	8.5	44813.6	4.99	HUMAN	E9PBF6	Lamin-B1
21451	dirMS_041712_NAR_60mM_plus.21216.21216.3	3	5.08	1	4.03E+05		(R)KAIIIFVP	(R)K A I I I\F\V/P V P Q L K(S)		174.23	489.3205	1465.95	-0.0035	-2.4	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
21452	dirMS_041712_NAR_60mM_plus.4887.4887.3	3	5.08	1	2.77E+04		(R)AAEEED	(R)A A/E E E/D E A D|P K/R(Q)		80.98	453.872	1359.602	-0.0008	-0.6	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
21453	dirMS_041712_NAR_60mM_plus.9099.9099.2	2	5.08	1	4.14E+05		(R)ALSTGEI	(R)A/L|S T/G E K G F G Y K(G)		105.68	629.3259	1257.647	-0.0029	-2.3	8.54	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
21454	dirMS_041712_NAR_120mM_minus.14294.14294.4	4	5.07	2	6.24E+05		(K)MEIATKI	(K)M/E I A T K D/P L N P I K Q D/V K(K)		131.67	485.7686	1940.052	0.0004	0.2	5.88	33115.9	5.54	HUMAN	Q15181	Inorganic pyrophosphatase
21455	dirMS_041712_NAR_20mM_minus.14437.14437.2	2	5.07	0	2.52E+05		(R)APGSGL	(R)A P/G/S G/L/A\L L\P L K(I)		198.32	568.8551	1136.704	-0.0008	-0.7	8.8	266161	5.68	HUMAN	E9PPU0	Epiplakin
21456	dirMS_041712_NAR_30mM_minus2.11485.11485.2	2	5.07	0	4.63E+05		(K)EIAEAYL	(K)E I/A/E/A Y/L/G K(T)		115.67	497.265	993.525	-0.0024	-2.4	4.53	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
21457	dirMS_041712_NAR_30mM_minus2.14150.14150.2	2	5.07	0	2.16E+05		(R)GANDFI	(R)G A\N D|F/M/C D/E/M E/R(S)	C:Carbamidomethylation	130.03	737.7725	1474.54	-0.0018	-1.2	3.91	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
21458	dirMS_041712_NAR_30mM_minus2.16721.16721.2	2	5.07	0	3.69E+05		(K)MIFVGII	(K)M/I/F V G/I K(K)		145.18	404.2383	807.48	-0.0104	-12.9	8.5	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
21459	dirMS_041712_NAR_30mM_minus2.8709.8709.2	2	5.07	0	5.08E+05		(R)GYSFTTI	(R)G Y|S\F/T\T T A E/R(E)		101.4	566.7699	1132.527	0.0056	4.9	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
21460	dirMS_041712_NAR_60mM_minus.18567.18567.3	3	5.07	0	2.76E+05		(K)TFLVWV	(K)T F L/V/W/V N E E D H L R(V)		165.73	553.2818	1657.833	-0.0024	-1.5	4.65	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
21461	dirMS_041712_NAR_20mM_plus.15637.15637.3	3	5.07	0	8.77E+03		(R)SSFYVN(	(R)S S F\Y V N G L/T L G/G Q K(C)		179.37	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
21462	dirMS_041712_NAR_20mM_plus.17741.17741.2	2	5.07	0	8.14E+04		(R)TTLLPGL	(R)T T|L L/P G L L K(T)		193.85	478.3131	955.619	0.0003	0.3	8.41	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
21463	dirMS_041712_NAR_20mM_plus.17775.17775.2	2	5.07	1	6.24E+03		(R)DNEKAL	(R)D/N E K\A/L/P\V L K(R)		193.3	563.8196	1126.647	-0.0147	-13.1	6.07	19968.3	5.39	HUMAN	Q9NWS1-3	Isoform 3 of PCNA-interacting partner
21464	dirMS_041712_NAR_20mM_plus.8690.8723.2	2	5.07	0	1.10E+05	M118m	(R)mVVPA/	(R)m/V|V|P A A L/K(V)	m:Oxidized methionine	130.37	422.7485	828.501	15.9886	-7.5	8.5	23633.9	11.02	HUMAN	P40429	60S ribosomal protein L13a
21465	dirMS_041712_NAR_30mM_plus2.20533.20833.2	2	5.07	0	4.62E+05		(R)QINWT\	(R)Q I/N/W/T V/L/Y R(R)		162.88	596.8315	1192.647	0.0084	7	8.75	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
21466	dirMS_041712_NAR_30mM_plus2.21912.21912.2	2	5.07	0	1.03E+05		(K)NFYFLEI	(K)N F|Y|F/L E M N T/R(L)		170.5	667.8205	1334.62	0.0139	10.4	6	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
21467	dirMS_041712_NAR_40mM_plus2.5659.5659.2	2	5.07	0	1.28E+05		(K)INYTEGF	(K)I/N/Y/T/E G R(A)		90.6	426.7143	852.421	0.0003	0.4	6	16867	10.86	HUMAN	K7ELR7	Glucose-6-phosphate isomerase (Fragment)
21468	dirMS_041712_NAR_50mM_plus2.11185.11185.3	3	5.07	1	1.17E+06		(K)VGDKVL	(K)V G D K V L L/P E Y/G G T K(V)		126.95	492.6069	1475.81	-0.0043	-2.9	6.04	5189.9	4.56	HUMAN	B8ZZ54	10 kDa heat shock protein, mitochondrial

21469	dirMS_041712_NAR_50mM_plus2.11855.11855.3	3	5.07	1	1.45E+05	K868k	(K)LMEADK	(K)L M/E A D K|A/Q/T G Q V k(L)	k:Ubiquitin-K	130.77	511.6035	1418.731	114.0652	14.5	6.07	161690.4	6.32	HUMAN	I3L4X2	Multidrug resistance-associated protein 1 (Fragment)
21470	dirMS_041712_NAR_50mM_plus2.14118.14118.3	3	5.07	0	1.41E+05		(R)GLTSPS	(R)G L/T S P S/Q L L T S/E S I Q T K(E)		142.43	597.3178	1789.954	-0.0153	-8.6	6	261905	6.07	HUMAN	Q9P212	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase epsilon-1
21471	dirMS_041712_NAR_50mM_plus2.18934.18934.3	3	5.07	0	9.07E+05		(R)CRPDQL	(R)C R P D Q\L\T|G L S|L/L/P L S E K(A)	C:Carbamidomethylation	167.52	643.0148	1927.032	-0.0019	-1	6.07	533778	5.74	HUMAN	Q15149	Plectin
21472	dirMS_041712_NAR_50mM_plus2.20818.20818.3	3	5.07	1	8.31E+03		(R)VTRLPLL	(R)V T R L P\L\L\M/D T\L C L K(T)	C:Carbamidomethylation	178.12	558.3196	1672.949	-0.0046	-2.7	8.72	20868.8	9.29	HUMAN	B0QZD4	Rho guanine exchange factor (GEF) 16 (Fragment)
21473	dirMS_041712_NAR_60mM_plus.14297.14297.3	3	5.07	1	6.34E+05		(K)WKDSD	(K)W K D S D E/A/D L/V/L/A K(E)		131.07	497.2559	1489.753	-0.0002	-0.1	4.23	20982.2	5.23	HUMAN	Q13185	Chromobox protein homolog 3
21474	dirMS_041712_NAR_60mM_plus.17165.17165.3	3	5.07	0	1.58E+05		(R)SGGLGG	(R)S G G L/G G S H A L/L/L L/R(S)		146.32	450.9323	1350.785	-0.0029	-2.1	9.49	56801.9	8.81	HUMAN	B8ZZ38	Leucine-rich PPR motif-containing protein, mitochondrial
21475	dirMS_041712_NAR_60mM_plus.19639.19639.3	3	5.07	0	1.33E+05		(R)NSVSNF	(R)N/S/V/S N F L/H S L E R(G)		161.23	468.2401	1402.707	-0.0016	-1.1	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
21476	dirMS_041712_NAR_60mM_plus.9561.9561.2	2	5.07	0	1.93E+05		(K)GHENVE	(K)G H|E\N V E A A\Q\A\E Y/I/E K(F)		107.83	844.3982	1687.792	-0.0031	-1.8	4.48	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
21477	dirMS_041712_NAR_120mM_minus.9589.9589.3	3	5.06	0	4.38E+05		(K)QEYDES	(K)Q E Y D E S G/P S/I/V/H/R(K)		107.47	506.2424	1516.703	0.01	6.6	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
21478	dirMS_041712_NAR_20mM_minus.11772.11772.2	2	5.06	0	1.07E+05	M98m	(R)TLTIVDT	(R)T L\T I/V/D/T G/I G m T K(A)	m:Oxidized methionine	166.87	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
21479	dirMS_041712_NAR_30mM_minus2.16328.16328.2	2	5.06	0	1.09E+05		(K)FGVIFA	(K)F/G\V/I/F\A/G A Q K(N)		141.95	519.2901	1037.578	-0.0049	-4.7	8.75	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
21480	dirMS_041712_NAR_40mM_minus2.7237.7237.3	3	5.06	1	1.85E+04	M265m	(K)AVEEED	(K)A V/E E E D K m T/P E/Q L A I K(N)	m:Oxidized methionine	116.48	616.3078	1830.915	15.9935	-0.8	4.25	34747.6	6.06	HUMAN	O00487	26S proteasome non-ATPase regulatory subunit 14
21481	dirMS_041712_NAR_40mM_minus2.8324.8324.3	3	5.06	1	3.09E+03		(R)DYSGQ	(R)D Y|S G Q G/V V K L/D V Q P K(C)		129.8	544.958	1632.859	0.0003	0.2	5.96	66876.9	6.17	HUMAN	O75083	WD repeat-containing protein 1
21482	dirMS_041712_NAR_50mM_minus2.10334.10334.3	3	5.06	1	9.57E+03		(K)AELEIQK	(K)A E|L E I/Q K D A L E/P G Q R(V)		126.97	566.2988	1696.886	-0.0046	-2.7	4.41	14613.6	6.73	HUMAN	G5E9J2	Adenine phosphoribosyltransferase
21483	dirMS_041712_NAR_50mM_minus2.12549.12549.3	3	5.06	1	2.27E+05	M2709m	(K)ISmPDI	(K)I S/m/P/D I D L\N L K/G P K(V)	m:Oxidized methionine	139.5	519.6148	1540.84	15.9895	-3.5	5.96	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
21484	dirMS_041712_NAR_50mM_minus2.12967.12967.3	3	5.06	0	4.41E+04		(K)AASDIA	(K)A A/S D I/A M T E L/P/P\T H P I R(L)		141.1	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
21485	dirMS_041712_NAR_60mM_minus.15089.15089.3	3	5.06	0	3.51E+04		(K)AFSLNS	(K)A F S L/N S N L\V/L/H Q R(I)		143.9	500.2735	1498.813	-0.0065	-4.4	9.8	40178.9	9.55	HUMAN	B3KRF7	Zinc finger protein with KRAB and SCAN domains 1
21486	dirMS_041712_NAR_60mM_minus.15380.15380.3	3	5.06	1	2.23E+05		(R)GPIKFN	(R)G P I K F N\V|W|D/T A G Q E K(F)		146.48	563.9575	1689.86	-0.0015	-0.9	6.07	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
21487	dirMS_041712_NAR_60mM_minus.16674.16674.3	3	5.06	1	2.20E+05		(R)GQFSTD	(R)G Q|F S T D E/L/V/A E V E K R(N)		153.65	569.9569	1707.855	0.0013	0.8	4.41	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
21488	dirMS_041712_NAR_120mM_plus.10234.10234.2	2	5.06	0	5.25E+05		(R)VHIEIGP	(R)V/H\I\E/I\G P D/G R(V)		105.87	546.7931	1092.58	-0.0007	-0.6	5.32	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
21489	dirMS_041712_NAR_20mM_plus.10882.10882.2	2	5.06	0	4.96E+03		(K)VVLIGDS	(K)V V/L/I/G D/S G V/G\K(S)		146.02	522.3072	1043.61	-0.0024	-2.3	5.81	16628.4	5.19	HUMAN	B4DQU5	Ras-related protein Rab-11A
21490	dirMS_041712_NAR_20mM_plus.12643.12643.3	3	5.06	0	7.26E+04		(K)GTIQVIT	(K)G T\I\Q/V I T Q/G T S L K(N)		160.1	449.261	1345.769	-0.0001	-0.1	8.75	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
21491	dirMS_041712_NAR_30mM_plus2.15964.15964.2	2	5.06	0	8.88E+05		(R)GDLGIE	(R)G D/L G\I|E I/P A E K(V)		137.35	571.3087	1141.61	0.0002	0.2	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
21492	dirMS_041712_NAR_30mM_plus2.9921.9944.2	2	5.06	0	1.68E+06		(K)GSFSDT	(K)G S/F/S/D/T/G L/G D G K(M)		106.02	570.7598	1140.517	-0.0044	-3.9	4.21	108720.9	10.17	HUMAN	Q9Y2W1	Thyroid hormone receptor-associated protein 3
21493	dirMS_041712_NAR_40mM_plus2.10814.10814.3	3	5.06	1	4.32E+05		(R)DGKLVS	(R)D/G K\L V S E/S/S D V L|P K(-)		128.65	491.9315	1473.78	0.0004	0.3	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
21494	dirMS_041712_NAR_40mM_plus2.14986.14986.3	3	5.06	0	6.60E+04		(R)QAQEYE	(R)Q A\Q E Y E/A/L|L N I/K(V)		154.73	473.9204	1419.748	-0.0012	-0.8	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
21495	dirMS_041712_NAR_50mM_plus2.12999.12999.3	3	5.06	0	2.22E+04	S335s	(R)sNSVEK	(R)s N/S V E K P/V S S I L S R(T)	s:N-acetylglucosamine (S)	137.18	569.2948	1502.817	203.0525	-15.7	8.46	41747.8	9.58	HUMAN	B7Z3I5	Ena/VASP-like protein
21496	dirMS_041712_NAR_50mM_plus2.14018.14018.3	3	5.06	1	9.56E+03		(K)LLQSIGC	(K)L L|Q/S\I/G Q A/P E S I S E K\E L K(L)		141.2	657.3638	1970.08	-0.0036	-1.8	4.79	60972	5.25	HUMAN	A6NCK0	NEDD8-activating enzyme E1 regulatory subunit
21497	dirMS_041712_NAR_50mM_plus2.21589.21589.3	3	5.06	1	1.07E+04		(R)SKAEEL	(R)S K A E E L G L|P/I|L/G V L R(S)		183.92	532.3178	1594.953	-0.0138	-8.7	5.87	40725.2	9.61	HUMAN	C9JDE9	3-ketoacyl-CoA thiolase, peroxisomal
21498	dirMS_041712_NAR_60mM_plus.10967.10967.3	3	5.06	1	1.18E+06		(R)EKLEME	(R)E K L\E/M E/M E/A/A R(H)		115.43	446.2162	1336.623	0.0105	7.9	4.49	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)
21499	dirMS_041712_NAR_120mM_minus.17819.17819.4	4	5.05	1	2.52E+05		(K)SKNILFV	(K)S K N I L/F/V/I T K/P D V Y K(S)		151.37	442.0108	1765.026	-0.0045	-2.5	9.53	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
21500	dirMS_041712_NAR_20mM_minus.11226.11226.2	2	5.05	0	1.10E+05	M316m	(R)ISEQFTA	(R)I S\E/Q/F/T/A m F R(R)	m:Oxidized methionine	159.05	623.3005	1229.598	15.9954	0.4	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
21501	dirMS_041712_NAR_30mM_minus2.16682.16682.2	2	5.05	0	2.37E+05		(K)NAAGAL	(K)N/A|A/G A/L D L L K(E)		144.18	493.2881	985.568	0.0013	1.3	5.84	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
21502	dirMS_041712_NAR_30mM_minus2.16704.16704.2	2	5.05	0	4.52E+05	M834m T8	(R)mTQLtV	(R)m T/Q/L t V E K(V)	m:Oxidized methionine t:N-a	144.43	584.7961	949.502	219.0826	7.1	5.75	271875.5	5.65	HUMAN	A2RRP1	Neuroblastoma-amplified sequence
21503	dirMS_041712_NAR_30mM_minus2.17766.17766.2	2	5.05	0	2.91E+05		(K)EAFQLF	(K)E A F/Q/L F D/R(T)		151.6	513.2571	1025.505	0.0019	1.8	4.37	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
21504	dirMS_041712_NAR_30mM_minus2.19487.19487.2	2	5.05	0	3.36E+05		(R)ASLSLW	(R)A S L|S/L/W Q A M E K(G)		162.42	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
21505	dirMS_041712_NAR_50mM_minus2.12763.12763.3	3	5.05	0	1.05E+05		(R)NFDLTA	(R)N F|D\L T A/I P C A N H K(M)	C:Carbamidomethylation	140.93	500.914	1500.726	0.0011	0.7	6.74	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
21506	dirMS_041712_NAR_50mM_minus2.8115.8115.3	3	5.05	1	1.41E+05		(K)GILAAD	(K)G I/L/A/A D E S/T G S I A K R(L)		113.83	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
21507	dirMS_041712_NAR_60mM_minus.15725.15725.3	3	5.05	1	2.99E+05		(R)GFPTIYF	(R)G F/P T I Y/F S P A N K K(L)		147.22	490.5972	1469.779	-0.0017	-1.1	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
21508	dirMS_041712_NAR_60mM_minus.7915.7915.3	3	5.05	0	9.10E+04		(K)STGEPL	(K)S T|G E\P/L G H V P A R(M)		103.75	407.5515	1220.638	0.0017	1.4	6.47	9840	8.09	HUMAN	C9J1K7	Lipoma-preferred partner (Fragment)
21509	dirMS_041712_NAR_120mM_plus.20554.20554.3	3	5.05	0	3.50E+05		(K)VHLVGI	(K)V H L V\G I/D\I/F T/G K(K)		161.58	433.5874	1298.747	0.0009	0.7	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
21510	dirMS_041712_NAR_20mM_plus.10221.10221.2	2	5.05	0	6.33E+04		(K)GYDVIA	(K)G Y D V I/A|Q A/Q S G/T G K(T)		142.97	697.846	1394.691	-0.0063	-4.5	5.83	16071.1	4.8	HUMAN	B4E102	Eukaryotic initiation factor 4A-I
21511	dirMS_041712_NAR_20mM_plus.11435.11435.2	2	5.05	0	2.11E+05		(R)YALYDA	(R)Y/A\L/Y/D A T\Y E T K(E)		151.17	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
21512	dirMS_041712_NAR_20mM_plus.13537.13537.2	2	5.05	0	2.18E+05		(R)GALQNI	(R)G A/L/Q/N|I/I\P A S T G A A K(A)		166.53	706.3975	1411.79	-0.0026	-1.9	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
21513	dirMS_041712_NAR_20mM_plus.17773.17773.3	3	5.05	0	1.12E+04		(R)IINEPTA	(R)I I N\E P T A A A\I/A/Y/G L D R(T)		193.42	563.3055	1687.901	0.0006	0.3	4.37	25598.3	6.45	HUMAN	E7EP11	Heat shock 70 kDa protein 1A/1B
21514	dirMS_041712_NAR_30mM_plus2.15862.15862.2	2	5.05	0	4.03E+05		(R)MGPNIY	(R)M/G/P|N/I Y\E|L/R(T)		136.35	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
21515	dirMS_041712_NAR_40mM_plus2.13949.13949.3	3	5.05	1	1.95E+05		(R)GDVVPK	(R)G D V/V P K D V N A A I/A/T I K(T)		147.7	537.6381	1610.911	-0.0115	-7.1	5.96	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
21516	dirMS_041712_NAR_40mM_plus2.8023.8023.2	2	5.05	0	3.33E+04		(R)SGQGAF	(R)S G/Q/G\A/F\G N M C R(G)	C:Carbamidomethylation	107.53	592.7523	1184.494	0.0038	3.2	9.47	18988.7	11.2	HUMAN	H3BTP7	60S ribosomal protein L4 (Fragment)
21517	dirMS_041712_NAR_50mM_plus2.17605.17605.3	3	5.05	1	5.25E+05		(K)VKLAAV	(K)V K L A A V D A\T V/N Q/V|L/A S/R(Y)		160.33	585.6736	1755.012	-0.0061	-3.5	8.72	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
21518	dirMS_041712_NAR_50mM_plus2.6714.6714.3	3	5.05	1	4.03E+04		(R)AAPGAE	(R)A A/P G A E/F A/P N K R(R)		100.23	410.218	1228.643	-0.0038	-3.1	8.79	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
21519	dirMS_041712_NAR_50mM_plus2.9244.9244.3	3	5.05	0	1.91E+05		(K)TAVEHA	(K)T A/V E H/A/T D\E D I L A K(G)		115.42	504.9238	1512.754	0.0028	1.9	4.31	288852.1	5.33	HUMAN	E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein
21520	dirMS_041712_NAR_50mM_plus2.9986.9986.3	3	5.05	1	2.46E+06		(K)ATAVVD	(K)A T|A V V D G A F/K E V K(L)		120.07	445.5822	1334.731	0.0006	0.5	6.11	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
21521	dirMS_041712_NAR_60mM_plus.12946.12946.3	3	5.05	0	5.53E+05		(R)SGGME	(R)S/G/G|M/E R P F V L A R(A)		124.78	440.5673	1319.689	-0.0015	-1.2	9.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
21522	dirMS_041712_NAR_60mM_plus.18415.18415.3	3	5.05	0	2.10E+05		(K)DHGLEV	(K)D H G\L E\V|L/G L V/R(V)		153.62	403.2318	1207.679	0.0015	1.2	5.32	17732.8	5.85	HUMAN	F5GYJ1	U8 snoRNA-decapping enzyme
21523	dirMS_041712_NAR_60mM_plus.8262.8262.3	3	5.05	1	5.45E+05		(R)LSQIGV	(R)L/S/Q I/G V/E N T E E N R R(L)		101.4	548.9468	1644.83	-0.0041	-2.5	4.79	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
21524	dirMS_041712_NAR_30mM_minus2.12112.12112.2	2	5.04	0	4.12E+04		(K)GISQEQ	(K)G I/S Q/E Q M/Q E F/R(A)		119.47	676.8161	1352.626	-0.0014	-1	4.53	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
21525	dirMS_041712_NAR_40mM_minus2.12049.12049.3	3	5.04	1	1.80E+05		(K)AGTQIE	(K)A/G/T Q/I/E N/I D E D F R D G L K(L)		153.87	640.9843	1920.93	0.0086	4.5	4.11	59872.5	4.85	HUMAN	F5GXS2	Alpha-actinin-4
21526	dirMS_041712_NAR_50mM_minus2.13119.13119.3	3	5.04	0	7.05E+04	N382n	(K)NVALLA	(K)N V A L/L A|Y n R(W)	n:N-acetylglucosamine (N)	142.73	412.8971	1033.579	203.0978	14.9	8.75	45849.5	6.35	HUMAN	E7EVZ5	Prenylcysteine oxidase-like
21527	dirMS_041712_NAR_50mM_minus2.17846.17846.3	3	5.04	0	1.39E+05		(K)TTLLNYI	(K)T T/L/L\N Y\I/L T E Q H S K(R)		170.47	554.3024	1660.891	0.0022	1.3	6.41	42238.2	4.88	HUMAN	B4DNG9	COBW domain-containing protein 3
21528	dirMS_041712_NAR_50mM_minus2.9432.9432.3	3	5.04	0	6.17E+04		(R)DLSKPIG	(R)D L/S K/P I G A L N/P K(R)		121.75	418.2465	1252.726	-0.001	-0.8	8.59	84798.4	5.92	HUMAN	B7Z2H9	Neurobeachin
21529	dirMS_041712_NAR_60mM_minus.15477.15477.3	3	5.04	0	2.13E+05		(K)EGHVEV	(K)E G H V E\V V|S E L/L Q R(E)		145.9	498.9349	1494.791	-0.0009	-0.6	4.75	48586.6	9.32	HUMAN	D6RCB2	Ankyrin-3
21530	dirMS_041712_NAR_120mM_plus.21068.21068.3	3	5.04	1	1.96E+05		(K)IKYPENF	(K)I/K Y P E N F F/L/L/R(G)		164.05	480.6058	1439.805	-0.0017	-1.2	8.59	33222.3	5.74	HUMAN	A6NNR3	Serine/threonine-protein phosphatase
21531	dirMS_041712_NAR_120mM_plus.22563.22563.4	4	5.04	1	1.52E+04		(K)SKGLAP	(K)S K G L A\P D L/P/E D L Y H L I K(K)		172.08	478.0137	1909.043	-0.01	-5.2	5.36	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
21532	dirMS_041712_NAR_120mM_plus.4298.4298.2	2	5.04	0	2.79E+05	M46m M4	(R)HQGVm	(R)H Q/G V m V G m G/Q K(D)	m:Oxidized methionine	70.93	602.2829	1171.571	31.9875	-2	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
21533	dirMS_041712_NAR_20mM_plus.14124.14124.2	2	5.04	0	9.68E+04		(R)ELAVQI	(R)E L|A/V/Q I/Y E/E A R(K)		169.83	660.839	1320.679	-0.0087	-6.6	4.25	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
21534	dirMS_041712_NAR_20mM_plus.18479.18479.3	3	5.04	0	1.88E+04		(R)APVPAS	(R)A P V P A\S E L\L/A/S G/V/L/S R(A)		199.92	522.9655	1566.885	-0.003	-1.9	6.05	533778	5.74	HUMAN	Q15149	Plectin
21535	dirMS_041712_NAR_40mM_plus2.5707.5707.2	2	5.04	0	1.12E+05		(R)FSSSSGY	(R)F/S/S S/S|G Y|G G G S S R(V)		90.98	618.2686	1235.529	0.0012	1	8.75	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
21536	dirMS_041712_NAR_50mM_plus2.17734.17734.3	3	5.04	0	3.57E+05		(R)LLLDIPL	(R)L L L D I|P L/Q T/P H K(L)		160.8	463.2819	1387.831	0.0004	0.3	6.74	198852.6	5.95	HUMAN	A6NKT7	RanBP2-like and GRIP domain-containing protein 3
21537	dirMS_041712_NAR_50mM_plus2.19856.19856.3	3	5.04	1	4.75E+04		(K)AKINEA	(K)A K I\N E A\V/E C/L L S/L K(A)	C:Carbamidomethylation	172.82	529.9621	1587.878	-0.0057	-3.6	6.18	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
21538	dirMS_041712_NAR_50mM_plus2.21481.21481.3	3	5.04	1	1.45E+05		(K)ALFEEVF	(K)A L/F/E E V/P E/L L T E A E K K(E)		182.72	615.9987	1845.984	-0.0029	-1.6	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
21539	dirMS_041712_NAR_50mM_plus2.7880.7880.3	3	5.04	0	2.22E+04		(R)DGQVIN	(R)D G|Q V/I/N E\T S Q H H D D L E(-)		108.25	612.9457	1836.8	0.0231	12.6	4.28	53707.8	5.06	HUMAN	P08670	Vimentin
21540	dirMS_041712_NAR_50mM_plus2.8436.8436.3	3	5.04	1	1.45E+05		(R)TTKSPS	(R)T T K S P S D S\G|Y|S/Y E T/I/G K(T)		111.5	607.6222	1820.855	-0.0028	-1.5	5.74	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
21541	dirMS_041712_NAR_120mM_minus.18813.18813.4	4	5.03	1	4.17E+05	T119t	(R)KLSLGV	(R)K L S\L G V A E t A A\V M/S L L/T R(T)	t:Phosphorylated T	157.15	485.7686	1860.062	79.9903	12.3	8.75	14729.7	9.69	HUMAN	Q9H7H1	Putative uncharacterized protein encoded by RUNX1-IT1
21542	dirMS_041712_NAR_120mM_minus.8602.8602.3	3	5.03	1	5.01E+04		(R)LKVTEG	(R)L K V T E|G G E|P\Y/R(L)		101.15	416.885	1248.658	-0.0178	-14.3	6.14	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
21543	dirMS_041712_NAR_20mM_minus.14615.14615.3	3	5.03	0	3.68E+05		(K)LAVEALS	(K)L A/V E A L/S\S L D/G D L/A G R(Y)		201.3	529.6163	1586.838	-0.0041	-2.6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
21544	dirMS_041712_NAR_30mM_minus2.12448.12448.2	2	5.03	0	1.26E+05		(K)SIYYITG	(K)S I|Y Y/I/T G E S K(E)		121.13	580.7949	1160.583	-0.0009	-0.7	5.72	16789.1	8.77	HUMAN	H0Y5S7	Heat shock protein HSP 90-beta (Fragment)
21545	dirMS_041712_NAR_30mM_minus2.18544.18544.2	2	5.03	0	4.15E+04		(R)GIFPVLC	(R)G I|F|P V/L/C K(D)	C:Carbamidomethylation	155.43	467.2718	933.523	0.0137	14.7	8.75	53557.7	6.39	HUMAN	H3BTN5	Pyruvate kinase (Fragment)
21546	dirMS_041712_NAR_30mM_minus2.8584.8584.2	2	5.03	0	9.70E+04		(K)IDDVVN	(K)I/D|D|V/V N T R(-)		101.97	466.2472	931.484	0.0028	3	4.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
21547	dirMS_041712_NAR_50mM_minus2.12578.12578.3	3	5.03	1	3.53E+05		(K)NTVELL	(K)N/T\V/E/L/L/V E D K/G N Q V Y R(C)		140.3	626.3309	1876.976	0.0018	1	4.68	258215.9	5.48	HUMAN	E7EN95	Filamin-B
21548	dirMS_041712_NAR_50mM_minus2.13632.13632.3	3	5.03	0	5.40E+05		(K)LQMEAF	(K)L Q|M E A/P H I/I V/G/T P G R(V)		145.62	540.2947	1618.873	-0.0038	-2.4	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
21549	dirMS_041712_NAR_50mM_minus2.18191.18191.3	3	5.03	1	2.37E+05		(K)LKEAELL	(K)L K E A E L L|E|P\L\M/P A I R(A)		172.75	574.9957	1722.982	-0.0097	-5.6	4.79	56164.6	6.01	HUMAN	E9PP73	Coatomer subunit beta (Fragment)
21550	dirMS_041712_NAR_60mM_minus.17955.17955.3	3	5.03	1	5.33E+04		(K)VKLAAV	(K)V K L A A V D A T V/N\Q/V L/A S/R(Y)		161.3	585.6728	1755.012	-0.0085	-4.8	8.72	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
21551	dirMS_041712_NAR_60mM_minus.18042.18042.3	3	5.03	0	1.00E+05		(R)CRPQED	(R)C R P Q E D T\G W V/L/F P V N K(A)	C:Carbamidomethylation	161.85	649.3238	1945.959	-0.002	-1.1	6.07	558007.1	5.44	HUMAN	P58107	Epiplakin
21552	dirMS_041712_NAR_60mM_minus.7751.7751.3	3	5.03	1	7.39E+04		(R)MLQADI	(R)M/L/Q|A D/P N K V/S A R(A)		103.22	443.9018	1329.694	-0.0035	-2.6	8.5	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
21553	dirMS_041712_NAR_120mM_plus.16144.16144.4	4	5.03	1	1.07E+06		(R)YAEIVHL	(R)Y A/E I V H L/T L/P D/G T K/R(S)		138.78	428.9885	1712.933	-0.0008	-0.5	6.75	21230	6.36	HUMAN	H0YC04	V-type proton ATPase subunit B, brain isoform (Fragment)
21554	dirMS_041712_NAR_120mM_plus.4172.4172.3	3	5.03	1	1.73E+07	M310m	(R)TKTEISE	(R)T K T E I/S E/m N R(N)	m:Oxidized methionine	69.83	408.8687	1208.594	15.9976	2.2	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
21555	dirMS_041712_NAR_120mM_plus.4416.4416.3	3	5.03	1	3.08E+05		(K)AGADEE	(K)A/G\A D/E E/R/A E T A R(L)		71.55	425.869	1275.592	0.0001	0.1	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
21556	dirMS_041712_NAR_20mM_plus.10028.10028.2	2	5.03	0	1.71E+05		(K)GEATVS	(K)G E A/T\V/S/F/D D/P/P S A K(A)		140.67	710.8324	1420.659	-0.0015	-1.1	4.03	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
21557	dirMS_041712_NAR_30mM_plus2.22160.22160.2	2	5.03	0	1.39E+05		(K)ETLLAM	(K)E T\L/L/A/M F/K(Y)		171	476.7621	952.517	-0.0003	-0.3	6.1	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
21558	dirMS_041712_NAR_40mM_plus2.10251.10251.2	2	5.03	0	1.27E+05		(R)QINLSN	(R)Q I/N/L/S N/I R(A)		124.97	479.2747	957.548	-0.0055	-5.7	9.75	102679.8	6.75	HUMAN	Q7KZF4	Staphylococcal nuclease domain-containing protein 1
21559	dirMS_041712_NAR_40mM_plus2.12133.12133.3	3	5.03	1	2.39E+05		(R)VVDALG	(R)V V/D/A L G N/A I\D G K G P I G S K(T)		137.15	570.9838	1710.939	-0.0016	-1	5.93	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
21560	dirMS_041712_NAR_50mM_plus2.10616.10616.3	3	5.03	1	2.36E+06		(R)MQKEIT	(R)M Q K E I T A\L|A|P S T M K(I)		123.98	516.9418	1548.812	-0.0016	-1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
21561	dirMS_041712_NAR_50mM_plus2.11604.11604.3	3	5.03	0	3.55E+05		(K)SNMGH	(K)S N M/G/H\P E/P A/S G L/A A L A K(V)		128.5	550.9462	1650.827	-0.0028	-1.7	6.47	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
21562	dirMS_041712_NAR_50mM_plus2.19265.19265.3	3	5.03	1	1.15E+05		(K)GLKVNL	(K)G L K\V N L\F|P|G L S P S A/L K(A)		169.47	547.6608	1640.973	-0.0056	-3.4	10	182819.3	4.77	HUMAN	Q9C0C2	182 kDa tankyrase-1-binding protein
21563	dirMS_041712_NAR_50mM_plus2.20888.20888.3	3	5.03	1	1.93E+05		(R)GGGNQ	(R)G G/G N/Q/V/S L L N V/V M D L K K(C)		178.88	591.3291	1771.974	-0.0007	-0.4	8.59	218583	5.58	HUMAN	F5GWX5	Chromodomain-helicase-DNA-binding protein 4
21564	dirMS_041712_NAR_50mM_plus2.5269.5269.3	3	5.03	0	3.48E+05	M116m	(R)ATAPQT	(R)A T/A P Q T Q H/V/S P m R(Q)	m:Oxidized methionine	87.5	480.5727	1423.711	15.9925	-1.7	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
21565	dirMS_041712_NAR_60mM_plus.19495.19495.3	3	5.03	0	1.33E+05		(R)NSVSNF	(R)N S|V/S N/F L H S L E R(G)		161.23	468.2401	1402.707	-0.0016	-1.1	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
21566	dirMS_041712_NAR_60mM_plus.5095.5095.3	3	5.03	1	3.95E+05		(R)AAEDDE	(R)A/A/E D D E D D D V D T K/K(Q)		83.53	522.5529	1565.645	-0.0008	-0.5	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
21567	dirMS_041712_NAR_60mM_plus.8296.8296.3	3	5.03	1	5.99E+05		(K)AAYEAE	(K)A A/Y E/A E/L G D/A R K(T)		101.2	431.8884	1293.643	0.0073	5.6	4.68	74423.5	6.57	HUMAN	P02545	Prelamin-A/C
21568	dirMS_041712_NAR_60mM_plus.8581.8581.3	3	5.03	1	5.18E+05		(K)ICEPGYS	(K)I/C/E|P/G Y S P T Y\K Q D K(H)	C:Carbamidomethylation	102.07	562.5983	1685.784	-0.0036	-2.1	6.07	38790.8	5.88	HUMAN	P07858	Cathepsin B
21569	dirMS_041712_NAR_120mM_minus.9486.9486.3	3	5.02	1	1.75E+05		(K)IRSLQEC	(K)I R/S L/Q\E Q/A D/A/A E E R(A)		106.8	539.2683	1615.803	-0.0131	-8.1	4.41	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
21570	dirMS_041712_NAR_20mM_minus.10143.10143.3	3	5.02	0	3.04E+04		(K)IEDLSQC	(K)I/E D L S Q Q/A\Q/L/A/A A E K(F)		151.12	538.9478	1614.833	-0.0045	-2.8	4.14	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
21571	dirMS_041712_NAR_30mM_minus2.18326.18326.2	2	5.02	0	9.87E+03		(K)LNLGTV	(K)L/N|L/G/T V G\F Y R(T)		154.28	570.3115	1139.621	-0.005	-4.4	8.75	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
21572	dirMS_041712_NAR_40mM_minus2.14112.14112.3	3	5.02	0	6.60E+05		(R)IHFPLAT	(R)I H F P L A T Y|A|P V/I S A E K(A)		167.77	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
21573	dirMS_041712_NAR_40mM_minus2.14445.14445.3	3	5.02	1	1.30E+05		(R)LKLPSIP	(R)L K L P\S I/P L V/P V S A Q K(R)		169.43	530.6703	1589.999	-0.0025	-1.6	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
21574	dirMS_041712_NAR_50mM_minus2.13067.13067.3	3	5.02	1	1.64E+05		(R)NVIFQP	(R)N V|I F Q/P V A E L K K(Q)		142.7	462.6086	1385.815	-0.0039	-2.8	8.59	23167	8.94	HUMAN	B1APP8	6-phosphofructokinase type C
21575	dirMS_041712_NAR_50mM_minus2.16122.16122.2	2	5.02	1	1.53E+05		(R)VSFELFA	(R)V/S|F E/L F A D K/V|P K(T)		159.72	690.3821	1379.757	0	0	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
21576	dirMS_041712_NAR_50mM_minus2.9916.9916.3	3	5.02	0	1.19E+05	M392m	(K)EmNPAL	(K)E/m N P A L|G/I|D C L H K(G)	C:Carbamidomethylation m:Oxid	125.25	505.2416	1497.719	15.9914	-2.3	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
21577	dirMS_041712_NAR_60mM_minus.14759.14759.3	3	5.02	1	5.91E+05		(K)TDKTLV	(K)T D\K T L\V\L/L/M/G/K(E)		142.57	406.9088	1218.713	-0.0008	-0.6	8.26	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b

21578	dirMS_041712_NAR_60mM_minus.5151.5151.3	3	5.02	1	2.94E+03		(K)TSSDPT(	(K)T S/S/D/P T/C V E K\E/K(V)	C:Carbamidomethylation	82.53	460.8816	1380.631	-0.0009	-0.6	4.68	15390.6	7.96	HUMAN	C9J673	Exportin-1 (Fragment)
21579	dirMS_041712_NAR_60mM_minus.9778.9843.3	3	5.02	1	7.94E+05		(K)TLEDPDI	(K)T L|E/D/P D/L N V R R(V)		114.83	443.2407	1327.697	0.0111	8.4	4.55	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
21580	dirMS_041712_NAR_120mM_plus.4168.4168.2	2	5.02	1	1.45E+06	M310m	(R)TKTEISE	(R)T K|T E|I/S E m N R(N)	m:Oxidized methionine	69.8	612.7976	1208.594	15.994	-0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
21581	dirMS_041712_NAR_120mM_plus.4526.4526.3	3	5.02	0	5.96E+05		(R)THSQGG	(R)T H\S Q G\G\Y\G/S/Q G Y/K(Y)		74.03	457.2092	1369.613	-0.0001	-0.1	8.2	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
21582	dirMS_041712_NAR_20mM_plus.10466.10466.2	2	5.02	0	1.88E+05	M592m M!	(R)mGPAm	(R)m G/P A m|G/P A L/G A G I/E R(M)	m:Oxidized methionine	144.65	730.3568	1427.713	31.993	2.1	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
21583	dirMS_041712_NAR_20mM_plus.15614.15614.3	3	5.02	0	8.77E+03		(R)SSFYVN(	(R)S S F Y/V N\G\L/T|L/G G Q K(C)		179.37	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
21584	dirMS_041712_NAR_20mM_plus.18400.18400.3	3	5.02	0	7.58E+04		(K)ITSEALL\	(K)I T S E A L\L/V/T/Q Q L V K(A)		198.28	514.9762	1542.91	0.0039	2.5	6	50425	5.53	HUMAN	H0YH27	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
21585	dirMS_041712_NAR_40mM_plus2.20016.20016.3	3	5.02	1	5.56E+05		(K)EGGLGP	(K)E G G L|G/P L/N I/P L L A D V\T R R(L)		189.75	631.0288	1891.076	-0.0041	-2.2	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
21586	dirMS_041712_NAR_50mM_plus2.10295.10295.3	3	5.02	2	3.17E+04	Y831y	(R)LSGIEER	(R)L S G I/E E/R\y K E V\A E L T R(L)	y:Phosphorylated Y	121.53	658.3369	1893.008	79.9885	11.3	4.95	275403.1	5.39	HUMAN	Q01082	Spectrin beta chain, non-erythrocytic 1
21587	dirMS_041712_NAR_50mM_plus2.12472.12472.3	3	5.02	1	6.29E+05	S22s	(K)LVVFDT:	(K)L V V/F D T s L Q/V/K K(A)	s:Phosphorylated S	132.97	486.2644	1376.815	79.9639	-1.7	8.59	34254.3	8.79	HUMAN	B4DDT7	5'-AMP-activated protein kinase subunit gamma-1
21588	dirMS_041712_NAR_50mM_plus2.19954.19954.3	3	5.02	0	1.09E+05		(R)LLHLPLS	(R)L L H\L P\L/S/L T A L K(L)		173.43	440.2862	1318.846	-0.0016	-1.2	8.76	59982.4	4.94	HUMAN	Q9BTT6	Leucine-rich repeat-containing protein 1
21589	dirMS_041712_NAR_60mM_plus.17353.17353.3	3	5.02	1	1.90E+05	M332m	(R)AKFEELN	(R)A K\F E E/L/N/m/D/L/F R(S)	m:Oxidized methionine	147.92	510.2582	1512.752	16.0085	8.9	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
21590	dirMS_041712_NAR_60mM_plus.5459.5459.3	3	5.02	0	4.17E+05	M21m	(R)SGSmDF	(R)S G S/m D/P/S G A H P S V R(Q)	m:Oxidized methionine	86.32	467.5464	1384.627	15.9973	1.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
21591	dirMS_041712_NAR_60mM_plus.5564.5564.3	3	5.02	1	2.35E+04		(R)YYGGGS	(R)Y Y/G/G G S E/G G R A P K(R)		86.05	433.5425	1298.612	0.0006	0.4	8.5	64759.2	8.88	HUMAN	P14866	Heterogeneous nuclear ribonucleoprotein L
21592	dirMS_041712_NAR_120mM_minus.5485.5485.2	2	5.01	0	1.59E+05	M161m	(R)mQHLIA	(R)m/Q/H/L I A R(E)	m:Oxidized methionine	83.22	442.7426	868.482	15.9958	1	9.52	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
21593	dirMS_041712_NAR_120mM_minus.9475.9475.3	3	5.01	0	1.70E+06		(K)EFHLNE!	(K)E F H L N E|S/G D/P S S K(S)		106.18	482.8881	1446.65	0.0002	0.1	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
21594	dirMS_041712_NAR_20mM_minus.11643.11643.2	2	5.01	0	4.20E+05		(R)GALQNI	(R)G A L/Q/N I/I\P A S T G A A K(A)		164.77	706.3976	1411.79	-0.0024	-1.7	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
21595	dirMS_041712_NAR_20mM_minus.13867.13867.2	2	5.01	0	3.78E+05		(K)VLTPELY	(K)V L\T/P/E L Y A\E/L/R(A)		190.8	652.3653	1303.726	-0.0023	-1.8	4.53	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
21596	dirMS_041712_NAR_30mM_minus2.15156.15156.2	2	5.01	0	3.47E+05		(R)YPVNSV	(R)Y/P/V N S V N I/L K(A)		136.42	573.8282	1146.652	-0.0026	-2.3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
21597	dirMS_041712_NAR_30mM_minus2.5417.5417.2	2	5.01	0	9.57E+04		(K)DSYVGD	(K)D S Y\V|G D/E A Q S K(R)		83.82	599.7632	1198.522	-0.0031	-2.6	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
21598	dirMS_041712_NAR_50mM_minus2.18881.18881.3	3	5.01	1	2.09E+06		(R)LIALLEVI	(R)L I|A/L L E V/L S Q K R(M)		183.8	461.6289	1382.873	-0.0008	-0.6	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
21599	dirMS_041712_NAR_50mM_minus2.6930.6930.3	3	5.01	0	2.13E+04		(R)QSSGPG	(R)Q S S/G/P\G A/S S\G T S G D H G E L V V R(I)		106	662.3147	1984.932	-0.0023	-1.2	5.32	20818.7	4.89	HUMAN	E9PL71	Elongation factor 1-delta (Fragment)
21600	dirMS_041712_NAR_50mM_minus2.8481.8481.3	3	5.01	1	4.13E+04	M88m	(K)ALDDmI	(K)A/L|D D m/I S T/L K/K(I)	m:Oxidized methionine	116.17	417.5602	1234.671	15.9949	0	6	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
21601	dirMS_041712_NAR_60mM_minus.11555.11555.3	3	5.01	1	1.59E+05		(K)EIADYLA	(K)E I/A/D/Y/L A A G K D/E R(A)		124.38	484.2432	1450.717	-0.0022	-1.5	4.32	41736.1	5.41	HUMAN	A8KAH5	IST1 homolog
21602	dirMS_041712_NAR_60mM_minus.14138.14138.3	3	5.01	0	8.54E+04	T137t	(R)ASQFtIV	(R)A/S/Q/F t I V L E A M R(R)	t:N-acetylglucosamine (T)	138.52	523.6047	1365.719	203.08	0.4	6.05	22384.9	9.36	HUMAN	A8MTQ3	TCF3 fusion partner
21603	dirMS_041712_NAR_20mM_plus.11525.11525.2	2	5.01	0	4.86E+04		(K)IQIAPDS	(K)I Q|I A/P D S G G L/P E R(S)		151.68	676.8596	1352.717	-0.0049	-3.6	4.37	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
21604	dirMS_041712_NAR_20mM_plus.15590.15590.3	3	5.01	0	1.25E+05		(R)GNPTVE	(R)G N/P T\V E V D L/F/T S K(G)		179.65	469.577	1406.716	0.0003	0.2	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
21605	dirMS_041712_NAR_20mM_plus.17005.17005.3	3	5.01	0	2.41E+05		(K)VQIAVA	(K)V Q I\A\V A/N A\Q/E L L Q R(M)		188.13	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
21606	dirMS_041712_NAR_30mM_plus2.10828.10924.2	2	5.01	0	4.75E+05		(K)NLETPL(	(K)N L|E/T/P L/C/K(N)	C:Carbamidomethylation	110.43	487.7534	974.497	0.002	2	6	21283.1	6.45	HUMAN	F8VY04	Adenylate kinase 2, mitochondrial
21607	dirMS_041712_NAR_30mM_plus2.20225.20225.2	2	5.01	0	3.03E+05		(R)LTIAILR(	(R)L T|I/A I L/R(H)		158.95	400.2728	799.54	-0.0017	-2.1	9.75	87498	6.43	HUMAN	C9J266	E3 ubiquitin-protein ligase RNF123
21608	dirMS_041712_NAR_30mM_plus2.21386.21386.2	2	5.01	0	8.38E+04		(K)SFYGSTL	(K)S F/Y/G/S T/L/F L C R(R)	C:Carbamidomethylation	166.78	675.8282	1350.651	-0.002	-1.5	8.46	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
21609	dirMS_041712_NAR_40mM_plus2.10316.10316.2	2	5.01	0	9.40E+04		(K)IGGIGTV	(K)I G/G\I/G T V/P V G R(V)		125.75	513.3081	1025.61	-0.0013	-1.2	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
21610	dirMS_041712_NAR_40mM_plus2.9717.9717.3	3	5.01	0	2.39E+05	S1080s	(K)AAGARP	(K)A A|G A/R P L T S P E/S L s R(D)	s:N-acetylglucosamine (S)	121.07	572.6438	1512.813	203.104	14.3	9.64	119157.2	5.4	HUMAN	B0UX83	HLA-B associated transcript 3
21611	dirMS_041712_NAR_50mM_plus2.11998.11998.3	3	5.01	0	1.85E+04		(R)DLEAEH'	(R)D L|E A E/H V E V E/D/T/T L N R(C)		132.13	623.966	1869.882	0.001	0.5	4.07	10027.3	8.44	HUMAN	H3BTW0	Uncharacterized protein (Fragment)
21612	dirMS_041712_NAR_50mM_plus2.13198.13198.3	3	5.01	2	4.32E+05	T331t	(K)StFMDL/	(K)S\t F M D L A K E D/I K D N D R(T)	t:Phosphorylated T	137.6	659.9658	1897.896	79.9868	10.4	4.36	73117.8	5.33	HUMAN	B4DHX2	Cytosolic carboxypeptidase 1
21613	dirMS_041712_NAR_50mM_plus2.20688.20688.3	3	5.01	1	1.70E+05		(R)VNSKFD'	(R)V/N S K/F D T\I|Y/Q I L L K(K)		177.62	561.3209	1681.952	-0.0042	-2.5	8.47	72626.7	9.13	HUMAN	Q14258	E3 ubiquitin/ISG15 ligase TRIM25
21614	dirMS_041712_NAR_50mM_plus2.9143.9143.3	3	5.01	0	6.88E+04		(R)SSGPYG(	(R)S S G/P Y/G G G G Q\Y F A K|P R(N)		115.35	543.6023	1628.782	0.0108	6.6	9.7	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
21615	dirMS_041712_NAR_60mM_plus.12704.12704.3	3	5.01	0	4.54E+04		(R)LFGGNF.	(R)L/F/G G N F A/H Q/A S V A R(V)		121.93	492.2556	1474.755	-0.0027	-1.8	9.75	61760.3	6.01	HUMAN	O14773	Tripeptidyl-peptidase 1
21616	dirMS_041712_NAR_60mM_plus.18324.18324.3	3	5.01	0	7.87E+04		(R)LHSLLGI	(R)L H S L\L G\D\Y Y/Q A I/K(V)		153.02	507.607	1520.811	-0.0043	-2.8	6.74	71128.7	6.21	HUMAN	B0QY89	Eukaryotic translation initiation factor 3 subunit L
21617	dirMS_041712_NAR_20mM_minus.12602.12602.2	2	5	0	2.31E+05	M185m	(K)LAVNm\	(K)L A\V/N/m/V/P F P R(L)	m:Oxidized methionine	173.62	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
21618	dirMS_041712_NAR_20mM_minus.13045.13162.2	2	5	0	3.87E+05	M35m	(K)NDIAINE	(K)N D I/A|I|N E L m K(R)	m:Oxidized methionine	181.67	588.7948	1160.598	15.9843	-9	4.37	28354	7.11	HUMAN	B4DXI8	26S proteasome non-ATPase regulatory subunit 7
21619	dirMS_041712_NAR_20mM_minus.14649.14649.2	2	5	0	8.83E+04		(R)IITLTGPT	(R)I I\T\L|T|G/P T N A I F K(A)		201.33	694.9107	1388.815	-0.0007	-0.5	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
21620	dirMS_041712_NAR_50mM_minus2.14625.14644.3	3	5	1	1.70E+06		(K)AGTQIEI	(K)A G/T/Q/I/E N I D E D F R D G L K(L)		152	640.9832	1920.93	0.0053	2.8	4.11	59872.5	4.85	HUMAN	F5GXS2	Alpha-actinin-4
21621	dirMS_041712_NAR_50mM_minus2.17871.17871.3	3	5	0	2.19E+05		(R)LGFHLPI	(R)L G F H L\P L E\V/A/Y Q R(G)		170.25	514.953	1542.843	0.0017	1.1	6.75	533778	5.74	HUMAN	Q15149	Plectin
21622	dirMS_041712_NAR_120mM_plus.5332.5332.2	2	5	0	1.88E+05		(K)YLPHSA(	(K)Y L/P/H/S A G R(Y)		81.35	450.7388	900.469	0.0017	1.9	8.75	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
21623	dirMS_041712_NAR_120mM_plus.9589.9589.3	3	5	1	3.69E+05		(R)SRSGEG	(R)S R S G E\G E\V/S G/L M R(K)		102.8	455.5574	1364.659	-0.001	-0.8	5.87	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
21624	dirMS_041712_NAR_20mM_plus.7421.7421.2	2	5	0	7.99E+04		(R)GTSFDA.	(R)G T S F D/A/A/A|T S G G S A S S E/K(A)		119.65	815.8661	1630.719	0.0058	3.6	4.37	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
21625	dirMS_041712_NAR_30mM_plus2.15442.15442.2	2	5	0	4.29E+05		(R)YNFFTG(	(R)Y\N|F|F T G C P K(A)	C:Carbamidomethylation	133.38	567.2595	1133.508	0.0033	2.9	8.59	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
21626	dirMS_041712_NAR_30mM_plus2.5717.5717.2	2	5	0	1.34E+05	M57m	(K)EmGTPD	(K)E m/G T/P/D/V R(I)	m:Oxidized methionine	84.58	460.7158	904.419	16.005	11	4.37	15175.4	10.46	HUMAN	B7Z4C8	60S ribosomal protein L31
21627	dirMS_041712_NAR_30mM_plus2.9589.9589.2	2	5	0	5.86E+05		(K)EAESSPF	(K)E A/E/S S/P F V/E R(L)		104.93	575.7726	1150.537	0.0004	0.4	4.25	92752.5	4.76	HUMAN	P14625	Endoplasmin
21628	dirMS_041712_NAR_50mM_plus2.19133.19133.3	3	5	1	4.47E+05		(K)NLDKEYI	(K)N L D K E Y\L/P|I G G/L A E F C/K(A)	C:Carbamidomethylation	168.33	656.3389	1966.994	0.0079	4	4.68	47916.2	9.44	HUMAN	P00505	Aspartate aminotransferase, mitochondrial
21629	dirMS_041712_NAR_50mM_plus2.5553.5553.3	3	5	1	1.11E+05		(K)DSYVGD	(K)D S|Y/V/G D E/A Q S K R(G)		90.6	452.2114	1354.623	-0.0037	-2.7	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
21630	dirMS_041712_NAR_120mM_minus.7315.7315.2	2	4.99	1	8.79E+03		(K)EIGQKGI	(K)E I/G\Q K G/L/K(I)		94.15	436.7639	872.52	0.0005	0.6	8.69	10155.4	8.03	HUMAN	F8WB12	Protein TSSC1
21631	dirMS_041712_NAR_20mM_minus.7505.7505.3	3	4.99	0	7.64E+05	M239m	(K)EVDEQn	(K)E V D E Q|m/L\N V/Q/N/K(N)	m:Oxidized methionine	123.52	488.2327	1446.689	15.9942	-0.5	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
21632	dirMS_041712_NAR_30mM_minus2.11279.11279.2	2	4.99	0	1.68E+05		(R)GYSFTT1	(R)G Y|S/F/T/T T A/E/R(E)		114.92	566.7699	1132.527	0.0056	4.9	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
21633	dirMS_041712_NAR_30mM_minus2.18971.18971.2	2	4.99	0	2.11E+05		(K)SYELPD(	(K)S Y E\L/P D/G/Q V\I\T I/G N E R(F)		158.68	895.9492	1790.892	-0.0008	-0.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
21634	dirMS_041712_NAR_40mM_minus2.9173.9173.3	3	4.99	0	2.52E+05	M240m	(K)mLDAED	(K)m L/D/A/E/D I/V N T A R P D E K(A)	m:Oxidized methionine	136.73	611.627	1816.875	15.9919	-1.6	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
21635	dirMS_041712_NAR_50mM_minus2.11649.11649.3	3	4.99	0	1.02E+05		(K)AQIHDL'	(K)A Q I H D L\V|L|V G/G/S T R(I)		134.53	489.2711	1465.812	-0.0134	-9.1	6.79	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
21636	dirMS_041712_NAR_50mM_minus2.12868.12868.3	3	4.99	1	3.48E+05	M100m	(K)QGGLGF	(K)Q G G/L|G P m N\I|P L V S D P K R(T)	m:Oxidized methionine	140.62	598.988	1778.958	15.9913	-2	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
21637	dirMS_041712_NAR_60mM_minus.17610.17610.3	3	4.99	0	1.17E+05		(R)GGHVVE	(R)G/G H\V\V E G\L|A/G E/L E Q L R(A)		158.32	555.2959	1663.876	-0.0031	-1.8	4.75	106088.3	5.78	HUMAN	P10275	Androgen receptor
21638	dirMS_041712_NAR_60mM_minus.9777.9777.2	2	4.99	1	4.41E+05		(R)LQAEIEG	(R)L Q|A\E|I E/G L K G Q R(A)		114.13	671.3768	1341.748	-0.0022	-1.6	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
21639	dirMS_041712_NAR_60mM_minus.9950.9950.3	3	4.99	1	5.63E+05	M230m M:	(R)mSmKE\	(R)m/S m K E V D\E Q\M|L/N V Q/N K(N)	m:Oxidized methionine	114.97	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
21640	dirMS_041712_NAR_20mM_plus.17690.17690.2	2	4.99	0	8.56E+04		(R)GDGPICI	(R)G/D G P/I|C L|V/L/A\P T R(E)	C:Carbamidomethylation	193.13	684.8681	1368.73	-0.0015	-1.1	5.84	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
21641	dirMS_041712_NAR_30mM_plus2.14492.14492.2	2	4.99	0	5.73E+05		(K)CCSGAII'	(K)C C|S\G A I/I V/L/T K(S)	C:Carbamidomethylation	128.2	611.3189	1221.633	-0.0025	-2	8.75	58506.4	8.38	HUMAN	P14618	Pyruvate kinase isozymes M1/M2
21642	dirMS_041712_NAR_30mM_plus2.15695.15695.2	2	4.99	0	2.49E+05		(R)MAGAIA	(R)M A\G A|I/A Q/G L I/R(A)		134.7	550.816	1100.624	0.0002	0.2	9.5	4449.1	11.42	HUMAN	F8WEI0	Pyrroline-5-carboxylate reductase 3
21643	dirMS_041712_NAR_30mM_plus2.16304.16304.3	3	4.99	0	5.65E+05		(R)GLCAIA(	(R)G L C\A I A Q|A/E S/L R(Y)	C:Carbamidomethylation	138.48	430.2276	1288.668	0.0005	0.3	6	18529.2	9.98	HUMAN	E9PL45	40S ribosomal protein S3
21644	dirMS_041712_NAR_30mM_plus2.5276.5276.2	2	4.99	0	5.47E+05		(K)VSSFEEK	(K)V/S|S F E E K(M)		81.48	413.203	825.399	-0.0002	-0.2	4.53	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
21645	dirMS_041712_NAR_30mM_plus2.5945.5945.2	2	4.99	0	1.03E+05		(R)EAEEVYI	(R)E A|E E V/Y R(N)		85.05	448.2113	895.416	-0.0003	-0.3	4.25	54793.4	10.51	HUMAN	B7Z4Q3	Putative RNA-binding protein Luc7-like 2
21646	dirMS_041712_NAR_30mM_plus2.6833.6833.2	2	4.99	0	8.68E+03		(R)NGYDYG	(R)N/G|Y|D/Y G Q|C/R(L)	C:Carbamidomethylation	90.3	566.7271	1132.448	-0.0007	-0.6	5.83	25655.9	8.94	HUMAN	Q13242	Serine/arginine-rich splicing factor 9
21647	dirMS_041712_NAR_30mM_plus2.7742.7742.2	2	4.99	0	3.77E+05		(K)QTFGYG	(K)Q T/F/G/Y/G A/R(L)		94.05	450.2234	899.437	0.0025	2.8	8.75	23092.1	6.93	HUMAN	G3V438	Activator of 90 kDa heat shock protein ATPase homolog 1 (Fragment)
21648	dirMS_041712_NAR_40mM_plus2.9630.9630.2	2	4.99	0	5.54E+04		(R)NGYGFII	(R)N/G|Y/G/F|I N R(N)		120.03	470.7365	940.463	0.0022	2.3	8.75	23597.5	10.26	HUMAN	C9J5V9	Nuclease-sensitive element-binding protein 1 (Fragment)
21649	dirMS_041712_NAR_50mM_plus2.12659.12659.3	3	4.99	1	3.83E+05		(K)LPGGELI	(K)L P/G G E L N|P G E D E V E G L K R(L)		134.28	636.9936	1908.966	0.0001	0.1	4.25	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
21650	dirMS_041712_NAR_50mM_plus2.20091.20219.3	3	4.99	1	6.00E+05		(R)SKALGSI	(R)S K A L G S D H C P I T\L\Y\L/A|L(-)	C:Carbamidomethylation	174.58	620.3259	1858.973	-0.01	-5.4	6.46	5634.5	9.82	HUMAN	G3V574	DNA-(apurinic or apyrimidinic site) lyase
21651	dirMS_041712_NAR_60mM_plus.11065.11065.3	3	4.99	1	1.18E+06		(R)EKLEME	(R)E\K L E M E/M E/A A/R(H)		115.43	446.2162	1336.623	0.0105	7.9	4.49	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)
21652	dirMS_041712_NAR_60mM_plus.15731.16066.4	4	4.99	0	9.78E+05		(R)FCAHEN	(R)F C A H\E N C/S A D L Q/V S A/K(I)	C:Carbamidomethylation	139.6	459.9647	1836.8	0.0366	19.9	5.32	116323.9	6.05	HUMAN	P13612	Integrin alpha-4
21653	dirMS_041712_NAR_60mM_plus.17286.17286.3	3	4.99	0	6.20E+05		(R)DRPSVP.	(R)D R P\S V P/A P V Q A G G/R(S)		146.93	469.5946	1406.75	0.0194	13.8	9.6	160163.6	6.35	HUMAN	E9PFC1	Protein CEP170B
21654	dirMS_041712_NAR_60mM_plus.20207.20207.3	3	4.99	0	2.31E+04		(R)FYTLIPH	(R)F Y/T\L I P H/D F G M/K(K)		165.47	490.2529	1468.729	0.0148	10.1	6.74	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
21655	dirMS_041712_NAR_60mM_plus.9800.9800.3	3	4.99	1	3.71E+05		(K)VADWT(	(K)V A|D W/T/G A/T Y Q D K R(Y)		109.1	504.2484	1510.728	0.0022	1.4	5.93	31956.7	9.73	HUMAN	B0QYA5	Eukaryotic translation initiation factor 3 subunit D (Fragment)
21656	dirMS_041712_NAR_120mM_minus.8627.8627.3	3	4.98	0	1.99E+05		(R)GHQAFI	(R)G H Q/A F D\V/G Q/P/R(D)		100.92	404.5343	1211.592	-0.0032	-2.7	6.74	281330.5	5.64	HUMAN	P11717	Cation-independent mannose-6-phosphate receptor
21657	dirMS_041712_NAR_20mM_minus.12652.12652.3	3	4.98	0	1.60E+04	M73m	(R)AVLVDLI	(R)A V\L V\D L E/P G T m/D S V R(S)	m:Oxidized methionine	175.63	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
21658	dirMS_041712_NAR_30mM_minus2.15758.15758.2	2	4.98	0	1.75E+05		(K)STLDINE	(K)S\T|L/D/I/N E M/V R(T)		139.6	589.2997	1177.588	0.004	3.4	4.37	120522.3	5.57	HUMAN	F5H1H6	Cytospin-A
21659	dirMS_041712_NAR_50mM_minus2.14552.14552.3	3	4.98	0	1.91E+04		(K)VALLLLD	(K)V A|L L L/L D Q/G A/S P H A A A K(N)		150.97	558.9883	1674.954	-0.0034	-2	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
21660	dirMS_041712_NAR_60mM_minus.15396.15396.3	3	4.98	1	1.77E+05		(R)ASLISAV	(R)A/S L/I/S A V/S D K L R(W)		146.23	420.5811	1259.732	-0.003	-2.4	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
21661	dirMS_041712_NAR_60mM_minus.18254.18254.3	3	4.98	0	1.21E+05		(R)LGIEGLS	(R)L G\I/E/G L S/L H N V L K(L)		163.43	464.9423	1392.821	-0.0086	-6.2	6.75	177928	5.42	HUMAN	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1
21662	dirMS_041712_NAR_60mM_minus.19993.19993.3	3	4.98	0	2.25E+05		(R)EGGFLLI	(R)E G G F L|L/L H T L L R(G)		182.45	456.9372	1368.8	-0.0027	-2	6.85	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
21663	dirMS_041712_NAR_120mM_plus.4160.4160.2	2	4.98	1	1.45E+06	M310m	(R)TKTEISE	(R)T K/T|E/I/S E m N R(N)	m:Oxidized methionine	69.8	612.7976	1208.594	15.994	-0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
21664	dirMS_041712_NAR_40mM_plus2.19284.19284.3	3	4.98	0	1.75E+05		(R)LQQAQL	(R)L Q/Q|A Q\L Y P I A I F I/K P K(S)		180.67	624.3737	1871.115	-0.0088	-4.7	9.7	94175.4	6.59	HUMAN	Q5JUW8	Discs, large homolog 3 (Neuroendocrine-dlg, Drosophila)
21665	dirMS_041712_NAR_40mM_plus2.5668.5668.2	2	4.98	0	1.26E+05		(K)INYTEGF	(K)I/N/Y/T E G R(A)		90.63	426.7143	852.421	0.0003	0.4	6	16867	10.86	HUMAN	K7ELR7	Glucose-6-phosphate isomerase (Fragment)
21666	dirMS_041712_NAR_50mM_plus2.11144.11144.3	3	4.98	0	3.78E+05		(K)LQAEAP	(K)L Q|A E A P H|I V\V/G T/P G R(V)		126.57	515.6223	1544.854	-0.002	-1.3	6.75	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
21667	dirMS_041712_NAR_50mM_plus2.12481.12481.3	3	4.98	0	1.98E+05		(R)VNAIEH'	(R)V N/A I/E H V I I P R(I)		133.77	420.9182	1260.742	-0.0022	-1.8	6.72	21920.7	5.63	HUMAN	G3V2S6	V-type proton ATPase subunit D
21668	dirMS_041712_NAR_60mM_plus.10272.10272.3	3	4.98	1	2.30E+05	M142m	(K)VKEGMI	(K)V K E G M N\I|V/E A m E R(F)	m:Oxidized methionine	111.35	507.9187	1505.745	15.9965	1	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
21669	dirMS_041712_NAR_60mM_plus.10438.10438.3	3	4.98	1	8.41E+05		(R)LKNTLT(	(R)L K N T L T/Q/T T/E N L R(R)		112.28	511.2871	1531.844	0.0029	1.9	8.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
21670	dirMS_041712_NAR_60mM_plus.15384.15384.3	3	4.98	1	2.67E+04		(R)KVIGIEC	(R)K V I\G I E|C S/S/I/S D Y A V K(I)	C:Carbamidomethylation	136.72	590.3097	1768.915	-0.0004	-0.2	6.07	12798.3	6.06	HUMAN	E9PI83	Protein arginine N-methyltransferase 1 (Fragment)
21671	dirMS_041712_NAR_60mM_plus.5709.5709.3	3	4.98	0	1.46E+05	M116m	(R)ATAPQT	(R)A T/A/P Q T Q H V/S/P m R(Q)	m:Oxidized methionine	88.28	480.5724	1423.711	15.9916	-2.3	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
21672	dirMS_041712_NAR_120mM_minus.16517.16517.3	3	4.97	0	5.94E+05		(R)EHALLA\	(R)E H/A L\L A\Y/T/L G V K(Q)		144.88	438.9186	1314.742	-0.0004	-0.3	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
21673	dirMS_041712_NAR_30mM_minus2.15339.15339.2	2	4.97	0	3.06E+05		(R)IVFQEFR	(R)I/V/F/Q E F R(Q)		137.33	469.7582	938.509	-0.0003	-0.3	6	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
21674	dirMS_041712_NAR_30mM_minus2.9165.9165.2	2	4.97	0	1.43E+05		(R)LGEYED'	(R)L/G/E/Y E/D V S/R(V)		102.97	534.2599	1067.5	0.0121	11.4	4.14	23811.2	6.78	HUMAN	A8MVD5	Tubulin-folding cofactor B
21675	dirMS_041712_NAR_30mM_minus2.9368.9368.2	2	4.97	0	8.41E+04		(K)IMATPE(	(K)I M/A T/P E/Q V G/K(M)		105.43	537.2824	1073.566	-0.0084	-7.9	6	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
21676	dirMS_041712_NAR_40mM_minus2.13407.13407.3	3	4.97	1	1.92E+05		(K)LGVQVV	(K)L G V\Q/V/V/I T D/P E K L D Q I R(Q)		163.35	641.7007	1923.091	-0.0034	-1.8	4.56	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
21677	dirMS_041712_NAR_60mM_minus.8619.8619.3	3	4.97	1	2.05E+04	M227m M:	(R)mQKEIT.	(R)m Q/K E I T A\L|A/P S T m K(I)	m:Oxidized methionine	108.02	527.6044	1548.812	31.9862	-2.3	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
21678	dirMS_041712_NAR_120mM_plus.10136.10136.2	2	4.97	1	3.04E+04		(R)VKYETEI	(R)V K|Y/E/T E L A M/R(Q)		106.03	620.3237	1239.64	-0.0001	0	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
21679	dirMS_041712_NAR_120mM_plus.10367.10367.3	3	4.97	1	2.55E+05		(R)LRQLAEI	(R)L R Q L A\E\E/D L/A/Q Q R(A)		107.03	523.949	1569.834	-0.0019	-1.2	4.68	533778	5.74	HUMAN	Q15149	Plectin
21680	dirMS_041712_NAR_120mM_plus.13889.13889.4	4	4.97	1	9.40E+05		(K)AGKFPSI	(K)A G K F P/S/L/L/T H N E N M/V A K(V)		126.23	464.9972	1856.969	-0.0018	-0.9	8.64	25002	10.06	HUMAN	P62906	60S ribosomal protein L10a
21681	dirMS_041712_NAR_120mM_plus.14401.14401.4	4	4.97	1	4.26E+05		(R)LEAPELP	(R)L E/A P E L P\V K V/N P T K P R(R)		128.22	447.7616	1788.038	-0.0132	-7.4	8.59	10558	9.4	HUMAN	H0YE28	Protein C11orf31 (Fragment)
21682	dirMS_041712_NAR_20mM_plus.17498.17498.3	3	4.97	0	1.38E+04	M199m	(K)SmVPVC	(K)S m V|P V\Q V\Q|L/D V/P V V K(V)	m:Oxidized methionine	192.58	551.9759	1637.93	15.9837	-6.8	5.55	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
21683	dirMS_041712_NAR_30mM_plus2.17393.17393.2	2	4.97	0	7.91E+05		(R)IMNTFS'	(R)I M/N T/F/S V V/P S P K(V)		144.93	660.3537	1319.703	-0.0027	-2	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
21684	dirMS_041712_NAR_30mM_plus2.4261.4261.2	2	4.97	0	8.85E+05	M299m M:	(K)NmmAA	(K)N m|m/A/A C/D|P R(H)	C:Carbamidomethylation m:Oxid	69.93	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
21685	dirMS_041712_NAR_30mM_plus2.4662.4662.2	2	4.97	0	1.32E+05		(K)NCSETQ	(K)N C/S E/T/Q/Y E S K(V)	C:Carbamidomethylation	75.17	623.256	1245.505	-0.0005	-0.4	4.53	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
21686	dirMS_041712_NAR_30mM_plus2.7275.7275.2	2	4.97	0	4.47E+05		(K)ATSATG.	(K)A T S A/T/G A V P K(G)		92.6	451.7509	902.494	0.0004	0.4	8.8	65967.6	8.92	HUMAN	Q7L311	Armadillo repeat-containing X-linked protein 2

21687	dirMS_041712_NAR_40mM_plus2.17835.17835.3	3	4.97	1	5.38E+05		(R)GLLPGL	(R)G L L/P/G L L/P A/P A D K L T P K(G)		170.62	567.6811	1701.031	-0.0022	-1.3	8.59	153084.9	5.55	HUMAN	Q6P2E9	Enhancer of mRNA-decapping protein 4
21688	dirMS_041712_NAR_50mM_plus2.15380.15380.3	3	4.97	0	1.63E+05		(K)VALLLLD	(K)V/A\L\L/L/L D Q G/A/S P/H A A A K(N)		148.48	558.9877	1674.954	-0.0052	-3.1	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
21689	dirMS_041712_NAR_50mM_plus2.21173.21173.3	3	4.97	1	4.22E+05	M145m	(R)GVmLA	(R)G V|m\L A V/D/A V/I A E L K K(Q)	m:Oxidized methionine	181.53	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
21690	dirMS_041712_NAR_50mM_plus2.21781.21781.3	3	4.97	1	2.09E+04		(R)DLLGSD	(R)D L/L G S D A P R A|A/P E P G R P R(T)		185.73	625.6716	1874.983	0.0171	9.1	6.12	62355.5	11.3	HUMAN	E7ESL9	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3
21691	dirMS_041712_NAR_50mM_plus2.7173.7173.3	3	4.97	0	1.94E+05	T611t	(K)DSFQIST	(K)D S/F/Q I S T L V\C S t K(L)	C:Carbamidomethylation t:N-ace	103.85	563.6145	1485.725	203.1036	14.3	5.84	216311.9	7.33	HUMAN	Q14185	Dedicator of cytokinesis protein 1
21692	dirMS_041712_NAR_60mM_plus.17143.17143.3	3	4.97	1	1.38E+05		(R)MRIESLS	(R)M/R I E S L S\S Q/L/S/N L\Q/K(E)		146.5	578.6436	1733.921	-0.0052	-3	8.5	44813.6	4.99	HUMAN	E9PBF6	Lamin-B1
21693	dirMS_041712_NAR_60mM_plus.8762.8762.3	3	4.97	0	8.85E+04		(K)VSYGIGD	(K)V/S/Y/G/I/G D E E H D Q E G R(V)		103.63	564.2485	1690.73	0.0006	0.4	4.17	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
21694	dirMS_041712_NAR_20mM_minus.13525.13525.2	2	4.96	0	1.07E+05		(K)FIIPNVV	(K)F I|I/P N V V K(Y)		186.23	465.294	929.582	-0.0011	-1.2	8.75	17529.3	9.3	HUMAN	F5GXY2	L-lactate dehydrogenase A chain (Fragment)
21695	dirMS_041712_NAR_30mM_minus2.5919.5919.2	2	4.96	0	1.90E+05		(K)TSEVNC	(K)T S|E/V/N C Y R(C)	C:Carbamidomethylation	86.62	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
21696	dirMS_041712_NAR_40mM_minus2.13550.13550.3	3	4.96	0	1.40E+05		(K)VAIVKP	(K)V/A I/V K P G V|P/M E I V L N K(E)		163.27	569.6777	1707.024	-0.0052	-3	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
21697	dirMS_041712_NAR_40mM_minus2.5765.5765.3	3	4.96	1	6.96E+04		(R)AQLGGP	(R)A Q|L/G/G P E A\A K S D E T A A K(-)		95.1	548.612	1643.824	-0.0021	-1.3	4.68	3888.3	5	HUMAN	C9J3N8	Heat shock protein beta-1
21698	dirMS_041712_NAR_50mM_minus2.10903.10903.3	3	4.96	0	1.79E+05	M35m	(K)AASDIA	(K)A A|S D I A m T/E L/P/P T H P I R(L)	m:Oxidized methionine	130.27	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
21699	dirMS_041712_NAR_50mM_minus2.11266.11266.3	3	4.96	0	2.39E+05		(K)QADLYIS	(K)Q A D L/Y/I/S/E G L/H P R(I)		131.97	500.2598	1498.765	0	0	5.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
21700	dirMS_041712_NAR_60mM_minus.15570.15570.3	3	4.96	0	2.01E+04		(R)LGGLRP	(R)L G/G L R P E S P/E/S L T S V S R(T)		146.85	595.6552	1784.95	0.0009	0.5	6.14	9248	8.73	HUMAN	H0YG79	Coiled-coil domain-containing protein 86 (Fragment)
21701	dirMS_041712_NAR_60mM_minus.7171.7171.3	3	4.96	2	5.20E+04	M1m N9n	(-)mGSTDS	(-)m/G S/T D S K\L/n F R K(A)	m:Oxidized methionine n:N-	98.43	534.9257	1383.705	219.0576	-10.4	9.99	21682.3	9.62	HUMAN	E9PIM7	Protein HID1
21702	dirMS_041712_NAR_120mM_plus.7312.7312.3	3	4.96	1	1.14E+06		(R)EKVPGG	(R)E K V/P G G L/Q/G S Q D R(G)		92.32	457.5737	1370.702	0.0043	3.1	6.17	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
21703	dirMS_041712_NAR_120mM_plus.8696.8696.3	3	4.96	1	5.21E+05		(R)RTEEGP	(R)R T E E G\P/T|L/S\Y G R(D)		98.45	455.8929	1365.676	-0.0116	-8.5	6.14	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
21704	dirMS_041712_NAR_120mM_plus.8790.8790.3	3	4.96	1	4.30E+04		(R)RQQEEL	(R)R Q Q E E\L|L/A/E E N Q R(L)		99.1	548.2767	1642.814	0.0012	0.7	4.49	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
21705	dirMS_041712_NAR_20mM_plus.14938.14938.3	3	4.96	0	1.16E+05		(K)VLEQLT	(K)V L E Q L T G\Q|T P/V F S K(A)		174.55	516.2866	1546.848	-0.0023	-1.5	5.97	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
21706	dirMS_041712_NAR_20mM_plus.15545.15545.3	3	4.96	0	1.87E+05		(R)GVVDSE	(R)G V\V D S E D I/P/L N L S R(E)		179.25	505.2667	1513.786	-0.0001	-0.1	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
21707	dirMS_041712_NAR_20mM_plus.7802.7802.3	3	4.96	0	1.06E+05		(K)AQAAA	(K)A Q\A A A\P\A S V/P A Q A/P K(R)		123.6	459.9204	1377.748	-0.0018	-1.3	8.8	17808.8	11.77	HUMAN	P47914	60S ribosomal protein L29
21708	dirMS_041712_NAR_30mM_plus2.17333.17333.2	2	4.96	0	4.27E+05		(K)LMFEEL	(K)L/M/F/E E/L R(N)		144.73	469.2488	937.481	0.0092	9.8	4.53	19338.9	5.33	HUMAN	E7EQS9	tRNA-splicing ligase RtcB homolog
21709	dirMS_041712_NAR_30mM_plus2.8425.8425.2	2	4.96	0	5.88E+05		(R)LGLGEG	(R)L/G|L/G E/G A E E K(S)		98.35	501.7639	1002.51	0.0103	10.3	4.25	40096.8	9.24	HUMAN	C9JW69	Regulator of chromosome condensation (Fragment)
21710	dirMS_041712_NAR_50mM_plus2.17042.17042.2	2	4.96	1	4.01E+05		(R)VSFELFA	(R)V S/F E/L/F A D K V/P\K(T)		156.92	690.3803	1379.757	-0.0036	-2.6	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
21711	dirMS_041712_NAR_50mM_plus2.19917.19917.3	3	4.96	0	1.09E+05		(R)LLHLPLS	(R)L L H\L P\L/S L/T A/L K(L)		173.43	440.2862	1318.846	-0.0016	-1.2	8.76	59982.4	4.94	HUMAN	Q9BTT6	Leucine-rich repeat-containing protein 1
21712	dirMS_041712_NAR_50mM_plus2.8156.8156.3	3	4.96	0	3.65E+05		(K)IGNTGG	(K)I/G N/T G G M L D N I/L A S K(L)		110.28	501.9302	1503.784	-0.0075	-5	5.84	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
21713	dirMS_041712_NAR_50mM_plus2.8376.8376.3	3	4.96	0	2.54E+05	T623t	(R)DIGDTtI	(R)D I G D/T/t I Q L S W\S R(G)	t:N-acetylglucosamine (T)	110.47	565.6079	1491.744	203.0653	-8.3	4.21	114075.9	8.51	HUMAN	Q02246	Contactin-2
21714	dirMS_041712_NAR_50mM_plus2.8546.8546.3	3	4.96	1	2.38E+04	M22m	(K)LAEQAE	(K)L/A/E Q A/E R Y D D m A/A C M K(S)	C:Carbamidomethylation m:Oxid	113.12	639.9473	1901.819	16.0083	7	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
21715	dirMS_041712_NAR_60mM_plus.13204.13204.3	3	4.96	1	3.36E+06		(R)VVDLM	(R)V V|D/L/M A H M A S K/E(-)		126.55	444.2219	1330.649	0.0018	1.3	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
21716	dirMS_041712_NAR_120mM_minus.10350.10350.3	3	4.95	1	4.55E+05		(R)QRGGA	(R)Q R G G A\E\G\E\L/Q/A L R(A)		110.92	462.2462	1384.729	-0.0051	-3.7	6.14	533778	5.74	HUMAN	Q15149	Plectin
21717	dirMS_041712_NAR_120mM_minus.13941.13941.3	3	4.95	1	5.35E+05		(K)ASIHEA	(K)A S I/H/E A W/T/D/G/K E A M L/K(H)		130.1	596.2973	1786.879	-0.0019	-1.1	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
21718	dirMS_041712_NAR_120mM_minus.9663.9663.3	3	4.95	0	4.38E+05		(K)QEYDES	(K)Q E Y/D E S/G P S/I/V H R(K)		107.47	506.2424	1516.703	0.01	6.6	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
21719	dirMS_041712_NAR_20mM_minus.14458.14458.2	2	4.95	0	5.49E+04		(K)FIIPQIV	(K)F/I/I/P/Q I V K(Y)		198.77	479.3083	957.613	-0.0038	-4	8.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
21720	dirMS_041712_NAR_30mM_minus2.11499.11499.2	2	4.95	0	1.87E+05		(K)SCNCLLL	(K)S/C|N C L L/L/K(V)	C:Carbamidomethylation	116.4	504.2543	1007.501	0.0001	0.1	8.47	47510.4	7.04	HUMAN	P06733	Alpha-enolase
21721	dirMS_041712_NAR_40mM_minus2.11828.11828.2	2	4.95	1	4.21E+04		(R)IINEPTA	(R)I I/N/E/P T A A A I A Y G/L D K K(V)		153.28	894.4971	1787.99	-0.0033	-1.8	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
21722	dirMS_041712_NAR_50mM_minus2.7863.7863.3	3	4.95	1	1.46E+05		(K)TAVCDI	(K)T A/V/C D I/P P R G L K(M)	C:Carbamidomethylation	111.9	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
21723	dirMS_041712_NAR_120mM_plus.11410.11410.3	3	4.95	1	1.45E+06		(K)KAEAGA	(K)K A E A G A G\S\A|T E/F Q/F R(G)		112.88	523.9272	1569.766	0.0015	0.9	6.14	18897.4	10.15	HUMAN	P46783	40S ribosomal protein S10
21724	dirMS_041712_NAR_20mM_plus.13935.13935.3	3	4.95	0	2.82E+04	M348m	(K)VmQVL	(K)V m Q\V L\N|A/D A I/V V K(L)	m:Oxidized methionine	167.77	472.6031	1399.798	15.997	1.5	5.81	102679.8	6.75	HUMAN	Q7KZF4	Staphylococcal nuclease domain-containing protein 1
21725	dirMS_041712_NAR_20mM_plus.14727.14727.2	2	4.95	0	1.73E+05	M256m	(R)SLDmDS	(R)S L/D/m/D S I\I A E|V K(A)	m:Oxidized methionine	172.53	668.8371	1320.671	15.9954	0.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
21726	dirMS_041712_NAR_20mM_plus.18461.18461.2	2	4.95	0	7.26E+04		(R)VVVLGL	(R)V V/V L|G/L L P R(G)		198.8	483.3247	965.651	-0.0085	-8.8	9.72	25847.9	6.33	HUMAN	Q15102	Platelet-activating factor acetylhydrolase IB subunit gamma
21727	dirMS_041712_NAR_30mM_plus2.12236.12236.2	2	4.95	0	1.14E+05		(K)VLELDN	(K)V/L|E/L/D N V K(S)		117.15	465.2708	929.53	0.0041	4.4	4.37	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
21728	dirMS_041712_NAR_30mM_plus2.16834.16834.2	2	4.95	0	2.93E+05		(R)DIQTLLS	(R)D I|Q\T L/L/S R(M)		141.38	473.2687	945.536	-0.0062	-6.6	5.84	119157.2	5.4	HUMAN	B0UX83	HLA-B associated transcript 3
21729	dirMS_041712_NAR_30mM_plus2.5473.5473.3	3	4.95	0	2.01E+05		(R)NQGGY	(R)N\Q\G G Y G G S S S/S/S/S Y/G S G R(R)		83.03	565.5708	1694.7	-0.0022	-1.3	8.59	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
21730	dirMS_041712_NAR_40mM_plus2.10820.10820.3	3	4.95	1	4.29E+05		(R)DGKLVS	(R)D G K L V|S\E/S S|D V L P K(-)		128.67	491.9315	1473.78	0.0004	0.3	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
21731	dirMS_041712_NAR_40mM_plus2.6726.6726.2	2	4.95	0	1.68E+04		(K)SLAAEEE	(K)S L/A|A E E E A A/R(Q)		99.53	523.7589	1046.511	-0.0008	-0.7	4.25	533778	5.74	HUMAN	Q15149	Plectin
21732	dirMS_041712_NAR_50mM_plus2.12544.12544.2	2	4.95	1	2.99E+05		(K)KVPQVS	(K)K|V/P Q V/S T P T L V E V S R(N)		134.05	820.471	1639.938	-0.003	-1.8	8.75	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
21733	dirMS_041712_NAR_50mM_plus2.20666.20666.2	2	4.95	1	5.19E+05		(K)EFKYAL	(K)E F/K/Y|A L/V W|G L S V K(H)		177.02	770.4211	1539.857	-0.0221	-14.3	8.59	40826.7	9.22	HUMAN	Q9Y295	Developmentally-regulated GTP-binding protein 1
21734	dirMS_041712_NAR_50mM_plus2.21622.21622.3	3	4.95	1	1.07E+04		(R)SKAEEL	(R)S K A E E L G L|P I L/G V/L R(S)		183.92	532.3178	1594.953	-0.0138	-8.7	5.87	40725.2	9.61	HUMAN	C9JDE9	3-ketoacyl-CoA thiolase, peroxisomal
21735	dirMS_041712_NAR_50mM_plus2.8886.8886.3	3	4.95	0	3.97E+05		(R)ATQQQ	(R)A T\Q Q Q H\D\F\T|L/T/Q T A D/G R(S)		113.55	639.9699	1917.905	-0.0098	-5.1	5.21	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
21736	dirMS_041712_NAR_60mM_plus.12834.12834.3	3	4.95	1	9.04E+05	M232m	(R)MSmKE	(R)M S m K E V D E Q|M/L N V\Q/N K(N)	m:Oxidized methionine	123.57	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
21737	dirMS_041712_NAR_60mM_plus.5207.5207.3	3	4.95	0	2.64E+04		(R)TATEKP	(R)T/A|T E K|P G P A/E A A R(Q)		84.77	433.5671	1298.67	0.0168	13	5.81	49823.3	9.39	HUMAN	B4DQQ4	NADPH:adrenodoxin oxidoreductase, mitochondrial
21738	dirMS_041712_NAR_20mM_minus.7834.7834.2	2	4.94	0	1.69E+05		(K)SVEAAA	(K)S V|E A/A/A E\L|S A K(D)		128.45	538.2838	1075.563	-0.0027	-2.5	4.53	12131.5	11.14	HUMAN	F5GXR3	Parathymosin
21739	dirMS_041712_NAR_30mM_minus2.10819.10819.2	2	4.94	0	5.46E+03	M50m	(K)LYANm	(K)L/Y/A/N m F E R(L)	m:Oxidized methionine	114.13	530.2501	1043.498	15.995	0.1	6	9740.1	10.08	HUMAN	H0YFG2	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed (Fragment)
21740	dirMS_041712_NAR_40mM_minus2.13384.13384.3	3	4.94	1	7.49E+03	M148m	(R)LDLAGR	(R)L D/L A/G R D L/T\D Y L m K(I)	m:Oxidized methionine	162.48	547.2822	1623.841	15.991	-2.4	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
21741	dirMS_041712_NAR_40mM_minus2.15308.15308.3	3	4.94	0	1.86E+04		(R)ETSSDV	(R)E T S S/D V A\L A/S/H/I/L T A/L R(E)		176.72	595.3178	1783.955	-0.016	-9	5.32	36920.6	4.68	HUMAN	O00273	DNA fragmentation factor subunit alpha
21742	dirMS_041712_NAR_50mM_minus2.10279.10279.3	3	4.94	2	1.71E+05	S1986s	(R)LSHGDR	(R)L S\H G D R G/T D/G K A s R(D)	s:N-acetylglucosamine (S)	127.75	553.9474	1456.725	203.1025	13.9	8.75	231702.4	6.52	HUMAN	Q92576	PHD finger protein 3
21743	dirMS_041712_NAR_50mM_minus2.12701.12701.3	3	4.94	1	2.79E+05		(R)LSEDYG	(R)L/S E/D Y/G V L K/T D E G I A Y R(G)		141.18	643.6561	1928.96	-0.0063	-3.2	4.32	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
21744	dirMS_041712_NAR_120mM_plus.15429.15429.4	4	4.94	2	4.59E+05		(K)LLVGVD	(K)L L V/G V D E K L N/P E/D I K K(H)		133.73	453.2599	1810.032	-0.0143	-7.9	4.79	121749.9	6.97	HUMAN	P53396	ATP-citrate synthase
21745	dirMS_041712_NAR_20mM_plus.15049.15049.2	2	4.94	0	2.46E+03		(K)GILFVGS	(K)G I L F|V/G S G/V S/G G/E E G A R(Y)		175.22	796.4002	1591.807	-0.0143	-9	4.53	52385	7.18	HUMAN	B4DQJ8	6-phosphogluconate dehydrogenase, decarboxylating
21746	dirMS_041712_NAR_20mM_plus.6637.6637.2	2	4.94	0	7.77E+04	M357m	(K)AELDDT	(K)A/E|L/D D|T/P m\R(G)	m:Oxidized methionine	110.62	532.24	1047.478	15.9952	0.3	4.03	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
21747	dirMS_041712_NAR_20mM_plus.8069.8069.3	3	4.94	0	4.57E+05	M239m	(K)EVDEQ	(K)E V D E Q m|L/N V/Q N K(N)	m:Oxidized methionine	125.12	488.2328	1446.689	15.9945	-0.3	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
21748	dirMS_041712_NAR_30mM_plus2.15378.15378.2	2	4.94	0	7.45E+05		(R)YIEIFK(S	(R)Y I/E I/F/K(S)		134.2	406.7314	812.455	0.0003	0.3	6	24249.1	6.99	HUMAN	D6RBM0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
21749	dirMS_041712_NAR_50mM_plus2.18086.18086.3	3	4.94	0	2.70E+04		(R)TIRPMD	(R)T I/R P M D M\E T|I/E/A S V M/K(T)		163.03	617.9711	1851.901	-0.0026	-1.4	4.68	39089.4	7.08	HUMAN	C9J634	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial
21750	dirMS_041712_NAR_50mM_plus2.19714.19714.3	3	4.94	1	1.99E+05		(R)KAIIIFVP	(R)K A I I\I\F\V/P V P Q L K(S)		172.13	489.3212	1465.95	-0.0014	-1	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
21751	dirMS_041712_NAR_120mM_minus.11031.11031.3	3	4.93	0	2.80E+04		(K)GSYVSI	(K)G S/Y/V S I H S S G/F R(D)		114.25	432.8784	1296.633	-0.0125	-9.6	8.75	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
21752	dirMS_041712_NAR_20mM_minus.8527.8527.2	2	4.93	0	1.29E+04		(R)YEIEETE	(R)Y E|I|E/E T E T V T K(S)		134.38	671.3246	1341.642	-0.0001	-0.1	4.09	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
21753	dirMS_041712_NAR_30mM_minus2.16798.16798.2	2	4.93	0	1.34E+05		(R)IMNTFS	(R)I M|N T/F/S V V|P S P K(V)		145.47	660.3534	1319.703	-0.0033	-2.5	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
21754	dirMS_041712_NAR_30mM_minus2.7032.7032.2	2	4.93	0	1.08E+05		(R)ETQSQL	(R)E T Q/S/Q/L/E/T E/R(S)		92.9	610.7948	1220.575	0.007	5.7	4.25	334221.3	6.44	HUMAN	P15924	Desmoplakin
21755	dirMS_041712_NAR_40mM_minus2.10458.10458.3	3	4.93	0	1.35E+04	T170t	(R)YVVDLS	(R)Y V V D L S/V/M/t G L G K(T)	t:N-acetylglucosamine (T)	145.93	528.9384	1381.74	203.0611	-11.5	5.83	21701.3	9.39	HUMAN	A8MXJ6	Frataxin, mitochondrial
21756	dirMS_041712_NAR_50mM_minus2.14218.14218.3	3	4.93	0	1.43E+05		(K)IQVCIPE	(K)I Q/V C I P E/S I Y Q K(V)	C:Carbamidomethylation	149.17	493.2741	1477.772	0.0358	24.2	6	167754.1	5.86	HUMAN	Q5W026	Ankyrin repeat domain 30A
21757	dirMS_041712_NAR_50mM_minus2.18795.18795.3	3	4.93	1	2.08E+06		(R)LIALLEV	(R)L I A L/L/E V L S Q K R(M)		183.67	461.6289	1382.873	-0.0008	-0.6	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
21758	dirMS_041712_NAR_50mM_minus2.9474.9474.3	3	4.93	0	1.82E+05		(R)LQAQQ	(R)L Q/A Q\Q D A V N I|V/C H S K(T)	C:Carbamidomethylation	121.82	570.9573	1710.859	-0.0018	-1.1	6.74	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
21759	dirMS_041712_NAR_120mM_plus.8109.8109.2	2	4.93	0	4.29E+05		(K)AGEVFI	(K)A/G\E/V/F I/H K(D)		96.3	450.7531	900.494	0.0051	5.7	6.79	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
21760	dirMS_041712_NAR_20mM_plus.12630.12630.3	3	4.93	0	3.48E+05		(K)IISNASC	(K)I I\S N\A\S C T T/N C L/A/P\L A K(V)	C:Carbamidomethylation	159.53	611.9768	1833.92	-0.0039	-2.1	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
21761	dirMS_041712_NAR_20mM_plus.13717.13717.2	2	4.93	0	1.08E+05	M273m	(K)mISDAI	(K)m I/S/D A I/P E L\K(A)	m:Oxidized methionine	166.17	566.7967	1116.597	15.9892	-5	4.37	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
21762	dirMS_041712_NAR_20mM_plus.14165.14165.3	3	4.93	1	3.82E+04	Y737y	(K)IFyRKSE	(K)I F/y R K/S E L A Q H/Q R(S)	y:Phosphorylated Y	169.55	585.9641	1675.903	79.975	5	9.99	97863.7	9.18	HUMAN	F6TH33	Zinc finger protein 33A
21763	dirMS_041712_NAR_30mM_plus2.17375.17375.2	2	4.93	0	4.09E+05		(K)NAAGAL	(K)N A|A/G/A L D L/L K(E)		143.75	493.2867	985.568	-0.0015	-1.6	5.84	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
21764	dirMS_041712_NAR_30mM_plus2.6767.6767.2	2	4.93	0	2.50E+05	M529m	(R)MGLSm	(R)M/G|L|S m E R(M)	m:Oxidized methionine	89.82	420.1949	823.38	16.0025	9	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
21765	dirMS_041712_NAR_40mM_plus2.15998.15998.3	3	4.93	1	1.60E+05		(R)VYAEDP	(R)V/Y/A E D/P Y K S F G L/P S I G R(L)		161.13	633.6593	1898.965	-0.0013	-0.7	6.04	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
21766	dirMS_041712_NAR_50mM_plus2.10204.10204.3	3	4.93	1	3.56E+04		(K)YGEPGE	(K)Y G\E/P G E/V\F I N/K G/K(G)		121.27	479.9177	1437.737	0.0013	0.9	6.14	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
21767	dirMS_041712_NAR_50mM_plus2.15371.15371.3	3	4.93	1	7.67E+05		(K)EAFSLF	(K)E A F|S/L/F D/K D G D G T I T T K(E)		149.35	615.6348	1844.891	-0.0014	-0.8	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
21768	dirMS_041712_NAR_50mM_plus2.21008.21008.3	3	4.93	1	3.79E+05	S707s	(K)LsAALSS	(K)L s A A L S S/L\Q/R D M Q R(L)	s:N-acetylglucosamine (S)	179.75	593.6536	1575.827	203.1191	22.3	9.6	135546	8.99	HUMAN	Q9P1Y5	Calmodulin-regulated spectrin-associated protein 3
21769	dirMS_041712_NAR_60mM_plus.13076.13076.3	3	4.93	1	8.37E+05		(R)EFEVYG	(R)E F E V Y/G P I K R(I)		124.55	413.2246	1237.658	0.0017	1.4	6.24	51612.9	9.98	HUMAN	P08621	U1 small nuclear ribonucleoprotein 70 kDa
21770	dirMS_041712_NAR_60mM_plus.13892.13892.3	3	4.93	1	2.19E+05		(K)LSAEKV	(K)L/S\A/E K/V E I/A/T L T R(E)		129.57	477.6106	1430.821	-0.0041	-2.8	6.14	26661.1	7.81	HUMAN	H0YL69	Proteasome subunit alpha type (Fragment)
21771	dirMS_041712_NAR_60mM_plus.15899.15899.3	3	4.93	1	4.34E+05		(R)VTNRDI	(R)V T N R D I\I|C/Q I/A Y/A\R(I)	C:Carbamidomethylation	140.18	564.9631	1692.885	-0.0103	-6.1	8.71	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
21772	dirMS_041712_NAR_60mM_plus.21467.21467.3	3	4.93	0	1.40E+04		(R)LHFFMP	(R)L H F F M\P G F\A|P\L T S R(G)		178.02	540.9492	1620.835	-0.0025	-1.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
21773	dirMS_041712_NAR_60mM_plus.7675.7675.3	3	4.93	1	7.88E+05		(K)TPKGPS	(K)T P K G P S\S/V/E D/I K(A)		98.27	419.894	1257.669	-0.0011	-0.8	5.73	32745.6	4.64	HUMAN	P06748	Nucleophosmin
21774	dirMS_041712_NAR_60mM_plus.9401.9401.3	3	4.93	0	6.10E+05		(K)SVIHSGF	(K)S V/I H S G\P F/T E/S Q K(S)		107.38	472.9094	1416.712	0.0019	1.3	6.47	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
21775	dirMS_041712_NAR_120mM_minus.15549.15549.4	4	4.92	0	1.39E+05		(K)VTICIFV	(K)V T I C I F V S H/F T A P/Y S V/K(N)	C:Carbamidomethylation	139.4	493.0108	1969.025	-0.0038	-1.9	8.57	35679.7	9.6	HUMAN	Q9H1B4-4	Isoform D of Nuclear RNA export factor 5
21776	dirMS_041712_NAR_20mM_minus.11579.11579.2	2	4.92	0	3.10E+05		(R)GALQNI	(R)G A L\Q\N/I|I P A S/T G A A K(A)		164.45	706.3976	1411.79	-0.0024	-1.7	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
21777	dirMS_041712_NAR_30mM_minus2.18331.18331.2	2	4.92	0	1.57E+05		(K)FGAYIV	(K)F G\A/Y I/V/D/G L R(Q)		153.6	555.7984	1110.594	-0.0047	-4.2	5.83	269989.9	5.92	HUMAN	F8W8T8	Acetyl-CoA carboxylase 2
21778	dirMS_041712_NAR_40mM_minus2.13267.13267.2	2	4.92	0	9.94E+04		(K)SYELPD	(K)S Y E\L/P D G Q V I/T/I/G N E/R(F)		161.55	895.9483	1790.892	-0.0026	-1.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
21779	dirMS_041712_NAR_50mM_minus2.14506.14506.3	3	4.92	0	1.56E+04		(R)IDQVNQ	(R)I/D/Q/V/N Q\L L E L D H Q K(R)		150.7	564.9709	1692.892	0.0066	3.9	4.54	44513	5.59	HUMAN	B4DIH5	COP9 signalosome complex subunit 2
21780	dirMS_041712_NAR_60mM_minus.17064.17064.3	3	4.92	1	3.47E+04		(K)DREGFF	(K)D R E G F\F|T|N/G L/T L G A K(K)		155.48	542.6145	1625.828	0.0008	0.5	6.07	9954.3	9.57	HUMAN	C9J0J7	Profilin-2
21781	dirMS_041712_NAR_120mM_plus.13918.13940.3	3	4.92	1	1.29E+06	N1991n M:	(K)nYYRILm	(K)n Y Y|R I/L/m/R(R)	n:N-acetylglucosamine (N) m	126.75	449.8938	1128.598	219.0686	-4.2	9.99	254327.9	5.45	HUMAN	E9PGT0	Putative peptidyl-prolyl cis-trans isomerase
21782	dirMS_041712_NAR_20mM_plus.11594.11594.2	2	4.92	0	1.54E+05		(K)VGLQVV	(K)V/G\L|Q V/V A V K(A)		151.85	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
21783	dirMS_041712_NAR_20mM_plus.16048.16048.2	2	4.92	0	1.13E+05		(R)GLFIIDG	(R)G L/F/I I/D G K(G)		182.03	431.7544	862.503	-0.0018	-2	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
21784	dirMS_041712_NAR_20mM_plus.7579.7579.2	2	4.92	0	3.86E+04		(K)IAVAAQ	(K)I A|V|A/A Q\N C Y K(V)	C:Carbamidomethylation	121.72	569.2902	1137.572	0.001	0.9	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
21785	dirMS_041712_NAR_30mM_plus2.16520.16520.2	2	4.92	0	8.98E+04		(R)LIFSTITS	(R)L/I|F/S T I/T S K(M)		139.15	505.3008	1009.593	0.0015	1.5	8.75	47479.5	5.09	HUMAN	P43686	26S protease regulatory subunit 6B
21786	dirMS_041712_NAR_30mM_plus2.17227.17227.2	2	4.92	0	2.45E+05		(K)VSTLPA	(K)V S|T L/P A I T L K(L)		143.45	521.8272	1042.651	-0.0035	-3.4	8.72	20599.3	9.19	HUMAN	H7C1V0	Cathepsin D light chain (Fragment)
21787	dirMS_041712_NAR_30mM_plus2.17757.17757.2	2	4.92	0	1.26E+04		(R)AINIADE	(R)A I/N I A D/E/L/P\R(S)		146.6	556.3051	1111.611	-0.0077	-6.9	4.37	34746.4	9.67	HUMAN	Q8NFV4	Alpha/beta hydrolase domain-containing protein 11
21788	dirMS_041712_NAR_40mM_plus2.7047.7047.3	3	4.92	0	2.12E+04		(K)SNVSDA	(K)S N V S D A V/A Q/S T R(I)		101.47	412.2048	1234.602	-0.0024	-1.9	5.55	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
21789	dirMS_041712_NAR_40mM_plus2.7548.7548.3	3	4.92	0	1.52E+04		(R)EATNPP	(R)E A/T N/P/P V I Q E/E\K P K(K)		104.03	527.286	1579.833	0.0108	6.9	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
21790	dirMS_041712_NAR_50mM_plus2.7095.7095.3	3	4.92	1	3.65E+04	M92m	(K)LGEGEG	(K)L/G/E G E/G/S m T K E E F/T K(M)	m:Oxidized methionine	103.2	553.5925	1642.763	16.0001	3.1	4.49	14591.3	4.63	HUMAN	G3V2U1	Sorting nexin-6
21791	dirMS_041712_NAR_60mM_plus.13641.13641.2	2	4.92	1	3.15E+05		(R)VVDLM	(R)V V D L/M/A\H M/A/S\K E(-)		127.75	665.8295	1330.649	0.0024	1.8	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
21792	dirMS_041712_NAR_60mM_plus.15819.15819.3	3	4.92	1	2.45E+05		(R)TSFLDD	(R)T|S/F/L D D/A F R K(N)		139.9	400.5399	1199.605	-0.0004	-0.3	5.62	21195.7	6.97	HUMAN	H0YJ21	Cytoplasmic dynein 1 heavy chain 1 (Fragment)
21793	dirMS_041712_NAR_60mM_plus.19957.19957.3	3	4.92	1	1.35E+05		(R)TLLLDG	(R)T L/L\L/D/G N P F R V P R(A)		164.42	499.9559	1497.854	-0.0005	-0.3	9.26	68762.2	6.04	HUMAN	Q9H9A6	Leucine-rich repeat-containing protein 40
21794	dirMS_041712_NAR_60mM_plus.6946.6946.3	3	4.92	1	3.73E+05		(K)DGGFCE	(K)D/G|G F/C/E V C K K(L)	C:Carbamidomethylation	94.72	400.5114	1199.518	0.0013	1.1	6.07	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
21795	dirMS_041712_NAR_120mM_minus.14719.14719.3	3	4.91	0	1.01E+06		(-)MVNHF	(-)M/V/N H F I A E/F K(R)		134.9	412.5458	1235.624	-0.0013	-1	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein

21796	dirMS_041712_NAR_120mM_minus.4295.4295.3	3	4.91	1	5.31E+05		(R)EPGPAG	(R)E P/G P A G/R G D G D/S G/R(S)		70.73	443.2041	1327.599	-0.0008	-0.6	4.56	558007.1	5.44	HUMAN	P58107	Epiplakin
21797	dirMS_041712_NAR_120mM_minus.9095.9095.3	3	4.91	0	8.47E+05		(K)HTGPNS	(K)H T G P N\S\P D T\A/N D/G F V R(L)		103.3	562.2599	1684.767	-0.0022	-1.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
21798	dirMS_041712_NAR_40mM_minus2.14292.14292.3	3	4.91	1	1.61E+05		(K)TGISDVF	(K)T G I S/D V F A/K N D L/A/V\V D/V R(I)		168.48	640.3454	1919.023	-0.0016	-0.8	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
21799	dirMS_041712_NAR_40mM_minus2.8243.8243.3	3	4.91	1	3.04E+05	M119m	(R)SNTPILV	(R)S N\T|P I/L V/D/G K D V m P E V N K(V)	m:Oxidized methionine	128.4	658.0032	1956.011	15.9844	-5.3	4.56	18405.7	9.81	HUMAN	K7EP41	Glucose-6-phosphate isomerase (Fragment)
21800	dirMS_041712_NAR_50mM_minus2.10143.10143.3	3	4.91	1	9.36E+04		(R)VGEPVA	(R)V G/E/P/V A L S/E E E R L K(L)		125.62	519.2824	1555.833	0	0	4.49	8516.9	5.1	HUMAN	E9PIL8	Splicing factor 3B subunit 2 (Fragment)
21801	dirMS_041712_NAR_50mM_minus2.6146.6146.2	2	4.91	0	3.56E+04		(K)AGFAGD	(K)A G F/A/G/D D A P R(A)		97.78	488.7293	976.448	0.003	3.1	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
21802	dirMS_041712_NAR_50mM_minus2.6851.6851.3	3	4.91	0	8.00E+03	M233m	(K)SAAmLG	(K)S A A m|L/G/N S E D H\T A L S R(A)	m:Oxidized methionine	105.48	559.2593	1659.776	15.9878	-4.2	5.3	46211	6.76	HUMAN	B4DEK4	Sorting nexin-2
21803	dirMS_041712_NAR_60mM_minus.19999.19999.3	3	4.91	1	7.82E+05		(R)LIALLEVI	(R)L I|A L/L E/V L S Q K R(M)		182.07	461.6287	1382.873	-0.0014	-1	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
21804	dirMS_041712_NAR_60mM_minus.5337.5337.3	3	4.91	0	8.98E+04	M116m	(R)ATAPQT	(R)A T\A/P Q T Q H V/S/P m R(Q)	m:Oxidized methionine	85.37	480.5729	1423.711	15.9931	-1.3	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
21805	dirMS_041712_NAR_60mM_minus.7468.7468.3	3	4.91	1	1.06E+05		(R)AVTGYK	(R)A V/T/G Y K D/P Y S G K(L)		101.32	429.2175	1285.642	-0.0043	-3.4	8.47	533778	5.74	HUMAN	Q15149	Plectin
21806	dirMS_041712_NAR_120mM_plus.13575.13575.3	3	4.91	0	1.09E+06		(K)THINIVV	(K)T H\I N I\V\V|I/G H V/D\S G K(S)		124	530.2975	1588.881	-0.0026	-1.6	6.61	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
21807	dirMS_041712_NAR_20mM_plus.11547.11547.2	2	4.91	0	1.24E+05	M402m	(R)mAFGA	(R)m A|F|G A T/L D/V K(T)	m:Oxidized methionine	152.27	534.7743	1052.545	15.9968	1.8	5.59	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
21808	dirMS_041712_NAR_20mM_plus.18978.18978.2	2	4.91	1	5.61E+04	Y582y	(R)LVKVTLy	(R)L V/K V T/L|y G S Q I K(L)	y:Phosphorylated Y	201.58	714.8991	1348.82	79.9711	3.3	9.7	128647.2	6.02	HUMAN	D3DWF9	Exportin 6, isoform CRA_a
21809	dirMS_041712_NAR_20mM_plus.9856.9856.2	2	4.91	0	7.83E+04		(K)AIADTG	(K)A I\A|D T/G A N V V V/T G G K(V)		139.22	686.874	1372.743	-0.0023	-1.7	5.88	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
21810	dirMS_041712_NAR_30mM_plus2.15840.15840.2	2	4.91	0	3.11E+05		(R)YSVDIPL	(R)Y/S/V/D\I/P L D K(T)		136.1	525.2819	1049.551	0.0052	4.9	4.21	16471.9	10.59	HUMAN	K7ELC7	60S ribosomal protein L27 (Fragment)
21811	dirMS_041712_NAR_30mM_plus2.4816.4816.2	2	4.91	0	8.12E+05		(R)MGQTM	(R)M/G Q/T/M E R(I)		76.8	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
21812	dirMS_041712_NAR_40mM_plus2.8424.8424.2	2	4.91	0	8.22E+04		(K)DVNQQI	(K)D V/N Q Q E/F/V R(A)		110.82	567.78	1134.554	-0.0011	-1	4.37	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
21813	dirMS_041712_NAR_50mM_plus2.13801.13801.3	3	4.91	1	3.03E+05		(K)IWLAAH	(K)I W L A/A H W D/K K L T K(A)		140.87	537.3129	1609.921	0.0028	1.8	9.7	25908.6	4.65	HUMAN	E5RFV8	Double-strand-break repair protein rad21 homolog (Fragment)
21814	dirMS_041712_NAR_50mM_plus2.14913.14913.3	3	4.91	1	9.00E+05		(R)LYSILGT	(R)L/Y\S I/L/G T T L K D\E/G/K(L)		145.9	513.2859	1537.847	-0.0041	-2.6	6.07	66876.9	6.17	HUMAN	O75083	WD repeat-containing protein 1
21815	dirMS_041712_NAR_50mM_plus2.17335.17335.3	3	4.91	1	1.15E+05		(K)LLVYEAL	(K)L L/V/Y E A L E Y A K R(A)		160.62	489.9441	1467.821	-0.0028	-1.9	6.14	32535.6	9.19	HUMAN	B4DZW6	Regulator of microtubule dynamics protein 1
21816	dirMS_041712_NAR_50mM_plus2.7369.7369.3	3	4.91	1	2.01E+04	M236m M	(K)NSVTPD	(K)N\S|V/T P D/M m E\E m Y\K K(A)	m:Oxidized methionine	104.67	578.9161	1702.748	31.9853	-2.6	4.68	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
21817	dirMS_041712_NAR_60mM_plus.6692.6692.3	3	4.91	0	7.60E+04		(R)NIDEHA	(R)N I/D E H/A N/E/D V E R(M)		93.17	480.8866	1440.635	0.0103	7.1	4.17	22768.7	8.94	HUMAN	P61026	Ras-related protein Rab-10
21818	dirMS_041712_NAR_20mM_minus.11002.11002.3	3	4.9	1	2.29E+04	S11s	(-)MAKHGA	(-)M A K H G\A/D|E P S s/R(S)	s:N-acetylglucosamine (S)	157.83	496.895	1285.595	203.0751	-2.9	6.51	76676.1	6.47	HUMAN	A1IGU5	Rho guanine nucleotide exchange factor 37
21819	dirMS_041712_NAR_20mM_minus.13382.13382.3	3	4.9	2	1.16E+04	S212s M22	(K)sTERLSP	(K)s T E R L/S/P/L m K D I K(S)	s:Phosphorylated S m:Oxidiz	184.68	538.6093	1517.836	95.9778	10.2	8.31	91964.4	9.32	HUMAN	F8WE45	Leucine-rich repeat-containing protein 7
21820	dirMS_041712_NAR_20mM_minus.14361.14361.2	2	4.9	0	2.33E+05		(K)DAGVIA	(K)D A\G/V|I/A|G/L N V L R(I)		198.12	599.3503	1197.695	-0.0017	-1.4	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
21821	dirMS_041712_NAR_20mM_minus.8248.8248.2	2	4.9	0	1.72E+04	K201k	(K)LATEDV	(K)L/A T/E D V/Y/I N k(V)	k:Ubiquitin-K	132.37	640.3296	1165.61	114.042	-0.7	4.37	35471	8.91	HUMAN	A6NMU1	Putative olfactory receptor 52A4
21822	dirMS_041712_NAR_30mM_minus2.13934.13934.2	2	4.9	0	2.95E+05	M313m	(K)NSLESYA	(K)N/S|L\E/S/Y A F N m K(A)	m:Oxidized methionine	128.95	660.3011	1303.599	15.9962	1	6	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
21823	dirMS_041712_NAR_30mM_minus2.14461.14461.2	2	4.9	0	1.34E+04	M1m	(-)mQHSGI	(-)m Q/H\S G I P T\K(T)	m:Oxidized methionine	133.57	507.7594	998.509	16.0027	7.7	8.52	90424.8	9.82	HUMAN	F5GZL2	Centrosomal protein C10orf90
21824	dirMS_041712_NAR_50mM_minus2.11423.11423.3	3	4.9	0	9.65E+04	K252k M25	(K)EkLSAm	(K)E k L/S A/m Q A H L A G K(M)	k:Ubiquitin-K m:Oxidized me	132.95	505.2683	1383.741	130.0491	7.4	8.69	47756.9	10.05	HUMAN	Q9BZS1	Forkhead box protein P3
21825	dirMS_041712_NAR_50mM_minus2.13521.13521.3	3	4.9	1	1.26E+05		(R)SEGVVA	(R)S/E G\V/V/A V L L T K K(S)		145.45	415.255	1243.762	-0.0116	-9.3	8.31	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
21826	dirMS_041712_NAR_50mM_minus2.14154.14154.3	3	4.9	1	1.29E+04	T1164t	(R)VLDDVS	(R)V L/D/D V S I R S P E t K(C)	t:N-acetylglucosamine (T)	148.55	554.6378	1458.78	203.119	23.8	4.56	310748.8	5.77	HUMAN	E7ETD6	Nucleosome-remodeling factor subunit BPTF
21827	dirMS_041712_NAR_60mM_minus.15487.15487.3	3	4.9	0	1.83E+05		(K)LKPQYLE	(K)L K\P/Q Y\L E/E\L/P G Q L K(Q)		146.18	552.6501	1655.937	-0.0009	-0.6	6.14	27015.5	5.37	HUMAN	P21266	Glutathione S-transferase Mu 3
21828	dirMS_041712_NAR_60mM_minus.18510.18510.3	3	4.9	0	3.17E+05		(R)GIITWGI	(R)G I/I/T W G L L P G P/Y H/R(G)		165.42	527.2975	1579.874	0.0036	2.3	8.75	35021.8	6.18	HUMAN	B4DF47	Protein misato homolog 1
21829	dirMS_041712_NAR_120mM_plus.10606.10632.3	3	4.9	0	6.93E+05		(R)AHSSM	(R)A H S S M V|G\V/N/L/P Q K(A)		108.48	456.5762	1367.71	0.0041	3	8.8	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
21830	dirMS_041712_NAR_120mM_plus.6236.6236.3	3	4.9	0	7.54E+05		(K)QRPQAT	(K)Q R P\Q\A|T/A E Q/I R(L)		86.02	433.2367	1297.697	-0.0016	-1.2	9.6	113668.7	6.2	HUMAN	F8W726	Ubiquitin-associated protein 2-like
21831	dirMS_041712_NAR_120mM_plus.7672.7672.3	3	4.9	0	3.68E+05		(R)NADHSN	(R)N A D H/S M N|Y Q Y/R(-)		93.8	466.8673	1398.585	0.0018	1.3	6.74	96205.6	9.06	HUMAN	G5E9M5	Interleukin enhancer binding factor 3, 90kDa, isoform CRA_b
21832	dirMS_041712_NAR_40mM_plus2.16126.16126.3	3	4.9	1	1.93E+05		(R)VYAEDP	(R)V Y/A E D/P Y K S F G L/P S/I G R(L)		161.62	633.6593	1898.965	-0.0013	-0.7	6.04	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
21833	dirMS_041712_NAR_60mM_plus.7367.7367.3	3	4.9	1	1.93E+06		(R)SEEKISD	(R)S E E K/I/S/D\S E G F K(A)		96.8	452.5501	1355.632	0.0032	2.4	4.41	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
21834	dirMS_041712_NAR_120mM_minus.13427.13427.4	4	4.89	0	3.61E+05		(R)VLSAPP	(R)V L S A/P P H/F H/F/G Q T N R(T)		127.58	427.7219	1707.871	-0.0056	-3.3	9.74	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
21835	dirMS_041712_NAR_120mM_minus.19900.19900.3	3	4.89	1	2.47E+05		(R)AKFEEL	(R)A K F E E E L N/M/D/L/F R(S)		164.85	504.9216	1512.752	-0.0013	-0.8	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
21836	dirMS_041712_NAR_120mM_minus.9562.9562.2	2	4.89	0	5.89E+05		(K)HVVFIA	(K)H V|V/F I A Q R(R)		105.95	485.2837	969.563	-0.0027	-2.8	9.75	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
21837	dirMS_041712_NAR_30mM_minus2.18012.18012.3	3	4.89	0	6.94E+04		(R)SSFYVN	(R)S\S F\Y V N G L/T L G/G Q K(C)		152.48	490.9238	1470.759	-0.0019	-1.3	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
21838	dirMS_041712_NAR_40mM_minus2.12210.12210.3	3	4.89	1	2.69E+05		(K)DVAIKE	(K)D V\A I/K/E P L|V D V V D P K(Q)		156.03	546.3068	1636.916	-0.0098	-6	4.23	24376.8	6.08	HUMAN	E9PIX6	Protein arginine N-methyltransferase 1 (Fragment)
21839	dirMS_041712_NAR_40mM_minus2.8149.8149.3	3	4.89	0	2.15E+05	M35m	(K)AASDIA	(K)A A|S D/I A|m T E L/P P T H P I R(L)	m:Oxidized methionine	128.43	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
21840	dirMS_041712_NAR_50mM_minus2.16778.16778.3	3	4.89	0	2.38E+05		(R)LGIEGLS	(R)L G\I E/G L/S L/H N V L K(L)		164.13	464.9452	1392.821	0.0001	0.1	6.75	177928	5.42	HUMAN	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1
21841	dirMS_041712_NAR_50mM_minus2.18311.18311.3	3	4.89	0	4.19E+05		(K)ALIEVLQ	(K)A L\I/E V L Q/P L/I A E H Q A R(R)		175.35	601.0139	1801.033	-0.0059	-3.3	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
21842	dirMS_041712_NAR_50mM_minus2.8759.8759.3	3	4.89	0	1.19E+06		(R)EIVHIQA	(R)E/I/V H I Q A G\Q|C G N Q I G A K(F)	C:Carbamidomethylation	117.03	608.3087	1822.923	-0.0113	-6.2	6.85	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
21843	dirMS_041712_NAR_60mM_minus.12405.12405.3	3	4.89	1	5.26E+05		(R)EMDRET	(R)E M D/R E T L I/D/V A R(T)		128.95	483.2454	1447.721	0.0007	0.5	4.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
21844	dirMS_041712_NAR_60mM_minus.16630.16630.3	3	4.89	0	1.67E+05		(R)LLIHQSL	(R)L L I H Q\S/L/A|G/G I/I/G V K(G)		153.32	506.9823	1518.937	-0.0043	-2.8	8.76	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
21845	dirMS_041712_NAR_60mM_minus.8630.8630.3	3	4.89	1	2.05E+04	M227m M	(R)mQKEIT	(R)m Q\K E I T A L|A|P S T m K(I)	m:Oxidized methionine	108.02	527.6044	1548.812	31.9862	-2.3	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
21846	dirMS_041712_NAR_120mM_plus.14581.14581.4	4	4.89	0	8.39E+05	S106s	(R)YQVLLSL	(R)Y Q/V\L L/S L M L\S s Q T/K(D)	s:N-acetylglucosamine (S)	130.45	454.2533	1610.882	203.1092	16.4	8.59	23944	9.9	HUMAN	H3BRL9	Endonuclease III-like protein 1 (Fragment)
21847	dirMS_041712_NAR_120mM_plus.4279.4279.3	3	4.89	0	6.53E+05	M77m M7	(R)LTNSMn	(R)L/T|N S M m\m H/G R(N)	m:Oxidized methionine	71.17	403.8446	1177.527	31.9918	1.6	9.75	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
21848	dirMS_041712_NAR_20mM_plus.11027.11027.2	2	4.89	0	1.04E+05	M188m	(K)VVEILAD	(K)V V E|I/L/A D m T A R(D)	m:Oxidized methionine	148.63	617.3237	1217.656	15.9843	-8.6	4.37	68200.1	8.69	HUMAN	Q13322	Growth factor receptor-bound protein 10
21849	dirMS_041712_NAR_20mM_plus.14473.14473.2	2	4.89	0	1.27E+05		(K)LVILAN	(K)L V\I\L|A|N/N C|P A L R(K)	C:Carbamidomethylation	171.45	677.3851	1353.767	-0.0042	-3.1	9.75	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
21850	dirMS_041712_NAR_20mM_plus.14493.14493.3	3	4.89	2	9.06E+04		(R)TAAWRT	(R)T A A W R T|T S E E K K(A)		171.62	469.9095	1407.723	-0.0087	-6.2	8.26	51294.7	5.64	HUMAN	B4DUX5	Methionine aminopeptidase
21851	dirMS_041712_NAR_20mM_plus.16594.16594.2	2	4.89	0	7.60E+04		(R)LGSTVF	(R)L G\S T V/F\V/A N L D Y K(V)		185	713.8819	1426.758	-0.0011	-0.8	5.83	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
21852	dirMS_041712_NAR_20mM_plus.18958.18958.3	3	4.89	0	4.52E+04		(K)GLVQAL	(K)G L V Q A|L G L/S N/F N S R(Q)		201.73	492.6019	1475.796	-0.0054	-3.6	9.75	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
21853	dirMS_041712_NAR_20mM_plus.7595.7595.2	2	4.89	0	2.49E+05		(K)VLTPTQ	(K)V/L|T/P T Q V K(N)		121.73	443.2734	885.54	-0.0009	-1	8.72	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
21854	dirMS_041712_NAR_30mM_plus2.10430.10430.2	2	4.89	0	2.93E+05		(R)DPYGFG	(R)D P/Y/G/F G\D/S\R(D)		108.67	507.2274	1013.432	0.0152	15	4.21	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
21855	dirMS_041712_NAR_30mM_plus2.17074.17074.3	3	4.89	0	5.02E+05	M313m	(R)TVQSLEI	(R)T\V Q S L E/I/D/L/D/S m R(N)	m:Oxidized methionine	142.1	508.2535	1506.747	15.9991	2.8	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
21856	dirMS_041712_NAR_30mM_plus2.17359.17359.2	2	4.89	0	5.74E+04		(K)GPLMM	(K)G/P|L/M/M Y I S K(M)		143.65	520.2659	1039.532	-0.007	-6.7	8.59	96306.4	6.41	HUMAN	P13639	Elongation factor 2
21857	dirMS_041712_NAR_30mM_plus2.22778.22778.2	2	4.89	0	2.69E+05		(R)ELSDFIS	(R)E L/S D F|I\S\Y L Q/R(E)		177.22	685.8507	1370.695	-0.0009	-0.7	4.37	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
21858	dirMS_041712_NAR_30mM_plus2.7635.7635.2	2	4.89	0	1.34E+05		(K)LSENSV	(K)L S|E N S/V A K(G)		94.17	424.2304	847.452	0.0016	1.8	6	163852.7	5.43	HUMAN	C9JJN9	Vacuolar protein sorting-associated protein 8 homolog
21859	dirMS_041712_NAR_30mM_plus2.9243.9243.2	2	4.89	0	2.25E+05		(R)ALELEQ	(R)A L/E/L E/Q/E R(K)		101.35	494.2566	987.511	-0.0046	-4.7	4.25	67933	6.08	HUMAN	P26038	Moesin
21860	dirMS_041712_NAR_40mM_plus2.11125.11125.3	3	4.89	0	9.07E+04		(R)VLVASS	(R)V L|V|A/S S V V A G E S Q K P E L K(A)		131.88	614.3443	1841.038	-0.0195	-10.6	6.11	61441.6	5.93	HUMAN	G8JLE9	Fragile X mental retardation protein 1
21861	dirMS_041712_NAR_40mM_plus2.6034.6034.2	2	4.89	0	1.26E+05		(R)SPDNPN	(R)S P/D\N/P M N Q R(A)		93.73	529.7368	1058.468	-0.002	-1.9	5.55	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
21862	dirMS_041712_NAR_40mM_plus2.8045.8045.2	2	4.89	0	1.89E+05		(K)SFYVCR	(K)S F/Y/V C R(A)	C:Carbamidomethylation	108.43	416.1954	831.382	0.0017	2.1	8.46	130841	9.05	HUMAN	Q9UNY4	Transcription termination factor 2
21863	dirMS_041712_NAR_50mM_plus2.20458.20458.3	3	4.89	1	2.26E+05		(K)VKIPEGT	(K)V K I|P E G T I/L/T/M/D M L T\V K(V)		176.9	630.3524	1889.049	-0.006	-3.2	6.04	40763.2	6.29	HUMAN	Q9NR45	Sialic acid synthase
21864	dirMS_041712_NAR_50mM_plus2.5122.5122.3	3	4.89	1	3.11E+04		(R)MQNDT	(R)M Q/N/D T A E N E T T E K E E K(S)		85.33	632.9398	1896.813	-0.0079	-4.2	4.14	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
21865	dirMS_041712_NAR_50mM_plus2.7704.7704.3	3	4.89	0	6.60E+04	M378m M	(K)mIVDPV	(K)m I\V/D/P V E/P/H G E m/K(F)	m:Oxidized methionine	106.6	505.2419	1481.713	31.9984	5.7	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
21866	dirMS_041712_NAR_50mM_plus2.8090.8090.3	3	4.89	0	1.26E+05		(K)QLAVAE	(K)Q L A/V/A E G K/P/P E A P K(G)		109.72	478.9337	1434.795	-0.0086	-6	6.14	24364.9	9.64	HUMAN	H0YIP0	Methionine--tRNA ligase, cytoplasmic (Fragment)
21867	dirMS_041712_NAR_60mM_plus.9897.9897.2	2	4.89	0	4.34E+05		(R)QSVEND	(R)Q S/V E/N D/I/H/G L/R(K)		109.77	634.3217	1267.639	-0.0028	-2.2	5.32	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
21868	dirMS_041712_NAR_120mM_minus.5447.5447.2	2	4.88	1	1.34E+05		(K)MKGDY	(K)M/K|G D/Y Y R(Y)		82.75	466.7187	932.429	0.0007	0.7	8.25	18789.1	6.77	HUMAN	A2IDB2	14-3-3 protein eta (Fragment)
21869	dirMS_041712_NAR_30mM_minus2.10982.10982.2	2	4.88	0	5.48E+04		(K)MLVIEQ	(K)M L|V|I/E Q C/K(N)	C:Carbamidomethylation	114.78	510.7635	1020.522	-0.0019	-1.9	5.75	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
21870	dirMS_041712_NAR_30mM_minus2.9416.9416.2	2	4.88	0	2.46E+06	N82n	(R)ITDnVGF	(R)I T|D n V G R(E)	n:N-acetylglucosamine (N)	106.1	489.2597	774.41	203.1017	22.8	5.84	19048.7	5.44	HUMAN	C9J636	Phospholipid scramblase 2 (Fragment)
21871	dirMS_041712_NAR_50mM_minus2.15339.15339.3	3	4.88	1	7.30E+05		(R)DVDFELI	(R)D V|D/F/E L I K V E/G K(V)		154.4	464.5852	1391.742	-0.0006	-0.4	4.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
21872	dirMS_041712_NAR_60mM_minus.16856.16856.3	3	4.88	1	1.76E+05		(K)NLTAAK	(K)N L/T A A K A\G/G T S D\S F\V K(G)		154.63	522.9452	1566.812	0.0088	5.6	8.59	76836	9.37	HUMAN	F8W9B9	Synaptotagmin-like protein 4
21873	dirMS_041712_NAR_120mM_plus.21940.21940.3	3	4.88	0	9.50E+04		(R)DFNHIN	(R)D F\N H I N\V\E|L/S L L/G K(K)		168.47	533.6224	1598.854	-0.001	-0.6	5.32	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
21874	dirMS_041712_NAR_20mM_plus.12329.12329.2	2	4.88	0	2.53E+04		(R)LGTLSPA	(R)L G T/L/S/P A F S T R(V)		158.03	575.3192	1149.626	0.0049	4.2	9.75	102679.8	6.75	HUMAN	Q7KZF4	Staphylococcal nuclease domain-containing protein 1
21875	dirMS_041712_NAR_20mM_plus.15805.15805.2	2	4.88	0	9.29E+03		(K)ALTLIAG	(K)A L T\L|I/A/G S P/L K(I)		180.12	542.3395	1083.677	-0.0055	-5.1	8.8	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
21876	dirMS_041712_NAR_20mM_plus.17849.17849.3	3	4.88	0	1.92E+05		(R)TVQSLEI	(R)T V Q|S L E I/D L/D S M R(N)		194.88	502.9236	1506.747	0.0094	6.2	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
21877	dirMS_041712_NAR_20mM_plus.18337.18337.2	2	4.88	0	1.68E+05		(R)LTGQLFL	(R)L T/G Q\L/F/L G G S I V/K(G)		197.02	666.8962	1332.789	-0.0034	-2.6	8.75	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
21878	dirMS_041712_NAR_20mM_plus.18708.18708.2	2	4.88	0	4.11E+04		(K)LLDAVD	(K)L L D A V/D\T Y/I/P V/P A R(D)		199.97	771.9239	1542.853	-0.0121	-7.8	4.21	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
21879	dirMS_041712_NAR_20mM_plus.8352.8352.2	2	4.88	0	1.59E+04		(R)FTEYETC	(R)F/T/E/Y/E/T Q V K(V)		127.72	572.782	1144.552	0.0046	4.1	4.53	33803.8	6.12	HUMAN	B1AKP7	TAR DNA binding protein
21880	dirMS_041712_NAR_20mM_plus.9297.9297.3	3	4.88	0	3.09E+04		(R)SVSLTG	(R)S V S/L/T/G\A/P E S V Q K(A)		135.52	434.9007	1302.69	-0.0024	-1.9	5.72	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
21881	dirMS_041712_NAR_30mM_plus2.10019.10019.2	2	4.88	0	1.51E+06		(R)GVNVSA	(R)G V/N\V S A L/S R(D)		105.73	451.7509	902.505	-0.0109	-12.1	9.75	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
21882	dirMS_041712_NAR_40mM_plus2.13656.13656.3	3	4.88	0	3.14E+05		(R)VAPDEH	(R)V/A/P D E H P I L L T E A/P L N/P K(I)		146.03	652.0252	1954.064	-0.0034	-1.7	4.65	42344.8	5.39	HUMAN	Q562R1	Beta-actin-like protein 2
21883	dirMS_041712_NAR_40mM_plus2.7426.7426.2	2	4.88	0	1.62E+04		(K)CGPITST	(K)C G P I/T S T T R(F)	C:Carbamidomethylation	102.32	496.7407	992.483	-0.0088	-8.9	9.75	98576.9	6.39	HUMAN	F5H2H5	Ankyrin repeat and LEM domain-containing protein 2
21884	dirMS_041712_NAR_40mM_plus2.9989.9989.2	2	4.88	0	1.16E+05		(K)SCAHDV	(K)S C A H D W\V|Y/E(-)	C:Carbamidomethylation	122.45	583.7327	1166.457	0.001	0.8	4.71	8782.8	5.3	HUMAN	F6XY72	Nucleoside diphosphate kinase
21885	dirMS_041712_NAR_50mM_plus2.13570.13570.3	3	4.88	0	1.13E+06		(K)AASDIA	(K)A A|S D/I A/M/T E L/P/P T H P I R(L)		139.33	607.3177	1819.937	0.0015	0.8	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
21886	dirMS_041712_NAR_50mM_plus2.19918.19918.3	3	4.88	0	1.93E+04		(R)EAILEYIL	(R)E A I/L E Y I/L H Q K(K)		173.2	452.9215	1356.752	-0.0022	-1.6	5.4	33684.9	9.52	HUMAN	Q9Y314	Nitric oxide synthase-interacting protein
21887	dirMS_041712_NAR_50mM_plus2.6467.6467.3	3	4.88	1	3.41E+04		(K)IIVGDAT	(K)I I/V/G D/A/T E K D A S K(K)		98.78	449.5766	1346.716	-0.0009	-0.7	4.56	45188.9	5.76	HUMAN	Q96I25	Splicing factor 45
21888	dirMS_041712_NAR_60mM_plus.14040.14040.3	3	4.88	0	2.84E+05		(R)LYFLQCE	(R)L Y|F/L Q C E/T C H S R(C)	C:Carbamidomethylation	129.48	538.5788	1613.72	0.0019	1.2	6.75	38730.1	5.6	HUMAN	P20042	Eukaryotic translation initiation factor 2 subunit 2
21889	dirMS_041712_NAR_60mM_plus.15850.15850.3	3	4.88	1	1.17E+06		(R)MSMKE	(R)M S M K E V D E\Q|M/L/N V\Q N/K(N)		140.23	641.9696	1923.897	-0.003	-1.6	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
21890	dirMS_041712_NAR_60mM_plus.17280.17280.3	3	4.88	0	2.04E+05		(K)THLPGF	(K)T\H L\P G F\V|E Q/A E A L/K(A)		147.35	513.9442	1539.817	0.0015	1	5.37	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
21891	dirMS_041712_NAR_60mM_plus.9335.9335.3	3	4.88	1	2.16E+05		(R)AYQKQP	(R)A Y Q K Q/P T/I/F Q/N K(K)		106.18	489.2643	1465.78	-0.0014	-1	9.7	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
21892	dirMS_041712_NAR_120mM_minus.15861.15861.3	3	4.87	1	1.98E+05		(R)TSFLDD	(R)T S|F/L\D/D/A F\R/K(N)		140.05	400.5402	1199.605	0.0005	0.4	5.62	21195.7	6.97	HUMAN	H0YJ21	Cytoplasmic dynein 1 heavy chain 1 (Fragment)
21893	dirMS_041712_NAR_30mM_minus2.12313.12313.2	2	4.87	0	1.33E+05		(K)SIYYITGE	(K)S I/Y|Y I/T G E S K(E)		121.08	580.7949	1160.583	-0.0009	-0.7	5.72	16789.1	8.77	HUMAN	H0Y5S7	Heat shock protein HSP 90-beta (Fragment)
21894	dirMS_041712_NAR_50mM_minus2.10936.10936.3	3	4.87	1	1.10E+04		(K)ALELDP	(K)A L|E|L D/P D N E T Y K S N L K(I)		130.67	617.3102	1849.918	-0.0018	-0.9	4.32	34290.7	4.81	HUMAN	O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha
21895	dirMS_041712_NAR_50mM_minus2.11789.11789.3	3	4.87	0	6.96E+04	M425m M	(R)VFITDDF	(R)V F|I/T D/D\F H D m m P K(Y)	m:Oxidized methionine	135.23	543.2416	1595.723	31.987	-1.7	4.41	92752.5	4.76	HUMAN	P14625	Endoplasmin
21896	dirMS_041712_NAR_50mM_minus2.18010.18010.3	3	4.87	1	2.22E+05	M116m	(R)ELAILLG	(R)E L\A I L/L G m L D/P A E/K D E K(G)	m:Oxidized methionine	170.85	634.3353	1884.999	15.9927	-1.2	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
21897	dirMS_041712_NAR_60mM_minus.15662.15662.3	3	4.87	1	3.11E+05		(R)GFPTIYF	(R)G F/P T I Y/F S/P A N K K(L)		147.17	490.5972	1469.779	-0.0017	-1.1	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
21898	dirMS_041712_NAR_60mM_minus.6860.6860.3	3	4.87	1	1.11E+05	M281m	(R)SRAEAE	(R)S R A E\A E|S m/Y/Q I K(Y)	m:Oxidized methionine	96.73	476.895	1412.684	15.9866	-5.8	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
21899	dirMS_041712_NAR_60mM_minus.6900.6900.3	3	4.87	1	5.61E+05	M286m M	(R)VVDLmA	(R)V V/D/L m/A H m A/S K E(-)	m:Oxidized methionine	96.77	454.8843	1330.649	31.989	-0.6	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
21900	dirMS_041712_NAR_120mM_plus.6141.6141.2	2	4.87	2	3.38E+05	Y18y	(K)SIYTREK	(K)S\I/Y T/R E K\S y K(C)	y:Phosphorylated Y	86.27	677.815	1274.674	79.9488	-12.9	9.52	23729	10.36	HUMAN	Q15940	Putative zinc finger protein 726P1
21901	dirMS_041712_NAR_20mM_plus.14117.14117.2	2	4.87	0	2.23E+05		(R)AALQELI	(R)A A/L/Q/E L L/S K(G)		168.87	486.789	972.572	-0.0017	-1.7	6.05	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
21902	dirMS_041712_NAR_20mM_plus.9991.9991.2	2	4.87	0	1.01E+05		(R)IASPEGC	(R)I/A\S|P/E/G Q D\Y L K(G)		140.32	610.8101	1220.616	-0.0028	-2.3	4.37	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
21903	dirMS_041712_NAR_40mM_plus2.11274.11274.3	3	4.87	1	7.87E+04	S682s	(R)IDIsPSTF	(R)I D\I/s/P S T F R K(H)	s:Phosphorylated S	133.02	415.2087	1163.642	79.9696	2.7	8.75	108720.9	10.17	HUMAN	Q9Y2W1	Thyroid hormone receptor-associated protein 3
21904	dirMS_041712_NAR_40mM_plus2.13577.13577.3	3	4.87	0	1.81E+05		(K)NLPPSG	(K)N L/P/P S G A V P V/T G I/P P H V V K(V)		145.88	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1

21905	dirMS_041712_NAR_50mM_plus2.17297.17297.3	3	4.87	0	1.24E+05		(R)FGVPVI	(R)F G\V/P V/I A D G G I Q N V G H I A K(A)		159.7	631.3464	1892.039	-0.0142	-7.5	6.74	51583.4	8.8	HUMAN	H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)
21906	dirMS_041712_NAR_60mM_plus.17767.17767.3	3	4.87	2	4.32E+05	S109s	(K)DGAKsLI	(K)D/G A/K s L K G D V P A S E V(-)	s:N-acetylglucosamine (S)	150.02	559.288	1472.759	203.0903	6.5	4.56	12506.3	4.51	HUMAN	K7EL14	Zinc finger protein 532 (Fragment)
21907	dirMS_041712_NAR_60mM_plus.5541.5541.3	3	4.87	0	1.11E+06		(K)TATPQQ	(K)T A|T P Q Q A\Q E V H\E K(L)		87.6	489.5727	1466.723	-0.0198	-13.5	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
21908	dirMS_041712_NAR_120mM_minus.12604.12604.3	3	4.86	0	3.35E+05	N182n	(R)IVLAnD	(R)I/V L A n/D P D/A D/R(L)	n:N-acetylglucosamine (N)	122.72	467.9028	1198.606	203.0876	5.9	3.93	32837.5	6.16	HUMAN	B4E0G8	Phosphoglucomutase-2
21909	dirMS_041712_NAR_20mM_minus.13758.13758.2	2	4.86	0	1.20E+05		(K)ALQQGL	(K)A L\Q/Q|G L\V/G L E/L K(E)		187.97	634.8811	1268.757	-0.0023	-1.8	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
21910	dirMS_041712_NAR_20mM_minus.13835.13835.2	2	4.86	0	2.47E+04	M882m	(K)NLEISID	(K)N L/E/I/S I D T L m A K(I)	m:Oxidized methionine	189.73	682.3615	1347.719	15.9969	1.5	4.37	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
21911	dirMS_041712_NAR_30mM_minus2.16606.16606.2	2	4.86	0	2.63E+04		(R)SSGLTA	(R)S S\G L/T/A/V/W\V\A R(N)		144.03	573.8112	1146.627	-0.0115	-10	9.47	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
21912	dirMS_041712_NAR_30mM_minus2.6611.6611.2	2	4.86	0	1.27E+04		(R)LQDTSS	(R)L/Q|D T/S S Y/A K(I)		91.78	506.7468	1012.495	-0.0082	-8.1	5.83	334221.3	6.44	HUMAN	P15924	Desmoplakin
21913	dirMS_041712_NAR_50mM_minus2.12944.12944.3	3	4.86	1	5.62E+05		(K)VLAGDK	(K)V L|A G D K\N F\I/T/A E E L R(R)		142.62	559.3044	1675.901	-0.0027	-1.6	4.68	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
21914	dirMS_041712_NAR_50mM_minus2.8531.8531.3	3	4.86	1	1.70E+05	S81s	(K)LFLDFQs	(K)L F L/D F Q\s M K/I I/K(E)	s:Phosphorylated S	117.1	521.6128	1482.839	79.985	11.9	8.59	42336	9.92	HUMAN	Q9NTX9	Protein FAM217B
21915	dirMS_041712_NAR_50mM_minus2.9583.9583.3	3	4.86	0	3.07E+05	T1246t	(R)SPQtLA	(R)S P/Q/t L A P V G E D/A M K(T)	t:N-acetylglucosamine (T)	122.18	549.6072	1443.715	203.0922	7.8	4.37	142001.7	5.82	HUMAN	Q92797	Symplekin
21916	dirMS_041712_NAR_120mM_plus.14769.14769.3	3	4.86	0	1.31E+06		(-)MVNHFI	(-)M V/N/H/F I/A E F K(R)		131.5	412.5446	1235.624	-0.0049	-4	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
21917	dirMS_041712_NAR_120mM_plus.6849.6849.3	3	4.86	0	2.36E+04		(R)GPEGQ	(R)G P E G Q G L P/E/V E/T R(E)		89.17	456.902	1368.675	0.0161	11.7	4.25	73325.4	8.16	HUMAN	F8W9X7	Coiled-coil domain-containing protein 93
21918	dirMS_041712_NAR_30mM_plus2.20253.20253.2	2	4.86	0	1.18E+05		(R)MLDMG	(R)M L/D\M/G F E/P Q I R(K)		159.28	668.8241	1336.639	0.0021	1.6	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
21919	dirMS_041712_NAR_30mM_plus2.21646.21646.2	2	4.86	0	4.75E+04		(K)EIIDLVL	(K)E I|I/D/L/V/L D R(I)		168.75	543.3133	1085.62	-0.0008	-0.7	4.03	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
21920	dirMS_041712_NAR_30mM_plus2.5554.5554.2	2	4.86	0	6.44E+04	M299m M	(K)NmmAA	(K)N/m m A A C D|P/R(H)	C:Carbamidomethylation m:Oxid	83.2	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
21921	dirMS_041712_NAR_30mM_plus2.6377.6377.2	2	4.86	0	8.62E+04		(K)EVYPEAI	(K)E V/Y/P E/A R(K)		87.3	432.2218	863.426	0.0106	12.2	4.53	17921.1	9.84	HUMAN	H7BZW6	Histone deacetylase complex subunit SAP18 (Fragment)
21922	dirMS_041712_NAR_40mM_plus2.19318.19318.3	3	4.86	0	1.75E+05		(R)LQQAQL	(R)L Q\Q/A Q L Y/P\I A I/F I K P K(S)		180.67	624.3737	1871.115	-0.0088	-4.7	9.7	94175.4	6.59	HUMAN	Q5JUW8	Discs, large homolog 3 (Neuroendocrine-dlg, Drosophila)
21923	dirMS_041712_NAR_50mM_plus2.17604.17604.3	3	4.86	1	5.25E+05		(K)VKLAAV	(K)V K L A A V D A T V/N/Q/V/L A S R(Y)		160.33	585.6736	1755.012	-0.0061	-3.5	8.72	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
21924	dirMS_041712_NAR_60mM_plus.11535.11535.2	2	4.86	0	8.24E+05	T191t	(R)LTAGVP	(R)L T|A G V\P D t/P T R(L)	t:N-acetylglucosamine (T)	117.02	665.8295	1127.605	203.0462	-24.9	5.84	24092.5	8.08	HUMAN	J3QS11	Integrin beta-4 (Fragment)
21925	dirMS_041712_NAR_60mM_plus.13251.13378.3	3	4.86	1	7.69E+05	M49m	(R)KNLTVD	(R)K\N L T V D/E G T/m/K(V)	m:Oxidized methionine	125.97	417.8778	1235.63	15.9888	-4.9	6.07	25797.2	10.26	HUMAN	E7EN93	Hydroxyacylglutathione hydrolase, mitochondrial
21926	dirMS_041712_NAR_60mM_plus.18289.18289.3	3	4.86	1	9.38E+05		(K)QLDDLK	(K)Q L/D/D L K V E/L|S Q/L R(V)		153.72	519.6254	1556.864	-0.0026	-1.7	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
21927	dirMS_041712_NAR_60mM_plus.18465.18465.3	3	4.86	1	1.48E+05		(K)ISISDSIK	(K)I S\I S D\S/I K\V L T G R(L)		154.42	463.6084	1388.811	-0.0001	-0.1	8.75	159535.7	5.58	HUMAN	H0YA93	NEDD4-binding protein 2 (Fragment)
21928	dirMS_041712_NAR_60mM_plus.5826.5826.3	3	4.86	1	8.67E+04		(R)CLSSAT	(R)C L|S S A T D/P Q T K/R(K)	C:Carbamidomethylation	88.38	455.226	1363.663	0	0	8.75	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
21929	dirMS_041712_NAR_60mM_plus.7503.7522.3	3	4.86	1	6.48E+05		(R)VALSEP	(R)V/A|L/S E/P Q P E R/R(-)		97.35	427.8995	1281.691	-0.007	-5.5	6.11	5611.6	11.62	HUMAN	H7C1K0	Serrate RNA effector molecule homolog (Fragment)
21930	dirMS_041712_NAR_60mM_plus.8596.8596.2	2	4.86	0	4.27E+05		(R)FACHSA	(R)F A/C/H/S/A\S L T V R(N)	C:Carbamidomethylation	102.73	624.8118	1248.615	0.001	0.8	9.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
21931	dirMS_041712_NAR_120mM_minus.13499.13499.3	3	4.85	1	2.25E+05		(R)VIDRELY	(R)V I D R E\L\Y|Q/Q L Q R(G)		128.15	520.955	1560.849	0.0012	0.8	6.04	533778	5.74	HUMAN	Q15149	Plectin
21932	dirMS_041712_NAR_120mM_minus.17471.17471.4	4	4.85	2	3.00E+05		(R)NLKASL	(R)N L K A/S\L\E/N S L R\E V E/A R(Y)		150.28	458.0011	1828.988	-0.005	-2.7	6.23	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
21933	dirMS_041712_NAR_120mM_minus.19994.19994.3	3	4.85	1	2.47E+05		(R)AKFEEL	(R)A K F E E\L/N M/D/L/F R(S)		164.85	504.9216	1512.752	-0.0013	-0.8	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
21934	dirMS_041712_NAR_120mM_minus.6655.6655.2	2	4.85	0	7.62E+04		(K)LLNPLV	(K)L L/N P/L V/R(Q)		90.7	412.7706	824.535	-0.0013	-1.6	9.75	38703.5	9.25	HUMAN	A8MQ23	Serine/threonine-protein kinase WNK2
21935	dirMS_041712_NAR_20mM_minus.11746.11746.2	2	4.85	1	1.70E+05	T647t	(K)IDLNDW	(K)I D L N D/W K/S N t R(L)	t:N-acetylglucosamine (T)	166.77	782.8828	1361.681	203.0775	-1.2	5.96	86967.8	6.57	HUMAN	Q9HCE7	E3 ubiquitin-protein ligase SMURF1
21936	dirMS_041712_NAR_20mM_minus.11782.11782.2	2	4.85	0	1.10E+05	M98m	(R)TLTIVDT	(R)T L|T|I/V D T G I/G m T K(A)	m:Oxidized methionine	166.9	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
21937	dirMS_041712_NAR_20mM_minus.7247.7247.2	2	4.85	0	1.47E+04	M33m	(R)IDEmPE	(R)I D|E|m|P E A A/V/K(S)	m:Oxidized methionine	120.43	559.7733	1102.545	15.9944	-0.4	4.14	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
21938	dirMS_041712_NAR_30mM_minus2.15234.15234.2	2	4.85	0	7.26E+05	M2249m	(K)MSIYQA	(K)M/S I/Y/Q/A/m W K(G)	m:Oxidized methionine	135.75	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
21939	dirMS_041712_NAR_30mM_minus2.17145.17169.2	2	4.85	0	1.88E+05		(R)SMVEDI	(R)S M|V/E/D I/T G L R(L)		146.82	560.7932	1120.567	0.0124	11.1	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
21940	dirMS_041712_NAR_40mM_minus2.8350.8350.3	3	4.85	1	4.74E+03		(R)IAEFTTN	(R)I A|E F/T T N L/T E E E E/K S K(S)		129.48	623.6417	1868.912	-0.0018	-1	4.32	227783.5	5.5	HUMAN	P35579	Myosin-9
21941	dirMS_041712_NAR_50mM_minus2.12943.12943.3	3	4.85	1	5.62E+05		(K)VLAGDK	(K)V L/A/G D K N F\I/T A E E/L R(R)		142.62	559.3044	1675.901	-0.0027	-1.6	4.68	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
21942	dirMS_041712_NAR_60mM_minus.10130.10130.3	3	4.85	0	1.13E+05		(K)YQYGGL	(K)Y/Q/Y/G G L N S G R P V T P P R(T)		115.72	587.9726	1761.903	0.0002	0.1	9.99	37984.9	5.84	HUMAN	P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit
21943	dirMS_041712_NAR_60mM_minus.8987.8987.3	3	4.85	1	3.60E+05	M232m M	(R)MSmKE	(R)M/S/m K E V D E Q/m|L/N V Q N K(N)	m:Oxidized methionine	110.3	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
21944	dirMS_041712_NAR_120mM_plus.10425.10425.4	4	4.85	1	7.05E+05		(K)VLSKEF	(K)V L S K E F H L N E S G D|P/S/S K(S)		107.85	469.2379	1873.929	0.0007	0.4	5.45	30992.3	4.14	HUMAN	B2REB8	Protein SET
21945	dirMS_041712_NAR_120mM_plus.18512.18512.3	3	4.85	1	6.09E+04	M75m	(R)RFDEILE	(R)R F D E\I\L\E\A/S D G I/m\V|A R(G)	m:Oxidized methionine	149.78	613.3075	1821.916	15.9916	-1.8	4.32	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
21946	dirMS_041712_NAR_20mM_plus.7894.7894.2	2	4.85	0	1.40E+05	M316m	(R)AmGEQ	(R)A m|G/E Q/A/V A L/A R(A)	m:Oxidized methionine	123.73	566.7967	1116.583	16.0031	7.2	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
21947	dirMS_041712_NAR_30mM_plus2.14292.14292.2	2	4.85	0	3.43E+05		(R)ELAFQIS	(R)E L/A F/Q/I/S K(E)		128.2	468.2629	935.52	-0.0011	-1.2	6.1	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
21948	dirMS_041712_NAR_40mM_plus2.14851.14851.3	3	4.85	1	2.18E+05		(R)VVVDAL	(R)V V|V/D/A/L/S G L K G D L A G R(Y)		154.27	523.9701	1569.896	-0.0001	-0.1	5.93	26949.2	7.99	HUMAN	C9JSQ1	Creatine kinase U-type, mitochondrial (Fragment)
21949	dirMS_041712_NAR_40mM_plus2.19593.19593.3	3	4.85	0	3.40E+04		(K)GAEILEV	(K)G A/E|I\L E V L/H/S L/P A V R(Q)		183.02	535.3088	1603.917	-0.0048	-3	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
21950	dirMS_041712_NAR_50mM_plus2.11269.11269.3	3	4.85	0	9.26E+05		(R)TFIAIKP	(R)T F/I/A I K/P D G V Q R(G)		126.32	448.9241	1344.763	-0.0057	-4.2	8.41	6640.6	8.25	HUMAN	C9K028	Nucleoside diphosphate kinase A (Fragment)
21951	dirMS_041712_NAR_50mM_plus2.5760.5760.3	3	4.85	1	9.72E+04		(R)AAPTAA	(R)A A|P/T A/A S D Q/P D S A A T T E K A K(K)		93.32	644.3093	1930.935	-0.0219	-11.3	4.56	22655.1	9.45	HUMAN	Q9BRP8	Partner of Y14 and mago
21952	dirMS_041712_NAR_60mM_plus.15666.15666.3	3	4.85	0	5.06E+04		(R)AITHLN	(R)A I T H L N N\N F|M F/G Q K(L)		138.55	545.6107	1634.811	0.0068	4.1	8.8	64759.2	8.88	HUMAN	P14866	Heterogeneous nuclear ribonucleoprotein L
21953	dirMS_041712_NAR_20mM_minus.8920.8920.2	2	4.84	0	1.34E+05		(R)LEQYTS	(R)L E/Q/Y T S A|I E/G T K(S)		138.02	670.3403	1339.674	-0.0007	-0.5	4.53	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
21954	dirMS_041712_NAR_30mM_minus2.5527.5527.2	2	4.84	0	1.73E+05		(R)LYQAGE	(R)L Y/Q/A/G E G/R(L)		84.55	447.2217	893.448	-0.0114	-12.8	6	38089.6	6.79	HUMAN	B4DT77	Annexin
21955	dirMS_041712_NAR_30mM_minus2.5984.5984.2	2	4.84	0	1.17E+05		(R)AQAEQ	(R)A Q|A|E|Q A/A L R(Q)		86.97	479.2592	957.511	-0.0001	-0.1	6.05	533778	5.74	HUMAN	Q15149	Plectin
21956	dirMS_041712_NAR_50mM_minus2.10101.10101.3	3	4.84	1	9.80E+04		(R)VGEPVA	(R)V/G E/P V A/L S E E/E R L K(L)		125.42	519.2824	1555.833	0	0	4.49	8516.9	5.1	HUMAN	E9PIL8	Splicing factor 3B subunit 2 (Fragment)
21957	dirMS_041712_NAR_50mM_minus2.15507.15507.3	3	4.84	0	2.83E+05	M118m	(R)AGKPVI	(R)A G K P V\I\C A|T Q|M/L/E/S m I K(K)	C:Carbamidomethylation m:Oxid	155.87	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
21958	dirMS_041712_NAR_50mM_minus2.9656.9656.3	3	4.84	1	2.35E+05		(R)ALEEAM	(R)A L|E E A M/E Q K/A E L E R(L)		122.4	549.6072	1646.805	0.0016	1	4.33	227783.5	5.5	HUMAN	P35579	Myosin-9
21959	dirMS_041712_NAR_60mM_minus.15693.15693.3	3	4.84	1	3.53E+05	K362k	(R)IQQIAE	(R)I Q Q I A/E G/E/K V/k(Q)	k:Ubiquitin-K	146.5	452.9148	1242.705	114.0246	-13.5	6.14	53935.2	5.17	HUMAN	E7EMK3	Flotillin-2
21960	dirMS_041712_NAR_120mM_plus.18971.18971.4	4	4.84	1	5.99E+05	K150k	(K)DKAIAG	(K)D K\A I/A G T V k V Q N L A F/E K(T)	k:Ubiquitin-K	153.18	487.2719	1832.028	114.0381	-2.5	8.5	33094	5.86	HUMAN	Q86XI6	Protein phosphatase 1 regulatory subunit 3B
21961	dirMS_041712_NAR_120mM_plus.7435.7435.2	2	4.84	0	3.16E+05		(K)NAKPLSI	(K)N A K/P L/S F/K(V)		92	452.767	904.525	0.0016	1.8	10	25233.4	9.34	HUMAN	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3
21962	dirMS_041712_NAR_20mM_plus.18784.18784.3	3	4.84	0	1.15E+05		(K)VIGNQS	(K)V I G N Q\S L/V N E\L|A/F T/A R(K)		200.72	577.9842	1731.939	-0.0008	-0.4	5.97	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
21963	dirMS_041712_NAR_20mM_plus.19052.19052.2	2	4.84	0	1.05E+05		(K)DTSYLFI	(K)D T S Y|L\F\I|T/G P\D V V K(S)		201.92	777.9049	1554.805	-0.0025	-1.6	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
21964	dirMS_041712_NAR_20mM_plus.7856.7856.2	2	4.84	0	1.18E+05		(K)VEIIAND	(K)V E|I|I/A N D\Q G N R(T)		124.48	614.8177	1228.628	0.0001	0.1	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
21965	dirMS_041712_NAR_30mM_plus2.6203.6203.2	2	4.84	0	5.49E+05		(R)VINEEY	(R)V/I|N E E/Y K(I)		87.1	447.7285	894.457	-0.007	-7.8	4.53	4534.2	4.75	HUMAN	C9JAJ9	Histone-binding protein RBBP7 (Fragment)
21966	dirMS_041712_NAR_40mM_plus2.7232.7232.2	2	4.84	0	1.06E+05		(R)SGYFDEI	(R)S G|Y/F D/E R(Y)		102.97	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
21967	dirMS_041712_NAR_60mM_plus.16295.16295.3	3	4.84	0	4.88E+05		(K)TTITMAI	(K)T T|I/T M/A H/L L A A R(E)		141.72	433.5839	1298.725	0.0122	9.4	9.44	37589.6	5.96	HUMAN	Q52LJ0	Protein FAM98B
21968	dirMS_041712_NAR_60mM_plus.17539.17539.3	3	4.84	1	7.56E+05		(R)FTDEES	(R)F/T/D/E/E S R V F L L D R(G)		148.33	542.9482	1626.812	0.0178	11	4.32	83344.9	10.18	HUMAN	E9PK09	Bcl-2-associated transcription factor 1 (Fragment)
21969	dirMS_041712_NAR_60mM_plus.20760.20760.3	3	4.84	1	1.09E+05		(R)GLFIIDD	(R)G L/F I/I/D D K G I L R(Q)		169.52	453.9368	1359.8	-0.0036	-2.7	5.96	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
21970	dirMS_041712_NAR_120mM_minus.7408.7408.3	3	4.83	0	1.20E+05		(R)NIDEHA	(R)N I/D/E/H A/N E D/V E R(M)		94.67	480.884	1440.635	0.0025	1.7	4.17	22768.7	8.94	HUMAN	P61026	Ras-related protein Rab-10
21971	dirMS_041712_NAR_40mM_minus2.12214.12214.3	3	4.83	0	1.84E+05		(R)LQQELD	(R)L Q|Q E L/D D\L/T V/D L D H Q R(Q)		154.77	646.6596	1937.956	0.0079	4.1	4.03	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
21972	dirMS_041712_NAR_50mM_minus2.13689.13689.3	3	4.83	1	3.85E+05		(K)ITDIIGK	(K)I/T D I I/G K E E G I/G/P E N L R(G)		146.88	618.665	1853.997	-0.0163	-8.8	4.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
21973	dirMS_041712_NAR_50mM_minus2.14952.14952.3	3	4.83	1	4.45E+04		(R)VRLGDV	(R)V R L G D\V\I\S I\Q|P C/P D V K(Y)	C:Carbamidomethylation	153.03	599.3283	1795.974	-0.0031	-1.7	5.93	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
21974	dirMS_041712_NAR_50mM_minus2.17735.17735.3	3	4.83	0	2.76E+06		(R)IHFPLAT	(R)I H\F P L A T\Y/A/P V I/S A E K(A)		168.65	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
21975	dirMS_041712_NAR_60mM_minus.9032.9032.3	3	4.83	1	1.11E+05	M754m	(K)TCVFEK	(K)T C|V/F E K E N D/P S V/m R(S)	C:Carbamidomethylation m:Oxid	110.18	576.5915	1711.778	15.9821	-7.4	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
21976	dirMS_041712_NAR_120mM_plus.6109.6109.2	2	4.83	1	2.26E+06		(K)IREEYPD	(K)I R/E E/Y\P D|R(I)		84.95	539.2694	1077.532	-0.0008	-0.8	4.68	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
21977	dirMS_041712_NAR_120mM_plus.7144.7144.3	3	4.83	1	1.73E+06		(R)RQLETL	(R)R Q L E|T|L/G Q/E K(L)		91.05	401.2207	1201.653	-0.006	-5	6.14	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
21978	dirMS_041712_NAR_120mM_plus.7299.7299.3	3	4.83	1	4.35E+05		(R)ESNCYD	(R)E S/N/C Y D/P E R V K(N)	C:Carbamidomethylation	91.78	466.2133	1396.616	0.0092	6.6	4.68	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
21979	dirMS_041712_NAR_120mM_plus.9873.9873.3	3	4.83	1	1.73E+06		(K)SKFDNL	(K)S K F D N\L/Y/G C/R(E)	C:Carbamidomethylation	104.62	420.5351	1259.584	0.007	5.6	8.31	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
21980	dirMS_041712_NAR_20mM_plus.14283.14283.2	2	4.83	0	8.58E+04		(R)VFSGLV	(R)V F|S G L/V/S T G L K(V)		170.27	554.3224	1107.641	-0.0033	-3	8.72	96306.4	6.41	HUMAN	P13639	Elongation factor 2
21981	dirMS_041712_NAR_20mM_plus.14797.14797.2	2	4.83	0	1.25E+05		(K)LSTGCT	(K)L S/T G C T G T L|V A E K(H)	C:Carbamidomethylation	172.82	668.8371	1336.678	-0.0108	-8.1	6	40040.2	9.87	HUMAN	B4E2J3	Serine protease 23
21982	dirMS_041712_NAR_20mM_plus.18276.18276.3	3	4.83	0	8.15E+04		(K)LVAIVD	(K)L V A|I V D V I/D Q/N R(A)		197.4	452.2607	1354.769	-0.0013	-1	4.21	14671.9	10.44	HUMAN	E7EPB3	60S ribosomal protein L14
21983	dirMS_041712_NAR_30mM_plus2.16470.16470.3	3	4.83	0	4.35E+05		(K)LLDLVQ	(K)L L\D\L V/Q/Q/S C N Y K(Q)	C:Carbamidomethylation	139.08	494.2566	1480.746	0.0088	5.9	5.83	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
21984	dirMS_041712_NAR_40mM_plus2.12262.12262.3	3	4.83	0	3.42E+04	M1115m	(K)NHKPSV	(K)N H K P/S V L/L G F D m S E\L K(N)	m:Oxidized methionine	137.8	610.9868	1814.947	15.9989	2.2	6.75	124371.4	9.72	HUMAN	Q6IQ32	ADNP homeobox protein 2
21985	dirMS_041712_NAR_40mM_plus2.6287.6287.2	2	4.83	1	2.84E+05		(R)YSGGNY	(R)Y S/G G N Y R D\N\Y\D\N(-)		95.58	719.2857	1437.567	-0.0024	-1.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
21986	dirMS_041712_NAR_50mM_plus2.16802.16802.3	3	4.83	1	1.87E+05	M132m	(R)TLAEIAK	(R)T L|A E I A K V E L D/N m\P L R(G)	m:Oxidized methionine	155.92	610.3302	1812.989	15.9873	-4.2	4.68	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
21987	dirMS_041712_NAR_50mM_plus2.19932.19932.3	3	4.83	1	4.83E+05		(R)LFLDRDI	(R)L F/L/D R D L M T\L|P I Q\N K(L)		173.57	606.3362	1816.999	-0.0049	-2.7	5.96	18188.9	10.98	HUMAN	K7EKP7	Ferrochelatase, mitochondrial (Fragment)
21988	dirMS_041712_NAR_60mM_plus.10837.10837.3	3	4.83	1	2.86E+05		(R)QQEGFK	(R)Q Q E G F K G T F/P D/A R(E)		114.17	494.2424	1480.718	-0.0053	-3.6	6.07	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
21989	dirMS_041712_NAR_60mM_plus.16335.16335.3	3	4.83	1	3.28E+06		(R)MSMKE	(R)M S M K E V D E Q|M|L/N V Q N K(N)		141.5	641.9696	1923.897	-0.003	-1.6	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
21990	dirMS_041712_NAR_60mM_plus.5090.5090.3	3	4.83	1	3.95E+05		(R)AAEDDE	(R)A/A/E/D D E D D D V/D/T K K(Q)		83.53	522.5529	1565.645	-0.0008	-0.5	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
21991	dirMS_041712_NAR_60mM_plus.8517.8517.3	3	4.83	1	4.93E+05	M2747m	(K)TLQEVT	(K)T L/Q/E V/T E m D S V K R(Y)	m:Oxidized methionine	102.37	517.9269	1535.773	15.9928	-1.4	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
21992	dirMS_041712_NAR_120mM_minus.8255.8255.3	3	4.82	0	1.10E+05	N580n	(K)HNVIVG	(K)H N/V I V G/n E/R(V)	n:N-acetylglucosamine (N)	99.23	414.2125	1037.549	203.0743	-4.1	6.75	88339.6	4.96	HUMAN	Q8IV76	PAS domain-containing protein 1
21993	dirMS_041712_NAR_120mM_minus.9970.9970.3	3	4.82	1	8.35E+04		(R)RLDECE	(R)R L D E C\E/E/A/F Q G T/K(V)	C:Carbamidomethylation	108.6	528.2437	1582.717	0	0	4.41	22568.6	6.35	HUMAN	B3KQ25	Proteasome activator complex subunit 3
21994	dirMS_041712_NAR_20mM_minus.13190.13190.2	2	4.82	0	1.01E+05	M329m	(K)ALELNm	(K)A L|E/L/N m/L S L K(G)	m:Oxidized methionine	182.82	574.3232	1131.644	15.9949	0	6.05	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
21995	dirMS_041712_NAR_30mM_minus2.14856.14856.2	2	4.82	0	3.41E+05	T10t	(R)LSIPtYGI	(R)L S I/P t/Y G L Q C T R(G)	C:Carbamidomethylation t:Phosp	134.55	744.839	1408.725	79.9454	-14.1	8.75	8533.6	12.23	HUMAN	J3KTF0	Enoyl-[acyl-carrier-protein] reductase (Fragment)
21996	dirMS_041712_NAR_30mM_minus2.8991.8991.2	2	4.82	0	1.12E+05	M27m	(R)mVTHY	(R)m V|T H Y A/V S K(G)	m:Oxidized methionine	103.58	526.2618	1035.529	15.9871	-7.4	8.37	58021	6.41	HUMAN	Q9NSB4	Keratin, type II cuticular Hb2
21997	dirMS_041712_NAR_40mM_minus2.7484.7484.2	2	4.82	0	1.86E+05		(K)MEENV	(K)M/E|E/N V Q L|N K(E)		120.2	552.7711	1104.535	-0.0005	-0.4	4.53	29749.8	6.04	HUMAN	F5H4M0	Vacuolar protein sorting-associated protein 37B (Fragment)
21998	dirMS_041712_NAR_50mM_minus2.8661.8661.3	3	4.82	0	1.19E+05		(R)LGYAVY	(R)L G/Y/A V Y E/T/P T A H N G A K(N)		117.08	564.6215	1691.839	0.0112	6.6	6.75	25016.4	5.65	HUMAN	B3KR28	Toll-interacting protein
21999	dirMS_041712_NAR_60mM_minus.17184.17184.3	3	4.82	1	8.69E+04	M148m	(R)LDLAGR	(R)L D/L/A/G R D L T|D Y L m K(I)	m:Oxidized methionine	156.05	547.2829	1623.841	15.9931	-1.1	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
22000	dirMS_041712_NAR_60mM_minus.7453.7453.3	3	4.82	1	4.87E+04	M807m	(R)NVmEE	(R)N/V m E E G K D F/Q/P S R(S)	m:Oxidized methionine	100.9	518.2403	1536.711	15.9952	0.2	4.68	99900.1	5.04	HUMAN	B4DZI8	Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b
22001	dirMS_041712_NAR_120mM_plus.10838.10838.3	3	4.82	1	1.21E+06		(R)QQEGFK	(R)Q/Q\E G F K G T F/P D/A/R(E)		109.43	494.2435	1480.718	-0.002	-1.3	6.07	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
22002	dirMS_041712_NAR_120mM_plus.20457.20457.4	4	4.82	1	7.46E+04		(R)DYLHLP	(R)D Y L H L\P\P E I/V/P A T L R/R(S)		160.4	473.2689	1890.06	-0.0058	-3.1	6.75	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
22003	dirMS_041712_NAR_120mM_plus.24001.24001.3	3	4.82	1	3.26E+05	M145m	(R)GVmLA	(R)G V m/L/A V/D/A\V I/A E L K/K(Q)	m:Oxidized methionine	179.97	524.9713	1556.908	15.9913	-2.3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
22004	dirMS_041712_NAR_120mM_plus.5180.5180.3	3	4.82	1	2.51E+05		(R)YEREQY	(R)Y E/R E/Q Y/A D R(A)		80.98	410.5196	1229.555	-0.0103	-8.4	4.68	37433.2	9.17	HUMAN	B0LM41	Protein RBM14-RBM4
22005	dirMS_041712_NAR_20mM_plus.12020.12020.2	2	4.82	2	1.44E+04		(-)MAAQV	(-)M A A/Q V A A R E A R D F R(E)		155.77	796.4095	1591.812	-0.0004	-0.3	9.26	525198.5	6.03	HUMAN	Q96DT5	Dynein heavy chain 11, axonemal
22006	dirMS_041712_NAR_20mM_plus.12756.12756.2	2	4.82	1	1.02E+05	N86n	(K)LVnDKP	(K)L V/n D K P/H/K F K(D)	n:N-acetylglucosamine (N)	161.23	714.8991	1225.705	203.0858	4.5	9.7	19677.9	6	HUMAN	G3V5D4	SH3 and cysteine-rich domain-containing protein 3 (Fragment)
22007	dirMS_041712_NAR_20mM_plus.8740.8740.2	2	4.82	0	5.31E+03		(R)AVLIAG	(R)A V L|I/A/G Q P G T G K(T)		130.05	556.3256	1111.647	-0.0031	-2.8	8.8	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
22008	dirMS_041712_NAR_30mM_plus2.10257.10257.2	2	4.82	0	3.23E+05		(K)GMPGF	(K)G M/P/G F S/T S K(K)		106.95	456.2155	911.429	-0.0054	-5.9	8.75	16060.3	9.43	HUMAN	H0YKV0	Isovaleryl-CoA dehydrogenase, mitochondrial (Fragment)
22009	dirMS_041712_NAR_40mM_plus2.14780.14780.3	3	4.82	1	1.28E+05		(R)EGSVML	(R)E G S V/M/L/Q V/D V D T V/K G G L K(L)		153.67	625.6667	1874.989	-0.0036	-1.9	4.56	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
22010	dirMS_041712_NAR_40mM_plus2.18289.18289.3	3	4.82	1	5.57E+04		(R)GRLEQL	(R)G/R/L/E Q L G G L L A N V S G E L G G/R(L)		173.38	666.0306	1996.093	-0.0162	-8.1	6.14	107977.4	5.07	HUMAN	Q9Y6C2	EMILIN-1
22011	dirMS_041712_NAR_40mM_plus2.9647.9647.2	2	4.82	0	5.54E+04		(R)NGYGFI	(R)N G\Y|G F I N/R(N)		120.03	470.7365	940.463	0.0022	2.3	8.75	23597.5	10.26	HUMAN	C9J5V9	Nuclease-sensitive element-binding protein 1 (Fragment)
22012	dirMS_041712_NAR_50mM_plus2.15525.15525.3	3	4.82	0	3.05E+05		(R)LEGVEG	(R)L/E G V E G V A H I I D/P K(A)		150.03	492.9376	1476.806	-0.0074	-5	4.65	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
22013	dirMS_041712_NAR_50mM_plus2.17533.17533.3	3	4.82	1	4.72E+05		(R)ELELKVP	(R)E/L/E L K V/P/L V V/R(L)		159.85	432.2745	1294.809	-0.0004	-0.3	6.24	20422.4	5.35	HUMAN	H0Y852	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial (Fragment)

22014	dirMS_041712_NAR_50mM_plus2.9383.9383.3	3	4.82	1	1.27E+05	M230m M	(R)mSmKE	(R)m S m K E V\D E/Q\M/L/N V Q N K(N)	m:Oxidized methionine	116.6	652.6312	1923.897	31.9818	-4.1	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
22015	dirMS_041712_NAR_60mM_plus.8808.8808.3	3	4.82	0	2.96E+05		(K)SEHPGL	(K)S\E/H P G\L/S/I/G D T A K(K)		104.32	437.8898	1311.654	0.0009	0.7	5.3	15574.6	9.97	HUMAN	D6R9A6	High mobility group protein B2 (Fragment)
22016	dirMS_041712_NAR_120mM_minus.16342.16342.4	4	4.81	1	4.94E+04	M81m	(K)mQLGEL	(K)m Q L G E/L T R Q V/S/G\N S L N K(R)	m:Oxidized methionine	143.45	473.4926	1874.975	15.9733	-11.4	8.5	14484	9.39	HUMAN	B8ZZS1	Uncharacterized protein
22017	dirMS_041712_NAR_30mM_minus2.20429.20429.2	2	4.81	0	4.17E+05		(R)FLTWIL	(R)F L/T|W I\L N/R(Y)		175.82	531.8089	1062.61	0.001	1	9.75	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
22018	dirMS_041712_NAR_40mM_minus2.10666.10666.3	3	4.81	0	1.44E+05		(R)DLSHIG	(R)D L S H I G D A\V|V/I/S C A K(D)	C:Carbamidomethylation	146.63	528.9384	1584.805	-0.0044	-2.8	5.21	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
22019	dirMS_041712_NAR_40mM_minus2.12914.12914.3	3	4.81	0	1.42E+05		(K)IEVIKPG	(K)I/E|V I K/P G D/L G V D L T/S K(L)		159.03	561.989	1683.953	-0.0003	-0.2	4.56	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
22020	dirMS_041712_NAR_40mM_minus2.7816.7816.3	3	4.81	0	7.49E+04	M47m M5	(K)SGTGIA	(K)S G T/G I/A A M S V m R P E Q/I m K(S)	m:Oxidized methionine	125.22	646.9867	1906.955	31.9908	0.5	8.46	8797.3	9.3	HUMAN	H3BR50	V-type proton ATPase 16 kDa proteolipid subunit
22021	dirMS_041712_NAR_60mM_minus.13473.13473.3	3	4.81	2	1.16E+05	M218m M	(K)GAKmm	(K)G A K/m\m K L/Y I D N/A/A P/D K(L)	m:Oxidized methionine	135.43	599.9744	1765.898	32.0111	11.8	8.43	482399.6	5.8	HUMAN	H0Y7V4	Dynein heavy chain 8, axonemal
22022	dirMS_041712_NAR_60mM_minus.8336.8336.3	3	4.81	0	1.07E+05		(R)DSLFIN	(R)D S L F\I N/G/Y A P Q N L S I R(G)		106.7	603.3097	1807.934	-0.0192	-10.6	5.83	1521202	5.13	HUMAN	B5ME49	Mucin-16
22023	dirMS_041712_NAR_120mM_plus.6923.6923.3	3	4.81	0	4.61E+05		(K)SQFSDK	(K)S Q/F/S/D K/P V Q D R(G)		89.77	436.2209	1306.639	0.0095	7.3	5.68	13194	9.99	HUMAN	E9PI70	Chitinase domain-containing protein 1 (Fragment)
22024	dirMS_041712_NAR_20mM_plus.15692.15692.3	3	4.81	0	1.63E+05		(R)GNPTVE	(R)G N P T V E V D/L F T S/K(G)		179.93	469.577	1406.716	0.0003	0.2	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
22025	dirMS_041712_NAR_30mM_plus2.16625.16625.2	2	4.81	0	2.54E+05		(K)LLDLVQ	(K)L L D|L/V/Q Q/S/C N Y K(Q)	C:Carbamidomethylation	139.32	740.8751	1480.746	-0.0035	-2.4	5.83	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
22026	dirMS_041712_NAR_30mM_plus2.21888.21888.3	3	4.81	0	1.73E+05		(K)GLVQAL	(K)G L V Q A/L G/L/S/N F N S R(Q)		169.5	492.6036	1475.796	-0.0003	-0.2	9.75	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
22027	dirMS_041712_NAR_30mM_plus2.4917.4917.2	2	4.81	0	7.31E+05		(R)MGQTM	(R)M/G/Q|T/M E R(I)		77.33	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
22028	dirMS_041712_NAR_50mM_plus2.12358.12358.3	3	4.81	0	1.16E+05		(K)GPLLYC	(K)G P|L/L Y C A R/P P Q D L K(I)	C:Carbamidomethylation	132.63	543.2913	1627.863	-0.0031	-1.9	8.59	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
22029	dirMS_041712_NAR_60mM_plus.10765.10765.3	3	4.81	1	3.21E+04		(R)LRQLAE	(R)L R Q L A\E\E\D/L/A/Q Q/R(A)		112.7	523.9486	1569.834	-0.0031	-2	4.68	533778	5.74	HUMAN	Q15149	Plectin
22030	dirMS_041712_NAR_60mM_plus.13433.13433.3	3	4.81	0	3.12E+04		(R)AELPLS	(R)A E/L P L S W S V/S S/K(L)		127.68	435.2389	1303.689	0.0129	9.9	6.05	48792.8	5.24	HUMAN	P48051	G protein-activated inward rectifier potassium channel 2
22031	dirMS_041712_NAR_60mM_plus.15699.15699.3	3	4.81	0	4.13E+04		(R)VWYVS	(R)V/W|Y/V S N I/D G T H I A K(T)		138.42	534.9464	1602.828	-0.0028	-1.8	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
22032	dirMS_041712_NAR_60mM_plus.18105.18105.3	3	4.81	1	7.59E+05		(K)EVNKFQ	(K)E V/N K F Q M A/Y S N/L L R(A)		152.52	571.6293	1712.879	-0.0055	-3.2	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
22033	dirMS_041712_NAR_60mM_plus.18648.18648.3	3	4.81	1	1.39E+05		(R)CRVDLP	(R)C R V D\L/P L/A V L/S K(M)	C:Carbamidomethylation	154.55	457.599	1370.782	0	0	8.75	7765.6	8.23	HUMAN	H3BSA6	dCTP pyrophosphatase 1
22034	dirMS_041712_NAR_60mM_plus.6412.6412.3	3	4.81	0	2.57E+05		(R)QAGEVT	(R)Q A G E/V/T Y/A D A H K(G)		92.2	430.5486	1289.612	0.0192	14.9	5.32	56791.5	11.56	HUMAN	Q08170	Serine/arginine-rich splicing factor 4
22035	dirMS_041712_NAR_120mM_minus.9645.9645.3	3	4.8	1	4.06E+05		(R)ALSTGE	(R)A/L/S\T/G E K G/F G Y/K(G)		107.15	419.8868	1257.647	-0.0015	-1.2	8.54	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
22036	dirMS_041712_NAR_20mM_minus.10815.10815.2	2	4.8	0	2.18E+04	M92m	(R)ImNTFS	(R)I m|N T\F/S V V P/S/P K(V)	m:Oxidized methionine	155.92	668.3513	1319.703	15.9925	-1.8	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
22037	dirMS_041712_NAR_40mM_minus2.15307.15307.3	3	4.8	1	1.59E+05		(R)GGPNIIT	(R)G G P/N/I/I T L A D I V K D/P V S R(T)		177.15	622.3523	1865.049	-0.0067	-3.6	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
22038	dirMS_041712_NAR_40mM_minus2.8357.8357.3	3	4.8	1	8.96E+04	K507k	(R)KTVkDE	(R)K\T/V\k D E A/H Q A/Q K(D)	k:Ubiquitin-K	130.35	499.5936	1382.739	114.0276	-10.2	8.51	64633.4	6.29	HUMAN	F5GWP3	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform
22039	dirMS_041712_NAR_40mM_minus2.9236.9236.3	3	4.8	0	1.31E+05		(K)VQASLA	(K)V Q|A/S L A A N T F T I T\G H A E T/K(Q)		137.35	654.0087	1960.013	-0.0019	-1	6.72	11802.2	5.6	HUMAN	D6RDG3	Transcription factor BTF3 (Fragment)
22040	dirMS_041712_NAR_50mM_minus2.11182.11182.3	3	4.8	1	1.86E+05		(R)DNKQA	(R)D N K Q A G|V|F E P T I V K(V)		132.05	515.9485	1545.827	0.0038	2.5	6.07	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
22041	dirMS_041712_NAR_50mM_minus2.11331.11331.3	3	4.8	1	2.04E+05		(K)MLVSG	(K)M L|V/S/G A G D I/K L T K(D)		132.4	444.9227	1332.756	-0.002	-1.5	8.35	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
22042	dirMS_041712_NAR_50mM_minus2.16661.16661.3	3	4.8	1	1.30E+05		(R)DLKVEN	(R)D L K V E N\L\L/L/S N Q/G T I K(L)		162.67	595.6712	1785.012	-0.0126	-7.1	6.07	135773.5	5.53	HUMAN	E9PGR2	Cyclin-G-associated kinase
22043	dirMS_041712_NAR_60mM_minus.18990.18990.3	3	4.8	1	3.05E+05	T1627t	(K)TKYHtPL	(K)T K Y H/t P L|D M V S V T A A K(K)	t:N-acetylglucosamine (T)	168.07	655.6847	1761.92	203.1192	20.3	8.2	990583.7	9.16	HUMAN	F8WCL5	Nebulin
22044	dirMS_041712_NAR_60mM_minus.6812.6812.3	3	4.8	1	2.18E+05		(K)IDDIRKP	(K)I/D D/I R K P G E S E E(-)		96.37	463.2294	1387.67	0.0037	2.7	4.37	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
22045	dirMS_041712_NAR_120mM_plus.12383.12383.4	4	4.8	2	8.44E+05		(K)KGTVEG	(K)K G T V E/G\F\E|P A D N K C L L R(A)	C:Carbamidomethylation	118.8	484.2468	1933.98	-0.0147	-7.6	6.18	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
22046	dirMS_041712_NAR_120mM_plus.4142.4142.3	3	4.8	1	1.77E+06	M54m	(K)SLDEmE	(K)S/L/D E m E K/Q Q/R(E)	m:Oxidized methionine	69.95	427.2032	1263.6	15.9953	0.3	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
22047	dirMS_041712_NAR_120mM_plus.9472.9472.3	3	4.8	1	5.95E+05		(R)NYRDNY	(R)N Y/R D N Y|Q/A F/C K(W)	C:Carbamidomethylation	103.37	493.5549	1478.648	0.002	1.4	8.49	334221.3	6.44	HUMAN	P15924	Desmoplakin
22048	dirMS_041712_NAR_20mM_plus.12500.12500.2	2	4.8	0	9.66E+03		(K)VNQIGS	(K)V N Q\I/G/S/V/T E S I/Q A C/K(L)	C:Carbamidomethylation	159.1	817.4114	1633.821	-0.0059	-3.6	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
22049	dirMS_041712_NAR_20mM_plus.7453.7453.2	2	4.8	1	7.83E+04	M181m K1	(R)RQTSmT	(R)R Q T/S m T/D F Y H S k(R)	m:Oxidized methionine k:Ub	119.68	815.8661	1500.69	130.0349	-1.8	8.6	22410.7	9.96	HUMAN	J3KQV0	Cyclin-dependent kinase inhibitor 1
22050	dirMS_041712_NAR_20mM_plus.8130.8130.3	3	4.8	0	2.29E+05	M346m M	(K)mGGmE	(K)m G G m E G P F/G/G/G\m/E N m G R(F)	m:Oxidized methionine	126.28	593.558	1714.68	63.979	-0.4	4.53	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
22051	dirMS_041712_NAR_30mM_plus2.13325.13339.2	2	4.8	0	3.38E+05		(R)FTVAEL	(R)F/T|V/A E/L K(Q)		123.32	404.2298	807.461	-0.0088	-10.8	6	98282.7	5.49	HUMAN	E9PPJ0	Splicing factor 3B subunit 2
22052	dirMS_041712_NAR_30mM_plus2.15806.15806.3	3	4.8	0	7.59E+04		(K)VAAIEAL	(K)V A\A I\E\A L/N D G E L Q K(A)		135.4	490.9251	1470.78	-0.0191	-13	4.14	18141.9	4.7	HUMAN	F6VDH7	Hsc70-interacting protein (Fragment)
22053	dirMS_041712_NAR_30mM_plus2.5186.5186.2	2	4.8	0	1.25E+05		(K)SACGVC	(K)S A|C/G V C/P G R(L)	C:Carbamidomethylation	80.28	482.2128	963.414	0.0048	5	9.47	13520.9	11.92	HUMAN	P49207	60S ribosomal protein L34
22054	dirMS_041712_NAR_30mM_plus2.6535.6535.2	2	4.8	0	1.47E+05		(R)AVVISG	(R)A V/V/I/S G A G/K(M)		88.42	401.2461	801.483	0.002	2.6	8.8	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
22055	dirMS_041712_NAR_40mM_plus2.17868.17868.3	3	4.8	0	1.03E+05		(R)APGPGL	(R)A P G/P G L A Q/G L/P Q L H S L V\L/R(R)		171.47	642.04	1924.113	-0.0072	-3.8	9.8	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
22056	dirMS_041712_NAR_60mM_plus.6386.6386.3	3	4.8	1	2.06E+05	M1m	(-)mDSETD	(-)m/D/S/E T/D M V R Q I R(A)	m:Oxidized methionine	91.9	499.5719	1480.688	16.0129	12	4.56	28693	5.27	HUMAN	E9PJ36	Vacuolar protein sorting-associated protein 51 homolog (Fragment)
22057	dirMS_041712_NAR_60mM_plus.6755.6755.2	2	4.8	1	1.82E+05		(K)SESPKEP	(K)S E|S|P/K/E P E Q L R(K)		93.92	650.3286	1299.654	-0.004	-3.1	4.78	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
22058	dirMS_041712_NAR_20mM_minus.10251.10251.3	3	4.79	1	5.72E+03		(R)AVSYPA	(R)A V S Y/P A S V R A N T/E E R(E)		152.13	550.6096	1649.824	-0.0099	-6	6.19	471334.6	5.19	HUMAN	P22105	Tenascin-X
22059	dirMS_041712_NAR_20mM_minus.12376.12376.2	2	4.79	0	9.78E+04		(R)AVAQAL	(R)A V A Q|A/L E V/I P R(T)		172.33	583.8469	1166.689	-0.0027	-2.3	6.05	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
22060	dirMS_041712_NAR_20mM_minus.12543.12543.2	2	4.79	0	4.08E+05	M73m	(R)AVLVDL	(R)A V L|V|D\L/E|P G T\m D S V\R(S)	m:Oxidized methionine	172.97	809.4088	1601.82	15.99	-3	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
22061	dirMS_041712_NAR_50mM_minus2.16475.16475.3	3	4.79	0	8.79E+04		(K)VSHLLG	(K)V S H L L\G\I N\V/T D/F T R(G)		162.08	524.6237	1571.854	0.0025	1.6	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
22062	dirMS_041712_NAR_60mM_minus.15644.15644.3	3	4.79	1	1.72E+05		(R)GRLPLL	(R)G R L P L\L/A/V/C D/Y K(Q)	C:Carbamidomethylation	146.87	468.9273	1404.767	0.0006	0.4	8.59	533778	5.74	HUMAN	Q15149	Plectin
22063	dirMS_041712_NAR_60mM_minus.15933.15933.3	3	4.79	1	3.10E+05		(K)ELKIDIIP	(K)E L K\I D I\I/P/N/P Q E R(T)		148.9	522.2935	1564.869	-0.0034	-2.2	4.68	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
22064	dirMS_041712_NAR_60mM_minus.19226.19226.3	3	4.79	1	1.02E+06	T459t	(R)ILQtEKI	(R)I L Q/t/E K/I H Q G G/K(T)	t:N-acetylglucosamine (T)	171.22	518.9484	1351.769	203.0614	-11.5	8.6	99514.3	9.8	HUMAN	Q96J94	Piwi-like protein 1
22065	dirMS_041712_NAR_120mM_plus.12752.12752.3	3	4.79	1	8.84E+05		(R)GYVKEQ	(R)G Y/V K/E\Q F/A W R(H)		121.42	428.5561	1283.653	0.0006	0.5	8.59	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
22066	dirMS_041712_NAR_120mM_plus.9071.9071.3	3	4.79	1	4.91E+05		(R)SGRGGN	(R)S G R G G N F\G|F G D/S/R(G)		101.07	438.538	1313.598	0.0013	1	9.32	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
22067	dirMS_041712_NAR_20mM_plus.11548.11548.2	2	4.79	0	1.44E+04	M94m	(K)mLLYTE	(K)m L|L/Y/T E V/T R(Y)	m:Oxidized methionine	152.37	571.3075	1125.597	16.0105	13.6	5.75	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
22068	dirMS_041712_NAR_20mM_plus.15330.15330.2	2	4.79	0	3.23E+05	M583m	(K)mEPEDA	(K)m E P E D A T E|E/I|S G F L(-)	m:Oxidized methionine	177.08	792.3469	1567.683	16.0033	5.3	3.45	66028	9.35	HUMAN	F5H640	YY1-associated protein 1
22069	dirMS_041712_NAR_20mM_plus.16014.16014.2	2	4.79	0	2.40E+05		(K)DAGTIA	(K)D A G T/I/A/G L N V L/R(I)		182.48	600.3422	1199.674	0.0029	2.4	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
22070	dirMS_041712_NAR_20mM_plus.17232.17232.3	3	4.79	0	2.46E+05		(K)VLAQNS	(K)V L A Q N S G F D|L Q E T L V/K(I)		190.65	587.9829	1761.938	-0.004	-2.3	4.37	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
22071	dirMS_041712_NAR_20mM_plus.17351.17351.3	3	4.79	0	3.74E+05		(K)VLAQNS	(K)V L A Q N S G/F/D L/Q E T L V/K(I)		191.22	587.9829	1761.938	-0.004	-2.3	4.37	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
22072	dirMS_041712_NAR_20mM_plus.18302.18302.2	2	4.79	0	1.22E+05		(R)GVVQEL	(R)G V|V Q/E L Q Q A/I/S K(L)		198.05	650.3656	1299.727	-0.0028	-2.1	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
22073	dirMS_041712_NAR_20mM_plus.6459.6459.2	2	4.79	0	1.60E+05		(K)DSYVGD	(K)D S/Y/V/G D E A Q S/K(R)		107.17	599.7645	1198.522	-0.0005	-0.4	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
22074	dirMS_041712_NAR_30mM_plus2.22772.22772.2	2	4.79	0	2.69E+05		(R)ELSDFIS	(R)E L/S D F\I S Y/L/Q/R(E)		177.22	685.8507	1370.695	-0.0009	-0.7	4.37	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
22075	dirMS_041712_NAR_40mM_plus2.9687.9687.2	2	4.79	0	2.98E+05		(K)SCNCLLL	(K)S C/N/C L/L/L K(V)	C:Carbamidomethylation	120.77	504.2542	1007.501	-0.0001	-0.1	8.47	47510.4	7.04	HUMAN	P06733	Alpha-enolase
22076	dirMS_041712_NAR_50mM_plus2.10008.10008.3	3	4.79	0	7.46E+05		(R)GISEETT	(R)G I|S/E E T/T T G V/H N L Y/K(M)		120.05	550.2759	1648.818	-0.0045	-2.8	5.4	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
22077	dirMS_041712_NAR_50mM_plus2.12362.12362.3	3	4.79	0	6.29E+05		(K)GIHPTIIS	(K)G I H|P T\I\I/S E\S F Q K(A)		132.97	486.2644	1456.78	-0.0008	-0.6	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
22078	dirMS_041712_NAR_60mM_plus.18043.18043.3	3	4.79	1	1.53E+05		(R)IRGETLG	(R)I R G E T L G L I/G/F/G R(T)		151.38	463.6084	1388.801	0.0098	7	9.6	49457.5	6.47	HUMAN	P56545	C-terminal-binding protein 2
22079	dirMS_041712_NAR_120mM_minus.19025.19025.4	4	4.78	1	1.84E+05		(R)SLRDLT	(R)S L R D|L T/P E H L/P/L L R(N)		158.82	415.7434	1659.954	-0.0023	-1.4	6.47	38779.2	5.93	HUMAN	Q96C86	m7GpppX diphosphatase
22080	dirMS_041712_NAR_120mM_minus.8611.8611.3	3	4.78	0	1.54E+05		(R)SQLLGS	(R)S Q/L/L/G S A H E V Q R(F)		101.63	442.2355	1324.697	-0.0048	-3.7	6.47	285798.6	5.23	HUMAN	A6NG51	Spectrin alpha chain, non-erythrocytic 1
22081	dirMS_041712_NAR_30mM_minus2.13998.13998.2	2	4.78	0	3.02E+05		(K)CDFPIM	(K)C D/F|P I/M/K(F)	C:Carbamidomethylation	129.53	455.7144	910.416	0.0054	5.9	5.84	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
22082	dirMS_041712_NAR_40mM_minus2.10878.10878.3	3	4.78	0	4.63E+05		(R)DAGEGL	(R)D A|G/E|G L L A V Q I/T D Q E G\K\P K(R)		147.63	657.0157	1969.024	0.0089	4.5	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
22083	dirMS_041712_NAR_40mM_minus2.6705.6705.2	2	4.78	0	4.17E+05		(R)LASYLD	(R)L/A/S/Y L D R(V)		108.32	419.2267	837.447	-0.0004	-0.4	5.83	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
22084	dirMS_041712_NAR_50mM_minus2.14798.14798.3	3	4.78	0	6.25E+04	T21t	(R)ItEGIYG	(R)I/t/E G I\Y G/S T/F/L Y/L K(F)	t:N-acetylglucosamine (T)	152.55	603.3247	1604.857	203.1025	12.8	6	76746.7	9.39	HUMAN	Q8N5G2	Macoilin
22085	dirMS_041712_NAR_50mM_minus2.17179.17179.3	3	4.78	0	1.66E+05	M195m	(R)LHFFmP	(R)L H F F m|P G\F/A/P L T S R(G)	m:Oxidized methionine	165.48	546.2872	1620.835	16.0115	10.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
22086	dirMS_041712_NAR_60mM_minus.17341.17341.3	3	4.78	1	3.46E+05		(R)KAPSDL	(R)K\A/P S D\L|Y/Q/I I L K(A)		156.37	463.6095	1388.815	-0.0008	-0.6	8.5	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
22087	dirMS_041712_NAR_20mM_plus.16198.16198.2	2	4.78	0	7.18E+04		(R)LLDAQL	(R)L L/D A Q/L\A T G G I/V/D/P R(L)		183.93	769.9362	1538.854	0.0114	7.4	4.21	533778	5.74	HUMAN	Q15149	Plectin
22088	dirMS_041712_NAR_30mM_plus2.16014.16014.2	2	4.78	0	3.64E+05		(K)GVLFYG	(K)G V L|F\Y/G/P P/G C G K(T)	C:Carbamidomethylation	136.92	626.3175	1251.619	0.0087	6.9	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
22089	dirMS_041712_NAR_30mM_plus2.18996.18996.2	2	4.78	0	2.57E+05		(K)LAFNSLL	(K)L/A|F\N\S L L E/K(A)		152.9	517.7928	1034.588	-0.0097	-9.4	6	109088.4	7.19	HUMAN	O75400	Pre-mRNA-processing factor 40 homolog A
22090	dirMS_041712_NAR_30mM_plus2.22303.22303.2	2	4.78	0	2.00E+05		(K)AFPAFL	(K)A F|P A F/L/Q T E I K(D)		171.48	632.8481	1264.694	-0.0047	-3.7	6.05	18176.5	8.78	HUMAN	B4DW83	NADH dehydrogenase (ubiquinone) complex I, assembly factor 6
22091	dirMS_041712_NAR_30mM_plus2.4828.4828.2	2	4.78	0	2.26E+05		(K)NCSETQ	(K)N C|S/E T Q/Y E/S K(V)	C:Carbamidomethylation	76.75	623.256	1245.505	-0.0005	-0.4	4.53	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
22092	dirMS_041712_NAR_30mM_plus2.5339.5339.2	2	4.78	0	5.67E+04		(R)TDTGEP	(R)T D|T/G E P M G R(G)		81.95	482.2128	963.42	-0.0017	-1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
22093	dirMS_041712_NAR_30mM_plus2.6944.6944.2	2	4.78	0	1.02E+05	M357m	(K)AELDDT	(K)A E|L\D D\T/P m R(G)	m:Oxidized methionine	90.5	532.2416	1047.478	15.9984	3.3	4.03	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
22094	dirMS_041712_NAR_40mM_plus2.13455.13455.3	3	4.78	0	3.86E+04		(K)EALGGQ	(K)E A L/G G/Q/A L Y/P H V L V K(N)		145.37	532.3012	1594.895	-0.0061	-3.8	6.85	86691.2	9.19	HUMAN	B7Z4B8	Heterogeneous nuclear ribonucleoprotein U-like protein 1
22095	dirMS_041712_NAR_40mM_plus2.5401.5401.2	2	4.78	0	4.44E+04		(R)SQESGY	(R)S/Q|E|S/G Y Y D R(M)		88.63	552.733	1104.459	-0.0005	-0.5	4.37	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
22096	dirMS_041712_NAR_50mM_plus2.18055.18055.3	3	4.78	1	1.60E+06		(R)ELIKVLE	(R)E L/I K V L E E A|N Q\A|I N/P K(L)		163.38	603.6741	1809.012	-0.0039	-2.2	4.79	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
22097	dirMS_041712_NAR_60mM_plus.15310.15310.3	3	4.78	1	5.71E+05		(R)MTGSEF	(R)M/T|G S E/F D/F E E M K R(K)		136.28	536.2355	1606.688	0.0043	2.7	4.41	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
22098	dirMS_041712_NAR_60mM_plus.16086.16086.3	3	4.78	0	3.62E+05		(K)MTHLPE	(K)M T\H L P E/L D|T/L|S/S E R(A)		141.95	543.6023	1628.795	-0.0025	-1.5	4.65	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
22099	dirMS_041712_NAR_60mM_plus.18813.18813.3	3	4.78	1	3.27E+04		(K)QLDDLK	(K)Q L/D D/L K V E L/S Q L R(V)		155.97	519.6254	1556.864	-0.0026	-1.7	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
22100	dirMS_041712_NAR_120mM_minus.7058.7058.3	3	4.77	1	3.74E+05		(K)DSYVGD	(K)D S/Y V/G D/E A Q S K R(G)		92.47	452.2134	1354.623	0.0023	1.7	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
22101	dirMS_041712_NAR_20mM_minus.11769.11769.2	2	4.77	0	5.30E+03		(R)ILFGDSC	(R)I/L/F G D S C Y P S N D S R(Q)	C:Carbamidomethylation	166.18	815.8697	1630.717	0.0155	9.5	4.21	75161.9	6.15	HUMAN	Q9UM07	Protein-arginine deiminase type-4
22102	dirMS_041712_NAR_30mM_minus2.15131.15131.2	2	4.77	0	7.03E+05		(K)SADTLW	(K)S A|D/T L/W\G I Q/K(E)		135.23	559.8008	1118.584	0.0103	9.2	5.55	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
22103	dirMS_041712_NAR_30mM_minus2.5508.5508.2	2	4.77	0	2.99E+05		(R)TDTGEP	(R)T D|T|G/E P M G\R(G)		83.1	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
22104	dirMS_041712_NAR_30mM_minus2.6318.6318.2	2	4.77	0	1.80E+05	M796m	(R)mNEAF	(R)m N|E/A\F/G D T/K(F)	m:Oxidized methionine	88.13	514.726	1012.44	16.0043	9.1	4.37	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
22105	dirMS_041712_NAR_40mM_minus2.14414.14414.3	3	4.77	0	2.04E+05		(R)DIKPQN	(R)D I K P Q N\L L/L/D/P D T A V L K(L)		169.47	631.6945	1893.069	-0.0002	-0.1	4.43	47257	9.38	HUMAN	P49841	Glycogen synthase kinase-3 beta
22106	dirMS_041712_NAR_50mM_minus2.11925.11925.3	3	4.77	0	3.00E+05	M351m K3	(R)SGADEL	(R)S G A D E L E N/N P E/m/k/C L/R(N)	C:Carbamidomethylation m:Oxid	136.35	664.9712	1862.837	130.0619	12.1	4.41	67349.2	5.75	HUMAN	Q6ZV50	DNA-binding protein RFX8
22107	dirMS_041712_NAR_50mM_minus2.14383.14383.3	3	4.77	1	2.78E+05	S13s	(K)LsRTGPE	(K)L/s R T G P E F\E|N V I K(R)	s:N-acetylglucosamine (S)	149.73	564.9709	1489.801	203.0972	10.5	6.14	18753.3	11.42	HUMAN	Q8IVJ8	AP20 region protein 1
22108	dirMS_041712_NAR_60mM_minus.18234.18234.3	3	4.77	1	4.80E+05		(K)TQLNLL	(K)T Q/L N L L/L/D/K/L R(S)		163.37	442.9403	1326.81	-0.004	-3	8.41	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
22109	dirMS_041712_NAR_20mM_plus.14401.14401.2	2	4.77	0	5.25E+04		(K)ATLEVSS	(K)A T|L/E/V/S S I I K(K)		170.97	530.8101	1060.625	-0.0119	-11.2	6.05	16689.5	9	HUMAN	B0QYV8	ADP-ribosylation factor GTPase activating protein 3 (Fragment)
22110	dirMS_041712_NAR_30mM_plus2.4527.4527.2	2	4.77	0	5.21E+05	M571m	(R)mGANSI	(R)m/G A/N/S L E R(M)	m:Oxidized methionine	73.77	447.2119	877.42	15.9969	2.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
22111	dirMS_041712_NAR_30mM_plus2.7507.7507.2	2	4.77	0	2.71E+05		(R)AAMGP	(R)A A/M/G/P G I/S/R(M)		93.57	430.2276	859.445	0.0025	2.9	9.79	22167.3	10.15	HUMAN	E7ENQ8	Phosphoglucomutase-2
22112	dirMS_041712_NAR_40mM_plus2.17671.17671.3	3	4.77	1	2.27E+05		(K)TGISDVF	(K)T G I/S D V/F A K\N D\L A\V/V D/V R(I)		169.65	640.3451	1919.023	-0.0025	-1.3	4.43	76670.1	4.6	HUMAN	P19338	Nucleolin
22113	dirMS_041712_NAR_40mM_plus2.18300.18300.3	3	4.77	0	1.04E+05		(K)VLSLPKP	(K)V L|S L/P K P T I I\L/S/A/Y Q R(K)		173.45	600.3613	1799.079	-0.0096	-5.3	9.99	80080.5	5.54	HUMAN	J3KMX1	Nuclear pore complex protein Nup88 (Fragment)
22114	dirMS_041712_NAR_40mM_plus2.5447.5447.2	2	4.77	0	1.51E+04		(R)GGSGGS	(R)G G S G\G S Y|G/G|G G S G G G Y/G G G S G S R(G)		88.82	896.3641	1791.728	-0.0068	-3.8	8.59	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
22115	dirMS_041712_NAR_50mM_plus2.12023.12023.3	3	4.77	0	2.31E+04		(R)DLEAEH	(R)D L/E/A\E H V/E V E D T T L N R(C)		132.58	623.966	1869.882	0.001	0.5	4.07	10027.3	8.44	HUMAN	H3BTW0	Uncharacterized protein (Fragment)
22116	dirMS_041712_NAR_50mM_plus2.13195.13195.3	3	4.77	1	5.39E+05		(R)VFDKDG	(R)V/F D K D G N G Y\I/S A A E L R(H)		137.5	585.6264	1754.871	-0.0061	-3.5	4.56	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
22117	dirMS_041712_NAR_50mM_plus2.14627.14627.3	3	4.77	0	2.14E+05		(R)LTEDLEY	(R)L/T|E/D/L E/Y H E L L D R(A)		145.27	549.2742	1645.807	0.0013	0.8	4.17	19946.4	5.79	HUMAN	H0YCV6	Oxysterol-binding protein 1 (Fragment)
22118	dirMS_041712_NAR_50mM_plus2.5194.5194.3	3	4.77	0	2.68E+05	M21m	(R)SGSmDF	(R)S G S m\D/P S G A|H/P S V/R(Q)	m:Oxidized methionine	86.13	467.5461	1384.627	15.9964	1	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
22119	dirMS_041712_NAR_50mM_plus2.8199.8199.3	3	4.77	1	7.95E+04		(R)DTGEKL	(R)D T/G E K L T\V/A E N E/A/E T K(L)		109.95	578.9478	1734.839	-0.0104	-6	4.25	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
22120	dirMS_041712_NAR_60mM_plus.6775.6775.2	2	4.77	1	1.82E+05		(K)SESPKEP	(K)S E\S/P/K/E P E Q L R(K)		93.92	650.3286	1299.654	-0.004	-3.1	4.78	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
22121	dirMS_041712_NAR_120mM_minus.9461.9461.2	2	4.76	0	1.53E+05		(K)EFHLNE	(K)E F/H\L N/E S G/D|P S/S K(S)		106.17	723.8269	1446.65	-0.003	-2.1	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
22122	dirMS_041712_NAR_20mM_minus.8322.8322.2	2	4.76	0	1.41E+05		(K)DVGSLA	(K)D V/G S/L/A/S V Q R(Y)		132.4	516.2772	1031.548	-0.0009	-0.8	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin

22123	dirMS_041712_NAR_20mM_minus.9057.9057.2	2	4.76	0	6.54E+04	M68m M7!	(R)NLAmG\	(R)N L\A/m/G/V N L|T S m S K(I)	m:Oxidized methionine	139.73	699.34	1365.687	31.9862	-2.6	8.75	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
22124	dirMS_041712_NAR_30mM_minus2.13829.13829.2	2	4.76	0	3.56E+05		(R)LAGLFNI	(R)L A|G L/F/N/E Q R(K)		128.93	524.2789	1047.558	-0.0076	-7.3	6	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
22125	dirMS_041712_NAR_40mM_minus2.11602.11602.3	3	4.76	1	4.75E+04		(R)QVFGEA	(R)Q V/F/G E A T K Q/P G I T F I/A A K(F)		152.53	636.0167	1906.043	-0.0077	-4.1	8.59	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
22126	dirMS_041712_NAR_50mM_minus2.17140.17140.3	3	4.76	1	3.18E+05		(K)AILILDNI	(K)A I/L/I/L D N/D G D R L F A K(Y)		165.27	558.6442	1673.922	-0.004	-2.4	4.43	18430.9	4.79	HUMAN	F8VS17	Coatomer subunit zeta-1
22127	dirMS_041712_NAR_60mM_minus.16518.16518.3	3	4.76	1	1.29E+05		(K)KLSTIAL/	(K)K L S T I A\L A/L/G V E R(T)		151.82	457.6153	1370.837	-0.0052	-3.8	8.75	52669.1	4.73	HUMAN	A8MY67	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform
22128	dirMS_041712_NAR_60mM_minus.17091.17091.3	3	4.76	0	1.15E+05		(K)DGLGFC	(K)D G\L|G/F/C A L I H R(H)	C:Carbamidomethylation	155.8	420.2191	1258.636	0.0066	5.3	6.74	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
22129	dirMS_041712_NAR_60mM_minus.5329.5353.3	3	4.76	0	8.98E+04	M116m	(R)ATAPQT	(R)A/T|A/P Q T Q H V/S P m R(Q)	m:Oxidized methionine	85.37	480.5729	1423.711	15.9931	-1.3	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
22130	dirMS_041712_NAR_120mM_plus.5110.5110.3	3	4.76	1	1.28E+05		(K)MSSPED	(K)M/S/S/P E\D D/S D T K R(L)		79.25	456.5294	1367.574	-0.0007	-0.5	4.23	103309.5	5.34	HUMAN	A0AV56	SAFB protein
22131	dirMS_041712_NAR_120mM_plus.6262.6262.2	2	4.76	1	3.49E+05		(K)DSYVGD	(K)D/S/Y V/G D/E A Q S K R(G)		86.28	677.815	1354.623	-0.0006	-0.5	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
22132	dirMS_041712_NAR_20mM_plus.19023.19023.3	3	4.76	0	6.93E+04		(K)LQNVQI.	(K)L Q N V\Q|I/A L/D Y L R(H)		202.85	482.6066	1445.811	-0.0058	-4	5.83	20181.7	9.9	HUMAN	E9PIA2	Plectin (Fragment)
22133	dirMS_041712_NAR_30mM_plus2.11896.11896.2	2	4.76	0	1.45E+06		(R)NTDEM\	(R)N T|D/E/M|V E/L R(I)		114.92	553.7615	1106.515	0.0011	1	4.14	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
22134	dirMS_041712_NAR_40mM_plus2.6573.6573.2	2	4.76	2	4.31E+04		(K)RSGEQG	(K)R S/G E Q G K K(K)		98.25	445.2395	889.485	-0.0133	-14.9	9.99	65526.5	10.39	HUMAN	Q02086	Transcription factor Sp2
22135	dirMS_041712_NAR_50mM_plus2.10555.10555.3	3	4.76	0	5.29E+04		(R)LQAQQI	(R)L Q|A Q Q D|A V N I/V C/H S K(T)	C:Carbamidomethylation	123.17	570.9571	1710.859	-0.0024	-1.4	6.74	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
22136	dirMS_041712_NAR_50mM_plus2.15252.15252.3	3	4.76	0	5.18E+05		(K)LHIIEVG	(K)L H I I E\V G T|P P T G N Q/P F P K(K)		147.45	649.0216	1945.054	-0.0039	-2	6.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
22137	dirMS_041712_NAR_50mM_plus2.20751.20751.3	3	4.76	1	1.16E+05		(K)SVLTGGI	(K)S V/L/T/G G L/D A L E F I G K K(T)		177.8	549.9834	1647.932	0.004	2.5	5.79	40220	4.95	HUMAN	Q6MZV4	Protein NOXP20
22138	dirMS_041712_NAR_50mM_plus2.5533.5533.3	3	4.76	1	1.11E+05		(K)DSYVGD	(K)D S Y V/G D E A/Q S K/R(G)		90.6	452.2114	1354.623	-0.0037	-2.7	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
22139	dirMS_041712_NAR_60mM_plus.19096.19096.3	3	4.76	1	3.50E+04		(K)SELVAM	(K)S E|L|V/A M L E E E E L R K(A)		158.07	559.288	1675.857	-0.0077	-4.6	4.32	18679.2	5.61	HUMAN	B4DWW1	ADP-ribosylation factor-like protein 1
22140	dirMS_041712_NAR_60mM_plus.6999.6999.3	3	4.76	1	1.17E+05		(K)KAEGEP	(K)K A E G E/P Q/E/E S/P L/K(S)		95.1	481.2429	1441.717	-0.0028	-1.9	4.49	53030.7	11.3	HUMAN	E9PJA7	Bcl-2-associated transcription factor 1
22141	dirMS_041712_NAR_120mM_minus.4895.4895.3	3	4.75	1	3.49E+05		(R)AAEEED	(R)A/A/E E E D E A D/P K R(Q)		78.73	453.8716	1359.602	-0.002	-1.5	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
22142	dirMS_041712_NAR_20mM_minus.7165.7165.2	2	4.75	0	1.39E+05		(R)AAQVA(	(R)A A/Q|V/A/Q D E E I A R(L)		119.03	650.8255	1300.649	-0.0054	-4.2	4.14	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
22143	dirMS_041712_NAR_30mM_minus2.17105.17105.2	2	4.75	0	2.34E+05		(R)FFMGN(	(R)F F/M/G N Q V L K(V)		146.27	542.2866	1083.566	0.0004	0.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
22144	dirMS_041712_NAR_40mM_minus2.15369.15369.3	3	4.75	1	3.30E+05		(R)GGPNIIT	(R)G G P\N\I/I|T L A D I V K D/P V S R(T)		177.93	622.3523	1865.049	-0.0067	-3.6	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
22145	dirMS_041712_NAR_50mM_minus2.10627.10627.3	3	4.75	0	2.90E+05	M35m	(K)AASDIAr	(K)A A/S D I/A m T E L/P P T H/P I R(L)	m:Oxidized methionine	128.37	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
22146	dirMS_041712_NAR_50mM_minus2.14653.14653.3	3	4.75	1	1.31E+05	M405m	(K)LSKNEVI	(K)L/S K N E V L m\V\N\I/G S L/S T G G R(V)	m:Oxidized methionine	151.43	664.3565	1975.064	15.9909	-2	8.75	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
22147	dirMS_041712_NAR_50mM_minus2.4941.4941.3	3	4.75	1	4.33E+05		(R)AAEDDE	(R)A A/E/D D E D D D V D T K K(Q)		82.37	522.5522	1565.645	-0.0029	-1.8	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
22148	dirMS_041712_NAR_50mM_minus2.5620.5620.3	3	4.75	1	9.00E+03		(K)DSYVGD	(K)D S\Y/V/G D E A Q S K R(G)		92.38	452.2119	1354.623	-0.0022	-1.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
22149	dirMS_041712_NAR_60mM_minus.10958.10958.3	3	4.75	1	1.26E+05		(K)KVEAQL	(K)K V E A Q/L\Q/E/L Q V K(F)		121.12	471.6068	1412.811	-0.0049	-3.5	6.14	227783.5	5.5	HUMAN	P35579	Myosin-9
22150	dirMS_041712_NAR_60mM_minus.13577.13577.3	3	4.75	0	2.13E+05		(K)EMNPAI	(K)E M N/P A/L/G/I D C L/H K(G)	C:Carbamidomethylation	135.33	499.9146	1497.719	0.0104	6.9	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
22151	dirMS_041712_NAR_60mM_minus.16890.16890.3	3	4.75	1	3.13E+05		(R)LKLPAV\	(R)L K L P A V\V/T/A D/L/R(L)		154.02	432.6056	1295.805	-0.0023	-1.8	8.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
22152	dirMS_041712_NAR_60mM_minus.19452.19452.3	3	4.75	0	3.63E+05		(K)HSQFIG\	(K)H S Q\F I G\Y/P I T L Y L E K(E)		173.42	603.6548	1808.958	-0.0083	-4.6	6.75	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
22153	dirMS_041712_NAR_120mM_plus.21680.21680.4	4	4.75	1	2.92E+05		(K)GDVREP	(K)G D V R/E\P F H\S I\L S\V L K(G)		166.93	424.9891	1696.938	-0.0035	-2.1	6.75	27027.7	6.85	HUMAN	Q5T3I4	Apolipoprotein A-I binding protein
22154	dirMS_041712_NAR_20mM_plus.15618.15618.2	2	4.75	0	9.29E+03		(K)ALTLIAG	(K)A L/T\L/I/A/G S P L K(I)		180.12	542.3395	1083.677	-0.0055	-5.1	8.8	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
22155	dirMS_041712_NAR_20mM_plus.16492.16492.2	2	4.75	0	1.33E+05		(R)ELLIIGG\	(R)E L\L I|I/G/G V A A\R(D)		185.67	556.3437	1111.683	-0.0032	-2.9	6.1	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
22156	dirMS_041712_NAR_20mM_plus.17447.17447.2	2	4.75	0	1.59E+05		(K)DVDLEFI	(K)D V/D L E F L/A K(M)		192.67	525.2795	1049.551	0.0004	0.4	4.03	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
22157	dirMS_041712_NAR_20mM_plus.18104.18104.2	2	4.75	0	9.83E+04		(R)APGSGL	(R)A/P G S G/L/A L L/P L K(I)		196.67	568.8548	1136.704	-0.0014	-1.3	8.8	266161	5.68	HUMAN	E9PPU0	Epiplakin
22158	dirMS_041712_NAR_30mM_plus2.10869.11039.2	2	4.75	0	5.54E+05		(R)AYLQQL	(R)A Y|L/Q\Q L/R(Q)		110.53	446.2501	891.505	-0.0118	-13.2	8.79	20774.5	9.1	HUMAN	O15145	Actin-related protein 2/3 complex subunit 3
22159	dirMS_041712_NAR_30mM_plus2.11795.11795.2	2	4.75	0	4.85E+05		(R)AMGEQ	(R)A/M/G E/Q|A/V/A/L A R(A)		114.22	558.7944	1116.583	-0.0015	-1.3	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
22160	dirMS_041712_NAR_30mM_plus2.14603.14603.3	3	4.75	0	7.47E+04		(K)VNQIGS'	(K)V N Q\I G S V/T/E/S/I Q/A C K(L)	C:Carbamidomethylation	129.65	545.28	1633.821	0.0041	2.5	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
22161	dirMS_041712_NAR_30mM_plus2.18468.18468.2	2	4.75	1	2.69E+04		(K)IPRTLQT	(K)I P R/T/L Q\T A P E K(E)		150.02	627.3688	1253.721	0.0091	7.3	8.75	93078.6	9.36	HUMAN	A6NJZ9	Nucleolar complex protein 3 homolog
22162	dirMS_041712_NAR_50mM_plus2.6207.6207.3	3	4.75	0	9.31E+04		(K)AGYSTD	(K)A G Y S/T/D E S S/S S S L/H/A T R(T)		97.42	585.9333	1755.778	0.0073	4.2	5.32	74564.3	5.95	HUMAN	P51116	Fragile X mental retardation syndrome-related protein 2
22163	dirMS_041712_NAR_120mM_minus.17781.17781.4	4	4.74	1	2.71E+05		(K)SKNILFV	(K)S K N I L F\V I/T K P D/V/Y K(S)		151.3	442.0108	1765.026	-0.0045	-2.5	9.53	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
22164	dirMS_041712_NAR_120mM_minus.20125.20125.3	3	4.74	0	1.97E+05		(K)KPGGFD	(K)K P G G F D\I|S/L/F Y R(D)		166.17	467.2504	1399.737	-0.0002	-0.2	8.59	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
22165	dirMS_041712_NAR_120mM_minus.9662.9662.3	3	4.74	0	7.94E+05		(K)SPQYCQ	(K)S/P Q Y C\Q V I|H/R(L)	C:Carbamidomethylation	106.43	429.8855	1287.626	0.0157	12.2	8.49	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
22166	dirMS_041712_NAR_30mM_minus2.11818.11818.2	2	4.74	0	3.78E+05		(K)MTISQQ	(K)M T/I/S Q/Q E/F/G R(T)		117.88	598.7911	1196.573	0.0021	1.7	5.75	21119.9	4.34	HUMAN	H0Y3Y9	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
22167	dirMS_041712_NAR_50mM_minus2.10811.10811.3	3	4.74	0	2.02E+05	M35m	(K)AASDIAr	(K)A A\S D I/A m T E L/P P T H P I R(L)	m:Oxidized methionine	129.75	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
22168	dirMS_041712_NAR_50mM_minus2.13094.13094.3	3	4.74	1	1.63E+05		(R)NVIFQP\	(R)N V/I/F Q/P V A E L/K K(Q)		142.78	462.6086	1385.815	-0.0039	-2.8	8.59	23167	8.94	HUMAN	B1APP8	6-phosphofructokinase type C
22169	dirMS_041712_NAR_50mM_minus2.16636.16636.3	3	4.74	1	1.61E+05		(K)TVTAMI	(K)T V|T A M D/V/V Y A L K R(Q)		162.78	489.6051	1466.804	-0.0028	-1.9	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
22170	dirMS_041712_NAR_50mM_minus2.5332.5332.3	3	4.74	0	8.24E+05		(K)TATPQQ	(K)T A\T/P Q/Q A Q\E V/H E K(L)		88.02	489.5768	1466.723	-0.0075	-5.1	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
22171	dirMS_041712_NAR_50mM_minus2.7577.7577.3	3	4.74	1	6.20E+05	M289m	(R)VVDLM/	(R)V/V/D L/M A H m A S K E(-)	m:Oxidized methionine	110.2	449.5526	1330.649	15.9939	-0.8	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
22172	dirMS_041712_NAR_120mM_plus.7774.7774.2	2	4.74	1	9.82E+05		(R)AQYDEL	(R)A Q/Y/D/E L A R K(N)		93.47	547.2874	1093.564	0.0039	3.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
22173	dirMS_041712_NAR_20mM_plus.17057.17057.2	2	4.74	0	9.70E+04		(R)AIVAIEN	(R)A I\V/A I/E/N/P A D V/S\V I S S R(N)		188.97	870.9764	1740.949	-0.0035	-2	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
22174	dirMS_041712_NAR_30mM_plus2.13195.13195.2	2	4.74	0	1.13E+06		(K)NDLAVV	(K)N D\L|A/V/V\D/V R(I)		121.8	500.7769	1000.542	0.0043	4.3	4.21	76670.1	4.6	HUMAN	P19338	Nucleolin
22175	dirMS_041712_NAR_30mM_plus2.16069.16069.2	2	4.74	0	5.33E+05		(R)IFIGTFK(	(R)I/F|I/G T F/K(A)		137.65	413.2445	825.487	-0.0052	-6.3	8.75	25246.3	11.45	HUMAN	B3KVR1	Small nuclear ribonucleoprotein-associated protein
22176	dirMS_041712_NAR_30mM_plus2.21483.21483.2	2	4.74	0	3.90E+05		(R)VNQAIW	(R)V N Q A I/W L L C/T/G A R(E)	C:Carbamidomethylation	166.88	751.3976	1501.794	-0.0065	-4.3	9.72	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
22177	dirMS_041712_NAR_30mM_plus2.4263.4263.2	2	4.74	0	1.52E+05		(R)SYTSGP(	(R)S/Y/T S/G/P G S R(I)		71.13	456.2155	911.422	0.002	2.2	8.46	19288.4	10.19	HUMAN	F8VQY3	Keratin, type II cytoskeletal 8 (Fragment)
22178	dirMS_041712_NAR_50mM_plus2.10698.10698.3	3	4.74	1	4.93E+05		(R)DGKLVS	(R)D G K L V S E|S/S/D V L/P/K(-)		124.1	491.9313	1473.78	-0.0002	-0.1	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
22179	dirMS_041712_NAR_60mM_plus.10212.10212.3	3	4.74	0	6.25E+05		(K)TPVEPE\	(K)T/P/V\E P E/V/A/I/H R(I)		111.5	416.5628	1247.674	-0.0004	-0.3	5.37	5429.1	9.6	HUMAN	E5RIP1	40S ribosomal protein S20
22180	dirMS_041712_NAR_60mM_plus.19343.19343.3	3	4.74	1	4.46E+04		(R)SLADIAR	(R)S L|A/D/I A R E E A/S N F R(S)		159.53	526.9346	1578.787	0.0022	1.4	4.68	20458.8	4.99	HUMAN	G3V4X5	Proteasome subunit alpha type-3
22181	dirMS_041712_NAR_120mM_minus.12821.12821.4	4	4.73	0	3.76E+05		(K)SLGTRPI	(K)S/L G T R P P H\V F\A\I A/D K(A)		124.95	402.9764	1608.886	-0.0019	-1.2	8.49	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
22182	dirMS_041712_NAR_20mM_minus.10087.10087.2	2	4.73	0	1.53E+04		(R)IVLQIDN	(R)I V|L|Q/I D\N A R(L)		150.52	521.3059	1041.605	-0.0006	-0.6	5.84	20842.9	5.32	HUMAN	C9JM50	Keratin, type I cytoskeletal 19 (Fragment)
22183	dirMS_041712_NAR_30mM_minus2.14271.14271.2	2	4.73	0	4.54E+05		(R)RPLDPVI	(R)R P|L D P V/K(V)		130.5	412.7522	824.499	-0.0017	-2.1	8.75	59001.4	5.76	HUMAN	Q6ZU67	BEN domain-containing protein 4
22184	dirMS_041712_NAR_30mM_minus2.6803.6803.2	2	4.73	0	1.71E+05		(R)GCLDEE'	(R)G/C|L/D E E\T S R(A)	C:Carbamidomethylation	91.75	533.7297	1066.447	0.0052	4.8	4.14	533778	5.74	HUMAN	Q15149	Plectin
22185	dirMS_041712_NAR_50mM_minus2.12614.12614.3	3	4.73	1	2.05E+04	M320m	(K)YmACCL	(K)Y m/A/C/C L L Y R G D V/V/P K(E)	C:Carbamidomethylation m:Oxid	139.78	620.9644	1844.886	15.9931	-1	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
22186	dirMS_041712_NAR_20mM_plus.17905.17905.2	2	4.73	0	1.94E+05		(R)YISPDQL	(R)Y I|S/P D Q L A|D L Y K(S)		194.27	713.3667	1425.726	0.0001	0.1	4.21	47510.4	7.04	HUMAN	P06733	Alpha-enolase
22187	dirMS_041712_NAR_20mM_plus.6671.6671.2	2	4.73	1	2.51E+04	M84m	(R)GVEEEEI	(R)G V\E E|E/E/E D G E m R E(-)	m:Oxidized methionine	110.62	777.2997	1537.596	15.9963	0.9	3.88	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F
22188	dirMS_041712_NAR_30mM_plus2.11366.11366.2	2	4.73	0	9.73E+04		(R)VEFMDI	(R)V E|F/M D D T S/R(S)		112.67	550.2401	1099.473	0.0005	0.4	4.03	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
22189	dirMS_041712_NAR_30mM_plus2.21414.21414.2	2	4.73	0	3.00E+05		(R)NSYLEVI	(R)N S|Y|L E V/L L K(L)		167.62	539.8092	1078.614	-0.0032	-2.9	6	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
22190	dirMS_041712_NAR_30mM_plus2.8454.8454.2	2	4.73	0	1.02E+05		(R)YNYIEGT	(R)Y/N|Y/I/E G T K(M)		99.03	494.2448	987.478	0.0041	4.2	6	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
22191	dirMS_041712_NAR_50mM_plus2.13870.13870.3	3	4.73	1	9.30E+05		(K)ALQQGL	(K)A L/Q\Q\G L/V/G L E L K\E/K(L)		141.73	509.3022	1525.895	-0.0028	-1.8	6.18	266161	5.68	HUMAN	E9PPU0	Epiplakin
22192	dirMS_041712_NAR_50mM_plus2.15292.15292.3	3	4.73	1	5.42E+05		(R)AALDKA	(R)A/A/L D K A/T\V L/L S M S K(G)		148.57	483.2728	1447.819	-0.015	-10.4	8.64	50974.6	5.31	HUMAN	B5ME91	Programmed cell death protein 4
22193	dirMS_041712_NAR_50mM_plus2.16248.16248.3	3	4.73	0	1.03E+06		(R)LSFQHD	(R)L S F Q H D\P E/T/S/V\L V L/R(K)		152.45	580.9801	1740.928	-0.0022	-1.2	5.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
22194	dirMS_041712_NAR_50mM_plus2.18420.18420.3	3	4.73	0	8.26E+05		(K)VAHALA	(K)V A H/A L A E G L G\V/I/A/C I G E K(L)	C:Carbamidomethylation	166.05	603.3265	1807.974	-0.0085	-4.7	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
22195	dirMS_041712_NAR_60mM_plus.13905.13905.3	3	4.73	1	9.19E+05		(K)TTVKDL!	(K)T T V K D L S/E|L/G/S V R(T)		129.45	468.9268	1404.769	-0.0034	-2.4	5.74	533778	5.74	HUMAN	Q15149	Plectin
22196	dirMS_041712_NAR_60mM_plus.18576.18576.3	3	4.73	1	2.52E+05		(R)RGDINLI	(R)R G D I N L\L|M L/G D/P G T A K(S)		154.57	557.6331	1670.889	-0.0047	-2.8	5.96	78390.7	9.27	HUMAN	B1AHB1	DNA replication licensing factor MCM5
22197	dirMS_041712_NAR_120mM_minus.8624.8624.3	3	4.72	2	2.56E+05		(R)KDGKDP	(R)K|D/G K D P N Q/F T I S R(R)		101.53	502.5853	1505.771	-0.0293	-19.5	8.59	28000.3	9.32	HUMAN	A6NE42	Homeobox protein TGIF1
22198	dirMS_041712_NAR_20mM_minus.8455.8455.3	3	4.72	0	5.22E+03		(R)EGQGE(	(R)E G Q G E G E T Q E|A\A/A/A/A A/A/A R(R)		134.03	596.6099	1787.815	-0.0003	-0.2	4.09	558007.1	5.44	HUMAN	P58107	Epiplakin
22199	dirMS_041712_NAR_30mM_minus2.6527.6527.2	2	4.72	0	1.68E+05		(R)QGEAEF	(R)Q G E/A/E/F N/R(I)		90.03	475.7203	950.433	0.0007	0.7	4.53	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
22200	dirMS_041712_NAR_50mM_minus2.8680.8680.3	3	4.72	1	2.35E+05	S38s	(R)ASAGPD	(R)A/S A/G/P D R L S L A L s R(A)	s:N-acetylglucosamine (S)	116.58	539.6119	1413.781	203.0403	-24.2	9.64	16873.6	11.88	HUMAN	Q5VSH5	Chromosome 1 open reading frame 122
22201	dirMS_041712_NAR_50mM_minus2.9536.9536.3	3	4.72	0	2.36E+05		(K)TSEVDL/	(K)T S/E V/D L/A K P L V K(F)		123.12	433.9205	1299.752	-0.0049	-3.8	5.73	17178.3	5.63	HUMAN	C9IZF9	Programmed cell death 6-interacting protein (Fragment)
22202	dirMS_041712_NAR_20mM_plus.11950.11950.2	2	4.72	0	4.27E+04	M108m	(K)LATQLT(	(K)L A T Q/L/T G/P V m/P V R(N)	m:Oxidized methionine	155.58	699.8907	1382.782	15.9917	-2.3	9.75	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
22203	dirMS_041712_NAR_20mM_plus.18877.18877.2	2	4.72	0	2.38E+05		(K)IYVDDGI	(K)I/Y|V/D D G L|I S L Q V K(Q)		200.77	731.9068	1462.815	-0.0088	-6	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
22204	dirMS_041712_NAR_40mM_plus2.17567.17567.3	3	4.72	0	6.01E+04		(R)GTEDITS	(R)G T/E/D I/T S\P H G I/P L/D\L L D R(V)		169.88	650.3372	1948.997	-0.0004	-0.2	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
22205	dirMS_041712_NAR_50mM_plus2.19934.19934.3	3	4.72	0	1.09E+05		(R)LLHLPLS	(R)L L H L P L|S/L/T A L K(L)		173.43	440.2862	1318.846	-0.0016	-1.2	8.76	59982.4	4.94	HUMAN	Q9BTT6	Leucine-rich repeat-containing protein 1
22206	dirMS_041712_NAR_120mM_minus.12646.12646.3	3	4.71	0	4.66E+05	T85t	(R)GSSLPGI	(R)G S S L\P G K P t/S P H/N(-)	t:N-acetylglucosamine (T)	123	494.5729	1278.644	203.0605	-12.8	8.76	10021.4	5.81	HUMAN	D6R9U3	Protein SMIM14 (Fragment)
22207	dirMS_041712_NAR_120mM_minus.5775.5775.3	3	4.71	0	1.05E+05	M434m M4	(R)LESGmC	(R)L E/S G m Q N m/S I H T/K(T)	m:Oxidized methionine	85.03	503.2345	1475.698	31.9908	0.7	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
22208	dirMS_041712_NAR_120mM_minus.7453.7453.3	3	4.71	1	3.19E+05		(K)IYEDGDI	(K)I Y|E D/G D/D D M K R(T)		94.63	452.8645	1356.574	0.0053	3.9	4.03	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
22209	dirMS_041712_NAR_30mM_minus2.10387.10387.2	2	4.71	0	1.27E+06		(K)TFEINPR	(K)T/F|E/I/N P R(H)		111.35	438.7375	876.457	0.0103	11.8	5.66	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
22210	dirMS_041712_NAR_40mM_minus2.6902.6902.2	2	4.71	0	5.56E+05		(R)GYSFTTI	(R)G Y|S\F/T/T T A E R(E)		111.9	566.7661	1132.527	-0.002	-1.8	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
22211	dirMS_041712_NAR_50mM_minus2.11160.11160.3	3	4.71	1	6.21E+05		(R)ISVYYNE	(R)I/S/V\Y/Y N E A T G G K Y/V P R(A)		131.08	606.3119	1816.923	-0.0017	-0.9	8.43	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
22212	dirMS_041712_NAR_50mM_minus2.12442.12442.3	3	4.71	1	2.16E+05	M4131m	(K)ISmPEVI	(K)I S\m/P E V D L/N L/K G P K(M)	m:Oxidized methionine	139.38	519.6148	1540.84	15.9895	-3.5	6.07	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
22213	dirMS_041712_NAR_50mM_minus2.6884.6884.3	3	4.71	1	2.38E+04	M185m	(K)ALIEmEI	(K)A L|I/E/m/E K Q Q Q D Q V D R(N)	m:Oxidized methionine	105.48	616.2995	1830.901	15.9825	-6.7	4.32	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)
22214	dirMS_041712_NAR_60mM_minus.11581.11581.3	3	4.71	2	1.42E+06	N15n	(K)MDNRD'	(K)M D/N R D V/A G K/A n R(W)	n:N-acetylglucosamine (N)	123.6	517.2449	1346.659	203.0608	-12	8.5	20563.9	9.69	HUMAN	B4DVK3	SURP and G-patch domain-containing protein 1
22215	dirMS_041712_NAR_60mM_minus.15561.15561.3	3	4.71	1	1.92E+05		(R)ASLISAV	(R)A/S/L I/S A V/S D\K L/R(W)		146.22	420.5811	1259.732	-0.003	-2.4	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
22216	dirMS_041712_NAR_60mM_minus.16513.16513.3	3	4.71	0	2.44E+05		(R)SLESLHS	(R)S L/E S\L H/S F V/A A A T K(E)		151.68	487.5978	1460.774	0.0045	3.1	6.47	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
22217	dirMS_041712_NAR_60mM_minus.16676.16676.3	3	4.71	1	7.73E+03		(R)KGTQCV	(R)K G T Q C\V E Q\I\Q E|L/V\L R(F)	C:Carbamidomethylation	152.3	600.9904	1800.964	-0.007	-3.9	6.14	36321.2	4.51	HUMAN	Q9P287	BRCA2 and CDKN1A-interacting protein
22218	dirMS_041712_NAR_60mM_minus.18699.18699.3	3	4.71	0	2.89E+05		(K)LHDNLII!	(K)L H D\N\L\I\I/S D/L E N T V K(K)		166	575.3117	1723.922	-0.0019	-1.1	4.54	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
22219	dirMS_041712_NAR_60mM_minus.19959.19959.3	3	4.71	1	8.17E+05		(R)LIALLEVI	(R)L I/A L/L E/V/L S Q K R(M)		182.02	461.6287	1382.873	-0.0014	-1	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
22220	dirMS_041712_NAR_120mM_plus.18968.18968.3	3	4.71	2	4.83E+05		(R)KIEEIKDI	(R)K\I/E E I K D F/L/L/T A/R(R)		152.4	525.9746	1575.911	-0.0012	-0.8	6.18	2559	9.99	HUMAN	J3KSP2	60S ribosomal protein L38 (Fragment)
22221	dirMS_041712_NAR_120mM_plus.7173.7173.2	2	4.71	1	2.31E+05		(R)SDYDGI(	(R)S D/Y D/G I G S R G D/R(S)		91.02	649.291	1297.577	-0.002	-1.5	4.43	15031.5	6.72	HUMAN	B4DLA0	ATP-dependent RNA helicase DDX3X
22222	dirMS_041712_NAR_20mM_plus.11486.11486.2	2	4.71	0	1.77E+05		(R)YALYDA'	(R)Y A|L/Y/D A/T Y E T K(E)		151.52	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
22223	dirMS_041712_NAR_20mM_plus.11883.11883.3	3	4.71	0	6.79E+04	M108m	(K)LATQLT(	(K)L A T Q L T/G P V/m P V R(N)	m:Oxidized methionine	155.43	466.9291	1382.782	15.9903	-3.3	9.75	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
22224	dirMS_041712_NAR_20mM_plus.18583.18583.2	2	4.71	0	7.26E+04		(K)STLINTLI	(K)S T/L/I/N T L/F K(S)		199.07	518.8058	1036.604	0.0006	0.6	8.47	18010.4	9.42	HUMAN	K7EIE4	Septin-9 (Fragment)
22225	dirMS_041712_NAR_20mM_plus.7366.7366.2	2	4.71	0	2.44E+05		(R)TVGIVGI	(R)T V|G I/V G N Q/P K(V)		119.85	506.7922	1012.579	-0.0014	-1.4	8.41	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
22226	dirMS_041712_NAR_30mM_plus2.16910.16910.2	2	4.71	0	3.92E+05		(R)DFFLAN.	(R)D F|F|L A|N A S R(A)		141.77	520.7632	1040.516	0.0032	3	5.84	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
22227	dirMS_041712_NAR_30mM_plus2.17075.17392.2	2	4.71	0	6.08E+05		(K)NAAGAL	(K)N A|A|G A/L D L L K(E)		143.23	493.2867	985.568	-0.0015	-1.6	5.84	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
22228	dirMS_041712_NAR_50mM_plus2.7669.7669.3	3	4.71	1	2.65E+05		(K)AQQLEV	(K)A/Q Q/L E/W/V K S R(Y)		106.62	415.5609	1244.675	-0.0064	-5.2	8.79	105657.6	6	HUMAN	H3BMX2	Alpha-mannosidase 2C1
22229	dirMS_041712_NAR_50mM_plus2.7955.7955.3	3	4.71	0	2.47E+04		(K)QLAVAE	(K)Q L\A V\A\E/G K P P E/A/P K(G)		108.23	478.9337	1434.795	-0.0086	-6	6.14	24364.9	9.64	HUMAN	H0YIP0	Methionine--tRNA ligase, cytoplasmic (Fragment)
22230	dirMS_041712_NAR_60mM_plus.11307.11307.2	2	4.71	0	7.25E+05		(R)GSAVHC	(R)G S A/V/H\Q L\S E E L R(C)		116.43	663.3438	1325.681	-0.0005	-0.4	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
22231	dirMS_041712_NAR_60mM_plus.11813.11813.2	2	4.71	1	2.66E+05		(K)TLQEVTI	(K)T L|Q/E/V/T E M D S V K/R(Y)		118.98	768.3889	1535.773	-0.0029	-1.9	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin

22232	dirMS_041712_NAR_60mM_plus.20652.20652.3	3	4.71	0	4.44E+05		(R)CRPDQL	(R)C R P D Q\L T G\L/S|L/L P L S E K(A)	C:Carbamidomethylation	168.32	643.0146	1927.032	-0.0025	-1.3	6.07	533778	5.74	HUMAN	Q15149	Plectin
22233	dirMS_041712_NAR_60mM_plus.5611.5611.3	3	4.71	0	7.32E+04		(K)AAGPSL!	(K)A/A/G\P S L S/H/T S G G T Q S K(V)		87.67	495.9135	1485.729	-0.0033	-2.2	8.8	68764.6	6.96	HUMAN	P27694	Replication protein A 70 kDa DNA-binding subunit
22234	dirMS_041712_NAR_120mM_minus.15073.15073.3	3	4.7	0	1.99E+05		(R)HGLEAIS	(R)H G\L\E A\I|S|I/M/D/S R(G)		136.3	443.5593	1328.663	0.0006	0.5	5.32	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
22235	dirMS_041712_NAR_120mM_minus.6074.6074.3	3	4.7	1	5.64E+05		(K)TCEESSF	(K)T C/E E S/S F/C K R(Q)	C:Carbamidomethylation	86.8	435.1849	1303.541	-0.0004	-0.3	5.81	10576.1	11.44	HUMAN	E9PRF8	Neutral alpha-glucosidase AB
22236	dirMS_041712_NAR_120mM_minus.8608.8608.3	3	4.7	1	2.56E+05	S133s	(R)AGDLLEI	(R)A/G|D\L|L E D s P K R/P K(E)	s:Phosphorylated S	101.53	502.5853	1425.77	79.9717	3.6	6.17	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
22237	dirMS_041712_NAR_20mM_minus.10712.10712.3	3	4.7	0	2.92E+05	M494m	(R)GAHImN	(R)G A H/I m N S|T C A A M\P K(L)	C:Carbamidomethylation m:Oxid	155.45	502.2275	1488.676	15.9923	-1.7	8.76	114220.9	9.14	HUMAN	O43303	Centriolar coiled-coil protein of 110 kDa
22238	dirMS_041712_NAR_20mM_minus.14520.14520.2	2	4.7	0	2.97E+04		(R)LSVEEA\	(R)L S V E E A V A/A G V/V/G G E I Q/E K(L)		199.53	942.996	1884.991	-0.0066	-3.5	4.09	266161	5.68	HUMAN	E9PPU0	Epiplakin
22239	dirMS_041712_NAR_20mM_minus.9827.9827.2	2	4.7	0	1.52E+05		(K)LSELEPG	(K)L S E/L/E/P G T G D/L R(F)		147.82	643.8318	1286.659	-0.0023	-1.8	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
22240	dirMS_041712_NAR_40mM_minus2.11396.11396.3	3	4.7	1	9.72E+04	S13s	(R)SLGKGs/	(R)S L/G K G/s A P\P G P/V P E G S I R(I)	s:N-acetylglucosamine (S)	149.57	637.0132	1705.923	203.1019	11.8	8.46	23993.4	6.77	HUMAN	F5H7H0	Glutathione S-transferase omega-1
22241	dirMS_041712_NAR_40mM_minus2.12032.12032.3	3	4.7	1	1.25E+05		(K)LDVSNV.	(K)L/D\V/S N/V A T D T E/R L E/L K(A)		153.87	601.6499	1802.949	-0.0143	-7.9	4.32	288852.1	5.33	HUMAN	E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein
22242	dirMS_041712_NAR_40mM_minus2.8407.8407.3	3	4.7	1	1.95E+03	S88s	(K)KLsGLN/	(K)K L s G L N A F/D/I A E E L V K(T)	s:N-acetylglucosamine (S)	130.18	650.6771	1746.964	203.0531	-13.5	4.68	26493.4	4.72	HUMAN	K7EIE8	Methyl-CpG binding domain protein 3, isoform CRA_b
22243	dirMS_041712_NAR_50mM_minus2.9444.9444.3	3	4.7	0	6.93E+03	M44m M5:	(K)SGTGIA/	(K)S G T/G/I/A/A m S V M R P E Q I m K(S)	m:Oxidized methionine	121.8	646.9807	1906.955	31.9728	-8.8	8.46	8797.3	9.3	HUMAN	H3BR50	V-type proton ATPase 16 kDa proteolipid subunit
22244	dirMS_041712_NAR_60mM_minus.14568.14568.3	3	4.7	1	2.18E+05	K791k	(R)LKPGkEI	(R)L K/P G k E/D K/L F R(K)	k:Ubiquitin-K	141.12	482.2774	1330.784	114.0335	-6.5	9.7	147219.5	9.31	HUMAN	Q8NHM5-4	Isoform 4 of Lysine-specific demethylase 2B
22245	dirMS_041712_NAR_60mM_minus.8943.8943.2	2	4.7	0	9.67E+05		(K)QEYDES	(K)Q E Y\D|E S G/P S I V/H/R(K)		110.35	758.8539	1516.703	-0.0021	-1.4	4.65	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
22246	dirMS_041712_NAR_120mM_plus.10043.10043.3	3	4.7	0	1.84E+05		(K)LTFYALS	(K)L T/F Y A L S A P E K(L)		105.65	413.8849	1239.662	-0.0218	-17.6	6	89371.2	6.26	HUMAN	E7ESK9	Protein EFR3 homolog B
22247	dirMS_041712_NAR_120mM_plus.4683.4683.3	3	4.7	0	6.09E+05		(R)THSQGG	(R)T H S Q G G/Y/G/S Q G Y K(Y)		74.08	457.2092	1369.613	-0.0001	-0.1	8.2	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
22248	dirMS_041712_NAR_20mM_plus.16428.16428.3	3	4.7	2	6.48E+04	S205s M21	(K)GPsKAQ	(K)G P/s K A Q R G/S/L E H/m/K(L)	s:N-acetylglucosamine (S) m:	185.8	582.2872	1525.79	219.0567	-10.1	9.99	101858.5	5.1	HUMAN	H7C0P0	Centrosome-associated protein CEP250 (Fragment)
22249	dirMS_041712_NAR_20mM_plus.17019.17019.2	2	4.7	0	7.91E+04		(K)VNIIPIIA	(K)V N|I/I/P I/I A K(A)		189.17	490.8283	980.65	-0.001	-1	8.72	51212	5.84	HUMAN	A6NFQ9	Septin-8
22250	dirMS_041712_NAR_20mM_plus.19028.19028.2	2	4.7	0	8.73E+04		(R)EGDVLT	(R)E G D\V/L|T L/L/E S E R(E)		203	680.8536	1360.696	0.0045	3.3	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
22251	dirMS_041712_NAR_20mM_plus.7539.7539.2	2	4.7	0	2.35E+05		(K)VLTPTQ\	(K)V L|T/P/T Q V K(N)		121.68	443.2734	885.54	-0.0009	-1	8.72	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
22252	dirMS_041712_NAR_30mM_plus2.21685.21685.2	2	4.7	0	1.65E+05		(K)AINDAIS	(K)A I|N D\A\I/S Q S G R(V)		169.43	566.2872	1131.575	-0.0082	-7.2	5.88	108208.7	5.5	HUMAN	B9EGE7	ZNF507 protein
22253	dirMS_041712_NAR_30mM_plus2.21749.21749.2	2	4.7	0	1.76E+04		(K)NGFLLD	(K)N G\F\L/L|D G F/P R(T)		169.18	568.3022	1135.59	0.0077	6.7	5.84	21283.1	6.45	HUMAN	F8VY04	Adenylate kinase 2, mitochondrial
22254	dirMS_041712_NAR_30mM_plus2.22284.22284.3	3	4.7	0	2.96E+05		(K)NSSYFVE	(K)N S\S Y F V/E/W I/P N N V K(V)		171.98	566.2872	1696.833	0.0141	8.3	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
22255	dirMS_041712_NAR_40mM_plus2.5511.5511.2	2	4.7	0	1.50E+05		(R)GSNGAF	(R)G S|N/G A F Y K(A)		89.17	422.2033	843.399	-0.0002	-0.3	8.59	66105.7	7.3	HUMAN	A8MQB8	Fragile X mental retardation protein 1
22256	dirMS_041712_NAR_50mM_plus2.9268.9268.3	3	4.7	1	7.87E+04		(K)ITNDFYF	(K)I T\N D/F Y/P E E D G K T K(G)		115.57	552.9296	1656.775	-0.0009	-0.5	4.32	33438.6	4.25	HUMAN	C9JZG1	Eukaryotic translation initiation factor 3 subunit B (Fragment)
22257	dirMS_041712_NAR_60mM_plus.17156.17156.3	3	4.7	0	2.04E+05		(K)THLPGF\	(K)T\H L P G F/V|E/Q/A\E A/L K(A)		147.35	513.9442	1539.817	0.0015	1	5.37	22314.2	9.39	HUMAN	P30044	Peroxiredoxin-5, mitochondrial
22258	dirMS_041712_NAR_60mM_plus.5636.5636.3	3	4.7	0	7.68E+04		(R)TAEHEA.	(R)T A E H E A A Q/Q D L Q/S K(F)		87.8	519.2487	1555.735	-0.0031	-2	4.65	156557.7	5.52	HUMAN	Q86UP2	Kinectin
22259	dirMS_041712_NAR_120mM_minus.17120.17120.4	4	4.69	1	5.17E+05		(K)YYVTIID/	(K)Y Y V T I/I/D/A/P G H\R D F I/K(N)		147.97	477.7556	1908.001	-0.0008	-0.4	6.75	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
22260	dirMS_041712_NAR_120mM_minus.5663.5663.3	3	4.69	0	2.27E+05		(K)ADQEEC	(K)A D/Q|E E/Q I H/P\R(S)		84.5	408.2002	1222.581	0.005	4.1	4.65	43303.4	8.7	HUMAN	F8VRN8	LIM domain and actin-binding protein 1
22261	dirMS_041712_NAR_120mM_minus.6598.6598.3	3	4.69	1	6.21E+04		(K)QMNDE	(K)Q M\N D/E K T/A A/D/Y/K(I)		90.38	471.8802	1413.632	-0.0054	-3.8	4.56	9786.1	5.52	HUMAN	E9PS38	Protein NEDD8-MDP1
22262	dirMS_041712_NAR_120mM_minus.8848.8848.3	3	4.69	0	2.90E+05	M148m	(R)AHSSm\	(R)A H S\S m|V/G|V/N L/P Q/K(A)	m:Oxidized methionine	103.02	461.9056	1367.71	15.9923	-1.9	8.8	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
22263	dirMS_041712_NAR_20mM_minus.13559.13559.2	2	4.69	0	1.33E+05		(K)DIYALISI	(K)D I|Y/A/L/I/S D Q K(H)		186.48	583.3076	1165.61	-0.002	-1.7	4.21	266161	5.68	HUMAN	E9PPU0	Epiplakin
22264	dirMS_041712_NAR_120mM_plus.3698.3698.3	3	4.69	1	2.01E+06	M139m	(R)QREmEE	(R)Q R E m/E E/Q M R(R)	m:Oxidized methionine	61.28	418.1852	1236.546	15.9951	0.1	4.79	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
22265	dirMS_041712_NAR_20mM_plus.12242.12242.2	2	4.69	0	1.54E+05		(K)LLQLVEI	(K)L L/Q/L V/E/D R(G)		157.65	493.2863	985.568	-0.0023	-2.4	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
22266	dirMS_041712_NAR_20mM_plus.18051.18051.2	2	4.69	0	1.31E+05	M153m	(K)VVTYGm	(K)V V T/Y|G m/A N L L T G P K(R)	m:Oxidized methionine	196.32	740.3997	1463.793	15.9995	3.1	8.56	28454.5	6.24	HUMAN	B0AZP7	Synaptic vesicle membrane protein VAT-1 homolog
22267	dirMS_041712_NAR_20mM_plus.18948.18948.2	2	4.69	0	2.13E+04		(K)LLVYEAL	(K)L L/V/Y E A L E/Y A K(R)		201.67	656.3664	1311.719	0.006	4.6	4.53	32535.6	9.19	HUMAN	B4DZW6	Regulator of microtubule dynamics protein 1
22268	dirMS_041712_NAR_30mM_plus2.18020.18020.3	3	4.69	0	1.41E+05		(R)VNPALA	(R)V N P A\L A E/L N/L/R(S)		147.58	403.9019	1209.695	-0.0039	-3.2	5.97	20026.6	4.67	HUMAN	E9PIK5	Ribonuclease inhibitor (Fragment)
22269	dirMS_041712_NAR_30mM_plus2.9294.9294.2	2	4.69	0	6.84E+05		(K)TAVCDIF	(K)T A|V/C D/I/P P R(G)	C:Carbamidomethylation	101.18	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
22270	dirMS_041712_NAR_30mM_plus2.9397.9397.2	2	4.69	0	3.22E+05		(R)LAAVDV	(R)L A|A/V/D\V/S A R(A)		102.88	451.2545	901.51	-0.0084	-9.4	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin
22271	dirMS_041712_NAR_40mM_plus2.16254.16254.3	3	4.69	1	3.74E+05		(R)EPGTSN:	(R)E P G T S N S L L V P D\S/L/R/G T D K(R)		163.12	662.6815	1986.014	0.0161	8.1	4.56	84112.2	6.8	HUMAN	Q04724	Transducin-like enhancer protein 1
22272	dirMS_041712_NAR_40mM_plus2.5837.5837.2	2	4.69	1	1.68E+05		(R)SKQAEE	(R)S K Q A E\E\E|F(-)		92.1	484.2219	967.437	-0.0002	-0.2	4.25	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
22273	dirMS_041712_NAR_40mM_plus2.5913.5913.2	2	4.69	0	2.43E+04		(K)GEGQLG	(K)G E G Q/L/G/P A E R(A)		92.77	507.2532	1013.501	-0.0019	-1.9	4.53	96306.4	6.41	HUMAN	P13639	Elongation factor 2
22274	dirMS_041712_NAR_50mM_plus2.13421.13421.3	3	4.69	0	8.41E+05		(R)VLVVHD	(R)V/L\V/V/H D G F E G L A K(G)		139.35	461.9229	1383.763	-0.0089	-6.5	5.32	18719.9	6.91	HUMAN	F8VP00	6-phosphofructokinase, muscle type (Fragment)
22275	dirMS_041712_NAR_50mM_plus2.17999.17999.3	3	4.69	1	2.83E+05		(K)AKIGLIQ	(K)A K I G L\I Q/F/C L S A/P K(T)	C:Carbamidomethylation	162.33	515.9649	1545.882	-0.002	-1.3	10	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
22276	dirMS_041712_NAR_50mM_plus2.22450.22450.3	3	4.69	1	1.26E+06		(R)GVMLA\	(R)G V/M L A V/D A V I A E/L K K(Q)		195.7	519.6393	1556.908	-0.0047	-3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
22277	dirMS_041712_NAR_50mM_plus2.5387.5387.3	3	4.69	0	3.32E+04	M453m K4	(K)mDVYIC	(K)m D|V/Y I C N D C k(R)	C:Carbamidomethylation m:Oxid	88.92	483.1881	1317.527	130.0225	-10.6	4.21	73680.1	9.14	HUMAN	E9PE19	Nucleosome-remodeling factor subunit BPTF (Fragment)
22278	dirMS_041712_NAR_50mM_plus2.9970.9970.3	3	4.69	1	2.46E+06		(K)ATAVVD	(K)A T/A/V/V D G A F K E V/K(L)		120.07	445.5822	1334.731	0.0006	0.5	6.11	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
22279	dirMS_041712_NAR_120mM_minus.5084.5084.3	3	4.68	1	1.03E+06	M194m	(R)CREmDE	(R)C R/E\m/D E Q I/R(L)	C:Carbamidomethylation m:Oxid	80.33	418.1844	1236.546	15.9927	-1.8	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
22280	dirMS_041712_NAR_20mM_minus.14583.14583.3	3	4.68	0	1.76E+04		(K)LAVEALS	(K)L A V E A L S S/L|D G D/L/A G R(Y)		199.98	529.6163	1586.838	-0.0041	-2.6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
22281	dirMS_041712_NAR_30mM_minus2.16684.16684.2	2	4.68	0	1.62E+05		(R)NPSAAF	(R)N P/S/A/A/F F/C V A R(L)	C:Carbamidomethylation	144.27	620.3013	1239.594	0.0014	1.1	9.75	18626.5	5.64	HUMAN	B8ZZK2	Gamma-glutamylcyclotransferase
22282	dirMS_041712_NAR_50mM_minus2.10098.10098.3	3	4.68	0	1.79E+05	M392m	(K)EmNPAL	(K)E m/N P A/L|G I|D C L H K(G)	C:Carbamidomethylation m:Oxid	125.8	505.2416	1497.719	15.9914	-2.3	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
22283	dirMS_041712_NAR_50mM_minus2.16045.16045.2	2	4.68	1	7.60E+05	M148m	(R)LDLAGR	(R)L D/L A G R D\L T/D\Y|L m K(I)	m:Oxidized methionine	159.95	820.4201	1623.841	15.9919	-1.9	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
22284	dirMS_041712_NAR_60mM_minus.11064.11064.3	3	4.68	1	4.59E+05		(K)GSITISAI	(K)G S/I/T/I/S A E E I K D N R(V)		121.13	511.6045	1532.792	0.0075	4.9	4.68	27142.4	5.34	HUMAN	E5RG68	Copine-3 (Fragment)
22285	dirMS_041712_NAR_60mM_minus.14834.14834.3	3	4.68	1	2.31E+05	M284m	(R)GLLLRG/	(R)G L/L L R G A V D G I L H m F|T/P\K(L)	m:Oxidized methionine	142.98	652.0241	1938.099	15.9584	-18.7	8.76	81798.7	5.68	HUMAN	Q9H1V8	Sodium-dependent neutral amino acid transporter SLC6A17
22286	dirMS_041712_NAR_60mM_minus.7821.7821.3	3	4.68	1	3.76E+05	M230m M:	(R)mSmKE\	(R)m S\m K\E V D E\Q|m|L N V|Q N K(N)	m:Oxidized methionine	103.82	657.9647	1923.897	47.9823	-1.3	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
22287	dirMS_041712_NAR_60mM_minus.8716.8716.3	3	4.68	0	3.02E+05		(K)EFHLNE!	(K)E\F H L N E S/G D/P S/S K(S)		108.08	482.8882	1446.65	0.0005	0.3	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
22288	dirMS_041712_NAR_60mM_minus.9181.9181.3	3	4.68	1	1.00E+05		(K)ELQAAG	(K)E L/Q|A A\G K S/P E D/L E R(L)		110.7	514.9252	1542.776	-0.0148	-9.6	4.41	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
22289	dirMS_041712_NAR_120mM_plus.20267.20267.3	3	4.68	0	5.28E+05	S986s	(R)IIHsLIAE	(R)I I H s/L I A/E F S L E E L K(K)	s:Phosphorylated S	159.85	607.9762	1741.974	79.9406	-14.1	4.75	149959.2	6.73	HUMAN	C9JKF1	Sterile alpha motif domain-containing protein 9 (Fragment)
22290	dirMS_041712_NAR_120mM_plus.8544.8544.3	3	4.68	0	8.76E+05		(K)QHTFVE	(K)Q H T F\V/E/T/E/S V R(Y)		97.77	444.8857	1332.654	-0.0117	-8.8	5.4	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
22291	dirMS_041712_NAR_20mM_plus.16585.16585.3	3	4.68	0	6.48E+04	T232t	(R)LLVVDPI	(R)L L\V V/D/P E t D E/H F/K(R)	t:N-acetylglucosamine (T)	185.8	582.2872	1541.785	203.0624	-9.7	4.31	36381	8.8	HUMAN	D3DU85	Na(+)/H(+) exchange regulatory cofactor NHE-RF2
22292	dirMS_041712_NAR_30mM_plus2.6746.6746.2	2	4.68	0	2.53E+05	M529m	(R)MGLSmI	(R)M/G|L/S m E R(M)	m:Oxidized methionine	89.8	420.1949	823.38	16.0025	9	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
22293	dirMS_041712_NAR_40mM_plus2.6136.6136.2	2	4.68	0	8.59E+03	M157m	(R)MGYmD	(R)M/G/Y m D|P R(E)	m:Oxidized methionine	94.83	443.1854	869.364	15.9991	4.7	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
22294	dirMS_041712_NAR_50mM_plus2.13942.13942.3	3	4.68	0	5.93E+05		(K)QMVID\	(K)Q M V I D/V/L H P\G/K(A)		142.07	412.894	1236.677	-0.0095	-7.6	6.74	32886.5	10.63	HUMAN	E7EPK6	40S ribosomal protein S24
22295	dirMS_041712_NAR_50mM_plus2.8424.8424.3	3	4.68	1	6.44E+04		(K)IALEDVP	(K)I/A|L E D V/P E K Q K(N)		111.17	423.9063	1269.705	-0.0005	-0.4	4.68	55527.8	6.3	HUMAN	O43148	mRNA cap guanine-N7 methyltransferase
22296	dirMS_041712_NAR_60mM_plus.10950.10950.3	3	4.68	1	2.07E+05		(R)VKYETEL	(R)V K Y E T E/L/A/M R(Q)		114.87	413.8859	1239.64	0.003	2.4	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
22297	dirMS_041712_NAR_60mM_plus.8276.8276.3	3	4.68	1	4.58E+05		(K)AALSEEE	(K)A/A|L/S E E E L E K K(S)		101.08	416.221	1246.652	-0.0041	-3.3	4.49	176357.7	5.25	HUMAN	D3DNT2	Eukaryotic translation initiation factor 4 gamma 1
22298	dirMS_041712_NAR_60mM_plus.8617.8617.2	2	4.68	0	4.27E+05		(R)FACHSA:	(R)F A/C H/S/A S/L T\V R(N)	C:Carbamidomethylation	102.73	624.8118	1248.615	0.001	0.8	9.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
22299	dirMS_041712_NAR_120mM_minus.13620.13620.3	3	4.67	2	9.83E+05		(R)AQKDEE	(R)A Q|K/D/E E/K M E I Q/E/I Q L/K(E)		128.13	654.0058	1960.006	-0.0027	-1.4	4.58	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
22300	dirMS_041712_NAR_120mM_minus.4878.4878.3	3	4.67	1	5.47E+05		(K)AGADEE	(K)A/G/A D|E E R/A E T A R(L)		77.67	425.8687	1275.592	-0.0008	-0.7	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
22301	dirMS_041712_NAR_120mM_minus.9273.9273.3	3	4.67	0	1.47E+05	T148t	(R)IASGEEC	(R)I A S/G/E E/Q/t Y R(K)	t:N-acetylglucosamine (T)	104.9	452.8778	1153.548	203.0705	-6.6	4.53	55929	8.6	HUMAN	Q0VAM2	Ras-GEF domain-containing family member 1B
22302	dirMS_041712_NAR_20mM_minus.11851.11851.2	2	4.67	0	1.25E+05	M98m	(R)TLTIVDT	(R)T L/T I/V D T/G I G/m T K(A)	m:Oxidized methionine	167.03	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
22303	dirMS_041712_NAR_50mM_minus2.10120.10120.3	3	4.67	1	9.68E+04		(R)VGEPVA	(R)V/G E/P/V/A/L S E E E R L K(L)		125.5	519.2824	1555.833	0	0	4.49	8516.9	5.1	HUMAN	E9PIL8	Splicing factor 3B subunit 2 (Fragment)
22304	dirMS_041712_NAR_50mM_minus2.10910.10910.3	3	4.67	1	1.10E+04		(K)ALELDPI	(K)A L/E/L/D/P D N E T Y K S N L K(I)		130.67	617.3102	1849.918	-0.0018	-0.9	4.32	34290.7	4.81	HUMAN	O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha
22305	dirMS_041712_NAR_50mM_minus2.7354.7354.3	3	4.67	0	7.38E+04		(K)QLAVAE	(K)Q L\A/V/A\E G K/P P E A/P K(G)		108.58	478.9368	1434.795	0.0007	0.5	6.14	24364.9	9.64	HUMAN	H0YIP0	Methionine--tRNA ligase, cytoplasmic (Fragment)
22306	dirMS_041712_NAR_50mM_minus2.9747.9747.3	3	4.67	0	8.67E+04	M73m	(K)NFVVVn	(K)N F V/V V/m V T K P K(A)	m:Oxidized methionine	123.18	426.5785	1261.734	15.9873	-6	10	43227.5	4.79	HUMAN	P54727	UV excision repair protein RAD23 homolog B
22307	dirMS_041712_NAR_60mM_minus.15609.15609.3	3	4.67	1	3.12E+05		(K)VAAIRGI	(K)V/A/A/I R G E V T\A|A D|L F N S R(V)		147.35	597.3237	1789.956	0.001	0.6	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
22308	dirMS_041712_NAR_60mM_minus.17384.17384.2	2	4.67	1	1.82E+05		(R)KAPSDL\	(R)K|A/P S D L Y|Q I I\L\K(A)		156.37	694.9105	1388.815	-0.0011	-0.8	8.5	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
22309	dirMS_041712_NAR_60mM_minus.8022.8022.3	3	4.67	1	3.66E+05	M230m M:	(R)mSmKE\	(R)m S m K E V/D E\Q m/L/N V\Q/N K(N)	m:Oxidized methionine	103.87	657.9647	1923.897	47.9823	-1.3	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
22310	dirMS_041712_NAR_20mM_plus.17753.17753.2	2	4.67	0	6.39E+04		(K)TGLIDYN	(K)T G\L|I/D Y N Q/L/A L T A R(L)		193.7	774.9178	1548.838	-0.0097	-6.3	5.5	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
22311	dirMS_041712_NAR_30mM_plus2.19309.19309.2	2	4.67	0	2.05E+05		(K)NFSGAE	(K)N F|S/G A/E/L E/G L V R(A)		155.2	646.3361	1291.664	0.0008	0.6	4.53	71924.9	6.25	HUMAN	B4DFA2	Vesicle-fusing ATPase
22312	dirMS_041712_NAR_30mM_plus2.7844.7844.3	3	4.67	0	1.54E+05		(K)SNVSDA	(K)S N/V S/D A/V/A Q S T/R(I)		94.92	412.2004	1234.602	-0.0156	-12.6	5.55	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
22313	dirMS_041712_NAR_40mM_plus2.11081.11081.3	3	4.67	1	1.63E+05	S13s	(R)RsAFPTE	(R)R\s A F/P/T E A R(G)	s:N-acetylglucosamine (S)	131.92	413.2151	1034.538	203.093	11	9.6	35633.2	10.94	HUMAN	J3KT39	Uncharacterized protein
22314	dirMS_041712_NAR_40mM_plus2.14036.14036.3	3	4.67	0	8.09E+04		(K)TVVSHSI	(K)T V/V S H S L\T\T L/G L E V\A K(Q)		149.07	552.3142	1654.937	-0.0094	-5.7	6.41	76061.2	7.76	HUMAN	P42166	Lamina-associated polypeptide 2, isoform alpha
22315	dirMS_041712_NAR_50mM_plus2.10660.10660.2	2	4.67	1	1.49E+06		(R)DGKLVS	(R)D G/K/L|V S E/S S D V/L\P K(-)		122.87	737.3925	1473.78	-0.0018	-1.2	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
22316	dirMS_041712_NAR_50mM_plus2.12985.12985.3	3	4.67	0	5.97E+05		(R)FDAERP'	(R)F D/A E R P V D C S V/I/V V N/K(Q)	C:Carbamidomethylation	135.82	616.6476	1847.932	-0.0038	-2	4.56	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
22317	dirMS_041712_NAR_50mM_plus2.20456.20456.3	3	4.67	1	1.59E+05		(R)QALQDL	(R)Q A/L Q/D L/L/S E Y/M G N A G R K(E)		176.35	631.9902	1893.949	0.0073	3.9	6.07	89360.3	5.63	HUMAN	F8W845	Catenin alpha-1
22318	dirMS_041712_NAR_50mM_plus2.20879.20879.3	3	4.67	1	4.35E+04		(R)ITSEAED	(R)I/T S E A/E D L\V/A N F F P K/K(L)		178	603.6541	1808.943	0.0049	2.7	4.68	14931.6	5.53	HUMAN	B7Z8D3	Proteasome activator complex subunit 3
22319	dirMS_041712_NAR_50mM_plus2.8693.8693.3	3	4.67	1	2.37E+04		(R)GGSDDS	(R)G G/S D/D\S S K D/P I/D V N Y/E K(L)		114.08	609.2765	1825.809	0.0063	3.5	4.03	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
22320	dirMS_041712_NAR_60mM_plus.4741.4741.3	3	4.67	1	3.16E+05		(K)AGADEE	(K)A/G A/D E/E R A/E T A R(L)		79.4	425.868	1275.592	-0.0029	-2.3	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
22321	dirMS_041712_NAR_120mM_minus.13151.13151.4	4	4.66	2	1.36E+06		(R)AQKDEE	(R)A Q K D E E/K M E\I\Q/E/I Q L K(E)		126.48	490.7539	1960.006	-0.0118	-6	4.58	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
22322	dirMS_041712_NAR_30mM_minus2.4967.4967.2	2	4.66	0	1.22E+05		(R)ENDEFC	(R)E N/D/E F/C/K(M)	C:Carbamidomethylation	80.23	471.188	941.367	0.0018	1.9	4.14	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
22323	dirMS_041712_NAR_60mM_minus.12424.12424.3	3	4.66	0	1.82E+05		(K)QADLYIS	(K)Q A D L/Y/I/S E/G L H P/R(I)		129.37	500.2603	1498.765	0.0015	1	5.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
22324	dirMS_041712_NAR_60mM_minus.15744.15744.3	3	4.66	1	3.91E+05		(K)KANLQII	(K)K A N L Q I D\Q\I/N/T/D L N L E R(S)		148.05	666.6911	1998.061	-0.0027	-1.3	4.56	227783.5	5.5	HUMAN	P35579	Myosin-9
22325	dirMS_041712_NAR_60mM_minus.18597.18597.3	3	4.66	0	1.21E+05		(R)IDILDSA	(R)I/D/I|L/D S A L L/R/P G R(I)		165.17	480.2832	1438.838	-0.0026	-1.8	5.96	44954.5	8.44	HUMAN	A8K3Z3	26S protease regulatory subunit 8
22326	dirMS_041712_NAR_120mM_plus.15304.15304.3	3	4.66	1	5.79E+05		(K)NREPVQ	(K)N R E P\V\Q/L|E/T/L/S I R(G)		133.42	518.9599	1554.86	0.0053	3.4	6.14	8392.6	11.84	HUMAN	J3QLI9	Small nuclear ribonucleoprotein Sm D1
22327	dirMS_041712_NAR_120mM_plus.4157.4157.2	2	4.66	1	1.45E+06	M310m	(R)TKTEISE	(R)T/K|T E/I/S E m N R(N)	m:Oxidized methionine	69.8	612.7976	1208.594	15.994	-0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
22328	dirMS_041712_NAR_120mM_plus.8089.8089.2	2	4.66	0	4.29E+05		(K)AGEVFIH	(K)A/G E/V/F/I/H|K(D)		96.3	450.7531	900.494	0.0051	5.7	6.79	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
22329	dirMS_041712_NAR_120mM_plus.8626.8626.3	3	4.66	0	3.43E+05	S192s	(K)sNHEQE	(K)s/N H E Q/E V/N T/L R(C)	s:Phosphorylated S	97.83	469.5419	1326.64	79.9715	3.7	5.38	48662.6	4.84	HUMAN	Q15323	Keratin, type I cuticular Ha1
22330	dirMS_041712_NAR_20mM_plus.11936.11936.2	2	4.66	0	4.20E+04	M108m	(K)LATQLT(	(K)L A T Q\L|T/G\P V m P V/R(N)	m:Oxidized methionine	155.55	699.8907	1382.782	15.9917	-2.3	9.75	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
22331	dirMS_041712_NAR_20mM_plus.15110.15110.2	2	4.66	0	6.42E+04	T5t	(R)AtLSAAF	(R)A t/L/S A A P S N P R(L)	t:N-acetylglucosamine (T)	175.7	644.346	1084.574	203.1102	23.9	9.79	11616.7	11.75	HUMAN	P19875	C-X-C motif chemokine 2
22332	dirMS_041712_NAR_20mM_plus.15181.15181.2	2	4.66	0	8.68E+04		(K)GVEGLII	(K)G V\E G L|I|D|I/E\N P\N R(V)		176.27	713.3667	1425.733	-0.0071	-5	4.14	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
22333	dirMS_041712_NAR_20mM_plus.15926.15926.2	2	4.66	0	1.02E+04		(K)ALTLIAG	(K)A L\T/L/I A/G S P L K(I)		180.78	542.3395	1083.677	-0.0055	-5.1	8.8	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
22334	dirMS_041712_NAR_30mM_plus2.21723.21723.2	2	4.66	0	1.15E+05		(R)IITLAGP'	(R)I I/T/L/A/G/P T N A I F K(A)		168.47	679.9016	1358.804	-0.0083	-6.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
22335	dirMS_041712_NAR_50mM_plus2.18006.18006.3	3	4.66	0	2.70E+04		(R)TIRPMD	(R)T I|R P M D\M\E|T|I/E A S/V M K(T)		163.03	617.9711	1851.901	-0.0026	-1.4	4.68	39089.4	7.08	HUMAN	C9J634	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial
22336	dirMS_041712_NAR_50mM_plus2.20899.20899.3	3	4.66	0	3.09E+05		(K)HSQFIG\	(K)H S Q F I\G\Y|P/I/T L F V E K(E)		179.23	593.6536	1778.948	-0.0013	-0.8	6.75	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
22337	dirMS_041712_NAR_60mM_plus.11179.11179.3	3	4.66	1	4.49E+05	M230m M:	(R)mSmKE\	(R)m S m K E V D\E Q|M|L/N\V\Q N K(N)	m:Oxidized methionine	115.73	652.6326	1923.897	31.986	-2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
22338	dirMS_041712_NAR_60mM_plus.12697.12697.3	3	4.66	0	5.74E+05		(K)GSYSLSH	(K)G S/Y/S L/S H V\Y T P N D/V R(M)		123.12	565.6098	1694.813	0.0016	0.9	6.74	63566.6	6.3	HUMAN	P07686	Beta-hexosaminidase subunit beta
22339	dirMS_041712_NAR_60mM_plus.7816.7816.3	3	4.66	1	1.31E+06		(K)KGTVEG	(K)K\G T V E\G/F\E|P A D N K(C)		98.42	464.5649	1391.68	0	0	4.68	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
22340	dirMS_041712_NAR_60mM_plus.8063.8063.3	3	4.66	0	8.71E+05		(K)VNTLIRP	(K)V/N/T/L/I R P D G E/K(K)		100.73	414.5622	1241.685	-0.0128	-10.3	6.04	22029.9	10.62	HUMAN	A8MUS3	60S ribosomal protein L23a

22341	dirMS_041712_NAR_120mM_minus.10531.10531.2	2	4.65	0	2.67E+05	M103m M:	(R)LmmDFI	(R)L/m m D/F/D G/K(N)	m:Oxidized methionine	112.05	494.7161	956.422	32.0033	13.7	4.21	64554.4	7.74	HUMAN	A0AV96	RNA-binding protein 47
22342	dirMS_041712_NAR_120mM_minus.14788.14788.4	4	4.65	0	1.44E+04	T29t	(R)ITEANLT	(R)I T/E A N L T G H E/E/K/P t A R(C)	t:N-acetylglucosamine (T)	134.6	493.2474	1766.903	203.0646	-7.5	5.5	5441.8	4.68	HUMAN	E9PKU3	Ribosomal protein S6 kinase alpha-4
22343	dirMS_041712_NAR_120mM_minus.5815.5815.3	3	4.65	0	4.17E+03	S1068s	(R)HITESVN	(R)H I T E/S V/N|s I/R(R)	s:Phosphorylated S	84.23	412.5267	1155.612	79.9539	-10.1	6.75	132001.8	5.66	HUMAN	G5E960	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3
22344	dirMS_041712_NAR_120mM_minus.7552.7552.3	3	4.65	1	2.18E+05		(K)SKAEAES	(K)S K A E A\E/S\L/Y/Q S K(Y)		95.33	447.558	1340.669	-0.0098	-7.3	5.86	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
22345	dirMS_041712_NAR_120mM_minus.8289.8289.3	3	4.65	0	3.55E+05		(R)AAHSEG	(R)A A H S E G N T\T/A/G L/D/M R(E)		99.15	510.9036	1530.697	-0.0003	-0.2	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
22346	dirMS_041712_NAR_20mM_minus.13115.13115.2	2	4.65	0	3.25E+05	M35m	(K)NDIAINE	(K)N D I|A\I|N E L m K(R)	m:Oxidized methionine	181.9	588.7948	1160.598	15.9843	-9	4.37	28354	7.11	HUMAN	B4DXI8	26S proteasome non-ATPase regulatory subunit 7
22347	dirMS_041712_NAR_30mM_minus2.15233.15233.2	2	4.65	0	7.26E+05	M2249m	(K)MSIYQA	(K)M S|I/Y/Q A m W K(G)	m:Oxidized methionine	135.75	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
22348	dirMS_041712_NAR_30mM_minus2.16869.16869.2	2	4.65	0	3.12E+05		(K)LNLGGD	(K)L/N|L|G G\D F/I K(E)		146.4	488.7803	976.546	0.0071	7.3	5.84	6447	4.24	HUMAN	H7C0D5	Protein YIPF4 (Fragment)
22349	dirMS_041712_NAR_30mM_minus2.17969.17969.2	2	4.65	0	1.70E+05		(R)YVANIFF	(R)Y V/A N/I\F P Y K(G)		151.43	557.7997	1114.593	-0.001	-0.9	8.5	23312.3	5.53	HUMAN	B4DFH3	Inorganic pyrophosphatase 2, mitochondrial
22350	dirMS_041712_NAR_50mM_minus2.13343.13343.3	3	4.65	1	1.92E+05	M17m	(K)GAEEmE	(K)G A/E/E/m E T V/I/P V D V M R R(A)	m:Oxidized methionine	143.83	616.6435	1831.904	16.0119	9.2	4.41	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
22351	dirMS_041712_NAR_50mM_minus2.13454.13454.3	3	4.65	1	1.37E+05		(K)IDSRLEQ	(K)I/D S R/L E Q\Y/T/S A I E G T K(S)		144.62	604.3145	1810.918	0.0108	6	4.68	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
22352	dirMS_041712_NAR_50mM_minus2.5998.5998.3	3	4.65	1	2.09E+04		(R)VVSSIEC	(R)V V|S S/I E Q K T E G A E K(K)		96.9	502.2662	1504.785	-0.0013	-0.9	4.79	8491.4	6.28	HUMAN	E5RIR4	14-3-3 protein zeta/delta (Fragment)
22353	dirMS_041712_NAR_50mM_minus2.9436.9436.3	3	4.65	1	1.88E+04	M127m T1	(K)LmtVmC	(K)L m t V/m/G L/R E S\A F(-)	m:Oxidized methionine t:N-a	122.27	530.5989	1354.686	235.0964	17.1	6	16127.5	8.87	HUMAN	H0YBL8	ATP-binding cassette sub-family A member 10 (Fragment)
22354	dirMS_041712_NAR_60mM_minus.12155.12155.3	3	4.65	1	3.77E+05		(K)AAAGKA	(K)A A|A G K A E L\E|L E/L G R(I)		127.53	476.5974	1427.785	-0.0076	-5.3	4.79	533778	5.74	HUMAN	Q15149	Plectin
22355	dirMS_041712_NAR_60mM_minus.18663.18663.3	3	4.65	1	1.17E+05		(K)IILDLISE	(K)I I/L/D L/I S E S P I K G R(A)		166	518.6442	1553.926	-0.0081	-5.2	6.07	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
22356	dirMS_041712_NAR_60mM_minus.19535.19535.3	3	4.65	1	9.88E+04		(R)VISGVLC	(R)V I/S G V L Q/L G N I V\F K/K(E)		175.05	539.0023	1614.994	-0.0018	-1.1	10	227783.5	5.5	HUMAN	P35579	Myosin-9
22357	dirMS_041712_NAR_60mM_minus.8367.8367.3	3	4.65	1	1.55E+05		(R)TPPGVT	(R)T P|P G V T F S/A K D N K(G)		107.03	454.5795	1361.706	0.018	13.2	8.26	78036.1	4.83	HUMAN	Q7Z6P3	Ras-related protein Rab-44
22358	dirMS_041712_NAR_20mM_plus.11288.11288.3	3	4.65	0	1.10E+05		(R)GCITIIG(	(R)G C I\T I I G G G D/T/A/T C C A K(W)	C:Carbamidomethylation	150.23	585.5999	1754.787	-0.0019	-1.1	5.84	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
22359	dirMS_041712_NAR_20mM_plus.14628.14628.3	3	4.65	0	1.30E+05		(R)LQEAGIL	(R)L Q E A G I L/S/A/E/E L Q R(L)		172.17	519.6131	1556.828	-0.0031	-2	4.25	533778	5.74	HUMAN	Q15149	Plectin
22360	dirMS_041712_NAR_20mM_plus.6939.6939.2	2	4.65	0	8.44E+04	M29m	(K)IVQmTE	(K)I V Q m/T E/A E V R(G)	m:Oxidized methionine	114.35	596.3035	1175.609	15.9908	-3.4	4.53	14493.5	5.23	HUMAN	C9J9S3	Serine/threonine-protein phosphatase (Fragment)
22361	dirMS_041712_NAR_30mM_plus2.20773.20773.2	2	4.65	0	1.27E+05		(K)SVVTSIF	(K)S V|V/T/S I F G V K(N)		162.85	518.799	1036.604	-0.013	-12.5	8.47	132902.3	5.82	HUMAN	J3KR24	Isoleucine--tRNA ligase, cytoplasmic
22362	dirMS_041712_NAR_30mM_plus2.4862.4862.2	2	4.65	1	2.34E+05		(R)NTKGGD	(R)N T/K G G D A\P\A|A/G/E/D A(-)		77	637.286	1273.565	-0.0008	-0.6	4.03	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
22363	dirMS_041712_NAR_30mM_plus2.9478.9478.2	2	4.65	0	2.50E+05		(R)LLTYNA	(R)L L/T/Y/N\A A R(L)		103.73	461.2586	921.515	-0.0053	-5.8	8.75	36309.7	5.86	HUMAN	B4DQ51	Short/branched chain-specific acyl-CoA dehydrogenase, mitochondrial
22364	dirMS_041712_NAR_40mM_plus2.13536.13536.3	3	4.65	0	1.42E+04		(K)LTEVPVE	(K)L/T/E V|P V E P V L T V H P E\S K(S)		146.12	625.3454	1874.027	-0.0053	-2.8	4.75	81726.4	6.71	HUMAN	Q9H307	Pinin
22365	dirMS_041712_NAR_40mM_plus2.6460.6460.2	2	4.65	0	1.35E+05		(K)SLESINSI	(K)S L/E|S I N/S R(L)		96.88	453.2358	905.469	-0.0044	-4.8	5.72	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
22366	dirMS_041712_NAR_40mM_plus2.9711.9711.3	3	4.65	0	2.32E+05		(R)AAEDPV	(R)A A\E D|P/V A/A A P R P L P A G G R(L)		121.05	572.6438	1715.919	-0.0019	-1.1	6.12	73966.7	10.21	HUMAN	B3KWK6	Alpha-L-iduronidase
22367	dirMS_041712_NAR_50mM_plus2.9726.9726.3	3	4.65	0	5.15E+05		(K)GAVDG(	(K)G A\V\D|G G L|S\I P H S T K(R)		117.32	446.9057	1338.701	0.0013	1	6.74	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
22368	dirMS_041712_NAR_50mM_plus2.9877.9877.3	3	4.65	0	1.07E+05	M180m	(R)VVVLmC	(R)V V|V|L/m G S T S D L G H C E K(I)	C:Carbamidomethylation m:Oxid	119.17	583.2837	1731.84	15.9961	0.7	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
22369	dirMS_041712_NAR_60mM_plus.17390.17390.3	3	4.65	2	3.44E+05		(R)DYVRLF(	(R)D Y V R L F|G I K C A K(C)	C:Carbamidomethylation	147.37	490.5979	1469.793	-0.0142	-9.7	9.7	16984.2	8.11	HUMAN	H0YKY2	Insulin gene enhancer protein ISL-2 (Fragment)
22370	dirMS_041712_NAR_60mM_plus.19085.19085.3	3	4.65	0	1.04E+04		(K)SLLKPFC	(K)S L/L/K P F C A A L L K(H)	C:Carbamidomethylation	157.23	454.2724	1360.802	0.0005	0.4	10	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
22371	dirMS_041712_NAR_60mM_plus.8968.8968.3	3	4.65	1	5.09E+05	M194m M:	(K)IAVSKmI	(K)I/A/V S K m M m V L G A/K(W)	m:Oxidized methionine	104.88	470.9225	1378.762	31.9911	0.9	10	218583	5.58	HUMAN	F5GWX5	Chromodomain-helicase-DNA-binding protein 4
22372	dirMS_041712_NAR_120mM_minus.11268.11268.3	3	4.64	0	1.39E+05		(R)GFCLPPI	(R)G F/C L/P/P H C S R(G)	C:Carbamidomethylation	114.32	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
22373	dirMS_041712_NAR_120mM_minus.14086.14086.3	3	4.64	0	4.54E+05		(K)NRPTSIS	(K)N R P T S I\S\W/D/G L D S G K(L)		130.58	544.9369	1632.798	-0.0015	-0.9	5.96	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
22374	dirMS_041712_NAR_20mM_minus.7573.7573.2	2	4.64	0	8.36E+05	M239m	(K)EVDEQn	(K)E V/D/E\Q m\L|N V Q/N K(N)	m:Oxidized methionine	124.27	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
22375	dirMS_041712_NAR_20mM_minus.9646.9646.2	2	4.64	0	5.91E+03		(K)DVNAAL	(K)D V/N A/A|I/A T I K(T)		146.73	508.2919	1015.578	-0.0017	-1.7	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
22376	dirMS_041712_NAR_30mM_minus2.19824.19824.2	2	4.64	0	7.44E+03		(R)EMEIWL	(R)E M/E I/W L S V|K(E)		165.08	567.804	1134.586	0.0144	12.7	4.53	60014.5	4.62	HUMAN	Q8N0Z9	V-set and immunoglobulin domain-containing protein 10
22377	dirMS_041712_NAR_50mM_minus2.5680.5680.3	3	4.64	0	1.44E+05		(K)FDDQGD	(K)F D|D Q G D S E G S V Y F(-)		92.85	489.1898	1465.575	-0.0205	-14	3.38	29631.3	10.25	HUMAN	Q9H607	Occludin/ELL domain-containing protein 1
22378	dirMS_041712_NAR_60mM_minus.12228.12228.3	3	4.64	1	2.17E+05		(K)SGYLAGI	(K)S G Y/L|A G D/K/L L P Q R(V)		127.73	473.258	1417.78	-0.0203	-14.3	8.31	67933	6.08	HUMAN	P26038	Moesin
22379	dirMS_041712_NAR_60mM_minus.18834.18834.3	3	4.64	0	2.50E+05		(K)LHDNLII	(K)L H D N L\I I/S/D L E N T V/K(K)		166.18	575.3117	1723.922	-0.0019	-1.1	4.54	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
22380	dirMS_041712_NAR_60mM_minus.19334.19334.3	3	4.64	1	1.56E+04		(K)AKINEA\	(K)A K I N E A\V/E/C/L L S L/K(A)	C:Carbamidomethylation	172.08	529.9633	1587.878	-0.0021	-1.3	6.18	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
22381	dirMS_041712_NAR_60mM_minus.7380.7380.3	3	4.64	1	2.06E+04		(R)IVDGKV	(R)I/V|D G K/V V/S E T N D T K(V)		100.4	502.2642	1504.785	-0.0073	-4.8	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
22382	dirMS_041712_NAR_60mM_minus.7583.7583.3	3	4.64	0	4.90E+04		(R)QSLGHP	(R)Q S L G H P P P E/P G/P D R(V)		101.33	495.2483	1483.729	0.0015	1	5.32	12758.7	4.21	HUMAN	C9J830	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
22383	dirMS_041712_NAR_120mM_plus.9242.9242.3	3	4.64	0	5.51E+05		(K)SPQYCQ	(K)S P Q|Y C/Q V/I/H R(L)	C:Carbamidomethylation	102.12	429.8865	1287.626	0.0187	14.5	8.49	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
22384	dirMS_041712_NAR_20mM_plus.18060.18060.3	3	4.64	0	1.71E+05		(R)LSVLGAI	(R)L S\V L G A/I/T/S V Q Q/R(L)		196.13	457.9354	1371.795	-0.0038	-2.8	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
22385	dirMS_041712_NAR_20mM_plus.9185.9185.2	2	4.64	0	7.02E+04		(K)ATAVVD	(K)A T A/V/V D G A F K(E)		134.42	489.7674	978.525	0.0021	2.1	5.88	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
22386	dirMS_041712_NAR_30mM_plus2.20203.20203.2	2	4.64	0	1.37E+05		(R)MLDMG	(R)M L\D\M/G/F E/P Q I R(K)		159.15	668.8241	1336.639	0.0021	1.6	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
22387	dirMS_041712_NAR_30mM_plus2.4260.4260.2	2	4.64	0	4.77E+05	M558m	(R)mGANN	(R)m/G A/N/N L E R(M)	m:Oxidized methionine	70.22	460.7158	904.431	15.9938	-1.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
22388	dirMS_041712_NAR_40mM_plus2.7956.7956.2	2	4.64	0	3.62E+03		(R)LFEQNV	(R)L/F/E Q N V/Q R(S)		106.87	517.2733	1033.543	-0.0032	-3.1	6	21184.9	7.82	HUMAN	P61081	NEDD8-conjugating enzyme Ubc12
22389	dirMS_041712_NAR_40mM_plus2.9206.9206.3	3	4.64	0	7.25E+03	M115m	(R)VmLGET	(R)V m/L G E|T N/P/A D S K/P G T I R(G)	m:Oxidized methionine	117.13	601.3077	1785.916	15.9922	-1.5	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
22390	dirMS_041712_NAR_50mM_plus2.10772.10772.3	3	4.64	1	2.12E+05		(K)AQALRD	(K)A Q/A L/R D N S T/M/G Y M M A/K(K)		123.72	596.6125	1787.824	-0.0008	-0.4	8.63	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
22391	dirMS_041712_NAR_50mM_plus2.12820.12820.3	3	4.64	1	4.62E+04	M1m	(-)mDIPLDL	(-)m D/I P\L D L S/S S A\G S G\K R R(R)	m:Oxidized methionine	135.27	602.6508	1789.922	16.0153	11.3	8.5	28000.3	9.32	HUMAN	A6NE42	Homeobox protein TGIF1
22392	dirMS_041712_NAR_50mM_plus2.20672.20672.3	3	4.64	1	2.60E+05		(R)NLQNLL	(R)N L|Q N/L/L/I L T A I K A D R(T)		178.05	566.0067	1696.012	-0.006	-3.6	8.75	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
22393	dirMS_041712_NAR_50mM_plus2.6252.6252.3	3	4.64	0	1.09E+05	M39m K43	(K)TPLQES/	(K)T P|L Q E S A T m A V V k(G)	m:Oxidized methionine k:Ub	96.73	502.2651	1374.73	130.051	8.8	5.66	54205.2	9.51	HUMAN	J3KTQ2	ATP-dependent DNA helicase Q5 (Fragment)
22394	dirMS_041712_NAR_60mM_plus.20185.20185.3	3	4.64	2	2.62E+05	M297m K3	(R)KVmVD(	(R)K V m/V D G D/I P P R/V k(K)	m:Oxidized methionine k:Ub	165.83	528.6238	1453.82	130.0373	-0.3	8.59	80924.6	8.42	HUMAN	Q8WWL2	Protein spire homolog 2
22395	dirMS_041712_NAR_120mM_minus.4400.4400.3	3	4.63	0	1.34E+05		(R)QELMQ\	(R)Q E\L M Q/V/H G E K(R)		72.95	400.1991	1198.589	-0.0057	-4.8	5.4	167865.2	5.34	HUMAN	Q08378	Golgin subfamily A member 3
22396	dirMS_041712_NAR_120mM_minus.5558.5558.2	2	4.63	1	6.56E+05		(K)CDVDIRI	(K)C/D V/D|I R/K(D)	C:Carbamidomethylation	84.02	453.2291	905.451	0	0	5.96	42675.9	5.9	HUMAN	I3L3I4	Actin, cytoplasmic 2, N-terminally processed
22397	dirMS_041712_NAR_120mM_minus.7194.7194.3	3	4.63	1	1.49E+06		(R)CREMDE	(R)C R\E\M D|E/Q/I/R(L)	C:Carbamidomethylation	93.97	412.8591	1236.546	0.0168	13.6	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
22398	dirMS_041712_NAR_20mM_minus.13330.13330.2	2	4.63	0	7.15E+04		(K)SILFVPT	(K)S I\L|F/V/P T S A/P R(G)		183.58	594.3411	1187.678	-0.0034	-2.8	9.47	92752.5	4.76	HUMAN	P14625	Endoplasmin
22399	dirMS_041712_NAR_30mM_minus2.15890.15890.2	2	4.63	0	2.59E+04		(R)ALQASA	(R)A L Q|A\S A/L/N/A W R(G)		139.9	600.8272	1200.648	-0.0013	-1	9.79	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
22400	dirMS_041712_NAR_30mM_minus2.20250.20250.2	2	4.63	0	5.37E+03		(R)VIFGLFG	(R)V I|F|G L F G K(T)		172.22	440.768	880.529	-0.0004	-0.4	8.72	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
22401	dirMS_041712_NAR_30mM_minus2.6118.6118.2	2	4.63	0	9.83E+04		(R)EAEEVYI	(R)E A/E/E/V/Y R(N)		87.62	448.2136	895.416	0.0043	4.8	4.25	54793.4	10.51	HUMAN	B7Z4Q3	Putative RNA-binding protein Luc7-like 2
22402	dirMS_041712_NAR_30mM_minus2.6173.6173.2	2	4.63	0	1.23E+05		(K)MAGAM	(K)M/A\G A/M/S T/T A K(T)		87.73	484.7299	968.454	-0.0014	-1.5	8.5	23963.2	8.9	HUMAN	Q9UQN3	Charged multivesicular body protein 2b
22403	dirMS_041712_NAR_50mM_minus2.13345.13345.3	3	4.63	1	5.93E+05		(K)LVEENKI	(K)L V/E/E N K N L Q I S F N K(E)		143.13	559.3044	1675.901	-0.0027	-1.6	6.14	129614.1	6.59	HUMAN	Q8NCX0	Coiled-coil domain-containing protein 150
22404	dirMS_041712_NAR_50mM_minus2.13579.13579.3	3	4.63	0	1.13E+04		(R)DLEAEH	(R)D L E A E H V L P S P G G V G Q V R(G)		146.82	620.658	1859.961	-0.0016	-0.8	4.65	8567.5	6.95	HUMAN	H3BPT9	BolA-like protein 2 (Fragment)
22405	dirMS_041712_NAR_50mM_minus2.15489.15489.3	3	4.63	0	2.99E+05	M118m	(R)AGKPVI(	(R)A G K\P/V I\C A\T Q\M|L/E/S m I K(K)	C:Carbamidomethylation m:Oxid	155.8	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
22406	dirMS_041712_NAR_50mM_minus2.6134.6134.2	2	4.63	0	3.56E+04		(K)AGFAGD	(K)A/G F/A/G/D\D A/P R(A)		97.78	488.7293	976.448	0.003	3.1	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
22407	dirMS_041712_NAR_60mM_minus.10838.10838.3	3	4.63	1	1.45E+05		(R)WMVAC	(R)W/M V\A G/K A D P/E M P/K(R)		120.88	487.236	1459.707	-0.0138	-9.4	6.07	79786.8	8.62	HUMAN	O15119	T-box transcription factor TBX3
22408	dirMS_041712_NAR_60mM_minus.13797.13797.3	3	4.63	0	1.42E+05		(K)ADFCIIH	(K)A D F/C/I/I/H/Y A/G K(V)	C:Carbamidomethylation	137.43	432.2132	1294.625	0.0002	0.1	6.79	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
22409	dirMS_041712_NAR_60mM_minus.17449.17449.3	3	4.63	0	2.98E+05		(K)GSDHSA	(K)G S D H S A S L E|P G/E|L A\E/L V R(S)		156.93	622.9764	1866.919	-0.0045	-2.4	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
22410	dirMS_041712_NAR_120mM_plus.8077.8077.3	3	4.63	2	2.08E+05	M53m	(K)LTDCVV	(K)L T/D/C V V m R D/P A/S K R(S)	C:Carbamidomethylation m:Oxid	95.88	555.2807	1647.831	15.997	1.3	8.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
22411	dirMS_041712_NAR_20mM_plus.12718.12718.3	3	4.63	0	4.87E+04	M17m M2(	(K)GAEEmE	(K)G A E/E m E T V/I|P V D V m R(R)	m:Oxidized methionine	160.27	569.9346	1675.803	31.9863	-2.1	4	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
22412	dirMS_041712_NAR_20mM_plus.6439.6439.3	3	4.63	0	5.31E+04		(R)GPQVQ(	(R)G P Q V Q Q/P/P/P S N R(F)		107.1	435.561	1304.671	-0.0021	-1.6	9.75	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
22413	dirMS_041712_NAR_30mM_plus2.15630.15630.2	2	4.63	0	6.93E+05		(R)YPVNSV	(R)Y/P|V/N S V N I/L/K(A)		134.57	573.8278	1146.652	-0.0034	-3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
22414	dirMS_041712_NAR_30mM_plus2.15659.15659.2	2	4.63	0	3.77E+04		(R)NNNTDI	(R)N N|N\T/D L\M I/L/K(N)		133.52	588.3046	1175.609	-0.007	-5.9	5.84	106861.4	5.24	HUMAN	Q99460	26S proteasome non-ATPase regulatory subunit 1
22415	dirMS_041712_NAR_30mM_plus2.18294.18294.2	2	4.63	0	1.72E+05	N94n	(K)SLDLnK(	(K)S L/D/L/n/K(N)	n:N-acetylglucosamine (N)	149.5	446.7383	689.383	203.0865	8	5.55	43365.4	8.69	HUMAN	C9J7B8	GRAM domain-containing protein 1C (Fragment)
22416	dirMS_041712_NAR_30mM_plus2.20411.20411.2	2	4.63	0	2.38E+04		(R)TVQSLEI	(R)T V|Q S|L\E I D L D\S M R(N)		161.05	753.8768	1506.747	-0.0005	-0.3	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
22417	dirMS_041712_NAR_30mM_plus2.20920.20920.2	2	4.63	0	4.39E+04		(R)EMVLEII	(R)E M/V/L E/I I R(E)		163.4	501.7877	1002.565	0.0029	2.9	4.53	61981.6	8.97	HUMAN	Q96I24	Far upstream element-binding protein 3
22418	dirMS_041712_NAR_50mM_plus2.21794.21794.3	3	4.63	1	2.30E+05		(K)LGFAGL\	(K)L/G/F/A/G L V Q E/I S F G T T K D K(M)		184.87	637.6781	1911.022	-0.0025	-1.3	6.07	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
22419	dirMS_041712_NAR_50mM_plus2.22048.22048.3	3	4.63	1	5.77E+05		(K)AGFLDLI	(K)A/G F/L D|L K D|F\L P K(E)		188.87	455.2587	1363.762	-0.0005	-0.3	6	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
22420	dirMS_041712_NAR_50mM_plus2.6680.6680.3	3	4.63	1	1.46E+04		(K)SMSVDE	(K)S M/S V/D E/T D/K S P C E/A G R(V)	C:Carbamidomethylation	99.83	590.2548	1768.748	0.0022	1.2	4.32	135657.7	6.27	HUMAN	G8JL86	Cordon-bleu protein-like 1
22421	dirMS_041712_NAR_60mM_plus.16579.16579.3	3	4.63	1	5.21E+05	M224m	(K)LLVKmP	(K)L L/V K m P F\Q T/S P/G G K(A)	m:Oxidized methionine	144.2	506.9426	1502.84	15.9733	-14.2	10	52610.9	10.02	HUMAN	P51608	Methyl-CpG-binding protein 2
22422	dirMS_041712_NAR_60mM_plus.20168.20168.3	3	4.63	1	1.54E+05		(R)ELIKVLEI	(R)E L I K V\L E E A|N/Q/A I N|P K(L)		165.17	603.6768	1809.012	0.0042	2.3	4.79	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
22423	dirMS_041712_NAR_50mM_minus2.13538.13538.3	3	4.62	0	3.51E+04		(K)EAFTNKI	(K)E A/F T/N K/P N V|F T V V T R(G)		145.15	574.9724	1722.917	-0.0147	-8.5	8.85	258215.9	5.48	HUMAN	E7EN95	Filamin-B
22424	dirMS_041712_NAR_60mM_minus.12681.13171.3	3	4.62	1	4.47E+05		(R)YLYLTPC	(R)Y/L/Y L/T/P Q/D Y K R(V)		131.83	487.2585	1459.758	0.003	2	8.43	6336.9	5.38	HUMAN	K7EPF1	Acetyl-CoA carboxylase 1 (Fragment)
22425	dirMS_041712_NAR_60mM_minus.6601.6601.3	3	4.62	1	1.04E+05	M199m	(R)mLQADI	(R)m L/Q A D/P N/K/V/S A|R(A)	m:Oxidized methionine	95.18	449.2329	1329.694	15.9898	-3.8	8.5	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
22426	dirMS_041712_NAR_60mM_minus.6854.6854.3	3	4.62	1	5.61E+05	M286m M:	(R)VVDLmA	(R)V/V|D L m A H m A S K E(-)	m:Oxidized methionine	96.77	454.8843	1330.649	31.989	-0.6	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
22427	dirMS_041712_NAR_60mM_minus.7448.7448.3	3	4.62	2	1.90E+05		(K)TPDAMI	(K)T\P|D A M/K A A M A L E K K(L)		101.43	502.2642	1504.786	-0.0081	-5.4	8.17	20076.4	5.51	HUMAN	P02792	Ferritin light chain
22428	dirMS_041712_NAR_20mM_plus.10897.10897.2	2	4.62	0	1.31E+04	M1m	(-)mSVLNN	(-)m S|V/L N N S E V/K(L)	m:Oxidized methionine	147.52	568.7909	1120.567	16.0078	11.4	5.75	35758.7	9.77	HUMAN	Q8NH64	Olfactory receptor 51A7
22429	dirMS_041712_NAR_40mM_plus2.13329.13329.2	2	4.62	0	8.98E+04		(K)FFVGGN	(K)F/F/V/G\G N W K(M)		144.42	477.7448	954.483	-0.0009	-0.9	8.75	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
22430	dirMS_041712_NAR_40mM_plus2.17864.17864.3	3	4.62	0	3.79E+04	K183k	(K)QLHEEV	(K)Q L/H E E V N L L k S N I|A K(Y)	k:Ubiquitin-K	170.98	617.3431	1735.97	114.0446	0.9	6.76	53023.5	5.92	HUMAN	Q6ZUS6	Coiled-coil domain-containing protein 149
22431	dirMS_041712_NAR_40mM_plus2.18974.18974.3	3	4.62	1	1.09E+05		(K)NLGIPIIT	(K)N L|G|I/P I I T V L G D S K N N V R(A)		178.08	641.701	1923.102	-0.0137	-7.1	8.75	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
22432	dirMS_041712_NAR_40mM_plus2.7389.7389.2	2	4.62	0	3.09E+05		(K)VIDDTNI	(K)V I|D/D T/N I/T R(L)		103.53	523.7788	1046.548	0.0027	2.5	4.21	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
22433	dirMS_041712_NAR_50mM_plus2.17156.17156.3	3	4.62	0	4.56E+05		(R)DLKPSNI	(R)D L/K P S N L\L|I/N T T C D L K(I)	C:Carbamidomethylation	158.4	615.664	1844.979	-0.0012	-0.6	5.96	30925	5.63	HUMAN	B3KR49	Mitogen-activated protein kinase 3
22434	dirMS_041712_NAR_50mM_plus2.17495.17495.3	3	4.62	1	5.25E+05		(K)VKLAAV	(K)V K L A A V D A T\V/N Q/V/L\A S R(Y)		160.33	585.6736	1755.012	-0.0061	-3.5	8.72	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
22435	dirMS_041712_NAR_60mM_plus.12562.12562.3	3	4.62	1	6.43E+05		(K)GIADIMI	(K)G I A/D/I M\I A F R T R(V)		122.07	455.257	1363.752	0.005	3.7	9.6	59367.1	9.07	HUMAN	Q9H306	Matrix metalloproteinase-27
22436	dirMS_041712_NAR_20mM_minus.10265.10265.2	2	4.61	0	2.40E+04		(R)AQAALA	(R)A Q|A/A L/A\V N I S A A R(G)		152.12	628.3558	1255.712	-0.0074	-5.9	9.79	58479.6	6.23	HUMAN	P40227	T-complex protein 1 subunit zeta
22437	dirMS_041712_NAR_20mM_minus.10355.10355.2	2	4.61	0	3.52E+04		(K)AGLAPLI	(K)A G L|A/P L E V R(V)		152.42	463.2776	925.547	0.0014	1.5	6.05	258215.9	5.48	HUMAN	E7EN95	Filamin-B
22438	dirMS_041712_NAR_20mM_minus.14544.14544.2	2	4.61	0	6.76E+04	M332m	(R)IVSQLLT	(R)I V S Q/L/L/T/L m D G L K(Q)	m:Oxidized methionine	200.23	723.9145	1430.829	15.993	-1.3	5.84	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
22439	dirMS_041712_NAR_30mM_minus2.18930.18930.2	2	4.61	0	1.91E+05		(K)CFSVLGI	(K)C F/S V|L/G F/C/K(S)	C:Carbamidomethylation	157.42	559.2673	1117.517	0.0104	9.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
22440	dirMS_041712_NAR_40mM_minus2.11572.11572.3	3	4.61	1	1.33E+04		(R)DLAALG	(R)D L\A|A L/G D K V N S L/G E T A E R(L)		151.8	620.3199	1858.95	-0.0053	-2.9	4.32	285798.6	5.23	HUMAN	A6NG51	Spectrin alpha chain, non-erythrocytic 1
22441	dirMS_041712_NAR_60mM_minus.16102.16102.3	3	4.61	2	1.54E+05	M92m T93	(R)EKLQKL(	(R)E\K L Q K L\G E/G E G S|m/t K(E)	m:Oxidized methionine t:N-a	149.28	618.6483	1634.842	219.0885	7.7	6.33	14591.3	4.63	HUMAN	G3V2U1	Sorting nexin-6
22442	dirMS_041712_NAR_60mM_minus.19066.19066.3	3	4.61	0	2.71E+05		(R)CRPDQL	(R)C R P D Q L\T/G|L S L/L|P\L S E K(A)	C:Carbamidomethylation	168.17	643.0129	1927.032	-0.0076	-3.9	6.07	533778	5.74	HUMAN	Q15149	Plectin
22443	dirMS_041712_NAR_20mM_plus.14170.14170.3	3	4.61	0	7.24E+03		(K)SYTISPN	(K)S Y T I S P N|S|H/F/H I K(M)		169.75	510.9348	1530.77	0.0199	13	8.35	87543.2	4.74	HUMAN	Q9Y5F2	Protocadherin beta-11
22444	dirMS_041712_NAR_30mM_plus2.12759.12759.2	2	4.61	0	5.53E+05		(R)CNNVLY	(R)C N\N/V|L/Y I R(G)	C:Carbamidomethylation	120.78	526.2726	1051.535	0.0026	2.5	8.75	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F
22445	dirMS_041712_NAR_30mM_plus2.17390.17390.3	3	4.61	0	1.06E+06		(R)ASLEAAI	(R)A S L E A A\I/A/D/A/E Q R(G)		144.38	448.8963	1344.675	-0.001	-0.8	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
22446	dirMS_041712_NAR_30mM_plus2.19074.19074.2	2	4.61	0	4.55E+05		(R)SSIAGLL	(R)S S/I/A G L/L L K(A)		154.37	451.2894	901.572	-0.0002	-0.2	8.47	533778	5.74	HUMAN	Q15149	Plectin
22447	dirMS_041712_NAR_30mM_plus2.21073.21073.2	2	4.61	0	1.70E+05		(R)QTLMW	(R)Q T|L/M/W/S A T W P\K(E)		165.3	674.8389	1348.672	-0.0013	-1	8.75	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
22448	dirMS_041712_NAR_40mM_plus2.10304.10304.3	3	4.61	0	7.42E+04		(R)ISMSEVI	(R)I S M S E V/D/L N\V A A/P/K(V)		125.02	491.9315	1473.762	0.0182	12.3	4.37	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
22449	dirMS_041712_NAR_40mM_plus2.8877.8877.2	2	4.61	0	1.19E+05		(R)GYSFTTI	(R)G Y|S/F/T/T T A E R(E)		114.9	566.7672	1132.527	0.0002	0.2	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)

22450	dirMS_041712_NAR_50mM_plus2.10737.10737.3	3	4.61	1	5.79E+04		(R)VCEEIAII	(R)V/C\E E I/A I/I P S K K(L)	C:Carbamidomethylation	123.9	462.9247	1386.766	-0.0066	-4.7	6.11	21927.8	9.55	HUMAN	H0YK46	40S ribosomal protein S17 (Fragment)
22451	dirMS_041712_NAR_50mM_plus2.10814.10814.3	3	4.61	1	4.68E+05		(R)ALRETLF	(R)A L R E T L|P\A\E Q D L T T K(N)		125.08	562.6377	1685.907	-0.0083	-4.9	4.68	26790	6.25	HUMAN	F5GX11	Proteasome subunit alpha type-1
22452	dirMS_041712_NAR_50mM_plus2.14269.14269.3	3	4.61	0	1.56E+06		(K)EALEPS	(K)E A/L E/P S G E N V I Q N K(E)		143.63	509.9193	1527.765	-0.0216	-14.1	4.25	39096.3	7.78	HUMAN	O75477	Erlin-1
22453	dirMS_041712_NAR_50mM_plus2.6047.6047.3	3	4.61	1	4.28E+04		(R)QSNVAA	(R)Q S N/V/A/A\P G D A T/P P A E K K(Y)		95.88	560.9581	1680.855	0.0046	2.7	6.07	34828	9.96	HUMAN	F5H5K4	Serine/threonine-protein phosphatase 1 regulatory subunit 10
22454	dirMS_041712_NAR_60mM_plus.21123.21123.3	3	4.61	1	1.05E+05		(K)AKINEA	(K)A K I N E A|V/E C L L S L K(A)	C:Carbamidomethylation	173.75	529.9643	1587.878	0.0009	0.6	6.18	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
22455	dirMS_041712_NAR_60mM_plus.6175.6175.3	3	4.61	1	4.61E+05	M22m	(K)EmDEED	(K)E m/D E/E D K A F K(Q)	m:Oxidized methionine	91.48	419.8479	1241.535	15.9937	-1	4.18	7066.2	10	HUMAN	Q9Y2S6	Translation machinery-associated protein 7
22456	dirMS_041712_NAR_60mM_plus.6806.6806.3	3	4.61	0	3.84E+05		(K)ASPNVE	(K)A S/P N V E\A/P Q/P H R(H)		94	434.8867	1302.655	-0.0094	-7.2	6.79	288852.1	5.33	HUMAN	E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein
22457	dirMS_041712_NAR_120mM_minus.16319.16319.3	3	4.6	2	1.19E+05		(K)KQGGLG	(K)K Q G\G L G P M N\I/P L/V S D P K R(T)		143.52	636.3552	1907.053	-0.0021	-1.1	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
22458	dirMS_041712_NAR_120mM_minus.16932.16932.3	3	4.6	0	4.29E+05		(K)HLEINPD	(K)H L/E I N P D\H/S\I/I E T L R(Q)		146.85	596.3176	1786.945	-0.0064	-3.6	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
22459	dirMS_041712_NAR_20mM_minus.10397.10397.2	2	4.6	0	4.90E+04		(K)ILQDGG	(K)I L\Q D/G G L/Q\V/V E/K(Q)		152.72	649.8694	1298.731	0.0001	0.1	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
22460	dirMS_041712_NAR_20mM_minus.14559.14559.3	3	4.6	0	1.76E+04		(K)LAVEALS	(K)L A V E A L S S L/D/G D L A/G R(Y)		199.98	529.6163	1586.838	-0.0041	-2.6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
22461	dirMS_041712_NAR_30mM_minus2.16811.16811.2	2	4.6	0	2.88E+05	M2243m	(K)mSIYQA	(K)m/S\I/Y Q/A/M W K(G)	m:Oxidized methionine	145.07	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
22462	dirMS_041712_NAR_30mM_minus2.5063.5063.2	2	4.6	0	1.31E+05		(R)AAEQYT	(R)A A|E/Q Y/T P K(A)		80.97	454.2271	907.452	-0.005	-5.6	6.04	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
22463	dirMS_041712_NAR_50mM_minus2.17088.17088.3	3	4.6	1	1.97E+05		(K)GYPPED	(K)G Y/P P E D I/F\N L V/G K K(V)		166.3	526.2832	1576.837	-0.0019	-1.2	6.07	40763.2	6.29	HUMAN	Q9NR45	Sialic acid synthase
22464	dirMS_041712_NAR_60mM_minus.17120.17120.3	3	4.6	0	8.20E+04		(K)LLDSSTV	(K)L L/D/S S T V/T H L/F/K(I)		155.38	454.2519	1360.747	-0.0059	-4.4	6.74	25746.2	6.77	HUMAN	B4DXJ9	Proteasome (Prosome, macropain) subunit, alpha type, 6, isoform CRA_a
22465	dirMS_041712_NAR_120mM_plus.14389.14389.4	4	4.6	1	6.34E+05		(R)ETNLDSI	(R)E T\N L D S L/P L V D T/H/S K/R(T)		128.35	456.9906	1824.945	-0.0044	-2.4	5.38	53707.8	5.06	HUMAN	P08670	Vimentin
22466	dirMS_041712_NAR_120mM_plus.14817.14817.2	2	4.6	0	9.17E+04		(R)DWSHYF	(R)D W/S H/Y F/K(I)		130.68	491.725	982.442	0.001	1	6.74	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
22467	dirMS_041712_NAR_120mM_plus.7979.7979.2	2	4.6	0	4.64E+05		(K)STTTGHI	(K)S T|T/T G H L I|Y K(C)		95.25	560.8014	1120.6	-0.0042	-3.7	8.34	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
22468	dirMS_041712_NAR_20mM_plus.6665.6665.2	2	4.6	0	7.77E+04	M357m	(K)AELDDTI	(K)A E|L/D D T P m R(G)	m:Oxidized methionine	110.62	532.24	1047.478	15.9952	0.3	4.03	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
22469	dirMS_041712_NAR_20mM_plus.8172.8172.2	2	4.6	0	7.77E+03		(K)TVGATA	(K)T V|G A/T A L P R(L)		125.67	443.2571	885.515	-0.0083	-9.4	9.41	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
22470	dirMS_041712_NAR_20mM_plus.9485.9485.2	2	4.6	0	1.54E+04		(R)TLIQNC	(R)T L|I|Q|N C G\A S T I/R(L)	C:Carbamidomethylation	136.63	667.3458	1333.689	-0.0049	-3.7	9.41	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
22471	dirMS_041712_NAR_30mM_plus2.22300.22300.2	2	4.6	0	1.54E+05		(K)GLSSLLC	(K)G L/S S/L L C N|F T K(S)	C:Carbamidomethylation	171.95	620.3199	1239.64	-0.0077	-6.2	8.75	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
22472	dirMS_041712_NAR_40mM_plus2.10661.10661.3	3	4.6	0	3.47E+04		(K)TASTLLK	(K)T A|S T L L K/P A P S G L/P S E R(K)		127.9	575.6528	1724.954	-0.0103	-6	8.41	268433.7	6.24	HUMAN	A4D212	DKFZP586J0619 protein
22473	dirMS_041712_NAR_40mM_plus2.13606.13606.3	3	4.6	0	1.65E+05		(K)NLPPSG	(K)N L/P/P S/G A V P V/T G I/P P H V V K(V)		146.07	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
22474	dirMS_041712_NAR_40mM_plus2.7961.7961.2	2	4.6	0	1.39E+05		(R)ELNITAA	(R)E L N|I T/A/A|K(E)		106.92	430.2474	859.488	-0.0008	-1	6.1	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
22475	dirMS_041712_NAR_40mM_plus2.9025.9025.3	3	4.6	1	9.66E+04	T2397t	(R)VSGRtSF	(R)V/S/G R t S/P/P L/L D R(A)	t:Phosphorylated T	115.02	459.8999	1297.722	79.9629	-2.5	9.57	300351.7	12.1	HUMAN	Q9UQ35	Serine/arginine repetitive matrix protein 2
22476	dirMS_041712_NAR_50mM_plus2.12745.12745.3	3	4.6	0	2.87E+05		(K)EMNPAL	(K)E M/N/P A L|G I D C L H K(G)	C:Carbamidomethylation	135.32	499.9106	1497.719	-0.0016	-1.1	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
22477	dirMS_041712_NAR_50mM_plus2.12900.12900.3	3	4.6	0	2.03E+05		(K)ILDAVVA	(K)I L/D A V/V/A Q E P L H/R(G)		135.72	487.6117	1460.822	-0.0014	-1	5.32	15036.9	7.16	HUMAN	K7EJ74	116 kDa U5 small nuclear ribonucleoprotein component (Fragment)
22478	dirMS_041712_NAR_50mM_plus2.9805.9805.3	3	4.6	1	4.40E+04		(R)IAEQQK	(R)I/A|E/Q Q K A Q A/E V E G L G K(G)		119.08	566.9707	1698.902	-0.0045	-2.7	4.79	533778	5.74	HUMAN	Q15149	Plectin
22479	dirMS_041712_NAR_60mM_plus.10463.10463.3	3	4.6	0	9.83E+05		(K)YAVTTG	(K)Y/A|V/T T/G D/H G I I R(T)		112.42	434.9004	1302.68	0.0066	5	6.74	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
22480	dirMS_041712_NAR_60mM_plus.14395.14395.3	3	4.6	1	1.29E+06		(R)LSEATQ	(R)L S E/A T Q A P G L/E G R/K(V)		131.32	486.2646	1456.775	0.0038	2.6	6.14	140166.4	6.25	HUMAN	B5MCJ9	Tripartite motif-containing protein 66
22481	dirMS_041712_NAR_60mM_plus.16306.16306.3	3	4.6	0	3.17E+05		(R)FVFDRPI	(R)F/V/F D R/P L P V S/R(L)		142.47	444.917	1332.742	-0.0058	-4.4	9.6	18685.5	9.45	HUMAN	B4DEV8	Proteasome subunit alpha type
22482	dirMS_041712_NAR_20mM_minus.14048.14048.3	3	4.59	0	2.47E+05		(R)TTVPQLI	(R)T T V P/Q L L|A/S V Q R(W)		192.73	438.2582	1312.758	0.0017	1.3	9.41	266161	5.68	HUMAN	E9PPU0	Epiplakin
22483	dirMS_041712_NAR_30mM_minus2.17407.17407.2	2	4.59	0	2.57E+05		(R)NGGQIL	(R)N G\G\Q|I/L I/A D L R(G)		148.82	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
22484	dirMS_041712_NAR_30mM_minus2.18060.18060.2	2	4.59	1	3.94E+04	M170m	(R)DQKEmL	(R)D/Q/K/E m L E V S G/I(-)	m:Oxidized methionine	152.85	632.8097	1248.614	15.9981	2.5	4.14	19926	9.56	HUMAN	C9JJ63	Transmembrane protein 176A
22485	dirMS_041712_NAR_30mM_minus2.4998.4998.2	2	4.59	0	4.35E+04		(R)VGQTIEI	(R)V/G/Q/T I E R(M)		80.82	401.7227	802.442	-0.0036	-4.5	5.97	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
22486	dirMS_041712_NAR_50mM_minus2.14510.14510.3	3	4.59	0	2.67E+03		(R)SAVDQA	(R)S A V/D Q|A/G/G A Q I V I D/H L R(S)		149.5	583.9833	1749.924	0.0111	6.4	5.19	17202.4	4.79	HUMAN	D6REZ0	Rap1 GTPase-GDP dissociation stimulator 1 (Fragment)
22487	dirMS_041712_NAR_50mM_minus2.15338.15338.3	3	4.59	0	3.28E+05		(R)LSFQHD	(R)L S|F Q H D\P E/T S V/L V L R(K)		156.07	580.9793	1740.928	-0.0046	-2.6	5.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
22488	dirMS_041712_NAR_50mM_minus2.7299.7299.3	3	4.59	2	6.43E+03		(R)YYLRNN	(R)Y Y L/R/N N/Y G S R Y/K(W)		108.53	532.9391	1596.792	0.011	6.9	9.82	120222.5	9.83	HUMAN	Q9NS56	E3 ubiquitin-protein ligase Topors
22489	dirMS_041712_NAR_20mM_plus.17998.17998.2	2	4.59	1	1.16E+05		(R)VPGASS	(R)V P|G A S S F K/L K(N)		195.05	517.3039	1033.604	-0.0035	-3.4	10	99203.4	5.88	HUMAN	P29590	Protein PML
22490	dirMS_041712_NAR_20mM_plus.8471.8471.2	2	4.59	0	1.70E+05		(K)TAVCDIF	(K)T A/V|C/D I/P/P R(G)	C:Carbamidomethylation	127.77	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
22491	dirMS_041712_NAR_30mM_plus2.20108.20108.2	2	4.59	0	2.07E+04		(R)SPTWFG	(R)S P\T W/F/G\I P R(L)		159.2	530.785	1060.557	0.0053	5	9.47	112927.8	6.09	HUMAN	P78347	General transcription factor II-I
22492	dirMS_041712_NAR_30mM_plus2.20554.20554.2	2	4.59	0	1.61E+05		(R)ASLSLW	(R)A S/L S/L/W/Q A M E K(G)		162.53	632.3231	1263.64	-0.0013	-1	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
22493	dirMS_041712_NAR_40mM_plus2.7028.7028.2	2	4.59	0	3.88E+04		(R)QGYGEC	(R)Q G/Y/G/E/G F R(W)		101.27	457.2098	913.416	-0.0039	-4.3	6	17613.9	5.58	HUMAN	B4DQ19	GTP-binding protein SAR1a
22494	dirMS_041712_NAR_40mM_plus2.9575.9575.2	2	4.59	0	5.93E+04		(R)NYYEQV	(R)N/Y/Y E Q W G K(L)		119.3	544.2469	1087.484	0.0022	2	6	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
22495	dirMS_041712_NAR_50mM_plus2.11881.11881.3	3	4.59	1	2.94E+05		(K)VEAQVY	(K)V/E/A Q V Y I/L/S/K E E G G R(H)		130.53	559.9637	1677.881	-0.0041	-2.4	4.79	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
22496	dirMS_041712_NAR_60mM_plus.18872.18872.3	3	4.59	2	2.25E+05	N456n	(K)LVnDKF	(K)L V n D K F/T R M/Y F/K(H)	n:N-acetylglucosamine (N)	156.15	588.9744	1561.82	203.0891	5.5	9.7	78298.8	5.26	HUMAN	Q7L1I2	Synaptic vesicle glycoprotein 2B
22497	dirMS_041712_NAR_120mM_minus.6628.6628.3	3	4.58	1	1.32E+05		(K)AMKEYE	(K)A M/K E Y E/E E E/R(K)		90.45	438.5284	1313.568	0.0028	2.2	4.32	11829.2	4.96	HUMAN	K7EIU0	Hsp90 co-chaperone Cdc37 (Fragment)
22498	dirMS_041712_NAR_120mM_minus.7953.7953.2	2	4.58	1	1.16E+05		(R)DRELALF	(R)D/R E/L|A\L|R(I)		97.63	436.7508	872.495	-0.0005	-0.6	6.07	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
22499	dirMS_041712_NAR_30mM_minus2.16061.16061.2	2	4.58	1	1.39E+05		(R)FVLSQAI	(R)F/V|L/S Q A K D E/L(-)		141.3	575.3113	1149.615	0.0003	0.3	4.37	41053.3	5.58	HUMAN	Q86UY0	TXNDC5 protein
22500	dirMS_041712_NAR_30mM_minus2.17442.17442.2	2	4.58	0	1.11E+04		(R)EQLAIAE	(R)E Q/L A/I/A/E F A R(S)		148.28	574.3084	1147.611	-0.0011	-0.9	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
22501	dirMS_041712_NAR_30mM_minus2.18394.18394.2	2	4.58	1	2.04E+05		(R)EPISVKE	(R)E P I/S V K|E Q H K(R)		154.58	597.8249	1194.648	-0.0052	-4.3	6.85	80179.4	9.28	HUMAN	G3V1N1	NF-kappa-B-repressing factor
22502	dirMS_041712_NAR_40mM_minus2.13273.13273.3	3	4.58	1	1.40E+05		(K)LGVQVV	(K)L G V|Q/V/V I T D/P E K L D Q I R(Q)		162.02	641.7007	1923.091	-0.0034	-1.8	4.56	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
22503	dirMS_041712_NAR_60mM_minus.13237.13237.3	3	4.58	1	4.52E+05		(K)TKEVYEL	(K)T K E\V Y E/L|L/D/S/P G K(V)		134.33	493.5966	1478.774	0.0015	1	4.68	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
22504	dirMS_041712_NAR_60mM_minus.15659.15659.3	3	4.58	1	6.80E+05		(R)FLQDYFI	(R)F L|Q D Y\F/D G N/L K/R(Y)		147.7	505.924	1515.759	-0.0016	-1.1	5.96	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
22505	dirMS_041712_NAR_60mM_minus.6153.6153.3	3	4.58	1	7.65E+05		(K)DSYVGD	(K)D S Y/V G D E/A Q/S K R(G)		92.4	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
22506	dirMS_041712_NAR_120mM_plus.6451.6451.2	2	4.58	1	5.24E+05	M25m K29	(K)KHAAEm	(K)K H|A A E m/A T/A/k(K)	m:Oxidized methionine k:Ub	87.48	594.2868	1057.546	130.0204	-14.7	8.6	7226.8	5.82	HUMAN	F8VWZ9	Homeobox protein Nkx-6.1 (Fragment)
22507	dirMS_041712_NAR_20mM_plus.18669.18669.2	2	4.58	0	1.96E+05		(R)IITLAGP	(R)I I T L/A|G/P T N A I F K(A)		200.85	679.9039	1358.804	-0.0037	-2.7	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
22508	dirMS_041712_NAR_20mM_plus.18896.18896.3	3	4.58	0	4.57E+05		(K)LAVEALS	(K)L A V E A\L S/S L/D G D/L A G R(Y)		200.58	529.6164	1586.838	-0.0038	-2.4	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
22509	dirMS_041712_NAR_20mM_plus.18957.18957.2	2	4.58	0	1.91E+05		(R)STGEAF	(R)S T G E A/F|V/Q\F\A\S Q E I\A E K(A)		202.2	921.4477	1841.892	-0.0035	-1.9	4.25	24249.1	6.99	HUMAN	D6RBM0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
22510	dirMS_041712_NAR_20mM_plus.19361.19361.2	2	4.58	0	4.97E+03		(R)ASVILAG	(R)A S V I L/A G L G\F T P K(M)		205.17	637.3763	1273.751	-0.0061	-4.8	8.8	80142.6	5.95	HUMAN	Q9NUQ8	ATP-binding cassette sub-family F member 3
22511	dirMS_041712_NAR_20mM_plus.8615.8615.2	2	4.58	0	2.04E+05		(R)VPPPPPI	(R)V/P/P/P P P I A\R(A)		130.42	472.2851	943.572	-0.0094	-10	9.72	32085.2	8.93	HUMAN	B4DY08	Heterogeneous nuclear ribonucleoproteins C1/C2
22512	dirMS_041712_NAR_20mM_plus.9833.9833.2	2	4.58	0	2.30E+05	S1699s	(R)AIVNsLA	(R)A I V N s L A Q A|L\G/R(Q)	s:Phosphorylated S	138.62	646.8319	1212.706	79.9506	-12.1	9.79	539796.2	6.25	HUMAN	Q96M86	Dynein heavy chain domain-containing protein 1
22513	dirMS_041712_NAR_30mM_plus2.20357.20357.2	2	4.58	0	2.16E+04		(R)ILLLGLDI	(R)I L|L|L/G L D N A G K(T)		161.85	563.8448	1126.683	-0.0007	-0.6	5.84	20626.3	6.76	HUMAN	P36405	ADP-ribosylation factor-like protein 3
22514	dirMS_041712_NAR_30mM_plus2.20613.20613.2	2	4.58	0	7.09E+04		(K)YLLDSCA	(K)Y L/L|D S/C A P L L/R(Y)	C:Carbamidomethylation	161.9	660.8437	1320.698	-0.0179	-13.6	5.83	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
22515	dirMS_041712_NAR_40mM_plus2.11042.11042.2	2	4.58	0	7.20E+03		(R)GDFCIQ	(R)G D/F/C/I/Q/V G R(-)	C:Carbamidomethylation	131.12	526.2539	1051.499	0.0016	1.5	5.84	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
22516	dirMS_041712_NAR_40mM_plus2.20097.20097.3	3	4.58	0	1.76E+05		(R)IWEDYY	(R)I W E D Y Y I L L T/K(C)		190.72	486.2654	1456.772	0.0094	6.5	4.37	42144.3	6.54	HUMAN	B4DV59	REST corepressor 3
22517	dirMS_041712_NAR_60mM_plus.17984.17984.3	3	4.58	1	8.54E+04	S618s	(K)GGTLHA	(K)G G T L H A D A/Q L/s G K/D A D/R(F)	s:N-acetylglucosamine (S)	151.25	638.979	1711.836	203.0866	3.8	5.3	148987.1	5.83	HUMAN	Q86UW7	Calcium-dependent secretion activator 2
22518	dirMS_041712_NAR_60mM_plus.5444.5444.3	3	4.58	0	1.66E+05		(R)TGIYSST	(R)T G I/Y S/S/T S C H K(T)	C:Carbamidomethylation	86.43	414.1936	1240.563	0.0036	2.9	8.28	38077.6	8.9	HUMAN	P09668	Pro-cathepsin H
22519	dirMS_041712_NAR_120mM_minus.14804.14804.4	4	4.57	0	1.01E+05		(R)LLLEGIS	(R)L L L E/G I S S T H V N H L R(C)		134.63	422.9909	1688.944	-0.0025	-1.5	6.92	44588.7	5.61	HUMAN	B7ZC38	Endophilin-B2
22520	dirMS_041712_NAR_20mM_minus.13478.13478.3	3	4.57	0	7.62E+05	M221m	(R)ALTVPEL	(R)A L\T\V/P E L T Q/Q m/F D A K(N)	m:Oxidized methionine	186.18	569.9577	1691.867	15.9913	-2.1	4.37	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
22521	dirMS_041712_NAR_20mM_minus.7026.7026.2	2	4.57	0	2.13E+05	M33m	(R)IDEmPE	(R)I/D E\m/P E/A A/V/K(S)	m:Oxidized methionine	117.98	559.7733	1102.545	15.9944	-0.4	4.14	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
22522	dirMS_041712_NAR_30mM_minus2.6503.6503.2	2	4.57	0	1.83E+05		(R)ASFNNP	(R)A S/F/N|N/P D R(A)		89.57	460.7171	920.422	0.0049	5.3	5.88	35061.2	4.66	HUMAN	G5E9P0	RAD23 homolog B (S. cerevisiae), isoform CRA_a
22523	dirMS_041712_NAR_30mM_minus2.7155.7155.2	2	4.57	0	3.80E+05		(R)ASYISSA	(R)A S/Y I S/S A/R(L)		94.13	427.7216	854.437	-0.0007	-0.9	8.79	59288.4	7.16	HUMAN	Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)
22524	dirMS_041712_NAR_40mM_minus2.14884.14884.3	3	4.57	0	1.07E+05		(R)EAVELPI	(R)E A V E/L/P L/T H F E L/Y K(Q)		173.08	563.6324	1688.889	-0.0068	-4	4.75	47479.5	5.09	HUMAN	P43686	26S protease regulatory subunit 6B
22525	dirMS_041712_NAR_50mM_minus2.15130.15130.3	3	4.57	0	2.63E+05	M118m	(R)AGKPVI	(R)A G K\P V I\C A T/Q/M/L/E S m I K(K)	C:Carbamidomethylation m:Oxid	154.53	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
22526	dirMS_041712_NAR_60mM_minus.14160.14160.3	3	4.57	1	1.40E+05		(R)TEMENE	(R)T E|M/E N E/F/V/L I K K(D)		138.83	494.2594	1480.772	-0.0079	-5.4	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
22527	dirMS_041712_NAR_60mM_minus.18289.18289.2	2	4.57	1	6.97E+04		(K)SLLGKD	(K)S L L/G\K D V L/F/L/K(D)		163.4	616.8819	1232.761	-0.0048	-3.9	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
22528	dirMS_041712_NAR_60mM_minus.5075.5075.3	3	4.57	1	3.69E+04		(K)KTGSPG	(K)K T\G S P G S P G A/G G V Q/S T A K(K)		83.02	529.6145	1586.813	0.0157	9.9	10	45232	5.78	HUMAN	B4DZP4	Cytoplasmic dynein 1 light intermediate chain 2
22529	dirMS_041712_NAR_60mM_minus.7189.7189.3	3	4.57	0	7.47E+04		(R)VETQFQ	(R)V/E/T Q F Q N/G H/Y D K(C)		98.7	489.232	1465.671	0.0108	7.4	5.32	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
22530	dirMS_041712_NAR_120mM_plus.10067.10067.2	2	4.57	0	2.92E+05		(K)HGINCFI	(K)H/G|I/N C F I N/R(Q)	C:Carbamidomethylation	106.15	565.7803	1130.552	0.001	0.8	9.75	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
22531	dirMS_041712_NAR_20mM_plus.14597.14597.2	2	4.57	0	1.36E+05		(R)FIDTTLA	(R)F I|D/T T/L/A I T S R(F)		171.98	619.3413	1237.679	-0.0034	-2.7	5.84	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
22532	dirMS_041712_NAR_20mM_plus.17450.17450.2	2	4.57	0	4.62E+03		(K)LLYAFAE	(K)L L|Y A\F/A E A T V P K(V)		190.97	661.8712	1322.736	-0.0003	-0.3	6	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
22533	dirMS_041712_NAR_20mM_plus.18204.18204.3	3	4.57	0	1.04E+05	N706n	(R)LLQALVI	(R)L L Q A L V/D I L N E E/n(-)	n:N-acetylglucosamine (N)	197.35	562.9694	1483.8	203.0934	8.3	3.57	79464.8	5.81	HUMAN	E9PHA1	Neuroendocrine convertase 1
22534	dirMS_041712_NAR_20mM_plus.7024.7024.2	2	4.57	0	1.09E+05		(K)AGFAGD	(K)A G F/A/G D D/A P R(A)		114.77	488.7307	976.448	0.0058	6	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
22535	dirMS_041712_NAR_30mM_plus2.11067.11099.2	2	4.57	0	1.19E+06		(R)GLTSVIN	(R)G L|T/S V/I/N Q K(L)		110.87	480.2785	959.552	-0.0023	-2.4	8.75	36923.1	5.71	HUMAN	P07195	L-lactate dehydrogenase B chain
22536	dirMS_041712_NAR_30mM_plus2.15086.15086.2	2	4.57	0	8.64E+05		(K)NMVLFT	(K)N/M/V/L F|T/R(Q)		131.23	440.7384	880.471	-0.0014	-1.6	9.75	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1
22537	dirMS_041712_NAR_30mM_plus2.19099.19099.2	2	4.57	0	1.18E+05		(K)IYVISLAE	(K)I Y/V|I S/L A/E P R(L)		152.93	580.8349	1160.667	-0.0049	-4.2	6	20139.7	9.34	HUMAN	C9J7S3	Aspartate--tRNA ligase, cytoplasmic (Fragment)
22538	dirMS_041712_NAR_30mM_plus2.5971.5971.2	2	4.57	0	1.01E+05		(R)EAEEVYI	(R)E A E E/V/Y/R(N)		85.07	448.2113	895.416	-0.0003	-0.3	4.25	54793.4	10.51	HUMAN	B7Z4Q3	Putative RNA-binding protein Luc7-like 2
22539	dirMS_041712_NAR_40mM_plus2.17971.17971.3	3	4.57	1	2.69E+04		(K)ALEVAE	(K)A L/E\V/A E/Y L T P V L K E S K(F)		171.98	597.3336	1789.995	-0.0083	-4.7	4.79	8368.5	5.85	HUMAN	F8WDI0	Ubiquitin-like-conjugating enzyme ATG3
22540	dirMS_041712_NAR_50mM_plus2.21212.21212.3	3	4.57	1	9.64E+03		(R)AQGGE	(R)A Q/G G/E V|M E Y T T I L R L R(E)		181.1	612.9957	1836.964	0.0089	4.8	6.19	70204.4	9.14	HUMAN	C9K080	Leucine-rich repeats and immunoglobulin-like domains protein 3
22541	dirMS_041712_NAR_60mM_plus.11617.11617.3	3	4.57	1	5.33E+05	M406m	(R)QLREYQ	(R)Q L R E Y\Q/E|L m/N V K(L)	m:Oxidized methionine	116.82	522.9381	1550.8	16.0002	3.4	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
22542	dirMS_041712_NAR_60mM_plus.17327.17327.3	3	4.57	1	1.69E+04	M81m	(K)EVNKFQ	(K)E V/N K F Q m A/Y/S N L L R(A)	m:Oxidized methionine	147.48	576.9649	1712.879	16.0013	3.7	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
22543	dirMS_041712_NAR_60mM_plus.6751.6751.3	3	4.57	0	1.20E+05		(K)EQMQP	(K)E Q/M\Q/P T H/P I R(L)		93.8	412.8762	1236.615	-0.0013	-1.1	6.85	18789.1	6.77	HUMAN	A2IDB2	14-3-3 protein eta (Fragment)
22544	dirMS_041712_NAR_120mM_minus.12026.12026.4	4	4.56	1	1.95E+05		(R)KVSQPIE	(R)K V S Q/P I/E G H A A S F/A Q F K(M)		119.47	461.9967	1844.965	-0.0004	-0.2	8.6	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
22545	dirMS_041712_NAR_120mM_minus.6585.6585.2	2	4.56	1	2.24E+05		(R)KLLEGEE	(R)K|L|L E G E E/S R(I)		89.75	530.7845	1060.563	-0.0016	-1.5	4.79	49709.6	5.19	HUMAN	B0YJC4	Vimentin
22546	dirMS_041712_NAR_20mM_minus.10130.10130.3	3	4.56	1	6.90E+03	M34m	(R)SVNDPG	(R)S V N D P G N m/S F V/K E/T V D K(L)	m:Oxidized methionine	150.72	628.3083	1866.89	16.0201	13.4	4.56	54663	9.39	HUMAN	P28472-2	Isoform 2 of Gamma-aminobutyric acid receptor subunit beta-3
22547	dirMS_041712_NAR_20mM_minus.14083.14083.3	3	4.56	0	7.22E+05		(K)SYELPD	(K)S Y\E/L/P D\G Q V\I/T I G N E R(F)		193.9	597.6345	1790.892	-0.003	-1.7	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
22548	dirMS_041712_NAR_30mM_minus2.16589.16589.2	2	4.56	0	2.38E+04		(R)FFMGN	(R)F/F/M/G N Q\V L/K(V)		144.32	542.2866	1083.566	0.0004	0.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
22549	dirMS_041712_NAR_30mM_minus2.16857.16857.2	2	4.56	0	4.10E+05		(K)NSLESYA	(K)N S/L/E S/Y A/F/N M K(A)		146.48	652.3031	1303.599	0.0002	0.2	6	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
22550	dirMS_041712_NAR_30mM_minus2.7257.7257.2	2	4.56	0	3.86E+05		(K)QQTLEA	(K)Q Q\T/L/E/A/E E A K(R)		93.4	573.7846	1146.564	-0.0018	-1.6	4.25	76925.9	4.46	HUMAN	A8MV58	Drebrin
22551	dirMS_041712_NAR_50mM_minus2.16158.16158.3	3	4.56	1	4.43E+06		(R)VSFELFA	(R)V S\F E L F/A D K V/P K(T)		159.72	460.5908	1379.757	0.0009	0.7	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
22552	dirMS_041712_NAR_50mM_minus2.16623.16623.3	3	4.56	1	1.87E+04		(R)EVQLEEI	(R)E V Q|L E/E/L E A A R D L/V S K(E)		161.82	610.3273	1828.965	0.0023	1.2	4.25	45984.6	6.24	HUMAN	B4E1G6	Galactokinase
22553	dirMS_041712_NAR_60mM_minus.10264.10264.3	3	4.56	1	2.36E+04	M88m	(K)DVDEAY	(K)D V|D/E A Y m/N K V/E L E S R(L)	m:Oxidized methionine	116.03	605.2791	1797.832	15.9904	-2.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
22554	dirMS_041712_NAR_60mM_minus.13529.13529.3	3	4.56	1	2.23E+05		(R)NDEELN	(R)N D/E E L/N K/L/L|G K(V)		135.13	424.8995	1272.679	0.0045	3.6	4.68	9975.4	9.7	HUMAN	H0YFX9	Histone H2A (Fragment)
22555	dirMS_041712_NAR_60mM_minus.7599.7599.3	3	4.56	0	5.31E+04	M141m	(K)mAEIPSS	(K)m A E/I P S S P\Y E P G Q\R(G)	m:Oxidized methionine	101.43	526.5879	1561.732	16.0176	14.4	4.53	94804.4	7.8	HUMAN	P84550-2	Isoform 2 of SKI family transcriptional corepressor 1
22556	dirMS_041712_NAR_60mM_minus.9641.9641.2	2	4.56	1	4.41E+05		(R)LQAEIE	(R)L Q/A E I/E G L K/G Q R(A)		114.13	671.3768	1341.748	-0.0022	-1.6	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
22557	dirMS_041712_NAR_20mM_plus.11044.11044.2	2	4.56	0	1.51E+06		(K)DVNAAI	(K)D V|N A/A I/A T I K(T)		149.55	508.292	1015.578	-0.0015	-1.5	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
22558	dirMS_041712_NAR_20mM_plus.14510.14510.3	3	4.56	0	9.32E+04	M326m M	(K)FTVLLmI	(K)F T\V L/L m/P N/G/P m R(I)	m:Oxidized methionine	171.65	469.9095	1375.723	31.9915	1.2	9.75	42088	5.39	HUMAN	F8VTY8	Proliferation-associated protein 2G4

22559	dirMS_041712_NAR_20mM_plus.15133.15133.2	2	4.56	0	5.88E+04		(R)EQLAIAE	(R)E Q L/A/I A E F A/R(S)		176.1	574.312	1147.611	0.0061	5.3	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
22560	dirMS_041712_NAR_20mM_plus.15267.15267.2	2	4.56	0	6.89E+04		(K)DVLSVAI	(K)D V\L\S V/A/F/S S D N R(Q)		175.98	655.3293	1309.638	0.0131	10	4.21	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
22561	dirMS_041712_NAR_20mM_plus.17794.17794.2	2	4.56	0	7.54E+04	M224m	(R)FVFSLVD	(R)F V|F/S L/V D A m N G K(E)	m:Oxidized methionine	194.18	672.3393	1327.671	15.9998	3.7	5.84	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
22562	dirMS_041712_NAR_30mM_plus2.16099.16099.2	2	4.56	0	2.35E+05		(K)APILIATI	(K)A P|I/L|I|A/T D V A/S R(G)		137.4	613.8551	1226.71	-0.0074	-6	5.88	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
22563	dirMS_041712_NAR_30mM_plus2.17225.17458.2	2	4.56	0	1.27E+05		(K)GPLMM	(K)G/P|L|M/M Y/I S K(M)		144.93	520.2659	1039.532	-0.007	-6.7	8.59	96306.4	6.41	HUMAN	P13639	Elongation factor 2
22564	dirMS_041712_NAR_30mM_plus2.20418.20418.2	2	4.56	0	3.12E+05		(R)FEELNAI	(R)F E|E|L|N A D L F R(G)		161.05	627.3106	1253.616	-0.0022	-1.7	4.14	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
22565	dirMS_041712_NAR_50mM_plus2.15624.15624.3	3	4.56	1	1.00E+06		(R)KVPGVT	(R)K\V P G V T A\I|E|L/D E D T/G T F R(I)		149.88	650.0048	1948.002	-0.0024	-1.2	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
22566	dirMS_041712_NAR_50mM_plus2.18930.18930.3	3	4.56	1	2.70E+05		(K)LALFQAI	(K)L/A|L F/Q A I/G K E V V D/R(A)		167.87	520.3019	1558.895	-0.004	-2.6	6.07	266161	5.68	HUMAN	E9PPU0	Epiplakin
22567	dirMS_041712_NAR_60mM_plus.13882.13882.3	3	4.56	1	4.89E+05		(R)VRTVTV	(R)V R T V/T V/T/L/G D E/K(G)		129.2	439.9237	1317.737	0.0193	14.6	6.04	567942.4	5.76	HUMAN	H0YGL9	Ryanodine receptor 2
22568	dirMS_041712_NAR_60mM_plus.18121.18121.3	3	4.56	0	3.33E+05		(R)SGHEQV	(R)S G H E Q V/V E/M/L L/D R(A)		151.43	504.9258	1512.747	0.0153	10.1	4.65	48586.6	9.32	HUMAN	D6RCB2	Ankyrin-3
22569	dirMS_041712_NAR_120mM_minus.13850.13850.3	3	4.55	1	5.35E+05		(K)ASIHEAV	(K)A/S/I H/E A\W T D/G K E A M L\K(H)		130.1	596.2973	1786.879	-0.0019	-1.1	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
22570	dirMS_041712_NAR_120mM_minus.18261.18261.4	4	4.55	2	1.95E+05	S233s	(K)LKFVAAS	(K)L K F/V A A s Y D I R/G/N F L/K(W)	s:Phosphorylated S	154.23	481.2594	1842.027	79.9885	11.6	9.7	45057.2	5.1	HUMAN	C9JRQ8	Meckelin (Fragment)
22571	dirMS_041712_NAR_120mM_minus.18264.18264.4	4	4.55	2	2.27E+05		(K)IPDHVRE	(K)I P D H\V R E R A W/L T W E K(V)		154.08	484.763	1936.019	0.0114	5.9	6.76	107013.3	8.48	HUMAN	P06400	Retinoblastoma-associated protein
22572	dirMS_041712_NAR_120mM_minus.5704.5704.3	3	4.55	1	3.31E+04		(R)KLSSETY	(R)K L S S E\T/Y S Q/A K(D)		84.58	414.5544	1241.637	0.0114	9.2	8.5	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b
22573	dirMS_041712_NAR_120mM_minus.7061.7061.3	3	4.55	0	5.83E+05		(K)NILGTAT	(K)N/I L/G T A\T/W A E R(L)		93.1	411.2157	1231.643	-0.0104	-8.5	6	36488	9.61	HUMAN	Q8NH59	Olfactory receptor 51Q1
22574	dirMS_041712_NAR_120mM_minus.7837.7837.3	3	4.55	1	3.52E+05		(K)AYAGDK	(K)A Y/A/G D K A/E E I G/R(H)		97.23	427.2156	1279.628	0.0045	3.5	4.68	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
22575	dirMS_041712_NAR_20mM_minus.11095.11217.3	3	4.55	0	5.64E+05	S380s	(R)YGTsPCS	(R)Y G\T s\P C S S A V T R(T)	C:Carbamidomethylation s:N-ace	159.3	496.895	1285.584	203.0863	4.7	8.75	75584.8	7.92	HUMAN	O14640	Segment polarity protein dishevelled homolog DVL-1
22576	dirMS_041712_NAR_20mM_minus.12103.12103.3	3	4.55	1	4.05E+05		(-)XSTDTSM	(-)X S T D T S M/N R/S P K(L)		170.55	446.227	1336.652	0.0139	10.4	8.75	4969.6	8.59	HUMAN	K7ELN8	Matrix metalloproteinase-28 (Fragment)
22577	dirMS_041712_NAR_20mM_minus.9266.9266.2	2	4.55	0	1.25E+05	M55m	(R)VLGmTL	(R)V L|G m T L I/Q K(C)	m:Oxidized methionine	142.9	509.8017	1002.602	15.9945	-0.4	8.72	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
22578	dirMS_041712_NAR_40mM_minus2.10692.10692.3	3	4.55	0	4.28E+04		(R)DAGEGL	(R)D A/G E G L/L A V/Q I T D Q E G K P K(R)		147.53	657.0157	1969.024	0.0089	4.5	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
22579	dirMS_041712_NAR_50mM_minus2.9037.9037.3	3	4.55	0	5.99E+04	S88s	(R)AAGGPA	(R)A A G G P A G P A s G/G/V Q L P R(C)	s:Phosphorylated S	119.88	514.9262	1462.776	79.9879	14	9.79	14385.2	11.75	HUMAN	Q6NT52-2	Isoform 2 of Choriogonadotropin subunit beta variant 2
22580	dirMS_041712_NAR_60mM_minus.17098.17098.3	3	4.55	1	3.47E+04		(K)DREGFF	(K)D R E G F\F/T/N G L/T L G A K(K)		155.48	542.6145	1625.828	0.0008	0.5	6.07	9954.3	9.57	HUMAN	C9J0J7	Profilin-2
22581	dirMS_041712_NAR_120mM_plus.13975.13975.4	4	4.55	0	7.94E+05	N644n	(R)VGAVLLI	(R)V G A V L L N L/Q H G D S/n L/R(E)	n:N-acetylglucosamine (N)	126.32	478.0137	1705.934	203.0986	10.1	6.71	73369.4	4.48	HUMAN	E7EMG8	Protocadherin-15
22582	dirMS_041712_NAR_120mM_plus.7972.7972.4	4	4.55	2	1.13E+05	M347m	(K)AEEEKGI	(K)A E E E K G N/D/L L/S R V N m L K(N)	m:Oxidized methionine	95.17	491.2553	1946.001	15.9982	1.7	4.87	96757.6	5.95	HUMAN	C9JYJ6	Filamin A-interacting protein 1-like (Fragment)
22583	dirMS_041712_NAR_120mM_plus.8758.8758.3	3	4.55	0	1.08E+06		(R)RPELEDS	(R)R P E L\E|D S T/L/R(Y)		98.58	405.8796	1215.633	-0.0085	-7	4.68	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
22584	dirMS_041712_NAR_120mM_plus.9202.9202.4	4	4.55	1	5.90E+05	T1481t	(R)GLRYHP	(R)G L R\Y H P/I D I E t S V S R(I)	t:N-acetylglucosamine (T)	101.47	487.2578	1742.918	203.091	6	6.75	173713.6	9.03	HUMAN	Q9P265	Disco-interacting protein 2 homolog B
22585	dirMS_041712_NAR_20mM_plus.15328.15328.2	2	4.55	0	2.38E+04	M73m	(R)AILVDLE	(R)A I L\V D\L/E/P G T m/D S V R(S)	m:Oxidized methionine	176.97	816.4181	1615.836	15.9929	-1.2	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
22586	dirMS_041712_NAR_20mM_plus.6680.6680.2	2	4.55	0	7.62E+04	M1m M2m	(-)mmEVAA	(-)m\m|E V A A A D/V/K(Q)	m:Oxidized methionine	110.9	548.754	1064.512	31.9892	-0.5	4.37	9475.6	4.64	HUMAN	J3KRD5	Cytosolic non-specific dipeptidase (Fragment)
22587	dirMS_041712_NAR_30mM_plus2.12822.12822.2	2	4.55	0	2.73E+05		(K)LDADYP	(K)L/D/A\D/Y P L R(V)		120.7	481.7538	962.494	0.0062	6.4	4.21	18169.4	9.62	HUMAN	F8VVL1	Density-regulated protein
22588	dirMS_041712_NAR_30mM_plus2.19495.19495.2	2	4.55	0	2.99E+05		(K)ILAGQHI	(K)I L/A G Q H/E D A R(E)		156.58	555.2902	1109.57	0.0033	3	5.32	218451.1	8.24	HUMAN	Q8TF72	Protein Shroom3
22589	dirMS_041712_NAR_40mM_plus2.10577.10577.2	2	4.55	0	1.56E+05		(R)GLQDVL	(R)G L/Q/D V L R(T)		128.1	400.7336	800.462	-0.0026	-3.2	5.84	54099	7.15	HUMAN	B4DX20	T-complex protein 1 subunit zeta-2
22590	dirMS_041712_NAR_40mM_plus2.5264.5264.2	2	4.55	0	1.31E+05		(R)DYSGYQ	(R)D Y/S G Y Q/R(D)		87.43	444.6967	888.385	0.0015	1.7	5.83	70523.3	4.94	HUMAN	G3V153	Caprin-1
22591	dirMS_041712_NAR_40mM_plus2.7145.7145.2	2	4.55	0	3.41E+04		(K)VYYYNA	(K)V/Y|Y Y N/A R(T)		101.85	474.7301	948.457	-0.0045	-4.7	8.47	116336.3	8.59	HUMAN	G3V220	Transcription elongation regulator 1
22592	dirMS_041712_NAR_40mM_plus2.8282.8282.2	2	4.55	1	4.32E+04		(R)ESQNGE	(R)E S/Q/N/G E H R N R(G)		109.47	613.7818	1226.562	-0.0058	-4.7	6.86	61229.6	6.22	HUMAN	H7C022	WD repeat-containing protein 60 (Fragment)
22593	dirMS_041712_NAR_50mM_plus2.12253.12253.3	3	4.55	0	2.98E+05		(K)IISSLSSA	(K)I I|S S L S S/A F H V F\E D G N K(E)		132.42	617.6485	1850.928	0.0026	1.4	5.32	116924.5	6.11	HUMAN	E9PC26	Mitotic checkpoint serine/threonine-protein kinase BUB1
22594	dirMS_041712_NAR_50mM_plus2.19328.19328.3	3	4.55	0	1.27E+05		(R)LSPISHG	(R)L S/P I/S H G N T I/A L F F R(S)		169.75	558.3077	1672.917	-0.0084	-5	9.75	77292.9	5.96	HUMAN	Q9BQ70	Transcription factor 25
22595	dirMS_041712_NAR_60mM_plus.11956.11956.3	3	4.55	1	1.08E+06		(R)QKAQVE	(R)Q K A Q V E Q/E/L/T/T L R(L)		120.05	515.2865	1543.844	0.0011	0.7	6.14	533778	5.74	HUMAN	Q15149	Plectin
22596	dirMS_041712_NAR_60mM_plus.16823.16823.3	3	4.55	1	8.61E+05	K302k	(K)IPAPDKV	(K)I P/A P D K\V\P T P E k(M)	k:Ubiquitin-K	145.52	469.2606	1291.726	114.0416	-0.9	6.07	70689.1	5.6	HUMAN	A4FU49	SH3 domain-containing protein 21
22597	dirMS_041712_NAR_120mM_minus.7356.7356.3	3	4.54	0	3.10E+04		(R)TLHGQE	(R)T L H G Q E/T/Y T/P R(L)		94.37	434.8858	1302.644	-0.0008	-0.6	6.41	35021.8	6.18	HUMAN	B4DF47	Protein misato homolog 1
22598	dirMS_041712_NAR_20mM_minus.8730.8730.2	2	4.54	1	9.88E+04		(R)SYRDLDI	(R)S Y/R/D L\D K P R(R)		137.25	575.3098	1149.601	0.0112	9.8	8.31	37704.1	10.13	HUMAN	Q8NAV1	Pre-mRNA-splicing factor 38A
22599	dirMS_041712_NAR_30mM_minus2.16819.16819.2	2	4.54	1	1.51E+05		(R)LGTSGTA	(R)L G/T/S G T A K/K(T)		145.58	431.7497	862.499	-0.0071	-8.3	10	19068	5.9	HUMAN	Q13522	Protein phosphatase 1 regulatory subunit 1A
22600	dirMS_041712_NAR_30mM_minus2.17245.17245.2	2	4.54	0	2.06E+04		(K)MIFVGIK	(K)M I/F V/G I K(K)		147.95	404.2383	807.48	-0.0104	-12.9	8.5	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
22601	dirMS_041712_NAR_30mM_minus2.5163.5163.2	2	4.54	0	1.56E+05		(R)AAEQYT	(R)A A/E/Q Y T P K(A)		81.5	454.2271	907.452	-0.005	-5.6	6.04	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
22602	dirMS_041712_NAR_50mM_minus2.12765.12765.3	3	4.54	0	2.74E+05		(K)AASDIAN	(K)A A S D I/A M T\E L/P P/T H P I R(L)		140.63	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
22603	dirMS_041712_NAR_50mM_minus2.13752.13752.3	3	4.54	1	2.01E+04		(R)YGSDIVF	(R)Y/G S/D I|V/P F S K V D E E Q M K(Y)		146.8	657.9852	1971.937	0.0042	2.1	4.32	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
22604	dirMS_041712_NAR_50mM_minus2.15678.15678.3	3	4.54	1	2.35E+05		(K)DVLFLKD	(K)D V/L\F L K/D C V/G/P E/V/E K(A)	C:Carbamidomethylation	156.5	583.3014	1747.893	-0.0039	-2.2	4.32	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
22605	dirMS_041712_NAR_50mM_minus2.16149.16149.3	3	4.54	0	1.99E+05		(R)DEPIHILI	(R)D E/P I H I L N V A I K(T)		160.45	454.5974	1361.779	-0.0011	-0.8	5.32	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
22606	dirMS_041712_NAR_50mM_minus2.17981.17981.3	3	4.54	1	1.42E+04		(K)GVPTGF	(K)G V/P/T/G F I L P I R D|I R(A)		171.02	518.6444	1553.916	0.0024	1.6	9.6	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
22607	dirMS_041712_NAR_60mM_minus.15150.15150.3	3	4.54	1	2.35E+04		(K)IREIADG	(K)I R E/I A D G\L\C|L/E V E G/K(M)	C:Carbamidomethylation	143.95	567.965	1701.884	-0.0035	-2.1	4.41	18253.3	4.7	HUMAN	E9PJF7	Translationally-controlled tumor protein (Fragment)
22608	dirMS_041712_NAR_60mM_minus.18587.18587.3	3	4.54	0	2.72E+05		(K)LHDNLII	(K)L H D/N L I|I/S\D L E N/T V K(K)		165.78	575.3117	1723.922	-0.0019	-1.1	4.54	88624.6	5.09	HUMAN	C9J8U1	Cytospin-A (Fragment)
22609	dirMS_041712_NAR_60mM_minus.7047.7047.3	3	4.54	0	1.04E+05		(K)TQAYQD	(K)T Q/A/Y Q D Q K/P G T S G L R(K)		97.58	550.6109	1649.824	-0.006	-3.7	8.25	61733.3	6.3	HUMAN	P36871	Phosphoglucomutase-1
22610	dirMS_041712_NAR_60mM_minus.7733.7733.3	3	4.54	1	5.55E+05		(R)YLAEVA	(R)Y L/A E|V A A G D D K K(G)		102.08	427.222	1279.653	-0.0014	-1.1	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
22611	dirMS_041712_NAR_60mM_minus.8889.9160.3	3	4.54	0	1.87E+06	M451m	(R)HSSLHTS	(R)H S S\L\H T/S/D V m Q E K(N)	m:Oxidized methionine	110.22	505.5677	1498.696	15.9931	-1.2	5.99	61322.5	9.53	HUMAN	Q9GZX5	Zinc finger protein 350
22612	dirMS_041712_NAR_120mM_plus.6820.6820.3	3	4.54	1	1.39E+05		(R)RQQEVE	(R)R/Q\Q\E\V/E/T E/L K(M)		88.68	420.5562	1259.659	-0.005	-3.9	4.79	51612.9	9.98	HUMAN	P08621	U1 small nuclear ribonucleoprotein 70 kDa
22613	dirMS_041712_NAR_20mM_plus.14048.14048.2	2	4.54	0	1.13E+05	K54k	(K)QFIPNVA	(K)Q/F I/P/N V A E k(T)	k:Ubiquitin-K	169.77	580.3169	1045.568	114.0589	13.7	6	50005.7	8.51	HUMAN	Q15465	Sonic hedgehog protein
22614	dirMS_041712_NAR_20mM_plus.17162.17162.3	3	4.54	1	1.17E+04	M1033m	(K)NRLVNIm	(K)N R L/V N\I m P/Y E/L T R(V)	m:Oxidized methionine	189.77	545.6246	1618.873	15.9859	-5.5	8.75	144181.4	6.29	HUMAN	F2Z3B8	Receptor-type tyrosine-protein phosphatase F
22615	dirMS_041712_NAR_30mM_plus2.16573.16573.2	2	4.54	0	5.92E+05		(K)LVAAFG	(K)L V A|A F G|E L R(S)		139.45	488.28	975.562	-0.0095	-9.7	6	215847.5	7.03	HUMAN	A3KMH1	von Willebrand factor A domain-containing protein 8
22616	dirMS_041712_NAR_40mM_plus2.10189.10189.3	3	4.54	0	1.35E+05	M1087m	(R)mPLPAP	(R)m P|L|P A P S L S\H Q/P P P A P R(V)	m:Oxidized methionine	124.5	603.6536	1792.953	15.9936	-0.7	9.52	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
22617	dirMS_041712_NAR_40mM_plus2.10830.10830.3	3	4.54	0	2.22E+05		(R)LLEAQAC	(R)L L|E/A/Q A C/T G G I I H P T T/G Q K(L)	C:Carbamidomethylation	128.95	665.6807	1995.033	-0.0052	-2.6	6.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
22618	dirMS_041712_NAR_50mM_plus2.13128.13128.3	3	4.54	0	3.85E+05		(K)VQASLA	(K)V Q/A S L/A A N T/F T\I/T G H A/E T K(Q)		137.68	654.0087	1960.013	-0.0019	-1	6.72	11802.2	5.6	HUMAN	D6RDG3	Transcription factor BTF3 (Fragment)
22619	dirMS_041712_NAR_50mM_plus2.8577.8577.3	3	4.54	1	1.35E+05		(K)EAALSTA	(K)E A\A L/S/T A/L S E K R(T)		112.45	425.8966	1275.69	-0.0151	-11.8	6.24	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
22620	dirMS_041712_NAR_50mM_plus2.9969.9969.3	3	4.54	1	2.46E+06		(K)ATAVVD	(K)A T|A V/V D/G A F K E V/K(L)		120.07	445.5822	1334.731	0.0006	0.5	6.11	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
22621	dirMS_041712_NAR_60mM_plus.17634.17634.3	3	4.54	1	4.48E+05		(R)AKELLGC	(R)A K E\L L\G\Q|G L/L L R(S)		148.85	437.6093	1310.815	-0.0021	-1.6	8.79	106155.7	5.45	HUMAN	B5ME19	Eukaryotic translation initiation factor 3 subunit C
22622	dirMS_041712_NAR_120mM_minus.4378.4378.3	3	4.53	1	1.50E+07	M310m	(R)TKTEISEm	(R)T\K T E I/S E/m N R(N)	m:Oxidized methionine	72.87	408.8693	1208.594	15.9994	3.7	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
22623	dirMS_041712_NAR_20mM_minus.12488.12488.3	3	4.53	0	2.42E+05	M256m	(R)SLDmDS	(R)S L D m D S/I/I A E/V K(A)	m:Oxidized methionine	172.42	446.227	1320.671	15.9949	0	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
22624	dirMS_041712_NAR_20mM_minus.7534.7534.2	2	4.53	0	6.81E+05	M239m	(K)EVDEQm	(K)E V|D E Q m L|N V/Q N\K(N)	m:Oxidized methionine	123.75	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
22625	dirMS_041712_NAR_30mM_minus2.11424.11424.2	2	4.53	0	1.11E+05		(R)VVLLAEC	(R)V V|L L A E G R(L)		116.5	428.7653	856.525	-0.0018	-2	5.97	60034.4	6.5	HUMAN	O43865	Putative adenosylhomocysteinase 2
22626	dirMS_041712_NAR_30mM_minus2.12198.12198.2	2	4.53	0	4.11E+04		(K)QALSGF	(K)Q/A/L/S/G F G/Y R(L)		119.07	499.7499	998.505	-0.0129	-12.9	8.75	21925.1	5.16	HUMAN	O75340	Programmed cell death protein 6
22627	dirMS_041712_NAR_50mM_minus2.13870.13870.3	3	4.53	0	3.05E+04		(K)EAFTNKI	(K)E A|F T/N K/P N V/F T V V T R(G)		147.05	574.9724	1722.917	-0.0147	-8.5	8.85	258215.9	5.48	HUMAN	E7EN95	Filamin-B
22628	dirMS_041712_NAR_50mM_minus2.14732.14732.3	3	4.53	0	3.94E+05		(K)YPIEHGI	(K)Y/P/I E H G I I/T N|W D/D/M E K(I)		152.43	654.3084	1960.911	-0.0003	-0.1	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
22629	dirMS_041712_NAR_50mM_minus2.18128.18128.3	3	4.53	0	8.78E+04		(R)EAVELPL	(R)E A\V/E L/P L/T H F E L/Y/K(Q)		171.98	563.634	1688.889	-0.002	-1.2	4.75	47479.5	5.09	HUMAN	P43686	26S protease regulatory subunit 6B
22630	dirMS_041712_NAR_60mM_minus.17423.17423.3	3	4.53	1	1.68E+05		(R)TKEEALE	(R)T\K E E A L E L\I/N/G\Y I Q K(I)		157.78	583.6501	1748.943	-0.0071	-4.1	4.78	16245.7	9.47	HUMAN	K7EMU7	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1
22631	dirMS_041712_NAR_120mM_plus.12363.12363.3	3	4.53	0	5.06E+04		(R)HVFGES	(R)H V F G E/S D E/L/I/G Q K(V)		117.77	486.9124	1458.722	0.0003	0.2	4.65	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
22632	dirMS_041712_NAR_120mM_plus.14684.14684.4	4	4.53	2	1.37E+06		(R)YLYTLVI	(R)Y L Y/T/L V/I/T D K E K/A E K(L)		130.85	454.2533	1813.995	-0.0032	-1.8	6.18	7621.9	10.1	HUMAN	J3KT73	60S ribosomal protein L38
22633	dirMS_041712_NAR_120mM_plus.5322.5322.3	3	4.53	1	7.52E+04		(R)GSQGGN	(R)G S/Q/G/G N/F E G P N K R(R)		81.23	449.8829	1347.64	-0.0059	-4.3	8.75	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
22634	dirMS_041712_NAR_120mM_plus.9295.9295.4	4	4.53	0	1.57E+05	K43k	(K)TIkTNDP	(K)T I k T/N D/P G V\L Q A A R(Y)	k:Ubiquitin-K	101.58	400.2199	1483.823	114.0351	-4.9	8.41	16910.2	9.64	HUMAN	O76096	Cystatin-F
22635	dirMS_041712_NAR_20mM_plus.17493.17493.2	2	4.53	0	7.39E+05		(R)VLITTDL	(R)V L|I/T/T D L L A R(G)		191.58	557.8442	1114.683	-0.0019	-1.7	5.81	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
22636	dirMS_041712_NAR_20mM_plus.18326.18326.3	3	4.53	0	2.70E+04		(K)EGPAVV	(K)E G/P/A V\V G/Q/F/I Q D V K(N)		197.33	496.2646	1486.79	-0.0108	-7.2	4.37	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
22637	dirMS_041712_NAR_20mM_plus.7538.7538.2	2	4.53	0	2.30E+04		(R)TVGIVGI	(R)T V|G I/V G N Q P K(V)		121	506.7922	1012.579	-0.0014	-1.4	8.41	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
22638	dirMS_041712_NAR_30mM_plus2.22201.22201.2	2	4.53	0	9.50E+04		(-)MLPLSLL	(-)M/L/P L S L L K(T)		171.97	457.7881	914.574	-0.0054	-5.9	8.5	15520.6	10.36	HUMAN	Q9Y4Z0	U6 snRNA-associated Sm-like protein LSm4
22639	dirMS_041712_NAR_30mM_plus2.8171.8171.3	3	4.53	0	4.58E+05		(K)SNVSDA	(K)S N\V S D A V/A/Q/S T R(I)		96.4	412.2004	1234.602	-0.0156	-12.6	5.55	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
22640	dirMS_041712_NAR_50mM_plus2.10747.10747.3	3	4.53	0	4.20E+05		(K)TSEVDLA	(K)T/S/E/V D L/A K P L V K(F)		123.78	433.922	1299.752	-0.0004	-0.3	5.73	17178.3	5.63	HUMAN	C9IZF9	Programmed cell death 6-interacting protein (Fragment)
22641	dirMS_041712_NAR_50mM_plus2.17182.17182.3	3	4.53	0	7.10E+05		(K)VLISSLQ	(K)V L I/S/S L Q D C L H G I E S K(S)	C:Carbamidomethylation	159.15	600.3189	1798.937	0.0054	3	5.32	52440.1	6	HUMAN	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6
22642	dirMS_041712_NAR_60mM_plus.5613.5613.3	3	4.53	0	7.68E+04		(R)TAEHEA	(R)T A/E H E/A\A Q|Q/D L Q/S/K(F)		87.8	519.2487	1555.735	-0.0031	-2	4.65	156557.7	5.52	HUMAN	Q86UP2	Kinectin
22643	dirMS_041712_NAR_60mM_plus.6118.6118.3	3	4.53	0	3.55E+05	S277s	(K)NACTAIL	(K)N/A C T/A I L s\V E K(R)	C:Carbamidomethylation s:Phosp	89.45	429.2022	1205.619	79.9726	4.9	6	38984.4	5.08	HUMAN	H3BTF5	Methyltransferase-like protein 22
22644	dirMS_041712_NAR_120mM_minus.18177.18177.4	4	4.52	1	1.95E+05		(K)YYITIIDA	(K)Y Y\I/T I/I/D/A P G/H R D F I K(N)		154.23	481.2594	1922.017	-0.0013	-0.7	6.75	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
22645	dirMS_041712_NAR_120mM_minus.20364.20364.4	4	4.52	0	2.45E+05		(K)ALEHAFC	(K)A L E/H A F\Q/L E H/I/M/D L T R(L)		167.78	481.7478	1923.975	-0.0052	-2.7	5.27	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
22646	dirMS_041712_NAR_20mM_minus.11457.11457.2	2	4.52	0	2.34E+05		(R)LSEYNGY	(R)L S\E|Y N G Y G K(S)		162.23	515.7416	1030.484	-0.0081	-7.8	6	70321.2	9.88	HUMAN	F8WEL6	Zinc finger protein 567
22647	dirMS_041712_NAR_30mM_minus2.17486.17486.2	2	4.52	0	2.29E+05		(R)NGGQIL	(R)N G\G Q/I|L I A D L R(G)		149.22	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
22648	dirMS_041712_NAR_50mM_minus2.5781.5781.3	3	4.52	1	4.10E+04		(R)ATEGMV	(R)A/T|E G M/V V/A D K N C S K(I)	C:Carbamidomethylation	94.57	503.9058	1509.704	-0.0007	-0.5	6.11	15607.8	9.99	HUMAN	B4E0P1	Proteasome (Prosome, macropain) subunit, beta type, 7, isoform CRA_b
22649	dirMS_041712_NAR_60mM_minus.18242.18242.3	3	4.52	1	1.92E+04		(R)ELRVEQI	(R)E L R V E Q E\S/L|L T\A F R(C)		162.8	564.3094	1690.912	0.0014	0.8	4.79	54229.5	5.12	HUMAN	Q9UBB4	Ataxin-10
22650	dirMS_041712_NAR_60mM_minus.9413.9413.3	3	4.52	0	1.04E+05	M409m	(K)VLAmSG	(K)V/L|A m|S G D P N Y/L H R(M)	m:Oxidized methionine	112.23	496.9147	1472.732	15.9981	2.1	6.71	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
22651	dirMS_041712_NAR_20mM_plus.11084.11084.2	2	4.52	0	2.17E+05		(K)LVIITAGA	(K)L V|I I/T A/G A/R(Q)		147.98	457.2945	913.583	-0.0012	-1.3	9.75	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
22652	dirMS_041712_NAR_20mM_plus.13447.13447.2	2	4.52	0	1.18E+05	M98m	(R)TLTIVDT	(R)T L|T/I/V/D T G\I G/m T K(A)	m:Oxidized methionine	165.38	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
22653	dirMS_041712_NAR_20mM_plus.9302.9302.2	2	4.52	0	5.23E+03	Y144y	(R)LEVNTLy	(R)L/E/V N/T/L y Y R(Y)	y:Phosphorylated Y	135.38	625.7909	1170.615	79.9592	-5.7	6	20048.4	6.84	HUMAN	F8W8D9	Peptidyl-alpha-hydroxyglycine alpha-amidating lyase
22654	dirMS_041712_NAR_30mM_plus2.18335.18335.2	2	4.52	0	1.64E+04		(K)VVNSILA	(K)V V|N/S I L/A F/R(E)		149.52	509.8031	1018.604	-0.0055	-5.4	9.72	56564.1	6.56	HUMAN	B4DNW0	Aminoacylase-1
22655	dirMS_041712_NAR_30mM_plus2.21269.21269.2	2	4.52	0	3.90E+05		(R)VNQAIW	(R)V N Q/A/I/W/L/L/C T G A R(E)	C:Carbamidomethylation	166.88	751.3976	1501.794	-0.0065	-4.3	9.72	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
22656	dirMS_041712_NAR_40mM_plus2.13034.13034.3	3	4.52	0	5.72E+04		(R)LQAYHT	(R)L Q/A Y H T Q T T/P L/I E Y Y R(K)		143.12	666.3423	1997.013	-0.0004	-0.2	6.75	21283.1	6.45	HUMAN	F8VY04	Adenylate kinase 2, mitochondrial
22657	dirMS_041712_NAR_50mM_plus2.10594.10594.2	2	4.52	1	1.53E+06		(R)DGKLVS	(R)D G K\L/V|S E S S D/V L/P K(-)		122.85	737.3925	1473.78	-0.0018	-1.2	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
22658	dirMS_041712_NAR_50mM_plus2.10733.10733.3	3	4.52	0	4.29E+05		(K)MIVDPV	(K)M I/V D/P V/E/P H G E/M K(F)		123.43	494.5783	1481.713	0.0076	5.2	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
22659	dirMS_041712_NAR_50mM_plus2.12584.12584.3	3	4.52	0	2.08E+05		(K)TVTSATI	(K)T V/T/S A/T I/V Y H L A R(Q)		133.68	477.9357	1431.795	-0.0029	-2	8.44	125655.3	6.18	HUMAN	Q92900	Regulator of nonsense transcripts 1
22660	dirMS_041712_NAR_50mM_plus2.12920.12920.3	3	4.52	0	1.82E+05		(K)SLLVPDH	(K)S L\L V/P/D H V/I T R(L)		136.25	417.2467	1249.726	-0.0008	-0.6	6.46	19837.4	6.59	HUMAN	D3DQ64	Adenylate kinase isoenzyme 4, mitochondrial
22661	dirMS_041712_NAR_50mM_plus2.14026.14026.3	3	4.52	1	5.24E+05		(R)VLELVSI	(R)V L/E L|V\S I/T A N K N T C P G D R(S)	C:Carbamidomethylation	141.7	663.0129	1987.028	-0.0036	-1.8	6.04	45186.1	9.89	HUMAN	B4DLV4	Serine hydroxymethyltransferase
22662	dirMS_041712_NAR_50mM_plus2.7073.7073.3	3	4.52	1	6.78E+04	S40s	(R)sRDIDAL	(R)s R D/I D/A/L L/A R(E)	s:N-acetylglucosamine (S)	102.53	444.9099	1129.632	203.0828	2.5	5.68	44449.6	9.98	HUMAN	Q03113	Guanine nucleotide-binding protein subunit alpha-12
22663	dirMS_041712_NAR_120mM_minus.10012.10012.3	3	4.51	0	5.96E+05		(R)HGESAW	(R)H G E S A W\N/L/E/N R(F)		109.4	438.2098	1312.603	0.012	9.1	5.4	28917.5	6.68	HUMAN	P18669	Phosphoglycerate mutase 1
22664	dirMS_041712_NAR_120mM_minus.14133.14133.4	4	4.51	2	6.24E+05		(K)MEIATKI	(K)M/E I A T K D P L N/P/I K/Q D/V/K(K)		131.67	485.7686	1940.052	0.0004	0.2	5.88	33115.9	5.54	HUMAN	Q15181	Inorganic pyrophosphatase
22665	dirMS_041712_NAR_20mM_minus.9222.9222.2	2	4.51	0	1.58E+04		(R)IITEGFEA	(R)I/I/T E G/F E/A\A K(E)		142.02	539.7915	1078.578	-0.0022	-2	4.53	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
22666	dirMS_041712_NAR_30mM_minus2.18588.18588.2	2	4.51	0	2.10E+04		(R)LDFNLIR	(R)L/D/F/N L I R(V)		155.7	445.759	890.509	0.0013	1.5	5.84	18956.4	6.97	HUMAN	C9JLK0	Phosphoribosylaminoimidazolecarboxamide formyltransferase (Fragment)
22667	dirMS_041712_NAR_30mM_minus2.20010.20010.2	2	4.51	0	8.99E+05	M224m S2	(K)TVmGIG	(K)T V m|G I G s G G E R(A)	m:Oxidized methionine s:N-a	168.33	641.8137	1063.52	219.1001	20.1	5.66	35782.1	9.87	HUMAN	Q9H340	Olfactory receptor 51B6

22668	dirMS_041712_NAR_40mM_minus2.14738.14738.3	3	4.51	0	8.80E+04		(K)LVLIGSN	(K)L V/L I/G S N H\S L P F L/K(F)		171.6	513.3088	1537.91	0.0018	1.2	8.76	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
22669	dirMS_041712_NAR_50mM_minus2.12821.12821.3	3	4.51	0	6.74E+05	M114m M:	(R)AGKPVI(	(R)A G K\P V I\C A/T/Q m|L E S m I K(K)	C:Carbamidomethylation m:Oxid	140.27	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
22670	dirMS_041712_NAR_50mM_minus2.16368.16368.3	3	4.51	0	5.32E+04		(K)TTIENIQ	(K)T T/I E/N I/Q/L/P H T L L S R(F)		161.2	579.326	1735.97	-0.0067	-3.8	6.41	95792.4	6.36	HUMAN	J3KPV4	DNA replication licensing factor MCM4
22671	dirMS_041712_NAR_60mM_minus.13808.13808.3	3	4.51	1	2.00E+05		(R)GLTESR\	(R)G L T E S R V L/V G/G/L/R(A)		137.73	452.9408	1356.796	0.0121	8.9	9.6	82367	6.46	HUMAN	J3KQU5	Ephrin type-B receptor 6
22672	dirMS_041712_NAR_60mM_minus.14430.14430.3	3	4.51	2	2.19E+05	K184k	(R)AKVIAAE	(R)A K V I A A E G E M/N A|S R A L k(E)	k:Ubiquitin-K	140.22	625.0044	1758.953	114.0456	1.4	8.63	26077.8	6.86	HUMAN	B4E2V5	Erythrocyte band 7 integral membrane protein
22673	dirMS_041712_NAR_60mM_minus.15541.15541.3	3	4.51	1	1.97E+05		(R)ASLISAV	(R)A S|L/I S A V/S D K L R(W)		146.18	420.5811	1259.732	-0.003	-2.4	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
22674	dirMS_041712_NAR_60mM_minus.16612.16612.3	3	4.51	1	1.13E+05		(K)KLSTIAL/	(K)K L S T I A L|A/L/G V E R(T)		151.93	457.6153	1370.837	-0.0052	-3.8	8.75	52669.1	4.73	HUMAN	A8MY67	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform
22675	dirMS_041712_NAR_120mM_plus.20720.20720.4	4	4.51	1	2.82E+06		(K)AAIDWF	(K)A A|I/D W/F D G K E F H G N I/I K(V)		160.7	491.0027	1960.992	-0.0026	-1.3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
22676	dirMS_041712_NAR_120mM_plus.5083.5083.3	3	4.51	1	2.82E+05	M163m	(K)IYEDGDI	(K)I/Y E/D G/D D D m K/R(T)	m:Oxidized methionine	79.62	458.195	1356.574	15.9968	1.4	4.03	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
22677	dirMS_041712_NAR_20mM_plus.13907.13907.3	3	4.51	0	3.12E+04		(R)GLCAIA(	(R)G L C A\I A/Q/A E/S L/R(Y)	C:Carbamidomethylation	167.38	430.2281	1288.668	0.002	1.5	6	18529.2	9.98	HUMAN	E9PL45	40S ribosomal protein S3
22678	dirMS_041712_NAR_20mM_plus.17893.17893.2	2	4.51	0	1.97E+05	S99s	(R)VDGLAF	(R)V D G L/A F|V N E D/I V A s K(G)	s:N-acetylglucosamine (S)	195.15	890.4414	1576.822	203.0538	-14.4	4.03	27007.4	5.06	HUMAN	H7C5N7	Leucine-rich repeat and WD repeat-containing protein 1 (Fragment)
22679	dirMS_041712_NAR_30mM_plus2.12205.12205.3	3	4.51	2	3.42E+05		(R)AEATAG	(R)A E A T A G R G/A D/R/A/R(T)		116.8	434.558	1301.667	-0.0074	-5.7	9.56	46321.6	6.17	HUMAN	B4DNX3	Advanced glycosylation end product-specific receptor
22680	dirMS_041712_NAR_40mM_plus2.11397.11397.2	2	4.51	0	4.95E+04	M320m	(K)YmACCL	(K)Y m|A|C C L L Y R(G)	C:Carbamidomethylation m:Oxid	133.18	633.2788	1249.553	15.9977	2.2	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
22681	dirMS_041712_NAR_40mM_plus2.15211.15211.3	3	4.51	0	1.32E+05		(R)IETMLGI	(R)I E|T M L G D V/A V/A V H P K(D)		156.07	527.286	1579.851	-0.0078	-4.9	5.32	141718.6	7.8	HUMAN	B0V043	Valine--tRNA ligase
22682	dirMS_041712_NAR_40mM_plus2.5822.5822.2	2	4.51	1	1.68E+05		(R)SKQAEE	(R)S K Q A E\E\E|F(-)		92.1	484.2219	967.437	-0.0002	-0.2	4.25	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
22683	dirMS_041712_NAR_50mM_plus2.13821.13821.3	3	4.51	1	5.33E+05	K461k	(K)DAKYEL\	(K)D/A K Y\E L/V k A\L A N/S/K(T)	k:Ubiquitin-K	140.47	555.3007	1549.858	114.0291	-8.3	8.43	56594.1	5.35	HUMAN	Q16401	26S proteasome non-ATPase regulatory subunit 5
22684	dirMS_041712_NAR_50mM_plus2.7154.7154.3	3	4.51	1	2.89E+04	T391t Y396	(K)GDYStKI	(K)G D Y S t K K/H V y G N G/Y S K(A)	t:Phosphorylated T y:Phosph	103.15	655.273	1803.866	159.9384	2.9	9.31	57499.4	5.77	HUMAN	Q15223	Poliovirus receptor-related protein 1
22685	dirMS_041712_NAR_120mM_minus.12457.12457.3	3	4.5	1	2.91E+05		(K)ARLENEI	(K)A R L E N E I/A\T/Y/R(N)		121.97	445.9006	1335.701	-0.0143	-10.7	6.19	51115.6	4.9	HUMAN	O76014	Keratin, type I cuticular Ha7
22686	dirMS_041712_NAR_120mM_minus.9675.9675.3	3	4.5	1	1.97E+05		(K)IRSLQEC	(K)I R/S L\Q\E\Q/A/D/A A E/E R(A)		106.9	539.2683	1615.803	-0.0131	-8.1	4.41	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
22687	dirMS_041712_NAR_20mM_minus.10161.10161.3	3	4.5	0	3.04E+04		(K)IEDLSQC	(K)I/E D L S Q Q A/Q/L A A/A E K(F)		151.12	538.9478	1614.833	-0.0045	-2.8	4.14	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
22688	dirMS_041712_NAR_40mM_minus2.13571.13571.3	3	4.5	1	1.19E+05		(R)CITDPQT	(R)C I|T D/P Q T/G L C L L/P L K E K(K)	C:Carbamidomethylation	164.02	662.684	1986.04	-0.0024	-1.2	6.07	533778	5.74	HUMAN	Q15149	Plectin
22689	dirMS_041712_NAR_40mM_minus2.15638.15638.3	3	4.5	0	1.90E+05		(K)GAEILEV	(K)G A/E I/L/E V L/H S L/P A V R(Q)		182.13	535.3104	1603.917	0	0	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
22690	dirMS_041712_NAR_50mM_minus2.12304.12304.3	3	4.5	2	2.06E+04	T208t M21	(K)LAGtEAI	(K)L/A G t E A P R/m R S\D N K(E)	t:N-acetylglucosamine (T) m:	138.1	588.9539	1545.78	219.0669	-4.2	8.75	47309.8	10.2	HUMAN	Q15697	Zinc finger protein 174
22691	dirMS_041712_NAR_50mM_minus2.17807.17807.3	3	4.5	1	2.28E+05	M116m	(R)ELAILLG	(R)E L|A I/L/L/G m L D P A E K D E K(G)	m:Oxidized methionine	170.82	634.3353	1884.999	15.9927	-1.2	4.18	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
22692	dirMS_041712_NAR_50mM_minus2.17946.17946.3	3	4.5	0	1.99E+05		(R)IHFPLAT	(R)I H F P L A T Y A/P V I/S A E K(A)		170.4	586.3248	1756.963	-0.0034	-1.9	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
22693	dirMS_041712_NAR_60mM_minus.11842.11842.3	3	4.5	1	4.61E+05	M232m	(R)MSmKE\	(R)M S m K E V\D E\Q|M/L/N V Q/N K(N)	m:Oxidized methionine	125.58	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
22694	dirMS_041712_NAR_60mM_minus.14762.14762.3	3	4.5	1	4.06E+05		(R)IKIGDPL	(R)I K\I G D P\L|L/E D/T R(M)		142.42	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
22695	dirMS_041712_NAR_60mM_minus.16961.16961.3	3	4.5	1	2.52E+05		(K)YAVLYQ	(K)Y A|V L/Y Q/P L F D K R(F)		154.6	504.9409	1512.821	-0.0128	-8.4	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
22696	dirMS_041712_NAR_60mM_minus.7562.7562.3	3	4.5	1	6.22E+04	T93t	(R)ITtTAAC	(R)I/T/t T A A C M M D L R R(Y)	C:Carbamidomethylation t:N-ace	101.22	581.6072	1539.744	203.063	-9.4	9.6	47729.5	9.33	HUMAN	E7EV50	Gamma-aminobutyric acid receptor subunit beta-2
22697	dirMS_041712_NAR_60mM_minus.8355.8355.3	3	4.5	0	7.55E+04		(K)HTGPNS	(K)H T G P N|S P D\T A/N/D G F/V R(L)		106.42	562.2608	1684.767	0.0005	0.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
22698	dirMS_041712_NAR_120mM_plus.6460.6460.2	2	4.5	0	1.42E+05		(R)LTEDEVE	(R)L/T/E/D E V E K(L)		87.23	481.7305	962.468	-0.014	-14.5	4	22102.8	5.03	HUMAN	P08590	Myosin light chain 3
22699	dirMS_041712_NAR_20mM_plus.11622.11622.2	2	4.5	0	1.09E+05		(K)LITPAVV	(K)L I|T/P A V V/S\E R(L)		151.6	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
22700	dirMS_041712_NAR_20mM_plus.9288.9288.2	2	4.5	0	6.34E+03	M388m	(R)IITVSmE	(R)I I|T/V/S m E D V/K(I)	m:Oxidized methionine	135.23	575.8029	1134.608	15.991	-3.4	4.37	59953.2	6.14	HUMAN	G3V1R4	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b
22701	dirMS_041712_NAR_50mM_plus2.12587.12587.3	3	4.5	1	2.82E+05		(R)YMVADI	(R)Y/M/V A D K F T E L Q/K(A)		134.55	491.5877	1472.745	0.0032	2.2	6.07	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
22702	dirMS_041712_NAR_50mM_plus2.17962.17962.3	3	4.5	0	2.49E+05		(R)VTMLFL	(R)V/T/M L F L G L H\N V R(Q)		162.78	467.267	1399.788	-0.0014	-1	9.73	21721.5	5.37	HUMAN	H7BZ35	Aspartate--tRNA ligase, cytoplasmic (Fragment)
22703	dirMS_041712_NAR_60mM_plus.10737.10737.3	3	4.5	1	6.85E+05		(R)KAGNFY	(R)K A G N F\Y V/P/A E|P K(L)		114.58	440.9074	1320.695	0.013	9.8	8.5	24489.6	10.74	HUMAN	A8MUD9	60S ribosomal protein L7
22704	dirMS_041712_NAR_60mM_plus.20486.20486.3	3	4.5	1	6.94E+05		(K)IKYPENF	(K)I K/Y/P E N\F F/L L R(G)		167.97	480.6056	1439.805	-0.0023	-1.6	8.59	33222.3	5.74	HUMAN	A6NNR3	Serine/threonine-protein phosphatase
22705	dirMS_041712_NAR_120mM_minus.10961.10961.3	3	4.49	1	2.36E+05		(R)TNEKVE	(R)T N|E K V E L\Q/E L/N D R(F)		114.1	529.9368	1587.797	-0.0014	-0.9	4.41	49709.6	5.19	HUMAN	B0YJC4	Vimentin
22706	dirMS_041712_NAR_120mM_minus.16592.16592.3	3	4.49	0	6.43E+05		(R)EHALLA\	(R)E H A\L\L/A/Y/T L G V K(Q)		145.08	438.9186	1314.742	-0.0004	-0.3	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
22707	dirMS_041712_NAR_120mM_minus.18574.18574.3	3	4.49	1	1.33E+05		(R)ARFEELI	(R)A R F E E\L|N/A/D L/F R(G)		155.98	494.2561	1480.754	-0.0006	-0.4	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
22708	dirMS_041712_NAR_20mM_minus.9023.9023.2	2	4.49	0	3.02E+05	T27t M30n	(R)QPEWtV	(R)Q P E W\t V P m/G H V(-)	t:N-acetylglucosamine (T) m:	139.95	750.3397	1280.609	219.0629	-7.6	5.24	3896.4	6.92	HUMAN	K7EJH9	ATP-dependent RNA helicase DHX8 (Fragment)
22709	dirMS_041712_NAR_30mM_minus2.6045.6045.2	2	4.49	0	2.56E+05		(K)TSEVNC	(K)T/S/E/V/N C Y R(C)	C:Carbamidomethylation	87.2	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
22710	dirMS_041712_NAR_60mM_minus.14226.14226.3	3	4.49	0	2.34E+05		(K)DLAGCII	(K)D L|A G C I/H G L S N V K(L)	C:Carbamidomethylation	138.65	461.9064	1383.705	-0.0003	-0.2	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
22711	dirMS_041712_NAR_120mM_plus.14584.14584.4	4	4.49	2	8.39E+05		(R)YLYTLVI	(R)Y L Y\T/L V I/T D K E K A E/K(L)		130.45	454.2533	1813.995	-0.0032	-1.8	6.18	7621.9	10.1	HUMAN	J3KT73	60S ribosomal protein L38
22712	dirMS_041712_NAR_120mM_plus.23653.23653.3	3	4.49	0	7.17E+05		(R)LHFFMP	(R)L H F F\M\P/G\F\A/P\L T S R(G)		179.03	540.9492	1620.835	-0.0025	-1.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
22713	dirMS_041712_NAR_20mM_plus.8224.8224.2	2	4.49	0	8.52E+04		(K)TAVCDII	(K)T A/V/C D/I/P\P R(G)	C:Carbamidomethylation	127.53	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
22714	dirMS_041712_NAR_30mM_plus2.20165.20165.2	2	4.49	0	2.05E+05		(R)ALFLIPRI	(R)A L/F/L I\P R(N)		159.05	415.2703	829.529	0.0039	4.7	9.79	40728.4	6.05	HUMAN	C9J338	TRAF2 and NCK-interacting protein kinase (Fragment)
22715	dirMS_041712_NAR_30mM_plus2.20551.20551.2	2	4.49	0	8.79E+04		(K)SVVTSIF	(K)S V|V/T S I F G V K(N)		162.57	518.799	1036.604	-0.013	-12.5	8.47	132902.3	5.82	HUMAN	J3KR24	Isoleucine--tRNA ligase, cytoplasmic
22716	dirMS_041712_NAR_30mM_plus2.4900.4900.2	2	4.49	0	1.86E+05		(K)NCSETQ	(K)N C/S E/T Q Y/E S K(V)	C:Carbamidomethylation	77	623.256	1245.505	-0.0005	-0.4	4.53	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
22717	dirMS_041712_NAR_30mM_plus2.8177.8177.2	2	4.49	0	5.88E+05		(R)LAEAAV.	(R)L/A|E/A/A V A E K(R)		97.15	451.2545	901.499	0.0028	3.1	4.53	268433.7	6.24	HUMAN	A4D212	DKFZP586J0619 protein
22718	dirMS_041712_NAR_40mM_plus2.16131.16131.3	3	4.49	1	1.28E+05	M253m S2	(K)LLIHmR\	(K)L L I H m R V H s/G/E K P N K(C)	m:Oxidized methionine s:N-a	161.52	660.0113	1758.98	219.0398	-17.4	9.99	67401.6	7.99	HUMAN	Q8NBF1	Zinc finger protein GLIS1
22719	dirMS_041712_NAR_40mM_plus2.6391.6391.2	2	4.49	0	1.22E+04		(R)LYLNGD	(R)L/Y|L/N G D G T G K(R)		96.83	519.2719	1037.526	0.0103	9.9	5.83	47132.7	5.78	HUMAN	Q13077	TNF receptor-associated factor 1
22720	dirMS_041712_NAR_50mM_plus2.14164.14164.3	3	4.49	1	3.82E+05		(R)NVIFQP\	(R)N V/I F\Q/P\V A E/L K K(Q)		142.4	462.6094	1385.815	-0.0015	-1.1	8.59	23167	8.94	HUMAN	B1APP8	6-phosphofructokinase type C
22721	dirMS_041712_NAR_60mM_plus.15034.15034.3	3	4.49	0	5.61E+05		(R)YLDLHD	(R)Y/L|D L/H D C Y L K(Y)	C:Carbamidomethylation	135	447.2169	1339.635	0.001	0.8	5.21	52796.2	5.19	HUMAN	E7EUT8	Splicing factor 3A subunit 3
22722	dirMS_041712_NAR_60mM_plus.18699.18699.3	3	4.49	1	9.11E+04		(R)YEEIVKE	(R)Y/E/E I V K E V S T Y I/K(K)		155.43	534.2888	1600.847	0.005	3.1	4.79	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
22723	dirMS_041712_NAR_60mM_plus.8303.8303.3	3	4.49	2	2.30E+05		(K)NLKVPS(	(K)N L\K\V\P|S G Q\N A/D V Q K T D N(-)		101.57	609.9803	1827.92	0.0068	3.7	5.96	11018.4	8.89	HUMAN	B0AZT5	N-alpha-acetyltransferase 50
22724	dirMS_041712_NAR_60mM_plus.9091.9091.3	3	4.49	0	2.11E+06		(K)NCPHIV	(K)N C|P H I V|V G T P G/R(I)	C:Carbamidomethylation	106.15	436.2272	1306.669	-0.0014	-1.1	9.75	28185.1	10.76	HUMAN	B4DIJ6	Spliceosome RNA helicase DDX39B
22725	dirMS_041712_NAR_120mM_minus.10099.10099.4	4	4.48	0	1.65E+05	T3t	(-)XDtLVNV	(-)X D t L V\N W/D F V E Q V/R(I)	t:N-acetylglucosamine (T)	109.07	484.9989	1733.886	203.0881	4.5	4.03	21374.4	6.38	HUMAN	H0YFN9	RING finger protein 10 (Fragment)
22726	dirMS_041712_NAR_120mM_minus.17195.17195.4	4	4.48	2	5.34E+05		(K)KDEKTD	(K)K D E K T D T L E|D\L\F/P T/T K(I)		149.03	470.9848	1880.949	-0.0314	-16.7	4.44	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
22727	dirMS_041712_NAR_120mM_minus.19342.19342.3	3	4.48	1	3.72E+05		(K)NLRDIDI	(K)N L R D I D\E\V|S/S L L/R(T)		161.42	510.614	1529.828	-0.0007	-0.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
22728	dirMS_041712_NAR_120mM_minus.8301.8301.3	3	4.48	1	3.19E+05		(K)DSIFFRD	(K)D/S/I F F R/D/G I R(Q)		99.6	409.2126	1225.632	-0.0091	-7.5	5.96	107927.3	6.37	HUMAN	Q75V66	Anoctamin-5
22729	dirMS_041712_NAR_30mM_minus2.16125.16125.2	2	4.48	0	1.30E+05		(R)SLVSGLI	(R)S L|V|S G/L I R(L)		141.85	422.7649	844.525	-0.0026	-3	9.47	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
22730	dirMS_041712_NAR_30mM_minus2.6868.6868.2	2	4.48	1	1.31E+05	K273k	(K)SKDSMG	(K)S\K/D S M G/A/D k(E)	k:Ubiquitin-K	91.83	526.7389	938.425	114.0458	2.7	5.68	35627.8	8.96	HUMAN	Q9NQN1	Olfactory receptor 2S2
22731	dirMS_041712_NAR_40mM_minus2.13257.13257.3	3	4.48	1	1.24E+05	T486t	(K)VTNSTEI	(K)V T/N S T E L Q/H/Q/L D K t K(Q)	t:N-acetylglucosamine (T)	160.9	648.9911	1741.908	203.0508	-14.7	6.72	163432.8	5.55	HUMAN	Q15075	Early endosome antigen 1
22732	dirMS_041712_NAR_50mM_minus2.7922.7922.3	3	4.48	1	6.36E+04		(R)GSTGSSI	(R)G S T G S S/D L/N D/Q E P G P R T P K(S)		112.08	648.3014	1942.91	-0.0204	-10.5	4.56	82206.1	9.28	HUMAN	Q8TDW5	Synaptotagmin-like protein 5
22733	dirMS_041712_NAR_50mM_minus2.8666.8666.3	3	4.48	1	4.19E+04	M88m	(K)DVDEAY	(K)D V/D E A Y/m N/K V E/L E S R(L)	m:Oxidized methionine	117.5	605.2717	1797.832	15.9682	-14.7	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
22734	dirMS_041712_NAR_50mM_minus2.9618.9618.3	3	4.48	0	1.73E+05	M329m	(K)SNmGHI	(K)S N/m G H P E/P A/S\G L A/A L A K(V)	m:Oxidized methionine	122.73	556.279	1650.827	15.9956	0.4	6.47	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
22735	dirMS_041712_NAR_120mM_plus.10748.10748.3	3	4.48	1	5.01E+06	S306s	(R)DHHMS(	(R)D H H M S G W s/Y/K R V E K(S)	s:N-acetylglucosamine (S)	108.87	654.972	1759.833	203.0681	-5.7	8.51	51648.4	5.55	HUMAN	B7XGB9	Protein phosphatase 1M
22736	dirMS_041712_NAR_120mM_plus.11646.11646.3	3	4.48	1	1.18E+06		(K)MKEIAE/	(K)M K E I A/E A Y/L/G K(T)		114.3	418.2253	1252.661	0.0008	0.6	5.9	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
22737	dirMS_041712_NAR_120mM_plus.13158.13158.3	3	4.48	1	4.96E+05		(R)KQITME	(R)K Q I T M\E|E/L V/R(S)		122.25	416.2263	1246.682	-0.018	-14.5	6.14	533778	5.74	HUMAN	Q15149	Plectin
22738	dirMS_041712_NAR_120mM_plus.13199.13199.3	3	4.48	1	8.52E+05	M316m	(K)RISEQFT	(K)R I S E\Q\F/T|A m F\R(R)	m:Oxidized methionine	122.3	467.9029	1385.699	15.9947	-0.1	9.6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
22739	dirMS_041712_NAR_120mM_plus.15175.15175.4	4	4.48	2	6.75E+05		(K)TVGVEP.	(K)T V/G V E/P|A A D G K G V V V V I K R(R)		132.43	474.2836	1894.112	0.0005	0.3	8.26	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
22740	dirMS_041712_NAR_20mM_plus.11619.11619.2	2	4.48	0	9.38E+04		(R)AQAALA	(R)A Q\A\A L|A|V N I/S A A R(G)		153.22	628.3565	1255.712	-0.006	-4.8	9.79	58479.6	6.23	HUMAN	P40227	T-complex protein 1 subunit zeta
22741	dirMS_041712_NAR_20mM_plus.17159.17159.2	2	4.48	0	6.47E+04		(R)EGGSIP\	(R)E G G S\I|P V/T\L T F/Q E A T|G K(N)		189.4	867.9453	1734.891	-0.0075	-4.3	4.53	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
22742	dirMS_041712_NAR_20mM_plus.8257.8257.2	2	4.48	0	3.33E+05	M176m	(K)VLEGmE	(K)V L|E|G m E V V\R(K)	m:Oxidized methionine	126.95	524.278	1031.555	15.9933	-1.5	4.53	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
22743	dirMS_041712_NAR_20mM_plus.9146.9146.2	2	4.48	0	2.11E+05		(R)VLTVIN(	(R)V L/T V/I|N Q T Q K(E)		133.33	572.3399	1143.673	-0.0007	-0.6	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
22744	dirMS_041712_NAR_30mM_plus2.5736.5736.2	2	4.48	0	1.78E+05	M57m	(K)EmGTPD	(K)E m/G T/P/D/V R(I)	m:Oxidized methionine	84.45	460.7158	904.419	16.005	11	4.37	15175.4	10.46	HUMAN	B7Z4C8	60S ribosomal protein L31
22745	dirMS_041712_NAR_30mM_plus2.6285.6285.2	2	4.48	0	2.52E+05		(K)GEGQLG	(K)G E|G Q/L/G/P A E R(A)		87.53	507.2537	1013.501	-0.0009	-0.9	4.53	96306.4	6.41	HUMAN	P13639	Elongation factor 2
22746	dirMS_041712_NAR_40mM_plus2.12387.12387.3	3	4.48	1	3.43E+04	M357m	(R)ALAEIAK	(R)A L/A/E I/A\K A E L D D T/P m R(G)	m:Oxidized methionine	139.65	587.3006	1743.895	15.9927	-1.3	4.32	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
22747	dirMS_041712_NAR_40mM_plus2.5278.5278.2	2	4.48	0	1.31E+05		(R)DYSGYQ	(R)D Y/S/G Y Q/R(D)		87.43	444.6967	888.385	0.0015	1.7	5.83	70523.3	4.94	HUMAN	G3V153	Caprin-1
22748	dirMS_041712_NAR_40mM_plus2.8944.8944.2	2	4.48	1	5.34E+04	M447m	(K)QRIDEFE	(K)Q R I D\E/F E/A|m(-)	m:Oxidized methionine	114.6	577.7598	1138.52	15.9926	-2	4.14	52734.7	5.88	HUMAN	F5H1A7	Radixin
22749	dirMS_041712_NAR_50mM_plus2.10816.10816.3	3	4.48	1	4.68E+05		(R)ALRETLF	(R)A L\R E T\L|P A\E/Q D/L T T K(N)		125.08	562.6377	1685.907	-0.0083	-4.9	4.68	26790	6.25	HUMAN	F5GX11	Proteasome subunit alpha type-1
22750	dirMS_041712_NAR_50mM_plus2.12569.12569.3	3	4.48	0	1.77E+05		(R)DLNYCF!	(R)D L|N Y C F S G/M S D/H R(Y)	C:Carbamidomethylation	133.72	534.5542	1601.647	0.0009	0.6	5.21	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
22751	dirMS_041712_NAR_50mM_plus2.7314.7314.3	3	4.48	1	1.93E+05		(R)IVEQDTI	(R)I/V/E Q D/T M/P P K G V R(H)		104.88	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
22752	dirMS_041712_NAR_50mM_plus2.7596.7596.3	3	4.48	0	4.08E+04		(K)VDNDEN	(K)V/D/N/D E/N E H Q L/S L R(T)		105.65	523.5793	1568.73	-0.0066	-4.2	4.31	6862.5	4.32	HUMAN	E5RGW4	Nucleophosmin (Fragment)
22753	dirMS_041712_NAR_60mM_plus.18863.18863.3	3	4.48	0	1.52E+05		(R)NHPGLL	(R)N H/P G L L L|M/D T T F R(D)		156.58	505.6001	1514.778	0.0073	4.8	6.74	130372.9	6.37	HUMAN	P11498	Pyruvate carboxylase, mitochondrial
22754	dirMS_041712_NAR_60mM_plus.5249.5249.3	3	4.48	1	3.55E+05		(K)MSSPED	(K)M/S S/P E D/D S D T K R(L)		85.33	456.5289	1367.574	-0.0022	-1.6	4.23	103309.5	5.34	HUMAN	A0AV56	SAFB protein
22755	dirMS_041712_NAR_20mM_minus.14370.14370.2	2	4.47	0	2.52E+05		(R)APGSGL.	(R)A/P G S G/L A/L\L/P L K(I)		198.32	568.8551	1136.704	-0.0008	-0.7	8.8	266161	5.68	HUMAN	E9PPU0	Epiplakin
22756	dirMS_041712_NAR_20mM_minus.14636.14636.2	2	4.47	0	8.83E+04		(R)IITLTGPT	(R)I I/T\L T/G P T N A I F K(A)		201.33	694.9107	1388.815	-0.0007	-0.5	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
22757	dirMS_041712_NAR_30mM_minus2.15660.15660.2	2	4.47	0	1.24E+05		(K)APGFAQ	(K)A/P|G F A Q M L/K(E)		139.2	481.7625	962.513	0.0049	5.1	8.8	60047.9	5.54	HUMAN	G5E9B2	Chaperonin containing TCP1, subunit 8 (Theta), isoform CRA_a
22758	dirMS_041712_NAR_30mM_minus2.6158.6158.2	2	4.47	1	9.06E+04	M433m	(K)VMAQQ	(K)V/M A/Q Q m K K(V)	m:Oxidized methionine	87.87	490.2513	963.511	15.9839	-11.2	10	116341.2	5.72	HUMAN	H3BUD4	Inactive phospholipase C-like protein 1 (Fragment)
22759	dirMS_041712_NAR_30mM_minus2.6710.6710.2	2	4.47	0	2.34E+05		(R)QQYESV	(R)Q Q/Y/E/S V A A/K(N)		89.95	512.2534	1023.511	-0.011	-10.8	6	49709.6	5.19	HUMAN	B0YJC4	Vimentin
22760	dirMS_041712_NAR_40mM_minus2.12550.12550.3	3	4.47	1	4.81E+04		(K)ALLQDK	(K)A L L Q D K D V\I|A\I/N Q D P L G K(Q)		157.28	651.0317	1951.086	-0.0053	-2.7	4.43	49507.6	5.35	HUMAN	P06280	Alpha-galactosidase A
22761	dirMS_041712_NAR_50mM_minus2.6165.6165.3	3	4.47	0	5.69E+04		(R)ASAAPK	(R)A S/A/A P K/P E P/V P V Q K(V)		97.78	473.6033	1418.8	-0.0048	-3.4	8.64	23930.8	10.06	HUMAN	F5H0X8	PDZ and LIM domain protein 5
22762	dirMS_041712_NAR_50mM_minus2.8763.8763.2	2	4.47	1	2.25E+05	M88m	(K)DVDEAY	(K)D V D/E A Y m/N K V\E/L E S R(L)	m:Oxidized methionine	117.97	907.4161	1797.832	15.9926	-1.3	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
22763	dirMS_041712_NAR_60mM_minus.7279.7279.3	3	4.47	0	1.06E+05		(K)NEDSVE	(K)N/E D S V|E L/L V L G R(T)		99.57	448.5786	1343.717	0.0047	3.5	4.14	66506.5	9.04	HUMAN	E9PNU3	Immunoglobulin-like domain-containing receptor 2
22764	dirMS_041712_NAR_20mM_plus.10920.10920.2	2	4.47	0	1.17E+05		(K)EITALAP	(K)E I|T A/L A P S T M K(I)		148.15	581.3129	1161.618	0.0001	0.1	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
22765	dirMS_041712_NAR_20mM_plus.13771.13771.2	2	4.47	0	5.87E+04		(K)ASAELAI	(K)A S A E L/A\L|G E\N S E/V L K(S)		166.93	765.8991	1530.801	-0.0101	-6.6	4.25	47916.2	9.44	HUMAN	P00505	Aspartate aminotransferase, mitochondrial
22766	dirMS_041712_NAR_20mM_plus.16280.16280.2	2	4.47	0	9.81E+04		(R)LLDAQL/	(R)L L\D\A/Q\L\A T G G\I/V\D/P R(L)		184.28	769.9362	1538.854	0.0114	7.4	4.21	533778	5.74	HUMAN	Q15149	Plectin
22767	dirMS_041712_NAR_20mM_plus.16506.16506.2	2	4.47	0	8.23E+04		(R)LGSTVF\	(R)L G\S/T\V/F V/A N L D Y K(V)		184.92	713.8819	1426.758	-0.0011	-0.8	5.83	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
22768	dirMS_041712_NAR_30mM_plus2.20711.20711.2	2	4.47	0	1.14E+04	K24k	(K)kVHFGSI	(K)k V H F/G/S I H D A/V R(A)	k:Ubiquitin-K	162.1	740.3971	1365.739	114.0483	3.7	8.76	59764.7	5.89	HUMAN	E9PIL2	Ankyrin repeat domain-containing protein 42
22769	dirMS_041712_NAR_30mM_plus2.23458.23458.2	2	4.47	0	4.40E+05		(R)IAIYELLF	(R)I A/I/Y E/L\L F K(E)		190.4	555.3331	1109.661	-0.0016	-1.4	6	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
22770	dirMS_041712_NAR_30mM_plus2.8074.8074.2	2	4.47	0	1.63E+05		(R)MYSYPA	(R)M/Y|S/Y P A R(V)		96.25	444.2085	887.408	0.0017	1.9	8.35	32085.2	8.93	HUMAN	B4DY08	Heterogeneous nuclear ribonucleoproteins C1/C2
22771	dirMS_041712_NAR_40mM_plus2.7175.7175.2	2	4.47	0	4.46E+04		(R)QGANIN	(R)Q G/A\N I/N E/I/R(Q)		101.92	507.7713	1014.533	0.0026	2.6	6	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
22772	dirMS_041712_NAR_50mM_plus2.11335.11335.3	3	4.47	1	4.13E+05		(R)MLFKDI	(R)M L/F/K D D Y P S S/P P K(C)		127.05	508.9188	1524.74	0.0016	1	5.71	20685.4	9.18	HUMAN	B0QYN7	SUMO-conjugating enzyme UBC9
22773	dirMS_041712_NAR_50mM_plus2.21112.21112.3	3	4.47	0	3.08E+05		(K)HSQFIG\	(K)H S Q\F\I G\Y/P\I/T L F V E K(E)		180.18	593.6536	1778.948	-0.0013	-0.8	6.75	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
22774	dirMS_041712_NAR_50mM_plus2.22331.22331.3	3	4.47	1	2.09E+04		(K)WLNKYF	(K)W/L/N/K Y F S L/G N S K(T)		192.93	486.2644	1456.758	0.0203	13.9	9.7	55783	9.52	HUMAN	Q15464	SH2 domain-containing adapter protein B
22775	dirMS_041712_NAR_50mM_plus2.7432.7432.3	3	4.47	1	6.13E+04		(K)MIYASSI	(K)M/I/Y/A S/S K/D A I K(K)		104.95	409.554	1226.645	0.0025	2	8.26	22956	8.8	HUMAN	E9PK25	Cofilin-1
22776	dirMS_041712_NAR_60mM_plus.10002.10002.3	3	4.47	0	1.94E+06		(K)TPVEPE\	(K)T/P V\E P E/V/A/I H R(I)		109.87	416.5628	1247.674	-0.0004	-0.3	5.37	5429.1	9.6	HUMAN	E5RIP1	40S ribosomal protein S20

22777	dirMS_041712_NAR_60mM_plus.17284.17284.3	3	4.47	1	3.92E+05		(R)GFPTIYF	(R)G F/P T I Y F/S/P A N K K(L)		147.2	490.5979	1469.779	0.0004	0.3	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
22778	dirMS_041712_NAR_60mM_plus.7990.7990.3	3	4.47	0	3.83E+04		(R)SLMIQTI	(R)S L M/I/Q T L E A/V K(R)		99.75	411.5685	1232.692	-0.0009	-0.8	5.72	18501.5	10.31	HUMAN	J3KSI8	28S ribosomal protein S7, mitochondrial (Fragment)
22779	dirMS_041712_NAR_60mM_plus.8027.8027.3	3	4.47	1	4.28E+05		(R)FEPYANI	(R)F E/P/Y/A N/P T K R(Y)		100.72	408.2176	1222.622	0.0167	13.7	8.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
22780	dirMS_041712_NAR_30mM_minus2.5751.5751.2	2	4.46	0	8.69E+04		(R)YLSEWK	(R)Y L/S E W/K(H)		85.48	413.2129	825.414	0.0044	5.3	6	55584.4	6.4	HUMAN	Q8IZP7	Heparan-sulfate 6-O-sulfotransferase 3
22781	dirMS_041712_NAR_30mM_minus2.7872.7872.2	2	4.46	0	4.01E+04		(K)TDEGIA\	(K)T D|E/G I/A Y R(G)		97.15	462.7203	924.442	-0.0088	-9.5	4.37	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
22782	dirMS_041712_NAR_40mM_minus2.6656.6656.2	2	4.46	0	3.95E+05		(K)LAADDF	(K)L/A/A/D D/F R(T)		107.52	404.2037	807.399	0.0006	0.7	4.21	48845.9	4.72	HUMAN	C4AM86	Keratin, type I cuticular Ha5
22783	dirMS_041712_NAR_50mM_minus2.9232.9232.3	3	4.46	0	2.32E+04		(R)ADSILAY	(R)A D\S\I/L A Y/H Q Q N V P R(A)		120.72	537.9453	1611.824	-0.0024	-1.5	6.79	157526.3	9.07	HUMAN	Q86UU0	B-cell CLL/lymphoma 9-like protein
22784	dirMS_041712_NAR_50mM_minus2.9265.9265.3	3	4.46	0	1.57E+05		(K)EVVKPV	(K)E V V K P V/P I/T/S/P A V S K(V)		121.18	517.639	1550.915	-0.0128	-8.2	8.69	65142.1	9.24	HUMAN	Q96HC4	PDZ and LIM domain protein 5
22785	dirMS_041712_NAR_50mM_minus2.9875.9875.3	3	4.46	0	8.97E+04	M392m	(K)EmNPAL	(K)E m/N P A/L\G I/D C L H K(G)	C:Carbamidomethylation m:Oxid	124.98	505.2416	1497.719	15.9914	-2.3	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
22786	dirMS_041712_NAR_60mM_minus.15569.15569.3	3	4.46	1	4.03E+05		(R)LLDAQL	(R)L L D\A Q/L A/T G G L V C P A R R(L)	C:Carbamidomethylation	146.22	604.3344	1810.996	-0.007	-3.8	9.6	266161	5.68	HUMAN	E9PPU0	Epiplakin
22787	dirMS_041712_NAR_120mM_plus.12980.12980.4	4	4.46	1	1.55E+06		(K)GVIVDKI	(K)G V/I/V D K D\F S H P Q M/P K(K)		121.9	425.2229	1697.868	0.0018	1.1	6.75	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
22788	dirMS_041712_NAR_20mM_plus.10087.10087.2	2	4.46	0	1.98E+05		(K)GEATVSI	(K)G E/A T V/S F D/D\P P S A K(A)		141.33	710.8324	1420.659	-0.0015	-1.1	4.03	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
22789	dirMS_041712_NAR_20mM_plus.11232.11232.2	2	4.46	0	4.63E+04		(K)STGGAP	(K)S T/G G/A|P\T F/N V T V T K(T)		150.08	690.3592	1379.717	-0.0054	-3.9	8.47	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
22790	dirMS_041712_NAR_20mM_plus.13502.13502.2	2	4.46	0	4.02E+03		(K)SPILVAT	(K)S P I\L/V A T A V A/A R(G)		165.7	584.8517	1168.705	-0.0087	-7.5	9.47	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
22791	dirMS_041712_NAR_20mM_plus.9233.9233.2	2	4.46	0	1.61E+05	M209m	(K)AGAGSA	(K)A G A G S/A T/L/S m A Y A G A/R(F)	m:Oxidized methionine	135.33	735.851	1454.706	15.9891	-4	8.79	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
22792	dirMS_041712_NAR_30mM_plus2.15420.15420.2	2	4.46	0	1.37E+05		(R)LVQLLVI	(R)L V|Q/L/L V R(A)		133.77	420.7864	840.567	-0.001	-1.2	9.75	85391.9	5.57	HUMAN	B4DGU4	Catenin beta-1
22793	dirMS_041712_NAR_30mM_plus2.4858.4858.2	2	4.46	0	3.07E+05	M71m	(K)ETmQSL	(K)E/T/m/Q S L N/D R(L)	m:Oxidized methionine	77.28	555.2469	1093.494	15.9923	-2.4	4.37	48845.9	4.72	HUMAN	C4AM86	Keratin, type I cuticular Ha5
22794	dirMS_041712_NAR_50mM_plus2.17260.17260.3	3	4.46	1	8.98E+05		(R)VYAEDP	(R)V/Y/A/E D|P Y K S F G L/P S I G R(L)		159.22	633.6509	1898.965	-0.0265	-14	6.04	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
22795	dirMS_041712_NAR_50mM_plus2.7333.7333.3	3	4.46	0	1.68E+05		(R)SGSSQEI	(R)S G S S Q/E/L/D V/K/P S A S P Q E R(S)		103.85	634.6443	1901.92	-0.0016	-0.8	4.68	227779.5	12.08	HUMAN	I3L2L6	Serine/arginine repetitive matrix protein 2
22796	dirMS_041712_NAR_120mM_minus.10025.10025.2	2	4.45	1	1.62E+05		(R)KNGFVV	(R)K\N G/F V/V|L/K(G)		108.88	452.7844	904.562	0.0001	0.1	10	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
22797	dirMS_041712_NAR_120mM_minus.12363.12363.2	2	4.45	1	1.50E+05		(-)MPVRAA	(-)M P/V/R/A A D/K(L)		120.97	444.2406	887.477	-0.0028	-3.2	8.5	43388.2	9.74	HUMAN	G3V4X8	SNW domain-containing protein 1
22798	dirMS_041712_NAR_20mM_minus.10740.10740.2	2	4.45	1	7.04E+04	Y372y	(K)yNHHISS	(K)y N H H I/S/S H K E S K(E)	y:Phosphorylated Y	155.32	773.8407	1466.714	79.9606	-3.7	8.52	108059.4	9.53	HUMAN	E9PPC4	Endonuclease RAG1
22799	dirMS_041712_NAR_20mM_minus.11485.11485.2	2	4.45	0	1.40E+05	M98m	(R)TLTIVDT	(R)T L T\I/V/D/T G I/G m/T/K(A)	m:Oxidized methionine	163.17	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
22800	dirMS_041712_NAR_30mM_minus2.15896.15896.2	2	4.45	0	2.40E+05		(K)EGALDLS	(K)E/G A L/D L/S/G L R(A)		139.27	515.7847	1030.553	0.0094	9.1	4.37	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
22801	dirMS_041712_NAR_30mM_minus2.16347.16347.2	2	4.45	0	1.37E+05		(K)STFVNIL	(K)S T|F/V/N I L K(Q)		142.58	461.2712	921.54	-0.0053	-5.7	8.47	23232.7	5.07	HUMAN	D6RCP9	Deoxycytidine kinase
22802	dirMS_041712_NAR_40mM_minus2.9524.9524.3	3	4.45	0	9.99E+04		(K)AASDIAI	(K)A A S D I/A M T E L P/P T/H P I R(L)		138.25	607.3174	1819.937	0.0006	0.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
22803	dirMS_041712_NAR_50mM_minus2.10474.10474.3	3	4.45	0	1.12E+05	M271m	(R)DLSYCLS	(R)D L/S Y/C/L S G m Y D/H R(Y)	C:Carbamidomethylation m:Oxid	128.07	544.8966	1616.683	15.9921	-1.7	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
22804	dirMS_041712_NAR_50mM_minus2.11787.11787.3	3	4.45	1	3.31E+05		(K)AVLFCLS	(K)A V/L F/C L S E D K/K(N)	C:Carbamidomethylation	135.95	437.2326	1309.682	0.0012	0.9	6.11	22956	8.8	HUMAN	E9PK25	Cofilin-1
22805	dirMS_041712_NAR_50mM_minus2.5778.5778.3	3	4.45	1	4.10E+04		(R)ATEGM\	(R)A T/E G M V V/A D K N/C/S K(I)	C:Carbamidomethylation	94.57	503.9058	1509.704	-0.0007	-0.5	6.11	15607.8	9.99	HUMAN	B4E0P1	Proteasome (Prosome, macropain) subunit, beta type, 7, isoform CRA_b
22806	dirMS_041712_NAR_50mM_minus2.6153.6153.3	3	4.45	1	7.30E+03	M365m	(R)IVEQDTı	(R)I/V|E\Q D T m/P P K G V R(H)	m:Oxidized methionine	97.75	495.9271	1469.778	15.9887	-4.2	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
22807	dirMS_041712_NAR_50mM_minus2.8141.8141.3	3	4.45	1	1.88E+05		(K)GILAADI	(K)G I/L|A/A D E S T G S/I/A K R(L)		114.12	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
22808	dirMS_041712_NAR_60mM_minus.10580.10605.3	3	4.45	1	6.53E+05		(K)TAVCDIF	(K)T A|V/C/D I/P/P R G L K(M)	C:Carbamidomethylation	118.72	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
22809	dirMS_041712_NAR_60mM_minus.13061.13061.3	3	4.45	0	6.54E+05		(K)GIHPTIIS	(K)G I H/P T I\I/S E/S F Q K(A)		132.97	486.2642	1456.78	-0.0014	-1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
22810	dirMS_041712_NAR_60mM_minus.13795.13795.3	3	4.45	1	6.66E+05		(K)LLYNLRA	(K)L L Y\N L R\A S\L N K(N)		136.17	435.5926	1304.768	-0.0052	-4	9.99	25189.6	6.21	HUMAN	G3V2D4	NADP-dependent oxidoreductase domain-containing protein 1 (Fragment)
22811	dirMS_041712_NAR_60mM_minus.16140.16140.3	3	4.45	0	2.57E+05		(R)HDPTSEI	(R)H D\P T S\E\N\I/L Q/L V K(A)		150.22	498.6051	1493.796	0.0049	3.3	5.32	13564.4	5.9	HUMAN	F8VZ98	Serine/threonine-protein kinase D1 (Fragment)
22812	dirMS_041712_NAR_60mM_minus.6991.6991.3	3	4.45	0	1.16E+05	S25s	(R)QTGALM	(R)Q T|G A L M A s/S P Q D I K(F)	s:N-acetylglucosamine (S)	97.45	550.6109	1446.726	203.0924	7.9	5.84	59048.7	9.04	HUMAN	P04053	DNA nucleotidylexotransferase
22813	dirMS_041712_NAR_120mM_plus.10851.10851.3	3	4.45	1	5.19E+05		(K)GFVEFA	(K)G F/V/E F A A K/P P A R K(A)		110	473.2689	1417.795	-0.0029	-2	9.99	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
22814	dirMS_041712_NAR_120mM_plus.13274.13274.2	2	4.45	0	8.76E+04		(R)DYLHYIR	(R)D Y/L/H\Y I R(K)		122.77	490.2536	979.5	0.0003	0.3	6.74	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
22815	dirMS_041712_NAR_20mM_plus.11964.11964.3	3	4.45	0	3.52E+05		(K)ITFDDYI	(K)I T F D D Y I A C C\V K(L)	C:Carbamidomethylation	155.65	502.2264	1504.681	-0.0164	-10.9	4.21	20629.9	5.11	HUMAN	A8MTH6	Sorcin
22816	dirMS_041712_NAR_20mM_plus.6420.6420.2	2	4.45	0	4.23E+04		(R)GPQVQ(	(R)G P Q V|Q Q|P P P S N R(F)		107.15	652.8373	1304.671	-0.0033	-2.5	9.75	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
22817	dirMS_041712_NAR_20mM_plus.7545.7545.2	2	4.45	0	2.93E+04		(K)VTLTSEE	(K)V T/L/T S/E E E A R(L)		120.93	567.7865	1134.564	0.002	1.8	4.25	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
22818	dirMS_041712_NAR_20mM_plus.9464.9464.2	2	4.45	0	1.86E+05		(K)SVTNED	(K)S V/T N E\D/V T\Q/E E L G G A K(T)		136	838.9014	1676.797	-0.0018	-1.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
22819	dirMS_041712_NAR_30mM_plus2.18090.18090.2	2	4.45	1	6.20E+05	M1060m	(K)IDEmDK	(K)I D/E/m D K/I L K(K)	m:Oxidized methionine	146.98	560.7925	1104.597	15.9808	-12.6	4.56	156850.5	5.11	HUMAN	H0YCZ2	Protein CASC5 (Fragment)
22820	dirMS_041712_NAR_40mM_plus2.10442.10442.2	2	4.45	0	9.40E+04		(K)IGGIGTV	(K)I/G G I|G T/V P V G R(V)		125.75	513.3081	1025.61	-0.0013	-1.2	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
22821	dirMS_041712_NAR_40mM_plus2.17791.17791.3	3	4.45	0	1.06E+05		(R)MPVIKP	(R)M/P V|I K P D I A\N W/E L S V K(L)		170.78	613.999	1840.004	-0.0213	-11.6	5.82	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
22822	dirMS_041712_NAR_40mM_plus2.6748.6748.2	2	4.45	0	1.78E+05		(R)LSEHTQI	(R)L S|E/H T Q R(Y)		98.8	435.7189	870.443	-0.0123	-14.1	6.75	384118.5	5.99	HUMAN	A4UGR9	Xin actin-binding repeat-containing protein 2
22823	dirMS_041712_NAR_50mM_plus2.17817.17817.3	3	4.45	0	2.36E+05		(R)ILVTLLH	(R)I L|V/T L/L H/T L E R(M)		162.35	436.6064	1307.805	0.0001	0.1	6.75	45212.4	9.41	HUMAN	B7Z233	Acetyl-CoA acetyltransferase, cytosolic
22824	dirMS_041712_NAR_50mM_plus2.20614.20614.3	3	4.45	1	1.70E+05		(R)VNSKFD	(R)V N S K F D T/I|Y/Q I L/L K(K)		177.62	561.3209	1681.952	-0.0042	-2.5	8.47	72626.7	9.13	HUMAN	Q14258	E3 ubiquitin/ISG15 ligase TRIM25
22825	dirMS_041712_NAR_60mM_plus.16919.16919.3	3	4.45	1	6.33E+06		(K)LKVPEW	(K)L K V/P E/W|V/D T V K(L)		145.72	438.5872	1313.746	0.0007	0.5	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
22826	dirMS_041712_NAR_60mM_plus.8704.8704.3	3	4.45	0	5.38E+04	K102k	(K)LEAQETI	(K)L E/A/Q/E T L N k G R(Q)	k:Ubiquitin-K	104.95	458.2494	1258.675	114.0587	11.5	6.14	78815.5	4.7	HUMAN	F8W785	Golgi integral membrane protein 4
22827	dirMS_041712_NAR_120mM_minus.16456.16456.3	3	4.44	1	4.15E+05	S678s	(K)LSsFEETI	(K)L/S/s F E/E T N K K(Q)	s:N-acetylglucosamine (S)	144.55	462.5714	1182.6	203.0996	14.6	6.14	162453.6	5.36	HUMAN	Q5TB80	Protein QN1 homolog
22828	dirMS_041712_NAR_120mM_minus.9553.9553.3	3	4.44	0	3.45E+05		(K)NCPHIV\	(K)N C/P H/I V/V/G T/P G R(I)	C:Carbamidomethylation	107.37	436.2293	1306.669	0.0049	3.7	9.75	28185.1	10.76	HUMAN	B4DIJ6	Spliceosome RNA helicase DDX39B
22829	dirMS_041712_NAR_30mM_minus2.12295.12295.2	2	4.44	0	1.70E+05		(R)MLVELS	(R)M L/V E L/S/K(A)		121.17	410.242	819.465	0.0123	15	5.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
22830	dirMS_041712_NAR_30mM_minus2.8963.8963.2	2	4.44	0	1.98E+05		(K)TSSAGP	(K)T/S/S\A G P S T/A/K(L)		103.2	453.7335	906.453	0.007	7.7	8.41	49263.1	9.93	HUMAN	Q96CB8	Integrator complex subunit 12
22831	dirMS_041712_NAR_50mM_minus2.16513.16513.3	3	4.44	1	1.87E+04		(R)EVQLEEI	(R)E V/Q|L/E E L E A A R D L V S K(E)		161.82	610.3273	1828.965	0.0023	1.2	4.25	45984.6	6.24	HUMAN	B4E1G6	Galactokinase
22832	dirMS_041712_NAR_50mM_minus2.9210.9210.3	3	4.44	0	2.32E+04		(R)ADSILAY	(R)A D/S\I/L/A Y H Q Q N V/P R(A)		120.72	537.9453	1611.824	-0.0024	-1.5	6.79	157526.3	9.07	HUMAN	Q86UU0	B-cell CLL/lymphoma 9-like protein
22833	dirMS_041712_NAR_60mM_minus.13986.13986.3	3	4.44	1	9.95E+05	S161s	(K)TFSGLSL	(K)T F S G L S L D V T T K/s A K(E)	s:Phosphorylated S	136.97	545.603	1554.837	79.9571	-5.7	8.26	19365.3	6.73	HUMAN	H0YGG3	Caprin-2 (Fragment)
22834	dirMS_041712_NAR_60mM_minus.17713.17713.3	3	4.44	0	1.40E+05		(R)GGHVVE	(R)G G H V\V E G\L/A/G E/L E Q L R(A)		158.98	555.2959	1663.876	-0.0031	-1.8	4.75	106088.3	5.78	HUMAN	P10275	Androgen receptor
22835	dirMS_041712_NAR_60mM_minus.18989.18989.3	3	4.44	0	2.76E+05		(R)CRPDQL	(R)C R P D Q L/T\G\L\S/L/L/P L S E K(A)	C:Carbamidomethylation	168.15	643.0129	1927.032	-0.0076	-3.9	6.07	533778	5.74	HUMAN	Q15149	Plectin
22836	dirMS_041712_NAR_60mM_minus.6873.6873.3	3	4.44	1	1.09E+05	M281m	(R)SRAEAE	(R)S R A E|A E\S m/Y/Q\I K(Y)	m:Oxidized methionine	96.73	476.895	1412.684	15.9866	-5.8	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
22837	dirMS_041712_NAR_120mM_plus.14447.14447.3	3	4.44	1	2.45E+06		(R)QLREYQ	(R)Q L R E Y\Q|E L/M N V K(L)		128.9	517.6042	1550.8	-0.0015	-1	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
22838	dirMS_041712_NAR_120mM_plus.16179.16179.4	4	4.44	1	1.20E+06		(R)ALEHFTI	(R)A L/E H F T D L/Y D/I/K R(A)		138.48	405.9647	1620.838	-0.0011	-0.7	5.38	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
22839	dirMS_041712_NAR_120mM_plus.6394.6394.3	3	4.44	0	6.55E+04		(K)ILGTAGT	(K)I L/G T A G T E/E G Q K(I)		87.03	401.882	1203.622	0.0099	8.2	4.53	31698.9	8.83	HUMAN	A6NN60	Quinone oxidoreductase
22840	dirMS_041712_NAR_20mM_plus.15945.15945.2	2	4.44	0	6.73E+04		(R)FVNVVP	(R)F V|N V/V\P T/F G K(K)		181.48	554.3056	1107.62	-0.0158	-14.3	8.75	10904.6	11.56	HUMAN	E9PR30	40S ribosomal protein S30
22841	dirMS_041712_NAR_20mM_plus.7947.7947.2	2	4.44	0	1.40E+05	M316m	(R)AmGEQ	(R)A m/G E|Q/A|V/A L A R(A)	m:Oxidized methionine	123.73	566.7967	1116.583	16.0031	7.2	6.05	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
22842	dirMS_041712_NAR_30mM_plus2.7152.7152.2	2	4.44	0	2.12E+04		(R)FYSLLDR	(R)F/Y|S L/L D R(H)		91.88	457.2405	913.478	-0.0041	-4.5	5.83	80603.6	6.78	HUMAN	F5H2E3	Oligophrenin-1
22843	dirMS_041712_NAR_30mM_plus2.8007.8007.3	3	4.44	0	6.82E+05		(K)SNVSDA	(K)S/N\V S D A\V/A Q/S T R(I)		95.82	412.2004	1234.602	-0.0156	-12.6	5.55	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
22844	dirMS_041712_NAR_40mM_plus2.15719.15719.3	3	4.44	1	5.12E+04		(R)IILPPEKI	(R)I I|L/P P E K E L A M/P G E D L K(F)		158.48	631.6874	1893.04	0.0075	4	4.41	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
22845	dirMS_041712_NAR_40mM_plus2.7322.7322.2	2	4.44	0	1.54E+05		(R)SGYFDEI	(R)S G Y/F D/E/R(Y)		103.57	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
22846	dirMS_041712_NAR_60mM_plus.15714.15714.3	3	4.44	1	9.16E+04		(R)KGVEGL	(R)K G V E G L I|D I/E/N P N R(V)		138.8	518.6115	1553.828	-0.0082	-5.3	4.68	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
22847	dirMS_041712_NAR_60mM_plus.20640.20640.3	3	4.44	1	7.00E+05		(K)IKYPENF	(K)I/K Y P E\N F/F L/L R(G)		167.98	480.6056	1439.805	-0.0023	-1.6	8.59	33222.3	5.74	HUMAN	A6NNR3	Serine/threonine-protein phosphatase
22848	dirMS_041712_NAR_120mM_minus.19131.19131.3	3	4.43	1	2.76E+05	M148m	(R)LDLAGR	(R)L/D/L/A G R D L T D/Y L\m K(I)	m:Oxidized methionine	159.78	547.2876	1623.841	16.0072	7.5	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
22849	dirMS_041712_NAR_120mM_minus.20289.20289.3	3	4.43	0	3.63E+05		(K)VHLVGII	(K)V H\L V G\I\D|I/F T G K(K)		166.53	433.5866	1298.747	-0.0015	-1.1	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
22850	dirMS_041712_NAR_120mM_minus.5130.5130.3	3	4.43	1	1.03E+06	M194m	(R)CREmDE	(R)C R E\m/D\E Q/I/R(L)	C:Carbamidomethylation m:Oxid	80.33	418.1844	1236.546	15.9927	-1.8	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
22851	dirMS_041712_NAR_120mM_minus.8443.8443.3	3	4.43	0	1.85E+05		(K)LFQECCI	(K)L F/Q E C C P/H S T D R(V)	C:Carbamidomethylation	99.98	517.2227	1549.652	0.0013	0.9	5.32	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
22852	dirMS_041712_NAR_120mM_minus.8505.8505.3	3	4.43	1	1.51E+05		(K)SKKPAG	(K)S K K P A G G V D\F D E|T(-)		100.87	450.8934	1350.654	0.0121	8.9	4.56	21981.5	5.39	HUMAN	Q9BUH6	Uncharacterized protein C9orf142
22853	dirMS_041712_NAR_30mM_minus2.16429.16429.3	3	4.43	0	6.11E+05		(R)ASLEAAI	(R)A S\L E A A\I/A/D/A E Q R(G)		143.53	448.8965	1344.675	-0.0004	-0.3	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
22854	dirMS_041712_NAR_30mM_minus2.16531.16531.3	3	4.43	0	7.21E+05		(R)ASLEAAI	(R)A S\L E A A\I A/D/A E/Q/R(G)		143.7	448.8965	1344.675	-0.0004	-0.3	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
22855	dirMS_041712_NAR_30mM_minus2.6088.6088.2	2	4.43	0	1.87E+05		(R)VVSSIEC	(R)V V|S S I/E/Q/K(T)		86.83	445.2523	889.499	-0.0016	-1.8	5.97	8491.4	6.28	HUMAN	E5RIR4	14-3-3 protein zeta/delta (Fragment)
22856	dirMS_041712_NAR_50mM_minus2.15656.15656.3	3	4.43	0	1.81E+05		(R)QVVQGI	(R)Q V\V Q|G L L S E/T/Y L E A/H/R(I)		156.92	614.9953	1842.971	0.0005	0.3	5.4	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
22857	dirMS_041712_NAR_50mM_minus2.15791.15791.3	3	4.43	0	8.21E+04	K136k	(R)VGMLGI	(R)V G M L G E k\L E/A|A I/Q R(S)	k:Ubiquitin-K	158.97	543.6248	1514.836	114.0239	-11.7	6.11	45250.9	6.42	HUMAN	G3V0F0	Putative uncharacterized protein MGC45438
22858	dirMS_041712_NAR_50mM_minus2.17779.17779.3	3	4.43	1	2.20E+05		(R)LEEAGG.	(R)L E E A G G A T S A/Q V E L N K/K R(E)		170.8	634.3353	1901.009	-0.0173	-9.1	6.23	223728.5	5.59	HUMAN	P13535	Myosin-8
22859	dirMS_041712_NAR_60mM_minus.16105.16105.3	3	4.43	0	2.48E+05		(R)HDPTSEI	(R)H D\P T S E N|I/L Q/L V/K(A)		150.08	498.6051	1493.796	0.0049	3.3	5.32	13564.4	5.9	HUMAN	F8VZ98	Serine/threonine-protein kinase D1 (Fragment)
22860	dirMS_041712_NAR_60mM_minus.18120.18120.3	3	4.43	0	9.48E+04		(R)NSVSNF	(R)N/S|V|S N F L H S L E R(G)		162.5	468.2409	1402.707	0.0008	0.6	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
22861	dirMS_041712_NAR_60mM_minus.19673.19673.3	3	4.43	1	2.41E+05		(R)NLQNLL	(R)N L/Q N L L I L T A/I/K A D/R(T)		177.3	566.0075	1696.012	-0.0036	-2.1	8.75	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
22862	dirMS_041712_NAR_60mM_minus.7154.7154.3	3	4.43	1	5.31E+04		(R)KSCPSA	(R)K|S C/P S A S\S L E I/H M R(S)	C:Carbamidomethylation	98.4	534.9257	1602.773	-0.0101	-6.3	8.76	106540.7	8.87	HUMAN	Q8IX07	Zinc finger protein ZFPM1
22863	dirMS_041712_NAR_60mM_minus.9556.9556.3	3	4.43	1	2.46E+05		(R)QERYEIE	(R)Q E R Y E\I|E\E/T E/T V/T K(S)		112.57	585.6185	1754.844	-0.0034	-1.9	4.32	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
22864	dirMS_041712_NAR_120mM_plus.17745.17745.3	3	4.43	1	1.44E+06	S56s	(K)GLDYLH	(K)G L D Y L H|s E R K(I)	s:N-acetylglucosamine (S)	146.07	474.2314	1217.627	203.0523	-19	6.75	39436.2	8.5	HUMAN	A8K6Z3	Serine/threonine-protein kinase 25
22865	dirMS_041712_NAR_120mM_plus.6020.6020.3	3	4.43	0	1.67E+05		(R)TFSGHEI	(R)T/F|S G/H E D C V R(G)	C:Carbamidomethylation	84.88	403.1797	1207.516	0.0085	7	5.29	67874.3	5.65	HUMAN	E5RIM3	Phospholipase A-2-activating protein
22866	dirMS_041712_NAR_120mM_plus.6343.6343.2	2	4.43	1	3.49E+05		(K)DSYVGD	(K)D/S Y V/G/D/E A Q/S K R(G)		86.28	677.815	1354.623	-0.0006	-0.5	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
22867	dirMS_041712_NAR_120mM_plus.7604.7604.3	3	4.43	0	3.18E+05	M1277m	(K)mADHW	(K)m A D H\W/E T A P R(H)	m:Oxidized methionine	93.13	410.5196	1213.542	16.0024	6.1	5.3	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
22868	dirMS_041712_NAR_20mM_plus.13314.13314.3	3	4.43	1	1.24E+04	S37s	(K)LSDQVK	(K)L/S\D Q/V K I s E E A L R(A)	s:N-acetylglucosamine (S)	165.15	564.2873	1487.806	203.0409	-22.7	4.68	15284.3	5.74	HUMAN	I3L0W4	Diamine acetyltransferase 2
22869	dirMS_041712_NAR_30mM_plus2.15678.15678.2	2	4.43	0	2.63E+05		(R)MAGAIA	(R)M A/G\A|I/A/Q/G/L I R(A)		134.53	550.816	1100.624	0.0002	0.2	9.5	4449.1	11.42	HUMAN	F8WEI0	Pyrroline-5-carboxylate reductase 3
22870	dirMS_041712_NAR_30mM_plus2.6291.6291.2	2	4.43	0	8.58E+04		(R)YTGAGL	(R)Y/T/G A\G L/S G R(Q)		86.93	441.2249	881.448	-0.005	-5.7	8.75	49155.6	6.13	HUMAN	Q05048	Cleavage stimulation factor subunit 1
22871	dirMS_041712_NAR_40mM_plus2.13145.13145.3	3	4.43	1	1.97E+05	S104s	(R)VGSDMI	(R)V G S D M L T/R F|s/I R(M)	s:N-acetylglucosamine (S)	144.35	528.9395	1381.726	203.0783	-0.7	9.57	48375.6	9.01	HUMAN	A6NFU0	Ig-like V-type domain-containing protein FAM187A
22872	dirMS_041712_NAR_40mM_plus2.5520.5520.2	2	4.43	1	2.40E+04		(R)RGGGSC	(R)R G G G S G G G E\E S E G E/E\V|D/E\D(-)		89.22	926.3584	1851.711	-0.0016	-0.9	3.81	33411.4	5.35	HUMAN	Q96QR8	Transcriptional activator protein Pur-beta
22873	dirMS_041712_NAR_40mM_plus2.9261.9261.2	2	4.43	0	1.48E+05		(R)QTVAVG	(R)Q T/V\A/V/G V/I K(A)		116.83	457.7854	914.567	-0.0034	-3.7	8.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
22874	dirMS_041712_NAR_50mM_plus2.19241.19241.3	3	4.43	0	8.39E+05	S112s	(R)LSHLLsE	(R)L S/H L L s E K/P E D K(G)	s:N-acetylglucosamine (S)	170.08	533.6223	1395.748	203.1045	15.7	5.44	14254.3	8.14	HUMAN	C9J347	Protein TBRG4 (Fragment)
22875	dirMS_041712_NAR_50mM_plus2.21440.21440.3	3	4.43	1	4.09E+05	M145m	(R)GVmLA\	(R)G V/m/L A\V D A V/I A E L K K(Q)	m:Oxidized methionine	182.55	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
22876	dirMS_041712_NAR_50mM_plus2.8431.8431.3	3	4.43	0	5.51E+04		(K)EAAYHP	(K)E A/A Y H P E V A/P D/V R(L)		111.45	485.2423	1453.707	0.0053	3.7	4.65	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
22877	dirMS_041712_NAR_50mM_plus2.8496.8496.3	3	4.43	0	2.07E+05		(K)IASSVTA	(K)I/A\S S\V T A G V A S|S L S E K(I)		111.28	502.9329	1506.801	-0.0168	-11.2	6	73336.3	8.57	HUMAN	G3V3F1	Neural cell expressed, developmentally down-regulated 1, isoform CRA_c
22878	dirMS_041712_NAR_60mM_plus.13649.13649.3	3	4.43	2	5.41E+05		(R)NDLDRL	(R)N D/L D R L F V K V|E K(I)		128.32	492.6101	1475.822	-0.0059	-4	6.12	66135.4	5.63	HUMAN	Q07065	Cytoskeleton-associated protein 4
22879	dirMS_041712_NAR_60mM_plus.13654.13654.3	3	4.43	0	4.98E+05		(R)IHQIEYA	(R)I H Q\I\E\Y A/M E/A V K(Q)		128.4	477.9163	1431.73	0.0043	3	5.4	18685.5	9.45	HUMAN	B4DEV8	Proteasome subunit alpha type
22880	dirMS_041712_NAR_60mM_plus.14806.14806.3	3	4.43	0	1.61E+05		(R)NVVALD	(R)N V/V A L D T E/V A S N R(I)		134.32	463.2467	1387.718	0.008	5.7	4.37	98684.5	4.84	HUMAN	H0YLU8	Low-density lipoprotein receptor
22881	dirMS_041712_NAR_60mM_plus.7969.7969.3	3	4.43	0	1.73E+05		(R)EATNPP	(R)E A/T N/P P V I Q E E K/P K(K)		99.68	527.2793	1579.833	-0.0093	-5.9	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
22882	dirMS_041712_NAR_60mM_plus.8185.8185.3	3	4.43	1	2.68E+06	M174m	(R)VKYETEL	(R)V/K Y E T E|L/A m R(Q)	m:Oxidized methionine	101.47	419.2169	1239.64	15.996	0.8	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
22883	dirMS_041712_NAR_120mM_minus.16536.16536.3	3	4.42	0	5.94E+05		(R)EHALLA\	(R)E H A L L A\Y/T/L/G V K(Q)		144.88	438.9186	1314.742	-0.0004	-0.3	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
22884	dirMS_041712_NAR_20mM_minus.11188.11188.2	2	4.42	0	6.00E+04		(R)LLAEPVI	(R)L/L/A\E/P V P G I K(A)		158.75	518.822	1036.64	-0.0034	-3.3	6	12039.9	9.34	HUMAN	F8VSD4	Ubiquitin-conjugating enzyme E2 N
22885	dirMS_041712_NAR_20mM_minus.14505.14505.3	3	4.42	0	4.72E+03		(R)AAVEEG	(R)A A V E E\G I\V L/G/G/G/C A L L R(C)	C:Carbamidomethylation	199.5	562.3053	1684.905	-0.0037	-2.2	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial

22886	dirMS_041712_NAR_20mM_minus.8903.8903.2	2	4.42	0	1.36E+05		(R)LEQYTS/	(R)L E\Q\Y/T S A/I/E G T K(S)		137.98	670.3403	1339.674	-0.0007	-0.5	4.53	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
22887	dirMS_041712_NAR_20mM_minus.9645.9645.2	2	4.42	0	5.91E+03		(K)DVNAAI.	(K)D/V/N A/A I A T I K(T)		146.73	508.2919	1015.578	-0.0017	-1.7	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
22888	dirMS_041712_NAR_30mM_minus2.10025.10025.2	2	4.42	0	6.28E+05	M53m	(K)LmVELSI	(K)L m|V\E L/S/K(S)	m:Oxidized methionine	108.82	418.2306	819.465	15.9895	-6.5	6	55804.4	5.33	HUMAN	B7ZAR1	T-complex protein 1 subunit epsilon
22889	dirMS_041712_NAR_30mM_minus2.12008.12008.2	2	4.42	0	2.68E+05		(K)NGQDL(	(K)N G Q/D L\G V/A/F/K(I)		118.93	524.7749	1048.542	0.0003	0.3	5.84	91324.5	5.75	HUMAN	Q00839	Heterogeneous nuclear ribonucleoprotein U
22890	dirMS_041712_NAR_30mM_minus2.15240.15240.2	2	4.42	0	7.16E+04		(K)ETWGP/	(K)E T/W/G P A T P R(A)		137.6	507.7594	1014.5	0.0112	11	6.1	16507.7	10.09	HUMAN	Q9UFV1	Putative TBC1 domain family member 29
22891	dirMS_041712_NAR_40mM_minus2.15106.15106.3	3	4.42	0	6.96E+05		(K)ALIEVLQ	(K)A L|I E V/L Q/P L I A E H Q A R(R)		175.25	601.0146	1801.033	-0.0038	-2.1	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
22892	dirMS_041712_NAR_40mM_minus2.15326.15326.3	3	4.42	1	1.93E+05		(R)GGPNIIT	(R)G G/P N I/I T L A D I V/K D P V S R(T)		177.33	622.3523	1865.049	-0.0067	-3.6	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
22893	dirMS_041712_NAR_40mM_minus2.6251.6251.3	3	4.42	0	5.09E+04		(R)EATNPP'	(R)E A T N/P/P V/I Q/E E K P K(K)		102.47	527.2804	1579.833	-0.006	-3.8	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
22894	dirMS_041712_NAR_50mM_minus2.14522.14522.3	3	4.42	1	2.01E+05		(R)IIDSLFN	(R)I I/D/S L F/N/T V T D K K(I)		150.67	498.612	1493.821	0.0005	0.3	5.96	44813.4	7.79	HUMAN	B4DN25	UDP-glucose 6-dehydrogenase
22895	dirMS_041712_NAR_50mM_minus2.15115.15115.3	3	4.42	0	2.48E+05	M118m	(R)AGKPVI(	(R)A G K\P V I\C A T\Q|M/L/E S m I K(K)	C:Carbamidomethylation m:Oxid	154.47	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
22896	dirMS_041712_NAR_50mM_minus2.17132.17132.3	3	4.42	0	9.82E+02		(K)YLITTFSI	(K)Y L/I T T/F/S L A/H E L Q K(I)		166.25	555.3037	1663.905	-0.0088	-5.3	6.75	17831.3	7.91	HUMAN	F5H5B1	NACHT, LRR and PYD domains-containing protein 2 (Fragment)
22897	dirMS_041712_NAR_50mM_minus2.6733.6733.3	3	4.42	1	7.07E+04	M230m M2	(R)mSmKE\	(R)m S m K E\V D E/Q/m/L|N V Q\N/K(N)	m:Oxidized methionine	104.68	657.9643	1923.897	47.9811	-1.9	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
22898	dirMS_041712_NAR_50mM_minus2.7641.7641.3	3	4.42	1	1.78E+04	M23m M2	(K)LAEQAE	(K)L\A/E/Q A E R Y D E/m/V E S m K(K)	m:Oxidized methionine	110.62	654.2933	1928.873	31.9925	1.4	4.25	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
22899	dirMS_041712_NAR_50mM_minus2.9276.9276.3	3	4.42	1	5.66E+03		(R)TGLIKGS	(R)T\G L I K G S/G T\A/E V E/L K(K)		120.57	501.6147	1502.842	-0.0129	-8.6	5.81	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
22900	dirMS_041712_NAR_60mM_minus.10098.10098.3	3	4.42	0	1.36E+05		(R)ILATMN	(R)I L A T M N\P G/G/D F G K(K)		115.73	440.8942	1320.662	0.0064	4.8	5.84	638399.7	5.46	HUMAN	Q9NU22	Midasin
22901	dirMS_041712_NAR_60mM_minus.13616.13616.3	3	4.42	1	1.80E+05		(K)QMADT	(K)Q M/A/D/T/G/K L/N T L L Q R(A)		135.92	530.2846	1588.848	-0.0083	-5.2	8.75	91324.5	5.75	HUMAN	Q00839	Heterogeneous nuclear ribonucleoprotein U
22902	dirMS_041712_NAR_60mM_minus.15461.15461.3	3	4.42	1	5.72E+05	M81m	(K)EVNKFQ	(K)E V/N/K F Q m/A/Y/S N L L R(A)	m:Oxidized methionine	146.68	576.9619	1712.879	15.9923	-1.5	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
22903	dirMS_041712_NAR_60mM_minus.17778.17778.3	3	4.42	1	6.14E+05	Y252y	(R)ITRYQG\	(R)I T\R Y Q G V N L/y/V/K(N)	y:Phosphorylated Y	159.9	511.9372	1453.816	79.9809	9.5	9.7	65918.2	9.74	HUMAN	E7EQV3	Polyadenylate-binding protein 1
22904	dirMS_041712_NAR_60mM_minus.18981.18981.3	3	4.42	0	3.00E+05		(K)HNQLPL	(K)H N/Q L\P L V\I E/F T E Q T/A/P K(I)		168.05	655.6847	1965.044	-0.0045	-2.3	5.4	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
22905	dirMS_041712_NAR_60mM_minus.5495.5495.2	2	4.42	1	2.77E+04	Y31y	(K)SGKYVL(	(K)S G\K\Y/V/L G y K(Q)	y:Phosphorylated Y	86.67	547.7622	1014.562	79.9553	-10.1	9.52	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
22906	dirMS_041712_NAR_60mM_minus.6727.6727.3	3	4.42	0	9.17E+04	S89s	(R)EsSIPGA	(R)E s/S/I P G A G/L G V W A K(R)	s:Phosphorylated S	96.62	484.5732	1371.727	79.9784	8.3	6.1	140198.5	5.85	HUMAN	D3YTA5	PR domain zinc finger protein 16
22907	dirMS_041712_NAR_120mM_plus.10855.10855.2	2	4.42	1	2.27E+06		(R)LASYLDF	(R)L A/S/Y L D/R V/R(S)		109.83	546.8117	1092.616	0.0001	0.1	8.75	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
22908	dirMS_041712_NAR_120mM_plus.16931.16931.3	3	4.42	1	1.33E+06		(K)LKVPEW	(K)L K V\P E W/V/D/T V K(L)		141.93	438.5868	1313.746	-0.0005	-0.4	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
22909	dirMS_041712_NAR_20mM_plus.10103.10103.2	2	4.42	0	1.96E+05		(R)VLLPTGI	(R)V L|L/P T G N Q R(A)		141.53	499.2863	997.579	-0.0136	-13.6	9.72	99570.4	9.54	HUMAN	P53814	Smoothelin
22910	dirMS_041712_NAR_20mM_plus.10357.10357.2	2	4.42	0	1.14E+05	M297m M	(K)mAILQIr	(K)m A I|L/Q I/m K(E)	m:Oxidized methionine	144.63	490.2722	947.542	31.9955	5.8	8.5	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
22911	dirMS_041712_NAR_20mM_plus.16021.16021.2	2	4.42	0	1.19E+05		(K)SILFVPT!	(K)S I\L/F/V|P T/S A P R(G)		181.33	594.3403	1187.678	-0.005	-4.2	9.47	92752.5	4.76	HUMAN	P14625	Endoplasmin
22912	dirMS_041712_NAR_30mM_plus2.17693.17693.3	3	4.42	1	6.16E+05		(R)LENGNC	(R)L E N G N Q/A/R S E A R(R)		145.08	448.8963	1344.661	0.0129	9.6	6.14	185718.4	8.45	HUMAN	F5GX68	Cytosine-specific methyltransferase
22913	dirMS_041712_NAR_30mM_plus2.18699.18699.2	2	4.42	0	6.67E+05		(R)SYNDEL(	(R)S Y|N/D E/L Q F L E K(I)		152.13	693.335	1385.658	0.0044	3.2	4.14	19338.9	5.33	HUMAN	E7EQS9	tRNA-splicing ligase RtcB homolog
22914	dirMS_041712_NAR_50mM_plus2.21353.21353.3	3	4.42	1	1.67E+05		(K)TGLSSE(	(K)T G L|S/S E Q/T V N V L A Q I L K R(L)		182.97	653.0385	1957.108	-0.0067	-3.4	8.41	48481.7	6.95	HUMAN	E7EUG6	General transcription factor IIF subunit 1
22915	dirMS_041712_NAR_60mM_plus.13615.13615.2	2	4.42	1	3.30E+05		(R)VVDLM/	(R)V V|D/L/M/A H M A S\K|E(-)		127.7	665.8295	1330.649	0.0024	1.8	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
22916	dirMS_041712_NAR_60mM_plus.21221.21221.3	3	4.42	1	4.03E+05		(R)KAIIIFVP	(R)K A I I I F|V/P/V P Q L K(S)		174.23	489.3205	1465.95	-0.0035	-2.4	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
22917	dirMS_041712_NAR_30mM_minus2.18998.18998.3	3	4.41	0	1.53E+05		(K)SYELPD(	(K)S Y E L P D G Q\V/I T/I/G N E R(F)		158.72	597.6343	1790.892	-0.0036	-2	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
22918	dirMS_041712_NAR_30mM_minus2.7507.7507.2	2	4.41	1	1.53E+06		(K)SYNEQR	(K)S Y|N E Q/R I R(Q)		95.12	533.2797	1065.544	0.0085	8	8.46	34175.8	9.07	HUMAN	B4DK69	Aldo-keto reductase family 1 member C2
22919	dirMS_041712_NAR_40mM_minus2.11996.11996.3	3	4.41	1	4.71E+04		(R)SLGEIPI\	(R)S L\G E I/P I V E S/E I\K K(E)		153.62	514.6302	1541.879	-0.0025	-1.6	4.78	108281.4	5.72	HUMAN	P53618	Coatomer subunit beta
22920	dirMS_041712_NAR_40mM_minus2.5341.5341.2	2	4.41	0	1.64E+05		(R)FLEQQN	(R)F L/E Q/Q\N K(I)		88.28	453.7371	906.468	-0.001	-1.1	6	49709.6	5.19	HUMAN	B0YJC4	Vimentin
22921	dirMS_041712_NAR_40mM_minus2.8210.8210.3	3	4.41	0	1.68E+05		(R)LLEAQA(	(R)L L\E/A/Q/A|C T G G I I H P T T G Q K(L)	C:Carbamidomethylation	128.68	665.6822	1995.033	-0.0007	-0.4	6.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
22922	dirMS_041712_NAR_60mM_minus.14594.14594.3	3	4.41	1	3.21E+05		(K)TDKTLVI	(K)T/D K T L V/L/L M G K(E)		142.15	406.9088	1218.713	-0.0008	-0.6	8.26	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
22923	dirMS_041712_NAR_60mM_minus.18863.18863.3	3	4.41	0	1.43E+05		(K)VAHALA	(K)V A H A L A E\G L/G V/I/A C I G/E K(L)	C:Carbamidomethylation	166.95	603.3262	1807.974	-0.0094	-5.2	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
22924	dirMS_041712_NAR_60mM_minus.19939.19939.3	3	4.41	1	8.24E+05		(K)EIIDLVLI	(K)E I/I D/L V L D R I R(K)		180.57	452.2739	1354.805	0.0019	1.4	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
22925	dirMS_041712_NAR_60mM_minus.8257.8257.3	3	4.41	1	1.02E+05		(R)AAERNP	(R)A A E R N\P\A|L|A/G S A I R(C)		106.15	466.2587	1396.766	-0.004	-2.9	9.64	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
22926	dirMS_041712_NAR_60mM_minus.8260.8260.2	2	4.41	0	5.97E+04	M809m	(K)NIPPSDr	(K)N/I|P P S/D m P Q I\K(A)	m:Oxidized methionine	106.05	628.3198	1239.64	15.9921	-2.2	5.84	117466.9	9.38	HUMAN	B0I1T2	Unconventional myosin-Ig
22927	dirMS_041712_NAR_120mM_plus.6387.6387.2	2	4.41	1	3.34E+05		(K)DSYVGD	(K)D S\Y|V|G/D/E/A Q S K R(G)		86.33	677.815	1354.623	-0.0006	-0.5	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
22928	dirMS_041712_NAR_30mM_plus2.19916.19916.3	3	4.41	0	1.72E+05		(R)TTVPQLI	(R)T T V P Q L|L/A/S V Q R(W)		158.23	438.2563	1312.758	-0.004	-3	9.41	266161	5.68	HUMAN	E9PPU0	Epiplakin
22929	dirMS_041712_NAR_30mM_plus2.21613.21613.2	2	4.41	0	1.79E+05		(R)TTNFAG	(R)T T/N F A G|I L\S Q G L R(I)		169.17	689.3749	1377.748	-0.006	-4.3	9.41	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
22930	dirMS_041712_NAR_30mM_plus2.8147.8147.3	3	4.41	0	4.74E+05		(K)SNVSDA	(K)S N V S D A V/A/Q S/T/R(I)		96.35	412.2004	1234.602	-0.0156	-12.6	5.55	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
22931	dirMS_041712_NAR_30mM_plus2.8580.8580.2	2	4.41	0	6.80E+05		(R)ALANSL/	(R)A/L\A/N/S L A/C Q G K(Y)	C:Carbamidomethylation	98.3	566.7922	1132.578	-0.0008	-0.7	8.8	13951.6	9.48	HUMAN	H3BR68	Fructose-bisphosphate aldolase A (Fragment)
22932	dirMS_041712_NAR_30mM_plus2.9293.9293.2	2	4.41	0	6.84E+05		(K)TAVCDIF	(K)T A|V\C/D I/P/P/R(G)	C:Carbamidomethylation	101.18	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
22933	dirMS_041712_NAR_50mM_plus2.10225.10225.3	3	4.41	0	3.78E+05		(R)MVQVH	(R)M/V Q\V/H E L S C E/G I S K(S)	C:Carbamidomethylation	121.6	539.5992	1616.777	0.006	3.7	5.38	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
22934	dirMS_041712_NAR_50mM_plus2.19888.19888.3	3	4.41	0	1.72E+05		(R)QLPAM1	(R)Q L/P/A M T A L/Q T L H L R(S)		172.75	531.635	1592.894	-0.0037	-2.3	9.75	78827.3	5.92	HUMAN	J3KS54	Protein flightless-1 homolog
22935	dirMS_041712_NAR_50mM_plus2.8851.8851.3	3	4.41	1	6.36E+04		(K)ATFIKVP	(K)A T/F I/K V/P Q N Q N G K(S)		113.77	482.2676	1444.791	-0.0024	-1.7	10	32503.1	5.29	HUMAN	H7BY16	Nucleolin (Fragment)
22936	dirMS_041712_NAR_60mM_plus.18952.18952.3	3	4.41	0	3.09E+05		(R)GGHVVE	(R)G G H/V V E G\L A|G\E/L E/Q L R(A)		156.17	555.2949	1663.876	-0.0061	-3.6	4.75	106088.3	5.78	HUMAN	P10275	Androgen receptor
22937	dirMS_041712_NAR_120mM_minus.17817.17817.4	4	4.4	0	3.17E+05		(R)LDHALY/	(R)L D H A L Y A L/P G/P/T I V/D L R(K)		151.6	466.7676	1864.033	0.0159	8.5	5.21	17079.4	5.66	HUMAN	Q12988	Heat shock protein beta-3
22938	dirMS_041712_NAR_20mM_minus.13348.13348.2	2	4.4	0	5.64E+04	M511m	(K)LmDVGI	(K)L/m/D V/G L|I A I R(-)	m:Oxidized methionine	184.12	558.8267	1100.65	15.9965	1.4	5.84	60404.6	6.4	HUMAN	F5H0T1	Stress-induced-phosphoprotein 1
22939	dirMS_041712_NAR_30mM_minus2.15243.15243.2	2	4.4	0	4.79E+04		(K)LCDFGF/	(K)L/C|D/F/G F A/R(A)	C:Carbamidomethylation	135.8	493.2343	985.456	0.0053	5.4	5.84	143554.7	5.57	HUMAN	A8MU99	Serine/threonine-protein kinase 36
22940	dirMS_041712_NAR_30mM_minus2.15640.15640.2	2	4.4	0	1.98E+05		(R)IGSGFDI	(R)I/G|S G F D N/I/D I K(S)		138.83	589.8069	1178.605	0.0013	1.1	4.21	20631.5	6.98	HUMAN	D6RAX2	C-terminal-binding protein 1 (Fragment)
22941	dirMS_041712_NAR_50mM_minus2.12477.12477.3	3	4.4	0	9.86E+05	M114m M	(R)AGKPVI(	(R)A G K\P V I/C A T/Q/m/L E S m I K(K)	C:Carbamidomethylation m:Oxid	139.75	636.9917	1876.969	31.9912	0.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
22942	dirMS_041712_NAR_50mM_minus2.13641.13641.3	3	4.4	2	9.39E+03		(K)DCGKAF	(K)D C G K A/F R W G S/S L V I H K(R)	C:Carbamidomethylation	146.82	620.9953	1860.954	0.0176	9.5	9.99	55392.3	9.77	HUMAN	Q9NQX6	Zinc finger protein 331
22943	dirMS_041712_NAR_50mM_minus2.17509.17509.3	3	4.4	1	2.59E+04		(R)FWLVIKI	(R)F W L/V I K E D/G H/M V T A R(Q)		169.05	601.3217	1801.942	0.0088	4.9	6.75	38593.3	9.81	HUMAN	Q969Z3	MOSC domain-containing protein 2, mitochondrial
22944	dirMS_041712_NAR_120mM_plus.14800.14800.3	3	4.4	1	9.20E+05		(K)LDKSQIH	(K)L D/K S Q I H D I|V|L\V|G G S T R(I)		130.88	613.3369	1838.013	-0.0169	-9.2	6.75	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
22945	dirMS_041712_NAR_120mM_plus.15724.15724.3	3	4.4	1	2.47E+05		(K)KGTPWE	(K)K G T P W\E/G G L/F K(L)		136.17	407.2187	1219.647	-0.0054	-4.5	8.59	20685.4	9.18	HUMAN	B0QYN7	SUMO-conjugating enzyme UBC9
22946	dirMS_041712_NAR_120mM_plus.5057.5057.3	3	4.4	1	1.21E+05		(K)MSSPED	(K)M S S/P E/D D S D T K R(L)		79.18	456.5294	1367.574	-0.0007	-0.5	4.23	103309.5	5.34	HUMAN	A0AV56	SAFB protein
22947	dirMS_041712_NAR_20mM_plus.12119.12119.3	3	4.4	0	7.99E+03	M54m M5	(K)TVVGQI	(K)T V\V G Q I T V D m m Y/G G m R(G)	m:Oxidized methionine	156.67	602.6103	1757.838	47.978	-3.7	5.5	50659.2	7.87	HUMAN	B4DJV2	Citrate synthase
22948	dirMS_041712_NAR_30mM_plus2.16072.16072.2	2	4.4	0	4.67E+05		(K)GVLFYGI	(K)G V L\F|Y/G/P P G C G K(T)	C:Carbamidomethylation	137.4	626.3175	1251.619	0.0087	6.9	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
22949	dirMS_041712_NAR_40mM_plus2.10203.10203.2	2	4.4	0	6.81E+04		(R)GYFDEEI	(R)G Y/F/D|E E/M N R(V)		124.8	580.7366	1160.468	-0.0018	-1.5	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
22950	dirMS_041712_NAR_40mM_plus2.14457.14457.3	3	4.4	1	1.51E+05		(K)IMASSPI	(K)I/M/A/S S/P D M/D L A T V/S A L R K(M)		151.42	635.9975	1905.977	0.0007	0.4	5.96	36208.1	7.21	HUMAN	B4DMU0	Pyrroline-5-carboxylate reductase
22951	dirMS_041712_NAR_40mM_plus2.15876.15876.3	3	4.4	0	1.34E+05	M1242m	(K)IFTYIFILE	(K)I F/T|Y I F\I L E m/L\L K(W)	m:Oxidized methionine	160.1	553.9799	1643.948	15.977	-10.8	6	228580.5	6.56	HUMAN	E9PBA5	Sodium channel protein type 9 subunit alpha
22952	dirMS_041712_NAR_40mM_plus2.6223.6223.2	2	4.4	0	5.91E+04		(R)AYSSFG(	(R)A/Y/S S F/G G G R(G)		95.42	451.2127	901.416	0.0019	2.1	8.79	27441.6	6.68	HUMAN	Q15056	Eukaryotic translation initiation factor 4H
22953	dirMS_041712_NAR_50mM_plus2.13204.13204.3	3	4.4	1	9.78E+05		(K)ASLAETI	(K)A/S/L/A E/T D K/I T L\E V A K(L)		137.42	530.2925	1588.879	-0.0163	-10.2	4.68	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
22954	dirMS_041712_NAR_50mM_plus2.15333.15333.3	3	4.4	1	4.95E+05		(K)TKDGQII	(K)T K D\G Q I\L/P V/P N V V V R(D)		148.7	545.6573	1634.959	-0.0015	-0.9	8.41	56825.2	9.49	HUMAN	Q9P258	Protein RCC2
22955	dirMS_041712_NAR_50mM_plus2.6184.6184.3	3	4.4	0	4.66E+04		(R)LQVEQA	(R)L Q|V/E Q A P/H/S S P G/A K(L)		96.6	483.5916	1448.749	0.011	7.6	6.75	16834.6	6.3	HUMAN	H0YKT9	Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase MESH1 (Fragment)
22956	dirMS_041712_NAR_50mM_plus2.9352.9352.3	3	4.4	0	1.33E+05		(K)AEITLVA	(K)A E\I T/L/V/A T/K P E K(L)		116.23	433.922	1299.752	-0.0004	-0.3	6.18	98761.7	5.56	HUMAN	Q9UBF2	Coatomer subunit gamma-2
22957	dirMS_041712_NAR_60mM_plus.7006.7006.3	3	4.4	0	1.08E+06		(K)SLQALTI	(K)S L Q\A\L\T E M D G Q R(C)		94.88	450.2236	1348.652	0.0037	2.7	4.37	75321.9	6.17	HUMAN	O95628-7	Isoform 7 of CCR4-NOT transcription complex subunit 4
22958	dirMS_041712_NAR_60mM_plus.8618.8618.3	3	4.4	0	2.80E+05		(K)AVMSNI	(K)A V/M/S N L S A H G V K(L)		103.63	405.2162	1213.636	-0.0017	-1.4	8.8	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
22959	dirMS_041712_NAR_120mM_minus.6527.6527.3	3	4.39	0	1.77E+04	M669m	(R)MLHWn	(R)M/L H W m/V V A E/G K(K)	m:Oxidized methionine	90.92	439.5579	1300.654	16.0051	7.7	6.5	139368.3	5.68	HUMAN	Q16827	Receptor-type tyrosine-protein phosphatase O
22960	dirMS_041712_NAR_20mM_minus.10673.10673.3	3	4.39	0	1.40E+05		(K)VNQIGS'	(K)V N Q\I G S\V\T|E/S I Q A C K(L)	C:Carbamidomethylation	155.38	545.2807	1633.821	0.0062	3.8	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
22961	dirMS_041712_NAR_20mM_minus.7218.7218.2	2	4.39	0	1.38E+05		(K)VTLTSEE	(K)V/T/L T/S E E E A/R(L)		119.77	567.785	1134.564	-0.001	-0.9	4.25	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
22962	dirMS_041712_NAR_30mM_minus2.19283.19283.2	2	4.39	0	2.40E+05		(R)LTIAILR(	(R)L T|I/A I L R(H)		159.4	400.2731	799.54	-0.0011	-1.3	9.75	87498	6.43	HUMAN	C9J266	E3 ubiquitin-protein ligase RNF123
22963	dirMS_041712_NAR_30mM_minus2.6042.6042.2	2	4.39	0	2.56E+05		(K)TSEVNC'	(K)T S|E|V/N C Y R(C)	C:Carbamidomethylation	87.2	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
22964	dirMS_041712_NAR_40mM_minus2.8882.8882.3	3	4.39	2	3.40E+04	M470m	(R)IPPLGER	(R)I P P L G E R Q S E/S m/P D R K(M)	m:Oxidized methionine	135.18	619.3102	1839.938	15.9779	-9.2	6.18	62866	5.73	HUMAN	C9IZH7	Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 11 protein
22965	dirMS_041712_NAR_50mM_minus2.10585.10585.3	3	4.39	0	1.83E+05		(K)SQIHDIV	(K)S Q I H D I V\L/V/G G S T/R(I)		128.62	494.6068	1481.807	-0.0012	-0.8	6.46	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
22966	dirMS_041712_NAR_50mM_minus2.6190.6190.3	3	4.39	0	4.44E+05	M434m	(R)LESGmC	(R)L E/S G m Q N\M S I H/T K(T)	m:Oxidized methionine	97.77	497.9018	1475.698	15.9927	-1.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
22967	dirMS_041712_NAR_50mM_minus2.6932.6932.3	3	4.39	2	2.38E+04	S621s T62(	(K)SPLVSPS	(K)S P/L/V S P S/K/s L E/E G t K K(T)	s:Phosphorylated S t:Phosph	105.48	616.2995	1686.927	159.9567	13	8.22	81309.2	5.66	HUMAN	P35612	Beta-adducin
22968	dirMS_041712_NAR_50mM_minus2.7295.7295.3	3	4.39	1	7.81E+04	M1506m	(R)TEmEDL	(R)T E\m/E D L M S S K D D/V G K(S)	m:Oxidized methionine	108.5	567.5829	1684.74	15.9937	-0.7	4.1	227783.5	5.5	HUMAN	P35579	Myosin-9
22969	dirMS_041712_NAR_50mM_minus2.8734.8735.3	3	4.39	1	7.70E+04	M227m	(R)mQKEIT.	(R)m Q K E I T|A|L/A/P S T M K(I)	m:Oxidized methionine	117.62	522.2727	1548.812	15.9911	-2.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
22970	dirMS_041712_NAR_120mM_plus.20404.20404.4	4	4.39	1	6.05E+05	T254t	(R)GAGRG1	(R)G A G/R G T V T A t P/G L Q A A D V R P(-)	t:Phosphorylated T	159.93	494.4975	1895.009	79.9588	-3.8	9.6	27899.4	9.81	HUMAN	K7ERR6	Lon protease homolog, mitochondrial (Fragment)
22971	dirMS_041712_NAR_120mM_plus.25719.25719.3	3	4.39	1	4.37E+05		(R)GVMLA\	(R)G V M L/A V/D A V/I A E L K K(Q)		193.37	519.6402	1556.908	-0.002	-1.3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
22972	dirMS_041712_NAR_120mM_plus.4289.4289.2	2	4.39	1	1.14E+06	M310m	(R)TKTEISEI	(R)T K|T E/I S/E m N R(N)	m:Oxidized methionine	70.07	612.7976	1208.594	15.994	-0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
22973	dirMS_041712_NAR_120mM_plus.7147.7147.2	2	4.39	0	7.27E+05	N75n	(R)GHSnAD	(R)G/H S n|A D A A|K(L)	n:N-acetylglucosamine (N)	91.05	537.248	870.406	203.0823	2.7	6.74	16706.1	5.7	HUMAN	F5GYS3	Bcl2 antagonist of cell death
22974	dirMS_041712_NAR_120mM_plus.9225.9225.3	3	4.39	1	5.51E+05	S907s	(R)sTLNGVI	(R)s T L N G V\L\K/G Y/R(V)	s:Phosphorylated S	102.12	429.8865	1207.679	79.9656	-0.6	9.99	202703.7	9.01	HUMAN	G3V1B5	Down syndrome cell adhesion molecule like 1, isoform CRA_a
22975	dirMS_041712_NAR_20mM_plus.11464.11464.2	2	4.39	0	2.39E+05		(K)LITPAVV	(K)L I/T|P A V V S E R(L)		151.05	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
22976	dirMS_041712_NAR_20mM_plus.13919.13919.2	2	4.39	0	5.72E+04	M348m	(K)VmQVLI	(K)V m|Q/V\L/N/A D A I V V K(L)	m:Oxidized methionine	167.57	708.3968	1399.798	15.9886	-4.5	5.81	102679.8	6.75	HUMAN	Q7KZF4	Staphylococcal nuclease domain-containing protein 1
22977	dirMS_041712_NAR_20mM_plus.15092.15092.3	3	4.39	0	2.24E+04		(R)TQILCSH	(R)T Q I L\C/S H L E/G/H R(V)	C:Carbamidomethylation	175.22	484.2492	1450.722	0.0111	7.6	6.61	101430.7	8.88	HUMAN	O76024	Wolframin
22978	dirMS_041712_NAR_20mM_plus.15196.15196.2	2	4.39	0	6.89E+04		(K)DVLSVAI	(K)D V|L S V/A/F S/S D N R(Q)		175.98	655.3293	1309.638	0.0131	10	4.21	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
22979	dirMS_041712_NAR_20mM_plus.6874.6874.2	2	4.39	0	4.15E+05	M132m	(R)DmVGIA	(R)D m|V/G I/A Q T G S G K(T)	m:Oxidized methionine	112.87	590.2864	1163.573	15.993	-1.6	5.84	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
22980	dirMS_041712_NAR_30mM_plus2.21357.21357.2	2	4.39	0	4.14E+04		(R)SPVTFLS	(R)S P/V/T/F L|S/D/L R(S)		165.5	567.8152	1134.615	0.0078	6.9	5.55	269273.3	6.66	HUMAN	A5YKK6	CCR4-NOT transcription complex subunit 1
22981	dirMS_041712_NAR_30mM_plus2.21711.21711.2	2	4.39	1	1.12E+05		(K)IYFKINK(	(K)I Y/F/K I N/K(L)		169.92	463.2766	925.551	-0.0046	-5	9.7	46656.7	9.19	HUMAN	Q5JVF3	PCI domain-containing protein 2
22982	dirMS_041712_NAR_30mM_plus2.4685.4685.2	2	4.39	0	4.80E+05		(R)MGQTM	(R)M/G Q/T M/E/R(I)		75.47	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
22983	dirMS_041712_NAR_30mM_plus2.4718.4718.2	2	4.39	0	1.76E+05		(K)NCSETQ	(K)N/C|S/E/T Q Y E/S K(V)	C:Carbamidomethylation	75.85	623.256	1245.505	-0.0005	-0.4	4.53	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
22984	dirMS_041712_NAR_30mM_plus2.5796.5796.2	2	4.39	0	3.34E+05		(R)EMEEQI	(R)E M/E/E/Q M R(R)		84	476.6984	952.386	0.0032	3.4	4.25	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
22985	dirMS_041712_NAR_30mM_plus2.6306.6306.2	2	4.39	0	3.51E+05		(K)NQCTQ\	(K)N Q|C\T Q V V|Q/E R(E)	C:Carbamidomethylation	87	631.3039	1261.595	0.0052	4.1	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
22986	dirMS_041712_NAR_50mM_plus2.11588.11588.3	3	4.39	0	2.53E+05		(K)GLCTSV1	(K)G L C/T S V T L A A S E\G R(N)	C:Carbamidomethylation	128.2	474.5801	1421.705	0.0204	14.4	6	103708.4	5.24	HUMAN	Q9HCI5	Melanoma-associated antigen E1
22987	dirMS_041712_NAR_50mM_plus2.16284.16284.3	3	4.39	1	7.13E+04		(R)WFQQK'	(R)W F Q Q K/Y/D G I/I L/P G K(-)		154.48	564.9788	1692.911	0.011	6.5	8.5	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
22988	dirMS_041712_NAR_50mM_plus2.22278.22278.3	3	4.39	0	8.73E+05		(R)GGHPP/	(R)G G H P P A I/Q\S\L|I/N\L\L A D N R(Y)		191.4	629.3448	1886.024	-0.0044	-2.3	6.74	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
22989	dirMS_041712_NAR_50mM_plus2.9779.9779.3	3	4.39	1	4.35E+05		(K)TAVCDIF	(K)T A/V/C D I/P P R G L K(M)	C:Carbamidomethylation	119.35	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
22990	dirMS_041712_NAR_60mM_plus.7770.7770.3	3	4.39	1	5.04E+04		(K)CSESIPK	(K)C S/E S I P/K/D/S L R(M)	C:Carbamidomethylation	98.85	431.2198	1291.631	0.0138	10.7	6.07	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
22991	dirMS_041712_NAR_60mM_plus.8127.8127.3	3	4.39	0	6.92E+05	M1m	(-)mPSLSPT	(-)m P\S/L/S P T M/E E G N I V K(W)	m:Oxidized methionine	100.53	550.2735	1632.797	16.0088	8.4	4.53	16243.3	5.13	HUMAN	E9PLU0	Pyruvate dehydrogenase protein X component, mitochondrial (Fragment)
22992	dirMS_041712_NAR_20mM_minus.9590.9590.3	3	4.38	0	9.16E+03	M175m	(R)LEQGQ/	(R)L E Q G Q A|I/D/D L m/P A Q K(-)	m:Oxidized methionine	146.8	558.2794	1656.826	15.9975	1.5	4.03	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
22993	dirMS_041712_NAR_30mM_minus2.16473.16473.2	2	4.38	0	4.51E+05		(R)DFFLAN.	(R)D F|F/L A N/A S R(A)		142.42	520.763	1040.516	0.0028	2.6	5.84	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
22994	dirMS_041712_NAR_30mM_minus2.17092.17092.2	2	4.38	0	8.47E+04		(R)IMNTFS'	(R)I M/N/T/F/S V V P S P K(V)		146.05	660.3534	1319.703	-0.0033	-2.5	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f

22995	dirMS_041712_NAR_30mM_minus2.18738.18738.2	2	4.38	0	1.04E+05		(K)GFGGIG	(K)G F|G G\I|G G/I L R(Y)		156.73	473.7762	946.547	-0.0018	-1.9	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
22996	dirMS_041712_NAR_30mM_minus2.5101.5101.2	2	4.38	0	4.31E+05		(R)TDTGEP	(R)T D|T/G|E\P M G R(G)		81.38	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
22997	dirMS_041712_NAR_30mM_minus2.7897.7897.2	2	4.38	0	2.89E+05		(K)SLAAEEE	(K)S L|A/A E E E/A/A R(Q)		96.52	523.7597	1046.511	0.0008	0.8	4.25	533778	5.74	HUMAN	Q15149	Plectin
22998	dirMS_041712_NAR_30mM_minus2.9746.9746.2	2	4.38	0	1.33E+05		(R)DPLQQD	(R)D/P L Q Q D\G|T/P K(S)		107.12	549.7705	1098.543	-0.0089	-8.1	4.21	555035.4	6.1	HUMAN	Q9Y6V0	Protein piccolo
22999	dirMS_041712_NAR_60mM_minus.10960.10960.3	3	4.38	0	1.26E+05		(K)TLPIPVQ	(K)T/L|P I P V Q I/T L R(F)		121.03	417.5985	1250.783	-0.0021	-1.7	9.41	30375.1	9.92	HUMAN	E9PRL6	Histone acetyltransferase KAT5 (Fragment)
23000	dirMS_041712_NAR_20mM_plus.10016.10016.2	2	4.38	0	1.69E+05		(K)GEATVS	(K)G E/A/T V/S F D D/P P S/A K(A)		140.63	710.8324	1420.659	-0.0015	-1.1	4.03	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
23001	dirMS_041712_NAR_20mM_plus.16193.16193.2	2	4.38	0	5.41E+04		(K)ALLTPVA	(K)A L L/T|P V A I A A G R(K)		182.97	576.8573	1152.71	-0.0026	-2.3	9.79	56826.6	9.16	HUMAN	P00390	Glutathione reductase, mitochondrial
23002	dirMS_041712_NAR_20mM_plus.7360.7360.3	3	4.38	0	2.14E+05		(K)TGQAPG	(K)T G Q/A\P G Y/S/Y/T A A N K(N)		119.53	476.8963	1428.675	-0.001	-0.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
23003	dirMS_041712_NAR_20mM_plus.7485.7485.2	2	4.38	0	1.26E+04	M136m M	(K)EGmNIV	(K)E G m/N I/V\E/A/m E/R(F)	m:Oxidized methionine	121.47	655.7891	1278.582	31.9892	-0.4	4.25	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
23004	dirMS_041712_NAR_20mM_plus.9877.9877.2	2	4.38	0	7.15E+04		(R)TDYNAS	(R)T D Y N A\S V/S\V/P D S S G P E R(I)		139.05	890.9015	1780.798	-0.0027	-1.5	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
23005	dirMS_041712_NAR_30mM_plus2.13574.13575.2	2	4.38	0	7.98E+05		(K)DLSELGS	(K)D L|S\E/L/G S V R(T)		125.25	488.2554	975.511	-0.007	-7.2	4.37	533778	5.74	HUMAN	Q15149	Plectin
23006	dirMS_041712_NAR_30mM_plus2.15268.15268.2	2	4.38	0	5.89E+05		(K)NIELAVM	(K)N/I/E|L A/V M R(R)		132.3	473.2687	945.519	0.0115	12.2	6	21330	9.14	HUMAN	H0Y586	Proteasome subunit alpha type-7 (Fragment)
23007	dirMS_041712_NAR_40mM_plus2.10958.10958.3	3	4.38	0	6.44E+04		(K)SLYVAEY	(K)S L/Y/V|A E Y H S E P V E D E K P(-)		130.75	664.6419	1991.923	-0.0121	-6.1	4.25	54815.2	9.17	HUMAN	P26196	Probable ATP-dependent RNA helicase DDX6
23008	dirMS_041712_NAR_40mM_plus2.11739.11739.2	2	4.38	0	2.07E+05		(R)FPGQLN	(R)F/P/G/Q/L/N A D/L R(K)		135.52	565.7995	1130.595	-0.0036	-3.1	5.84	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
23009	dirMS_041712_NAR_40mM_plus2.6097.6097.2	2	4.38	0	5.66E+04		(R)QAFPNT	(R)Q/A/F|P N/T\N R(W)		94.88	474.2383	947.469	0	0	9.75	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
23010	dirMS_041712_NAR_50mM_plus2.15634.15634.3	3	4.38	0	1.18E+05		(K)NLDYVA	(K)N L/D/Y/V A/T S I H E A V T K(I)		150.87	554.2887	1660.854	-0.0025	-1.5	5.32	44431.6	8.52	HUMAN	B7Z7E9	Aspartate aminotransferase
23011	dirMS_041712_NAR_50mM_plus2.18112.18112.3	3	4.38	1	1.09E+05		(K)DLEIKIP	(K)D L/E/I\K I/P V V V/R(L)		163.5	427.6021	1280.794	-0.0019	-1.5	6.07	44183.5	5.64	HUMAN	F5GXC8	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial
23012	dirMS_041712_NAR_50mM_plus2.20539.20539.3	3	4.38	2	1.50E+05		(R)ARGLLD	(R)A/R/G/L/L D R S F A N M A E P F K(V)		175.73	641.6672	1922.991	-0.0035	-1.8	8.79	54259.1	5.04	HUMAN	B8ZZ60	Acid trehalase-like protein 1
23013	dirMS_041712_NAR_50mM_plus2.21372.21372.3	3	4.38	1	4.32E+03	T357t	(K)ItKQQVF	(K)I t K Q Q|V F I D V I N K(L)	t:N-acetylglucosamine (T)	182.82	583.67	1545.9	203.0955	9.2	8.59	65679.7	4.98	HUMAN	D6RCC6	Cancer-associated gene 1 protein (Fragment)
23014	dirMS_041712_NAR_120mM_minus.6619.6619.3	3	4.37	0	3.90E+05	S1313s	(R)DGNsNL	(R)D/G N s N L E E A/G K(Q)	s:N-acetylglucosamine (S)	91.13	446.2012	1133.507	203.0821	2.1	4.14	409090.1	5.82	HUMAN	Q15911	Zinc finger homeobox protein 3
23015	dirMS_041712_NAR_120mM_minus.8112.8112.3	3	4.37	1	3.18E+05		(R)KYPEAA	(R)K Y P E\A A|A/C/Y G R(A)	C:Carbamidomethylation	98.67	429.2036	1285.599	-0.0031	-2.4	8.5	24827.2	5.74	HUMAN	H3BS86	E3 ubiquitin-protein ligase CHIP (Fragment)
23016	dirMS_041712_NAR_20mM_minus.11603.11603.2	2	4.37	0	1.40E+05		(R)VEVTEFE	(R)V/E|V/T/E F E D I K(S)		164.38	604.8043	1208.604	-0.0032	-2.6	4	30992.3	4.14	HUMAN	B2REB8	Protein SET
23017	dirMS_041712_NAR_20mM_minus.9604.9604.2	2	4.37	0	3.43E+05		(R)LQAEIEG	(R)L/Q/A E/I E/G L K(G)		146.05	500.7862	1000.567	-0.0022	-2.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
23018	dirMS_041712_NAR_30mM_minus2.12238.12238.2	2	4.37	0	4.21E+05		(R)SGYLLPD	(R)S G Y|L|L/P D T K(A)		119.03	497.265	993.525	-0.0024	-2.4	5.55	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
23019	dirMS_041712_NAR_50mM_minus2.10807.10807.3	3	4.37	1	2.11E+04		(K)LAEQAE	(K)L/A/E Q A/E R Y D D M A A/A M K(A)		128.58	604.9489	1812.825	0.0067	3.7	4.32	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
23020	dirMS_041712_NAR_50mM_minus2.6593.6593.3	3	4.37	0	1.33E+05	M185m M	(R)DFTVSA	(R)D F T/V/S A m H G D m D Q K(E)	m:Oxidized methionine	103.42	538.5571	1581.667	31.9895	-0.2	4.41	26945.8	8.07	HUMAN	J3KSZ0	Eukaryotic initiation factor 4A-I (Fragment)
23021	dirMS_041712_NAR_50mM_minus2.7215.7215.3	3	4.37	1	4.43E+04		(R)LGTPELS	(R)L/G/T/P E/L S T A E R K(E)		107.93	434.572	1301.706	-0.0045	-3.5	6.14	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
23022	dirMS_041712_NAR_60mM_minus.11407.11407.3	3	4.37	1	9.32E+04		(R)EIAQDFK	(R)E I/A/Q/D F K T D/L R(F)		123.83	445.9007	1335.69	-0.0028	-2.1	4.56	14166.5	11.62	HUMAN	B4DEB1	Histone H3
23023	dirMS_041712_NAR_60mM_minus.14116.14116.3	3	4.37	0	3.03E+05		(K)YGYTHLS	(K)Y/G Y\T H L/S T/G D/L L R(S)		138.93	499.2614	1495.754	0.0157	10.5	6.74	21748.6	8.92	HUMAN	P00568	Adenylate kinase isoenzyme 1
23024	dirMS_041712_NAR_60mM_minus.8382.8382.3	3	4.37	1	6.45E+04		(K)QGIETPE	(K)Q G\I/E/T/P E/D Q N D L R\K(M)		106.97	548.2737	1642.803	0.0034	2.1	4.32	46648.4	9.67	HUMAN	B4DX42	Splicing factor 1
23025	dirMS_041712_NAR_120mM_plus.7076.7076.3	3	4.37	1	5.15E+05		(R)NTEEEG	(R)N T/E E E/G/L K Y K(S)		90.52	404.2038	1210.595	0.0018	1.5	4.79	83344.9	10.18	HUMAN	E9PK09	Bcl-2-associated transcription factor 1 (Fragment)
23026	dirMS_041712_NAR_20mM_plus.14404.14404.2	2	4.37	0	1.70E+03	M118m	(R)ATLPQA	(R)A T L P Q/A/A m G V\A T V E R(D)	m:Oxidized methionine	169.57	765.8991	1514.8	15.9914	-2.3	6.05	38189.2	9.55	HUMAN	Q8IXV7	Kelch domain-containing protein 8B
23027	dirMS_041712_NAR_20mM_plus.14887.14887.2	2	4.37	0	1.45E+05		(K)VLEQLT	(K)V L E Q/L|T/G\Q/T P V/F/S K(A)		174.65	773.9244	1546.848	-0.006	-3.9	5.97	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
23028	dirMS_041712_NAR_20mM_plus.15779.15779.3	3	4.37	0	8.77E+03		(R)SSFYVN	(R)S S F Y V/N G\L/T L/G G Q K(C)		179.37	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
23029	dirMS_041712_NAR_20mM_plus.17338.17338.2	2	4.37	1	2.81E+05	M38m	(R)ImLKGD	(R)I m L K G D\N I T\L\L|Q/S\V/S N(-)	m:Oxidized methionine	191.2	881.4709	1745.947	15.9879	-4	5.84	5981.8	5.64	HUMAN	A6NHK2	Small nuclear ribonucleoprotein E
23030	dirMS_041712_NAR_20mM_plus.18705.18705.2	2	4.37	0	9.82E+04		(K)LTVYTTL	(K)L T V/Y T T L I/D V T K(G)		200.78	683.8948	1366.783	-0.0005	-0.4	5.83	42194.9	8.75	HUMAN	E7EMM4	Acid ceramidase
23031	dirMS_041712_NAR_20mM_plus.9187.9187.2	2	4.37	0	7.20E+04		(K)ATAVVD	(K)A T\A/V/V/D/G A F K(E)		134.45	489.7674	978.525	0.0021	2.1	5.88	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
23032	dirMS_041712_NAR_30mM_plus2.14315.14315.2	2	4.37	0	8.90E+05	M320m	(K)YmACCL	(K)Y/m|A\C C L/L/Y R(G)	C:Carbamidomethylation m:Oxid	127.25	633.2777	1249.553	15.9955	0.5	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
23033	dirMS_041712_NAR_30mM_plus2.21992.21992.2	2	4.37	0	1.95E+04		(R)VIFGLFG	(R)V I/F G L/F G K(T)		170.62	440.7682	880.529	0	0	8.72	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
23034	dirMS_041712_NAR_40mM_plus2.20150.20150.3	3	4.37	0	1.66E+05		(R)DALSDL	(R)D A/L S/D L A L H/F L/N K(M)		190.77	486.2654	1456.78	0.0022	1.5	5.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
23035	dirMS_041712_NAR_40mM_plus2.7110.7110.2	2	4.37	0	3.89E+04		(K)VTLTSEE	(K)V T/L/T/S E/E E A R(L)		101.7	567.78	1134.564	-0.011	-9.7	4.25	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
23036	dirMS_041712_NAR_50mM_plus2.10738.10738.3	3	4.37	0	2.02E+05		(R)ILDEIEE	(R)I L/D/E I/E E H N I/K(I)		123.78	451.5743	1352.706	0.0027	2	4.4	37167.8	5.8	HUMAN	B5MCX3	Septin-2
23037	dirMS_041712_NAR_50mM_plus2.16279.16279.3	3	4.37	1	4.50E+05		(R)YRVPDV	(R)Y R V P D\V L\V/A/D/P P I A R(L)		152.55	560.9825	1680.943	-0.0102	-6.1	5.96	96499.9	5.43	HUMAN	F5H6X6	Neutral alpha-glucosidase AB
23038	dirMS_041712_NAR_60mM_plus.13239.13239.3	3	4.37	1	2.80E+04		(K)AAAGKA	(K)A/A/A G K A/E L E/L E L G/R(I)		126.13	476.5985	1427.785	-0.0043	-3	4.79	533778	5.74	HUMAN	Q15149	Plectin
23039	dirMS_041712_NAR_60mM_plus.16510.16510.3	3	4.37	0	6.81E+05		(K)SPYQEF	(K)S P Y/Q E/F/T\D H L V/K(T)		142.77	488.5776	1463.717	0.0017	1.2	5.3	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
23040	dirMS_041712_NAR_60mM_plus.17151.17151.3	3	4.37	1	3.54E+05		(K)YQLDKD	(K)Y Q|L D K D/G V V L F K(K)		146.62	475.5976	1424.778	-0.0001	-0.1	5.96	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
23041	dirMS_041712_NAR_120mM_minus.9530.9530.3	3	4.36	1	1.52E+05		(R)FVKQDC	(R)F V/K Q D\Q/V|C I A/R(L)	C:Carbamidomethylation	107	455.2407	1363.715	-0.0075	-5.5	8.75	53458.1	5.47	HUMAN	H3BR35	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A (Fragment)
23042	dirMS_041712_NAR_20mM_minus.8518.8518.2	2	4.36	0	1.29E+04		(R)YEIEETE	(R)Y E|I/E E/T E T V T K(S)		134.38	671.3246	1341.642	-0.0001	-0.1	4.09	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
23043	dirMS_041712_NAR_30mM_minus2.6711.6711.2	2	4.36	0	1.92E+05		(R)QGEAEF	(R)Q G|E A/E/F N/R(I)		90.7	475.7203	950.433	0.0007	0.7	4.53	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
23044	dirMS_041712_NAR_40mM_minus2.10838.10838.3	3	4.36	0	4.26E+05		(R)DAGEGL	(R)D A/G/E/G/L/L A V Q I T D Q E G\K\P K(R)		147.47	657.0157	1969.024	0.0089	4.5	4.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
23045	dirMS_041712_NAR_50mM_minus2.10458.10458.3	3	4.36	0	1.12E+05	M271m	(R)DLSYCLS	(R)D L/S/Y/C L S G m Y D/H R(Y)	C:Carbamidomethylation m:Oxid	128.07	544.8966	1616.683	15.9921	-1.7	5.21	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
23046	dirMS_041712_NAR_50mM_minus2.11045.11045.3	3	4.36	0	8.01E+04		(K)ITKPGSI	(K)I T/K P G S I D S N N/Q/L F A/P G G R(L)		131.03	658.0062	1972.025	-0.0206	-10.5	8.75	176357.7	5.25	HUMAN	D3DNT2	Eukaryotic translation initiation factor 4 gamma 1
23047	dirMS_041712_NAR_50mM_minus2.13477.13477.3	3	4.36	1	1.56E+05		(R)LAIKLPD	(R)L A/I K L/P D D Q/I/P K(T)		145.3	450.9376	1350.799	-0.0009	-0.7	5.96	26413	9.18	HUMAN	B1APP6	6-phosphofructokinase type C (Fragment)
23048	dirMS_041712_NAR_60mM_minus.6283.6283.3	3	4.36	0	6.78E+04	M385m	(R)AQLmN	(R)A Q\L/m/N C H V/S/A G T R(H)	C:Carbamidomethylation m:Oxid	93.77	487.5623	1444.678	15.994	-0.6	9.8	57941.9	5.52	HUMAN	Q96RE7	Nucleus accumbens-associated protein 1
23049	dirMS_041712_NAR_20mM_plus.18620.18620.2	2	4.36	0	1.56E+05		(R)IITLTGP	(R)I I|T\L/T|G P T N A I F K(A)		200.3	694.9091	1388.815	-0.0039	-2.8	8.75	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
23050	dirMS_041712_NAR_20mM_plus.7276.7276.2	2	4.36	0	2.85E+04		(R)VLEEGS	(R)V L|E/E/G/S V E A R(T)		118.03	544.7829	1088.558	0.0003	0.3	4.25	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
23051	dirMS_041712_NAR_50mM_plus2.14195.14195.3	3	4.36	0	2.91E+05	S1730s	(K)ALNTPV	(K)A/L/N T P\V L s V/L/K(E)	s:Phosphorylated S	143.27	412.2315	1154.714	79.9656	-0.6	8.8	526822	6.64	HUMAN	Q9NZJ4	Sacsin
23052	dirMS_041712_NAR_120mM_minus.11881.11881.3	3	4.35	0	5.73E+05	S1925s	(R)FYsDSH	(R)F/Y|s D/S/H H L/K(R)	s:N-acetylglucosamine (S)	118.85	446.2102	1133.537	203.0786	-0.6	6.92	231702.4	6.52	HUMAN	Q92576	PHD finger protein 3
23053	dirMS_041712_NAR_120mM_minus.12858.12858.4	4	4.35	0	6.71E+04	T507t	(K)HIPPAP	(K)H I P P A P Q A S S P/t/F C/K(T)	C:Carbamidomethylation t:N-ace	124.18	460.9843	1637.81	203.1049	13.9	8.76	69228.1	7.89	HUMAN	J3KPP5	Potassium voltage-gated channel subfamily C member 2
23054	dirMS_041712_NAR_120mM_minus.9289.9289.3	3	4.35	1	1.47E+05		(R)EQAEEE	(R)E Q/A/E E/E R Y F R(A)		104.9	452.8778	1356.618	0.001	0.7	4.5	12248.6	9.34	HUMAN	Q9UII2	ATPase inhibitor, mitochondrial
23055	dirMS_041712_NAR_20mM_minus.11985.11985.3	3	4.35	1	1.00E+06	M271m	(K)TAAELR	(K)T A A/E L R/K C I G m Q E(-)	C:Carbamidomethylation m:Oxid	169.73	508.2517	1506.74	16.0002	3.5	5.95	32434.1	6.55	HUMAN	Q5T0U0	Coiled-coil domain-containing protein 122
23056	dirMS_041712_NAR_20mM_minus.12000.12000.3	3	4.35	0	1.12E+04	N303n	(R)GSDVAS	(R)G S D/V A S A Q/L P n/F R(H)	n:N-acetylglucosamine (N)	168.1	522.2561	1361.681	203.0729	-4.1	5.84	42521.4	7.16	HUMAN	Q5T280	Uncharacterized protein C9orf114
23057	dirMS_041712_NAR_20mM_minus.13857.13857.2	2	4.35	0	2.84E+05		(K)LGGSAV	(K)L G G S/A V/I/S L E G/K/P L(-)		188.97	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
23058	dirMS_041712_NAR_20mM_minus.14093.14093.2	2	4.35	0	2.03E+05		(K)DVDLEFI	(K)D V|D\L E F\L A K(M)		193.58	525.278	1049.551	-0.0026	-2.5	4.03	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
23059	dirMS_041712_NAR_30mM_minus2.7114.7114.2	2	4.35	1	1.24E+05		(R)MEVRW	(R)M E/V R/W/G E K(G)		93.68	517.7527	1034.509	-0.0107	-10.3	5.9	63472.5	7.82	HUMAN	Q9H6X2	Anthrax toxin receptor 1
23060	dirMS_041712_NAR_30mM_minus2.8160.8160.2	2	4.35	0	2.09E+04		(K)TSEDIIK	(K)T S/E D/I I/K(S)		98.57	403.2183	805.43	-0.0009	-1.1	4.37	162453.6	5.36	HUMAN	Q5TB80	Protein QN1 homolog
23061	dirMS_041712_NAR_50mM_minus2.14468.14468.3	3	4.35	0	3.68E+05		(R)LASTLVH	(R)L A|S T L/V/H L G E Y Q A A V D G A R(K)		150.95	657.6803	1971.029	-0.0031	-1.6	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
23062	dirMS_041712_NAR_60mM_minus.13346.13346.3	3	4.35	2	2.47E+05		(R)IGEELKC	(R)I/G E E L/K Q A G R K(G)		134.28	410.2411	1228.701	0.0079	6.5	8.59	74442.6	9.6	HUMAN	Q9HDB9	HERV-K_3q12.3 provirus ancestral Gag polyprotein
23063	dirMS_041712_NAR_120mM_plus.8688.8688.3	3	4.35	1	2.05E+04	Y232y	(R)TIyAAHK	(R)T/I y/A A H/K Q A K(A)	y:Phosphorylated Y	98.83	404.2038	1130.632	79.9652	-1	9.7	150443.8	8.95	HUMAN	C9JFZ1	Synaptojanin-1
23064	dirMS_041712_NAR_20mM_plus.11482.11482.2	2	4.35	0	1.82E+05		(R)YALYDA	(R)Y A\L|Y D A T Y E/T K(E)		151.48	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
23065	dirMS_041712_NAR_20mM_plus.7985.7985.3	3	4.35	0	4.52E+05	M239m	(K)EVDEQm	(K)E V D E/Q m L/N V Q N K(N)	m:Oxidized methionine	125.12	488.2328	1446.689	15.9945	-0.3	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
23066	dirMS_041712_NAR_30mM_plus2.5664.5664.2	2	4.35	0	6.89E+04		(R)QLEDGD	(R)Q\L E D/G D/Q/P E S K(K)		83.85	623.2808	1245.559	-0.005	-4	3.91	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
23067	dirMS_041712_NAR_40mM_plus2.12072.12072.3	3	4.35	1	2.81E+05		(K)LIADVAF	(K)L I A D/V A P S A I R E N D/I K(S)		136.47	575.6528	1724.954	-0.0103	-6	4.56	18388.8	6.85	HUMAN	F5H1Y3	Flap endonuclease 1 (Fragment)
23068	dirMS_041712_NAR_40mM_plus2.9131.9131.2	2	4.35	0	8.93E+04		(K)GSDFDC	(K)G S/D/F/D C E/L R(L)	C:Carbamidomethylation	115.47	549.7296	1098.452	-0.0001	-0.1	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
23069	dirMS_041712_NAR_50mM_plus2.11190.11190.3	3	4.35	1	2.06E+05		(R)AVIGIGII	(R)A V|I/G/I G I E E E D/R K(H)		126.37	476.9255	1428.769	-0.0073	-5.1	4.41	107721.8	8.85	HUMAN	O94906	Pre-mRNA-processing factor 6
23070	dirMS_041712_NAR_50mM_plus2.15310.15310.3	3	4.35	1	1.38E+05		(R)VEKIPG	(R)V E K I P G G I\I/E/D S C V\L R(G)	C:Carbamidomethylation	147.18	595.6548	1784.958	-0.0076	-4.3	4.68	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
23071	dirMS_041712_NAR_50mM_plus2.17585.17585.3	3	4.35	2	3.82E+05	S319s	(R)LLsVEGS	(R)L L s V/E G S T|L R E A L T H R K(I)	s:Phosphorylated S	160.62	664.0289	1910.082	79.9904	12.1	8.75	119791	9.69	HUMAN	F5H6E2	Unconventional myosin-Ic
23072	dirMS_041712_NAR_60mM_plus.19457.19457.3	3	4.35	1	1.08E+05	M2755m	(K)AAAVLG	(K)A A A/V L G m D/K A V A E P V S/R(L)	m:Oxidized methionine	160.07	567.6349	1684.905	15.9851	-5.8	6.12	351590.8	5.81	HUMAN	P42858	Huntingtin
23073	dirMS_041712_NAR_60mM_plus.20765.20765.3	3	4.35	1	1.09E+05		(R)GLFIIDD	(R)G L|F I/I D D K/G I L R(Q)		169.52	453.9368	1359.8	-0.0036	-2.7	5.96	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
23074	dirMS_041712_NAR_60mM_plus.20991.20991.3	3	4.35	1	1.11E+04	S2742s	(R)RLLNFD	(R)R L L N F D T/E|L\s T K(E)	s:N-acetylglucosamine (S)	172.07	547.293	1436.774	203.0901	6.5	6.07	378709.3	6.48	HUMAN	H3BLU6	E3 ubiquitin-protein ligase RNF213
23075	dirMS_041712_NAR_120mM_minus.12718.12718.3	3	4.34	1	2.35E+05		(R)NKQEVN	(R)N K Q E/V M\I/S D/L/E/E/R(L)		123.4	530.9318	1590.779	0.0016	1	4.41	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
23076	dirMS_041712_NAR_20mM_minus.10973.10973.3	3	4.34	0	8.33E+03	M92m	(R)ImNTFS	(R)I m N T\F\S/V/V/P S P/K(V)	m:Oxidized methionine	157.25	445.9027	1319.703	15.9908	-3.1	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
23077	dirMS_041712_NAR_20mM_minus.12660.12660.2	2	4.34	0	1.65E+05	M185m	(K)LAVNm	(K)L/A|V/N m V/P F P R(L)	m:Oxidized methionine	174.95	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
23078	dirMS_041712_NAR_20mM_minus.9449.9449.2	2	4.34	0	9.12E+04		(K)NAGVEG	(K)N A\G\V|E G S L I/V E K(I)		144.07	608.3299	1215.658	-0.0054	-4.5	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
23079	dirMS_041712_NAR_30mM_minus2.17810.17810.3	3	4.34	0	1.27E+05		(R)SLAALSC	(R)S L\A\A L\S Q/I/A/Y/Q R(N)		150.78	440.9139	1320.727	0.0001	0.1	8.46	64225	6.66	HUMAN	E7EX44	Caldesmon
23080	dirMS_041712_NAR_30mM_minus2.5083.5083.2	2	4.34	0	1.38E+05		(R)AAEQYT	(R)A/A\E/Q Y/T\P K(A)		81.13	454.2271	907.452	-0.005	-5.6	6.04	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
23081	dirMS_041712_NAR_30mM_minus2.7396.7396.2	2	4.34	1	1.06E+05		(R)EANKLA	(R)E\A/N|K/L A E/K(R)		94.58	451.7442	902.494	-0.013	-14.5	6.24	51805.7	5.16	HUMAN	B3KXD6	Pescadillo homolog
23082	dirMS_041712_NAR_40mM_minus2.13560.13560.3	3	4.34	1	3.72E+04		(K)VTLVVG	(K)V T\L V V/G/A S Q D I I/P Q L K K(K)		163.58	603.696	1809.084	-0.011	-6.1	8.56	25180.2	5.34	HUMAN	E7EMS6	Catechol O-methyltransferase (Fragment)
23083	dirMS_041712_NAR_50mM_minus2.10727.10727.3	3	4.34	1	1.92E+05		(R)QKNGTT	(R)Q K N G T/T A L I H A A E K(N)		128.88	494.6068	1481.807	-0.0012	-0.8	8.6	97694	5.81	HUMAN	Q99549	M-phase phosphoprotein 8
23084	dirMS_041712_NAR_50mM_minus2.12154.12154.3	3	4.34	0	1.95E+05		(K)FADEHV	(K)F A D E H\V|P\G S/P F T V K(I)		137.67	510.9256	1530.759	0.0035	2.3	5.32	258215.9	5.48	HUMAN	E7EN95	Filamin-B
23085	dirMS_041712_NAR_50mM_minus2.15941.15941.3	3	4.34	0	9.45E+04	M55m	(R)DIKPDNI	(R)D I\K P D N\F|L m/G I/G/R(H)	m:Oxidized methionine	158.05	497.9267	1475.767	15.998	2.1	5.96	27968.7	9.69	HUMAN	D6REM4	Casein kinase I isoform alpha
23086	dirMS_041712_NAR_50mM_minus2.5783.5783.3	3	4.34	0	1.15E+05		(K)TVEAEA	(K)T V/E/A E A A H/G T V T/R(H)		94.6	447.8956	1341.676	-0.0035	-2.6	5.37	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
23087	dirMS_041712_NAR_60mM_minus.17381.17381.3	3	4.34	1	7.12E+05		(K)QLDDLK	(K)Q L/D D L K/V/E L S/Q L R(V)		156.22	519.6267	1556.864	0.0013	0.8	4.56	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
23088	dirMS_041712_NAR_60mM_minus.8116.8116.3	3	4.34	1	8.45E+04		(K)VDATAE	(K)V/D/A/T A E T D L A K R(F)		105.18	430.5619	1289.67	0.0016	1.2	4.56	73273.4	4.96	HUMAN	P13667	Protein disulfide-isomerase A4
23089	dirMS_041712_NAR_60mM_minus.8639.8639.3	3	4.34	1	6.84E+03	M52m K59	(R)RAPSSV	(R)R A P S S V A H T S m/S/D\N G G F k(R)	m:Oxidized methionine k:Ub	108.07	660.3034	1848.866	130.0299	-4	8.76	13961.3	8.26	HUMAN	A6NCC9	Protein TSSC4
23090	dirMS_041712_NAR_60mM_minus.8669.8669.3	3	4.34	1	5.21E+04	M227m M	(R)mQKEIT	(R)m Q K\E I T A L/A|P S T m K(I)	m:Oxidized methionine	108.17	527.6044	1548.812	31.9862	-2.3	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
23091	dirMS_041712_NAR_120mM_plus.17924.17924.3	3	4.34	0	1.18E+06		(R)SLSEGHI	(R)S L S E G H P T A/Q H E/K(M)		146.27	474.2314	1420.681	-0.0019	-1.3	5.95	73325.2	9.19	HUMAN	F5H2A9	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial
23092	dirMS_041712_NAR_20mM_plus.10866.10866.2	2	4.34	0	2.06E+04		(K)DVNAAI	(K)D V|N A|A I\A T I K(T)		147.28	508.292	1015.578	-0.0015	-1.5	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
23093	dirMS_041712_NAR_20mM_plus.16321.16321.3	3	4.34	0	3.16E+04		(K)TIIPLISQ	(K)T I I\P L\I/S/Q C T P/K(V)	C:Carbamidomethylation	184.13	457.5994	1370.771	0.0124	9.1	8.41	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
23094	dirMS_041712_NAR_20mM_plus.17488.17488.2	2	4.34	0	5.88E+04		(K)LAAVDA	(K)L A\A V/D A/T V/N Q V L A/S R(Y)		192.27	764.4257	1527.849	-0.0048	-3.1	5.84	53659.5	5.35	HUMAN	B5MCQ5	Protein disulfide-isomerase A6
23095	dirMS_041712_NAR_20mM_plus.8351.8351.2	2	4.34	0	2.18E+04		(K)GDATVS	(K)G D/A T\V S Y E D|P P/T/A K(A)		127.62	725.8358	1450.67	-0.0053	-3.7	4.03	65213.5	9.57	HUMAN	B0QYK0	Ewing sarcoma breakpoint region 1
23096	dirMS_041712_NAR_20mM_plus.9094.9094.2	2	4.34	0	4.59E+03	M1901m	(R)AEmEVL	(R)A E m/E V L L/A|S/K(A)	m:Oxidized methionine	133.03	553.7889	1090.581	15.9893	-5.1	4.53	533778	5.74	HUMAN	Q15149	Plectin
23097	dirMS_041712_NAR_30mM_plus2.16642.16642.2	2	4.34	0	2.65E+05		(K)NAFSLL	(K)N A\F S L/L/G K(Q)		139.48	425.239	849.483	-0.0122	-14.3	8.75	344060.7	5.87	HUMAN	F5H269	DmX-like protein 1
23098	dirMS_041712_NAR_30mM_plus2.16847.16847.2	2	4.34	1	1.66E+05		(K)ICIKESG	(K)I/C/I/K E S G Q/K(L)	C:Carbamidomethylation	140.52	531.7842	1062.561	-0.0001	-0.1	8.59	539122.1	5.69	HUMAN	Q15751	Probable E3 ubiquitin-protein ligase HERC1
23099	dirMS_041712_NAR_30mM_plus2.21422.21422.2	2	4.34	0	2.86E+05		(R)EADDIVI	(R)E A\D D I|V/N/W L/K(K)		167.47	601.81	1202.605	0.0075	6.3	4.03	26363.4	4.91	HUMAN	I3L312	Protein disulfide-isomerase (Fragment)
23100	dirMS_041712_NAR_40mM_plus2.13197.13197.2	2	4.34	0	1.70E+05		(R)VAPEEH	(R)V A/P E E H/P V L/L T E/A P L N P K(A)		143.78	977.5344	1954.064	-0.0029	-1.5	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
23101	dirMS_041712_NAR_40mM_plus2.14758.14758.3	3	4.34	1	1.29E+05		(R)EGSVML	(R)E G/S\V/M/L Q V D V D/T V/K G G L K(L)		153.6	625.6667	1874.989	-0.0036	-1.9	4.56	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
23102	dirMS_041712_NAR_40mM_plus2.6981.6981.2	2	4.34	0	2.31E+05		(K)NMMAA	(K)N M|M/A A C D/P R(H)	C:Carbamidomethylation	101.42	533.2182	1065.427	0.0017	1.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
23103	dirMS_041712_NAR_40mM_plus2.7788.7788.2	2	4.34	0	4.23E+04		(R)VLNTNI	(R)V L|N/T/N I D G R(R)		105.73	501.2719	1001.537	-0.0009	-0.9	5.81	17718.4	10.99	HUMAN	P62269	40S ribosomal protein S18

23104	dirMS_041712_NAR_40mM_plus2.8183.8183.2	2	4.34	0	3.13E+04		(K)LIEVDDE	(K)L I/E V/D D E R(K)		108.03	494.7521	988.495	0.0024	2.4	3.91	10471.9	5.4	HUMAN	A2A3R7	40S ribosomal protein S6
23105	dirMS_041712_NAR_50mM_plus2.21517.21517.3	3	4.34	1	1.66E+05		(R)LLSLAAP	(R)L L/S L A A P K M A S/I M\E G P L S K(W)		183.03	653.0385	1957.086	0.0149	7.6	8.59	84468.7	6.03	HUMAN	B1AKJ6	Oxysterol-binding protein
23106	dirMS_041712_NAR_60mM_plus.10078.10078.2	2	4.34	0	2.03E+06		(K)GIVEFSG	(K)G I\V|E/F/S G K P A A R(K)		111.3	616.3425	1231.679	-0.0016	-1.3	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
23107	dirMS_041712_NAR_60mM_plus.18541.18541.3	3	4.34	1	2.31E+05		(K)DANAKL	(K)D A/N A\K L S E\L E/A/A L Q/R(A)		154.38	543.6241	1628.86	-0.0025	-1.5	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
23108	dirMS_041712_NAR_60mM_plus.7582.7582.3	3	4.34	0	7.88E+05		(K)AVEAAQ	(K)A V E A A Q L/A/E D/L/K(V)		98.27	419.894	1257.669	-0.0011	-0.8	4.14	79575.8	8.86	HUMAN	F8W8Z4	E3 ubiquitin-protein ligase BRE1B
23109	dirMS_041712_NAR_120mM_minus.15265.15265.4	4	4.33	0	1.28E+04	K63k	(K)AQKPNG	(K)A Q K P N G Q/L V N P N N F/W k(N)	k:Ubiquitin-K	137.83	493.0108	1854.961	114.0604	8.9	10	46499.8	9.63	HUMAN	Q8NFL0	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7
23110	dirMS_041712_NAR_120mM_minus.9168.9168.3	3	4.33	0	6.83E+05		(K)HTGPNS	(K)H T G P N S\P D/T/A/N D G F\V\R(L)		103.45	562.2599	1684.767	-0.0022	-1.3	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
23111	dirMS_041712_NAR_20mM_minus.10931.10931.2	2	4.33	0	7.01E+04		(R)LAVEAL	(R)L/A/V/E/A L V R(T)		157.07	435.7738	870.541	-0.0004	-0.5	6	65558.6	9.87	HUMAN	G3V1S7	Hyaluronan synthase 1
23112	dirMS_041712_NAR_20mM_minus.14019.14019.3	3	4.33	0	9.84E+04		(K)VLAQNS	(K)V L|A Q N S G F/D/L/Q E T L V K(I)		192.37	587.9823	1761.938	-0.0058	-3.3	4.37	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
23113	dirMS_041712_NAR_20mM_minus.9916.9916.2	2	4.33	0	9.49E+04	M196m	(K)DAGTIA	(K)D A\G T/I/A/G\L\N V m R(I)	m:Oxidized methionine	149.33	617.3216	1217.631	16.0052	8.4	5.84	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
23114	dirMS_041712_NAR_30mM_minus2.16820.16820.2	2	4.33	0	2.21E+04		(K)NSLESYA	(K)N S|L/E/S Y/A F N M K(A)		144.5	652.3031	1303.599	0.0002	0.2	6	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
23115	dirMS_041712_NAR_40mM_minus2.13399.13399.3	3	4.33	1	1.92E+05		(K)LGVQVV	(K)L/G V/Q V/V/I T D P E K L D Q I R(Q)		163.35	641.7007	1923.091	-0.0034	-1.8	4.56	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
23116	dirMS_041712_NAR_50mM_minus2.10722.10722.3	3	4.33	1	3.70E+05		(R)DVVICP	(R)D V/V/I C/P D/A S L\E D A K K(E)	C:Carbamidomethylation	128.77	553.9474	1659.826	0.0018	1.1	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
23117	dirMS_041712_NAR_50mM_minus2.15171.15171.3	3	4.33	0	3.63E+05		(K)IAILTCP	(K)I A\I/L/T C P F E P P K P K(T)	C:Carbamidomethylation	153.82	537.6375	1610.898	0.0005	0.3	8.59	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
23118	dirMS_041712_NAR_50mM_minus2.5709.5709.3	3	4.33	1	5.51E+04		(K)TAGPIAS	(K)T A G P I A/S A Q K Q P A/G K(V)		93.67	475.5972	1424.786	-0.0086	-6	10	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
23119	dirMS_041712_NAR_50mM_minus2.7314.7314.3	3	4.33	1	8.39E+04		(K)ELQAAG	(K)E L/Q/A A G K/S/P E D L E R(L)		108.02	514.9262	1542.776	-0.0118	-7.6	4.41	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
23120	dirMS_041712_NAR_60mM_minus.16259.16259.3	3	4.33	1	4.40E+05		(K)NIYVLQE	(K)N I/Y V/L Q E L/D N/P G A K R(I)		150.77	577.3128	1729.923	0.0007	0.4	6.07	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
23121	dirMS_041712_NAR_60mM_minus.8204.8204.3	3	4.33	1	8.96E+04	M936m	(K)IEEFEKL	(K)I E E/F/E K L m S|R(E)	m:Oxidized methionine	105.82	433.2257	1281.651	16.0118	13	4.79	337747	5.95	HUMAN	Q9P2D1	Chromodomain-helicase-DNA-binding protein 7
23122	dirMS_041712_NAR_60mM_minus.8995.8995.3	3	4.33	1	1.44E+05		(R)AREQAE	(R)A R E Q\A E A|E|V/A/S/L N R(R)		110.27	515.2639	1543.782	-0.0052	-3.3	4.79	11017	4.8	HUMAN	D6R904	Tropomyosin alpha-3 chain
23123	dirMS_041712_NAR_20mM_plus.10703.10703.2	2	4.33	0	4.55E+04		(R)FGIVTSS	(R)F G I/V\T S S A/G/T/G T T E D T E A K(K)		146.4	936.4446	1871.887	-0.005	-2.7	4.14	59643.8	9.11	HUMAN	H0YHG0	Uncharacterized protein (Fragment)
23124	dirMS_041712_NAR_20mM_plus.12983.12983.3	3	4.33	1	5.56E+05	T648t	(R)tIPPDVI	(R)t I|P\P D/V I A K N R(I)	t:Phosphorylated T	162.02	435.2319	1223.711	79.9705	3.2	8.41	107120	9.75	HUMAN	Q7Z7M9	Polypeptide N-acetylgalactosaminyltransferase 5
23125	dirMS_041712_NAR_30mM_plus2.11885.11885.2	2	4.33	0	3.97E+06		(K)SCNCLLL	(K)S C|N C L|L/L/K(V)	C:Carbamidomethylation	114.8	504.2556	1007.501	0.0027	2.7	8.47	47510.4	7.04	HUMAN	P06733	Alpha-enolase
23126	dirMS_041712_NAR_30mM_plus2.6793.6793.2	2	4.33	0	1.50E+05		(K)VPLTQA	(K)V/P\L/T|Q A T R(G)		90.48	443.2607	885.515	-0.0011	-1.3	9.72	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
23127	dirMS_041712_NAR_40mM_plus2.5065.5065.2	2	4.33	0	2.32E+05	M154m M	(R)mGYmD	(R)m G/Y m/D|P R(E)	m:Oxidized methionine	84.82	451.1811	869.364	31.9905	0.7	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
23128	dirMS_041712_NAR_40mM_plus2.6811.6811.2	2	4.33	0	1.53E+04		(K)AGFAGD	(K)A G/F/A/G D D A P R(A)		101.45	488.728	976.448	0.0004	0.4	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
23129	dirMS_041712_NAR_40mM_plus2.9861.9861.2	2	4.33	0	2.29E+05		(K)EQFAW	(K)E Q/F A/W R(H)		122.8	418.706	836.405	-0.0002	-0.3	6.1	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
23130	dirMS_041712_NAR_50mM_plus2.16313.16313.3	3	4.33	1	7.02E+05		(K)CEFQDA	(K)C/E/F Q D A\Y V/L L S E K K(I)	C:Carbamidomethylation	152.62	577.2866	1729.847	-0.0013	-0.8	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
23131	dirMS_041712_NAR_50mM_plus2.7502.7502.3	3	4.33	1	1.12E+04	M2747m	(K)TLQEVT	(K)T L\Q/E/V/T E m D S V K R(Y)	m:Oxidized methionine	105.53	517.9284	1535.773	15.9973	1.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
23132	dirMS_041712_NAR_60mM_plus.12583.12583.3	3	4.33	1	2.45E+05	K142k	(K)EGNHRF	(K)E/G N/H R F V A I k(T)	k:Ubiquitin-K	122.85	428.9017	1170.638	114.0527	7.6	8.85	64059.3	4.88	HUMAN	O75553	Disabled homolog 1
23133	dirMS_041712_NAR_60mM_plus.14198.14198.3	3	4.33	1	3.21E+05	N2180n	(R)DIVNPH	(R)D/I/V/N P H A Y K n N K(W)	n:N-acetylglucosamine (N)	131.17	539.2805	1412.728	203.0989	12.1	8.5	409988.3	5.51	HUMAN	Q70CQ2	Ubiquitin carboxyl-terminal hydrolase 34
23134	dirMS_041712_NAR_120mM_minus.4919.4919.3	3	4.32	0	1.22E+06	M46m M4	(R)HQGVm	(R)H Q G V m|V/G/m/G Q K(D)	m:Oxidized methionine	77.47	401.8604	1171.571	31.9956	4.8	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
23135	dirMS_041712_NAR_120mM_minus.5817.5817.3	3	4.32	0	2.02E+04		(R)QHGEQL	(R)Q H G E Q L G\G G/G\S/G\G/G G/Y N N S K(H)		85.18	620.9431	1860.822	-0.0072	-3.9	6.75	120240.2	6.45	HUMAN	B4DG92	Pumilio homolog 1
23136	dirMS_041712_NAR_120mM_minus.7926.7926.2	2	4.32	0	1.60E+05		(K)HFEALA	(K)H/F|E A\L A N/R(A)		97.5	479.2478	957.49	-0.0018	-1.8	6.75	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
23137	dirMS_041712_NAR_50mM_minus2.18028.18028.3	3	4.32	0	2.87E+05		(R)SLHDAL	(R)S L H D A L|C|V|L/A Q T V K(D)	C:Carbamidomethylation	171.73	518.9488	1554.831	0.001	0.6	6.46	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
23138	dirMS_041712_NAR_50mM_minus2.6159.6159.3	3	4.32	1	5.72E+03		(R)IVDGKV	(R)I/V/D/G K V V S E/T N D|T K(V)		99.03	502.2662	1504.785	-0.0013	-0.9	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
23139	dirMS_041712_NAR_50mM_minus2.8114.8114.3	3	4.32	1	1.41E+05		(K)GILAAD	(K)G I/L/A/A D E S T G S/I A K R(L)		113.83	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
23140	dirMS_041712_NAR_60mM_minus.11660.11660.3	3	4.32	0	7.55E+04		(R)LMPALG	(R)L M P A L G V S/V/A D Q/K(G)		124.88	443.5818	1328.724	0.0066	5	5.84	139455.1	9.44	HUMAN	Q6P4R8	Nuclear factor related to kappa-B-binding protein
23141	dirMS_041712_NAR_60mM_minus.12692.12692.3	3	4.32	1	1.29E+05		(R)TPSDVK	(R)T P\S D V K/E L V/L/D N/S R(S)		131.18	524.9451	1572.823	-0.002	-1.3	4.55	20111	4.47	HUMAN	H0YN26	Acidic leucine-rich nuclear phosphoprotein 32 family member A
23142	dirMS_041712_NAR_60mM_minus.14532.14532.3	3	4.32	1	1.80E+05		(R)KTTLQV	(R)K T T L Q\V D T L/N A/E/L/A A E R(S)		140.43	625.0044	1873.003	-0.0039	-2.1	4.68	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
23143	dirMS_041712_NAR_120mM_plus.21240.21240.4	4	4.32	0	5.96E+04	T203t	(K)NTVtLV	(K)N T V t L/V Q A T/P P\Q P I K(V)	t:N-acetylglucosamine (T)	165.15	453.2599	1606.916	203.1015	12.2	8.75	75480.3	9.78	HUMAN	Q96BD5	PHD finger protein 21A
23144	dirMS_041712_NAR_120mM_plus.9511.9511.4	4	4.32	2	2.99E+05		(K)LITYGSD	(K)L I/T Y/G S D R T E A L K R(M)		103.75	406.4764	1622.886	-0.0023	-1.4	8.59	15838.9	7.03	HUMAN	H0Y5U0	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment)
23145	dirMS_041712_NAR_20mM_plus.11867.11867.2	2	4.32	0	1.15E+05		(R)AQAALA	(R)A Q|A/A L/A/V N I S A A R(G)		154.77	628.3565	1255.712	-0.006	-4.8	9.79	58479.6	6.23	HUMAN	P40227	T-complex protein 1 subunit zeta
23146	dirMS_041712_NAR_20mM_plus.14464.14464.3	3	4.32	0	4.89E+04	M313m	(R)TVQSLE	(R)T V Q S L E I/D/L/D/S m/R(N)	m:Oxidized methionine	171.23	508.2519	1506.747	15.9943	-0.4	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
23147	dirMS_041712_NAR_20mM_plus.7127.7127.2	2	4.32	0	8.61E+04		(K)VAPAPA	(K)V A/P\A/P\A/V V K(K)		116.67	426.2703	851.535	-0.0016	-1.9	8.72	30166.2	10.79	HUMAN	P62424	60S ribosomal protein L7a
23148	dirMS_041712_NAR_20mM_plus.7749.7749.2	2	4.32	0	5.41E+04		(K)LAAIGE	(K)L A|A|I/G E A T R(L)		123.2	451.2557	901.51	-0.006	-6.7	6	533778	5.74	HUMAN	Q15149	Plectin
23149	dirMS_041712_NAR_40mM_plus2.6715.6715.2	2	4.32	1	6.44E+04		(R)GGRGN	(R)G G/R\G N G/A E/R(V)		99.47	437.2125	873.429	-0.0108	-12.4	9.6	297845.7	9.32	HUMAN	Q9UMN6	Histone-lysine N-methyltransferase MLL4
23150	dirMS_041712_NAR_60mM_plus.14515.14515.3	3	4.32	1	9.30E+05		(K)TKEVYE	(K)T K\E V Y\E\L/L/D S/P G K(V)		131.93	493.5959	1478.774	-0.0006	-0.4	4.68	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
23151	dirMS_041712_NAR_120mM_minus.5080.5080.3	3	4.31	1	4.70E+05		(R)AAEEED	(R)A A/E E E D E A D/P K/R(Q)		79.58	453.8716	1359.602	-0.002	-1.5	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
23152	dirMS_041712_NAR_120mM_minus.9761.9761.3	3	4.31	0	8.01E+05		(K)EFHLNE	(K)E F H L N/E S/G D/P S S K(S)		106.63	482.8881	1446.65	0.0002	0.1	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
23153	dirMS_041712_NAR_30mM_minus2.13665.13665.2	2	4.31	0	2.35E+05		(K)LTVEEA	(K)L/T|V/E E A F K(A)		127.65	468.7559	936.504	0.0008	0.9	4.53	266161	5.68	HUMAN	E9PPU0	Epiplakin
23154	dirMS_041712_NAR_50mM_minus2.7588.7588.3	3	4.31	1	1.66E+04	M22m	(K)LAEQAE	(K)L A/E/Q A E R Y D D m A/A C M K(S)	C:Carbamidomethylation m:Oxid	111.05	639.9402	1901.819	15.987	-4.1	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
23155	dirMS_041712_NAR_50mM_minus2.7818.7818.3	3	4.31	1	1.59E+04		(R)ALSTTA	(R)A L/S T/T A S T A/A F D/K Q/P Q S R(E)		111.67	627.319	1879.951	-0.0084	-4.5	8.79	48446.2	8.53	HUMAN	C9J8T0	Selenocysteine-specific elongation factor
23156	dirMS_041712_NAR_120mM_plus.11177.11177.4	4	4.31	0	1.39E+05		(K)SGLTPL	(K)S G L|T/P L H V A A H Y D N Q K(V)		111.67	438.4807	1750.887	0.0139	7.9	6.66	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
23157	dirMS_041712_NAR_120mM_plus.4678.4678.3	3	4.31	0	6.15E+05		(R)THSQG	(R)T H S Q G G/Y/G S\Q/G Y/K(Y)		74.07	457.2092	1369.613	-0.0001	-0.1	8.2	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
23158	dirMS_041712_NAR_120mM_plus.7840.7983.3	3	4.31	1	4.48E+05	M62m	(R)RmGES	(R)R\m G E|S D/D/S/I/L R(L)	m:Oxidized methionine	95.33	432.2104	1278.611	16.006	8.5	4.56	9225.3	9.16	HUMAN	P63220	40S ribosomal protein S21
23159	dirMS_041712_NAR_20mM_plus.17892.17892.2	2	4.31	0	1.94E+05		(R)YISPDQ	(R)Y/I/S/P D Q L A D L Y K(S)		194.27	713.3667	1425.726	0.0001	0.1	4.21	47510.4	7.04	HUMAN	P06733	Alpha-enolase
23160	dirMS_041712_NAR_20mM_plus.18271.18271.2	2	4.31	0	1.68E+05		(K)DAGVIA	(K)D A/G\V|I|A|G L N V L\R(I)		196.73	599.3505	1197.695	-0.0013	-1.1	5.84	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
23161	dirMS_041712_NAR_20mM_plus.9629.9629.2	2	4.31	0	6.00E+04		(K)ITLVSAA	(K)I T|L/V/S A/A P G K(V)		137.95	478.793	956.577	0.0012	1.3	8.75	12480.3	9.05	HUMAN	F5H2L4	Acyl-coenzyme A thioesterase 13
23162	dirMS_041712_NAR_20mM_plus.9981.9981.2	2	4.31	0	9.94E+04		(R)IASPEG	(R)I A S|P E/G/Q D Y L K(G)		140.27	610.8101	1220.616	-0.0028	-2.3	4.37	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
23163	dirMS_041712_NAR_30mM_plus2.10857.10955.2	2	4.31	0	2.20E+06		(K)SSFFSD	(K)S S/F/F/S D|R(G)		109.6	423.193	845.379	-0.0001	-0.1	5.55	15031.5	6.72	HUMAN	B4DLA0	ATP-dependent RNA helicase DDX3X
23164	dirMS_041712_NAR_30mM_plus2.4803.4803.2	2	4.31	0	8.21E+05	M67m	(K)SATPm	(K)S A/T P m|N\T/R(M)	m:Oxidized methionine	76.35	447.2119	877.42	15.9969	2.2	9.47	67469.1	8.66	HUMAN	Q96MW7	Tigger transposable element-derived protein 1
23165	dirMS_041712_NAR_30mM_plus2.7864.7864.2	2	4.31	0	1.42E+05		(R)AQYEEI	(R)A Q|Y/E/E I A\Q R(S)		94.78	554.2726	1107.543	-0.005	-4.5	4.53	54364	5.73	HUMAN	F5H8K9	Keratin, type II cytoskeletal 4
23166	dirMS_041712_NAR_30mM_plus2.9376.9376.2	2	4.31	0	4.41E+05		(R)GGGQII	(R)G G G Q/I|I|P/T A R(R)		103.85	485.2772	969.548	-0.0005	-0.5	9.75	15036.9	7.16	HUMAN	K7EJ74	116 kDa U5 small nuclear ribonucleoprotein component (Fragment)
23167	dirMS_041712_NAR_50mM_plus2.20634.20634.3	3	4.31	1	1.70E+05		(K)EELTRYL	(K)E E L T R Y L/L Y L Q/I/K(R)		177.62	561.3209	1681.952	-0.0042	-2.5	6.24	69683.6	5.97	HUMAN	A2A2Y4	FERM domain-containing protein 3
23168	dirMS_041712_NAR_60mM_plus.13200.13200.3	3	4.31	1	2.18E+06	S261s	(R)DSHLGP	(R)D S H L G|P|H R s T P E S R(A)	s:N-acetylglucosamine (S)	124.67	593.628	1575.762	203.1072	15.6	6.92	42309.7	5.34	HUMAN	E7ES96	Presenilin-1
23169	dirMS_041712_NAR_60mM_plus.7836.7836.3	3	4.31	1	5.67E+05		(K)EASKQA	(K)E A S K Q A D V|N L/V/N A/K(L)		98.85	496.2656	1486.786	-0.0038	-2.5	6.17	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
23170	dirMS_041712_NAR_20mM_minus.12301.12301.3	3	4.3	0	4.91E+05	M256m	(R)SLDmDS	(R)S\L\D m D\S\I|I A E V K(A)	m:Oxidized methionine	171.53	446.227	1320.671	15.9949	0	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
23171	dirMS_041712_NAR_30mM_minus2.11890.11890.2	2	4.3	0	4.10E+04		(R)QGAFLV	(R)Q G|A F/L/V/N A A/R(G)		117.48	523.7834	1046.574	-0.0146	-14	9.75	49457.5	6.47	HUMAN	P56545	C-terminal-binding protein 2
23172	dirMS_041712_NAR_30mM_minus2.12281.12281.2	2	4.3	0	4.11E+04	S35s	(R)IQASsV	(R)I Q A/S|s/V V S K(A)	s:Phosphorylated S	119.07	499.7499	918.525	79.9671	0.7	8.75	11845.1	9.77	HUMAN	F5H2Z5	Complement C1r subcomponent-like protein
23173	dirMS_041712_NAR_30mM_minus2.16550.16550.3	3	4.3	0	7.31E+05		(R)ASLEAA	(R)A S L E A/A I|A/D/A/E Q R(G)		143.75	448.8965	1344.675	-0.0004	-0.3	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
23174	dirMS_041712_NAR_30mM_minus2.5214.5214.2	2	4.3	0	6.25E+05		(R)TDTGEP	(R)T D|T|G/E P M G R(G)		82.03	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
23175	dirMS_041712_NAR_40mM_minus2.8057.8057.3	3	4.3	0	1.58E+05	M35m	(K)AASDIA	(K)A A/S D\I\A/m T\E L/P P T H P I R(L)	m:Oxidized methionine	128.13	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
23176	dirMS_041712_NAR_60mM_minus.17288.17288.3	3	4.3	1	1.56E+05		(K)SKDSLV	(K)S K D S L\V D I|I G I/C K(S)	C:Carbamidomethylation	156.22	483.2681	1447.783	0.0073	5	5.68	35399.1	5.17	HUMAN	I3L4R8	Replication protein A 70 kDa DNA-binding subunit (Fragment)
23177	dirMS_041712_NAR_60mM_minus.8138.8138.3	3	4.3	2	2.87E+05		(R)TARQAR	(R)T/A R/Q A R E E E\A R(R)		105.53	439.5636	1316.667	0.0097	7.4	5.9	235195.7	6.91	HUMAN	K7EKI0	Envoplakin
23178	dirMS_041712_NAR_60mM_minus.8900.8900.3	3	4.3	1	1.09E+05		(R)SRAEAE	(R)S R A\E A E|S|M/Y/Q I K(Y)		109.18	471.5706	1412.684	0.0134	9.5	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
23179	dirMS_041712_NAR_60mM_minus.9261.9261.3	3	4.3	0	2.51E+05		(K)QADNP	(K)Q A D N/P H V/A L Y/Q A R(F)		111.68	494.9197	1482.745	-0.0003	-0.2	6.74	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
23180	dirMS_041712_NAR_120mM_plus.6926.6926.3	3	4.3	1	2.82E+05		(R)VIEDRD	(R)V/I/E/D R/D S Q L R(S)		89.75	410.8828	1230.644	-0.0098	-8	4.56	94000.1	5.5	HUMAN	Q8N1F7	Nuclear pore complex protein Nup93
23181	dirMS_041712_NAR_30mM_plus2.21925.21925.2	2	4.3	0	2.18E+05		(R)NSILAQ	(R)N S\I\L|A/Q|V L D Q S A R(A)		170.2	707.8889	1414.765	0.0057	4	5.84	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
23182	dirMS_041712_NAR_40mM_plus2.10842.10842.3	3	4.3	0	2.22E+05		(R)LLEAQA	(R)L L/E/A Q A/C T G G I I H/P T T G Q K(L)	C:Carbamidomethylation	128.95	665.6807	1995.033	-0.0052	-2.6	6.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
23183	dirMS_041712_NAR_40mM_plus2.12193.12193.3	3	4.3	1	6.68E+04		(K)TSLVAT	(K)T S\L/V/A/T/P G I D K L/T E K(S)		137.8	524.9653	1572.884	-0.003	-1.9	5.73	89370.5	5.69	HUMAN	Q8IV36	Protein HID1
23184	dirMS_041712_NAR_40mM_plus2.5704.5704.2	2	4.3	1	5.58E+04		(R)ARGDSE	(R)A R G D S E A\L\D\E|E/S(-)		91.22	639.7736	1278.544	-0.0045	-3.5	3.83	74986.2	6.56	HUMAN	I3L080	Hepatoma-derived growth factor-related protein 2
23185	dirMS_041712_NAR_40mM_plus2.5844.5844.2	2	4.3	0	1.08E+05		(K)FNYSGS	(K)F N|Y|S|G S G G R(S)		92.48	472.7171	944.422	0.0049	5.1	8.75	96205.6	9.06	HUMAN	G5E9M5	Interleukin enhancer binding factor 3, 90kDa, isoform CRA_b
23186	dirMS_041712_NAR_40mM_plus2.8252.8252.2	2	4.3	0	6.73E+04		(K)NMGLY	(K)N M|G/L/Y/G E R(V)		109.63	470.2221	939.435	0.0016	1.8	6	43371.1	9.64	HUMAN	E7ERW2	Aspartate aminotransferase
23187	dirMS_041712_NAR_50mM_plus2.13702.13702.3	3	4.3	0	2.12E+05		(R)TPLHEIA	(R)T P L/H/E I A/L/S I K(L)		140.02	407.9109	1221.72	-0.002	-1.6	6.41	142268.2	6.41	HUMAN	Q08211	ATP-dependent RNA helicase A
23188	dirMS_041712_NAR_50mM_plus2.15798.15798.3	3	4.3	0	2.06E+05		(K)YPIEHGI	(K)Y/P I E H G I I|T/N/W D D M E K(I)		151.1	654.3085	1960.911	0	0	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
23189	dirMS_041712_NAR_50mM_plus2.21259.21259.3	3	4.3	1	5.54E+05	M145m	(R)GVmLA	(R)G V/m|L\A V/D/A V I A E L K/K(Q)	m:Oxidized methionine	181.93	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
23190	dirMS_041712_NAR_60mM_plus.15300.15300.3	3	4.3	0	1.93E+05		(K)HQTLQ	(K)H Q T L Q|G\V\A\F/P I S R(E)		136.23	485.2663	1453.791	-0.0067	-4.6	9.75	33635.5	6.01	HUMAN	F8VS81	Twinfilin-1 (Fragment)
23191	dirMS_041712_NAR_120mM_minus.7262.7262.2	2	4.29	0	2.68E+05		(R)HLTGEF	(R)H/L|T\G E\F E/K(K)		93.38	480.7433	960.479	0.0008	0.8	5.4	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
23192	dirMS_041712_NAR_20mM_minus.13871.13871.2	2	4.29	0	4.01E+05		(K)VLTPELY	(K)V L/T|P/E L Y A E L R(A)		190.87	652.3653	1303.726	-0.0023	-1.8	4.53	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
23193	dirMS_041712_NAR_20mM_minus.7979.7979.2	2	4.29	0	3.32E+03		(K)MDYNS	(K)M D Y N S F Q A|V/T I R(T)		128.55	722.8406	1444.689	-0.015	-10.4	5.59	135472.3	6.98	HUMAN	Q8IZF2-3	Isoform 3 of Probable G-protein coupled receptor 116
23194	dirMS_041712_NAR_20mM_minus.9086.9086.2	2	4.29	0	1.78E+04	M239m	(K)EITALAP	(K)E I/T/A/L/A/P S T m K(I)	m:Oxidized methionine	139.97	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
23195	dirMS_041712_NAR_30mM_minus2.5649.5649.2	2	4.29	0	1.48E+05		(K)YIDENQ	(K)Y I|D E/N Q D/R(Y)		84.52	526.7389	1052.464	0.0062	5.9	4.03	6412.4	9.52	HUMAN	J3KSS4	Cytosolic non-specific dipeptidase (Fragment)
23196	dirMS_041712_NAR_40mM_minus2.11052.11052.3	3	4.29	0	1.92E+04	N130n	(R)nLIWDI	(R)n/L/I W D I N/A/M L A M R(N)	n:N-acetylglucosamine (N)	149.23	588.6311	1560.803	203.0762	-1.8	5.84	16449.8	9.75	HUMAN	C6GKU9	Mediator of RNA polymerase II transcription subunit 30
23197	dirMS_041712_NAR_50mM_minus2.10565.10565.2	2	4.29	1	1.12E+05	S60s	(R)ETTSSTP	(R)E T/T S S/T P/R I S s K(T)	s:N-acetylglucosamine (S)	128.7	748.8859	1293.665	203.1	13.8	8.85	20145.6	9.6	HUMAN	C9J6P7	Nuclear valosin-containing protein-like (Fragment)
23198	dirMS_041712_NAR_50mM_minus2.15138.15138.3	3	4.29	1	1.67E+05		(R)SQPETT	(R)S Q P\E T T/E A A F K L T D L K(E)		153.45	593.6417	1778.917	-0.0065	-3.7	4.68	48885.9	7.05	HUMAN	F8W6H8	Cyclin-dependent kinase 15
23199	dirMS_041712_NAR_20mM_plus.10234.10234.3	3	4.29	0	1.27E+05	M281m M	(R)NmPQA	(R)N m P Q A D/A\m|V/L/V A R(N)	m:Oxidized methionine	143.37	483.2393	1415.713	31.99	0.1	5.84	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
23200	dirMS_041712_NAR_20mM_plus.19108.19108.2	2	4.29	0	1.45E+05		(R)EGDVLT	(R)E G D V L/T\L/L/E|S E R(E)		203.45	680.8536	1360.696	0.0045	3.3	4	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
23201	dirMS_041712_NAR_20mM_plus.8163.8163.3	3	4.29	0	2.31E+05	M346m M	(K)mGGmE	(K)m G G m\E/G P F/G/G/G|m E N m G R(F)	m:Oxidized methionine	126.28	593.558	1714.68	63.979	-0.4	4.53	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
23202	dirMS_041712_NAR_30mM_plus2.11258.11258.3	3	4.29	0	3.26E+05	M298m	(R)MGQm	(R)M G Q\m A M G G\A/M/G I/N N R(G)	m:Oxidized methionine	112.8	518.8921	1538.67	15.9923	-1.7	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
23203	dirMS_041712_NAR_30mM_plus2.19770.19770.3	3	4.29	0	1.09E+05		(K)GFAFVQ	(K)G F A F V Q/Y V/N E R(N)		157.68	443.8907	1329.659	-0.0011	-0.8	6	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
23204	dirMS_041712_NAR_40mM_plus2.7319.7319.2	2	4.29	0	1.45E+05		(R)SGYFDE	(R)S/G|Y|F D E/R(Y)		103.5	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
23205	dirMS_041712_NAR_40mM_plus2.9402.9402.2	2	4.29	0	8.85E+04		(R)INVYYN	(R)I/N/V/Y Y N E A T G G K(Y)		118.58	664.8342	1328.648	0.013	9.8	6	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
23206	dirMS_041712_NAR_50mM_plus2.11360.11360.3	3	4.29	1	2.98E+05		(R)ETGVDL	(R)E T/G V/D L T K/D N M A/L Q/R(V)		127.18	564.2856	1690.843	-0.0006	-0.4	4.56	73964.5	5.87	HUMAN	P38646	Stress-70 protein, mitochondrial
23207	dirMS_041712_NAR_50mM_plus2.13041.13041.3	3	4.29	1	4.07E+05		(K)DMESPT	(K)D M/E/S/P T K L D V T L A K(D)		136.88	516.6001	1547.799	-0.0128	-8.3	4.56	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
23208	dirMS_041712_NAR_50mM_plus2.13812.13812.3	3	4.29	0	1.46E+06		(K)STTSDIP	(K)S T/T/S D I/P H M/L/N Q V E/S K(V)		140.32	596.2908	1786.864	-0.0061	-3.4	5.3	11532.2	6.34	HUMAN	H0YNA1	Protein FAM98B (Fragment)
23209	dirMS_041712_NAR_50mM_plus2.22318.22318.3	3	4.29	0	5.52E+05		(R)GGHPPA	(R)G G H P P A I Q/S/L\I|N L L A D N R(Y)		191.85	629.3448	1886.024	-0.0044	-2.3	6.74	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
23210	dirMS_041712_NAR_50mM_plus2.9727.9727.3	3	4.29	1	8.03E+04		(K)LKGEAT	(K)L K G E\A/T V S/F D D\P P S A K(A)		117.67	554.6155	1661.838	-0.0061	-3.7	4.56	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
23211	dirMS_041712_NAR_60mM_plus.20036.20036.3	3	4.29	1	5.36E+05		(R)AKFEEL	(R)A K F E E\L/N/M/D/L F R(S)		165.08	504.9258	1512.752	0.0113	7.5	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
23212	dirMS_041712_NAR_120mM_minus.6111.6111.3	3	4.28	1	2.07E+04		(K)NVICDK	(K)N V I/C\D K\C/E/G R(G)	C:Carbamidomethylation	86.4	417.525	1250.562	-0.0012	-0.9	6.07	45609.1	6.66	HUMAN	P31689	DnaJ homolog subfamily A member 1

23213	dirMS_041712_NAR_20mM_minus.14621.14621.3	3	4.28	0	3.68E+05		(K)LAVEAL	(K)L A V E A\L/S S\L/D G D/L/A G R(Y)		201.3	529.6163	1586.838	-0.0041	-2.6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
23214	dirMS_041712_NAR_20mM_minus.8827.8827.2	2	4.28	0	1.60E+04		(K)VAGQD	(K)V A|G Q|D/G S V V Q/F K(I)		137.65	617.823	1234.643	-0.0039	-3.2	5.81	17127.4	10.05	HUMAN	A8MU27	Small ubiquitin-related modifier 3
23215	dirMS_041712_NAR_30mM_minus2.17595.17595.2	2	4.28	0	1.77E+05		(R)NGGQIL	(R)N G/G Q/I/L I/A D L/R(G)		149.52	585.3352	1169.664	-0.0006	-0.5	5.84	34524.7	5.4	HUMAN	A8MV37	Protein SEC13 homolog
23216	dirMS_041712_NAR_30mM_minus2.17711.17711.2	2	4.28	0	7.39E+04		(R)VAFTLLE	(R)V/A/F/T L L E K(V)		150.72	460.7759	920.545	-0.0006	-0.7	5.97	18751.1	6.84	HUMAN	B4DR94	Synaptobrevin homolog YKT6
23217	dirMS_041712_NAR_30mM_minus2.6754.6754.2	2	4.28	0	3.22E+05		(K)SPEYPE	(K)S/P/E|Y P E G R(D)		90.63	467.7219	934.427	0.01	10.7	4.53	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
23218	dirMS_041712_NAR_30mM_minus2.9426.9426.2	2	4.28	1	2.73E+06		(K)RGFLSPE	(K)R G/F L S/P E N K(N)		104.52	524.2789	1047.558	-0.0076	-7.3	8.75	45467.4	5.84	HUMAN	Q9HBI1-2	Isoform 2 of Beta-parvin
23219	dirMS_041712_NAR_40mM_minus2.11745.11745.3	3	4.28	2	4.53E+05		(K)TLPMVP	(K)T L/P M V P F/K T K D S P G V F S K(L)		151.5	660.3663	1979.067	0.0173	8.7	9.7	53857.3	10.03	HUMAN	E7EX35	ATP-binding cassette sub-family G member 5
23220	dirMS_041712_NAR_40mM_minus2.15261.15261.3	3	4.28	0	3.27E+04		(K)ALESPEF	(K)A L/E/S/P E R P/F L A I/L G G A K(V)		175.58	590.3353	1768.996	-0.0042	-2.4	6.19	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
23221	dirMS_041712_NAR_40mM_minus2.15787.15787.3	3	4.28	0	6.82E+05		(K)GLAPDLI	(K)G L\A/P D L/P E D L Y H L I K(K)		184.42	565.3111	1693.916	0.0028	1.7	4.54	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
23222	dirMS_041712_NAR_50mM_minus2.15901.15901.3	3	4.28	0	1.18E+05		(K)SLLSSAS	(K)S L/L/S S/A/S A T V/G H/G L T A V K(E)		158.37	566.9809	1698.939	-0.0103	-6.1	8.49	61083	4.61	HUMAN	Q8IWE2	Protein NOXP20
23223	dirMS_041712_NAR_50mM_minus2.7445.7445.3	3	4.28	0	4.22E+04	M289m	(K)ATVmD	(K)A/T/V/m D/V K P V D/Y R(E)	m:Oxidized methionine	108.9	470.5755	1393.714	15.9975	1.9	6	35399.1	5.17	HUMAN	I3L4R8	Replication protein A 70 kDa DNA-binding subunit (Fragment)
23224	dirMS_041712_NAR_20mM_plus.10768.10768.2	2	4.28	0	2.19E+05	M33m	(K)VAGmD	(K)V/A/G m D V/E L T/V/E E R(N)	m:Oxidized methionine	147.28	732.3555	1447.71	15.994	-0.6	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
23225	dirMS_041712_NAR_20mM_plus.14962.14962.3	3	4.28	0	1.15E+05		(K)VLEQLT	(K)V L E Q/L\T\G Q T|P V F S K(A)		174.57	516.2866	1546.848	-0.0023	-1.5	5.97	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
23226	dirMS_041712_NAR_30mM_plus2.5441.5441.2	2	4.28	0	1.84E+05		(R)TDTGEP	(R)T/D\T/G E/P M/G R(G)		82.82	482.2128	963.42	-0.0017	-1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
23227	dirMS_041712_NAR_30mM_plus2.6847.6847.2	2	4.28	0	2.27E+05		(R)NMGYV	(R)N/M|G/Y V/Q\Q R(R)		90.27	498.2399	995.473	-0.0002	-0.2	8.75	28637.7	6.66	HUMAN	B4DDM6	Mitotic checkpoint protein BUB3
23228	dirMS_041712_NAR_40mM_plus2.10150.10150.2	2	4.28	0	4.39E+04		(K)SKPVFSE	(K)S K\P V F S E\S L|S|D(-)		124.27	598.2943	1195.584	-0.0028	-2.3	4.67	11226.4	5.09	HUMAN	O60220	Mitochondrial import inner membrane translocase subunit Tim8 A
23229	dirMS_041712_NAR_40mM_plus2.5936.5936.2	2	4.28	0	1.13E+05		(R)SPDNP	(R)S/P D N/P M/N\Q R(A)		93.55	529.7368	1058.468	-0.002	-1.9	5.55	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
23230	dirMS_041712_NAR_50mM_plus2.19793.19793.3	3	4.28	1	1.83E+04	K72k	(R)TENSSLT	(R)T E/N S S L T k E/V Q D/L K A K(Q)	k:Ubiquitin-K	172.68	635.6611	1790.949	114.0193	-12.4	5.85	69285	5.2	HUMAN	G3V4Y7	Kinectin
23231	dirMS_041712_NAR_50mM_plus2.7197.7197.3	3	4.28	0	6.94E+03	M233m	(K)SAAmLG	(K)S A/A m L/G/N S E D H\T A L S R(A)	m:Oxidized methionine	103.72	559.2654	1659.776	16.0061	6.7	5.3	46211	6.76	HUMAN	B4DEK4	Sorting nexin-2
23232	dirMS_041712_NAR_60mM_plus.12419.12419.3	3	4.28	1	6.50E+05		(K)YGQISE	(K)Y/G\Q/I/S E/V V V V K D R(E)		121.42	497.9427	1491.817	-0.003	-2	6.07	28815.3	9.52	HUMAN	B4E2X2	Cold-inducible RNA-binding protein
23233	dirMS_041712_NAR_60mM_plus.13977.13977.3	3	4.28	0	1.49E+05		(K)LAQANG	(K)L A Q/A N G W G/V/M V/S H R(S)		130.15	509.2606	1525.769	-0.002	-1.3	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
23234	dirMS_041712_NAR_60mM_plus.15396.15396.3	3	4.28	0	6.30E+05	T2t	(-)MtAEEG	(-)M t A E E G\V/Q/L S Q/Q N A K(D)	t:N-acetylglucosamine (T)	137.77	612.9511	1633.785	203.0537	-14	4.53	4276.9	9.4	HUMAN	J3KS03	Nuclear prelamin A recognition factor (Fragment)
23235	dirMS_041712_NAR_60mM_plus.9230.9230.3	3	4.28	1	2.99E+05		(R)FVKQDC	(R)F V/K Q D|Q|V/C I A R(L)	C:Carbamidomethylation	106	455.2428	1363.715	-0.0012	-0.9	8.75	53458.1	5.47	HUMAN	H3BR35	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A (Fragment)
23236	dirMS_041712_NAR_20mM_minus.7547.7547.3	3	4.27	0	8.83E+05	M239m	(K)EVDEQ	(K)E V D E Q|m/L/N V Q N K(N)	m:Oxidized methionine	123.95	488.2327	1446.689	15.9942	-0.5	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
23237	dirMS_041712_NAR_20mM_minus.8888.8888.2	2	4.27	0	5.53E+04		(K)AIADTG	(K)A I|A/D T/G A N V V/V T G G K(V)		137.98	686.8733	1372.743	-0.0037	-2.7	5.88	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
23238	dirMS_041712_NAR_30mM_minus2.19266.19266.2	2	4.27	1	2.26E+04		(K)IATIGSD	(K)I/A|T I G/S D R/K(V)		160.23	480.7751	960.547	-0.0043	-4.5	8.75	56155.2	8.78	HUMAN	B4DWR9	Peptidylprolyl isomerase domain and WD repeat-containing protein 1
23239	dirMS_041712_NAR_30mM_minus2.5352.5352.2	2	4.27	0	7.86E+04		(R)LYQAGE	(R)L/Y/Q A G E/G R(L)		83.83	447.2217	893.448	-0.0114	-12.8	6	38089.6	6.79	HUMAN	B4DT77	Annexin
23240	dirMS_041712_NAR_40mM_minus2.13172.13172.2	2	4.27	0	9.44E+04		(K)SYELPD	(K)S Y\E L/P D\G Q V/I/T I/G N E R(F)		161.48	895.9483	1790.892	-0.0026	-1.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
23241	dirMS_041712_NAR_40mM_minus2.14763.14763.3	3	4.27	0	1.10E+05	M159m	(R)SVAAIH	(R)S V|A A I/H P S L E I/P m L I P K(E)	m:Oxidized methionine	171.37	611.3477	1816.04	15.9884	-3.5	6.47	31606.3	6.72	HUMAN	B4E329	Phosphoribosyl pyrophosphate synthase-associated protein 2
23242	dirMS_041712_NAR_40mM_minus2.9638.9638.2	2	4.27	1	1.41E+06	S921s	(R)GIsLLPD	(R)G I/s L L P D/K A D/L S T V G H K(K)	s:N-acetylglucosamine (S)	139.92	977.5343	1750.97	203.0915	6.2	6.75	196685.9	9.01	HUMAN	G3XAE9	KIAA0423, isoform CRA_a
23243	dirMS_041712_NAR_50mM_minus2.17158.17158.3	3	4.27	0	1.66E+05	M195m	(R)LHFFmP	(R)L H F F m\P G\F/A/P L T S R(G)	m:Oxidized methionine	165.48	546.2872	1620.835	16.0115	10.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
23244	dirMS_041712_NAR_60mM_minus.14606.14606.3	3	4.27	0	4.00E+05		(K)AVGHPF	(K)A V/G H P F\V|I|Q L G R(I)		141.87	431.9182	1293.743	-0.0026	-2	9.8	124524.8	5.71	HUMAN	O14980	Exportin-1
23245	dirMS_041712_NAR_60mM_minus.14991.14991.3	3	4.27	1	5.42E+04		(R)VAGGP	(R)V/A|G/G/P Q M I Q\L S L/D G K/R(L)		143.72	557.3065	1669.905	-0.0005	-0.3	8.72	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
23246	dirMS_041712_NAR_60mM_minus.17395.17395.3	3	4.27	0	1.10E+04	M251m M	(R)AHmGm	(R)A H m G m F T/E/L A|I L/Y S K(F)	m:Oxidized methionine	157.03	581.9563	1711.855	31.9997	5.7	6.79	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
23247	dirMS_041712_NAR_60mM_minus.9205.9205.3	3	4.27	0	2.35E+04		(K)QDYNQ	(K)Q D/Y N Q E/V D/A S I F K(A)		110.83	519.5852	1556.723	0.0183	11.8	4.03	18748.9	5.02	HUMAN	H3BQH6	Interferon regulatory factor 8 (Fragment)
23248	dirMS_041712_NAR_120mM_plus.5419.5419.3	3	4.27	0	3.85E+04		(R)TGIYSST	(R)T G/I/Y/S S T S C H K(T)	C:Carbamidomethylation	81.43	414.1962	1240.563	0.0114	9.2	8.28	38077.6	8.9	HUMAN	P09668	Pro-cathepsin H
23249	dirMS_041712_NAR_20mM_plus.14991.14991.2	2	4.27	0	8.31E+04		(K)VVNIVP	(K)V V|N\I/V P V I A/K(A)		174.67	526.3453	1051.687	-0.0041	-3.9	8.72	22387.6	9.64	HUMAN	K7EK18	Septin-9 (Fragment)
23250	dirMS_041712_NAR_20mM_plus.16049.16049.2	2	4.27	0	1.05E+05		(K)SILFVPT	(K)S I\L|F\V|P/T S A/P R(G)		181.45	594.3403	1187.678	-0.005	-4.2	9.47	92752.5	4.76	HUMAN	P14625	Endoplasmin
23251	dirMS_041712_NAR_20mM_plus.17716.17716.2	2	4.27	1	7.23E+04		(-)MGKGIP	(-)M G K G I|P L N D Q/D R(I)		194.03	672.3393	1343.674	-0.0023	-1.7	5.71	10060.5	8.08	HUMAN	E9PP74	Probable gluconokinase (Fragment)
23252	dirMS_041712_NAR_20mM_plus.6445.6445.2	2	4.27	0	2.02E+05	M216m	(R)DLmAC	(R)D L\m|A C A/Q/T G S G K(T)	C:Carbamidomethylation m:Oxid	107.72	627.776	1238.55	15.9943	-0.5	5.84	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
23253	dirMS_041712_NAR_20mM_plus.7793.7793.2	2	4.27	0	6.78E+04		(R)AQYDEL	(R)A Q|Y/D E/L A R(K)		123.52	483.2393	965.469	0.0026	2.7	4.37	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
23254	dirMS_041712_NAR_20mM_plus.9701.9737.2	2	4.27	0	1.93E+05		(K)IVVVTA	(K)I V|V|V T A G V R(Q)		139.03	457.2945	913.583	-0.0012	-1.3	9.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
23255	dirMS_041712_NAR_40mM_plus2.20108.20108.3	3	4.27	1	5.33E+05		(K)EGGLGP	(K)E G G L/G/P/L N I/P L L A D V T R R(L)		189.9	631.0288	1891.076	-0.0041	-2.2	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
23256	dirMS_041712_NAR_40mM_plus2.7621.7621.2	2	4.27	0	1.66E+05	T270t	(K)SGYtSR	(K)S G/Y t/S R(N)	t:N-acetylglucosamine (T)	104.47	437.1906	670.316	203.0584	-24	8.46	43752.5	9.34	HUMAN	B7WP89	Uncharacterized protein C4orf29
23257	dirMS_041712_NAR_40mM_plus2.9316.9316.2	2	4.27	1	2.47E+04		(K)IEKEWR	(K)I/E/K|E W R(Q)		117.67	430.7364	860.462	0.003	3.5	6.14	72177.3	5.72	HUMAN	H0YD93	RUN and FYVE domain-containing protein 2 (Fragment)
23258	dirMS_041712_NAR_50mM_plus2.6631.6631.3	3	4.27	0	1.97E+05	M8m	(-)MINTGT	(-)M I/N/T G T Q m D L E\V K(G)	m:Oxidized methionine	98.92	499.2426	1479.718	15.9951	0.1	4.37	54830.3	9.24	HUMAN	B9A061	Calcyphosin-2
23259	dirMS_041712_NAR_60mM_plus.15148.15148.3	3	4.27	0	8.87E+04	M120m	(R)IHDGEA	(R)I H D G E/A D I m I N F/G/R(W)	m:Oxidized methionine	134.4	535.2618	1587.758	16.0124	10.9	4.54	69799.9	5.14	HUMAN	E9PE45	PEX
23260	dirMS_041712_NAR_60mM_plus.21476.21476.3	3	4.27	0	1.02E+05		(R)LHFFMP	(R)L H F F M P G\F/A/P\L/T S R(G)		178.52	540.9492	1620.835	-0.0025	-1.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
23261	dirMS_041712_NAR_120mM_minus.10756.10897.3	3	4.26	1	3.57E+05		(R)LKYENE	(R)L K Y E N E/V/A L/R(Q)		113.43	412.2282	1234.679	-0.009	-7.3	6.14	59054.3	5.14	HUMAN	P13645	Keratin, type I cytoskeletal 10
23262	dirMS_041712_NAR_120mM_minus.15701.15701.4	4	4.26	2	3.36E+05	S510s	(R)LPRGKD	(R)L P R G K D/L I Y/F G s E\K(S)	s:N-acetylglucosamine (S)	141.02	457.2525	1622.89	203.0981	10.3	8.5	70463.1	5.36	HUMAN	H0Y9Y0	F-box/LRR-repeat protein 5 (Fragment)
23263	dirMS_041712_NAR_120mM_minus.4980.4980.3	3	4.26	1	2.92E+05		(K)AGADEE	(K)A/G\A\D/E E R A/E T A R(L)		78.62	425.8687	1275.592	-0.0008	-0.7	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
23264	dirMS_041712_NAR_20mM_minus.13629.13629.3	3	4.26	0	2.14E+05		(R)QAQEYE	(R)Q A Q\E Y E/A L/L/N I K(V)		187.02	473.9203	1419.748	-0.0015	-1	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
23265	dirMS_041712_NAR_20mM_minus.14543.14543.2	2	4.26	2	7.32E+04	S142s	(K)GKVKAL	(K)G K V K/A|L|I A E E T s S R(L)	s:Phosphorylated S	199.67	784.9166	1488.838	79.9879	13.7	8.59	133849.8	5.28	HUMAN	J3KQ40	TBC1 domain family member 8
23266	dirMS_041712_NAR_30mM_minus2.12098.12098.3	3	4.26	0	4.86E+05		(R)VASALS	(R)V/A S\A L S S\G S/E S S D R(S)		118.83	451.547	1352.629	-0.0024	-1.8	4.37	215614.3	9.97	HUMAN	B5MDS5	Adenomatous polyposis coli protein 2
23267	dirMS_041712_NAR_30mM_minus2.13076.13076.2	2	4.26	0	2.33E+05		(R)FTVAEL	(R)F/T/V/A E L K(Q)		124.95	404.2383	807.461	0.0082	10.2	6	98282.7	5.49	HUMAN	E9PPJ0	Splicing factor 3B subunit 2
23268	dirMS_041712_NAR_30mM_minus2.6467.6467.2	2	4.26	0	2.98E+05		(K)SPEYPE	(K)S/P|E/Y\P E G R(D)		90.05	467.7219	934.427	0.01	10.7	4.53	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
23269	dirMS_041712_NAR_40mM_minus2.9158.9158.2	2	4.26	0	6.99E+04		(K)WSLLQC	(K)W/S|L/L Q Q Q K(T)		136.32	515.7871	1030.568	-0.0011	-1.1	8.75	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
23270	dirMS_041712_NAR_60mM_minus.15539.15539.3	3	4.26	0	1.87E+05		(K)LKPQYL	(K)L K P Q Y L E|E\L|P G Q L K(Q)		146.37	552.6501	1655.937	-0.0009	-0.6	6.14	27015.5	5.37	HUMAN	P21266	Glutathione S-transferase Mu 3
23271	dirMS_041712_NAR_60mM_minus.8143.8143.3	3	4.26	1	1.31E+05	S133s	(R)AGDLLE	(R)A/G/D|L/L/E/D/s P K R\P K(E)	s:Phosphorylated S	105.57	502.5858	1425.77	79.9732	4.6	6.17	23020.5	4.53	HUMAN	A8K8G0	Hepatoma-derived growth factor
23272	dirMS_041712_NAR_120mM_plus.13141.13141.3	3	4.26	0	2.23E+04		(K)SHTFPE	(K)S H\T\F P/E/L/A Y R(K)		123.13	407.5358	1220.606	-0.013	-10.7	6.47	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
23273	dirMS_041712_NAR_30mM_plus2.16050.16050.2	2	4.26	0	4.26E+05		(K)GVLFYG	(K)G V\L|F Y/G/P P G/C G K(T)	C:Carbamidomethylation	137.25	626.3175	1251.619	0.0087	6.9	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
23274	dirMS_041712_NAR_30mM_plus2.6719.6719.2	2	4.26	0	2.58E+05	M529m	(R)MGLSm	(R)M/G L/S m/E R(M)	m:Oxidized methionine	89.77	420.1949	823.38	16.0025	9	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
23275	dirMS_041712_NAR_60mM_plus.12675.12675.3	3	4.26	0	5.66E+05		(K)GSYSLS	(K)G S/Y/S L/S H V Y/T/P N D V R(M)		123.05	565.6098	1694.813	0.0016	0.9	6.74	63566.6	6.3	HUMAN	P07686	Beta-hexosaminidase subunit beta
23276	dirMS_041712_NAR_60mM_plus.8933.8933.3	3	4.26	1	5.09E+05		(K)ELKSPD	(K)E L/K S P/D E G/F E/G/K(S)		104.78	445.8862	1335.643	0.0014	1	4.41	84557.3	6.5	HUMAN	Q04609	Glutamate carboxypeptidase 2
23277	dirMS_041712_NAR_60mM_plus.8936.8936.3	3	4.26	1	4.04E+05		(K)MQASIE	(K)M Q|A/S I E K G G S L/P K(V)		104.02	449.2449	1345.714	0.0057	4.3	8.35	32745.6	4.64	HUMAN	P06748	Nucleophosmin
23278	dirMS_041712_NAR_120mM_minus.15181.15181.4	4	4.25	1	1.02E+05	M89m K95	(K)KVTVRP	(K)K\V T V R\P G/E S V\m\V N I S\A k(A)	m:Oxidized methionine k:Ub	136.97	487.0126	1815.016	130.0129	-12.8	9.99	596825.2	5.14	HUMAN	Q9Y6R7	IgGFc-binding protein
23279	dirMS_041712_NAR_120mM_minus.9734.9734.3	3	4.25	1	3.01E+04		(R)SGGGEC	(R)S G G/G E C E/V R/Q D P R(S)	C:Carbamidomethylation	107.62	482.8881	1446.639	0.0107	7.4	4.68	22469.1	6.17	HUMAN	H7C4Y3	Poly [ADP-ribose] polymerase 14 (Fragment)
23280	dirMS_041712_NAR_20mM_minus.10970.10970.2	2	4.25	0	7.01E+04		(R)LAVEAL	(R)L A|V/E/A L V R(T)		157.07	435.7738	870.541	-0.0004	-0.5	6	65558.6	9.87	HUMAN	G3V1S7	Hyaluronan synthase 1
23281	dirMS_041712_NAR_20mM_minus.12462.12462.3	3	4.25	0	2.79E+05	M256m	(R)SLDmDS	(R)S L D m D S|I/I A E/V K(A)	m:Oxidized methionine	172.3	446.227	1320.671	15.9949	0	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
23282	dirMS_041712_NAR_40mM_minus2.8696.8696.3	3	4.25	2	2.27E+05	S209s	(R)RGKAPT	(R)R G/K A P T/D C A s G P A A A/G I K(K)	C:Carbamidomethylation s:N-ace	132.72	644.3329	1727.886	203.0984	9.9	9.99	60517.3	10.29	HUMAN	Q96T92	Insulinoma-associated protein 2
23283	dirMS_041712_NAR_50mM_minus2.13208.13208.3	3	4.25	1	6.04E+04		(R)IVLLDSS	(R)I V/L/L/D S S|L E Y K K(G)		143.35	469.9471	1407.809	0.0174	12.4	6.07	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
23284	dirMS_041712_NAR_50mM_minus2.17705.17705.3	3	4.25	1	2.19E+05		(R)GPLLWP	(R)G P L L W/P\E R G/P\P A\P R(H)		170.25	514.953	1542.854	-0.0095	-6.2	9.6	50503.8	6.31	HUMAN	B4DNN9	Zinc finger protein 500
23285	dirMS_041712_NAR_50mM_minus2.5793.5793.3	3	4.25	1	1.12E+05		(K)IQDKEGI	(K)I Q D K/E G I/P P D/Q Q/R(L)		95.13	508.597	1523.781	-0.0048	-3.1	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
23286	dirMS_041712_NAR_50mM_minus2.9755.9755.3	3	4.25	0	7.53E+04		(R)ELTLEKP	(R)E\L T/L/E K P E/L K(A)		123.75	400.5678	1199.688	0.0007	0.6	4.79	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
23287	dirMS_041712_NAR_60mM_minus.12793.12793.3	3	4.25	1	1.62E+05		(K)TIKVLLE	(K)T I K V L L E Y/A\D K(M)		131.18	431.5887	1292.746	0.0055	4.3	5.73	223636.2	5.43	HUMAN	E7ET19	Sodium channel protein type 5 subunit alpha
23288	dirMS_041712_NAR_60mM_minus.7521.7521.3	3	4.25	1	5.70E+04		(K)TEADAE	(K)T/E/A D A E K T F E/E K(Q)		101.08	466.5515	1397.643	-0.0031	-2.2	4.25	32503.1	5.29	HUMAN	H7BY16	Nucleolin (Fragment)
23289	dirMS_041712_NAR_60mM_minus.8268.8268.3	3	4.25	1	1.02E+05		(R)AAERNP	(R)A A E R\N/P A\L/A/G S A I R(C)		106.15	466.2587	1396.766	-0.004	-2.9	9.64	183049.2	5.32	HUMAN	Q9GZU2	Paternally-expressed gene 3 protein
23290	dirMS_041712_NAR_120mM_plus.7079.7079.3	3	4.25	0	1.73E+06	S985s	(K)TNYIsIC	(K)T/N/Y/I s I C K(M)	C:Carbamidomethylation s:N-ace	91.05	401.1974	998.497	203.0801	0.6	8.26	174809.4	9.08	HUMAN	Q5THR3	EF-hand calcium-binding domain-containing protein 6
23291	dirMS_041712_NAR_120mM_plus.8574.8574.3	3	4.25	1	2.67E+05		(R)RTEEGP	(R)R T E E G|P T\L/S/Y/G R(D)		97.93	455.8929	1365.676	-0.0116	-8.5	6.14	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
23292	dirMS_041712_NAR_20mM_plus.10725.10725.2	2	4.25	0	4.34E+04		(K)NVTELN	(K)N V/T\E L|N/E P L S N E E R(N)		146.47	822.3937	1643.787	-0.007	-4.3	4.09	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
23293	dirMS_041712_NAR_20mM_plus.13280.13280.2	2	4.25	0	1.15E+05		(R)YPVNSV	(R)Y/P/V\N\S V N/I/L K(A)		164.03	573.8278	1146.652	-0.0034	-3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
23294	dirMS_041712_NAR_20mM_plus.13785.13785.2	2	4.25	0	2.57E+05		(R)GDLGIEI	(R)G D L|G I|E I/P/A E K(V)		166.83	571.3075	1141.61	-0.0022	-1.9	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
23295	dirMS_041712_NAR_20mM_plus.6896.6896.2	2	4.25	0	9.09E+04		(R)VTDALN	(R)V T/D/A/L/N A T R(A)		113.88	480.7584	960.511	-0.0014	-1.4	5.81	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
23296	dirMS_041712_NAR_20mM_plus.7949.7949.2	2	4.25	0	5.64E+04		(K)SVTEQG	(K)S V\T E Q/G/A E/L S N\E E R(N)		124.88	774.8589	1548.714	-0.0031	-2	4.09	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
23297	dirMS_041712_NAR_20mM_plus.8268.8268.2	2	4.25	0	9.35E+04		(R)LATNTS	(R)L/A T N T/S A/P D L K(N)		127.33	565.806	1130.605	-0.0005	-0.4	5.84	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
23298	dirMS_041712_NAR_30mM_plus2.14460.14460.3	3	4.25	0	1.03E+04		(K)VNQIGS	(K)V N\Q\I G S V|T E S I/Q A C/K(L)	C:Carbamidomethylation	127.72	545.28	1633.821	0.0041	2.5	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
23299	dirMS_041712_NAR_40mM_plus2.18468.18468.3	3	4.25	1	8.70E+04		(R)VLEALLP	(R)V/L/E A L L/P L K G L E E R(V)		174.3	527.3177	1579.942	-0.0032	-2	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
23300	dirMS_041712_NAR_60mM_plus.10160.10160.3	3	4.25	0	6.66E+05		(K)TPVEPE	(K)T P V E\P/E/V/A I H/R(I)		111.47	416.5628	1247.674	-0.0004	-0.3	5.37	5429.1	9.6	HUMAN	E5RIP1	40S ribosomal protein S20
23301	dirMS_041712_NAR_60mM_plus.13777.13777.3	3	4.25	1	4.71E+05		(R)KYEMFA	(R)K\Y E M F\A Q/T/L/Q/Q S R(G)		128.72	543.9389	1629.805	-0.0032	-2	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
23302	dirMS_041712_NAR_60mM_plus.19954.19954.3	3	4.25	1	5.02E+05		(R)GFKDQI	(R)G F K\D Q|I/Y/D I/F Q K(L)		164.73	501.2609	1501.769	-0.0004	-0.3	5.96	26945.8	8.07	HUMAN	J3KSZ0	Eukaryotic initiation factor 4A-I (Fragment)
23303	dirMS_041712_NAR_60mM_plus.5730.5730.3	3	4.25	0	7.68E+04		(R)TAEHEA	(R)T A E H E A|A\Q/Q D/L Q S K(F)		87.8	519.2487	1555.735	-0.0031	-2	4.65	156557.7	5.52	HUMAN	Q86UP2	Kinectin
23304	dirMS_041712_NAR_60mM_plus.6070.6070.3	3	4.25	0	9.69E+04	N88n M94	(K)DnPTSC	(K)D n/P T S C F m/E/K(V)	C:Carbamidomethylation n:N-ac	90.17	483.1867	1228.497	219.0483	-18	4.37	11586	5.58	HUMAN	F8WC39	Glycerol kinase
23305	dirMS_041712_NAR_60mM_plus.8525.8525.3	3	4.25	1	2.30E+05	T123t	(R)LSRtSW	(R)L/S|R t\S/W/A Q L(-)	t:N-acetylglucosamine (T)	103.22	422.2223	1061.574	203.0785	-0.7	9.75	15082.2	5.65	HUMAN	B7Z6A4	Surfeit 4, isoform CRA_c
23306	dirMS_041712_NAR_120mM_minus.16111.16111.3	3	4.24	1	5.23E+04		(R)EPSKSL	(R)E P S K S L G I S/I V G G R(G)		141.05	467.2647	1399.79	-0.0108	-7.7	8.85	99157	5.28	HUMAN	B7ZB24	Multiple PDZ domain protein
23307	dirMS_041712_NAR_120mM_minus.7501.7501.3	3	4.24	1	8.01E+04	M462m	(R)KAYGGA	(R)K A Y G G\A\Y/D/V/m S/S K(H)	m:Oxidized methionine	95.07	464.8871	1376.651	15.9953	0.3	8.43	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
23308	dirMS_041712_NAR_120mM_minus.9295.9295.3	3	4.24	1	1.29E+05		(R)RADLNC	(R)R A D\L N Q G\I/G E|P Q S P S R(R)		105.1	575.6264	1724.867	-0.0028	-1.6	6.07	26810.9	5.15	HUMAN	Q96C19	EF-hand domain-containing protein D2
23309	dirMS_041712_NAR_20mM_minus.12327.12327.2	2	4.24	0	7.10E+05	M185m	(K)LAVNm	(K)L A|V/N m V|P F/P R(L)	m:Oxidized methionine	171.87	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
23310	dirMS_041712_NAR_20mM_minus.8084.8084.2	2	4.24	0	1.02E+05		(R)ATTGYP	(R)A T T/G Y|P D P Y G G E K(L)		130.38	678.3078	1355.611	-0.0031	-2.3	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
23311	dirMS_041712_NAR_20mM_minus.9973.9973.3	3	4.24	0	6.58E+04	M526m	(R)AmLAQ	(R)A m\L\A Q Q Y Q/E\G T L S V E K(L)	m:Oxidized methionine	149.72	604.632	1795.89	15.992	-1.6	4.53	266161	5.68	HUMAN	E9PPU0	Epiplakin
23312	dirMS_041712_NAR_30mM_minus2.13141.13204.2	2	4.24	0	2.52E+05		(R)FTVAEL	(R)F/T|V/A E L K(Q)		125.05	404.2383	807.461	0.0082	10.2	6	98282.7	5.49	HUMAN	E9PPJ0	Splicing factor 3B subunit 2
23313	dirMS_041712_NAR_30mM_minus2.14167.14167.2	2	4.24	0	3.70E+05		(R)TLGLGE	(R)T L|G L G/E E/W R(-)		130.48	530.7694	1060.542	-0.0107	-10.1	4.53	8429.6	8.25	HUMAN	C9JIX5	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 (Fragment)
23314	dirMS_041712_NAR_30mM_minus2.19082.19082.2	2	4.24	0	2.25E+05	K1325k	(K)SGMLQ	(K)S G|M L|Q/A E|k K(L)	k:Ubiquitin-K	158.95	553.2953	991.524	114.0592	14.7	8.31	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
23315	dirMS_041712_NAR_30mM_minus2.5816.5816.2	2	4.24	1	5.58E+05		(K)AYNEKG	(K)A Y/N E K/G/K(S)		86.38	405.2098	809.415	-0.0029	-3.5	8.54	4024332	6.06	HUMAN	K7ENY1	Titin
23316	dirMS_041712_NAR_50mM_minus2.13735.13735.3	3	4.24	2	1.01E+04	M130m	(K)QSRNLA	(K)Q S/R N L A E E L G K A V E I/m/G K(G)	m:Oxidized methionine	146.87	663.6836	1973.048	15.9878	-3.6	6.23	19331.2	7.03	HUMAN	I3L1W7	Protein disulfide-isomerase-like protein of the testis (Fragment)
23317	dirMS_041712_NAR_50mM_minus2.15999.15999.3	3	4.24	1	5.02E+05	S956s	(R)TVDSTPI	(R)T V D S T P L s V\H T P\T L R K(K)	s:Phosphorylated S	158.15	611.3086	1751.965	79.9462	-11	8.44	195742.6	6.27	HUMAN	F5H5N0	Serine/threonine-protein kinase MRCK alpha
23318	dirMS_041712_NAR_50mM_minus2.17583.17583.3	3	4.24	0	6.42E+05	M195m	(R)LHFFmP	(R)L H F F m P G/F A|P/L T S R(G)	m:Oxidized methionine	167.52	546.2872	1620.835	16.0115	10.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
23319	dirMS_041712_NAR_50mM_minus2.8909.8909.3	3	4.24	1	7.72E+04		(R)SATKVT	(R)S A/T\K V T A D|V/I N/A A/E K(L)		118.25	506.6094	1517.817	-0.0033	-2.2	5.79	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
23320	dirMS_041712_NAR_60mM_minus.11535.11535.3	3	4.24	1	2.79E+04	M1288m S	(K)VEEAmF	(K)V E E/A m F T/s L R R(L)	m:Oxidized methionine s:N-a	125.13	519.9211	1338.683	219.0653	-5.8	6.11	479967.7	5.72	HUMAN	Q9C0G6	Dynein heavy chain 6, axonemal
23321	dirMS_041712_NAR_60mM_minus.18287.18287.3	3	4.24	1	1.13E+05	M445m	(K)LVDPQE	(K)L V D/P Q\E m L/R L L G H(-)	m:Oxidized methionine	162.92	512.9419	1520.825	15.9858	-5.9	5.32	49823.3	9.39	HUMAN	B4DQQ4	NADPH:adrenodoxin oxidoreductase, mitochondrial

23322	dirMS_041712_NAR_60mM_minus.20176.20176.3	3	4.24	1	4.92E+05		(R)KEGGLG	(R)K E G G L G P L N/I|P L/L A D V T R(R)		186.08	621.6933	1863.07	-0.0045	-2.4	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
23323	dirMS_041712_NAR_60mM_minus.7907.7907.3	3	4.24	0	4.20E+04	T374t	(R)TAAtLAT	(R)T/A|A t L/A/T H E L R(A)	t:N-acetylglucosamine (T)	103.87	462.9072	1183.643	203.0641	-11	6.41	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
23324	dirMS_041712_NAR_60mM_minus.8121.8121.3	3	4.24	0	1.91E+05		(R)QYDISDI	(R)Q Y/D/I S D/P Q R/P R(L)		105.63	458.8971	1374.676	0.0007	0.5	5.96	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
23325	dirMS_041712_NAR_120mM_plus.11676.11676.4	4	4.24	2	3.85E+05		(R)YESLTDF	(R)Y E|S L/T D/P S K/L D S G K E L K(I)		114.12	478.2542	1909.975	0.0197	10.3	4.78	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
23326	dirMS_041712_NAR_120mM_plus.12305.12305.4	4	4.24	1	2.45E+06	S193s	(R)SsFLSGV	(R)S s F L\S/G V G L G P/M A K/N/K(A)	s:N-acetylglucosamine (S)	117.45	449.7412	1592.847	203.0965	9.5	10	39781	9.8	HUMAN	Q5SQS8	Uncharacterized protein C10orf120
23327	dirMS_041712_NAR_120mM_plus.9621.9621.4	4	4.24	1	3.67E+05	M581m	(K)KmYFIQI	(K)K\m Y F I Q H\G/V/V S V L T/K(G)	m:Oxidized methionine	104.02	442.2427	1749.972	15.9769	-10.2	9.7	97747.5	9.56	HUMAN	Q9UL51	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 2
23328	dirMS_041712_NAR_20mM_plus.15122.15122.2	2	4.24	0	5.77E+04		(K)DLGTES(	(K)D L G T|E/S Q/I/F I S R(T)		175.72	683.3505	1365.701	-0.0071	-5.2	4.37	51636.5	8.68	HUMAN	E7EU23	Rab GDP dissociation inhibitor beta
23329	dirMS_041712_NAR_20mM_plus.18531.18531.2	2	4.24	0	7.89E+04		(R)VVVLGLI	(R)V V|V/L G/L L P R(G)		198.95	483.3247	965.651	-0.0085	-8.8	9.72	25847.9	6.33	HUMAN	Q15102	Platelet-activating factor acetylhydrolase IB subunit gamma
23330	dirMS_041712_NAR_20mM_plus.8808.8808.2	2	4.24	0	3.05E+03		(R)DVAYQY	(R)D V/A|Y Q Y V K(K)		131.12	493.2543	985.499	0.0024	2.4	5.83	14130.9	9.56	HUMAN	C9K0U8	Single-stranded DNA-binding protein (Fragment)
23331	dirMS_041712_NAR_30mM_plus2.18438.18438.2	2	4.24	0	2.36E+05		(K)GNFNYII	(K)G N\F|N Y/I/E F\T/R(I)		150.27	630.8035	1260.601	-0.001	-0.8	6	20513.6	4.62	HUMAN	J3QRS3	Myosin regulatory light chain 12A
23332	dirMS_041712_NAR_40mM_plus2.15321.15321.3	3	4.24	1	2.11E+04		(R)TIAQDY(	(R)T I/A Q/D Y G|V L K/A D E G I S F R(G)		155.8	661.6783	1983.018	0.0022	1.1	4.56	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
23333	dirMS_041712_NAR_40mM_plus2.18807.18807.3	3	4.24	0	3.95E+05		(K)ALIEVLQ	(K)A L I E V/L Q/P L I A E H Q A R(R)		176.2	601.0146	1801.033	-0.0038	-2.1	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
23334	dirMS_041712_NAR_50mM_plus2.6943.6943.3	3	4.24	1	1.65E+05		(R)EGVLTG:	(R)E G V/L/T/G S P/E Q K E E A A K(A)		100.93	558.2837	1672.839	-0.0023	-1.4	4.49	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
23335	dirMS_041712_NAR_60mM_plus.10570.10570.3	3	4.24	1	6.84E+05		(R)LKAEAEI	(R)L K A\E A E L/L|Q/Q Q K(E)		112.97	466.9362	1398.795	-0.0011	-0.8	6.14	533778	5.74	HUMAN	Q15149	Plectin
23336	dirMS_041712_NAR_60mM_plus.17431.17431.3	3	4.24	1	3.74E+05		(R)KVPGVT	(R)K\V P G V\T A\I E/L/D E/D T G T F R(I)		148.18	650.0017	1948.002	-0.0117	-6	4.32	68668.3	5.77	HUMAN	B4DXZ6	Fragile X mental retardation syndrome-related protein 1
23337	dirMS_041712_NAR_60mM_plus.19975.19975.3	3	4.24	1	5.02E+05		(R)GFKDQI'	(R)G F/K D\Q I\Y D/I F Q/K(L)		164.73	501.2609	1501.769	-0.0004	-0.3	5.96	26945.8	8.07	HUMAN	J3KSZ0	Eukaryotic initiation factor 4A-I (Fragment)
23338	dirMS_041712_NAR_120mM_minus.10139.10139.4	4	4.23	1	2.50E+05	T102t T105	(R)LSFPSIKI	(R)L S\F P S I/K P/D t D/Q t L K K(E)	t:Phosphorylated T	109.3	495.2441	1818.001	159.9538	10.7	8.5	24054.6	6.98	HUMAN	B4DT58	Zinc finger protein ubi-d4
23339	dirMS_041712_NAR_120mM_minus.12364.12364.2	2	4.23	0	2.31E+05		(K)HLSVND	(K)H L/S/V N D|L P V G R(S)		121.13	603.8309	1206.659	-0.0044	-3.7	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
23340	dirMS_041712_NAR_120mM_minus.18253.18253.4	4	4.23	1	4.84E+05		(K)EMVELP	(K)E M V/E L/P L/R H P A L F K(A)		154.6	420.737	1679.93	-0.004	-2.4	6.86	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
23341	dirMS_041712_NAR_120mM_minus.5924.5924.3	3	4.23	2	3.11E+05	N151n	(K)InAERSR	(K)I n A E/R S/R G E G\P(-)	n:N-acetylglucosamine (N)	85.25	463.5589	1185.597	203.0651	-10.3	6.14	17724.2	5.2	HUMAN	E5RI90	Uncharacterized protein C1orf198 (Fragment)
23342	dirMS_041712_NAR_120mM_minus.6056.6056.3	3	4.23	0	2.07E+04	T427t	(R)NVtVNE	(R)N V/t V N E S|E R(E)	t:N-acetylglucosamine (T)	86.4	417.525	1047.507	203.0539	-20.4	4.53	67078.7	4.91	HUMAN	F5GYC0	Myelin-associated glycoprotein
23343	dirMS_041712_NAR_20mM_minus.11557.11557.2	2	4.23	0	8.48E+04		(R)ATLYVT/	(R)A T\L/Y/V/T A/I E D R(Q)		163.22	626.3282	1251.658	-0.0088	-7	4.37	24376.8	6.08	HUMAN	E9PIX6	Protein arginine N-methyltransferase 1 (Fragment)
23344	dirMS_041712_NAR_20mM_minus.7541.7541.3	3	4.23	0	8.44E+05	M239m	(K)EVDEQm	(K)E V D E Q m L/N V/Q N K(N)	m:Oxidized methionine	123.83	488.2327	1446.689	15.9942	-0.5	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
23345	dirMS_041712_NAR_30mM_minus2.14019.14019.2	2	4.23	0	2.85E+05		(K)CDFPIM	(K)C D|F P I/M/K(F)	C:Carbamidomethylation	129.62	455.7144	910.416	0.0054	5.9	5.84	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
23346	dirMS_041712_NAR_60mM_minus.10630.10630.3	3	4.23	0	9.21E+03		(K)FNGSHV	(K)F/N G/S H/V V/G S/P F K(V)		119.33	425.8906	1275.648	0.0092	7.2	8.76	258215.9	5.48	HUMAN	E7EN95	Filamin-B
23347	dirMS_041712_NAR_60mM_minus.13411.13411.3	3	4.23	0	3.40E+05	M4092m K	(K)LNHQGE	(K)L N/H/Q G E L m L k K(A)	m:Oxidized methionine k:Ub	134.98	480.9305	1310.725	130.052	9.8	8.6	609547	5.28	HUMAN	F5GZL7	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5
23348	dirMS_041712_NAR_60mM_minus.14033.14033.3	3	4.23	1	1.64E+05	M101m	(R)VIKDFm	(R)V I\K D F m\I/Q G G D F T R(G)	m:Oxidized methionine	138.1	548.2737	1626.831	15.9757	-11.7	5.93	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
23349	dirMS_041712_NAR_60mM_minus.16715.16715.3	3	4.23	1	3.82E+04		(K)KYDAFL/	(K)K Y D A/F\L/A/S E S L I K(Q)		152.88	495.6052	1484.8	0.0015	1	6.07	25002	10.06	HUMAN	P62906	60S ribosomal protein L10a
23350	dirMS_041712_NAR_60mM_minus.17110.17110.3	3	4.23	0	1.14E+04	S191s	(K)VLTANsI	(K)V/L/T A N s N P S S P S A A K(R)	s:N-acetylglucosamine (S)	155.37	549.6245	1443.744	203.1151	21.7	8.72	22587.9	5.57	HUMAN	Q9NV56	MRG/MORF4L-binding protein
23351	dirMS_041712_NAR_60mM_minus.9548.9548.3	3	4.23	1	4.47E+05		(K)TAVCDIF	(K)T A/V/C/D I/P P R G L K(M)	C:Carbamidomethylation	112.42	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
23352	dirMS_041712_NAR_120mM_plus.12304.12304.4	4	4.23	1	2.45E+06		(K)TLTTVQ(	(K)T L\T T V Q/G I/A\D D Y D K/K K(L)		117.45	449.7412	1795.944	-0.0006	-0.4	5.71	13778.5	7.96	HUMAN	K7EM18	Eukaryotic translation initiation factor 1
23353	dirMS_041712_NAR_120mM_plus.7274.7274.2	2	4.23	1	4.77E+05		(K)SLDEME	(K)S L/D E/M/E\K Q Q\R(E)		91.18	632.3059	1263.6	0.0047	3.8	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
23354	dirMS_041712_NAR_30mM_plus2.10825.10825.2	2	4.23	0	5.58E+05		(R)LASFYER	(R)L A|S F/Y E R(A)		110.48	443.2301	885.447	0.0064	7.3	6	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
23355	dirMS_041712_NAR_30mM_plus2.8468.8468.2	2	4.23	0	5.13E+05		(R)FSELTAE	(R)F/S|E/L/T A E K(L)		98.87	462.7408	924.467	0.007	7.6	4.53	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
23356	dirMS_041712_NAR_40mM_plus2.5907.5907.2	2	4.23	0	5.71E+03		(R)FGGSGS	(R)F/G G S G\S/Q V/D S A R(M)		92.85	584.273	1167.539	-0.0002	-0.1	5.84	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
23357	dirMS_041712_NAR_50mM_plus2.12492.12492.3	3	4.23	2	1.58E+04		(R)YERDLV(	(R)Y/E R/D L V Q/K L K(V)		133.18	431.2516	1291.737	0.0034	2.6	8.5	86967.8	6.57	HUMAN	Q9HCE7	E3 ubiquitin-protein ligase SMURF1
23358	dirMS_041712_NAR_60mM_plus.11912.11912.3	3	4.23	0	3.36E+04		(R)NSNLVG	(R)N S|N/L/V/G A A H E E L Q Q S R(I)		119.55	584.9576	1752.862	-0.0041	-2.3	5.4	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
23359	dirMS_041712_NAR_60mM_plus.13955.13955.3	3	4.23	0	1.56E+06		(K)LAQANG	(K)L A/Q/A/N G W G V/M V S H\R(S)		129.07	509.2606	1525.769	-0.002	-1.3	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
23360	dirMS_041712_NAR_60mM_plus.15677.15677.3	3	4.23	0	4.13E+04		(R)VWYVSI	(R)V W|Y|V/S N I/D G T H I A/K(T)		138.42	534.9464	1602.828	-0.0028	-1.8	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
23361	dirMS_041712_NAR_60mM_plus.21134.21134.3	3	4.23	0	1.67E+05		(K)NGGLGI	(K)N/G G L G H M N/I A/L/L/S D L T K(Q)		174.03	585.3126	1753.927	-0.0033	-1.9	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
23362	dirMS_041712_NAR_120mM_minus.8201.8201.3	3	4.22	2	1.08E+06		(K)KGAVAE	(K)K\G A\V/A E D G D E L R\T E\P E|A K(K)		99.27	638.9836	1914.94	-0.0041	-2.1	4.36	19284.3	5.23	HUMAN	G3V3C7	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
23363	dirMS_041712_NAR_30mM_minus2.5104.5104.2	2	4.22	0	1.42E+05		(R)AAEQYT	(R)A A|E/Q Y/T\P K(A)		81.22	454.2271	907.452	-0.005	-5.6	6.04	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
23364	dirMS_041712_NAR_30mM_minus2.5606.5606.2	2	4.22	0	1.00E+05		(R)LQDYEEI	(R)L/Q|D Y E E K(T)		84.57	462.7203	924.431	0.0024	2.6	4.14	65692.2	5.7	HUMAN	E7EQR4	Ezrin
23365	dirMS_041712_NAR_30mM_minus2.6481.6481.2	2	4.22	0	2.34E+05		(R)QQYESV	(R)Q Q/Y E/S V/A/A/K(N)		89.95	512.2534	1023.511	-0.011	-10.8	6	49709.6	5.19	HUMAN	B0YJC4	Vimentin
23366	dirMS_041712_NAR_30mM_minus2.7304.7304.2	2	4.22	1	4.14E+04	M278m	(K)NEGRmI	(K)N E/G/R m D A/E K(V)	m:Oxidized methionine	94.23	533.2399	1049.468	16.0045	9	4.68	102190.7	4.66	HUMAN	E7EUZ3	Zinc finger protein 638
23367	dirMS_041712_NAR_40mM_minus2.14987.14987.3	3	4.22	0	1.44E+05		(K)LFLFHTS	(K)L F\L F H T S L/P I/A E A/P G K(L)		173.92	580.9924	1740.968	-0.0057	-3.3	6.75	108105.4	6.57	HUMAN	E7EP00	Protein transport protein Sec24C
23368	dirMS_041712_NAR_50mM_minus2.10434.10434.3	3	4.22	0	7.23E+04		(R)LTSPIVS'	(R)L T/S/P/I V/S T H L D T R(N)		127.37	480.6	1439.785	0.0002	0.1	6.74	58760.2	5.26	HUMAN	Q6ZTN6	Ankyrin repeat domain-containing protein 13D
23369	dirMS_041712_NAR_50mM_minus2.11125.11125.3	3	4.22	0	4.11E+05		(R)DLPSAG	(R)D L/P/S A G E E I L E V/E S/E P R(A)		130.8	623.9684	1869.908	-0.017	-9.1	3.83	81886.4	6.72	HUMAN	P46199	Translation initiation factor IF-2, mitochondrial
23370	dirMS_041712_NAR_50mM_minus2.14797.14797.3	3	4.22	1	2.80E+05		(K)NIYVLQE	(K)N I|Y/V/L Q E L D N P G A K/R(I)		152.6	577.3116	1729.923	-0.0029	-1.7	6.07	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
23371	dirMS_041712_NAR_50mM_minus2.17128.17128.3	3	4.22	1	1.23E+05		(R)KHNLEL'	(R)K H/N L/E L T M S P/H C V P S K(L)	C:Carbamidomethylation	164.85	626.6531	1877.936	0.0087	4.6	8.61	75701.4	8.74	HUMAN	Q86WS4	Uncharacterized protein C12orf40
23372	dirMS_041712_NAR_60mM_minus.12180.12180.3	3	4.22	0	3.12E+05		(R)IELGDVT	(R)I E|L G D V/T/P H N I K(Q)		127.68	445.91	1335.727	-0.0112	-8.4	5.32	14942.8	8.71	HUMAN	C9J5D1	N-alpha-acetyltransferase 50
23373	dirMS_041712_NAR_60mM_minus.12677.12677.3	3	4.22	1	1.29E+05		(R)TPSDVKI	(R)T/P/S D V K\E L/V/L/D N S R(S)		131.18	524.9451	1572.823	-0.002	-1.3	4.55	20111	4.47	HUMAN	H0YN26	Acidic leucine-rich nuclear phosphoprotein 32 family member A
23374	dirMS_041712_NAR_60mM_minus.15293.15293.3	3	4.22	2	1.83E+05	N183n	(R)VRnKEA	(R)V R n K|E/A P A/G E/G T K(M)	n:N-acetylglucosamine (N)	145.4	520.6074	1356.723	203.0846	3.4	8.56	60836.6	9.59	HUMAN	O00294	Tubby-related protein 1
23375	dirMS_041712_NAR_60mM_minus.17251.17251.3	3	4.22	1	1.12E+05		(K)FLSPQD'	(K)F L|S/P Q D/T F E A L K/R(N)		156.22	517.9425	1551.817	-0.0036	-2.3	6.07	97622	8.94	HUMAN	Q9NTZ6	RNA-binding protein 12
23376	dirMS_041712_NAR_60mM_minus.18423.18423.3	3	4.22	1	7.22E+04		(K)AKIGLIQ	(K)A K I G L\I Q|F C L/S A/P K(T)	C:Carbamidomethylation	164.15	515.9647	1545.882	-0.0026	-1.7	10	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
23377	dirMS_041712_NAR_60mM_minus.9992.9992.3	3	4.22	1	1.97E+05	S303s	(R)DHHMs(	(R)D H H M s G W S/Y/K R V E K(S)	s:N-acetylglucosamine (S)	115.55	654.9721	1759.833	203.0684	-5.6	8.51	51648.4	5.55	HUMAN	B7XGB9	Protein phosphatase 1M
23378	dirMS_041712_NAR_120mM_plus.24440.24440.3	3	4.22	2	1.62E+05	K323k	(K)EEELLPK	(K)E E E L L\P K A M/D/E S/V A R k(L)	k:Ubiquitin-K	184.27	653.6605	1844.942	114.0247	-9.3	4.58	37206.4	9.51	HUMAN	Q9HBH5	Retinol dehydrogenase 14
23379	dirMS_041712_NAR_120mM_plus.4706.4706.3	3	4.22	0	3.31E+05		(K)ISRPGDS	(K)I/S R\P G D S\D D/S\R(S)		75.03	402.1896	1204.555	-0.001	-0.8	4.43	64759.2	8.88	HUMAN	P14866	Heterogeneous nuclear ribonucleoprotein L
23380	dirMS_041712_NAR_20mM_plus.10521.10521.2	2	4.22	0	1.93E+03		(R)AGGIGG	(R)A G G I/G G A T I\P E S A/P R(A)		145.9	677.3588	1353.712	-0.0018	-1.3	6.05	133030.9	10.9	HUMAN	F5H1R7	Protein FLJ22184
23381	dirMS_041712_NAR_20mM_plus.12033.12033.2	2	4.22	0	4.60E+04		(K)LVPVGY(	(K)L V|P/V/G Y/G/I R(K)		156.52	487.2934	973.583	-0.0034	-3.5	8.75	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
23382	dirMS_041712_NAR_20mM_plus.7552.7552.2	2	4.22	0	2.48E+05		(K)VLTPTQ'	(K)V L/T|P T Q/V K(N)		121.72	443.2734	885.54	-0.0009	-1	8.72	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
23383	dirMS_041712_NAR_20mM_plus.7697.7697.2	2	4.22	0	4.28E+04		(K)AVTEQG	(K)A V T E|Q|G A\E L S\N E E/R(N)		122.93	766.8616	1532.719	-0.0028	-1.8	4.09	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
23384	dirMS_041712_NAR_20mM_plus.7864.7864.3	3	4.22	0	1.14E+05		(K)VEIIAND	(K)V E I\I A/N D|Q G N R(T)		124.47	410.2139	1228.628	-0.0009	-0.7	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
23385	dirMS_041712_NAR_30mM_plus2.21324.21324.2	2	4.22	0	3.04E+05		(K)FDGILGI	(K)F D G I/L/G M/A Y/P R(I)		167.28	620.3199	1239.619	0.0135	10.9	5.83	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
23386	dirMS_041712_NAR_30mM_plus2.5849.5849.2	2	4.22	0	1.58E+04		(K)VLTAAG	(K)V L T/A/A|G N S C R(V)	C:Carbamidomethylation	85.88	524.764	1048.52	0.0003	0.3	9.72	38104.8	7.18	HUMAN	Q86W42	THO complex subunit 6 homolog
23387	dirMS_041712_NAR_40mM_plus2.12576.12576.3	3	4.22	0	3.76E+05		(K)AASDIAI	(K)A A/S D I\A M/T E L/P P T H P I R(L)		140.13	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
23388	dirMS_041712_NAR_50mM_plus2.13635.13635.3	3	4.22	2	7.89E+05		(K)LTTPSKT	(K)L T|T P S K T E G/S A G/Q/A E A K R(K)		139.13	611.3256	1831.951	0.0114	6.2	8.59	125387.1	10.17	HUMAN	F8VVT9	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2
23389	dirMS_041712_NAR_50mM_plus2.8253.8253.3	3	4.22	1	3.49E+05		(R)VAVEAK	(R)V A V E A K N|P A D L/P K(L)		110.53	451.2563	1351.758	-0.0036	-2.7	6.04	96306.4	6.41	HUMAN	P13639	Elongation factor 2
23390	dirMS_041712_NAR_60mM_plus.14814.14814.3	3	4.22	2	4.87E+04		(K)HRTLQK	(K)H/R\T L Q K D/C D/L Y/K(H)	C:Carbamidomethylation	133.95	526.2613	1576.79	-0.0207	-13.1	8.5	53721.7	7.88	HUMAN	B0QYC4	Caspase recruitment domain family, member 10 (Fragment)
23391	dirMS_041712_NAR_50mM_minus2.14760.14760.3	3	4.21	0	3.07E+04		(K)GQYFGE	(K)G Q|Y/F G E L/A/L V T N K P R(A)		152.52	564.9709	1692.907	-0.0086	-5.1	8.59	10305.6	6.94	HUMAN	H7C330	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
23392	dirMS_041712_NAR_60mM_minus.17545.17545.3	3	4.21	1	7.57E+03	K46k	(R)IIVWKRY	(R)I I V W K R Y S D F k(K)	k:Ubiquitin-K	157.63	523.6181	1454.815	114.0243	-11.9	9.7	118183.6	4.76	HUMAN	B1APS8	Ribosomal protein S6 kinase delta-1
23393	dirMS_041712_NAR_120mM_plus.7882.7882.2	2	4.21	0	5.08E+05		(K)STTTGHI	(K)S T|T/T/G H L I\Y K(C)		95.33	560.8014	1120.6	-0.0042	-3.7	8.34	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
23394	dirMS_041712_NAR_120mM_plus.9092.9092.3	3	4.21	1	4.91E+05		(R)SGRGGN	(R)S G R G G N\F/G|F G D/S R(G)		101.07	438.538	1313.598	0.0013	1	9.32	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
23395	dirMS_041712_NAR_20mM_plus.14946.14946.2	2	4.21	0	1.90E+05	M179m M:	(K)mFVLDE	(K)m F\V/L D\E A D/E/m/L S/R(G)	m:Oxidized methionine	173.63	794.3555	1555.713	31.9906	0.5	3.91	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
23396	dirMS_041712_NAR_30mM_plus2.12633.12633.2	2	4.21	0	8.98E+04		(R)LQLELSK	(R)L/Q|L E L/S K(V)		118.47	415.7543	830.498	0.0031	3.8	6	74423.5	6.57	HUMAN	P02545	Prelamin-A/C
23397	dirMS_041712_NAR_30mM_plus2.16639.16639.2	2	4.21	0	4.30E+05		(K)GCSFLPI	(K)G C/S/F|L/P D/P Y Q K(Q)	C:Carbamidomethylation	140.47	656.306	1311.604	0.0009	0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
23398	dirMS_041712_NAR_40mM_plus2.18099.18099.3	3	4.21	1	2.26E+04		(K)LVVVLNI	(K)L V|V/V L N K I D L L/P E G K(R)		172.68	550.678	1650.02	-0.0006	-0.3	6.07	48446.2	8.53	HUMAN	C9J8T0	Selenocysteine-specific elongation factor
23399	dirMS_041712_NAR_50mM_plus2.13657.13657.3	3	4.21	1	1.85E+06	M320m	(K)YmACCL	(K)Y m/A/C C L L Y R G D V V/P K(E)	C:Carbamidomethylation m:Oxid	140.47	620.9622	1844.886	15.9865	-4.5	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
23400	dirMS_041712_NAR_60mM_plus.10024.10024.3	3	4.21	0	1.03E+06		(K)LQNSAS.	(K)L Q N S A S A/T A L/V S/R(T)		109.93	439.9069	1317.712	-0.006	-4.5	9.75	47091.3	10.55	HUMAN	B4DKZ7	Transcriptional repressor p66-alpha
23401	dirMS_041712_NAR_60mM_plus.13051.13051.2	2	4.21	0	2.13E+05		(R)HGDLPD	(R)H/G\D L|P D|I|Q I/K(H)		124.9	568.3082	1135.611	-0.0015	-1.3	5.21	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
23402	dirMS_041712_NAR_60mM_plus.6106.6107.3	3	4.21	0	1.64E+05	M522m T5	(K)VADmts	(K)V A\D m/t s V L D P N/K(M)	m:Oxidized methionine t:Pho	90.27	489.1905	1289.641	175.9164	-7.6	4.21	279771.8	9.54	HUMAN	Q8NDH2	Coiled-coil domain-containing protein 168
23403	dirMS_041712_NAR_120mM_minus.16553.16553.3	3	4.2	0	6.11E+05		(R)EHALLA'	(R)E H\A\L L\A/Y/T/L G V K(Q)		144.95	438.9186	1314.742	-0.0004	-0.3	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
23404	dirMS_041712_NAR_20mM_minus.10533.10533.2	2	4.2	0	3.08E+04	M234m	(K)mVVESA	(K)m\V\V|E/S A/Y E V I K(L)	m:Oxidized methionine	153.82	642.3318	1267.66	15.9961	0.9	4.53	36923.1	5.71	HUMAN	P07195	L-lactate dehydrogenase B chain
23405	dirMS_041712_NAR_30mM_minus2.15379.15379.2	2	4.2	0	3.40E+04		(K)LCDFGF/	(K)L C/D/F/G F/A R(A)	C:Carbamidomethylation	135.87	493.2343	985.456	0.0053	5.4	5.84	143554.7	5.57	HUMAN	A8MU99	Serine/threonine-protein kinase 36
23406	dirMS_041712_NAR_50mM_minus2.13861.13861.3	3	4.2	1	3.29E+04		(R)ELISNAS	(R)E L/I/S/N/A S D A L D/K/I R(L)		146.95	515.6179	1544.828	0.0113	7.3	4.56	5582.4	4.81	HUMAN	F8W026	Endoplasmin (Fragment)
23407	dirMS_041712_NAR_50mM_minus2.7335.7335.3	3	4.2	1	8.39E+04		(K)ELQAAG	(K)E L Q|A/A G K/S/P E D L E R(L)		108.02	514.9262	1542.776	-0.0118	-7.6	4.41	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
23408	dirMS_041712_NAR_50mM_minus2.8497.8497.3	3	4.2	0	4.10E+04		(R)DNIQGI1	(R)D N|I Q G I/T K/P A I R(R)		116.12	442.5888	1325.754	-0.0017	-1.3	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
23409	dirMS_041712_NAR_60mM_minus.12920.12920.3	3	4.2	1	1.49E+05	N52n	(R)nSIWKN	(R)n S/I W/K N E\E\E K(V)	n:N-acetylglucosamine (N)	131.78	493.9126	1276.617	203.1064	18.3	4.79	27460.6	5.65	HUMAN	E9PN39	Protein MTFR2 (Fragment)
23410	dirMS_041712_NAR_60mM_minus.15925.15925.3	3	4.2	1	3.50E+04		(R)KDDPVT	(R)K D D\P V T N\L N|N/A F E V A E/K(Y)		148.48	635.317	1903.94	-0.0032	-1.7	4.32	21601.4	6.27	HUMAN	K7EJH8	Alpha-actinin-4 (Fragment)
23411	dirMS_041712_NAR_60mM_minus.16420.16420.3	3	4.2	1	1.31E+05		(K)WVAIQS	(K)W\V|A|I Q S/V S A/W P E K/R(G)		151.7	552.9674	1656.886	0.002	1.2	8.75	6412.4	9.52	HUMAN	J3KSS4	Cytosolic non-specific dipeptidase (Fragment)
23412	dirMS_041712_NAR_60mM_minus.6220.6220.3	3	4.2	1	2.64E+05		(K)ETEGDV'	(K)E T/E G/D V/T S V K D A K(I)		92.67	460.2267	1378.67	-0.0041	-3	4.32	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
23413	dirMS_041712_NAR_20mM_plus.19162.19162.3	3	4.2	0	2.19E+05		(R)LAGTQP	(R)L A G T Q P\L E/V/L/E/A V Q R(S)		204.08	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
23414	dirMS_041712_NAR_30mM_plus2.20359.20359.2	2	4.2	0	2.38E+04		(R)TVQSLEI	(R)T/V/Q/S L/E I/D L D S M R(N)		161.05	753.8768	1506.747	-0.0005	-0.3	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
23415	dirMS_041712_NAR_30mM_plus2.20428.20428.2	2	4.2	0	2.50E+03		(R)CSVLAA/	(R)C S V/L/A/A A N S/V F\G R(W)	C:Carbamidomethylation	162.43	676.3436	1351.679	0.0012	0.9	9.75	78390.7	9.27	HUMAN	B1AHB1	DNA replication licensing factor MCM5
23416	dirMS_041712_NAR_30mM_plus2.22299.22299.2	2	4.2	0	1.54E+05		(K)GLSSLLC	(K)G L/S S/L/L/C N\F T/K(S)	C:Carbamidomethylation	171.95	620.3199	1239.64	-0.0077	-6.2	8.75	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
23417	dirMS_041712_NAR_40mM_plus2.6804.6804.2	2	4.2	0	7.56E+04		(R)TALLGG(	(R)T A/L/L/G G G Q R(R)		99.97	436.7494	872.495	-0.0033	-3.8	9.41	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
23418	dirMS_041712_NAR_50mM_plus2.11048.11048.3	3	4.2	0	1.25E+05	M392m	(K)EmNPAL	(K)E m/N|P A L|G I|D C L/H K(G)	C:Carbamidomethylation m:Oxid	125.43	505.2419	1497.719	15.9923	-1.7	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
23419	dirMS_041712_NAR_50mM_plus2.12184.12184.3	3	4.2	0	2.97E+05		(R)VVVLMC	(R)V V V/L/M/G S T S D L G H C E K(I)	C:Carbamidomethylation	131.5	577.9512	1731.84	-0.0014	-0.8	5.32	37681.5	5.93	HUMAN	D6RF62	Phosphoribosylaminoimidazole carboxylase
23420	dirMS_041712_NAR_50mM_plus2.16808.16808.3	3	4.2	0	1.14E+05		(K)AQDGSH	(K)A Q|D/G S H/P L S L Q D L I E/K(V)		155.92	584.2981	1750.897	-0.0173	-9.9	4.54	128523.4	7.06	HUMAN	B7ZL00	Protein transport protein Sec31A
23421	dirMS_041712_NAR_120mM_minus.5866.5866.3	3	4.19	0	2.61E+04		(R)ADCHHL	(R)A/D C H H L H/G A/E R(L)	C:Carbamidomethylation	85.38	434.8643	1302.576	0.0027	2.1	6.27	25267.9	6.33	HUMAN	B4DQ88	EGF-like module-containing mucin-like hormone receptor-like 2
23422	dirMS_041712_NAR_20mM_minus.8019.8019.2	2	4.19	0	6.12E+03		(R)AAAGYP	(R)A A/A/G Y|P D/P Y S R(A)		129.75	584.2733	1167.543	-0.0036	-3.1	5.88	266161	5.68	HUMAN	E9PPU0	Epiplakin
23423	dirMS_041712_NAR_30mM_minus2.12890.12890.2	2	4.19	0	3.47E+05		(K)SQNTGL	(K)S Q/N T/G L T T K(K)		124.48	475.2457	949.495	-0.0108	-11.4	8.47	25101.1	10.03	HUMAN	D6RG09	Sentrin-specific protease 6 (Fragment)
23424	dirMS_041712_NAR_30mM_minus2.13813.13813.2	2	4.19	0	4.34E+05		(K)LSSLPFQ	(K)L/S/S L/P F Q K(I)		127.85	460.2646	919.525	-0.0028	-3.1	8.75	12272.7	5.08	HUMAN	H3BRV9	Nuclear transport factor 2 (Fragment)
23425	dirMS_041712_NAR_30mM_minus2.14500.14500.2	2	4.19	0	4.73E+05		(R)TFEDFVI	(R)T F/E/D F V R(I)		133.18	457.2246	913.441	0.0005	0.6	4.37	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
23426	dirMS_041712_NAR_40mM_minus2.7057.7057.3	3	4.19	0	2.36E+05	M115m	(R)VmLGET	(R)V m|L/G E/T N P A D S K P G T I R(G)	m:Oxidized methionine	113.92	601.3082	1785.916	15.9937	-0.7	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
23427	dirMS_041712_NAR_50mM_minus2.13577.13577.3	3	4.19	1	8.23E+04		(K)ITDIIGKE	(K)I T/D I/I/G K E/E G I/G P E N L R(G)		144.9	618.665	1853.997	-0.0163	-8.8	4.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
23428	dirMS_041712_NAR_50mM_minus2.17464.17464.3	3	4.19	0	2.57E+05		(R)LLLDGAI	(R)L L|L/D G A P L I A I H K(A)		168.5	458.6218	1373.852	-0.0007	-0.5	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
23429	dirMS_041712_NAR_60mM_minus.6517.6517.3	3	4.19	1	3.19E+04	M625m M6	(K)AQALRD	(K)A Q|A/L R D N S T m G Y m A A K(K)	m:Oxidized methionine	94.87	587.2735	1727.82	31.9856	-2.4	8.63	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
23430	dirMS_041712_NAR_60mM_minus.8140.8140.3	3	4.19	0	1.91E+05		(R)QYDISDI	(R)Q Y/D/I/S D/P Q/R P R(L)		105.63	458.8971	1374.676	0.0007	0.5	5.96	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1

23431	dirMS_041712_NAR_120mM_plus.4559.4559.3	3	4.19	0	2.15E+05	M77m M7	(R)LTNSM	(R)L/T N S M m/m/H G R(N)	m:Oxidized methionine	73.05	403.8446	1177.527	31.9918	1.6	9.75	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
23432	dirMS_041712_NAR_20mM_plus.13777.13777.2	2	4.19	0	1.24E+05	M256m	(R)SLDmDS	(R)S L D/m/D/S I\I|A E V/K(A)	m:Oxidized methionine	167.72	668.8371	1320.671	15.9954	0.3	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
23433	dirMS_041712_NAR_30mM_plus2.15992.15992.2	2	4.19	0	3.94E+05		(K)MDQAII	(K)M D/Q/A\I/I/F C R(T)	C:Carbamidomethylation	136.98	577.2809	1153.549	0.0053	4.6	5.59	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
23434	dirMS_041712_NAR_30mM_plus2.21927.21927.2	2	4.19	0	2.15E+05		(K)ALELNM	(K)A L E/L/N M/L/S L K(G)		170.23	566.3204	1131.644	-0.0107	-9.4	6.05	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
23435	dirMS_041712_NAR_40mM_plus2.11657.11657.2	2	4.19	0	7.03E+04		(K)IAWALS	(K)I A|W/A L S R(K)		134.97	408.7393	816.473	-0.0013	-1.6	9.75	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
23436	dirMS_041712_NAR_40mM_plus2.6536.6536.2	2	4.19	0	3.01E+04		(R)DGYQQ	(R)D G/Y/Q Q/N F\K(R)		97.77	500.2303	999.453	0.0003	0.3	5.83	70523.3	4.94	HUMAN	G3V153	Caprin-1
23437	dirMS_041712_NAR_40mM_plus2.8915.8915.2	2	4.19	0	1.05E+05		(K)FYEQFS	(K)F/Y|E/Q/F S K(N)		115.03	474.7301	948.446	0.0068	7.1	6	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
23438	dirMS_041712_NAR_50mM_plus2.10146.10146.3	3	4.19	0	3.78E+05		(R)MVQVH	(R)M/V|Q V H E/L/S C E G I S/K(S)	C:Carbamidomethylation	121.6	539.5992	1616.777	0.006	3.7	5.38	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
23439	dirMS_041712_NAR_50mM_plus2.10219.10219.3	3	4.19	1	1.28E+05		(K)ATAVVD	(K)A T|A V V/D G A F K E V K(L)		121.17	445.5822	1334.731	0.0006	0.5	6.11	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
23440	dirMS_041712_NAR_50mM_plus2.12015.12015.3	3	4.19	1	4.97E+05		(R)DNKQA	(R)D N K Q A\G\V/F/E/P T I V K(V)		131.35	515.9483	1545.827	0.0032	2.1	6.07	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
23441	dirMS_041712_NAR_50mM_plus2.21044.21044.3	3	4.19	0	3.66E+05		(K)HSQFIG	(K)H S Q F I\G\Y/P I|T L/F V E K(E)		179.9	593.6536	1778.948	-0.0013	-0.8	6.75	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
23442	dirMS_041712_NAR_50mM_plus2.9624.9624.3	3	4.19	0	7.71E+05		(R)DNIQGI	(R)D N\I Q/G I\T K/P A I R(R)		117.22	442.5902	1325.754	0.0025	1.9	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
23443	dirMS_041712_NAR_60mM_plus.11410.11410.2	2	4.19	0	8.24E+05		(R)TICSHV	(R)T/I/C\S H/V/Q N M\I|K(G)	C:Carbamidomethylation	117.02	665.8295	1330.661	-0.0089	-6.7	8.44	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
23444	dirMS_041712_NAR_60mM_plus.16953.16953.3	3	4.19	1	2.53E+05		(K)IKAIPQL	(K)I K A I/P\Q\L/Q/G Y L R(S)		145.68	467.2842	1399.842	-0.0039	-2.8	9.99	25891.4	10.67	HUMAN	F8W181	60S ribosomal protein L6 (Fragment)
23445	dirMS_041712_NAR_60mM_plus.17343.17343.3	3	4.19	2	1.96E+06	M348m	(K)KVKGW	(K)K\V/K G W L L P E m P(-)	m:Oxidized methionine	146.63	438.5872	1297.734	16.0134	14	8.59	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
23446	dirMS_041712_NAR_60mM_plus.21206.21206.3	3	4.19	1	4.03E+05		(R)KAIIIFVP	(R)K A I I I F\V|P V P Q/L K(S)		174.23	489.3205	1465.95	-0.0035	-2.4	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
23447	dirMS_041712_NAR_60mM_plus.5254.5254.3	3	4.19	1	1.86E+05	M163m	(K)IYEDGD	(K)I/Y|E/D G D/D D m K R(T)	m:Oxidized methionine	85.13	458.1946	1356.574	15.9956	0.5	4.03	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
23448	dirMS_041712_NAR_120mM_minus.20196.20196.3	3	4.18	0	3.87E+05		(K)VHLVGI	(K)V H\L\V G\I D I/F/T G K(K)		166.43	433.5866	1298.747	-0.0015	-1.1	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
23449	dirMS_041712_NAR_20mM_minus.13174.13174.2	2	4.18	0	2.77E+05	M35m	(K)NDIAINE	(K)N D I\A/I|N E L m K(R)	m:Oxidized methionine	182.05	588.7948	1160.598	15.9843	-9	4.37	28354	7.11	HUMAN	B4DXI8	26S proteasome non-ATPase regulatory subunit 7
23450	dirMS_041712_NAR_20mM_minus.6291.6291.2	2	4.18	0	4.47E+04		(K)DSYVGD	(K)D S\Y/V/G D E A\Q/S K(R)		104.83	599.7642	1198.522	-0.0011	-0.9	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
23451	dirMS_041712_NAR_30mM_minus2.11189.11189.2	2	4.18	0	1.23E+05		(K)SCNCLL	(K)S C|N/C L L L K(V)	C:Carbamidomethylation	114.5	504.2543	1007.501	0.0001	0.1	8.47	47510.4	7.04	HUMAN	P06733	Alpha-enolase
23452	dirMS_041712_NAR_30mM_minus2.15778.15778.2	2	4.18	0	2.77E+05		(R)LTIGSNL	(R)L T/I/G/S N L S I/R(I)		139.28	537.313	1073.631	-0.0126	-11.7	9.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
23453	dirMS_041712_NAR_30mM_minus2.5586.5586.2	2	4.18	0	8.90E+04		(K)DSYVGD	(K)D S\Y|V/G D E A Q S K(R)		84.18	599.7632	1198.522	-0.0031	-2.6	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
23454	dirMS_041712_NAR_30mM_minus2.6193.6193.2	2	4.18	0	1.20E+05		(K)MAGAM	(K)M/A|G\A/M S T T A K(T)		87.82	484.7299	968.454	-0.0014	-1.5	8.5	23963.2	8.9	HUMAN	Q9UQN3	Charged multivesicular body protein 2b
23455	dirMS_041712_NAR_40mM_minus2.14069.14069.3	3	4.18	0	4.48E+04		(K)LQAVEV	(K)L Q|A V E V\V I T H L A/P G/T K(H)		166.73	559.3273	1675.974	-0.0068	-4	6.75	16120	9.05	HUMAN	Q9Y2V2	Calcium-regulated heat stable protein 1
23456	dirMS_041712_NAR_50mM_minus2.4961.4961.3	3	4.18	1	2.84E+05	M137m	(R)mQNDT	(R)m/Q N/D T A/E/N E T T E K/E E K(S)	m:Oxidized methionine	83	638.2738	1896.813	15.9941	-0.4	4.14	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
23457	dirMS_041712_NAR_50mM_minus2.5797.5797.3	3	4.18	1	4.10E+04		(R)ATEGM	(R)A/T/E/G M V V/A/D K N C S K(I)	C:Carbamidomethylation	94.57	503.9058	1509.704	-0.0007	-0.5	6.11	15607.8	9.99	HUMAN	B4E0P1	Proteasome (Prosome, macropain) subunit, beta type, 7, isoform CRA_b
23458	dirMS_041712_NAR_50mM_minus2.9185.9185.3	3	4.18	2	4.09E+04		(K)SRLMSE	(K)S R/L M S E/L/E K T R(E)		120.33	450.5813	1349.721	0.0088	6.5	8.46	281207.5	4.95	HUMAN	P02549	Spectrin alpha chain, erythrocytic 1
23459	dirMS_041712_NAR_60mM_minus.14800.14800.3	3	4.18	1	5.91E+05		(K)TDKTLV	(K)T/D K T L|V\L/L/M G K(E)		142.57	406.9088	1218.713	-0.0008	-0.6	8.26	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
23460	dirMS_041712_NAR_60mM_minus.8796.8796.3	3	4.18	1	1.14E+05		(K)YAGKDG	(K)Y/A/G K/D G Y N/Y T L/S K(T)		109.12	493.9126	1479.711	0.0118	8	8.38	11854.4	6.57	HUMAN	P31949	Protein S100-A11
23461	dirMS_041712_NAR_120mM_plus.10686.10686.3	3	4.18	1	1.83E+05		(R)VKYETEL	(R)V K Y E T/E L/A M/R(Q)		109.23	413.8849	1239.64	0	0	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
23462	dirMS_041712_NAR_120mM_plus.10849.10849.3	3	4.18	0	2.01E+05		(K)ILEANM	(K)I L E A N M/D I V Y/K(D)		109.42	436.8969	1308.687	-0.0107	-8.1	4.37	40035.7	9.98	HUMAN	Q96AQ8	Mitochondrial calcium uniporter regulator 1
23463	dirMS_041712_NAR_20mM_plus.11411.11411.2	2	4.18	0	3.48E+05		(K)LITPAVV	(K)L I|T|P A V/V S E R(L)		151.05	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
23464	dirMS_041712_NAR_20mM_plus.8559.8559.2	2	4.18	0	3.02E+05		(R)DVEIPQ	(R)D V|E I/P Q/F M R(Q)		129.47	567.7865	1134.561	0.0045	4	4.37	120222.5	9.83	HUMAN	Q9NS56	E3 ubiquitin-protein ligase Topors
23465	dirMS_041712_NAR_30mM_plus2.4335.4335.2	2	4.18	0	2.49E+05		(R)SMPEQT	(R)S M|P E Q T G E K(-)		71.63	503.7289	1006.451	-0.0005	-0.5	4.53	12955	9.87	HUMAN	P62888	60S ribosomal protein L30
23466	dirMS_041712_NAR_30mM_plus2.5550.5551.2	2	4.18	0	5.19E+04		(R)LQDYEE	(R)L/Q|D/Y E E/K(T)		83.17	462.7168	924.431	-0.0046	-5	4.14	65692.2	5.7	HUMAN	E7EQR4	Ezrin
23467	dirMS_041712_NAR_30mM_plus2.6732.6732.2	2	4.18	0	2.48E+05		(K)ALDEME	(K)A/L/D/E/M E/K(Q)		90.07	418.1994	835.387	0.0049	5.9	4.14	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
23468	dirMS_041712_NAR_30mM_plus2.7183.7183.2	2	4.18	0	1.58E+05		(K)TGEGFY	(K)T/G/E/G F Y K(Y)		92.13	401.1973	801.378	0.0096	12	5.66	35407.1	6.73	HUMAN	E9PF18	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial
23469	dirMS_041712_NAR_40mM_plus2.6511.6511.2	2	4.18	0	1.10E+05		(K)YCQVIR	(K)Y/C|Q/V I R(V)	C:Carbamidomethylation	98.08	419.7152	838.424	-0.0009	-1	8.75	31471	10.11	HUMAN	B5MCW2	60S ribosomal protein L3 (Fragment)
23470	dirMS_041712_NAR_50mM_plus2.16346.16346.3	3	4.18	0	3.28E+04		(-)XEITSSP	(-)X E I T S S/P Q G L|D/N P A L L R(D)		154.37	608.6724	1823.986	0.0165	9	4.37	11963.3	4.8	HUMAN	H0YI90	Protein DDI1 homolog 2 (Fragment)
23471	dirMS_041712_NAR_50mM_plus2.8652.8652.3	3	4.18	0	4.30E+05		(R)AALAHS	(R)A A L A H S/E E\V\T/A/S/Q V\A A T K(T)		112.93	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
23472	dirMS_041712_NAR_60mM_plus.11968.11968.3	3	4.18	1	1.16E+06		(R)QKAQVE	(R)Q K A Q V E\Q/E/L/T T L R(L)		120.13	515.2865	1543.844	0.0011	0.7	6.14	533778	5.74	HUMAN	Q15149	Plectin
23473	dirMS_041712_NAR_120mM_minus.13198.13198.4	4	4.17	1	5.13E+05		(K)SVHSSV	(K)S V H S S V/P L/L N S K D/P/I D|R(I)		126.43	466.7525	1863.992	-0.0041	-2.2	6.47	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
23474	dirMS_041712_NAR_120mM_minus.14922.14922.4	4	4.17	1	3.27E+05		(K)LDKAQI	(K)L D K A Q I H D L V\L\V/G/G/S T R(I)		135.53	456.2581	1822.018	-0.0076	-4.1	6.75	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
23475	dirMS_041712_NAR_120mM_minus.5841.5841.2	2	4.17	1	1.01E+05		(K)MLPDK	(K)M L|P D/K D/C R(Y)	C:Carbamidomethylation	85.58	517.7407	1034.476	-0.0016	-1.6	5.71	22956	8.8	HUMAN	E9PK25	Cofilin-1
23476	dirMS_041712_NAR_20mM_minus.10331.10331.2	2	4.17	0	4.90E+04		(K)ILQDGG	(K)I L Q|D/G G L Q V/V E K(Q)		152.72	649.8694	1298.731	0.0001	0.1	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
23477	dirMS_041712_NAR_20mM_minus.7020.7020.2	2	4.17	0	2.07E+05	M33m	(R)IDEmPE	(R)I/D|E m|P E A A V/K(S)	m:Oxidized methionine	117.95	559.7733	1102.545	15.9944	-0.4	4.14	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
23478	dirMS_041712_NAR_30mM_minus2.13708.13708.2	2	4.17	0	7.04E+04		(K)SSLGSQ	(K)S S/L/G S Q M L C K(K)	C:Carbamidomethylation	127.77	555.7685	1110.528	0.0015	1.4	8.47	176787.5	8.48	HUMAN	Q9NRD8	Dual oxidase 2
23479	dirMS_041712_NAR_30mM_minus2.16266.16266.2	2	4.17	0	1.09E+05		(K)FGVIFA	(K)F G\V/I/F A/G/A Q K(N)		141.95	519.2901	1037.578	-0.0049	-4.7	8.75	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
23480	dirMS_041712_NAR_30mM_minus2.7274.7274.2	2	4.17	1	2.09E+04	S11s	(K)KGsEQE	(K)K G/s|E\Q E S V K(E)	s:N-acetylglucosamine (S)	93.12	597.7918	991.505	203.0709	-7.1	6.14	13776.6	9.99	HUMAN	K7ENJ5	cAMP-dependent protein kinase catalytic subunit alpha
23481	dirMS_041712_NAR_40mM_minus2.12534.12534.3	3	4.17	0	1.19E+05		(K)GLPQTA	(K)G L/P Q T A V C N L/N\I T L P A H K(K)	C:Carbamidomethylation	157.48	649.6858	1947.048	-0.0052	-2.7	8.76	112066.5	5.59	HUMAN	B1AQT2	Ankyrin 3, node of Ranvier (Ankyrin G)
23482	dirMS_041712_NAR_50mM_minus2.6095.6095.3	3	4.17	0	5.24E+03	M145m	(K)EQEPm	(K)E\Q E/P/m/P T V D S H E P R(L)	m:Oxidized methionine	97.45	556.5819	1651.738	15.9931	-1.1	4.4	18962.9	9.6	HUMAN	A6NGP5	Hematological and neurological-expressed 1-like protein
23483	dirMS_041712_NAR_50mM_minus2.9814.9814.3	3	4.17	1	5.81E+03	M239m	(R)MQKEIT	(R)M Q K E I T\A L/A/P S T m K(I)	m:Oxidized methionine	123.53	522.2727	1548.812	15.9911	-2.4	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
23484	dirMS_041712_NAR_60mM_minus.10076.10076.3	3	4.17	0	2.17E+05		(R)AVIEHN	(R)A V/I\E H N L/L/S A S K(L)		115.72	427.9103	1281.716	0.0002	0.2	6.79	40481.5	6.48	HUMAN	B3KST5	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis), isoform CRA_a
23485	dirMS_041712_NAR_60mM_minus.15520.15520.3	3	4.17	0	9.90E+04		(R)EHALLA	(R)E H A L\L/A|Y T L/G V K(Q)		146.22	438.9202	1314.742	0.0044	3.4	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
23486	dirMS_041712_NAR_60mM_minus.17209.17209.3	3	4.17	0	2.81E+05		(K)GSDHSA	(K)G S D H S A S L E/P G E/L/A E L V R(S)		156.7	622.9764	1866.919	-0.0045	-2.4	4.4	12626.3	5.59	HUMAN	Q5TBR0	N-acetylneuraminic acid synthase (Fragment)
23487	dirMS_041712_NAR_20mM_plus.15661.15661.3	3	4.17	0	1.93E+04		(R)IIDVVYN	(R)I I D\V V\Y N/A|S N/N\E L V R(T)		179.13	573.6388	1718.907	-0.0053	-3.1	4.37	24490	10.56	HUMAN	P62241	40S ribosomal protein S8
23488	dirMS_041712_NAR_20mM_plus.19307.19307.2	2	4.17	0	8.40E+04		(R)ALIAGG	(R)A L|I/A G G G/A/P E I E L A L R(L)		205.1	775.9467	1550.89	-0.0039	-2.5	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
23489	dirMS_041712_NAR_30mM_plus2.19532.19532.2	2	4.17	0	1.80E+05		(K)CALDFF	(K)C A|L|D/F/F R(Q)	C:Carbamidomethylation	155.92	464.7242	928.434	0.0066	7.1	5.84	15387.4	6.92	HUMAN	F5H7V7	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8
23490	dirMS_041712_NAR_30mM_plus2.22058.22058.2	2	4.17	0	1.47E+05		(K)GLSSLLC	(K)G L S/S/L/L/C N F T/K(S)	C:Carbamidomethylation	171.65	620.3199	1239.64	-0.0077	-6.2	8.75	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
23491	dirMS_041712_NAR_30mM_plus2.4868.4868.2	2	4.17	0	5.52E+05		(K)QASEGP	(K)Q A/S/E G P L/K(G)		77.48	415.225	829.441	0.0013	1.6	6	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
23492	dirMS_041712_NAR_30mM_plus2.5503.5503.2	2	4.17	0	6.24E+04		(K)QSQDEP	(K)Q S/Q/D E/P L/R(S)		83.02	486.741	972.475	0.0002	0.2	4.37	33803.8	6.12	HUMAN	B1AKP7	TAR DNA binding protein
23493	dirMS_041712_NAR_50mM_plus2.13294.13294.3	3	4.17	2	3.34E+05		(R)APTVDP	(R)A/P|T V/D P P R T D R I L M K(A)		138.17	570.655	1709.937	0.0137	8	8.79	50456.3	9.91	HUMAN	C9JLZ4	INO80 complex subunit D (Fragment)
23494	dirMS_041712_NAR_50mM_plus2.5411.5411.3	3	4.17	2	3.17E+04		(R)AVEDAK	(R)A V|E D A K G S S S D\S T/A G V/K E(-)		88.8	579.9425	1737.814	-0.0008	-0.4	4.54	67598.2	5.72	HUMAN	Q86TU7	Histone-lysine N-methyltransferase setd3
23495	dirMS_041712_NAR_60mM_plus.14644.14644.3	3	4.17	1	1.87E+05		(R)MLATLF	(R)M/L A T L/F K/D/E R(C)		132.97	408.5544	1223.645	0.0034	2.8	5.82	40481.5	6.48	HUMAN	B3KST5	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis), isoform CRA_a
23496	dirMS_041712_NAR_60mM_plus.14729.14729.3	3	4.17	0	2.65E+05		(R)SQSSHS	(R)S Q S S H S Y D D\S T|L/P L I D R(N)		133.68	640.9681	1920.893	-0.0036	-1.9	4.41	105417.2	6.41	HUMAN	C9JZR2	Catenin delta-1
23497	dirMS_041712_NAR_60mM_plus.16134.16134.3	3	4.17	0	5.46E+05		(R)ETHSAL	(R)E T H S A\L\G|P A/L/Q/A A F K(L)		141.77	514.2744	1540.812	-0.0032	-2.1	6.85	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
23498	dirMS_041712_NAR_120mM_minus.9910.9910.3	3	4.16	1	3.07E+05		(K)AYPLAD	(K)A Y|P L/A\D A H L T K K(L)		108.45	443.2499	1327.737	-0.0017	-1.3	8.55	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
23499	dirMS_041712_NAR_20mM_minus.10171.10172.2	2	4.16	0	1.06E+05		(K)DVNAAI	(K)D V|N|A/A/I A T I K(T)		151.03	508.2919	1015.578	-0.0017	-1.7	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
23500	dirMS_041712_NAR_20mM_minus.13430.13430.2	2	4.16	1	3.04E+05		(R)EPISVKE	(R)E P I/S V/K/E Q H K(R)		185.62	597.8271	1194.648	-0.0008	-0.7	6.85	80179.4	9.28	HUMAN	G3V1N1	NF-kappa-B-repressing factor
23501	dirMS_041712_NAR_20mM_minus.7185.7185.2	2	4.16	0	1.40E+05		(K)VTLTSEE	(K)V/T L/T/S/E E E A/R(L)		119.73	567.785	1134.564	-0.001	-0.9	4.25	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
23502	dirMS_041712_NAR_30mM_minus2.6641.6641.2	2	4.16	0	2.55E+04	K1356k	(K)DTNLAA	(K)D T N/L|A A G I M\Q/k(S)	k:Ubiquitin-K	90.43	638.3134	1161.593	114.0263	-13	5.84	292466.7	7.12	HUMAN	O75417	DNA polymerase theta
23503	dirMS_041712_NAR_40mM_minus2.15093.15093.3	3	4.16	0	3.73E+03		(K)ALIEVLQ	(K)A L\I/E\V L Q/P L I/A E H Q A R(R)		174.07	601.0146	1801.033	-0.0038	-2.1	5.4	53506.8	5.83	HUMAN	P23381	Tryptophan--tRNA ligase, cytoplasmic
23504	dirMS_041712_NAR_50mM_minus2.16584.16584.3	3	4.16	0	1.43E+05		(K)VSHLLGI	(K)V S H L L G I\N|V|T D/F T R(G)		162.17	524.6237	1571.854	0.0025	1.6	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
23505	dirMS_041712_NAR_50mM_minus2.8024.8024.3	3	4.16	1	1.15E+05		(K)TAVCDI	(K)T A|V/C D/I/P P R G L K(M)	C:Carbamidomethylation	112.25	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
23506	dirMS_041712_NAR_60mM_minus.10753.10753.3	3	4.16	0	7.44E+04	N944n	(R)LPnVDL	(R)L P n V D\L/V L S/Q T K(Q)	n:N-acetylglucosamine (N)	119.87	510.6099	1326.763	203.0524	-17.6	5.84	133450	7.41	HUMAN	Q13751	Laminin subunit beta-3
23507	dirMS_041712_NAR_60mM_minus.12098.12098.3	3	4.16	0	3.22E+05		(R)QLYVLG	(R)Q L/Y/V/L/G H E A M K(R)		127.72	430.2305	1288.672	0.0051	4	6.75	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
23508	dirMS_041712_NAR_60mM_minus.15610.15610.3	3	4.16	1	1.83E+05		(R)ASLISAV	(R)A/S L/I/S A V S D K L R(W)		146.25	420.5811	1259.732	-0.003	-2.4	8.79	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
23509	dirMS_041712_NAR_20mM_plus.12539.12539.2	2	4.16	0	8.34E+04		(K)VNQIGS	(K)V N Q\I|G S V/T/E S I Q A C K(L)	C:Carbamidomethylation	158.82	817.4114	1633.821	-0.0059	-3.6	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
23510	dirMS_041712_NAR_20mM_plus.14565.14565.2	2	4.16	0	1.19E+05		(R)LVNWPE	(R)L V|N W P E/H L R(S)		171.48	582.3166	1163.632	-0.0061	-5.2	6.75	25352.6	11.4	HUMAN	K7ENP0	Matrix metalloproteinase-28
23511	dirMS_041712_NAR_20mM_plus.14792.14792.2	2	4.16	0	1.54E+05		(K)VSTLPA	(K)V S/T/L/P A I/T L K(L)		172.87	521.8283	1042.651	-0.0013	-1.3	8.72	20599.3	9.19	HUMAN	H7C1V0	Cathepsin D light chain (Fragment)
23512	dirMS_041712_NAR_20mM_plus.16146.16165.3	3	4.16	1	1.84E+05		(R)RGSALG	(R)R\G S A L G\P D/E A G G E L E R(L)		183.12	538.6101	1613.788	0.028	17.3	4.41	134064.6	5.53	HUMAN	O75145	Liprin-alpha-3
23513	dirMS_041712_NAR_20mM_plus.16407.16407.3	3	4.16	0	4.95E+04		(R)LGGIPV	(R)L G G\I P\V G V\V A/V/E/T R(T)		184.27	456.2733	1366.805	0.0001	0.1	6	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
23514	dirMS_041712_NAR_20mM_plus.18341.18341.2	2	4.16	0	3.92E+04		(K)EGPAVV	(K)E G P A/V|V/G Q F I/Q D/V K(N)		197.32	743.8975	1486.79	-0.0023	-1.5	4.37	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
23515	dirMS_041712_NAR_20mM_plus.18657.18657.2	2	4.16	1	1.45E+04		(R)RRGTLQ	(R)R R G T L/Q S Y L D(-)		199.77	604.8302	1208.638	0.0149	12.3	8.75	48968.1	8.73	HUMAN	P50440	Glycine amidinotransferase, mitochondrial
23516	dirMS_041712_NAR_30mM_plus2.5654.5654.2	2	4.16	0	2.19E+05		(R)ENPVYE	(R)E N|P/V Y E/K(K)		83.65	439.717	878.425	0.0013	1.5	4.53	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
23517	dirMS_041712_NAR_30mM_plus2.5738.5738.2	2	4.16	0	1.58E+05		(K)LDDYQE	(K)L/D/D Y/Q E R(M)		84.77	469.719	938.421	0.0093	9.9	4.03	20235.4	6.77	HUMAN	E9PLA9	Caprin-1 (Fragment)
23518	dirMS_041712_NAR_40mM_plus2.7123.7123.2	2	4.16	0	1.54E+05		(K)TADEFV	(K)T A/D/E F V K(E)		102.42	405.2041	809.404	-0.003	-3.8	4.37	34971.5	9.33	HUMAN	P37058	Testosterone 17-beta-dehydrogenase 3
23519	dirMS_041712_NAR_40mM_plus2.7651.7651.2	2	4.16	0	6.28E+04		(R)AQYDEL	(R)A Q|Y|D E\L A R(K)		105.2	483.2372	965.469	-0.0016	-1.6	4.37	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
23520	dirMS_041712_NAR_40mM_plus2.8151.8151.2	2	4.16	0	1.26E+04		(R)FGSGM	(R)F/G S/G M N M G R(I)		108.37	478.706	956.408	-0.003	-3.1	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
23521	dirMS_041712_NAR_120mM_minus.8537.8537.3	3	4.15	0	1.11E+05	M303m	(R)WLHNE	(R)W/L H N\E D|Q/m/A V/E K(L)	m:Oxidized methionine	100.85	505.9019	1499.695	15.9964	1	4.65	37710.6	6.36	HUMAN	P37837	Transaldolase
23522	dirMS_041712_NAR_20mM_minus.14034.14034.2	2	4.15	0	5.22E+05		(K)SYELPD	(K)S Y E\L/P/D G Q V I T I G N E R(F)		193.55	895.9481	1790.892	-0.003	-1.7	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
23523	dirMS_041712_NAR_20mM_minus.9311.9311.2	2	4.15	0	5.62E+05		(K)YEELQS	(K)Y/E E L Q/S L A/G K(H)		143.23	569.2917	1137.579	-0.0025	-2.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
23524	dirMS_041712_NAR_30mM_minus2.15236.15236.2	2	4.15	1	1.19E+05		(K)QQMIV	(K)Q Q M/I/V R E K(T)		136.7	516.281	1031.567	-0.0119	-11.5	8.75	162210.8	6.8	HUMAN	Q9P241	Probable phospholipid-transporting ATPase VD
23525	dirMS_041712_NAR_30mM_minus2.17125.17125.2	2	4.15	0	1.92E+05		(R)SMVEDI	(R)S M|V/E/D I/T/G\L R(L)		146.77	560.7932	1120.567	0.0124	11.1	4.37	334221.3	6.44	HUMAN	P15924	Desmoplakin
23526	dirMS_041712_NAR_30mM_minus2.9405.9405.2	2	4.15	0	8.14E+04	T44t	(R)IAAQAV	(R)I/A|A/Q A/V t K(N)	t:Phosphorylated T	105.57	441.2255	801.483	79.9608	-6.2	8.75	35021.4	6.1	HUMAN	Q8NHV1	GTPase IMAP family member 7
23527	dirMS_041712_NAR_50mM_minus2.7019.7019.3	3	4.15	0	2.09E+05		(K)VSYGIG	(K)V S|Y/G I/G D E E/H D Q E G R(V)		106.65	564.249	1690.73	0.0021	1.3	4.17	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
23528	dirMS_041712_NAR_60mM_minus.11417.11417.3	3	4.15	1	8.45E+05	M232m	(R)MSmKE	(R)M S m K E V D\E Q|M/L|N V Q N K(N)	m:Oxidized methionine	122.85	647.3011	1923.897	15.9915	-1.8	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
23529	dirMS_041712_NAR_60mM_minus.17387.17387.3	3	4.15	1	1.68E+05		(R)TKEEALE	(R)T K E E A L E\L|I/N/G Y I Q K(I)		157.78	583.6501	1748.943	-0.0071	-4.1	4.78	16245.7	9.47	HUMAN	K7EMU7	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1
23530	dirMS_041712_NAR_60mM_minus.18602.18602.3	3	4.15	1	1.76E+05		(K)VVLDDK	(K)V V/L/D/D K/D Y F\L F R(D)		165.17	510.6099	1529.8	0.0153	10	4.43	5189.9	4.56	HUMAN	B8ZZ54	10 kDa heat shock protein, mitochondrial
23531	dirMS_041712_NAR_120mM_plus.15385.15385.4	4	4.15	1	9.61E+04		(K)LDKAQI	(K)L D K A Q I H D L V\L/V/G G S T R(I)		134.05	456.259	1822.018	-0.004	-2.2	6.75	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
23532	dirMS_041712_NAR_120mM_plus.20456.20456.3	3	4.15	1	7.97E+05		(R)RFDEILE	(R)R F D E I\L E\A\S/D/G I/M/V A R(G)		160.87	607.9762	1821.916	-0.0023	-1.3	4.32	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
23533	dirMS_041712_NAR_120mM_plus.4158.4158.2	2	4.15	1	1.45E+06	M310m	(R)TKTEISE	(R)T K|T/E I/S E m N R(N)	m:Oxidized methionine	69.8	612.7976	1208.594	15.994	-0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
23534	dirMS_041712_NAR_120mM_plus.5325.5325.3	3	4.15	1	4.80E+05		(R)QRQLAA	(R)Q R\Q L|A|A/E E E\R(R)		81.45	410.5424	1229.623	-0.0106	-8.7	4.79	533778	5.74	HUMAN	Q15149	Plectin
23535	dirMS_041712_NAR_120mM_plus.6735.6735.3	3	4.15	1	1.28E+05		(K)LGGVNA	(K)L G G/V N A V G H S R G G E|K(R)		88.5	479.9193	1437.756	-0.0124	-8.6	8.76	151497.3	6.37	HUMAN	Q2M1P5	Kinesin-like protein KIF7
23536	dirMS_041712_NAR_20mM_plus.14042.14042.2	2	4.15	0	1.56E+05	M98m	(R)TLTIVDT	(R)T L T/I/V|D T/G I G m T K(A)	m:Oxidized methionine	167.85	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
23537	dirMS_041712_NAR_20mM_plus.18401.18401.3	3	4.15	0	7.58E+04		(K)ITSEALL	(K)I T S E A L\L/V/T/Q Q L\V K(A)		198.28	514.9762	1542.91	0.0039	2.5	6	50425	5.53	HUMAN	H0YH27	Cullin-associated NEDD8-dissociated protein 1 (Fragment)
23538	dirMS_041712_NAR_20mM_plus.8868.8868.3	3	4.15	0	1.55E+04		(K)GVQQD	(K)G V Q Q D E A L Q L/P/K(D)		131.57	442.5729	1325.706	-0.0018	-1.4	4.37	80761.3	9.07	HUMAN	Q9Y2Z2	Protein MTO1 homolog, mitochondrial
23539	dirMS_041712_NAR_20mM_plus.8964.8964.2	2	4.15	0	1.27E+04		(K)VLEEAN	(K)V L|E/E A/N/Q\A I N P K(L)		132.33	663.353	1325.706	-0.0072	-5.5	4.53	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17

23540	dirMS_041712_NAR_30mM_plus2.18490.18490.2	2	4.15	0	8.06E+05		(K)QLLLQL	(K)Q\L\L|L|Q/L\N Q Q/R(T)		150.85	627.3688	1253.732	-0.0021	-1.7	9.75	67181.8	5.96	HUMAN	Q96JB3	Hypermethylated in cancer 2 protein
23541	dirMS_041712_NAR_30mM_plus2.20426.20426.2	2	4.15	0	2.38E+04		(R)TVQSLEI	(R)T V/Q S L|E/I D L D S M/R(N)		161.05	753.8768	1506.747	-0.0005	-0.3	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
23542	dirMS_041712_NAR_30mM_plus2.21452.21452.2	2	4.15	0	5.24E+05		(K)STLINTLI	(K)S T/L/I/N T L/F K(S)		166.65	518.799	1036.604	-0.013	-12.5	8.47	18010.4	9.42	HUMAN	K7EIE4	Septin-9 (Fragment)
23543	dirMS_041712_NAR_30mM_plus2.9435.9435.2	2	4.15	0	4.35E+05		(K)ATFDAIS	(K)A T/F/D A I/S K(T)		103.23	426.7266	852.446	-0.0002	-0.3	5.88	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
23544	dirMS_041712_NAR_40mM_plus2.6157.6157.2	2	4.15	0	1.40E+04		(R)NMGYV	(R)N/M|G/Y V/Q\Q R(R)		95	498.2392	995.473	-0.0016	-1.6	8.75	28637.7	6.66	HUMAN	B4DDM6	Mitotic checkpoint protein BUB3
23545	dirMS_041712_NAR_60mM_plus.10100.10100.2	2	4.15	0	2.03E+06		(K)GIVEFSG	(K)G I/V/E/F/S G K P A A R(K)		111.3	616.3425	1231.679	-0.0016	-1.3	8.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
23546	dirMS_041712_NAR_60mM_plus.11886.11886.3	3	4.15	1	7.07E+05	M144m S1	(R)SmDSAE	(R)S m/D/S A E K I M I Y s I K(E)	m:Oxidized methionine s:N-a	119.38	612.284	1615.807	219.0305	-23.9	5.79	44870.3	9.02	HUMAN	Q6ZR37	Pleckstrin homology domain-containing family G member 7
23547	dirMS_041712_NAR_60mM_plus.5844.5844.3	3	4.15	0	1.32E+05	M110m	(K)LmELHG	(K)L/m/E L H G E G S\S/S G K(A)	m:Oxidized methionine	88.53	449.8794	1331.626	15.9977	2	5.4	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
23548	dirMS_041712_NAR_120mM_minus.6808.6808.2	2	4.14	1	1.62E+05		(K)VQVEYK	(K)V Q/V|E/Y/K/G E\T K(S)		91.35	590.8128	1180.621	-0.0025	-2.1	6.11	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
23549	dirMS_041712_NAR_30mM_minus2.12300.12300.2	2	4.14	0	3.54E+05		(K)DISLSDY	(K)D I|S/L/S D Y K(G)		120.35	470.7357	940.462	0.0019	2	4.21	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
23550	dirMS_041712_NAR_30mM_minus2.12366.12366.2	2	4.14	0	9.20E+04		(K)YALSVG	(K)Y/A/L/S/V G Y/R(H)		121.55	464.7493	928.489	0.0026	2.8	8.59	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
23551	dirMS_041712_NAR_30mM_minus2.12566.12566.2	2	4.14	0	5.44E+05	M405m	(K)FDLmYA	(K)F/D/L\m Y A/K(R)	m:Oxidized methionine	122.48	452.2186	887.433	15.9968	2.1	5.83	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
23552	dirMS_041712_NAR_30mM_minus2.6191.6191.2	2	4.14	0	2.84E+05		(K)TSEVNC	(K)T\S/E|V/N C Y R(C)	C:Carbamidomethylation	88	514.726	1028.447	-0.0018	-1.8	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
23553	dirMS_041712_NAR_30mM_minus2.7258.7258.2	2	4.14	0	1.16E+05		(K)MQAVQ	(K)M Q|A\V/Q E A T R(L)		94	517.257	1033.509	-0.0028	-2.7	5.75	533778	5.74	HUMAN	Q15149	Plectin
23554	dirMS_041712_NAR_40mM_minus2.8283.8283.3	3	4.14	1	4.45E+04		(R)VGLQAC	(R)V G L Q\A Q\P V/P D E I V K K(I)		129.47	540.9825	1620.932	0.001	0.6	6.04	112066.5	5.59	HUMAN	B1AQT2	Ankyrin 3, node of Ranvier (Ankyrin G)
23555	dirMS_041712_NAR_50mM_minus2.12804.12804.3	3	4.14	0	1.89E+05		(R)LVVVLC	(R)L V/V/V/L/C N L K P Q K(M)	C:Carbamidomethylation	140.37	470.9508	1410.85	-0.0123	-8.7	10	59484.7	6.61	HUMAN	P54577	Tyrosine--tRNA ligase, cytoplasmic
23556	dirMS_041712_NAR_50mM_minus2.9580.9580.3	3	4.14	0	2.43E+05		(K)TSEVDL	(K)T/S E/V D L A K/P L V/K(F)		123.15	433.9205	1299.752	-0.0049	-3.8	5.73	17178.3	5.63	HUMAN	C9IZF9	Programmed cell death 6-interacting protein (Fragment)
23557	dirMS_041712_NAR_60mM_minus.10818.10818.3	3	4.14	1	3.89E+05		(K)TAVCDIF	(K)T A V/C D I/P/P R G L K(M)	C:Carbamidomethylation	119.88	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
23558	dirMS_041712_NAR_120mM_plus.5632.5632.3	3	4.14	1	2.35E+05	M1529m T	(K)EmEPKS	(K)E m E/P K S H H t L K(I)	m:Oxidized methionine t:Pho	82.2	478.2139	1336.668	95.9594	-1.3	7.02	291223.6	5.75	HUMAN	J3KNF5	Centrosomal protein of 290 kDa
23559	dirMS_041712_NAR_120mM_plus.9491.9491.3	3	4.14	1	6.95E+05		(R)RMGESI	(R)R M\G E\S\D\D S|I/L/R(L)		103.37	426.8756	1278.611	0.0016	1.2	4.56	9225.3	9.16	HUMAN	P63220	40S ribosomal protein S21
23560	dirMS_041712_NAR_120mM_plus.9866.9866.4	4	4.14	1	3.56E+06		(K)DTGKTP	(K)D T\G K T P V E/P/E/V\A I H R(I)		104.8	412.9719	1648.865	0.0005	0.3	5.45	5429.1	9.6	HUMAN	E5RIP1	40S ribosomal protein S20
23561	dirMS_041712_NAR_20mM_plus.13795.13795.2	2	4.14	0	4.19E+04		(K)IVLTNPV	(K)I V|L\T N|P V C/T/E V G E K(I)	C:Carbamidomethylation	167.07	779.9082	1558.815	-0.0054	-3.5	4.53	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3
23562	dirMS_041712_NAR_20mM_plus.13844.13844.2	2	4.14	0	2.33E+05	M98m	(R)TLTIVDT	(R)T L/T\I/V/D T G I G m T K(A)	m:Oxidized methionine	167.38	683.3671	1349.735	15.9924	-1.8	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
23563	dirMS_041712_NAR_20mM_plus.14596.14596.2	2	4.14	0	9.93E+04		(K)FLDGIYV	(K)F/L/D G\I/Y V S E K(G)		173.5	585.8066	1170.604	0.0018	1.5	4.37	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
23564	dirMS_041712_NAR_20mM_plus.17254.17254.2	2	4.14	0	2.51E+05	K44k	(K)FILkVLDI	(K)F I|L/k V L D/R(H)	k:Ubiquitin-K	189.97	559.3342	1003.63	114.0312	-10.5	8.75	43921.6	7.89	HUMAN	Q969G2	LIM/homeobox protein Lhx4
23565	dirMS_041712_NAR_30mM_plus2.4070.4070.2	2	4.14	0	8.47E+05	M299m M	(K)NmmAA	(K)N m/m A/A C D|P\R(H)	C:Carbamidomethylation m:Oxid	68.23	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
23566	dirMS_041712_NAR_30mM_plus2.6125.6125.2	2	4.14	0	9.08E+04		(K)SNALSAI	(K)S N/A L S A M E G K(F)		86.25	504.2397	1007.483	-0.0105	-10.4	5.72	41431.4	8.98	HUMAN	H3BPF5	Protein fantom (Fragment)
23567	dirMS_041712_NAR_30mM_plus2.6572.6572.2	2	4.14	0	2.06E+05		(K)ALDEME	(K)A/L/D E/M/E K(Q)		89.07	418.1994	835.387	0.0049	5.9	4.14	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
23568	dirMS_041712_NAR_40mM_plus2.7791.7791.2	2	4.14	0	1.19E+05	K151k	(K)SGYLAGI	(K)S G/Y|L/A/G D k(L)	k:Ubiquitin-K	106.37	462.7191	810.399	114.0317	-12.1	5.55	67933	6.08	HUMAN	P26038	Moesin
23569	dirMS_041712_NAR_50mM_plus2.11490.11490.3	3	4.14	1	2.53E+05		(R)ICCDLD	(R)I/C/C D L D/V/L A S K K(V)	C:Carbamidomethylation	128.2	474.5801	1421.713	0.013	9.2	5.96	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
23570	dirMS_041712_NAR_50mM_plus2.7598.7598.3	3	4.14	1	5.04E+04		(R)DLSTPGI	(R)D L S/T/P/G L E K D S G G/K(T)		105.95	468.5732	1403.701	0.0038	2.7	4.56	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
23571	dirMS_041712_NAR_60mM_plus.6476.6476.3	3	4.14	0	3.41E+05	M445m	(K)GPTSQE	(K)G P\T S/Q E S Q/L N A m/K(R)	m:Oxidized methionine	92.13	469.5621	1390.663	16.0086	9.8	6	49263.1	9.93	HUMAN	Q96CB8	Integrator complex subunit 12
23572	dirMS_041712_NAR_20mM_minus.11324.11324.2	2	4.13	0	2.06E+05		(K)LSELEAA	(K)L S\E/L E A/A|L Q R(A)		159.77	565.3134	1129.621	-0.0016	-1.5	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
23573	dirMS_041712_NAR_20mM_minus.9770.9770.2	2	4.13	0	3.36E+05		(K)IGGIGTV	(K)I G G\I/G/T V\P V G/R(V)		147.47	513.3075	1025.61	-0.0025	-2.4	9.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
23574	dirMS_041712_NAR_30mM_minus2.11483.11483.2	2	4.13	0	1.00E+05		(K)VVLQELI	(K)V V/L/Q E L R(R)		116.57	428.7653	856.525	-0.0018	-2	5.97	6608.5	9.69	HUMAN	E5RGE2	Ubiquitin-conjugating enzyme E2 variant 2
23575	dirMS_041712_NAR_30mM_minus2.6948.6948.2	2	4.13	0	3.65E+05		(R)STFSTNY	(R)S T|F|S T N Y/R(S)		91.98	488.2317	975.453	0.0031	3.2	8.46	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
23576	dirMS_041712_NAR_40mM_minus2.10451.10451.2	2	4.13	0	7.33E+05		(R)VAPEEH	(R)V A/P E E/H\P V/L L T E\A/P L N\P K(A)		144	977.5343	1954.064	-0.0031	-1.6	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
23577	dirMS_041712_NAR_50mM_minus2.12590.12590.3	3	4.13	2	1.02E+05	S917s M92	(K)IKsLVALI	(K)I\K/s/L V A L L V E T Q/m K/K(L)	s:N-acetylglucosamine (S) m:	139.55	640.7016	1701.034	219.056	-9.5	9.7	136581	5.5	HUMAN	F8VXC8	SWI/SNF complex subunit SMARCC2
23578	dirMS_041712_NAR_50mM_minus2.15855.15855.3	3	4.13	1	2.17E+05	M407m K4	(R)TGLFTPI	(R)T G/L/F/T P D m A F E T I\V K k(Q)	m:Oxidized methionine k:Ub	158.43	643.3412	1797.946	130.0635	13.3	5.73	97805.9	6.73	HUMAN	Q05193	Dynamin-1
23579	dirMS_041712_NAR_50mM_minus2.16132.16132.3	3	4.13	0	1.59E+05	M138m	(K)NGGLGH	(K)N G G L G H/m N I/A/L/L/S D L/T K(Q)	m:Oxidized methionine	160.02	590.6502	1753.927	16.0095	8.3	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
23580	dirMS_041712_NAR_60mM_minus.10999.10999.3	3	4.13	0	2.65E+05		(R)ALPESLG	(R)A L|P E S L G Q/H A L R(S)		121.37	431.2376	1291.712	-0.0135	-10.4	6.79	31463.6	5.53	HUMAN	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1
23581	dirMS_041712_NAR_60mM_minus.13442.13442.3	3	4.13	1	5.12E+05		(R)KLVIIESI	(R)K\L V\I\I\E/S D/L E|R(A)		135.33	438.9202	1314.763	-0.0167	-12.7	4.68	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
23582	dirMS_041712_NAR_60mM_minus.19309.19309.3	3	4.13	0	4.54E+05		(R)THNGES	(R)T/H N G E S V S Y L/F S/H\V/P L(-)		171.93	596.2923	1786.876	-0.0135	-7.6	5.92	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
23583	dirMS_041712_NAR_60mM_minus.5538.5538.3	3	4.13	1	3.61E+07		(K)DSYVGD	(K)D S Y/V/G D/E/A Q S K R(G)		87.62	452.2129	1354.623	0.0008	0.6	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
23584	dirMS_041712_NAR_120mM_plus.10078.10078.3	3	4.13	1	2.66E+05		(K)LKHNAD	(K)L K H/N A D A|L/S D R(F)		105.75	413.8849	1239.644	-0.0039	-3.1	6.75	127856.3	9.42	HUMAN	Q9UHB7	AF4/FMR2 family member 4
23585	dirMS_041712_NAR_20mM_plus.15010.15010.2	2	4.13	0	1.29E+05	S195s M20	(R)EIIsAAEI	(R)E I I s A A|E H/F S m I R(A)	s:Phosphorylated S m:Oxidiz	174.58	800.3664	1503.762	95.9631	1.2	5.4	55085.2	7.09	HUMAN	A1L020	RNA-binding protein MEX3A
23586	dirMS_041712_NAR_20mM_plus.16667.16667.2	2	4.13	0	2.56E+04		(R)LIDFLEC	(R)L I/D\F L E C/G K(T)	C:Carbamidomethylation	185.57	547.7827	1094.555	0.0031	2.8	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
23587	dirMS_041712_NAR_20mM_plus.5864.5864.2	2	4.13	0	7.42E+04	M283m	(R)DYDDm	(R)D Y|D D m S P R(R)	m:Oxidized methionine	97.63	507.6952	998.388	15.9947	-0.2	3.93	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
23588	dirMS_041712_NAR_20mM_plus.9806.9806.2	2	4.13	0	7.68E+04		(R)TDYNAS	(R)T D/Y N A/S|V S V/P D S S G P E R(I)		138.97	890.9015	1780.798	-0.0027	-1.5	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
23589	dirMS_041712_NAR_30mM_plus2.18951.18951.2	2	4.13	0	4.17E+05		(K)ALQFLEE	(K)A L|Q/F L E E V K(V)		152.42	538.8034	1076.599	0.0009	0.8	4.53	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
23590	dirMS_041712_NAR_40mM_plus2.9710.9710.2	2	4.13	0	1.28E+05	M14m	(R)NTFmVS	(R)N T/F|m/V S K(R)	m:Oxidized methionine	120.53	421.7119	826.413	16.0038	10.5	8.75	13026	9.97	HUMAN	A8MXJ9	Protein tweety homolog 3 (Fragment)
23591	dirMS_041712_NAR_50mM_plus2.6924.6924.3	3	4.13	1	1.73E+05		(R)EGVLTG	(R)E G V L/T/G S P E Q K E E A A K(A)		100.9	558.2837	1672.839	-0.0023	-1.4	4.49	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
23592	dirMS_041712_NAR_50mM_plus2.7032.7032.3	3	4.13	1	6.00E+05		(K)IVADKD	(K)I/V|A D\K D Y S V/T A/N S K(I)		101.95	504.2628	1510.775	-0.0009	-0.6	5.96	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
23593	dirMS_041712_NAR_50mM_plus2.8256.8256.3	3	4.13	0	3.07E+04	T88t	(K)TPQNQt	(K)T P/Q N Q t I/H L S K(S)	t:Phosphorylated T	110.1	449.5534	1266.68	79.9656	-0.6	8.44	23497.1	9.8	HUMAN	F5GZE4	Protein FAM216A
23594	dirMS_041712_NAR_120mM_minus.7090.7090.3	3	4.12	1	1.81E+05		(K)EAAEVL	(K)E/A\A/E V L/Q N N R R(L)		92.83	433.8957	1299.676	-0.0038	-3	6.24	21184.9	7.82	HUMAN	P61081	NEDD8-conjugating enzyme Ubc12
23595	dirMS_041712_NAR_30mM_minus2.12394.12394.2	2	4.12	0	5.81E+04		(R)GVVGPE	(R)G V/V/G|P E L Y G R(L)		121.18	523.7834	1046.563	-0.0034	-3.2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
23596	dirMS_041712_NAR_30mM_minus2.13959.13959.2	2	4.12	0	4.88E+04		(K)EYTLDV	(K)E Y/T L/D/V/Y R(L)		128.87	529.7691	1058.515	0.0156	14.8	4.37	59484.7	6.61	HUMAN	P54577	Tyrosine--tRNA ligase, cytoplasmic
23597	dirMS_041712_NAR_40mM_minus2.13189.13189.2	2	4.12	0	9.64E+04		(K)SYELPD	(K)S Y\E/L|P D G Q V\I/T I/G N E R(F)		161.5	895.9483	1790.892	-0.0026	-1.4	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
23598	dirMS_041712_NAR_50mM_minus2.14197.14197.3	3	4.12	1	2.08E+05	M2409m S	(R)DLEILSIn	(R)D L/E\I L S I m L Y S/s K K(E)	m:Oxidized methionine s:N-a	149.15	620.3204	1639.898	219.0491	-13.5	6.07	335976	5.62	HUMAN	O43149	Zinc finger ZZ-type and EF-hand domain-containing protein 1
23599	dirMS_041712_NAR_50mM_minus2.14219.14219.3	3	4.12	1	1.31E+05		(R)QFVPIK	(R)Q F V P I K|V/E Q I/E/A/G T P G R(L)		148.68	623.6775	1869.023	-0.0049	-2.6	6.14	55287.2	6.08	HUMAN	B2R5P6	Thioredoxin reductase 1, cytoplasmic
23600	dirMS_041712_NAR_50mM_minus2.6198.6198.3	3	4.12	0	4.44E+05	M434m	(R)LESGmC	(R)L E|S G m Q N/M S I/H/T K(T)	m:Oxidized methionine	97.77	497.9018	1475.698	15.9927	-1.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
23601	dirMS_041712_NAR_60mM_minus.11474.11474.3	3	4.12	0	2.59E+05	T179t	(R)IMDLPtL	(R)I M\D L\P/t/L L R(H)	t:N-acetylglucosamine (T)	124.48	425.5679	1071.623	203.0661	-10.4	5.84	30270.6	5.33	HUMAN	Q96K19	E3 ubiquitin-protein ligase RNF170
23602	dirMS_041712_NAR_60mM_minus.17899.17899.3	3	4.12	0	2.52E+05		(R)VLDPFTI	(R)V/L D/P/F T I K P L D R(K)		161.27	471.9394	1413.81	-0.0064	-4.5	5.93	63448.4	7.29	HUMAN	B4E022	Transketolase
23603	dirMS_041712_NAR_20mM_plus.12893.12893.2	2	4.12	0	6.06E+04		(R)LLAEPVI	(R)L L/A E/P V/P G I K(A)		161.5	518.823	1036.64	-0.0014	-1.3	6	12039.9	9.34	HUMAN	F8VSD4	Ubiquitin-conjugating enzyme E2 N
23604	dirMS_041712_NAR_30mM_plus2.10826.10826.2	2	4.12	0	4.56E+05	S247s	(R)EGSSsSN	(R)E G/S/S s S N/W(-)	s:N-acetylglucosamine (S)	109.65	528.7093	853.332	203.0791	-0.3	4	27838.7	9.05	HUMAN	H0Y6P4	Acyl-coenzyme A thioesterase THEM5 (Fragment)
23605	dirMS_041712_NAR_40mM_plus2.11327.11327.2	2	4.12	0	1.90E+04		(R)AFFSEVE	(R)A F/F/S E V E R(R)		132.42	492.7445	984.479	0.0032	3.3	4.53	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
23606	dirMS_041712_NAR_40mM_plus2.13071.13071.2	2	4.12	0	1.70E+05		(R)VAPEEH	(R)V/A/P E/E H P V/L L T E A/P L N P K(A)		143.78	977.5344	1954.064	-0.0029	-1.5	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
23607	dirMS_041712_NAR_40mM_plus2.6076.6076.2	2	4.12	0	6.05E+03		(R)ENPYYD	(R)E N/P/Y/Y/D/S R(V)		94.42	522.2253	1043.443	0.0005	0.4	4.37	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
23608	dirMS_041712_NAR_40mM_plus2.9549.9549.2	2	4.12	0	1.08E+05		(R)RPCTLSE	(R)R P C T L S E|L\E(-)	C:Carbamidomethylation	120.05	552.7699	1104.535	-0.0029	-2.6	4.85	61333.4	5.7	HUMAN	P13674	Prolyl 4-hydroxylase subunit alpha-1
23609	dirMS_041712_NAR_50mM_plus2.10534.10534.3	3	4.12	0	5.29E+04		(R)LQAQQI	(R)L Q|A/Q Q D A/V/N I/V C/H S K(T)	C:Carbamidomethylation	123.17	570.9571	1710.859	-0.0024	-1.4	6.74	21953.7	6.6	HUMAN	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
23610	dirMS_041712_NAR_50mM_plus2.12767.12767.3	3	4.12	0	4.50E+05		(K)YYVTIID	(K)Y Y/V T I I/D A/P/G H R(D)		135.38	468.9142	1404.727	0.001	0.7	6.74	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
23611	dirMS_041712_NAR_50mM_plus2.21569.21569.3	3	4.12	1	1.88E+05		(K)LKVNFLI	(K)L K V N F L/P E I I T L S K(E)		184.27	539.0011	1614.983	0.0058	3.6	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
23612	dirMS_041712_NAR_60mM_plus.19098.19098.3	3	4.12	0	7.89E+03		(K)HSMNPI	(K)H S M N P F C E I/A/V/E/E A V R(L)	C:Carbamidomethylation	158.15	630.2949	1888.868	0.0021	1.1	4.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
23613	dirMS_041712_NAR_60mM_plus.20605.20605.3	3	4.12	1	2.02E+05	M267m K2	(K)ITSKAAF	(K)I T S K A A F|I D H/F N V/m I\k(K)	m:Oxidized methionine k:Ub	168.03	655.6825	1834.988	130.0445	3.4	8.6	186240.8	8.58	HUMAN	Q8IVG5	Sterile alpha motif domain-containing protein 9-like
23614	dirMS_041712_NAR_60mM_plus.9722.9722.3	3	4.12	1	1.35E+06		(K)CAADLG	(K)C/A/A D L/G L/N K G Y R(M)	C:Carbamidomethylation	109.25	446.56	1337.663	0.0024	1.8	8.59	13915.8	6.43	HUMAN	P49773	Histidine triad nucleotide-binding protein 1
23615	dirMS_041712_NAR_120mM_minus.10407.10407.3	3	4.11	1	5.43E+05	M142m	(K)VKEGMI	(K)V K E G M N\I/V E A/m E R(F)	m:Oxidized methionine	110.18	507.9186	1505.745	15.9962	0.8	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
23616	dirMS_041712_NAR_120mM_minus.11723.11723.4	4	4.11	1	4.65E+05		(K)AAQASD	(K)A A Q/A/S/D/L E K I H L D E K(S)		117.83	417.7202	1667.86	-0.0009	-0.6	4.75	37710.6	6.36	HUMAN	P37837	Transaldolase
23617	dirMS_041712_NAR_120mM_minus.20862.20862.4	4	4.11	1	3.06E+05		(K)SKGLAPI	(K)S K G L A P D|L/P E D L Y H L I K(K)		174.07	478.0167	1909.043	0.002	1.1	5.36	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
23618	dirMS_041712_NAR_20mM_minus.13487.13487.3	3	4.11	0	8.09E+05	M221m	(R)ALTVPEI	(R)A L/T V/P E L T Q Q m F D A K(N)	m:Oxidized methionine	186.23	569.9577	1691.867	15.9913	-2.1	4.37	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
23619	dirMS_041712_NAR_20mM_minus.8519.8519.2	2	4.11	0	1.29E+04		(R)YEIEETE	(R)Y E|I/E/E/T E T V T K(S)		134.38	671.3246	1341.642	-0.0001	-0.1	4.09	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
23620	dirMS_041712_NAR_30mM_minus2.17761.17761.2	2	4.11	0	1.53E+05		(K)GFLIDGY	(K)G F|L/I/D G Y P/R(E)		150.42	519.2752	1037.542	0.0017	1.6	5.83	15567.5	8.13	HUMAN	H0Y4J6	Adenylate kinase isoenzyme 1 (Fragment)
23621	dirMS_041712_NAR_50mM_minus2.13247.13247.3	3	4.11	1	1.62E+05		(R)NVIFQP	(R)N V/I F Q P/V/A E L K/K(Q)		143.08	462.6086	1385.815	-0.0039	-2.8	8.59	23167	8.94	HUMAN	B1APP8	6-phosphofructokinase type C
23622	dirMS_041712_NAR_50mM_minus2.17427.17427.3	3	4.11	0	1.23E+05		(K)VHLVGII	(K)V H L V G\I D/I|F T/G K(K)		167.63	433.5856	1298.747	-0.0045	-3.4	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
23623	dirMS_041712_NAR_60mM_minus.12109.12109.3	3	4.11	1	3.03E+06	M72m	(R)TEmENE	(R)T\E/m/E N E F/V L I K K(D)	m:Oxidized methionine	126.87	499.5941	1480.772	15.9962	0.8	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
23624	dirMS_041712_NAR_60mM_minus.19446.19446.3	3	4.11	1	6.86E+05		(K)LASDLLE	(K)L/A/S D/L L E W I R R(T)		172.9	457.9288	1371.774	-0.0025	-1.8	6.07	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
23625	dirMS_041712_NAR_120mM_plus.20193.20193.4	4	4.11	1	4.98E+04		(R)AQKEGS	(R)A Q K E G S I A M/Q S S A T/H/L T S K(R)		158.85	494.4975	1974.991	-0.0231	-11.7	8.64	112563.1	6.05	HUMAN	E9PKB1	Coiled-coil domain-containing protein 15
23626	dirMS_041712_NAR_30mM_plus2.5044.5044.2	2	4.11	0	8.00E+04		(K)NASYYG	(K)N A/S/Y Y G N R(A)		78.92	472.7087	944.422	-0.0119	-12.6	8.59	30468.2	9.09	HUMAN	K7EIH8	DnaJ homolog subfamily C member 7 (Fragment)
23627	dirMS_041712_NAR_40mM_plus2.11359.11359.2	2	4.11	0	4.95E+04	M320m	(K)YmACCL	(K)Y m|A|C C L/L Y R(G)	C:Carbamidomethylation m:Oxid	133.18	633.2788	1249.553	15.9977	2.2	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
23628	dirMS_041712_NAR_40mM_plus2.13328.13328.3	3	4.11	0	3.78E+04		(R)LDNVPH	(R)L/D N V|P H T P S S Y/I/E T L/P K(A)		144.72	637.673	1910.986	0.0186	9.7	5.32	18209.2	5.03	HUMAN	A8MXH2	Nucleosome assembly protein 1-like 4 (Fragment)
23629	dirMS_041712_NAR_40mM_plus2.14633.14633.3	3	4.11	1	1.08E+05		(R)LPAAGV	(R)L P A A/G/V G D\M V M/A/T V K K(G)		153.2	529.9585	1587.86	0.0013	0.8	8.59	12270.4	11.49	HUMAN	B9ZVP7	60S ribosomal protein L23
23630	dirMS_041712_NAR_40mM_plus2.17539.17539.3	3	4.11	0	2.47E+04		(R)GTEDITS	(R)G T/E/D I/T/S P H G I P L D\L L D R(V)		169.42	650.3372	1948.997	-0.0004	-0.2	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
23631	dirMS_041712_NAR_40mM_plus2.17819.17819.3	3	4.11	0	1.60E+05		(K)LAKPLSS	(K)L A\K P L S S L|T/P L I M A A/K(E)		171.67	552.0052	1653.997	0.0039	2.3	10	24711.4	5.19	HUMAN	H7C1X3	PAK-2p34 (Fragment)
23632	dirMS_041712_NAR_40mM_plus2.8080.8080.2	2	4.11	0	2.00E+05		(K)LAADDF	(K)L/A/A/D D/F/R(T)		107.08	404.2049	807.399	0.003	3.7	4.21	48845.9	4.72	HUMAN	C4AM86	Keratin, type I cuticular Ha5
23633	dirMS_041712_NAR_40mM_plus2.8377.8377.2	2	4.11	0	2.86E+05		(R)FGSGMI	(R)F/G|S G M N M/G R(I)		109.45	478.706	956.408	-0.003	-3.1	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
23634	dirMS_041712_NAR_50mM_plus2.11507.11507.3	3	4.11	0	4.19E+05		(K)GFVEFA	(K)G F|V/E F/A A K P P A\R(K)		127.83	430.5716	1289.7	0.0002	0.1	8.75	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
23635	dirMS_041712_NAR_50mM_plus2.18974.18974.3	3	4.11	0	4.02E+05		(R)AGLGSG	(R)A G L|G/S G L S\L S G L V H\P E L S\R(S)		167.18	617.3412	1850.013	-0.004	-2.2	6.79	73325.2	9.19	HUMAN	F5H2A9	Very long-chain-specific acyl-CoA dehydrogenase, mitochondrial
23636	dirMS_041712_NAR_50mM_plus2.21979.21979.3	3	4.11	2	3.47E+05		(K)SADTLW	(K)S A|D/T L/W D I Q\K D\L K D L(-)		187.05	587.6346	1760.907	-0.0173	-9.8	4.14	36923.1	5.71	HUMAN	P07195	L-lactate dehydrogenase B chain
23637	dirMS_041712_NAR_50mM_plus2.5431.5431.3	3	4.11	1	5.11E+04		(R)DASTLQ	(R)D A|S T/L Q S Q/K/A E G T G D/A K(-)		89.17	569.61	1706.819	-0.0037	-2.2	4.56	9538.7	10.48	HUMAN	O00479	High mobility group nucleosome-binding domain-containing protein 4
23638	dirMS_041712_NAR_60mM_plus.17530.17530.3	3	4.11	1	8.46E+05		(R)DKLNNL	(R)D K L N\N\L/V/L F D K(A)		148.4	440.2499	1318.737	-0.0014	-1	5.96	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
23639	dirMS_041712_NAR_60mM_plus.8097.8097.3	3	4.11	1	4.67E+05		(R)FEPYANI	(R)F E/P Y A N P T K R(Y)		100.8	408.2176	1222.622	0.0167	13.7	8.59	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
23640	dirMS_041712_NAR_120mM_minus.17022.17022.3	3	4.1	1	5.08E+05		(K)RISEQFT	(K)R I S E\Q\F|T/A M F R(R)		147.73	462.5714	1385.699	0.0002	0.2	9.6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
23641	dirMS_041712_NAR_20mM_minus.13562.13562.2	2	4.1	0	1.03E+05		(K)FIIPNVV	(K)F I/I/P N V V K(Y)		186.3	465.294	929.582	-0.0011	-1.2	8.75	17529.3	9.3	HUMAN	F5GXY2	L-lactate dehydrogenase A chain (Fragment)
23642	dirMS_041712_NAR_40mM_minus2.14021.14021.3	3	4.1	1	1.12E+05	S799s	(R)SIDGSIV	(R)S I/D G S I/V/L P L A R G s P K(A)	s:N-acetylglucosamine (S)	166.87	605.0051	1609.927	203.0736	-3.2	8.46	134607	9.04	HUMAN	Q9HD20	Probable cation-transporting ATPase 13A1
23643	dirMS_041712_NAR_40mM_minus2.14654.14654.3	3	4.1	0	1.65E+05	M159m	(R)SVAAIHI	(R)S V|A/A/I H P S L E|I P m L I P K(E)	m:Oxidized methionine	171.3	611.3477	1816.04	15.9884	-3.5	6.47	31606.3	6.72	HUMAN	B4E329	Phosphoribosyl pyrophosphate synthase-associated protein 2
23644	dirMS_041712_NAR_40mM_minus2.8223.8223.3	3	4.1	1	3.04E+05	M119m	(R)SNTPILV	(R)S N|T/P I L V D/G K D V m/P E V N K(V)	m:Oxidized methionine	128.4	658.0032	1956.011	15.9844	-5.3	4.56	18405.7	9.81	HUMAN	K7EP41	Glucose-6-phosphate isomerase (Fragment)
23645	dirMS_041712_NAR_50mM_minus2.10107.10107.3	3	4.1	1	9.66E+04		(K)NVDILKI	(K)N V/D I/L K D/P E/T V K(Q)		125.43	457.5912	1370.753	0.0065	4.7	4.56	124524.8	5.71	HUMAN	O14980	Exportin-1
23646	dirMS_041712_NAR_50mM_minus2.13646.13646.3	3	4.1	0	5.43E+05		(K)LQMEAI	(K)L Q|M E A P H I/I V G T/P G R(V)		145.65	540.2947	1618.873	-0.0038	-2.4	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
23647	dirMS_041712_NAR_60mM_minus.17266.17266.2	2	4.1	1	1.88E+05		(R)KAPSDL	(R)K A|P S D\L Y Q I\I L K(A)		156.33	694.9105	1388.815	-0.0011	-0.8	8.5	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
23648	dirMS_041712_NAR_60mM_minus.17588.17588.3	3	4.1	1	1.01E+04		(K)RALIAG	(K)R A L I A\G G G\A|P\E I E L A/L R(L)		158.83	569.6652	1706.991	-0.0101	-5.9	6.14	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta

23649	dirMS_041712_NAR_60mM_minus.7893.7893.3	3	4.1	1	1.77E+05		(K)EASKQA	(K)E A S K Q\A D V/N/L/V N A K(L)		104.15	496.2639	1486.786	-0.0089	-6	6.17	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
23650	dirMS_041712_NAR_120mM_plus.10113.10113.3	3	4.1	1	3.34E+05		(R)LKNTLT	(R)L K N T L T/Q/T/T/E N L R(R)		105.95	511.2848	1531.844	-0.004	-2.6	8.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
23651	dirMS_041712_NAR_120mM_plus.14881.14881.4	4	4.1	1	6.41E+04	M251m	(K)FSHEEIA	(K)F S H E E I/A/m/A T/V T A L R R(T)	m:Oxidized methionine	131.28	462.7409	1831.948	15.9934	-0.8	6.76	39795.8	9.08	HUMAN	H3BQN4	Fructose-bisphosphate aldolase
23652	dirMS_041712_NAR_120mM_plus.5244.5244.3	3	4.1	0	3.09E+04	S2128s	(R)SQEPIYs	(R)S Q\E/P I Y s E E A S/G P R(S)	s:N-acetylglucosamine (S)	81.78	584.9277	1549.713	203.0557	-13.5	4.25	382015.9	5.85	HUMAN	Q5T011	Protein SZT2
23653	dirMS_041712_NAR_120mM_plus.6971.6971.3	3	4.1	0	7.24E+03	N176n	(K)MEASSS	(K)M/E A S S S/G/I T n G K(T)	n:N-acetylglucosamine (N)	89.1	462.218	1181.547	203.0928	9.7	5.75	39506.6	6.73	HUMAN	F5H834	Anoctamin-4
23654	dirMS_041712_NAR_120mM_plus.7796.7796.3	3	4.1	1	2.65E+05		(R)VAFERG	(R)V/A/F/E/R\G E E/P G K(S)		94.43	406.877	1218.611	0.0051	4.2	4.79	142268.2	6.41	HUMAN	Q08211	ATP-dependent RNA helicase A
23655	dirMS_041712_NAR_120mM_plus.8801.8801.2	2	4.1	0	5.19E+05		(R)NGVMP	(R)N G\V|M/P S H F S R(G)		99.72	566.274	1131.536	0.0043	3.8	9.75	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
23656	dirMS_041712_NAR_30mM_plus2.4192.4192.2	2	4.1	0	5.53E+05	M558m	(R)mGANN	(R)m/G A|N N L/E/R(M)	m:Oxidized methionine	69.97	460.7158	904.431	15.9938	-1.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
23657	dirMS_041712_NAR_30mM_plus2.8054.8173.2	2	4.1	0	1.13E+06		(K)ASLENSL	(K)A S|L/E/N S L R(E)		97.35	445.2405	889.474	0	-0.1	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
23658	dirMS_041712_NAR_40mM_plus2.9533.9533.2	2	4.1	1	1.08E+05		(R)ERNTAG	(R)E/R/N T A G S A G|G G K(L)		120.05	552.7699	1104.539	-0.0067	-6.1	8.85	34934.6	5.33	HUMAN	B1ARF3	Inositol polyphosphate-5-phosphatase, 75kDa
23659	dirMS_041712_NAR_50mM_plus2.11108.11108.3	3	4.1	0	2.78E+04	S69s	(K)IQPQEA	(K)I Q|P Q/E A s E E P P/A H K(D)	s:N-acetylglucosamine (S)	126.42	588.6053	1560.765	203.0361	-24.5	4.75	27274.5	4.58	HUMAN	Q8N402	Putative uncharacterized protein LOC388882
23660	dirMS_041712_NAR_50mM_plus2.12988.12988.3	3	4.1	0	4.58E+05		(K)VSHVST	(K)V S H V S T G G G A/S L/E|L/L E G/K(V)		137.07	580.9801	1740.913	0.0131	7.5	5.4	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
23661	dirMS_041712_NAR_50mM_plus2.7514.7514.3	3	4.1	1	3.21E+05		(R)IVEQDT	(R)I V/E Q D T M/P P K G V R(H)		105.43	490.5973	1469.778	-0.0007	-0.5	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
23662	dirMS_041712_NAR_50mM_plus2.8381.8381.3	3	4.1	0	3.33E+04	T406t	(R)IQDAGL	(R)I/Q D/A/G L V L A D t L R(K)	t:Phosphorylated T	110.98	488.9167	1384.78	79.9561	-7	4.21	50763.5	7.88	HUMAN	Q8IWW8	Hydroxyacid-oxoacid transhydrogenase, mitochondrial
23663	dirMS_041712_NAR_60mM_plus.15169.15169.3	3	4.1	0	2.48E+05	M156m	(R)ImNLIC	(R)I/m N L\I\C/D P D L\T K(V)	C:Carbamidomethylation m:Oxid	136.28	483.5686	1432.717	15.9738	-14.6	4.21	24489.1	10.1	HUMAN	F8VVC7	11-cis retinol dehydrogenase
23664	dirMS_041712_NAR_60mM_plus.5215.5215.3	3	4.1	1	1.25E+05	M50m	(K)QmNDE	(K)Q m/N D E K/T A A D/Y K(I)	m:Oxidized methionine	84.57	477.2136	1413.632	15.9948	-0.1	4.56	9786.1	5.52	HUMAN	E9PS38	Protein NEDD8-MDP1
23665	dirMS_041712_NAR_120mM_minus.10633.10633.3	3	4.09	0	5.97E+05		(R)GFCLPP	(R)G F/C L/P/P H C S R(G)	C:Carbamidomethylation	113.28	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
23666	dirMS_041712_NAR_20mM_minus.14105.14105.2	2	4.09	0	2.14E+05		(K)DVDLEF	(K)D V|D L/E/F L A K(M)		193.68	525.278	1049.551	-0.0026	-2.5	4.03	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
23667	dirMS_041712_NAR_20mM_minus.7099.7099.2	2	4.09	0	1.68E+05		(R)AAQVA	(R)A/A/Q\V\A Q D E E I/A R(L)		118.77	650.8255	1300.649	-0.0054	-4.2	4.14	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
23668	dirMS_041712_NAR_30mM_minus2.16666.16666.2	2	4.09	1	1.60E+05		(R)SPTIRD	(R)S P|T/I R D M A I R(C)		143.45	580.3178	1159.625	0.0031	2.7	9.32	204545.1	5.94	HUMAN	Q9Y6D5	Brefeldin A-inhibited guanine nucleotide-exchange protein 2
23669	dirMS_041712_NAR_30mM_minus2.17446.17446.2	2	4.09	0	1.11E+04		(R)EQLAIAE	(R)E Q|L/A I/A E F A R(S)		148.28	574.3084	1147.611	-0.0011	-0.9	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
23670	dirMS_041712_NAR_30mM_minus2.4722.4722.2	2	4.09	1	5.18E+05	M39m	(R)GYmMS	(R)G Y m M S K|Q R(E)	m:Oxidized methionine	77.97	508.732	1000.47	15.9864	-8.3	9.99	29695.2	4.39	HUMAN	B3KR75	Protein FAM134C
23671	dirMS_041712_NAR_30mM_minus2.8129.8129.2	2	4.09	0	5.16E+04		(K)LTALEER	(K)L T|A L E/E/R(E)		98.9	416.2371	831.457	0.0099	11.9	4.53	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
23672	dirMS_041712_NAR_60mM_minus.17719.17719.3	3	4.09	1	5.50E+05	S708s	(K)sKREPEN	(K)s K/R/E P/E/N E L T/K(Q)	s:N-acetylglucosamine (S)	159.73	511.9372	1330.696	203.1009	14.1	5.95	99897.9	6.43	HUMAN	B5MC89	Thyroid adenoma-associated protein
23673	dirMS_041712_NAR_60mM_minus.5378.5378.3	3	4.09	0	1.09E+05	T147t	(K)ELCPPG	(K)E L|C P P G K/P T t/S E K(I)	C:Carbamidomethylation t:Phosp	85.82	508.5661	1443.715	79.9689	1.7	6.24	21734	5.61	HUMAN	Q16385	Protein SSX2
23674	dirMS_041712_NAR_60mM_minus.6560.6560.3	3	4.09	1	9.46E+04	M436m	(R)TPGKEA	(R)T\P\G K E/A V A m/E S/Y A K(A)	m:Oxidized methionine	95.08	499.9146	1481.73	15.9988	2.6	5.81	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
23675	dirMS_041712_NAR_120mM_plus.12368.12368.4	4	4.09	1	1.30E+06	T266t	(R)GVSPSK	(R)G V S P S K A H G L/G S N L V t E V R(V)	t:Phosphorylated T	118.02	497.7567	1908.03	79.9752	4.5	8.76	50632.9	8.83	HUMAN	E0YMJ9	HNF1 beta A splice variant 4
23676	dirMS_041712_NAR_120mM_plus.18263.18263.3	3	4.09	1	7.11E+05		(K)GKAGTA	(K)G K/A G T A T|L|A M S E K(V)		148.25	422.22	1264.657	-0.0111	-8.8	8.59	120266.4	8.66	HUMAN	E7EWW0	UPF0505 protein C16orf62
23677	dirMS_041712_NAR_120mM_plus.9185.9185.3	3	4.09	0	4.32E+04	K477k	(K)DYEPPF	(K)D Y E/P/P F G S/k V R(E)	k:Ubiquitin-K	101.58	470.2372	1294.643	114.0544	8.2	6.07	65992.9	5.6	HUMAN	P37173	TGF-beta receptor type-2
23678	dirMS_041712_NAR_20mM_plus.10289.10289.2	2	4.09	0	3.85E+03	S455s	(R)GCATLL	(R)G C/A T/L/L/L s P/K(G)	C:Carbamidomethylation s:Phosp	143.1	570.276	1059.587	79.958	-7.3	8.75	71176.3	9.83	HUMAN	Q8IXW0	Uncharacterized protein C11orf35
23679	dirMS_041712_NAR_20mM_plus.10670.10670.2	2	4.09	0	3.71E+04		(K)STLTDSL	(K)S T/L/T/D/S L V C K(A)	C:Carbamidomethylation	146.22	562.2896	1123.566	0.0056	5	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
23680	dirMS_041712_NAR_20mM_plus.15861.15861.2	2	4.09	0	4.98E+03		(R)SSFYVN	(R)S S F|Y V|N/G\L T L G G Q K(C)		180.83	735.8818	1470.759	-0.0024	-1.6	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
23681	dirMS_041712_NAR_30mM_plus2.20964.20964.2	2	4.09	0	1.44E+05		(R)GVVQEL	(R)G V/V Q/E/L/Q/Q A/I/S K(L)		164.67	650.3632	1299.727	-0.0076	-5.8	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
23682	dirMS_041712_NAR_40mM_plus2.12615.12615.2	2	4.09	0	2.07E+05		(R)YIEIFK(S	(R)Y/I|E I/F K(S)		140.38	406.7302	812.455	-0.0021	-2.6	6	24249.1	6.99	HUMAN	D6RBM0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
23683	dirMS_041712_NAR_40mM_plus2.13705.13705.3	3	4.09	0	1.30E+05		(K)NLPPSG	(K)N L/P/P S G A V/P V/T/G I/P P H V V K(V)		146.72	627.031	1879.08	-0.0015	-0.8	8.76	31450.7	5.73	HUMAN	F5H4D6	Ras GTPase-activating protein-binding protein 1
23684	dirMS_041712_NAR_40mM_plus2.15963.15963.3	3	4.09	1	1.61E+04		(K)LGVQVV	(K)L/G V/Q/V V I T D/P E K L D Q I R(Q)		160.75	641.701	1923.091	-0.0025	-1.3	4.56	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
23685	dirMS_041712_NAR_50mM_plus2.10090.10090.3	3	4.09	1	2.46E+06		(K)ATAVVD	(K)A T/A V V D G A F K E/V K(L)		120.07	445.5822	1334.731	0.0006	0.5	6.11	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
23686	dirMS_041712_NAR_50mM_plus2.18865.18865.3	3	4.09	0	2.66E+05		(K)LAKPLSS	(K)L A K P L S S L T/P L I/M A A K(E)		167.48	552.004	1653.997	0.0003	0.2	10	24711.4	5.19	HUMAN	H7C1X3	PAK-2p34 (Fragment)
23687	dirMS_041712_NAR_50mM_plus2.19055.19055.3	3	4.09	1	1.38E+06		(R)SATLDRI	(R)S A T/L D R/I Q A C T Q Q/G L S S K(T)	C:Carbamidomethylation	167.13	655.3417	1963.987	0.024	12.2	8.46	342291.8	5.65	HUMAN	Q5TBA9	Protein furry homolog
23688	dirMS_041712_NAR_50mM_plus2.21729.21729.3	3	4.09	1	1.07E+04		(R)SKAEEL	(R)S K A E E L G L/P\I|L/G V L/R(S)		183.92	532.3178	1594.953	-0.0138	-8.7	5.87	40725.2	9.61	HUMAN	C9JDE9	3-ketoacyl-CoA thiolase, peroxisomal
23689	dirMS_041712_NAR_60mM_plus.11137.11137.3	3	4.09	0	1.25E+06		(R)EDITQS	(R)E D I/T Q/S A Q/H A L R(L)		115.1	456.9003	1368.687	-0.0003	-0.2	5.32	96205.6	9.06	HUMAN	G5E9M5	Interleukin enhancer binding factor 3, 90kDa, isoform CRA_b
23690	dirMS_041712_NAR_60mM_plus.5781.5781.3	3	4.09	0	1.32E+05	M110m	(K)LmELHG	(K)L/m|E L/H/G E G S\S S/G K(A)	m:Oxidized methionine	88.53	449.8794	1331.626	15.9977	2	5.4	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
23691	dirMS_041712_NAR_120mM_minus.11356.11356.3	3	4.08	1	4.30E+04	T719t	(R)HKQELtE	(R)H K Q E/L/t E K(D)	t:N-acetylglucosamine (T)	116.75	405.8796	1012.542	203.0821	2.2	6.76	134347.5	5.59	HUMAN	E9PF63	Rho-associated protein kinase 2
23692	dirMS_041712_NAR_20mM_minus.7985.7985.2	2	4.08	0	4.03E+04	M87m	(R)NDLSPT	(R)N D|L|S\P T T V m S E G A R(N)	m:Oxidized methionine	129.9	747.3477	1477.695	15.993	-1.3	4.37	22233.1	7.14	HUMAN	P30043	Flavin reductase (NADPH)
23693	dirMS_041712_NAR_30mM_minus2.18519.18519.2	2	4.08	0	1.34E+04		(R)LTAEDLF	(R)L/T/A/E/D L F E A R(I)		154.35	582.7922	1164.59	-0.0124	-10.7	4.14	533778	5.74	HUMAN	Q15149	Plectin
23694	dirMS_041712_NAR_30mM_minus2.18663.18663.2	2	4.08	0	2.09E+04		(R)QAQEYE	(R)Q A/Q/E Y E/A L\L\N I K(V)		156.48	710.3759	1419.748	-0.0033	-2.3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
23695	dirMS_041712_NAR_30mM_minus2.19022.19022.3	3	4.08	1	1.61E+05	T1331t	(K)DSNGTP	(K)D S N G T\P/S L/V/t I D G R R(S)	t:N-acetylglucosamine (T)	158.75	597.6343	1587.809	203.0798	0.3	5.96	224024.3	8.15	HUMAN	O60469	Down syndrome cell adhesion molecule
23696	dirMS_041712_NAR_50mM_minus2.11476.11476.3	3	4.08	0	2.90E+05	K678k	(K)ASEkVLD	(K)A S/E/k/V L D P A S/S D F T R(L)	k:Ubiquitin-K	134.03	579.6239	1622.802	114.0551	7	4.56	138538.3	9.36	HUMAN	E9PCK7	RRP12-like protein
23697	dirMS_041712_NAR_50mM_minus2.17150.17150.3	3	4.08	1	1.89E+04		(K)IILDLISE	(K)I I|L D L\I S/E S P I K G R(A)		166.68	518.6444	1553.926	-0.0075	-4.8	6.07	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
23698	dirMS_041712_NAR_50mM_minus2.8066.8066.3	3	4.08	0	5.89E+03		(R)VADTLN	(R)V A D T/L N N/W S I H P D P K(G)		112.63	569.6251	1706.85	0.0111	6.5	5.21	125121.9	5.42	HUMAN	Q6ZRK6	Coiled-coil domain-containing protein 73
23699	dirMS_041712_NAR_60mM_minus.14388.14388.3	3	4.08	0	1.89E+05		(R)GEAHLA	(R)G E/A H L A\V\N/D|F/E/L A R(A)		139.78	514.591	1541.771	-0.0122	-7.9	4.65	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
23700	dirMS_041712_NAR_60mM_minus.15852.15852.3	3	4.08	0	5.31E+05		(R)IYSHSLL	(R)I/Y S H S L\L/P/V L R(S)		148.57	433.2572	1297.763	-0.0056	-4.3	8.75	60871.9	6.3	HUMAN	B4DJ93	Phosphoribosylformylglycinamidine cyclo-ligase
23701	dirMS_041712_NAR_60mM_minus.6465.6465.3	3	4.08	1	8.87E+04		(K)SESPKEP	(K)S E\S P\K/E/P E Q L R(K)		94.9	433.8887	1299.654	-0.0024	-1.8	4.78	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
23702	dirMS_041712_NAR_60mM_minus.9658.9658.3	3	4.08	1	2.83E+05		(K)TAVCDI	(K)T A|V/C/D I/P P R G L K(M)	C:Carbamidomethylation	112.42	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
23703	dirMS_041712_NAR_120mM_plus.11228.11228.4	4	4.08	0	6.20E+05		(R)GAIQFV	(R)G A I\Q/F V/T H Y Q H/S S T Q R(R)		111.35	465.7339	1859.915	-0.0009	-0.5	8.76	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
23704	dirMS_041712_NAR_120mM_plus.11834.11834.3	3	4.08	0	5.14E+04	S8s	(-)XQAALP	(-)X Q A A/L P W/s\G\T A R(L)	s:N-acetylglucosamine (S)	114.62	491.9278	1270.69	203.0786	-0.5	9.75	23380.2	8.84	HUMAN	H0YDB7	Ras-related protein Rab-38 (Fragment)
23705	dirMS_041712_NAR_20mM_plus.10615.10615.2	2	4.08	0	6.78E+04		(K)VLQLYP	(K)V L\Q|L/Y|P N N K(A)		145.98	544.8057	1088.61	-0.0057	-5.3	8.56	9740.1	10.08	HUMAN	H0YFG2	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed (Fragment)
23706	dirMS_041712_NAR_20mM_plus.16742.16742.3	3	4.08	0	9.33E+04		(R)AAFTAF	(R)A A\F T A F/E E/A Q/L P R(L)		186.73	484.2492	1450.733	0.0005	0.4	4.53	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
23707	dirMS_041712_NAR_20mM_plus.18466.18466.3	3	4.08	0	1.05E+04		(R)AAVEEG	(R)A A V E E G I\V L/G/G G C A L L R(C)	C:Carbamidomethylation	198.63	562.3058	1684.905	-0.0022	-1.3	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
23708	dirMS_041712_NAR_30mM_plus2.5798.5798.2	2	4.08	0	4.03E+04	M66m	(R)AAmGP	(R)A/A/m/G/P G I/S/R(M)	m:Oxidized methionine	84.83	438.2226	859.445	15.9925	-2.8	9.79	22167.3	10.15	HUMAN	E7ENQ8	Phosphoglucomutase-2
23709	dirMS_041712_NAR_30mM_plus2.6855.6855.2	2	4.08	0	6.17E+04		(R)VYSTSV	(R)V/Y|S/T/S V T G S R(E)		90.47	528.7673	1056.532	-0.0047	-4.4	8.72	9437.4	9.69	HUMAN	Q5T123	SH3 domain binding glutamic acid-rich protein like 3
23710	dirMS_041712_NAR_40mM_plus2.7199.7199.2	2	4.08	0	2.44E+05		(R)VLDPTC	(R)V/L|D P T C T I K(T)	C:Carbamidomethylation	102.57	523.7788	1046.555	-0.0047	-4.5	5.81	37152.6	9.64	HUMAN	B4DU75	U3 small nucleolar RNA-associated protein 15 homolog
23711	dirMS_041712_NAR_40mM_plus2.9312.9312.2	2	4.08	0	4.56E+05		(R)GGNFGF	(R)G G N\F/G|F/G D S R(G)		116.57	507.2256	1013.444	0.0004	0.4	5.84	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
23712	dirMS_041712_NAR_50mM_plus2.16955.16955.3	3	4.08	1	5.24E+05		(K)LSKNEV	(K)L S K N E V L M\V N|I/G/S L|S T G G R(V)		157.05	659.0229	1975.064	-0.0099	-5	8.75	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
23713	dirMS_041712_NAR_60mM_plus.16369.16369.3	3	4.08	1	3.36E+04		(K)NLKVTA	(K)N L K V T A\V/P T L L K(Y)		143.5	432.9463	1296.825	-0.0006	-0.5	10	11462.8	5.18	HUMAN	I3L2R6	Thioredoxin domain-containing protein 17
23714	dirMS_041712_NAR_60mM_plus.18745.18745.3	3	4.08	1	9.11E+04		(R)YEEIVKE	(R)Y E/E I V K E/V/S T Y I K(K)		155.43	534.2888	1600.847	0.005	3.1	4.79	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
23715	dirMS_041712_NAR_60mM_plus.19136.19136.3	3	4.08	1	3.50E+04		(K)SELVAM	(K)S E/L|V/A M L/E E E E L R K(A)		158.07	559.288	1675.857	-0.0077	-4.6	4.32	18679.2	5.61	HUMAN	B4DWW1	ADP-ribosylation factor-like protein 1
23716	dirMS_041712_NAR_60mM_plus.9988.9988.3	3	4.08	1	1.28E+05		(K)DSQICEL	(K)D S/Q/I/C E L K/Y D K(Q)	C:Carbamidomethylation	109.98	466.8941	1398.657	0.0108	7.7	4.56	21156.2	9.41	HUMAN	P55145	Mesencephalic astrocyte-derived neurotrophic factor
23717	dirMS_041712_NAR_120mM_minus.6800.6800.3	3	4.07	1	2.31E+05		(R)TKTEISE	(R)T\K\T E I/S/E|M/N/R(N)		91.52	403.5363	1208.594	0.0004	0.3	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
23718	dirMS_041712_NAR_20mM_minus.10469.10469.2	2	4.07	1	6.73E+04		(K)AQEALD	(K)A Q/E A/L D|F Y G E/V R T R(D)		153.2	827.9072	1654.818	-0.0112	-6.8	4.68	47736	5.94	HUMAN	P60484	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN
23719	dirMS_041712_NAR_20mM_minus.11987.11987.3	3	4.07	0	1.00E+06	M313m	(R)TVQSLEI	(R)T V\Q S L E I/D/L D/S m R(N)	m:Oxidized methionine	169.73	508.2517	1506.747	15.9937	-0.8	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
23720	dirMS_041712_NAR_30mM_minus2.12409.12409.2	2	4.07	0	1.46E+05		(K)FDQLLA	(K)F/D|Q\L/L/A E E K(A)		121.23	546.7869	1092.557	0.0094	8.6	4.14	232239.1	5.52	HUMAN	F2Z2U8	Myosin-14
23721	dirMS_041712_NAR_30mM_minus2.16031.16031.2	2	4.07	0	1.41E+05		(K)GCSFLP	(K)G C/S F\L/P\D/P Y Q/K(Q)	C:Carbamidomethylation	141.02	656.3051	1311.604	-0.0009	-0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
23722	dirMS_041712_NAR_30mM_minus2.16471.16471.2	2	4.07	1	3.52E+05	K729k	(K)TFKNAC	(K)T F/K N A C S V k(I)	C:Carbamidomethylation k:Ubiqu	143.68	584.7961	1054.535	114.0499	6	10	111596.8	6.44	HUMAN	F5GY04	Zinc finger protein basonuclin-1
23723	dirMS_041712_NAR_30mM_minus2.5802.5802.2	2	4.07	0	8.23E+04		(R)QLEDGD	(R)Q L/E|D G D Q/P E/S K(K)		85.63	623.284	1245.559	0.0014	1.1	3.91	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
23724	dirMS_041712_NAR_40mM_minus2.10250.10250.3	3	4.07	1	5.31E+05		(K)TITLEVE	(K)T I/T L/E/V/E P S D\T I E N V K A K(I)		144.35	663.0226	1987.059	-0.0061	-3.1	4.41	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
23725	dirMS_041712_NAR_50mM_minus2.11884.11884.3	3	4.07	0	1.73E+05	M221m	(K)mLDAED	(K)m L/D A/E D I V/G T A R\P D E K(A)	m:Oxidized methionine	135.05	592.6214	1759.853	15.9966	0.9	4.1	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
23726	dirMS_041712_NAR_50mM_minus2.16318.16318.3	3	4.07	2	4.01E+04	N518n	(K)LDPHQK	(K)L/D|P H Q/K D D I n K K(A)	n:N-acetylglucosamine (N)	159.78	551.9429	1450.765	203.0493	-18.2	6.75	72508.6	9.07	HUMAN	Q99543	DnaJ homolog subfamily C member 2
23727	dirMS_041712_NAR_50mM_minus2.9202.9202.3	3	4.07	1	4.00E+04	S209s	(R)VKTSLN	(R)V K/T S L/N/Q S L F S I s K(E)	s:Phosphorylated S	120.57	544.6228	1551.874	79.9798	8.2	10	24613.4	9.3	HUMAN	H0YNM5	Pituitary-specific positive transcription factor 1 (Fragment)
23728	dirMS_041712_NAR_60mM_minus.10639.10639.3	3	4.07	1	6.48E+05		(K)ATAVVD	(K)A T/A/V/V D G A F K E V/K(L)		119.47	445.5804	1334.731	-0.0048	-3.6	6.11	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
23729	dirMS_041712_NAR_60mM_minus.18051.18051.3	3	4.07	0	8.31E+04	N4695n	(K)VALQA	(K)V/A/L Q A Q I E/n H K(V)	n:N-acetylglucosamine (N)	161.62	485.2617	1250.685	203.0854	4.1	6.72	794156.1	5.33	HUMAN	G3V5X4	Nesprin-2
23730	dirMS_041712_NAR_60mM_minus.4717.4717.3	3	4.07	0	8.39E+03	S244s S24	(K)TNQAILs	(K)T N Q A/I L s Q L/Y/Q s P N R(R)	s:Phosphorylated S	78.23	631.6171	1732.898	159.9391	3.4	8.41	42758.9	9.48	HUMAN	B1AM49	ELAV (Embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)
23731	dirMS_041712_NAR_120mM_plus.4094.4094.3	3	4.07	1	1.01E+07	T800t	(R)LtSNPSR	(R)L t S N P S/R V D R(L)	t:Phosphorylated T	69.47	408.8687	1144.607	79.9846	14.9	9.6	108754.9	6.69	HUMAN	A2RUB1	Uncharacterized protein C17orf104
23732	dirMS_041712_NAR_120mM_plus.5213.5213.3	3	4.07	2	2.11E+04	S110s	(K)ERGHKV	(K)E R G\H K V/G s Q P K(S)	s:Phosphorylated S	80.68	434.8849	1222.665	79.9751	6.7	10	68046.4	5.72	HUMAN	Q8N1W0	Transmembrane protein FLJ37396
23733	dirMS_041712_NAR_120mM_plus.9895.10108.3	3	4.07	0	1.88E+06	S138s	(K)LGsPDT	(K)L G/s P D/T V S P R(N)	s:N-acetylglucosamine (S)	105.1	411.2137	1028.537	203.0894	8.2	5.84	23075	9.52	HUMAN	H0Y9Y2	Biorientation of chromosomes in cell division protein 1-like 1 (Fragment)
23734	dirMS_041712_NAR_20mM_plus.14494.14494.3	3	4.07	0	4.89E+04	M313m	(R)TVQSLEI	(R)T/V Q S L E I D/L/D/S m R(N)	m:Oxidized methionine	171.23	508.2519	1506.747	15.9943	-0.4	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
23735	dirMS_041712_NAR_30mM_plus2.20811.20811.2	2	4.07	0	2.05E+05		(K)GGIVG	(K)G G I\V/G/M/T L|P I A R(D)		162.82	592.8453	1184.682	0.0013	1.1	9.75	27150.8	7.95	HUMAN	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2
23736	dirMS_041712_NAR_30mM_plus2.7175.7175.2	2	4.07	0	2.12E+04		(R)FYQQVT	(R)F/Y/Q/Q V T K(D)		91.88	457.2405	913.478	-0.0041	-4.5	8.59	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
23737	dirMS_041712_NAR_40mM_plus2.10320.10320.3	3	4.07	1	2.67E+05	Y287y	(K)ADRKSF	(K)A D/R K S F C T I H S T/G/y L K(S)	C:Carbamidomethylation y:Phos	125.1	655.3008	1883.943	79.9446	-11.1	9.7	60185.2	9.13	HUMAN	F8W6J9	Aryl hydrocarbon receptor nuclear translocator-like protein 1
23738	dirMS_041712_NAR_40mM_plus2.6230.6230.2	2	4.07	0	8.88E+04	M200m	(K)SFYmQR	(K)S/F/Y/m Q/R(C)	m:Oxidized methionine	95.47	424.1929	831.382	15.9967	2.2	8.46	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
23739	dirMS_041712_NAR_60mM_plus.16608.16608.3	3	4.07	1	6.42E+05		(R)TDGKVF	(R)T/D/G K/V/F Q F L/N A K(C)		143.48	456.5782	1367.732	-0.0117	-8.6	8.26	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
23740	dirMS_041712_NAR_60mM_plus.18061.18061.3	3	4.07	1	4.02E+04		(K)MFGIDR	(K)M/F|G I D R D A I\A Q A V R(G)		152.52	521.6038	1562.811	-0.0139	-8.9	5.71	63448.4	7.29	HUMAN	B4E022	Transketolase
23741	dirMS_041712_NAR_60mM_plus.7385.7385.2	2	4.07	1	2.33E+05		(R)SEEKISD	(R)S E E K/I|S/D/S E/G F K(A)		96.78	678.3205	1355.632	0.0012	0.9	4.41	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
23742	dirMS_041712_NAR_60mM_plus.9235.9235.3	3	4.07	0	2.11E+06		(K)NCPHIV	(K)N C P H I/V/V|G T/P G R(I)	C:Carbamidomethylation	106.15	436.2272	1306.669	-0.0014	-1.1	9.75	28185.1	10.76	HUMAN	B4DIJ6	Spliceosome RNA helicase DDX39B
23743	dirMS_041712_NAR_120mM_minus.11040.11040.3	3	4.06	0	6.08E+05		(R)ISNRPAF	(R)I/S N R\P A F\M|P S E/G K(M)		113.93	478.5776	1433.721	-0.0023	-1.6	8.75	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
23744	dirMS_041712_NAR_120mM_minus.15678.15678.3	3	4.06	1	2.70E+05		(R)MSMKE	(R)M S M K E V D\E Q\M/L/N V/Q N K(N)		139.48	641.9706	1923.897	0	0	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
23745	dirMS_041712_NAR_120mM_minus.8783.8783.3	3	4.06	2	2.48E+04	S214s	(K)LDPsKVF	(K)L D/P s K V F K S/K(N)	s:Phosphorylated S	102.15	410.2197	1148.667	79.9772	8.8	9.7	29835.1	6.18	HUMAN	B4DIX2	Tubulin polyglutamylase complex subunit 2
23746	dirMS_041712_NAR_20mM_minus.13182.13182.3	3	4.06	0	2.65E+05		(K)VGINYQ	(K)V G I N Y Q P P T V\V/P G G D L A K(V)		183.15	608.9971	1824.985	-0.0087	-4.8	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
23747	dirMS_041712_NAR_20mM_minus.9184.9184.2	2	4.06	0	9.72E+04	M267m	(R)LITLEEE	(R)L I|T L E/E E m T K(Y)	m:Oxidized methionine	142.02	611.8143	1206.629	15.9927	-1.8	4.25	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
23748	dirMS_041712_NAR_30mM_minus2.13984.13984.2	2	4.06	0	1.18E+05		(K)INLIAPP	(K)I N|L|I A P P R(Y)		129.67	447.2789	893.557	-0.0062	-6.9	9.75	31604.9	6.88	HUMAN	G3V4T5	Eukaryotic translation initiation factor 2 subunit 1 (Fragment)
23749	dirMS_041712_NAR_40mM_minus2.11616.11616.3	3	4.06	1	1.06E+05		(R)IINEPTA	(R)I I/N E/P T A A A/I A/Y G L D K K(V)		152.32	596.6671	1787.99	-0.0034	-1.9	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
23750	dirMS_041712_NAR_40mM_minus2.5722.5722.2	2	4.06	0	2.72E+05		(-)MGLEAQ	(-)M/G L E A Q R(L)		95.12	402.7052	804.403	-0.0001	-0.2	5.75	16053.1	6.05	HUMAN	F8WD21	Kinesin-like protein KIF7
23751	dirMS_041712_NAR_60mM_minus.10507.10507.3	3	4.06	0	1.66E+05		(K)TTLAHII	(K)T T|L A/H I I A/S N S/K(K)		118.72	419.2377	1255.7	-0.0019	-1.5	8.44	72873.4	5.73	HUMAN	Q96S55	ATPase WRNIP1
23752	dirMS_041712_NAR_60mM_minus.14823.14823.3	3	4.06	0	3.86E+05		(K)AVGHPF	(K)A V G H/P/F\V I Q/L G/R(I)		142.08	431.9182	1293.743	-0.0026	-2	9.8	124524.8	5.71	HUMAN	O14980	Exportin-1
23753	dirMS_041712_NAR_60mM_minus.6702.6702.3	3	4.06	1	2.18E+05		(K)IDDIRKP	(K)I/D/D/I R K P G E S E|E(-)		96.37	463.2294	1387.67	0.0037	2.7	4.37	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
23754	dirMS_041712_NAR_120mM_plus.10039.10039.4	4	4.06	2	1.97E+06		(K)MQASIE	(K)M Q/A S I E K/G G S L/P K V E/A K(F)		105.72	443.9944	1772.958	-0.0017	-1	8.25	32745.6	4.64	HUMAN	P06748	Nucleophosmin
23755	dirMS_041712_NAR_120mM_plus.4460.4460.3	3	4.06	1	3.04E+05		(R)AAEEED	(R)A A|E E/E D\E A D/P K/R(Q)		72.42	453.8721	1359.602	-0.0005	-0.4	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
23756	dirMS_041712_NAR_120mM_plus.4822.4822.3	3	4.06	1	3.66E+05		(K)ALKSES	(K)A L|K\S E\S A A/S S T G/K(E)		76.28	412.8845	1236.643	-0.0041	-3.3	8.64	31674	9.17	HUMAN	H3BR06	Telomeric repeat-binding factor 2 (Fragment)
23757	dirMS_041712_NAR_120mM_plus.5529.5529.2	2	4.06	0	4.33E+05	M1m S5s	(-)mGSFsS	(-)m G/S/F s\S H m T E F P|R(K)	m:Oxidized methionine s:N-a	82.05	874.8622	1513.656	235.0609	-4.8	6.5	62471.3	7.02	HUMAN	Q8WYA1-6	Isoform 6 of Aryl hydrocarbon receptor nuclear translocator-like protein 2

23758	dirMS_041712_NAR_120mM_plus.6498.6498.2	2	4.06	1	1.80E+05		(R)TKTEISEI	(R)T/K|T/E/I/S E/M N R(N)		87.52	604.8002	1208.594	-0.0008	-0.7	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
23759	dirMS_041712_NAR_120mM_plus.7320.7320.3	3	4.06	1	3.21E+05	M105m	(K)mERVSE	(K)m E R V S E/P/C P G S K(K)	C:Carbamidomethylation m:Oxid	91.37	464.8863	1376.63	16.0147	14.2	5.9	52682.9	9.2	HUMAN	Q969G9	Protein naked cuticle homolog 1
23760	dirMS_041712_NAR_120mM_plus.8663.8663.3	3	4.06	0	6.13E+05		(K)QHTFVE	(K)Q H T F V/E/T E S|V R(Y)		98.12	444.8857	1332.654	-0.0117	-8.8	5.4	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
23761	dirMS_041712_NAR_20mM_plus.7821.7821.3	3	4.06	0	1.06E+05		(K)AQAAAF	(K)A Q A A A\P A/S\V/P A Q A/P K(R)		123.6	459.9204	1377.748	-0.0018	-1.3	8.8	17808.8	11.77	HUMAN	P47914	60S ribosomal protein L29
23762	dirMS_041712_NAR_20mM_plus.9770.9770.3	3	4.06	2	1.54E+04		(K)KAKMPS	(K)K A K|M P S|A/S T E S R(R)		138.57	431.5577	1292.663	-0.0042	-3.2	9.99	91752.1	9.17	HUMAN	Q96PU4	E3 ubiquitin-protein ligase UHRF2
23763	dirMS_041712_NAR_30mM_plus2.20486.20486.2	2	4.06	0	4.24E+04		(K)LAVNM	(K)L A\V/N M/V/P F P R(L)		160.68	572.32	1143.634	-0.0016	-1.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
23764	dirMS_041712_NAR_40mM_plus2.4584.4584.2	2	4.06	0	1.96E+05		(R)YYGGGS	(R)Y Y/G\G/G S E G G R(A)		76.25	501.7171	1002.428	-0.0006	-0.6	6	64759.2	8.88	HUMAN	P14866	Heterogeneous nuclear ribonucleoprotein L
23765	dirMS_041712_NAR_40mM_plus2.9695.9695.3	3	4.06	0	2.22E+05		(R)AAEDPV	(R)A A/E/D/P V A A A P R P L P A G G R(L)		121.02	572.6438	1715.919	-0.0019	-1.1	6.12	73966.7	10.21	HUMAN	B3KWK6	Alpha-L-iduronidase
23766	dirMS_041712_NAR_50mM_plus2.14772.14772.3	3	4.06	1	2.19E+05		(R)ALSNLES	(R)A L/S\N L/E/S I P G G Y N A\L R R(M)		146.78	610.9972	1830.982	-0.005	-2.7	8.79	16443.8	5	HUMAN	H0YDS0	Ubiquilin-1 (Fragment)
23767	dirMS_041712_NAR_50mM_plus2.7824.7824.2	2	4.06	0	6.33E+04		(R)EGTLPTF	(R)E G T L/P T F D P/T K(V)		106.97	603.309	1205.605	0.0059	4.9	4.37	10156.7	4.12	HUMAN	Q5JUL1	G antigen family E member 1
23768	dirMS_041712_NAR_60mM_plus.17355.17355.3	3	4.06	1	1.80E+05		(R)LDTEELF	(R)L D/T/E E L/R L V E R(D)		147.43	458.2494	1372.743	-0.0094	-6.9	4.41	39931.9	4.74	HUMAN	E9PBI0	Zinc finger and SCAN domain-containing protein 18
23769	dirMS_041712_NAR_60mM_plus.5422.5422.3	3	4.06	0	1.56E+04	M111m	(R)MEELHN	(R)M/E/E L H N Q E m Q K(R)	m:Oxidized methionine	84.6	478.2118	1416.625	15.9962	0.9	4.75	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
23770	dirMS_041712_NAR_120mM_minus.12874.12874.3	3	4.05	0	1.57E+06	T61t	(R)LtQGRP	(R)L t Q/G R P A/E N L A K(V)	t:Phosphorylated T	125.02	459.8997	1297.722	79.9623	-2.9	8.75	18012.3	10.59	HUMAN	C9JY46	Golgi to ER traffic protein 4 homolog (Fragment)
23771	dirMS_041712_NAR_120mM_minus.5869.5869.3	3	4.05	0	1.04E+05	S1744s	(K)SsIALTAI	(K)S s I A L T A P/D/A A A D P/K(E)	s:Phosphorylated S	85.03	503.2345	1427.738	79.9513	-10	4.21	237639.1	6.17	HUMAN	G3XAA0	AT rich interactive domain 1B (SWI1-like), isoform CRA_a
23772	dirMS_041712_NAR_120mM_minus.6779.6779.2	2	4.05	1	1.62E+05		(K)VQVEYK	(K)V/Q|V E/Y\K G E|T K(S)		91.35	590.8128	1180.621	-0.0025	-2.1	6.11	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
23773	dirMS_041712_NAR_20mM_minus.13677.13677.2	2	4.05	0	1.55E+05		(K)ALQQGL	(K)A L|Q Q/G L V/G L E L K(E)		187.58	634.8811	1268.757	-0.0023	-1.8	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
23774	dirMS_041712_NAR_20mM_minus.7023.7023.2	2	4.05	0	2.11E+05	M33m	(R)IDEmPE	(R)I D|E m/P E A/A V K(S)	m:Oxidized methionine	117.97	559.7733	1102.545	15.9944	-0.4	4.14	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
23775	dirMS_041712_NAR_20mM_minus.8727.8727.2	2	4.05	0	1.91E+04	M149m	(K)ITLDNAY	(K)I/T|L/D N A Y m E K(C)	m:Oxidized methionine	136.55	607.2934	1197.582	15.9975	2.1	4.37	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
23776	dirMS_041712_NAR_30mM_minus2.17685.17685.2	2	4.05	0	2.08E+05		(R)TEMDW	(R)T E|M/D|W V/L K(H)		151.1	511.2565	1021.502	0.0034	3.4	4.37	46013.4	5.38	HUMAN	P52597	Heterogeneous nuclear ribonucleoprotein F
23777	dirMS_041712_NAR_30mM_minus2.6453.6453.2	2	4.05	1	1.03E+05		(R)KEEWER	(R)K E/E W|E/R(E)		89.35	438.7093	876.421	-0.0097	-11	4.79	109165.8	8.64	HUMAN	E7ERS3	Zinc finger CCCH domain-containing protein 18
23778	dirMS_041712_NAR_30mM_minus2.7179.7179.2	2	4.05	0	1.65E+05	M239m	(K)TVYPmE	(K)T V|Y/P m E R(L)	m:Oxidized methionine	93.98	456.2163	895.434	15.9911	-4.2	5.66	67446.5	5.63	HUMAN	F8VQE1	LIM domain and actin-binding protein 1
23779	dirMS_041712_NAR_40mM_minus2.10346.10346.2	2	4.05	0	9.91E+05		(R)VAPEEH	(R)V A/P E E H|P V L L T E/A P L N/P K(A)		143.67	977.5343	1954.064	-0.0031	-1.6	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
23780	dirMS_041712_NAR_40mM_minus2.6568.6568.2	2	4.05	0	2.25E+05		(K)LAADDF	(K)L/A A\D D\F/R(T)		107	404.2037	807.399	0.0006	0.7	4.21	48845.9	4.72	HUMAN	C4AM86	Keratin, type I cuticular Ha5
23781	dirMS_041712_NAR_50mM_minus2.17394.17394.3	3	4.05	2	1.49E+04		(R)NSSPIRN	(R)N S S P/I R M A K/I T H V E G K(K)		167.3	589.9831	1767.953	-0.0187	-10.6	9.99	191251.2	7.07	HUMAN	Q13029	PR domain zinc finger protein 2
23782	dirMS_041712_NAR_60mM_minus.19382.19382.3	3	4.05	1	1.89E+05		(R)KAIIIFVP	(R)K A I I I F\V/P V P Q/L K(S)		172.82	489.3209	1465.95	-0.0023	-1.6	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
23783	dirMS_041712_NAR_60mM_minus.6934.6934.3	3	4.05	1	4.25E+05		(K)LKENENI	(K)L/K E N/E N M M/E G N L\P K(C)		96.63	549.6071	1646.788	0.0191	11.6	4.79	93493.8	9.47	HUMAN	B4DZN9	Rho GTPase-activating protein 11A
23784	dirMS_041712_NAR_120mM_plus.11773.11773.4	4	4.05	1	3.91E+05		(K)ISSVEGK	(K)I S\S V\E G K K/I/P T/E S V K(E)		114.12	401.2306	1601.911	-0.0103	-6.4	8.5	104919.7	9.34	HUMAN	Q6ZXV5	Transmembrane and TPR repeat-containing protein 3
23785	dirMS_041712_NAR_20mM_plus.13625.13625.2	2	4.05	0	2.03E+05		(K)APILIATI	(K)A P\I/L|I|A/T D/V A S R(G)		166.55	613.8559	1226.71	-0.0058	-4.7	5.88	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
23786	dirMS_041712_NAR_30mM_plus2.4892.4892.2	2	4.05	0	1.89E+05		(K)NCSETQ	(K)N/C|S/E/T Q Y E\S K(V)	C:Carbamidomethylation	76.98	623.256	1245.505	-0.0005	-0.4	4.53	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
23787	dirMS_041712_NAR_40mM_plus2.11091.11091.3	3	4.05	0	9.54E+04	M35m	(K)AASDIA	(K)A A S D I/A m/T E L/P/P T H P I/R(L)	m:Oxidized methionine	131.15	612.652	1819.937	16.0044	5.1	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
23788	dirMS_041712_NAR_40mM_plus2.11342.11342.3	3	4.05	2	2.83E+04	S744s	(R)RAADVE	(R)R A/A D V E P s L P/E/P K R(R)	s:N-acetylglucosamine (S)	132.63	589.9796	1564.844	203.0801	0.4	6.18	84483.4	10.39	HUMAN	A8MQ56	Uncharacterized protein
23789	dirMS_041712_NAR_40mM_plus2.8315.8315.2	2	4.05	0	7.12E+04		(K)NMGLY	(K)N M|G|L/Y G E R(V)		109.7	470.2221	939.435	0.0016	1.8	6	43371.1	9.64	HUMAN	E7ERW2	Aspartate aminotransferase
23790	dirMS_041712_NAR_40mM_plus2.9281.9281.2	2	4.05	0	5.29E+05		(K)SSFFSDR	(K)S S|F/F/S D|R(G)		116.48	423.1935	845.379	0.0009	1.1	5.55	15031.5	6.72	HUMAN	B4DLA0	ATP-dependent RNA helicase DDX3X
23791	dirMS_041712_NAR_40mM_plus2.9814.9814.2	2	4.05	0	9.48E+04		(R)GYFSEEN	(R)G Y|F/S E E M N R(V)		121.53	566.7355	1132.473	-0.0091	-8	4.53	533778	5.74	HUMAN	Q15149	Plectin
23792	dirMS_041712_NAR_50mM_plus2.10668.10668.3	3	4.05	1	3.65E+05		(K)AQALRD	(K)A Q|A L R D N S T/M/G Y M M/A K(K)		123.58	596.6125	1787.824	-0.0008	-0.4	8.63	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
23793	dirMS_041712_NAR_50mM_plus2.10875.10875.3	3	4.05	1	4.28E+05		(K)NQLTSN	(K)N Q|L/T S N/P E/N/T/V F D A K R(L)		124.88	611.9758	1833.909	0.0039	2.1	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
23794	dirMS_041712_NAR_60mM_plus.12226.12226.3	3	4.05	0	6.89E+05		(K)TQIGMT	(K)T Q I G/M T E/S L L/K(A)		120.63	407.5532	1220.656	-0.0105	-8.6	5.66	794156.1	5.33	HUMAN	G3V5X4	Nesprin-2
23795	dirMS_041712_NAR_60mM_plus.13307.13307.3	3	4.05	0	1.81E+05		(K)LSLGTYA	(K)L S L/G T/Y/A S L H G R(I)		125.78	425.563	1274.685	-0.0107	-8.4	8.75	67446.5	5.63	HUMAN	F8VQE1	LIM domain and actin-binding protein 1
23796	dirMS_041712_NAR_120mM_minus.8628.8628.3	3	4.04	0	1.54E+05		(R)SQLLGSA	(R)S Q|L|L/G S A\H E V Q R(F)		101.63	442.2355	1324.697	-0.0048	-3.7	6.47	285798.6	5.23	HUMAN	A6NG51	Spectrin alpha chain, non-erythrocytic 1
23797	dirMS_041712_NAR_120mM_minus.8838.8838.2	2	4.04	0	5.09E+05		(K)HFVALST	(K)H F|V/A/L\S T N T\T/K(V)		103.17	609.8267	1218.648	-0.0016	-1.3	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
23798	dirMS_041712_NAR_20mM_minus.9190.9190.2	2	4.04	0	9.72E+04	M267m	(R)LITLEEE	(R)L I/T L/E/E E m T K(Y)	m:Oxidized methionine	142.02	611.8143	1206.629	15.9927	-1.8	4.25	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
23799	dirMS_041712_NAR_20mM_minus.9804.9804.2	2	4.04	0	1.80E+05	K566k	(K)TkSHGQ	(K)T k/S H/G/Q E K(T)	k:Ubiquitin-K	148.58	514.7668	914.469	114.0573	14	8.29	100681.3	9.34	HUMAN	A6NCI8	Uncharacterized protein C2orf78
23800	dirMS_041712_NAR_30mM_minus2.13263.13263.2	2	4.04	0	3.32E+04		(R)TSGSVYI	(R)T S|G S/V/Y/I T L K(K)		125.93	534.7976	1068.594	-0.0056	-5.3	8.26	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
23801	dirMS_041712_NAR_30mM_minus2.7976.7976.2	2	4.04	0	3.27E+05		(K)VYVVEG	(K)V/Y|V V\E/G S K(R)		98	440.7384	880.477	-0.0079	-9	5.97	55097.1	7.14	HUMAN	O75844	CAAX prenyl protease 1 homolog
23802	dirMS_041712_NAR_30mM_minus2.9927.9927.2	2	4.04	1	4.25E+05		(K)IERFTR(	(K)I E/R F T/R(D)		108.53	411.2348	821.463	-0.0005	-0.6	9.6	78521.8	9.1	HUMAN	G5E9B8	Zinc finger protein 180
23803	dirMS_041712_NAR_50mM_minus2.5700.5700.3	3	4.04	0	2.90E+04		(K)SVSSASE	(K)S V/S S A/S E H S T T E/P S P/A A R(R)		93.32	600.9511	1800.836	0.0029	1.6	5.38	133030.9	10.9	HUMAN	F5H1R7	Protein FLJ22184
23804	dirMS_041712_NAR_60mM_minus.18253.18253.3	3	4.04	0	9.33E+04		(R)LNVVAF	(R)L N/V V A F L/N E L P K(T)		162.73	452.9408	1356.789	0.0193	14.2	6	68619.5	9.37	HUMAN	E9PIN3	Nuclear RNA export factor 1 (Fragment)
23805	dirMS_041712_NAR_60mM_minus.8885.8885.3	3	4.04	0	4.32E+03		(R)TLHSDD	(R)T L H S D D E G T V/L D/D/S R(A)		109.43	553.919	1659.746	-0.0032	-1.9	4.03	23307.1	5.11	HUMAN	E9PMH2	Peptidyl-prolyl cis-trans isomerase (Fragment)
23806	dirMS_041712_NAR_120mM_plus.19439.19439.2	2	4.04	1	1.64E+05	T881t	(K)IKtEEIAA	(K)I K t E E/I|A A F/Q R(K)	t:Phosphorylated T	154.63	693.3483	1305.716	79.9732	5	6.14	151497.3	6.37	HUMAN	Q2M1P5	Kinesin-like protein KIF7
23807	dirMS_041712_NAR_120mM_plus.9356.9356.3	3	4.04	1	3.91E+05		(K)STFREES	(K)S T/F R E E S|P L R(I)		102.63	407.8773	1221.622	-0.0049	-4	5.87	53030.7	11.3	HUMAN	E9PJA7	Bcl-2-associated transcription factor 1
23808	dirMS_041712_NAR_20mM_plus.11615.11615.2	2	4.04	0	1.35E+05		(R)ANTFVA	(R)A N\T/F/V/A/E L K(G)		152.95	496.7735	992.541	-0.0014	-1.4	6.05	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
23809	dirMS_041712_NAR_20mM_plus.12143.12143.2	2	4.04	0	3.44E+04		(K)LQAFSA	(K)L Q|A\F\S/A/A I E S C N K(A)	C:Carbamidomethylation	156.63	719.8475	1438.699	-0.0118	-8.2	6	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
23810	dirMS_041712_NAR_20mM_plus.6712.6712.3	3	4.04	0	1.25E+05	M136m	(R)LVAGEm	(R)L V A G E m G Q N E|P D Q/G G Q/R(G)	m:Oxidized methionine	111.45	601.2753	1785.818	15.9929	-1.1	4.14	17508.7	8.03	HUMAN	Q5H928	3-hydroxyacyl-CoA dehydrogenase type-2
23811	dirMS_041712_NAR_20mM_plus.9811.9811.2	2	4.04	0	6.63E+03		(K)IIEEAPAI	(K)I I E/E/A/P|A/P G I K(S)		138.67	569.3276	1137.651	-0.0035	-3.1	4.53	66923.1	6.88	HUMAN	E9PG35	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (Fragment)
23812	dirMS_041712_NAR_30mM_plus2.14582.14582.2	2	4.04	1	4.35E+05		(K)QRIDEFE	(K)Q R I D E\F E|A|M(-)		129.5	569.7707	1138.52	0.0144	12.6	4.14	52734.7	5.88	HUMAN	F5H1A7	Radixin
23813	dirMS_041712_NAR_30mM_plus2.21062.21062.2	2	4.04	0	2.78E+04		(R)EMVLEII	(R)E M/V\L|E/I I R(E)		163.52	501.7877	1002.565	0.0029	2.9	4.53	61981.6	8.97	HUMAN	Q96I24	Far upstream element-binding protein 3
23814	dirMS_041712_NAR_40mM_plus2.11722.11722.2	2	4.04	0	5.70E+04		(R)GYIYWR	(R)G Y|I Y/W R(L)		135.38	429.2135	857.43	-0.0107	-12.5	8.59	66055.4	5.07	HUMAN	C9J1E7	AP-1 complex subunit beta-1 (Fragment)
23815	dirMS_041712_NAR_50mM_plus2.7039.7039.3	3	4.04	1	1.15E+04		(R)DLTTGYI	(R)D L/T/T/G Y D D/S Q P D K K(A)		102.95	528.2459	1582.723	0	0	4.14	51084.6	5.75	HUMAN	F5H6V2	Phosphoglucomutase-2
23816	dirMS_041712_NAR_60mM_plus.10239.10239.3	3	4.04	1	8.18E+05		(K)TAVCDIF	(K)T A|V/C D/I/P P R G L K(M)	C:Carbamidomethylation	111.95	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
23817	dirMS_041712_NAR_60mM_plus.6480.6480.3	3	4.04	1	9.73E+04	M725m	(K)GQIEEQI	(K)G Q|I E/E Q/K E M m E/K(A)	m:Oxidized methionine	92.43	499.2318	1479.682	15.9991	2.8	4.49	107721.8	8.85	HUMAN	O94906	Pre-mRNA-processing factor 6
23818	dirMS_041712_NAR_20mM_minus.13646.13646.3	3	4.03	0	1.57E+05		(R)ETTDTD	(R)E T T D T D T A|D/Q V I/A S F K(V)		186.55	581.2735	1741.813	-0.0067	-3.9	3.84	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
23819	dirMS_041712_NAR_30mM_minus2.19008.19008.2	2	4.03	0	2.13E+05		(R)TLLAILR(	(R)T/L/L A I L R(L)		158.98	400.2731	799.54	-0.0011	-1.3	9.41	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
23820	dirMS_041712_NAR_30mM_minus2.9276.9276.2	2	4.03	0	2.59E+05		(R)VLNTNII	(R)V/L/N/T/N/I D\G/R(R)		106.07	501.2667	1001.537	-0.0113	-11.3	5.81	17718.4	10.99	HUMAN	P62269	40S ribosomal protein S18
23821	dirMS_041712_NAR_40mM_minus2.6919.6919.3	3	4.03	0	2.26E+03		(K)VVQVSA	(K)V V/Q V/S A/G D S H T A A L T D D G R(V)		111	633.6417	1898.92	-0.0097	-5.1	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
23822	dirMS_041712_NAR_40mM_minus2.9518.9518.3	3	4.03	1	2.93E+04		(R)LSEDYG	(R)L S/E D/Y\G V L|K T D E G I A Y R(G)		138.48	643.6603	1928.96	0.0063	3.3	4.32	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
23823	dirMS_041712_NAR_50mM_minus2.10108.10108.3	3	4.03	0	1.11E+05		(K)TKPYIQV	(K)T K P Y I Q V/D|I/G G G Q T K(T)		125.82	535.6231	1604.864	-0.0095	-5.9	8.17	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
23824	dirMS_041712_NAR_50mM_minus2.13492.13492.3	3	4.03	1	5.10E+05		(K)ATLPSPI	(K)A T/L/P S/P D K L P G F K(M)		144.2	457.5912	1370.768	-0.0088	-6.4	8.64	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
23825	dirMS_041712_NAR_50mM_minus2.7428.7428.3	3	4.03	1	9.46E+04		(K)ATQPET	(K)A/T Q/P E T T E E/V T D L K R(Q)		109.53	573.2875	1717.86	-0.0123	-7.2	4.41	72152.1	5.27	HUMAN	A0MZ66	Shootin-1
23826	dirMS_041712_NAR_60mM_minus.10590.10590.3	3	4.03	1	1.42E+05		(R)SATKVT	(R)S A\T K V T A D\V|I/N/A|A E K(L)		118.78	506.6084	1517.817	-0.0063	-4.2	5.79	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
23827	dirMS_041712_NAR_60mM_minus.18503.18503.3	3	4.03	0	6.80E+04		(R)QFLFRP	(R)Q F/L/F R/P\W D/V T/K(L)		164.55	479.5947	1436.768	0.0011	0.7	8.75	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
23828	dirMS_041712_NAR_120mM_plus.9691.9691.2	2	4.03	2	2.30E+05	M814m	(R)KAMFAF	(R)K\A|M F A/R F T\E/m\E(-)	m:Oxidized methionine	104.13	688.8259	1360.639	16.0057	7.8	6.28	92665.7	5.94	HUMAN	P52756	RNA-binding protein 5
23829	dirMS_041712_NAR_20mM_plus.10562.10562.3	3	4.03	0	8.25E+04		(K)VLQATV	(K)V L Q A T V\V/A|V G S G S K(G)		145.63	439.2573	1315.758	-0.0006	-0.5	8.72	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
23830	dirMS_041712_NAR_20mM_plus.16654.16654.2	2	4.03	0	7.68E+04	M137m M:	(R)IIGATDS	(R)I I G A|T D S\S G E L m/F L\m/K(W)	m:Oxidized methionine	185.68	872.926	1712.86	31.985	-2.8	4.37	19439.5	4.97	HUMAN	B5MD17	Chromobox protein homolog 1 (Fragment)
23831	dirMS_041712_NAR_20mM_plus.17724.17724.2	2	4.03	0	8.14E+04		(R)TTLLPGL	(R)T T|L\L/P G L/L K(T)		193.85	478.3131	955.619	0.0003	0.3	8.41	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
23832	dirMS_041712_NAR_20mM_plus.9994.9994.2	2	4.03	0	1.64E+05		(R)ALGQNF	(R)A L G Q/N|P T N A E V L K(V)		140.22	677.8702	1354.733	0.0006	0.5	6.05	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
23833	dirMS_041712_NAR_30mM_plus2.5382.5382.3	3	4.03	0	6.70E+04		(R)GGSGGS	(R)G G S G G S Y G G G G/S G G G Y/G G/G/S G S R(G)		82.82	597.9128	1791.728	-0.0039	-2.2	8.59	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
23834	dirMS_041712_NAR_40mM_plus2.9739.9739.2	2	4.03	0	3.20E+05		(K)SCNCLLL	(K)S/C/N/C L L\L/K(V)	C:Carbamidomethylation	120.87	504.2542	1007.501	-0.0001	-0.1	8.47	47510.4	7.04	HUMAN	P06733	Alpha-enolase
23835	dirMS_041712_NAR_50mM_plus2.13985.13985.3	3	4.03	1	6.26E+05		(K)GGELVY	(K)G G\E L|V/Y T D S E A R D V F E K(A)		141.5	638.9735	1914.908	-0.002	-1.1	4.18	533778	5.74	HUMAN	Q15149	Plectin
23836	dirMS_041712_NAR_50mM_plus2.7149.7149.3	3	4.03	0	1.56E+04	M226m	(K)VEImPPI	(K)V E\I\m/P/P/P P K/P K(D)	m:Oxidized methionine	104.55	416.9025	1232.707	15.9858	-7.3	8.56	53885.5	9	HUMAN	P11182	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial
23837	dirMS_041712_NAR_60mM_plus.11682.11682.2	2	4.03	1	3.39E+05		(K)KAEAGA	(K)K|A E A|G A G S A/T E\F Q\F R(G)		118.3	785.3854	1569.766	-0.0021	-1.3	6.14	18897.4	10.15	HUMAN	P46783	40S ribosomal protein S10
23838	dirMS_041712_NAR_60mM_plus.18644.18644.3	3	4.03	1	2.30E+05		(K)DANAKL	(K)D A/N A K/L S E\L/E A A/L/Q R(A)		154.87	543.6241	1628.86	-0.0025	-1.5	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
23839	dirMS_041712_NAR_60mM_plus.5202.5202.3	3	4.03	1	4.46E+04		(K)GNSPPS	(K)G N|S/P/P/S S G E A C R E E K(G)	C:Carbamidomethylation	84.52	535.5678	1604.697	-0.0081	-5	4.79	24954.4	5.33	HUMAN	A6NM98	ARD1 homolog A, N-acetyltransferase (S. cerevisiae), isoform CRA_b
23840	dirMS_041712_NAR_60mM_plus.5542.5542.3	3	4.03	0	1.11E+06		(K)TATPQQ	(K)T A|T/P Q Q A/Q E V H E K(L)		87.6	489.5727	1466.723	-0.0198	-13.5	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
23841	dirMS_041712_NAR_120mM_minus.10319.10319.3	3	4.02	1	6.18E+04		(R)KEEELQ	(R)K E E E L Q|A/A/L A/R(A)		111.02	419.8975	1257.68	-0.0018	-1.4	4.79	232239.1	5.52	HUMAN	F2Z2U8	Myosin-14
23842	dirMS_041712_NAR_120mM_minus.12711.12711.3	3	4.02	0	5.78E+05		(K)TFTAWC	(K)T/F|T A/W C N S H/L/R(K)	C:Carbamidomethylation	122.47	464.8871	1392.648	-0.001	-0.7	9.44	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
23843	dirMS_041712_NAR_120mM_minus.17719.17719.3	3	4.02	1	1.82E+05		(R)AGKLDP	(R)A G K L D\P/H|L/V/L D Q\L R(C)		151.47	525.6385	1574.901	-0.0004	-0.2	6.79	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
23844	dirMS_041712_NAR_20mM_minus.14415.14415.3	3	4.02	0	2.19E+05		(K)LAAELSA	(K)L A A E L S A/T\L E Q A/A/A T A R(V)		198.9	562.9713	1686.902	-0.0027	-1.6	4.53	558007.1	5.44	HUMAN	P58107	Epiplakin
23845	dirMS_041712_NAR_30mM_minus2.8750.8750.2	2	4.02	0	1.78E+05		(K)EANEILC	(K)E A/N/E/I/L Q R(S)		102.45	486.7596	972.511	0.001	1.1	4.53	64718.1	6.56	HUMAN	A4D0Z6	Inosine-5'-monophosphate dehydrogenase
23846	dirMS_041712_NAR_40mM_minus2.11269.11269.3	3	4.02	0	5.33E+03		(K)DVTLHV	(K)D V T L/H V S A S N P A/M L L Y Q K(F)		148.28	663.0226	1987.032	0.0215	10.8	6.74	89583.9	6.14	HUMAN	Q9H8E8	Cysteine-rich protein 2-binding protein
23847	dirMS_041712_NAR_50mM_minus2.15583.15583.3	3	4.02	1	6.71E+04		(K)LALDIEI	(K)L A/L D/I E/I A/T Y R K(L)		156.43	469.2729	1405.805	-0.0008	-0.6	6.07	49564	5.84	HUMAN	E9PAX3	Glial fibrillary acidic protein
23848	dirMS_041712_NAR_50mM_minus2.6693.6693.3	3	4.02	2	7.27E+03	S250s	(R)KISQALA	(R)K I|S Q/A\L A s K E N S Y P K(E)	s:Phosphorylated S	105.55	581.9591	1663.901	79.9614	-2.8	9.53	76002.5	6.47	HUMAN	Q9H6T3	RNA polymerase II-associated protein 3
23849	dirMS_041712_NAR_60mM_minus.8823.8823.3	3	4.02	1	2.76E+05		(R)LGTPELS	(R)L/G T P E/L S T/A E/R K(E)		108.48	434.572	1301.706	-0.0045	-3.5	6.14	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
23850	dirMS_041712_NAR_120mM_plus.13179.13179.3	3	4.02	0	8.67E+05	M2365m	(R)WYPNIS	(R)W Y P N I S/T|V m F K(F)	m:Oxidized methionine	122.27	467.9029	1385.692	16.0019	5	8.59	353199.2	6.01	HUMAN	P24043	Laminin subunit alpha-2
23851	dirMS_041712_NAR_120mM_plus.14898.14898.4	4	4.02	2	1.54E+06		(R)YLYTLVI	(R)Y L Y/T L V/I/T D K E K A E K(L)		131.28	454.2533	1813.995	-0.0032	-1.8	6.18	7621.9	10.1	HUMAN	J3KT73	60S ribosomal protein L38
23852	dirMS_041712_NAR_20mM_plus.11299.11299.2	2	4.02	0	1.61E+04		(R)GCITIIG(	(R)G C I\T\I|I/G G G D T A T/C C A K(W)	C:Carbamidomethylation	150	877.8947	1754.787	-0.0049	-2.8	5.84	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
23853	dirMS_041712_NAR_20mM_plus.12258.12258.2	2	4.02	0	1.23E+04	M320m	(K)YmACCL	(K)Y m/A/C C L L/Y R(G)	C:Carbamidomethylation m:Oxid	157.45	633.2796	1249.553	15.9993	3.5	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
23854	dirMS_041712_NAR_20mM_plus.19247.19247.3	3	4.02	0	2.77E+05		(R)LAGTQP	(R)L A\G T Q P\L\E V/L|E A/V Q/R(S)		204.3	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
23855	dirMS_041712_NAR_20mM_plus.19316.19316.2	2	4.02	0	8.40E+04		(R)ALIAGG(	(R)A L\I A G\G G A|P E I/E/L/A L R(L)		205.1	775.9467	1550.89	-0.0039	-2.5	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
23856	dirMS_041712_NAR_30mM_plus2.20067.20067.3	3	4.02	0	1.29E+05		(R)SQNVM	(R)S Q N V M A\A A S I/A N I V K(S)		158.98	506.2751	1516.815	-0.0044	-2.9	8.47	47423	5.43	HUMAN	E7ERF2	T-complex protein 1 subunit alpha
23857	dirMS_041712_NAR_30mM_plus2.9584.9584.2	2	4.02	0	4.96E+05		(R)TSLGPN(	(R)T S|L/G/P N G L D K(M)		104.43	501.2717	1001.526	0.0099	9.9	5.5	55804.4	5.33	HUMAN	B7ZAR1	T-complex protein 1 subunit epsilon
23858	dirMS_041712_NAR_40mM_plus2.19048.19048.3	3	4.02	0	1.41E+05		(R)ETSSDV	(R)E T/S/S D V A/L/A S H I L T A L R(E)		178.68	595.3161	1783.955	-0.0211	-11.8	5.32	36920.6	4.68	HUMAN	O00273	DNA fragmentation factor subunit alpha
23859	dirMS_041712_NAR_40mM_plus2.7146.7146.2	2	4.02	0	5.90E+04	S73s	(R)MYVGsK	(R)M/Y/V G s K(D)	s:N-acetylglucosamine (S)	101.92	444.2105	684.338	203.0752	-4.7	8.34	10541	6.01	HUMAN	C9IYS6	Semaphorin-3F (Fragment)
23860	dirMS_041712_NAR_50mM_plus2.11822.11822.3	3	4.02	1	4.35E+05		(K)QIDLSTV	(K)Q I/D/L|S T/V/D L K K(L)		130.47	420.5781	1259.72	-0.0008	-0.6	5.96	21156.2	9.41	HUMAN	P55145	Mesencephalic astrocyte-derived neurotrophic factor
23861	dirMS_041712_NAR_50mM_plus2.9979.9979.3	3	4.02	1	3.08E+05		(R)SATKVT	(R)S A/T K V T A D V/I/N A/A E K(L)		119.68	506.6094	1517.817	-0.0033	-2.2	5.79	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
23862	dirMS_041712_NAR_60mM_plus.10059.10059.3	3	4.02	1	1.20E+06		(K)IFRDGEE	(K)I F R/D G E E A\G A|Y/D/G P R(T)		111.33	551.593	1652.766	-0.0019	-1.1	4.32	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
23863	dirMS_041712_NAR_60mM_plus.10719.10719.3	3	4.02	1	2.18E+05		(R)LKYENE	(R)L/K Y E N E V/A L/R(Q)		113.4	412.2319	1234.679	0.0021	1.7	6.14	59054.3	5.14	HUMAN	P13645	Keratin, type I cytoskeletal 10
23864	dirMS_041712_NAR_60mM_plus.18316.18316.3	3	4.02	0	1.94E+05		(K)DHGLEV	(K)D H G L E\V|L/G L\V/R(V)		153.45	403.2318	1207.679	0.0015	1.2	5.32	17732.8	5.85	HUMAN	F5GYJ1	U8 snoRNA-decapping enzyme
23865	dirMS_041712_NAR_60mM_plus.19289.19289.3	3	4.02	1	5.06E+05		(K)LEALKDI	(K)L E A L K/D\L/A S/L S R(D)		159.45	439.262	1315.758	0.0135	10.2	6.07	18679.9	4.7	HUMAN	C9IZR8	Engulfment and cell motility protein 1 (Fragment)
23866	dirMS_041712_NAR_60mM_plus.19951.19951.3	3	4.02	1	9.70E+04		(R)NLLSVA	(R)N L/L\S V A/Y/K N/V I G A R(R)		164.77	506.6285	1517.88	-0.0089	-5.9	9.99	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon

23867	dirMS_041712_NAR_60mM_plus.6665.6665.3	3	4.02	0	5.67E+05		(K)SQFSDK	(K)S Q/F S D K/P/V Q D/R(G)		93.3	436.218	1306.639	0.0008	0.6	5.68	13194	9.99	HUMAN	E9PI70	Chitinase domain-containing protein 1 (Fragment)
23868	dirMS_041712_NAR_120mM_minus.13652.13652.3	3	4.01	1	5.66E+05	T188t	(K)NYLAtR	(K)N Y/L A t R G L T W K(N)	t:Phosphorylated T	128.55	468.2346	1322.722	79.9677	1	9.99	33386	5.9	HUMAN	F5H7R8	E3 ubiquitin-protein ligase CHFR
23869	dirMS_041712_NAR_120mM_minus.7088.7088.2	2	4.01	0	4.18E+05		(K)HNAAFC	(K)H N|A A/F C Y K(L)	C:Carbamidomethylation	92.42	505.7282	1010.451	-0.0021	-2.1	8.6	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
23870	dirMS_041712_NAR_120mM_minus.8941.8941.3	3	4.01	0	3.33E+05		(K)GQVGSE	(K)G Q V G S\E Q|H S D I V\K(F)		103.18	461.9056	1383.686	0.016	11.5	5.32	22067.8	7.85	HUMAN	C9JTJ4	V-set and immunoglobulin domain-containing protein 4 (Fragment)
23871	dirMS_041712_NAR_20mM_minus.11760.11760.2	2	4.01	0	8.63E+04	S583s M58	(K)ALVAEs	(K)A L/V A E s H N m K(N)	s:N-acetylglucosamine (S) m:	166.72	659.8282	1099.556	219.0927	13.9	6.79	80540.3	8.34	HUMAN	Q92541	RNA polymerase-associated protein RTF1 homolog
23872	dirMS_041712_NAR_20mM_minus.13846.13846.2	2	4.01	0	3.15E+05		(K)LGGSAV	(K)L G G S A V|I/S L/E/G K|P L(-)		188.88	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
23873	dirMS_041712_NAR_30mM_minus2.12114.12114.2	2	4.01	0	4.12E+04		(K)GISQEQ	(K)G I/S Q/E/Q M/Q/E F R(A)		119.47	676.8161	1352.626	-0.0014	-1	4.53	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
23874	dirMS_041712_NAR_30mM_minus2.6720.6720.2	2	4.01	0	9.58E+04		(R)SQESGY	(R)S Q/E\S/G/Y Y D/R(M)		89.97	552.7321	1104.459	-0.0023	-2.1	4.37	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
23875	dirMS_041712_NAR_30mM_minus2.7180.7180.2	2	4.01	2	4.70E+05	S692s	(K)ELKEEKs	(K)E/L K/E|E K|s K(H)	s:Phosphorylated S	93.02	535.762	990.547	79.9701	3.5	6.33	152344.8	4.64	HUMAN	G3V599	Cutaneous T-cell lymphoma-associated antigen 5
23876	dirMS_041712_NAR_40mM_minus2.9479.9479.3	3	4.01	0	9.99E+04		(K)AASDIA	(K)A A S D I/A M/T E L/P P/T H P I R(L)		138.25	607.3174	1819.937	0.0006	0.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
23877	dirMS_041712_NAR_50mM_minus2.15412.15412.3	3	4.01	1	1.73E+05		(K)DVLFLK	(K)D V|L/F/L K D C\V/G P E/V E K(A)	C:Carbamidomethylation	156.42	583.3014	1747.893	-0.0039	-2.2	4.32	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
23878	dirMS_041712_NAR_50mM_minus2.17413.17413.3	3	4.01	1	2.59E+04	S65s	(K)SKTGLPL	(K)S K T/G/L P L s/T Y F S\A V K(L)	s:N-acetylglucosamine (S)	169.05	601.3217	1598.879	203.0717	-4.3	9.7	13157.7	10.2	HUMAN	H7C2A0	Glycerol kinase (Fragment)
23879	dirMS_041712_NAR_50mM_minus2.7154.7154.3	3	4.01	1	2.86E+04		(R)SQCLQV	(R)S Q/C L Q V P E R E A Q D A Q K(Q)	C:Carbamidomethylation	107.55	629.6378	1886.902	-0.0037	-1.9	4.68	23297.7	6.12	HUMAN	K7ESF4	Uncharacterized protein (Fragment)
23880	dirMS_041712_NAR_60mM_minus.10927.10927.3	3	4.01	1	1.03E+05		(K)TAVCDI	(K)T A/V C/D I/P P R G L K(M)	C:Carbamidomethylation	119.85	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
23881	dirMS_041712_NAR_60mM_minus.11241.11241.3	3	4.01	1	1.68E+05		(R)AEDEGG	(R)A E D E G/G A R/A Q/L/L K(S)		122.18	453.2461	1357.707	0.0167	12.3	4.68	232239.1	5.52	HUMAN	F2Z2U8	Myosin-14
23882	dirMS_041712_NAR_60mM_minus.14041.14041.3	3	4.01	0	2.39E+05		(K)IVNFLLQ	(K)I V N F/L/L Q H S A/K(V)		138.03	423.9167	1269.731	0.0042	3.3	8.76	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
23883	dirMS_041712_NAR_60mM_minus.15309.15309.2	2	4.01	0	4.13E+05		(R)EHALLA	(R)E H/A|L|L A/Y/T L G V\K(Q)		144.67	657.873	1314.742	-0.0029	-2.2	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
23884	dirMS_041712_NAR_120mM_plus.6049.6049.3	3	4.01	1	3.76E+04		(R)YDSNSG	(R)Y/D|S N S/G G\E R E I Q/R(T)		85.05	504.2287	1510.688	-0.0165	-10.9	4.68	41280.4	4.9	HUMAN	B4DR63	26S protease regulatory subunit 4
23885	dirMS_041712_NAR_120mM_plus.7284.7284.3	3	4.01	1	2.99E+04		(K)NRQEYD	(K)N R Q E\Y/D A L|A K(V)		91.33	403.2084	1207.607	0.0041	3.4	6.07	23970.7	5.47	HUMAN	Q6I9Y2	THO complex subunit 7 homolog
23886	dirMS_041712_NAR_120mM_plus.7418.7418.2	2	4.01	0	1.91E+05		(K)HQNVQ	(K)H/Q/N\V Q L/P/R(E)		92.48	496.2727	991.543	-0.0051	-5.1	9.75	21912.8	9.55	HUMAN	A6NLN1	Polypyrimidine tract binding protein 1, isoform CRA_e
23887	dirMS_041712_NAR_120mM_plus.9611.9611.4	4	4.01	1	6.40E+04	K385k	(R)ISYLVQ	(R)I S Y L V Q/H Q\R S H V G k(N)	k:Ubiquitin-K	102.98	442.2427	1651.903	114.0463	1.9	9.99	44933.5	7.98	HUMAN	H7BXX1	Zinc finger protein 306, isoform CRA_a
23888	dirMS_041712_NAR_120mM_plus.9788.9788.4	4	4.01	2	7.06E+05		(K)KMGIEK	(K)K\M G I E K L D I/L/T E L K(Y)		104.53	408.4892	1630.945	-0.0098	-6	6.18	79656.1	8.97	HUMAN	Q4G163	F-box only protein 43
23889	dirMS_041712_NAR_120mM_plus.9909.9909.4	4	4.01	1	3.56E+06		(K)DTGKTP	(K)D T G K T P V E P/E/V/A I/H/R(I)		104.8	412.9719	1648.865	0.0005	0.3	5.45	5429.1	9.6	HUMAN	E5RIP1	40S ribosomal protein S20
23890	dirMS_041712_NAR_20mM_plus.16056.16056.3	3	4.01	0	4.41E+03	M221m	(R)ALTVPE	(R)A L T V/P E L T Q Q/m F D/A K(N)	m:Oxidized methionine	182.08	569.9583	1691.867	15.9931	-1.1	4.37	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
23891	dirMS_041712_NAR_20mM_plus.19043.19043.3	3	4.01	0	7.26E+04		(K)LQNVQI	(K)L Q\N V Q I/A/L|D Y L R(H)		202.9	482.6066	1445.811	-0.0058	-4	5.83	20181.7	9.9	HUMAN	E9PIA2	Plectin (Fragment)
23892	dirMS_041712_NAR_20mM_plus.8439.8439.2	2	4.01	0	2.72E+04	M254m M	(R)LIDDmV	(R)L I/D D/m V A/Q A m/K(S)	m:Oxidized methionine	128.07	633.8075	1234.617	31.9907	0.7	4.21	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
23893	dirMS_041712_NAR_30mM_plus2.21635.21635.2	2	4.01	0	2.01E+05		(R)TTNFAG	(R)T T/N/F/A/G I L S/Q G L R(I)		169.25	689.3749	1377.748	-0.006	-4.3	9.41	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
23894	dirMS_041712_NAR_30mM_plus2.21824.21824.2	2	4.01	0	2.27E+05		(R)TTNFAG	(R)T T\N\F\A|G I L/S Q/G L R(I)		169.43	689.3749	1377.748	-0.006	-4.3	9.41	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
23895	dirMS_041712_NAR_30mM_plus2.7990.7990.2	2	4.01	0	2.62E+04		(K)EGALCE	(K)E G A\L/C/E/E N M R(G)	C:Carbamidomethylation	94.92	604.7561	1208.503	0.0015	1.2	4.25	96306.4	6.41	HUMAN	P13639	Elongation factor 2
23896	dirMS_041712_NAR_40mM_plus2.10600.10600.2	2	4.01	0	7.56E+04		(R)LSESQLS	(R)L/S|E/S Q L/S F R(R)		127.93	533.7789	1066.553	-0.0022	-2.1	6	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
23897	dirMS_041712_NAR_40mM_plus2.11702.11702.3	3	4.01	1	6.34E+04		(K)TVNVV	(K)T/V|N V\V Q F/E/P S K/G A I G K(A)		135.05	558.6431	1673.922	-0.0073	-4.4	8.26	83905.8	6.62	HUMAN	P41250	Glycine--tRNA ligase
23898	dirMS_041712_NAR_40mM_plus2.12136.12136.2	2	4.01	0	3.28E+03		(K)LYANM	(K)L Y|A/N M/F E\R(L)		137.6	522.2521	1043.498	-0.001	-0.9	6	9740.1	10.08	HUMAN	H0YFG2	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed (Fragment)
23899	dirMS_041712_NAR_40mM_plus2.17625.17625.3	3	4.01	1	6.01E+04		(R)SAEVTL	(R)S A/E/V\T L/E V A G K S W E L C G I(-)	C:Carbamidomethylation	169.88	650.3372	1948.968	0.0286	14.7	4.25	44226.9	6.5	HUMAN	O15533-2	Isoform 2 of Tapasin
23900	dirMS_041712_NAR_40mM_plus2.5175.5175.2	2	4.01	0	3.48E+05	M154m M	(R)mGYmD	(R)m G Y\m D/P R(E)	m:Oxidized methionine	85.57	451.1811	869.364	31.9905	0.7	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
23901	dirMS_041712_NAR_40mM_plus2.6963.6963.2	2	4.01	0	2.64E+04		(R)DYDDM	(R)D Y|D/D M S P R(R)		100.75	499.6964	998.388	-0.0029	-2.9	3.93	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
23902	dirMS_041712_NAR_40mM_plus2.7493.7493.3	3	4.01	0	6.28E+03	T40t	(K)HAEAtL	(K)H A E A\t L/G S/G N L R(M)	t:Phosphorylated T	104.08	435.8697	1225.628	79.9662	-0.1	6.75	14802.4	4.98	HUMAN	D6RCK3	MOB kinase activator 1B (Fragment)
23903	dirMS_041712_NAR_40mM_plus2.8726.8726.2	2	4.01	1	1.20E+05		(K)YLRDSG	(K)Y/L/R D S\G\F(-)		113.28	429.2135	857.415	0.0045	5.3	5.83	13902.7	5.73	HUMAN	C9J2N0	Profilin
23904	dirMS_041712_NAR_40mM_plus2.9277.9277.2	2	4.01	0	1.46E+05		(R)QTVAV	(R)Q T V|A V/G V/I/K(A)		116.85	457.7854	914.567	-0.0034	-3.7	8.75	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
23905	dirMS_041712_NAR_50mM_plus2.12175.12175.3	3	4.01	1	3.05E+05		(K)NQVAL	(K)N Q|V/A\L N/P Q N T V F D A K R(L)		131.65	605.6528	1814.951	-0.0069	-3.8	8.75	70336.2	5.48	HUMAN	P08107	Heat shock 70 kDa protein 1A/1B
23906	dirMS_041712_NAR_60mM_plus.10034.10034.3	3	4.01	0	1.94E+06		(K)TPVEPE	(K)T P V E P E V/A/I/H R(I)		109.87	416.5628	1247.674	-0.0004	-0.3	5.37	5429.1	9.6	HUMAN	E5RIP1	40S ribosomal protein S20
23907	dirMS_041712_NAR_60mM_plus.13517.13517.3	3	4.01	1	5.02E+05		(R)INVYYN	(R)I N|V/Y Y N E A/T G G K Y V P R(A)		126.65	615.3146	1843.934	-0.0045	-2.4	8.43	50286.6	4.79	HUMAN	P68371	Tubulin beta-4B chain
23908	dirMS_041712_NAR_60mM_plus.16209.16209.3	3	4.01	1	1.12E+06		(K)TDKTLV	(K)T/D K T\L\V|L/L/M G\K(E)		141.08	406.908	1218.713	-0.0032	-2.6	8.26	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
23909	dirMS_041712_NAR_60mM_plus.20545.20545.3	3	4.01	0	5.10E+03		(K)HLTVEE	(K)H L T V E E/L/F/G/T/S\L P K(E)		167.45	524.2918	1570.848	0.0133	8.5	5.4	63479.5	5.83	HUMAN	Q9NPI6	mRNA-decapping enzyme 1A
23910	dirMS_041712_NAR_60mM_plus.5595.5595.3	3	4.01	1	7.68E+04	M118m T1	(R)YAmRYF	(R)Y/A\m R Y/F A\t V/S K(S)	m:Oxidized methionine t:N-a	87.8	519.2487	1336.672	219.0597	-9.4	9.7	41977.7	6.73	HUMAN	E9PE01	Unconventional myosin-Vc
23911	dirMS_041712_NAR_60mM_plus.8833.8833.3	3	4.01	1	4.26E+05	M239m	(K)GIDGN	(K)G I D G N\m H/V/R M\G K(L)	m:Oxidized methionine	103.3	444.2219	1314.641	16.0106	11.8	8.76	83192.7	6.08	HUMAN	E9PES4	Kinesin-like protein KIF3A
23912	dirMS_041712_NAR_30mM_minus2.12203.12203.2	2	4	0	6.85E+05		(K)VLQLYP	(K)V L|Q|L\Y/P N/N K(A)		118.93	544.8076	1088.61	-0.0019	-1.8	8.56	9740.1	10.08	HUMAN	H0YFG2	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed (Fragment)
23913	dirMS_041712_NAR_30mM_minus2.15638.15638.2	2	4	0	1.54E+05		(K)AMTGV	(K)A M/T/G V E Q/W P Y R(A)		138.4	669.3172	1337.631	-0.0036	-2.7	6.04	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
23914	dirMS_041712_NAR_30mM_minus2.18672.18672.2	2	4	0	2.88E+05		(K)YPQLLP	(K)Y/P/Q L\L P G I R(G)		155.77	528.816	1056.62	0.0047	4.4	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
23915	dirMS_041712_NAR_30mM_minus2.7081.7081.2	2	4	0	1.72E+05		(R)ETQSQL	(R)E/T/Q/S/Q/L E T E R(S)		92.87	610.7948	1220.575	0.007	5.7	4.25	334221.3	6.44	HUMAN	P15924	Desmoplakin
23916	dirMS_041712_NAR_30mM_minus2.8094.8094.2	2	4	0	1.83E+05		(K)GSGTAE	(K)G S/G/T/A/E V E/L K(K)		98.32	495.7528	990.51	-0.0119	-12	4.53	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
23917	dirMS_041712_NAR_30mM_minus2.8762.8762.2	2	4	0	6.12E+04		(R)GAESPF	(R)G A|E S/P/F E E K(S)		100.83	497.2314	993.452	0.0032	3.2	4.25	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
23918	dirMS_041712_NAR_40mM_minus2.6895.6895.3	3	4	0	3.82E+04		(R)AALAHS	(R)A A/L A H S E E\V T/A/S Q V/A A T K(T)		111.18	595.3178	1783.919	0.0204	11.4	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
23919	dirMS_041712_NAR_50mM_minus2.14351.14351.3	3	4	0	3.37E+05		(K)LHIIEVG	(K)L H\I I E V G T|P/P T G N Q P F P K(K)		149.9	649.0215	1945.054	-0.0042	-2.2	6.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
23920	dirMS_041712_NAR_60mM_minus.14468.14468.3	3	4	1	2.21E+05	K794k	(R)LKPGKE	(R)L K/P G K E D k L F R(K)	k:Ubiquitin-K	140.65	482.2774	1330.784	114.0335	-6.5	9.7	147219.5	9.31	HUMAN	Q8NHM5-4	Isoform 4 of Lysine-specific demethylase 2B
23921	dirMS_041712_NAR_120mM_plus.18637.18637.4	4	4	1	6.08E+05	S626s	(R)CPsILGG	(R)C/P s I L/G G/L A\P E K/D Q/P K(S)	C:Carbamidomethylation s:N-ace	150.23	479.0094	1709.889	203.1267	24.7	6.07	269273.3	6.66	HUMAN	A5YKK6	CCR4-NOT transcription complex subunit 1
23922	dirMS_041712_NAR_120mM_plus.6977.6977.3	3	4	2	1.79E+04		(K)AKSRCT	(K)A K S R\C T E/L/E K(E)	C:Carbamidomethylation	89.97	407.8773	1221.626	-0.0083	-6.8	8.63	52484.4	4.97	HUMAN	B3KR21	GRIP and coiled-coil domain-containing protein 2 (Fragment)
23923	dirMS_041712_NAR_120mM_plus.7230.7230.2	2	4	1	1.06E+06		(R)LSVDYG	(R)L/S/V/D/Y G K K(S)		90.95	455.2548	909.504	-0.0017	-1.9	8.5	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
23924	dirMS_041712_NAR_20mM_plus.15801.15801.3	3	4	0	1.73E+05		(R)GNPTVE	(R)G/N P T V E V D L/F T/S K(G)		180.2	469.577	1406.716	0.0003	0.2	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
23925	dirMS_041712_NAR_20mM_plus.9186.9186.2	2	4	0	7.02E+04		(K)ATAVVD	(K)A T/A V/V\D G A F K(E)		134.42	489.7674	978.525	0.0021	2.1	5.88	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
23926	dirMS_041712_NAR_20mM_plus.9609.9609.2	2	4	0	7.76E+04		(K)AVDSQI	(K)A/V/D S Q I/L|P K(I)		137.17	485.7824	970.557	0.0008	0.8	5.88	25891.4	10.67	HUMAN	F8W181	60S ribosomal protein L6 (Fragment)
23927	dirMS_041712_NAR_30mM_plus2.9313.9313.2	2	4	0	4.71E+05		(K)TAVCDI	(K)T A\V C/D/I P P R(G)	C:Carbamidomethylation	101.32	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
23928	dirMS_041712_NAR_50mM_plus2.11649.11649.3	3	4	1	1.66E+05		(K)QIDLSTV	(K)Q I D L/S T V/D/L/K K(L)		128.98	420.5781	1259.72	-0.0008	-0.6	5.96	21156.2	9.41	HUMAN	P55145	Mesencephalic astrocyte-derived neurotrophic factor
23929	dirMS_041712_NAR_50mM_plus2.11985.11985.3	3	4	1	3.33E+06		(R)VVDLM	(R)V V|D L M A H M A S K/E(-)		130.52	444.2215	1330.649	0.0006	0.4	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
23930	dirMS_041712_NAR_50mM_plus2.20795.20795.3	3	4	1	1.67E+05		(R)GGGNQ	(R)G G\G N\Q V/S L L N V/V M D L K K(C)		178.62	591.3291	1771.974	-0.0007	-0.4	8.59	218583	5.58	HUMAN	F5GWX5	Chromodomain-helicase-DNA-binding protein 4
23931	dirMS_041712_NAR_60mM_plus.12563.12563.3	3	4	1	6.43E+05		(R)IKPVEEV	(R)I/K/P/V E E V/K Y\M K(N)		122.07	455.257	1363.765	-0.0089	-6.6	8.43	13979.2	5.17	HUMAN	Q9H246	Uncharacterized protein C1orf21
23932	dirMS_041712_NAR_60mM_plus.19165.19165.3	3	4	0	1.07E+05		(K)HSMNP	(K)H S M N P F C\E\I/A/V/E E A/V R(L)	C:Carbamidomethylation	157.47	630.2949	1888.868	0.0021	1.1	4.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
23933	dirMS_041712_NAR_60mM_plus.20552.20552.3	3	4	1	3.05E+05		(K)ITQDIFQ	(K)I/T|Q/D I/F Q/Q L L K R(G)		168	501.626	1502.869	-0.0055	-3.7	8.75	72796.9	6.75	HUMAN	A6NC17	Methionine--tRNA ligase, cytoplasmic
23934	dirMS_041712_NAR_60mM_plus.21272.21272.3	3	4	0	2.23E+05		(R)QARPTY	(R)Q A R P T Y\A T\A|M L/Q/S L L K(-)		175.57	597.9953	1791.979	-0.0072	-4	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
23935	dirMS_041712_NAR_60mM_plus.7027.7027.3	3	4	0	1.25E+06	N1298n	(K)nLLGSG	(K)n\L L G S/G/P A/L/R(L)	n:N-acetylglucosamine (N)	94.95	400.8875	997.579	203.069	-8.6	9.75	151851.5	9.27	HUMAN	O95789	Zinc finger MYM-type protein 6
23936	dirMS_041712_NAR_60mM_plus.9817.9817.3	3	4	0	1.22E+06		(R)ASGNYA	(R)A S|G/N/Y/A T V I S H N P E T K(K)		109.13	563.613	1688.824	0.0006	0.4	6.79	24115.6	11.59	HUMAN	E9PIZ3	60S ribosomal protein L8
23937	dirMS_041712_NAR_20mM_minus.7343.7343.3	3	3.99	0	8.31E+03	M13m M1	(K)ISGGSV	(K)I/S G G S V V/E m/Q/G/D E m T R(I)	m:Oxidized methionine	121.18	576.5901	1695.768	31.9881	-1	4.14	17833.3	8.73	HUMAN	C9J4N6	Isocitrate dehydrogenase [NADP] cytoplasmic (Fragment)
23938	dirMS_041712_NAR_30mM_minus2.16533.16533.2	2	3.99	0	2.46E+05		(K)NAAGAL	(K)N A|A|G A L D L L K(E)		143.65	493.2881	985.568	0.0013	1.3	5.84	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
23939	dirMS_041712_NAR_30mM_minus2.17570.17570.2	2	3.99	0	2.16E+05		(K)AQVEQE	(K)A Q V|E|Q E L T T L R(L)		149.7	644.3426	1287.69	-0.0124	-9.6	4.53	533778	5.74	HUMAN	Q15149	Plectin
23940	dirMS_041712_NAR_30mM_minus2.5868.5868.2	2	3.99	1	1.92E+04		(R)KLCDNL	(R)K L/C/D\N L/R(M)	C:Carbamidomethylation	85.95	459.7452	918.483	0.0006	0.6	8.75	163032.4	6.38	HUMAN	F5H335	Eukaryotic translation initiation factor 3 subunit A
23941	dirMS_041712_NAR_40mM_minus2.5353.5353.3	3	3.99	1	1.07E+05		(K)DSYVGD	(K)D S\Y/V/G D E/A Q S K/R(G)		89.5	452.2136	1354.623	0.0029	2.1	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
23942	dirMS_041712_NAR_40mM_minus2.7805.7805.3	3	3.99	2	1.94E+05	M131m T1	(R)LRmAQt	(R)L R m A Q t s L V E|V/Q K/E R(D)	m:Oxidized methionine t:Pho	125.23	655.3013	1787.98	175.9097	-9.1	8.75	40024.8	9.75	HUMAN	J3KPB0	Testis-expressed sequence 13A protein
23943	dirMS_041712_NAR_40mM_minus2.9340.9340.3	3	3.99	0	1.42E+05		(K)QLTEED	(K)Q L/T E/E/D G/V H S V I E E N I K(C)		137.88	647.3235	1939.961	-0.0048	-2.5	4.25	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
23944	dirMS_041712_NAR_50mM_minus2.11912.11912.3	3	3.99	1	1.60E+05	M264m	(K)TmTDV	(K)T m T D\V V G/N P\E/E E R R(A)	m:Oxidized methionine	135.73	550.2563	1632.765	15.9897	-3.1	4.41	37190.7	6.16	HUMAN	F8VRQ4	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1
23945	dirMS_041712_NAR_50mM_minus2.16212.16212.3	3	3.99	1	8.21E+04		(R)LGLSTL	(R)L/G L/S T L/G E L/K Q N L S R(S)		158.97	543.6477	1628.933	-0.0044	-2.7	8.75	22294.4	5.26	HUMAN	O43399	Tumor protein D54
23946	dirMS_041712_NAR_50mM_minus2.16798.16798.3	3	3.99	1	1.53E+05		(K)NIPIPTL	(K)N I\P I/P T L K D/F\A K(A)		163.45	452.9385	1356.789	0.0124	9.1	8.59	20960.6	7.05	HUMAN	H0YKU1	Tropomodulin-3 (Fragment)
23947	dirMS_041712_NAR_50mM_minus2.18164.18164.3	3	3.99	1	7.92E+05		(R)KAIIIFVP	(R)K A I I I/F V|P V P Q L K(S)		173.52	489.3206	1465.95	-0.0032	-2.2	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
23948	dirMS_041712_NAR_50mM_minus2.9251.9251.3	3	3.99	1	7.89E+04		(R)LAEFSS	(R)L/A/E|F/S S Q A A E E E E K V K(S)		120.68	598.964	1794.876	0.0018	1	4.32	232239.1	5.52	HUMAN	F2Z2U8	Myosin-14
23949	dirMS_041712_NAR_120mM_plus.8404.8404.4	4	3.99	2	4.26E+05	N112n	(K)IKIQLAn	(K)I K I Q/L A n E E/Y K/R(I)	n:N-acetylglucosamine (N)	97.37	427.7382	1504.848	203.0828	2	8.5	32432.6	11.01	HUMAN	E9PBQ3	Transmembrane protein 199
23950	dirMS_041712_NAR_20mM_plus.12269.12269.2	2	3.99	0	5.97E+04		(R)DLAPIGI	(R)D L|A/P/I G I R(V)		157.78	427.7587	854.509	0.0007	0.8	5.84	27150.8	7.95	HUMAN	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2
23951	dirMS_041712_NAR_20mM_plus.12556.12556.2	2	3.99	0	7.47E+04		(K)VNQIGS	(K)V N Q I/G\S/V/T E/S I\Q A C K(L)	C:Carbamidomethylation	158.92	817.4114	1633.821	-0.0059	-3.6	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
23952	dirMS_041712_NAR_20mM_plus.14125.14125.2	2	3.99	0	7.40E+04		(K)LSILYPA	(K)L S I/L/Y/P A/T T G R(N)		169.05	596.3406	1191.673	0.0007	0.6	8.75	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
23953	dirMS_041712_NAR_20mM_plus.15244.15244.2	2	3.99	0	2.33E+03		(R)LAQQNL	(R)L A/Q Q/N L E T L/K(K)		177.02	579.3248	1157.652	-0.0101	-8.8	6	58494.3	9.29	HUMAN	Q8N3R3	T-cell activation inhibitor, mitochondrial
23954	dirMS_041712_NAR_20mM_plus.17978.17978.3	3	3.99	0	1.89E+05		(R)TVQSLEI	(R)T V Q\S\L E I/D/L/D S M R(N)		195.05	502.9236	1506.747	0.0094	6.2	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
23955	dirMS_041712_NAR_30mM_plus2.12169.12169.2	2	3.99	0	3.17E+05		(R)LPLETAY	(R)L/P|L/E/T A Y R(R)		116.9	481.7661	962.531	-0.0056	-5.9	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
23956	dirMS_041712_NAR_30mM_plus2.12660.12660.2	2	3.99	0	5.00E+05		(R)QINLSNI	(R)Q I/N/L/S/N I R(A)		118.65	479.2725	957.548	-0.0099	-10.3	9.75	102679.8	6.75	HUMAN	Q7KZF4	Staphylococcal nuclease domain-containing protein 1
23957	dirMS_041712_NAR_30mM_plus2.20045.20045.2	2	3.99	0	1.80E+04		(R)TLMNLG	(R)T L/M/N\L|G G L A|V A R(D)		158.72	608.3434	1215.688	-0.0083	-6.8	9.41	22562.2	8.8	HUMAN	P37802	Transgelin-2
23958	dirMS_041712_NAR_30mM_plus2.22344.22344.3	3	3.99	0	5.20E+05		(R)VGNLGL	(R)V G N L G L\A T S/F/F|N E R(N)		172.8	508.9306	1524.781	-0.0033	-2.1	5.97	73641.5	6.74	HUMAN	O00571	ATP-dependent RNA helicase DDX3X
23959	dirMS_041712_NAR_40mM_plus2.14166.14166.3	3	3.99	1	1.07E+05		(K)VQGGAL	(K)V Q/G G A/L E D S Q L\V A G V A F K K(T)		148.83	639.6845	1917.044	-0.0051	-2.6	6.04	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
23960	dirMS_041712_NAR_40mM_plus2.4064.4064.2	2	3.99	0	1.74E+05	M299m M	(K)NmmAA	(K)N m m/A A C D|P/R(H)	C:Carbamidomethylation m:Oxid	67.68	549.2114	1065.427	31.9881	-1.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
23961	dirMS_041712_NAR_50mM_plus2.11196.11196.3	3	3.99	1	1.06E+04	M862m	(K)RNVEG	(K)R N V E G/Q\D\m L Y Q S L K(L)	m:Oxidized methionine	126.42	566.2937	1680.837	16.0292	20.2	6.07	102015.4	5.13	HUMAN	K7EJT8	AP-2 complex subunit beta
23962	dirMS_041712_NAR_50mM_plus2.21722.21722.3	3	3.99	1	1.78E+05		(K)LKVNFL	(K)L K V N F|L/P E I/I T L S K(E)		184.43	539.0011	1614.983	0.0058	3.6	8.59	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
23963	dirMS_041712_NAR_50mM_plus2.7360.7360.3	3	3.99	0	1.63E+05		(R)EATNPP	(R)E/A T|N/P P/V I Q E E K P K(K)		104.22	527.282	1579.833	-0.0012	-0.7	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
23964	dirMS_041712_NAR_120mM_minus.10423.10423.2	2	3.98	0	2.30E+05	S404s T411	(R)SsVFAD	(R)S s V F A D/V E t H F\R(T)	s:Phosphorylated S t:Phosph	111.13	777.8083	1394.67	159.9394	4.3	5.3	61899.1	9.58	HUMAN	P59817	Zinc finger protein 280A
23965	dirMS_041712_NAR_20mM_minus.10521.10521.2	2	3.98	0	1.59E+05		(R)TTPSYV	(R)T T\P S Y/V A F T D/T/E R(L)		154.47	744.3547	1487.701	0.0009	0.6	4.37	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
23966	dirMS_041712_NAR_20mM_minus.8032.8032.3	3	3.98	1	2.29E+05	S623s	(K)EYAQRI	(K)E Y A Q R|I P s G G D G K(T)	s:N-acetylglucosamine (S)	129.42	527.5948	1377.676	203.0941	9.3	6.17	132385.9	5.91	HUMAN	P56199	Integrin alpha-1
23967	dirMS_041712_NAR_20mM_minus.8420.8420.2	2	3.98	0	1.09E+05		(R)GYSFTT	(R)G Y/S/F/T T/T/A E R(E)		133.35	566.771	1132.527	0.0078	6.9	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
23968	dirMS_041712_NAR_30mM_minus2.6864.6864.2	2	3.98	0	1.89E+05		(K)DYNVTA	(K)D Y/N|V/T A N S K(L)		92	506.2404	1011.474	-0.0006	-0.6	5.83	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
23969	dirMS_041712_NAR_40mM_minus2.14969.14969.3	3	3.98	2	8.92E+05		(R)LLSTLGP	(R)L L S T L/G P\R/A E A L R/A H G E K(L)		172.33	640.3618	1919.082	-0.0113	-5.9	8.75	419509.2	6.23	HUMAN	Q9NRC6	Spectrin beta chain, non-erythrocytic 5
23970	dirMS_041712_NAR_40mM_minus2.8562.8562.3	3	3.98	0	2.85E+05		(R)SVIDPV	(R)S V\I/D P/V/P A P V G D S H V D G A A K(S)		132.48	644.3329	1930.987	-0.0027	-1.4	4.41	58326.8	5.7	HUMAN	Q13177	Serine/threonine-protein kinase PAK 2
23971	dirMS_041712_NAR_50mM_minus2.12420.12420.3	3	3.98	1	2.74E+04	K28k	(K)LESLKED	(K)L E S L K E D/I/k E F F K(I)	k:Ubiquitin-K	139.47	580.6487	1625.879	114.053	5.8	4.87	7921	8.05	HUMAN	D6RA60	TBC1 domain family member 19 (Fragment)
23972	dirMS_041712_NAR_50mM_minus2.17212.17212.3	3	3.98	1	2.93E+04	T301t	(K)ILLPELtP	(K)I L/L P E L t P R V/L L P(-)	t:Phosphorylated T	166.75	518.6444	1473.94	79.9783	7.7	6	33266.7	7.27	HUMAN	H7C4G6	Isovaleryl-CoA dehydrogenase, mitochondrial (Fragment)
23973	dirMS_041712_NAR_50mM_minus2.7620.7620.3	3	3.98	0	1.15E+03	M44m M4	(K)SGTGIA	(K)S G T G/I/A A m/S V m R P E Q I m K(S)	m:Oxidized methionine	111.57	652.3177	1906.955	47.9838	-0.5	8.46	8797.3	9.3	HUMAN	H3BR50	V-type proton ATPase 16 kDa proteolipid subunit
23974	dirMS_041712_NAR_50mM_minus2.9651.9651.3	3	3.98	1	8.78E+04	M27m	(K)LAEQAE	(K)L A E Q/A E R Y/D/E M/V E S m K(K)	m:Oxidized methionine	122.68	648.9602	1928.873	15.9932	-0.9	4.25	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
23975	dirMS_041712_NAR_60mM_minus.7481.7481.3	3	3.98	2	6.13E+05		(K)QSVDKV	(K)Q S/V D K V/T/S/P T K V(-)		100.82	430.241	1288.711	-0.0023	-1.8	8.59	64225	6.66	HUMAN	E7EX44	Caldesmon

23976	dirMS_041712_NAR_120mM_plus.4273.4273.2	2	3.98	1	1.17E+06	M310m	(R)TKTEISE	(R)T/K|T E I/S E m N R(N)	m:Oxidized methionine	70.03	612.7976	1208.594	15.994	-0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
23977	dirMS_041712_NAR_20mM_plus.14463.14463.2	2	3.98	0	1.54E+05		(K)VSTLPAI	(K)V/S T/L/P A I T L K(L)		171.87	521.8283	1042.651	-0.0013	-1.3	8.72	20599.3	9.19	HUMAN	H7C1V0	Cathepsin D light chain (Fragment)
23978	dirMS_041712_NAR_20mM_plus.17580.17580.3	3	3.98	0	6.52E+04		(K)ITNLTQC	(K)I T\N L T Q/Q L/E/Q A S I V/K(K)		192.92	562.6523	1685.943	-0.0009	-0.5	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
23979	dirMS_041712_NAR_30mM_plus2.18026.18026.2	2	3.98	0	7.89E+03		(K)NINLPEI	(K)N I|N L|P E I/P/R(N)		147.53	533.2996	1065.605	-0.0132	-12.4	6	44223.4	5.17	HUMAN	E2QRD5	Protein C15orf38-AP3S2
23980	dirMS_041712_NAR_30mM_plus2.19201.19201.2	2	3.98	0	4.65E+04		(R)NLLTPLN	(R)N L|L/T\P L M/E K(F)		153.12	529.8026	1058.591	0.0065	6.1	6	26268.8	7.96	HUMAN	F5GZM3	Exportin-T (Fragment)
23981	dirMS_041712_NAR_30mM_plus2.5502.5502.2	2	3.98	0	6.24E+04		(K)QSQDEP	(K)Q/S Q/D E/P L R(S)		83.02	486.741	972.475	0.0002	0.2	4.37	33803.8	6.12	HUMAN	B1AKP7	TAR DNA binding protein
23982	dirMS_041712_NAR_40mM_plus2.12678.12678.2	2	3.98	0	5.91E+04		(K)NYIFLR(I	(K)N Y/I/F L R(N)		141.12	413.2357	825.462	0.0024	2.9	8.75	41595	8.51	HUMAN	P78406	mRNA export factor
23983	dirMS_041712_NAR_40mM_plus2.14250.14250.3	3	3.98	1	6.67E+04		(R)STGLELE	(R)S T/G\L E L E T P S L V/P V K K(N)		149.58	566.6552	1697.968	-0.0173	-10.2	5.86	34828	9.96	HUMAN	F5H5K4	Serine/threonine-protein phosphatase 1 regulatory subunit 10
23984	dirMS_041712_NAR_40mM_plus2.15921.15921.3	3	3.98	1	1.18E+05	M428m	(R)DAALVY	(R)D A\A L V Y H K/L H Q L H T m G K(H)	m:Oxidized methionine	160.67	660.0113	1962.038	15.9815	-6.8	8.52	96861.1	9.96	HUMAN	B5MD58	Sterol regulatory element-binding protein 1
23985	dirMS_041712_NAR_40mM_plus2.15983.15983.2	2	3.98	0	9.23E+04		(R)YLTVAA	(R)Y L/T/V/A A V F R(G)		161.72	520.2997	1039.593	-0.0014	-1.3	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
23986	dirMS_041712_NAR_40mM_plus2.17993.17993.3	3	3.98	1	2.69E+04		(K)ALEVAE	(K)A L\E|V/A E Y L T/P V L K E S K(F)		171.98	597.3336	1789.995	-0.0083	-4.7	4.79	8368.5	5.85	HUMAN	F8WDI0	Ubiquitin-like-conjugating enzyme ATG3
23987	dirMS_041712_NAR_40mM_plus2.19148.19148.3	3	3.98	0	1.21E+05		(R)ETSSDV	(R)E T\S S/D V A\L/A S H I L T A L R(E)		178.87	595.3161	1783.955	-0.0211	-11.8	5.32	36920.6	4.68	HUMAN	O00273	DNA fragmentation factor subunit alpha
23988	dirMS_041712_NAR_40mM_plus2.19676.19676.3	3	3.98	1	3.80E+05		(R)ILDDDTI	(R)I L/D D D T I/I/T/T/L E N L K R(E)		185.02	625.0111	1873.028	-0.0089	-4.8	4.23	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
23989	dirMS_041712_NAR_50mM_plus2.15206.15206.3	3	3.98	1	7.88E+05		(R)GFPTIYF	(R)G F/P T I Y F/S P/A N K K(L)		148.63	490.5973	1469.779	-0.0014	-0.9	9.7	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
23990	dirMS_041712_NAR_50mM_plus2.7516.7516.3	3	3.98	1	2.35E+05		(R)LDHTFE	(R)L D H T F/E A L Q E R K R(K)		105.42	548.2865	1642.866	-0.021	-12.8	6.76	150311.9	6.33	HUMAN	B7ZKT6	SOS2 protein
23991	dirMS_041712_NAR_60mM_plus.13807.13807.3	3	3.98	0	2.15E+05		(R)LFFQPH	(R)L F\F Q/P H Q A G L/S K(V)		128.93	458.2494	1372.737	-0.0035	-2.6	8.76	8684.1	9.22	HUMAN	C9J0F6	Ubiquitin-like modifier-activating enzyme 5 (Fragment)
23992	dirMS_041712_NAR_60mM_plus.16917.16917.3	3	3.98	1	1.96E+04		(R)ARLGGII	(R)A R L G G I\P V G\V\V/A/V E/T R(T)		146.58	531.981	1593.944	-0.0151	-9.4	9.64	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
23993	dirMS_041712_NAR_60mM_plus.6371.6371.3	3	3.98	0	1.06E+05		(K)AFYYPEE	(K)A F Y Y P E E A G L/A F G/G P G S S R(Y)		91.83	659.3068	1975.919	-0.0126	-6.4	4.53	69919.5	5.97	HUMAN	P09172	Dopamine beta-hydroxylase
23994	dirMS_041712_NAR_120mM_minus.13057.13057.3	3	3.97	2	1.49E+05		(R)LRQKEA	(R)L R Q K E A/S V T T N(-)		125.65	416.2324	1246.675	0.0077	6.1	8.75	147757.2	9.22	HUMAN	H0YM30	Formin-1
23995	dirMS_041712_NAR_120mM_minus.14820.14820.4	4	3.97	1	4.07E+05		(K)AVELARI	(K)A V E L A R L/A F P V/E/V V/K(L)		134.37	411.0042	1640.973	0.0216	13.1	6.19	199341	5.78	HUMAN	Q9UG01	Intraflagellar transport protein 172 homolog
23996	dirMS_041712_NAR_120mM_minus.18287.18287.4	4	3.97	1	1.95E+05	T44t	(K)LNtTAILI	(K)L N t T A I L R E|G A L Y Q R(Q)	t:N-acetylglucosamine (T)	154.23	481.2594	1718.955	203.061	-9.6	8.75	52519.9	10.78	HUMAN	D6REC4	Uncharacterized protein
23997	dirMS_041712_NAR_20mM_minus.10928.10928.2	2	3.97	1	1.71E+05	S58s	(K)sKTSEAL	(K)s K/T\S E A L A/K(L)	s:Phosphorylated S	157.15	507.7443	934.52	79.9609	-5.3	8.31	72714	5.88	HUMAN	E7EQQ2	WND/140 kDa
23998	dirMS_041712_NAR_30mM_minus2.17149.17149.2	2	3.97	0	4.44E+04		(K)LGINSLC	(K)L/G/I/N S/L Q E L/K(Q)		146.95	557.8242	1114.647	-0.0055	-5	6	25978.5	4.91	HUMAN	C9J502	Prostate leucine zipper variant 2
23999	dirMS_041712_NAR_60mM_minus.10592.10592.3	3	3.97	0	1.26E+05		(R)VLGSGT	(R)V L G S G/T|W/P S A/P K(M)		119.07	400.5514	1199.642	-0.0023	-1.9	8.72	29805.8	10.73	HUMAN	Q9P0G3	Kallikrein-14
24000	dirMS_041712_NAR_60mM_minus.11235.11235.4	4	3.97	0	1.45E+05		(K)LFEVEEV	(K)L F E V E E/V/N C I C V D W K(K)	C:Carbamidomethylation	122.72	485.7316	1939.893	0.0117	6	4	15402.4	4.99	HUMAN	E9PMA6	Pancreatic lipase-related protein 1 (Fragment)
24001	dirMS_041712_NAR_60mM_minus.18140.18140.3	3	3.97	2	7.18E+04		(R)LDARGD	(R)L D/A R G D K S/T L L/R(N)		162.33	448.9308	1344.759	0.0185	13.7	8.75	58975.6	10.31	HUMAN	Q5T925	Novel protein (KIAA0894)
24002	dirMS_041712_NAR_60mM_minus.8932.8932.3	3	3.97	1	5.81E+03	S1277s	(K)ADPYVV	(K)A D P/Y V/V V s A G R E R(Q)	s:Phosphorylated S	110.88	500.2367	1418.739	79.9569	-6.3	6.11	202288.6	5.88	HUMAN	A9Z1Z3	Fer-1-like protein 4
24003	dirMS_041712_NAR_60mM_minus.9815.9815.3	3	3.97	1	4.34E+05	S139s	(R)LDVQLA	(R)L D/V Q L/A\S/R s L R(Q)	s:Phosphorylated S	114.55	446.5761	1257.727	79.9864	15	9.6	22801.8	6.25	HUMAN	Q86X83	COMM domain-containing protein 2
24004	dirMS_041712_NAR_20mM_plus.6996.6996.3	3	3.97	0	1.33E+05	M298m M	(R)MGQmA	(R)M G Q m A m\G\G A/m/G I/N N R(G)	m:Oxidized methionine	115.02	529.5557	1538.67	47.9831	-1.1	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
24005	dirMS_041712_NAR_20mM_plus.9436.9436.2	2	3.97	2	1.54E+04	K3010k	(K)RGGGKD	(K)R G/G G K/D G S V\T G T/k(R)	k:Ubiquitin-K	136.63	667.3458	1219.639	114.0454	1.8	9.99	360912.4	9.65	HUMAN	P46013	Antigen KI-67
24006	dirMS_041712_NAR_20mM_plus.9985.9985.2	2	3.97	0	1.82E+05		(K)IVVVTAC	(K)I V|V/V T A G V R(Q)		139.42	457.2945	913.583	-0.0012	-1.3	9.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
24007	dirMS_041712_NAR_30mM_plus2.5701.5701.2	2	3.97	0	1.44E+05		(K)LDDYQE	(K)L/D\D/Y|Q E R(M)		84.67	469.719	938.421	0.0093	9.9	4.03	20235.4	6.77	HUMAN	E9PLA9	Caprin-1 (Fragment)
24008	dirMS_041712_NAR_40mM_plus2.17953.17953.3	3	3.97	0	1.71E+05		(K)ISSIQSIV	(K)I S\S I Q/S I V/P A L/E I A N A H R(K)		172.4	640.3668	1919.071	0.015	7.8	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
24009	dirMS_041712_NAR_50mM_plus2.13446.13446.3	3	3.97	1	2.72E+05	S662s	(R)LMGAFA	(R)L M G A F/A s/L D/L K/S\Q R(K)	s:N-acetylglucosamine (S)	139.05	580.6491	1536.82	203.1125	19	8.75	85584.9	6.27	HUMAN	Q9ULH4	Leucine-rich repeat and fibronectin type-III domain-containing protein 2
24010	dirMS_041712_NAR_50mM_plus2.7270.7270.3	3	3.97	0	9.48E+03		(R)AQGASC	(R)A Q/G A S C P G T A D A G I A S P G R(A)	C:Carbamidomethylation	104.12	581.944	1743.808	0.0096	5.5	5.88	28749.3	12.05	HUMAN	E9PB92	Uncharacterized protein
24011	dirMS_041712_NAR_60mM_plus.11954.11954.3	3	3.97	0	8.89E+05	K233k	(K)LLSESAC	(K)L L S E S\A|Q P/L k K(V)	k:Ubiquitin-K	119.02	443.2516	1213.715	114.0252	-13.4	8.59	32190	4.91	HUMAN	Q9H3N1	Thioredoxin-related transmembrane protein 1
24012	dirMS_041712_NAR_60mM_plus.16573.16573.3	3	3.97	1	1.56E+05	N631n	(K)VALTKLH	(K)V A/L T K L H N/S L n E K(S)	n:N-acetylglucosamine (N)	143.02	557.3061	1466.833	203.0712	-4.9	8.57	90050.1	6.35	HUMAN	O94874	E3 UFM1-protein ligase 1
24013	dirMS_041712_NAR_60mM_plus.16806.16806.3	3	3.97	0	2.20E+05		(R)YQEALH	(R)Y/Q E A/L H/L G S Q L L/R(E)		144.43	509.946	1527.828	-0.0044	-2.9	6.75	47748.2	6.08	HUMAN	O00231	26S proteasome non-ATPase regulatory subunit 11
24014	dirMS_041712_NAR_60mM_plus.17425.17425.3	3	3.97	1	8.46E+05		(R)DKLNNL	(R)D K L N N\L\V/L F/D K(A)		148.4	440.2499	1318.737	-0.0014	-1	5.96	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
24015	dirMS_041712_NAR_60mM_plus.17794.17794.3	3	3.97	1	3.41E+05		(R)LMDLLG	(R)L M/D/L L/G E G L K R(S)		149.52	415.5712	1244.703	-0.0041	-3.3	6.07	52817.9	6.2	HUMAN	F5H3T8	Arginine--tRNA ligase, cytoplasmic
24016	dirMS_041712_NAR_120mM_minus.10560.10560.2	2	3.96	2	1.38E+04		(K)VKEAGS	(K)V/K/E A G\S S M R\K(R)		111.72	546.7932	1092.583	-0.0039	-3.6	9.99	31654.8	5.39	HUMAN	Q9Y3B9	RRP15-like protein
24017	dirMS_041712_NAR_120mM_minus.17701.17701.3	3	3.96	1	4.10E+05		(R)RAPFDLI	(R)R A\P F\D\L/F E/N/R(K)		152.18	422.2193	1264.643	0.0001	0	6.07	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
24018	dirMS_041712_NAR_120mM_minus.6963.6963.2	2	3.96	0	4.18E+05		(K)HNAAFC	(K)H/N\A/A|F/C\Y\K(L)	C:Carbamidomethylation	92.42	505.7282	1010.451	-0.0021	-2.1	8.6	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
24019	dirMS_041712_NAR_120mM_minus.8111.8111.3	3	3.96	1	3.18E+05		(R)KYPEAA	(R)K\Y P E A\A|A/C/Y G/R(A)	C:Carbamidomethylation	98.67	429.2036	1285.599	-0.0031	-2.4	8.5	24827.2	5.74	HUMAN	H3BS86	E3 ubiquitin-protein ligase CHIP (Fragment)
24020	dirMS_041712_NAR_20mM_minus.12034.12034.2	2	3.96	0	2.13E+05	M185m	(K)LAVNm\	(K)L A|V/N m/V|P F P R(L)	m:Oxidized methionine	170.08	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
24021	dirMS_041712_NAR_20mM_minus.7527.7527.2	2	3.96	0	6.66E+05	M239m	(K)EVDEQn	(K)E V/D E/Q m L/N V/Q/N K(N)	m:Oxidized methionine	123.67	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
24022	dirMS_041712_NAR_20mM_minus.9278.9278.2	2	3.96	0	2.52E+04		(K)IDATSAS	(K)I/D/A\T/S A S V L A S R(F)		142.23	595.8208	1190.638	-0.0032	-2.7	5.84	73273.4	4.96	HUMAN	P13667	Protein disulfide-isomerase A4
24023	dirMS_041712_NAR_30mM_minus2.16639.16639.2	2	3.96	1	9.48E+04		(R)LGTSGT	(R)L G|T\S G/T A K K(T)		144.22	431.7497	862.499	-0.0071	-8.3	10	19068	5.9	HUMAN	Q13522	Protein phosphatase 1 regulatory subunit 1A
24024	dirMS_041712_NAR_30mM_minus2.17577.17577.2	2	3.96	0	1.15E+05		(R)SGSNTG	(R)S G S N T/G L D Y I/K(F)		149.22	577.7894	1154.569	0.0027	2.4	5.55	56524.8	9.73	HUMAN	P35367	Histamine H1 receptor
24025	dirMS_041712_NAR_30mM_minus2.18657.18657.2	2	3.96	0	2.94E+05		(K)YPQLLPC	(K)Y P/Q L/L/P G I R(G)		155.65	528.816	1056.62	0.0047	4.4	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
24026	dirMS_041712_NAR_30mM_minus2.4616.4616.2	2	3.96	0	7.76E+05		(K)QASEGP	(K)Q A/S E G P/L/K(G)		76.28	415.2235	829.441	-0.0017	-2	6	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
24027	dirMS_041712_NAR_30mM_minus2.5955.5955.2	2	3.96	0	9.70E+04		(R)ISSSSFSI	(R)I/S|S/S S F S R(V)		86.57	435.7203	870.432	0.0018	2	9.75	19288.4	10.19	HUMAN	F8VQY3	Keratin, type II cytoskeletal 8 (Fragment)
24028	dirMS_041712_NAR_50mM_minus2.10604.10604.3	3	3.96	0	1.90E+05		(K)SQIHDIV	(K)S Q I H D\I V\L/V/G/G S T R(I)		128.67	494.6068	1481.807	-0.0012	-0.8	6.46	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
24029	dirMS_041712_NAR_50mM_minus2.11021.11021.3	3	3.96	0	1.66E+05	M35m	(K)AASDIAr	(K)A A\S D I/A m T/E/L/P P T H P I\R(L)	m:Oxidized methionine	130.68	612.6486	1819.937	15.9942	-0.4	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
24030	dirMS_041712_NAR_50mM_minus2.9918.9918.3	3	3.96	2	2.57E+03		(R)MNREEL	(R)M N/R E E L\E D S F/F R L R(E)		123.65	614.6369	1841.896	-0.0001	-0.1	4.87	108373.2	5.56	HUMAN	G3V236	X-linked retinitis pigmentosa GTPase regulator-interacting protein 1
24031	dirMS_041712_NAR_60mM_minus.19169.19169.3	3	3.96	0	1.10E+05		(K)HLLQAP	(K)H L L Q A\P L D D\A/Q/E I L Q A R(F)		169.72	644.347	1931.035	-0.0081	-4.2	4.54	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
24032	dirMS_041712_NAR_60mM_minus.6572.6572.3	3	3.96	1	2.56E+04		(K)TGQAPC	(K)T G Q A|P G Y S/Y T A A N K N K(G)		95.17	557.6064	1670.813	-0.0086	-5.2	9.52	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
24033	dirMS_041712_NAR_120mM_plus.14232.14232.3	3	3.96	1	2.78E+05	S602s	(K)WDPPKI	(K)W D P\P K/D N G G/s E I L/K(Y)	s:N-acetylglucosamine (S)	127.67	586.9652	1555.775	203.1059	15.1	4.56	135053.9	5.64	HUMAN	Q53EP0	Fibronectin type III domain-containing protein 3B
24034	dirMS_041712_NAR_120mM_plus.16543.16543.3	3	3.96	0	2.84E+05		(K)FFEHFIE	(K)F F E/H/F/I/E/G G R(T)		139.92	413.5361	1238.595	-0.0015	-1.2	5.4	32986.6	4.86	HUMAN	F5GYJ8	Ubiquitin thioesterase OTUB1
24035	dirMS_041712_NAR_120mM_plus.19175.19175.3	3	3.96	1	6.13E+05		(R)HGVQEL	(R)H G\V Q E\L E|I\E|L Q S Q L S K K(A)		153.85	656.0237	1966.06	-0.0038	-2	5.5	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
24036	dirMS_041712_NAR_120mM_plus.20549.20549.3	3	3.96	1	9.26E+05		(K)AAIDWF	(K)A A/I/D/W F D G K E F H/G N I I/K(V)		160.18	654.3334	1960.992	-0.0059	-3	5.38	49181	4.93	HUMAN	K7EPT6	TATA-binding protein-associated factor 2N
24037	dirMS_041712_NAR_120mM_plus.5544.5544.2	2	3.96	1	6.62E+05	M1m M2m	(-)mmTDLK	(-)m m T D L/K/Q s H S V\R(L)	m:Oxidized methionine s:Pho	82.1	772.8273	1432.704	111.9438	-8	8.52	17281.5	5.11	HUMAN	C9J5T8	Aldo-keto reductase family 1 member C-like protein 1 (Fragment)
24038	dirMS_041712_NAR_30mM_plus2.18038.18038.3	3	3.96	0	1.41E+05		(R)VNPALA	(R)V N P A\L A|E|L N L/R(S)		147.58	403.9019	1209.695	-0.0039	-3.2	5.97	20026.6	4.67	HUMAN	E9PIK5	Ribonuclease inhibitor (Fragment)
24039	dirMS_041712_NAR_30mM_plus2.6637.6637.2	2	3.96	0	2.22E+05		(K)ALDEME	(K)A L|D/E/M E K(Q)		89.35	418.1994	835.387	0.0049	5.9	4.14	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
24040	dirMS_041712_NAR_40mM_plus2.10225.10225.2	2	3.96	1	8.78E+05		(K)KITIADC	(K)K I T|I A D C G Q|L|E(-)	C:Carbamidomethylation	125.52	624.3146	1247.63	-0.0081	-6.5	4.75	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
24041	dirMS_041712_NAR_40mM_plus2.12115.12115.2	2	3.96	0	7.68E+03		(K)LWNTLG	(K)L W/N/T L G V/C K(Y)	C:Carbamidomethylation	137.6	545.791	1090.571	0.0033	3.1	8.75	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
24042	dirMS_041712_NAR_40mM_plus2.6432.6459.2	2	3.96	0	2.12E+05	M154m	(R)mGYMD	(R)m G\Y\M D|P R(E)	m:Oxidized methionine	96.87	443.1854	869.364	15.9991	4.7	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
24043	dirMS_041712_NAR_40mM_plus2.9594.9594.2	2	3.96	0	1.27E+05		(K)FYEAFSK	(K)F/Y|E/A F S K(N)		120.15	446.2159	891.425	-0.0002	-0.2	6	20127.1	9.4	HUMAN	H0Y598	Heat shock protein HSP 90-beta (Fragment)
24044	dirMS_041712_NAR_50mM_plus2.8093.8093.3	3	3.96	0	1.56E+04		(R)IEPADAI	(R)I E/P/A/D A H V L Q K(N)		108.3	407.5589	1220.663	-0.0012	-1	5.32	11018.4	8.89	HUMAN	B0AZT5	N-alpha-acetyltransferase 50
24045	dirMS_041712_NAR_50mM_plus2.9074.9074.3	3	3.96	1	4.63E+05		(K)TAVCDIF	(K)T A/V/C D I/P P R G L K(M)	C:Carbamidomethylation	115.2	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
24046	dirMS_041712_NAR_60mM_plus.10513.10513.3	3	3.96	0	1.38E+06		(K)VFEHDS	(K)V F/E H/D S\V E L N C K(M)	C:Carbamidomethylation	111.87	492.8967	1476.679	-0.0032	-2.2	4.65	31975.7	6.55	HUMAN	P10768	S-formylglutathione hydrolase
24047	dirMS_041712_NAR_60mM_plus.5164.5164.3	3	3.96	1	3.54E+05		(K)MSSPED	(K)M/S S/P E D D/S D T K R(L)		85.33	456.5289	1367.574	-0.0022	-1.6	4.23	103309.5	5.34	HUMAN	A0AV56	SAFB protein
24048	dirMS_041712_NAR_120mM_minus.19410.19410.3	3	3.95	1	2.15E+05		(K)EETKKLT	(K)E E T K\K L T\E/S/A E/I/R(I)		160.55	511.9444	1533.812	0.0068	4.4	4.95	81251.3	5.83	HUMAN	Q96NL6	Sodium channel and clathrin linker 1
24049	dirMS_041712_NAR_120mM_minus.7333.7333.3	3	3.95	1	7.89E+05		(K)IQDKEGI	(K)I Q D K E G/I/P/P D\Q Q/R(L)		94.87	508.5981	1523.781	-0.0015	-1	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
24050	dirMS_041712_NAR_30mM_minus2.11171.11171.2	2	3.95	0	1.23E+05		(K)SCNCLLL	(K)S C|N C L/L/L/K(V)	C:Carbamidomethylation	114.5	504.2543	1007.501	0.0001	0.1	8.47	47510.4	7.04	HUMAN	P06733	Alpha-enolase
24051	dirMS_041712_NAR_50mM_minus2.14738.14738.3	3	3.95	1	8.78E+04		(K)EFDPTIT	(K)E F D/P T/I/T/D/A S L S L P S R R(M)		150.93	635.6664	1904.971	0.0134	7	4.56	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
24052	dirMS_041712_NAR_50mM_minus2.14753.14753.3	3	3.95	0	4.12E+05		(K)QLEAIDC	(K)Q\L\E/A/I D Q/L H L E Y A/K(R)		152.43	557.6327	1670.875	0.0087	5.2	4.65	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
24053	dirMS_041712_NAR_50mM_minus2.16022.16022.3	3	3.95	1	5.14E+04	N751n	(K)nTKLQEI	(K)n/T K L/Q E L V/L/K(N)	n:N-acetylglucosamine (N)	159.03	463.6084	1185.72	203.0905	8	8.59	111703.3	4.91	HUMAN	H0YJD4	E3 ubiquitin-protein ligase HECTD1 (Fragment)
24054	dirMS_041712_NAR_60mM_minus.8070.8070.3	3	3.95	0	1.41E+04	S33s	(K)LAEHGG	(K)L/A|E/H G G s C F S F Q V L G R(L)	C:Carbamidomethylation s:Phos	104.78	615.611	1764.849	79.9698	1.9	6.75	8821.7	8.5	HUMAN	H0YHK7	Uncharacterized protein
24055	dirMS_041712_NAR_120mM_plus.4296.4296.3	3	3.95	0	6.69E+05	T85t S88s	(R)LTAtSTs	(R)L/T/A t S T s Q I K(-)	t:Phosphorylated T s:Phosph	71.18	403.8446	1049.584	159.9355	2.4	8.75	10563.9	9.98	HUMAN	E9PF88	Metastasis-associated protein MTA3
24056	dirMS_041712_NAR_120mM_plus.5493.5493.3	3	3.95	1	2.35E+05		(-)MEERGS	(-)M/E/E/R G S P D G D L/A R(S)		82.2	478.2139	1432.649	-0.0214	-14.9	4.32	71857	10.27	HUMAN	Q96FN5	Kinesin-like protein KIF12
24057	dirMS_041712_NAR_20mM_plus.10676.10676.3	3	3.95	0	2.82E+04		(K)SQLLAPI	(K)S Q L L A/P\P P/P S/A P P G N K(T)		146.3	524.2902	1570.859	-0.0027	-1.7	8.47	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
24058	dirMS_041712_NAR_20mM_plus.11711.11711.2	2	3.95	0	1.35E+05		(R)AQAALA	(R)A Q A/A\L|A/V/N I S A/A R(G)		153.67	628.3565	1255.712	-0.006	-4.8	9.79	58479.6	6.23	HUMAN	P40227	T-complex protein 1 subunit zeta
24059	dirMS_041712_NAR_20mM_plus.12203.12203.2	2	3.95	0	6.14E+04		(R)YVDIAIP	(R)Y V/D\I A I P/C N/N K(G)	C:Carbamidomethylation	157.03	653.8273	1306.646	0.0013	1	5.83	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
24060	dirMS_041712_NAR_20mM_plus.16782.16782.3	3	3.95	0	3.11E+05		(K)VQIAVA	(K)V Q\I A\V A\N/A Q/E/L L Q R(M)		187.02	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
24061	dirMS_041712_NAR_20mM_plus.7451.7451.2	2	3.95	0	1.17E+05		(K)AQYEDI	(K)A Q|Y/E D I A N R(S)		120.42	540.2601	1079.512	0.0013	1.2	4.37	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
24062	dirMS_041712_NAR_20mM_plus.9021.9021.2	2	3.95	0	4.59E+03	M1901m	(R)AEmEVL	(R)A E/m/E\V L/L A/S K(A)	m:Oxidized methionine	133.03	553.7889	1090.581	15.9893	-5.1	4.53	533778	5.74	HUMAN	Q15149	Plectin
24063	dirMS_041712_NAR_30mM_plus2.15553.15553.2	2	3.95	0	2.09E+05		(R)IDTGWL	(R)I D/T/G W/L D R(L)		133.77	488.2554	975.489	0.0141	14.5	4.21	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
24064	dirMS_041712_NAR_30mM_plus2.21774.21774.2	2	3.95	1	6.55E+03		(K)ALKMTD	(K)A L|K|M T D/A Q V K(T)		169.57	552.8032	1104.608	-0.009	-8.2	8.64	34706.5	9.94	HUMAN	P31314	T-cell leukemia homeobox protein 1
24065	dirMS_041712_NAR_30mM_plus2.22076.22076.2	2	3.95	2	1.51E+05	M302m	(R)NKEVTR	(R)N/K E V T R A/F m/K(I)	m:Oxidized methionine	171.68	620.3199	1223.657	15.976	-15.2	9.99	35454.4	9.15	HUMAN	Q8NG83	Olfactory receptor 2M3
24066	dirMS_041712_NAR_30mM_plus2.5454.5454.3	3	3.95	0	6.70E+04		(R)GGSGGS	(R)G G S G/G S Y G G G G S G G G|Y/G G/G S G S R(G)		82.82	597.9128	1791.728	-0.0039	-2.2	8.59	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
24067	dirMS_041712_NAR_40mM_plus2.6915.6915.2	2	3.95	0	7.26E+04		(R)LTEGCSI	(R)L/T/E G C S F/R(R)	C:Carbamidomethylation	101	485.2217	969.446	-0.0097	-10	6	5988.9	10.55	HUMAN	C9J1C5	40S ribosomal protein S27
24068	dirMS_041712_NAR_50mM_plus2.10780.10780.3	3	3.95	1	4.80E+04		(R)SVLGEAI	(R)S V/L/G E A D Q K G S L V/A P D R(L)		124.37	581.3036	1741.908	-0.0117	-6.7	4.56	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
24069	dirMS_041712_NAR_50mM_plus2.11632.11632.3	3	3.95	1	1.31E+05		(K)VTQLDLI	(K)V/T/Q L/D L D/G P K E L S R(R)		128.88	524.2855	1570.843	-0.0016	-1	4.56	20629.7	8.84	HUMAN	Q13442	28 kDa heat- and acid-stable phosphoprotein
24070	dirMS_041712_NAR_50mM_plus2.17163.17163.3	3	3.95	0	2.65E+05		(R)DEPIHILI	(R)D E/P/I H/I L N V A/I K(T)		158.45	454.6	1361.779	0.0067	4.9	5.32	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
24071	dirMS_041712_NAR_50mM_plus2.18164.18164.3	3	3.95	0	2.29E+05		(R)DIKPDNI	(R)D I K P D N F\L/M/G I G R(H)		163.4	492.5943	1475.767	0.0008	0.6	5.96	27968.7	9.69	HUMAN	D6REM4	Casein kinase I isoform alpha
24072	dirMS_041712_NAR_50mM_plus2.7574.7574.3	3	3.95	1	4.08E+04	M93m	(K)DITKWS	(K)D I T/K W S S N/D L m D K(I)	m:Oxidized methionine	105.65	523.5793	1552.731	15.9922	-1.8	4.43	117565.7	6.78	HUMAN	E7EQC3	Membrane-associated phosphatidylinositol transfer protein 2
24073	dirMS_041712_NAR_50mM_plus2.9099.9099.3	3	3.95	1	1.56E+05		(R)YLMEED	(R)Y L/M E E D E D A/Y K K(Q)		114.85	511.8989	1533.678	0.0044	2.9	4.18	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
24074	dirMS_041712_NAR_50mM_plus2.9205.9205.3	3	3.95	1	2.75E+05		(R)TNAENE	(R)T N/A E/N E F V T/I K|K(D)		115.83	465.2518	1393.732	0.0087	6.2	5.81	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
24075	dirMS_041712_NAR_60mM_plus.19790.19790.3	3	3.95	1	1.53E+05		(R)GMLRED	(R)G M L R E D A\V|L/E Y L K(I)		163.87	512.9411	1536.809	-0.0003	-0.2	4.68	67933	6.08	HUMAN	P26038	Moesin
24076	dirMS_041712_NAR_60mM_plus.4665.4665.3	3	3.95	1	4.77E+05	M54m	(K)SLDEmE	(K)S L/D E m/E K Q Q R(E)	m:Oxidized methionine	77.38	427.2032	1263.6	15.9953	0.3	4.68	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
24077	dirMS_041712_NAR_60mM_plus.5594.5594.3	3	3.95	0	7.68E+04		(R)TAEHEA	(R)T A E H E A A\Q/Q D\L Q/S K(F)		87.8	519.2487	1555.735	-0.0031	-2	4.65	156557.7	5.52	HUMAN	Q86UP2	Kinectin
24078	dirMS_041712_NAR_60mM_plus.5639.5639.3	3	3.95	1	1.53E+05	M131m	(R)QmGQP	(R)Q/m G\Q/P/C/D/A Y Q K R(L)	C:Carbamidomethylation m:Oxid	87.98	499.8898	1481.662	15.9925	-1.6	8.59	334221.3	6.44	HUMAN	P15924	Desmoplakin
24079	dirMS_041712_NAR_120mM_minus.14418.14418.3	3	3.94	1	1.13E+06		(R)RLEAAYI	(R)R L E A A\Y|L/D/L Q R(I)		132.53	449.9126	1347.738	-0.0147	-10.9	6.07	15962.5	9.61	HUMAN	B4DT30	Tubulin-specific chaperone A
24080	dirMS_041712_NAR_120mM_minus.7944.7944.3	3	3.94	1	4.27E+04		(K)GKGGEI	(K)G K\G G/E I Q/P V S V|K(V)		98.08	400.229	1198.679	-0.0066	-5.5	8.59	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
24081	dirMS_041712_NAR_20mM_minus.10069.10069.2	2	3.94	0	1.24E+05		(R)YALYDA	(R)Y A|L|Y D A T Y E T K(E)		150.82	669.3156	1337.626	-0.0021	-1.5	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
24082	dirMS_041712_NAR_20mM_minus.8458.8458.2	2	3.94	0	3.26E+05	M239m	(K)EITALAP	(K)E I|T A L/A/P/S T m K(I)	m:Oxidized methionine	133.58	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
24083	dirMS_041712_NAR_30mM_minus2.16479.16479.2	2	3.94	0	6.44E+04	M2243m	(K)mSIYQA	(K)m S\I|Y Q A M/W/K(G)	m:Oxidized methionine	144.38	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
24084	dirMS_041712_NAR_50mM_minus2.12001.12001.3	3	3.94	0	1.61E+05		(K)EMNPAI	(K)E M/N|P/A/L G I/D C L H K(G)	C:Carbamidomethylation	136.6	499.9082	1497.719	-0.0088	-5.9	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon

24085	dirMS_041712_NAR_50mM_minus2.12016.12016.3	3	3.94	0	2.85E+05	M22m	(K)QGPLHG	(K)Q G P L H G m L I/N T/P Y|V T K(D)	m:Oxidized methionine	136.62	595.6534	1768.941	16.0042	5.2	8.6	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
24086	dirMS_041712_NAR_60mM_minus.10057.10057.3	3	3.94	1	1.25E+05		(R)AGTGV	(R)A G/T/G V/D N V D L/E/A A T R K(G)		115.55	539.6117	1616.824	-0.0033	-2	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
24087	dirMS_041712_NAR_120mM_plus.23699.23699.4	4	3.94	1	2.02E+05	T347t	(R)SEVRSV	(R)S E V R/S\V/A V T H t F Q I/A K(A)	t:N-acetylglucosamine (T)	178.83	494.7707	1772.965	203.0956	8.2	8.49	47153.7	9.89	HUMAN	A6NKP2	Putative short-chain dehydrogenase/reductase family 42E member 2
24088	dirMS_041712_NAR_120mM_plus.7793.7793.3	3	3.94	0	4.72E+05		(R)SGSMD	(R)S G|S/M/D/P S G A H P S V R(Q)		94.15	462.218	1384.627	0.0121	8.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
24089	dirMS_041712_NAR_120mM_plus.8105.8127.2	2	3.94	0	1.42E+06		(R)HQGVM	(R)H|Q|G V/M\V G M/G Q K(D)		96.13	586.2888	1171.571	-0.0007	-0.6	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
24090	dirMS_041712_NAR_20mM_plus.13979.13979.2	2	3.94	0	1.34E+05		(R)GGIVDE	(R)G G I/V/D/E G A L L R(A)		167.83	550.3066	1099.611	-0.0047	-4.3	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
24091	dirMS_041712_NAR_20mM_plus.17853.17853.2	2	3.94	0	7.96E+04		(R)TTLLPGL	(R)T T|L/L/P G L L K(T)		193.87	478.3131	955.619	0.0003	0.3	8.41	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
24092	dirMS_041712_NAR_20mM_plus.18258.18258.2	2	3.94	0	5.11E+04		(K)FIIPQIV	(K)F I|I/P Q I V K(Y)		197.13	479.3081	957.613	-0.0042	-4.4	8.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
24093	dirMS_041712_NAR_20mM_plus.18817.18817.3	3	3.94	0	1.53E+04	M80m	(R)APLPDL	(R)A P L P D L Y/P/F/G\T m R(G)	m:Oxidized methionine	200.72	498.5865	1477.751	15.9941	-0.5	5.88	81122.9	9.03	HUMAN	H3BLZ8	Probable ATP-dependent RNA helicase DDX17
24094	dirMS_041712_NAR_20mM_plus.19302.19302.3	3	3.94	0	2.70E+05		(R)LAGTQP	(R)L A G T Q\P L E\V/L/E A V\Q/R(S)		204.33	541.9731	1623.906	-0.0017	-1	4.53	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
24095	dirMS_041712_NAR_30mM_plus2.11497.11497.2	2	3.94	0	2.32E+05		(-)MMEVA	(-)M M|E|V/A A A D V K(Q)		113.63	532.7609	1064.512	0.003	2.9	4.37	9475.6	4.64	HUMAN	J3KRD5	Cytosolic non-specific dipeptidase (Fragment)
24096	dirMS_041712_NAR_40mM_plus2.6319.6319.2	2	3.94	0	1.96E+05		(K)TEISEM	(K)T E|I/S E/M N R(N)		96.27	490.2292	979.451	-0.0002	-0.2	4.53	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
24097	dirMS_041712_NAR_40mM_plus2.8028.8028.2	2	3.94	0	2.11E+05		(K)VAVLSQ	(K)V A V/L|S Q N R(T)		108.22	443.7528	886.51	-0.0122	-13.7	9.72	45212.4	9.41	HUMAN	B7Z233	Acetyl-CoA acetyltransferase, cytosolic
24098	dirMS_041712_NAR_50mM_plus2.13100.13100.3	3	3.94	1	9.64E+05		(K)ASLAET	(K)A/S|L/A E T D K\I T L\E V A K(L)		137.32	530.2925	1588.879	-0.0163	-10.2	4.68	65077.2	5.47	HUMAN	B7Z1R5	V-type proton ATPase catalytic subunit A
24099	dirMS_041712_NAR_50mM_plus2.21193.21193.3	3	3.94	1	4.45E+05	M145m	(R)GVmLA	(R)G V|m L A V D A V/I/A E L K K(Q)	m:Oxidized methionine	181.6	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
24100	dirMS_041712_NAR_50mM_plus2.6867.6867.3	3	3.94	2	1.00E+05	S178s	(R)EVLKsKE	(R)E/V L K s K/E L G V A T N(-)	s:Phosphorylated S	100.83	489.9166	1387.779	79.9561	-7	6.24	19990.2	9.45	HUMAN	B4DY35	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial
24101	dirMS_041712_NAR_50mM_plus2.7024.7024.3	3	3.94	1	1.15E+04	T226t	(R)IHTAEKt	(R)I/H T A E/K t/Y E C K(Q)	C:Carbamidomethylation t:N-ace	102.95	528.2459	1379.662	203.0608	-11.8	6.75	75164.1	9.88	HUMAN	K7EQM2	Zinc finger protein 555
24102	dirMS_041712_NAR_50mM_plus2.7939.7939.3	3	3.94	1	3.43E+04	M250m	(K)TTDmA	(K)T T/D/m A P S K E T E M A/L A K(D)	m:Oxidized methionine	108.27	580.6104	1723.824	15.9925	-1.4	4.68	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
24103	dirMS_041712_NAR_60mM_plus.15416.15416.3	3	3.94	1	2.83E+05		(K)LNKITVP	(K)L N K I T/V P A S Q K(L)		137.35	400.2383	1198.715	-0.0151	-12.6	10	46651.1	6.62	HUMAN	F5GXS1	B-cell linker protein
24104	dirMS_041712_NAR_60mM_plus.20368.20368.3	3	3.94	1	3.74E+04	M354m	(K)LLmQLE	(K)L L m Q L E A R E|I K(M)	m:Oxidized methionine	166.93	453.9368	1343.772	16.0243	21.6	6.14	50534.1	8.72	HUMAN	Q5VX52	Spermatogenesis-associated protein 1
24105	dirMS_041712_NAR_60mM_plus.20917.20917.3	3	3.94	1	1.34E+05		(K)TFVNITP	(K)T F/V/N/I T P A E V G V L V G K D R(S)		170.6	639.0248	1915.065	-0.0049	-2.6	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
24106	dirMS_041712_NAR_60mM_plus.6737.6737.3	3	3.94	1	1.11E+06		(R)NTEEEG	(R)N T|E\E E G L K/Y\K(S)		93.37	404.2017	1210.595	-0.0045	-3.7	4.79	83344.9	10.18	HUMAN	E9PK09	Bcl-2-associated transcription factor 1 (Fragment)
24107	dirMS_041712_NAR_60mM_plus.9851.9851.3	3	3.94	0	7.13E+05		(R)QQEGF	(R)Q Q|E G F/K/P/N Y M E/N R(E)		109.4	547.5879	1640.749	0.0006	0.4	6.14	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
24108	dirMS_041712_NAR_120mM_minus.12082.12082.3	3	3.93	1	2.55E+06		(R)NLKASL	(R)N L/K A S L E/N/S L/R(E)		119.45	415.5698	1244.696	-0.0009	-0.7	8.75	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
24109	dirMS_041712_NAR_120mM_minus.5045.5045.3	3	3.93	1	6.76E+04	T526t	(K)AFNQSS	(K)A F/N/Q\S S|K L t K(H)	t:Phosphorylated T	78.53	401.8604	1123.611	79.956	-8.5	10	71017.4	9.95	HUMAN	Q03923	Zinc finger protein 85
24110	dirMS_041712_NAR_20mM_minus.10398.10398.2	2	3.93	0	4.24E+04		(K)AVLSLY	(K)A V|L/S/L/Y A S G R(T)		152.4	518.7929	1036.579	0	0	8.79	14579.3	5.13	HUMAN	K7EM38	Actin, cytoplasmic 2, N-terminally processed (Fragment)
24111	dirMS_041712_NAR_30mM_minus2.15337.15337.2	2	3.93	0	4.97E+05	M2249m	(K)MSIYQA	(K)M S I|Y/Q A m W K(G)	m:Oxidized methionine	136.03	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
24112	dirMS_041712_NAR_30mM_minus2.18722.18722.2	2	3.93	0	2.63E+05		(K)YPQLLP	(K)Y P|Q\L L/P G I/R(G)		156.17	528.816	1056.62	0.0047	4.4	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
24113	dirMS_041712_NAR_30mM_minus2.7268.7268.2	2	3.93	0	2.48E+05	T83t	(K)AVEGQt	(K)A V|E G\Q t R(L)	t:N-acetylglucosamine (T)	93.92	482.244	760.395	203.0859	6.8	6.05	36381	8.8	HUMAN	D3DU85	Na(+)/H(+) exchange regulatory cofactor NHE-RF2
24114	dirMS_041712_NAR_40mM_minus2.14595.14595.3	3	3.93	1	9.76E+04		(R)LKLPSIP	(R)L K L P S I P L/V/P V/S A/Q K(R)		169.73	530.6703	1589.999	-0.0025	-1.6	10	34958.1	9.42	HUMAN	Q15785	Mitochondrial import receptor subunit TOM34
24115	dirMS_041712_NAR_40mM_minus2.15860.15860.3	3	3.93	0	5.07E+05	M466m	(R)QLPQVL	(R)Q L/P/Q V/L H m S E L L N R(G)	m:Oxidized methionine	184.82	565.3111	1677.911	16.0083	7.9	6.75	121344.2	5.76	HUMAN	B4DM01	Helicase SKI2W
24116	dirMS_041712_NAR_50mM_minus2.6744.6744.3	3	3.93	1	3.56E+04	M1048m K	(K)LmPPDR	(K)L m P P D R\T/A V E k(L)	m:Oxidized methionine k:Ub	104.72	462.9052	1256.667	130.0343	-2.5	6.07	294551.9	5.56	HUMAN	O00507	Probable ubiquitin carboxyl-terminal hydrolase FAF-Y
24117	dirMS_041712_NAR_60mM_minus.10159.10159.3	3	3.93	2	8.31E+04		(R)GPDGFS	(R)G P D G/F S R G F A P D G R/R(A)		116.48	531.2693	1591.772	0.0209	13.2	9.51	14650.5	6.84	HUMAN	Q9H840	Gem-associated protein 7
24118	dirMS_041712_NAR_60mM_minus.9896.9896.3	3	3.93	1	2.88E+05		(R)KLDPGS	(R)K L D/P/G S/E\E\T Q/T/L V R(E)		114.75	524.9451	1572.823	-0.002	-1.3	4.68	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
24119	dirMS_041712_NAR_20mM_plus.10734.10734.2	2	3.93	0	4.55E+04		(R)FGIVTSS	(R)F G I V/T S/S A/G T G\T T E D/T E A K(K)		146.4	936.4446	1871.887	-0.005	-2.7	4.14	59643.8	9.11	HUMAN	H0YHG0	Uncharacterized protein (Fragment)
24120	dirMS_041712_NAR_20mM_plus.16590.16590.3	3	3.93	0	5.30E+04	M221m	(R)ALTVPE	(R)A L T V/P E L T Q/Q m F D/A K(N)	m:Oxidized methionine	185.5	569.9583	1691.867	15.9931	-1.1	4.37	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
24121	dirMS_041712_NAR_20mM_plus.16739.16739.2	2	3.93	0	1.22E+05		(K)IAFAITA	(K)I/A|F/A I T/A I K(G)		185.87	474.2987	947.592	-0.0023	-2.4	8.75	17718.4	10.99	HUMAN	P62269	40S ribosomal protein S18
24122	dirMS_041712_NAR_20mM_plus.8316.8316.2	2	3.93	0	3.67E+04	M130m	(R)ESLQQ	(R)E S/L Q/Q/m A E V T/R(E)	m:Oxidized methionine	127.77	654.3208	1291.631	16.0032	6.4	4.53	16719.5	5.02	HUMAN	K7EJ70	Glucosidase 2 subunit beta (Fragment)
24123	dirMS_041712_NAR_30mM_plus2.21648.21648.3	3	3.93	0	1.76E+05	N7n	(-)MAASVL	(-)M A\A S V L n T/V/L R(R)	n:N-acetylglucosamine (N)	169.22	459.9204	1174.661	203.0854	4.4	9.5	14276.1	10.12	HUMAN	B4DFG6	28S ribosomal protein S18b, mitochondrial
24124	dirMS_041712_NAR_30mM_plus2.6221.6221.2	2	3.93	0	1.91E+05	M169m	(R)MQSFG	(R)M Q|S F/G m/K(T)	m:Oxidized methionine	86.63	422.6944	828.374	16.0073	14.6	8.5	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
24125	dirMS_041712_NAR_40mM_plus2.11493.11493.3	3	3.93	1	4.38E+04		(K)DVDEAY	(K)D V/D E A Y M N K V/E L E S R(L)		133.62	599.9504	1797.832	0.0043	2.4	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
24126	dirMS_041712_NAR_50mM_plus2.12847.12847.3	3	3.93	0	4.23E+05		(K)YYVTIID	(K)Y Y V/T/I/I D/A/P G H R(D)		135.48	468.9142	1404.727	0.001	0.7	6.74	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
24127	dirMS_041712_NAR_50mM_plus2.21583.21583.3	3	3.93	1	9.83E+04	T400t	(R)TVLQPK	(R)T V|L Q P K K L/V t E/T\A/G K(E)	t:Phosphorylated T	184.12	564.9788	1612.963	79.9586	-4.6	9.7	65505.1	6.12	HUMAN	B7Z839	Exonuclease 3'-5' domain-containing protein 1
24128	dirMS_041712_NAR_60mM_plus.11069.11069.2	2	3.93	1	6.40E+05		(R)QQEGF	(R)Q Q/E G\F K/G T/F/P D/A R(E)		115.62	740.8612	1480.718	-0.0028	-1.9	6.07	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
24129	dirMS_041712_NAR_60mM_plus.19997.19997.3	3	3.93	1	3.34E+05		(K)GPVREG	(K)G P V R E G D\V\L T/L/L E S E R(E)		165.02	590.6485	1769.939	-0.0083	-4.7	4.41	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
24130	dirMS_041712_NAR_60mM_plus.6266.6266.3	3	3.93	1	2.17E+05		(K)QMNDE	(K)Q M N D E K T A A/D/Y/K(I)		91.65	471.8823	1413.632	0.0009	0.6	4.56	9786.1	5.52	HUMAN	E9PS38	Protein NEDD8-MDP1
24131	dirMS_041712_NAR_60mM_plus.6312.6312.3	3	3.93	0	2.52E+05	M480m	(R)AAHSEG	(R)A A H S E G N T T/A|G L D/m R(E)	m:Oxidized methionine	91.42	516.2346	1530.697	15.9927	-1.4	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
24132	dirMS_041712_NAR_60mM_plus.9251.9251.3	3	3.93	1	6.00E+04		(R)EALRAA	(R)E A L/R A A/T/M E V/K(V)		107.02	406.8878	1218.651	-0.0022	-1.8	6.24	558007.1	5.44	HUMAN	P58107	Epiplakin
24133	dirMS_041712_NAR_120mM_minus.13347.13347.4	4	3.92	2	3.54E+05	M100m	(K)KQGGL	(K)K Q G G L\G\P m N I/P L/V/S D/P K R(T)	m:Oxidized methionine	128.1	481.5173	1907.053	15.9942	-0.3	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
24134	dirMS_041712_NAR_120mM_minus.16998.16998.3	3	3.92	1	5.22E+05	S68s	(R)GGKAs	(R)G G K A s/Q L G/I F/I S K(V)	s:Phosphorylated S	147.63	462.5714	1305.753	79.9471	-13.9	10	16131	6.65	HUMAN	Q5EBL8	PDZ domain-containing protein 11
24135	dirMS_041712_NAR_20mM_minus.12981.12981.2	2	3.92	1	1.97E+05		(K)NADQSL	(K)N A D Q/S L I/R K(W)		181.02	522.7982	1044.58	0.0095	9.1	8.75	180011	6.83	HUMAN	A2A369	Dedicator of cytokinesis 8
24136	dirMS_041712_NAR_30mM_minus2.18721.18721.2	2	3.92	0	1.04E+05		(K)GFGGIG	(K)G F|G G I/G/G I L/R(Y)		156.73	473.7762	946.547	-0.0018	-1.9	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
24137	dirMS_041712_NAR_50mM_minus2.10073.10073.3	3	3.92	1	4.00E+03		(K)LAEQAE	(K)L A/E Q A E R/Y E D M A A F M K(G)		126	634.9586	1902.872	-0.0112	-5.9	4.41	27887.7	4.68	HUMAN	P31947	14-3-3 protein sigma
24138	dirMS_041712_NAR_50mM_minus2.16565.16565.3	3	3.92	0	8.91E+04		(R)LLLDIPL	(R)L L L/D/I P L Q/T P H K(L)		162.4	463.2805	1387.831	-0.0038	-2.7	6.74	198852.6	5.95	HUMAN	A6NKT7	RanBP2-like and GRIP domain-containing protein 3
24139	dirMS_041712_NAR_50mM_minus2.16866.16866.3	3	3.92	0	2.56E+05		(K)ALVSHN	(K)A L V S H\N G S L|I/N V/G S L L Q R(A)		164.02	626.6879	1878.056	-0.0064	-3.4	9.8	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
24140	dirMS_041712_NAR_50mM_minus2.6766.6766.3	3	3.92	1	4.19E+04	M22m M2	(K)LAEQAE	(K)L A|E Q/A|E R Y D D m A T C m K(A)	C:Carbamidomethylation m:Oxid	105.05	655.2831	1931.83	32.0052	7.8	4.32	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
24141	dirMS_041712_NAR_50mM_minus2.8124.8124.3	3	3.92	1	1.57E+05		(K)GILAAD	(K)G I/L A/A D E S/T G S I A K R(L)		113.93	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
24142	dirMS_041712_NAR_50mM_minus2.8836.8836.3	3	3.92	1	4.57E+04		(K)ATAAFS	(K)A T/A A/F/S/N V G/T A I S K K(F)		118.23	489.2711	1465.801	-0.0022	-1.5	10	18660.8	5.58	HUMAN	E9PNK6	Tumor protein D53
24143	dirMS_041712_NAR_60mM_minus.10212.10212.3	3	3.92	0	8.98E+03		(K)TLLLCSP	(K)T L/L L C S P Q P D G F K(S)	C:Carbamidomethylation	115.82	492.59	1475.756	-0.0008	-0.6	5.5	34044.7	8.8	HUMAN	E7EQB3	tRNA-splicing endonuclease subunit Sen34
24144	dirMS_041712_NAR_60mM_minus.11862.11862.3	3	3.92	1	8.97E+04	M546m	(K)QmADT	(K)Q m/A/D/T G K L N T L/L/Q R(A)	m:Oxidized methionine	126.07	535.6216	1588.848	16.0027	4.8	8.75	91324.5	5.75	HUMAN	Q00839	Heterogeneous nuclear ribonucleoprotein U
24145	dirMS_041712_NAR_60mM_minus.15872.15872.3	3	3.92	0	5.84E+05		(K)AVLIAES	(K)A V/L I A E\S T Q P I R(L)		148.73	433.2572	1297.747	0.0096	7.4	6.05	195078.7	6.9	HUMAN	E7EP56	Nuclear pore membrane glycoprotein 210-like
24146	dirMS_041712_NAR_60mM_minus.15960.15960.3	3	3.92	0	3.25E+05	K1450k	(K)GRPSLT	(K)G R/P/S L T G E\N L/E A k(M)	k:Ubiquitin-K	149.63	495.9328	1371.723	114.0612	12.3	6.14	197734.4	8.99	HUMAN	Q9BY89	Uncharacterized protein KIAA1671
24147	dirMS_041712_NAR_60mM_minus.17154.17154.3	3	3.92	1	3.56E+05		(R)KAPSDL	(R)K\A\P S/D\L\Y\Q I/I/L K(A)		156.15	463.6095	1388.815	-0.0008	-0.6	8.5	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
24148	dirMS_041712_NAR_60mM_minus.7570.7570.3	3	3.92	1	1.06E+05	T106t	(R)AVFGG	(R)A V/F G G G t K L S\V L G(-)	t:Phosphorylated T	101.32	429.2175	1205.689	79.9491	-13.4	8.8	11694.5	6.76	HUMAN	P04209	Ig lambda chain V-II region NIG-84
24149	dirMS_041712_NAR_60mM_minus.8102.8102.3	3	3.92	1	1.20E+05		(K)FAAKGE	(K)F/A A K G E G/Q|L G|P A E R(A)		105.55	477.5852	1430.739	0.0024	1.7	6.14	96306.4	6.41	HUMAN	P13639	Elongation factor 2
24150	dirMS_041712_NAR_120mM_plus.14794.14794.2	2	3.92	0	9.17E+04		(R)DWSHY	(R)D W/S/H\Y F/K(I)		130.68	491.725	982.442	0.001	1	6.74	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
24151	dirMS_041712_NAR_120mM_plus.7006.7006.3	3	3.92	1	9.66E+04		(K)SNKDG	(K)S N/K D G G N\Q/E|V E I A R(C)		89.93	506.2499	1516.735	0.0001	0.1	4.68	10305.6	6.94	HUMAN	H7C330	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
24152	dirMS_041712_NAR_120mM_plus.9208.9208.4	4	3.92	1	6.77E+04	Y193y	(K)VLVSLQ	(K)V L/V S L Q K A/E D y M K(T)	y:Phosphorylated Y	102.78	401.7053	1523.814	79.9856	12	6.04	114417.4	5.61	HUMAN	G3V5V3	Nuclear export mediator factor NEMF (Fragment)
24153	dirMS_041712_NAR_120mM_plus.9896.9896.3	3	3.92	1	3.87E+05		(R)RHTAYIS	(R)R H T A/Y I S E\L\K(A)		104.97	406.5624	1217.664	0.0089	7.4	8.6	66632.3	6.2	HUMAN	F2Z2K5	Janus kinase and microtubule-interacting protein 1
24154	dirMS_041712_NAR_20mM_plus.10307.10307.2	2	3.92	1	2.01E+05		(K)LSAAAG	(K)L/S/A\A A G K G V K(G)		143.02	451.2712	901.547	-0.0114	-12.7	10	26265.1	9.9	HUMAN	I3L4Z2	Uncharacterized protein
24155	dirMS_041712_NAR_20mM_plus.13575.13575.3	3	3.92	0	3.33E+04		(R)GALQNI	(R)G A L Q N I|I/P A S T G A A K(A)		165.95	471.2683	1411.79	0	0	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
24156	dirMS_041712_NAR_20mM_plus.18686.18686.2	2	3.92	0	4.18E+04	K553k	(K)ATASGI	(K)A T A S G I/M G\S\P K P/A I k(S)	k:Ubiquitin-K	199.9	771.9239	1428.788	114.0526	6.3	10	97319.1	9.36	HUMAN	Q5T670	MCM10 minichromosome maintenance deficient 10 (S. cerevisiae), isoform CRA_b
24157	dirMS_041712_NAR_20mM_plus.6394.6394.2	2	3.92	0	1.60E+05		(K)DSYVGD	(K)D S Y\V/G/D E A Q S K(R)		107.17	599.7645	1198.522	-0.0005	-0.4	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
24158	dirMS_041712_NAR_20mM_plus.8071.8071.2	2	3.92	1	7.44E+04	K348k	(R)EADVTR	(R)E A/D V T R I/k(K)	k:Ubiquitin-K	124.45	523.2843	931.521	114.0406	-2.2	6.17	128570.2	6.77	HUMAN	Q9H2K2	Tankyrase-2
24159	dirMS_041712_NAR_20mM_plus.8460.8460.2	2	3.92	1	5.51E+04		(R)SSFYCC	(R)S S F|Y/C C K E H Q R(Q)	C:Carbamidomethylation	128.65	751.3263	1501.631	0.0142	9.5	8.34	46876	9.38	HUMAN	Q9GZT9	Egl nine homolog 1
24160	dirMS_041712_NAR_20mM_plus.9181.9181.2	2	3.92	0	6.44E+04		(R)INVELST	(R)I/N V/E L\S/T K(G)		134.27	452.2607	903.515	-0.0004	-0.5	6	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
24161	dirMS_041712_NAR_30mM_plus2.11930.11948.2	2	3.92	0	3.03E+06		(R)EANLAA	(R)E A/N\L/A/A/S/F G/K(S)		115.1	504.2556	1007.516	-0.0117	-11.6	6.1	43928.7	6.58	HUMAN	B4DHG0	Dihydrolipoyl dehydrogenase, mitochondrial
24162	dirMS_041712_NAR_30mM_plus2.5787.5787.2	2	3.92	0	1.18E+05		(R)EAEEVY	(R)E/A E/E/V/Y R(N)		85.17	448.2113	895.416	-0.0003	-0.3	4.25	54793.4	10.51	HUMAN	B7Z4Q3	Putative RNA-binding protein Luc7-like 2
24163	dirMS_041712_NAR_40mM_plus2.19452.19452.3	3	3.92	0	1.01E+04		(K)GAEILEV	(K)G A E\I/L/E V L H/S L P A V/R(Q)		182.63	535.3088	1603.917	-0.0048	-3	5.4	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
24164	dirMS_041712_NAR_40mM_plus2.8275.8275.2	2	3.92	0	6.86E+04		(K)NMGLY	(K)N/M/G L/Y/G E R(V)		109.65	470.2221	939.435	0.0016	1.8	6	43371.1	9.64	HUMAN	E7ERW2	Aspartate aminotransferase
24165	dirMS_041712_NAR_50mM_plus2.14622.14622.3	3	3.92	0	2.95E+04		(R)EHALLA	(R)E H A\L\L A\Y/T\L\G V/K(Q)		143.53	438.9176	1314.742	-0.0034	-2.6	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
24166	dirMS_041712_NAR_50mM_plus2.19575.19575.3	3	3.92	0	2.46E+04		(R)DFNHIN	(R)D F N H I N|V\E/L S/L/L G K(K)		171.35	533.6223	1598.854	-0.0013	-0.8	5.32	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
24167	dirMS_041712_NAR_50mM_plus2.20947.20947.3	3	3.92	0	1.40E+05	T308t	(K)LGNGIN	(K)L/G N G I N/I I V/A t P G\R(L)	t:N-acetylglucosamine (T)	179.4	533.3084	1394.811	203.0992	12.4	9.75	75747.7	9.63	HUMAN	Q9NVP1	ATP-dependent RNA helicase DDX18
24168	dirMS_041712_NAR_50mM_plus2.22199.22199.3	3	3.92	0	1.19E+06		(R)DALSDL	(R)D A/L|S D/L A L H/F L N K(M)		191.6	486.2644	1456.78	-0.0008	-0.6	5.21	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
24169	dirMS_041712_NAR_60mM_plus.10761.10761.2	2	3.92	0	3.90E+05		(R)AHSSM	(R)A H|S/S M V|G V/N L/P Q K(A)		114.23	684.3577	1367.71	-0.0019	-1.4	8.8	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
24170	dirMS_041712_NAR_60mM_plus.19018.19018.3	3	3.92	0	1.62E+04		(K)HSMNP	(K)H S M N P F/C E\I/A V/E E A V R(L)	C:Carbamidomethylation	157.38	630.2949	1888.868	0.0021	1.1	4.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
24171	dirMS_041712_NAR_60mM_plus.7229.7229.2	2	3.92	1	1.84E+05		(K)EMDEE	(K)E M/D/E/E D/K/A F/K(Q)		96	621.2724	1241.535	0.0021	1.7	4.18	7066.2	10	HUMAN	Q9Y2S6	Translation machinery-associated protein 7
24172	dirMS_041712_NAR_120mM_minus.11851.11851.3	3	3.91	1	4.78E+05	K484k	(R)LFLRSPE	(R)L F\L R S P E\T/k(V)	k:Ubiquitin-K	118.68	402.2279	1090.626	114.0436	0.6	8.75	65641.8	9.29	HUMAN	Q96DL1	NXPE family member 2
24173	dirMS_041712_NAR_120mM_minus.15968.15968.3	3	3.91	1	1.40E+05		(K)QLEAID	(K)Q L|E|A/I D/Q L H L E Y A K R(A)		140.98	609.6614	1826.976	-0.0063	-3.4	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
24174	dirMS_041712_NAR_120mM_minus.6651.6651.3	3	3.91	1	1.52E+05		(R)RGETES	(R)R G E T E|S\E/E/F E/K(L)		90.5	447.5368	1340.597	-0.0006	-0.5	4.33	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
24175	dirMS_041712_NAR_30mM_minus2.19753.19753.2	2	3.91	0	3.53E+04	M730m	(K)LNGQL	(K)L N G Q|L/m P T E R(N)	m:Oxidized methionine	164.27	587.8058	1158.594	16.0108	13.5	6	85031.2	8.95	HUMAN	O00522	Krev interaction trapped protein 1
24176	dirMS_041712_NAR_40mM_minus2.15273.15273.3	3	3.91	1	1.31E+05		(R)VISGVL	(R)V I/S/G V L Q L G N I V F K/K(E)		176.82	539.0017	1614.994	-0.0036	-2.2	10	227783.5	5.5	HUMAN	P35579	Myosin-9
24177	dirMS_041712_NAR_40mM_minus2.7683.7683.3	3	3.91	0	6.54E+04		(K)EVVKPV	(K)E V V K P V/P I/T S/P A V S K(V)		123.68	517.6416	1550.915	-0.005	-3.2	8.69	65142.1	9.24	HUMAN	Q96HC4	PDZ and LIM domain protein 5
24178	dirMS_041712_NAR_50mM_minus2.13912.13912.3	3	3.91	1	1.32E+05		(K)NLKVTA	(K)N L K V T A\V/P/T L L K(Y)		147.1	432.9468	1296.825	0.0009	0.7	10	11462.8	5.18	HUMAN	I3L2R6	Thioredoxin domain-containing protein 17
24179	dirMS_041712_NAR_60mM_minus.11202.11202.3	3	3.91	0	2.55E+03		(R)EQLQLL	(R)E Q/L/Q L/L/E/E Q H R(A)		121.5	474.9156	1422.734	-0.0013	-0.9	4.75	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
24180	dirMS_041712_NAR_60mM_minus.19383.19383.3	3	3.91	0	3.41E+05		(K)HSQFIG	(K)H S Q F I/G\Y|P I/T L Y/L E K(E)		173.33	603.6548	1808.958	-0.0083	-4.6	6.75	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
24181	dirMS_041712_NAR_60mM_minus.8299.8299.3	3	3.91	1	1.04E+04		(R)SSPVPP	(R)S S/P V/P P V/P E R\R(G)		106.18	407.5617	1220.675	-0.004	-3.3	9.32	96735.1	9.2	HUMAN	J3KPS2	Protein FAM83H (Fragment)
24182	dirMS_041712_NAR_60mM_minus.9221.9221.3	3	3.91	1	2.34E+05		(R)IVDGKV	(R)I/V\D/G K V V/S E/T N D T K(V)		111.48	502.2642	1504.785	-0.0073	-4.8	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
24183	dirMS_041712_NAR_120mM_plus.10424.10424.3	3	3.91	1	2.55E+05		(R)LRQLAE	(R)L R Q L A\E E D\L/A/Q/Q R(A)		107.03	523.949	1569.834	-0.0019	-1.2	4.68	533778	5.74	HUMAN	Q15149	Plectin
24184	dirMS_041712_NAR_120mM_plus.12140.12140.4	4	3.91	0	5.53E+04		(K)QEESITV	(K)Q\E E S I T/V Q T M M/N T/L/R(D)		116.2	445.9748	1780.857	0.0206	11.6	4.53	47008.8	4.66	HUMAN	Q12765	Secernin-1
24185	dirMS_041712_NAR_120mM_plus.13196.13196.4	4	3.91	1	1.53E+06		(K)LCPSVQ	(K)L C P S V Q T/P Q V Q R/E R(G)	C:Carbamidomethylation	121.9	425.2229	1697.875	-0.0054	-3.2	9.6	210359.1	8.78	HUMAN	O14513	Nck-associated protein 5
24186	dirMS_041712_NAR_120mM_plus.4352.4352.3	3	3.91	1	2.27E+05		(R)AAEEED	(R)A A/E/E E/D\E/A D/P K/R(Q)		72.08	453.8721	1359.602	-0.0005	-0.4	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
24187	dirMS_041712_NAR_20mM_plus.16794.16794.2	2	3.91	0	9.92E+04		(K)IAFAITA	(K)I A/F/A/I\T A I K(G)		186.02	474.2987	947.592	-0.0023	-2.4	8.75	17718.4	10.99	HUMAN	P62269	40S ribosomal protein S18
24188	dirMS_041712_NAR_20mM_plus.17817.17817.2	2	3.91	0	8.58E+04		(K)VDFPQD	(K)V D F/P Q\D\Q L/T A L/T/G R(I)		194.7	780.9029	1560.802	-0.0031	-2	4.21	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
24189	dirMS_041712_NAR_20mM_plus.9432.9432.2	2	3.91	0	1.86E+05		(K)SVTNED	(K)S V|T N E/D V/T Q E E/L G G A K(T)		136	838.9014	1676.797	-0.0018	-1.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
24190	dirMS_041712_NAR_30mM_plus2.19539.19539.2	2	3.91	0	3.54E+05		(K)SNNVE	(K)S N|N/V/E/M D W V L K(H)		156.47	667.8205	1334.641	-0.0072	-5.4	4.37	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
24191	dirMS_041712_NAR_30mM_plus2.22364.22364.2	2	3.91	0	9.65E+04		(-)MLPLSLL	(-)M L/P L/S L L K(T)		172.95	457.7881	914.574	-0.0054	-5.9	8.5	15520.6	10.36	HUMAN	Q9Y4Z0	U6 snRNA-associated Sm-like protein LSm4
24192	dirMS_041712_NAR_40mM_plus2.15131.15131.3	3	3.91	0	3.88E+04	S2700s	(K)GGLPLA	(K)G G/L/P L A A L V L s C L D Q/K(T)	C:Carbamidomethylation s:N-ace	155.97	620.0038	1654.92	203.0772	-1.2	5.84	306975.2	7.12	HUMAN	Q8IYW2	Tetratricopeptide repeat protein 40
24193	dirMS_041712_NAR_40mM_plus2.17755.17755.3	3	3.91	0	3.15E+05		(R)DVCTEL	(R)D V/C T/E L L/P L I\K/P Q G R(V)	C:Carbamidomethylation	170.02	580.3213	1738.952	-0.0027	-1.5	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1

24194	dirMS_041712_NAR_40mM_plus2.8065.8065.2	2	3.91	0	6.58E+04	M1m	(-)mAPPAA	(-)m/A/P P A A P G/R(D)	m:Oxidized methionine	108.1	442.2237	867.451	15.9896	-6	9.5	12467.9	11.2	HUMAN	B8ZZA9	Transcription cofactor HES-6
24195	dirMS_041712_NAR_50mM_plus2.10843.10843.3	3	3.91	1	2.80E+05		(K)ILQIHAR	(K)I/L/Q/I H A R T H I G\E K(H)		124.22	505.9621	1515.875	-0.0037	-2.4	8.76	86938.2	9.77	HUMAN	K7EQV7	Zinc finger protein 700
24196	dirMS_041712_NAR_50mM_plus2.13805.13805.3	3	3.91	0	8.59E+05		(K)AASDIAI	(K)A A\S D/I/A\M T\E L/P P T H/P I R(L)		140.37	607.3177	1819.937	0.0015	0.8	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
24197	dirMS_041712_NAR_50mM_plus2.15259.15259.3	3	3.91	1	5.28E+05		(K)TKDGQII	(K)T K D G Q I\L|P\V/P N V V V R(D)		148.6	545.6573	1634.959	-0.0015	-0.9	8.41	56825.2	9.49	HUMAN	Q9P258	Protein RCC2
24198	dirMS_041712_NAR_50mM_plus2.16114.16114.3	3	3.91	1	5.02E+05		(K)LKLLLES	(K)L K/L/L L E S Y/T Q Q/K(K)		152.37	488.6224	1463.847	0.0058	4	8.5	49722.7	9.43	HUMAN	D6RF76	Coiled-coil domain-containing protein 112
24199	dirMS_041712_NAR_50mM_plus2.8406.8406.3	3	3.91	0	5.15E+05		(R)LEPKPQI	(R)L E\P/K P Q\P/P V/A E A T P R(S)		110.33	543.9631	1629.896	-0.0211	-13	6.14	14468.1	6.76	HUMAN	K7EJ51	Septin-9 (Fragment)
24200	dirMS_041712_NAR_50mM_plus2.8668.8668.3	3	3.91	1	9.99E+04		(R)SCMLTG	(R)S C|M/L/T G T/P E S V Q S A K R(L)	C:Carbamidomethylation	112.52	584.6157	1751.842	-0.0089	-5.1	8.46	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
24201	dirMS_041712_NAR_60mM_plus.18488.18488.3	3	3.91	1	1.59E+05		(R)KAPSDL	(R)K\A P S\D\L/Y Q\I I L K(A)		154.53	463.6084	1388.815	-0.0041	-3	8.5	21243.9	5.49	HUMAN	E9PL37	Calpain-1 catalytic subunit (Fragment)
24202	dirMS_041712_NAR_60mM_plus.18921.18921.3	3	3.91	1	1.42E+04		(K)LFTAESL	(K)L F/T/A E S L I/G L K N P E K(S)		156.12	553.9782	1659.932	-0.0116	-7	6.14	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
24203	dirMS_041712_NAR_60mM_plus.19250.19250.3	3	3.91	1	2.50E+04		(K)RSIQFVD	(K)R S I Q F\V|D|W C P T/G F K(V)	C:Carbamidomethylation	159.1	580.9558	1740.853	0.0002	0.1	8.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
24204	dirMS_041712_NAR_60mM_plus.21227.21227.3	3	3.91	1	4.03E+05		(R)KAIIIFVP	(R)K A I\I I\F V/P V P Q L K(S)		174.23	489.3205	1465.95	-0.0035	-2.4	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
24205	dirMS_041712_NAR_60mM_plus.5713.5713.3	3	3.91	0	1.90E+06	M21m	(R)SGSmDF	(R)S G S m/D P/S G\A H/P S V R(Q)	m:Oxidized methionine	87.5	467.5464	1384.627	15.9973	1.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
24206	dirMS_041712_NAR_120mM_minus.10340.10340.3	3	3.9	1	6.18E+04		(R)INAAEIE	(R)I N A A E I/E S/R V R(E)		111.02	419.8975	1257.691	-0.013	-10.4	6.14	12396.7	5.39	HUMAN	H0YF12	Tyrosine-protein phosphatase non-receptor type 11 (Fragment)
24207	dirMS_041712_NAR_120mM_minus.13014.13014.3	3	3.9	1	1.49E+05		(R)KQITME	(R)K\Q I T M\E/E/L V R(S)		125.65	416.2324	1246.682	0.0003	0.2	6.14	533778	5.74	HUMAN	Q15149	Plectin
24208	dirMS_041712_NAR_120mM_minus.20270.20270.3	3	3.9	1	3.80E+05	K435k	(K)IPIkRAD	(K)I P\I k/R A|D M L K(D)	k:Ubiquitin-K	166.5	433.5866	1184.718	114.0269	-12.4	9.99	81604.3	6.34	HUMAN	Q96JG8	Melanoma-associated antigen D4
24209	dirMS_041712_NAR_120mM_minus.6829.6829.2	2	3.9	0	4.18E+04		(K)LSGCQN	(K)L S G C Q/N/I T S T K(C)	C:Carbamidomethylation	91.5	604.8012	1208.594	0.0012	1	8.75	56672.2	5.65	HUMAN	B4DNT3	Interferon alpha/beta receptor 1
24210	dirMS_041712_NAR_120mM_minus.7278.7278.3	3	3.9	1	1.49E+06		(R)CREMDE	(R)C R E\M|D\E/Q I/R(L)	C:Carbamidomethylation	93.97	412.8591	1236.546	0.0168	13.6	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
24211	dirMS_041712_NAR_20mM_minus.14092.14092.2	2	3.9	0	6.21E+05		(R)VLITTDL	(R)V/L|I|T T D L/L A R(G)		192.28	557.8438	1114.683	-0.0027	-2.4	5.81	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
24212	dirMS_041712_NAR_30mM_minus2.17425.17425.2	2	3.9	0	1.11E+04		(R)EQLAIAE	(R)E Q\L A/I/A/E F A R(S)		148.28	574.3084	1147.611	-0.0011	-0.9	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
24213	dirMS_041712_NAR_30mM_minus2.7988.7988.2	2	3.9	0	1.83E+05		(K)GSGTAE	(K)G S/G T|A/E V E/L K(K)		98.32	495.7528	990.51	-0.0119	-12	4.53	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
24214	dirMS_041712_NAR_40mM_minus2.5509.5509.2	2	3.9	1	1.58E+05		(R)SKQAEE	(R)S K/Q A\E\E E|F(-)		91.33	484.2235	967.437	0.003	3.1	4.25	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
24215	dirMS_041712_NAR_40mM_minus2.8231.8231.3	3	3.9	0	2.47E+05	M35m	(K)AASDIA	(K)A A/S\D I/A/m T/E L/P P T H P I R(L)	m:Oxidized methionine	128.65	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
24216	dirMS_041712_NAR_60mM_minus.11304.11304.3	3	3.9	1	8.17E+05		(R)FPGQLN	(R)F/P/G Q L\N/A D L R K(L)		122.1	420.2346	1258.69	-0.001	-0.8	8.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
24217	dirMS_041712_NAR_60mM_minus.13982.13982.3	3	3.9	0	3.32E+05		(K)LHLGTT	(K)L H L G T T Q\N S\L/T/E/A D/F R(E)		137.52	601.6438	1802.903	0.0137	7.6	5.32	49472.3	6.75	HUMAN	O75351	Vacuolar protein sorting-associated protein 4B
24218	dirMS_041712_NAR_60mM_minus.14830.14830.3	3	3.9	1	2.72E+05		(R)KLQEEEL	(R)K L Q E E E L\L\A|T Q V D\M R(A)		142.8	601.6438	1802.932	-0.0148	-8.2	4.41	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
24219	dirMS_041712_NAR_60mM_minus.16107.16107.3	3	3.9	1	3.04E+04		(K)LPFPIID	(K)L/P F/P I/I D/D R N\R(E)		149.15	452.5849	1355.743	-0.0029	-2.1	5.96	25148.6	6	HUMAN	P30041	Peroxiredoxin-6
24220	dirMS_041712_NAR_60mM_minus.7734.7734.3	3	3.9	1	5.37E+05		(R)YLAEVA	(R)Y L A E V/A/A G D D K K(G)		102.12	427.222	1279.653	-0.0014	-1.1	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
24221	dirMS_041712_NAR_60mM_minus.8338.8338.3	3	3.9	1	2.81E+05		(K)EAIEGTY	(K)E A/I/E/G T Y I D K/K(C)		106.87	422.8919	1266.658	0.0035	2.8	4.68	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
24222	dirMS_041712_NAR_120mM_plus.15443.15443.4	4	3.9	2	1.54E+06		(R)FKGQIL	(R)F K G Q I\L|M/P N I G Y/G S N K K(T)		133.68	474.5115	1895.021	0.0034	1.8	10	15730.4	11.67	HUMAN	D3YTB1	60S ribosomal protein L32 (Fragment)
24223	dirMS_041712_NAR_120mM_plus.15953.15953.4	4	3.9	1	3.73E+05	M202m	(K)ILGSGIS	(K)I L G S G\I/S/S/S/S V L H G m V F K K(E)	m:Oxidized methionine	136.77	491.5215	1947.073	15.991	-2	10	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
24224	dirMS_041712_NAR_120mM_plus.17565.17565.4	4	3.9	2	6.05E+05		(K)LQASNV	(K)L Q A S N/V T/N K N D P K S I/N S R(V)		144.93	497.2584	1986.036	-0.0245	-12.3	9.99	24721.8	10.58	HUMAN	Q5QPL9	RNA binding protein, autoantigenic (HnRNP-associated with lethal yellow homolog (Mouse)) (Fragment)
24225	dirMS_041712_NAR_20mM_plus.11463.11463.2	2	3.9	0	2.39E+05		(K)LITPAVV	(K)L I/T|P/A V V S E R(L)		151.05	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
24226	dirMS_041712_NAR_20mM_plus.15858.15858.3	3	3.9	0	8.77E+03		(R)SSFYVN	(R)S S\F Y V N/G L T/L/G G Q K(C)		179.37	490.9251	1470.759	0.002	1.4	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
24227	dirMS_041712_NAR_20mM_plus.17909.17909.2	2	3.9	0	8.15E+04		(K)VNIIPIIA	(K)V N/I/I/P I I A K(A)		194.73	490.8283	980.65	-0.001	-1	8.72	51212	5.84	HUMAN	A6NFQ9	Septin-8
24228	dirMS_041712_NAR_20mM_plus.19324.19324.2	2	3.9	0	8.40E+04		(R)ALIAGG	(R)A L|I A/G\G/G A/P E I E L/A L R(L)		205.1	775.9467	1550.89	-0.0039	-2.5	4.53	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
24229	dirMS_041712_NAR_30mM_plus2.20269.20269.2	2	3.9	0	2.54E+05		(R)FEELNAI	(R)F E/E|L/N A/D L F R(G)		160.88	627.3106	1253.616	-0.0022	-1.7	4.14	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
24230	dirMS_041712_NAR_30mM_plus2.4752.4752.2	2	3.9	0	7.16E+05		(R)MGQTM	(R)M/G Q/T M E/R(I)		76.3	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
24231	dirMS_041712_NAR_30mM_plus2.6437.6437.2	2	3.9	0	1.03E+05	M514m M5	(K)NEEmm	(K)N E/E m m E\Q/K(E)	m:Oxidized methionine	88.55	535.7086	1038.423	31.9869	-2.8	4.25	67721.3	5.54	HUMAN	P32456	Interferon-induced guanylate-binding protein 2
24232	dirMS_041712_NAR_40mM_plus2.13659.13659.3	3	3.9	1	3.25E+05		(R)QVFGEA	(R)Q V/F G E A T K Q/P/G I T F I A A K(F)		147.4	636.0176	1906.043	-0.005	-2.6	8.59	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
24233	dirMS_041712_NAR_50mM_plus2.11567.11568.3	3	3.9	1	2.53E+05		(R)IDTACV	(R)I/D\T/A C/V C V L S R K(A)	C:Carbamidomethylation	128.2	474.5801	1421.724	0.0018	1.3	8.75	27300.6	10.52	HUMAN	P01138	Beta-nerve growth factor
24234	dirMS_041712_NAR_50mM_plus2.13937.13937.3	3	3.9	0	1.30E+06		(K)DLAGCI	(K)D L/A/G C I/H G L S N/V/K(L)	C:Carbamidomethylation	140.57	461.9061	1383.705	-0.0012	-0.8	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
24235	dirMS_041712_NAR_50mM_plus2.21548.21548.3	3	3.9	1	1.94E+05		(R)LIALLEVI	(R)L/I/A/L/L/E V L S Q K R(M)		183.27	461.6293	1382.873	0.0004	0.3	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
24236	dirMS_041712_NAR_60mM_plus.10667.10667.3	3	3.9	0	3.11E+06		(R)AHSSM	(R)A H S S M\V|G\V/N L/P Q K(A)		114.02	456.5782	1367.71	0.0101	7.3	8.8	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
24237	dirMS_041712_NAR_60mM_plus.13101.13101.2	2	3.9	1	6.28E+05	S107s	(R)RsSAWA	(R)R s S A\W A E/G G S/P R(S)	s:N-acetylglucosamine (S)	125.17	732.3483	1260.608	203.0814	1.4	9.6	112127.7	5.88	HUMAN	Q8N9B5	Junction-mediating and -regulatory protein
24238	dirMS_041712_NAR_60mM_plus.16283.16283.2	2	3.9	1	2.52E+05	S111s	(R)SQASSS	(R)S/Q A S S S R H s W/A E F L/K(F)	s:N-acetylglucosamine (S)	141.45	962.4515	1720.84	203.0556	-12.4	8.49	28439	12.22	HUMAN	Q5U4N7	Protein GDF5OS, mitochondrial
24239	dirMS_041712_NAR_60mM_plus.6753.6753.3	3	3.9	1	3.47E+05		(K)TQMTSA	(K)T Q|M T/S A V R E/P\K(L)		93.58	416.5533	1247.641	0.0041	3.3	8.41	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
24240	dirMS_041712_NAR_120mM_minus.11186.11186.3	3	3.89	0	4.97E+05		(R)GLHQSI	(R)G L H\Q\S I/E E/F R(A)		114.4	405.8796	1215.612	0.0126	10.4	5.4	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
24241	dirMS_041712_NAR_120mM_minus.14877.14877.4	4	3.89	1	4.81E+05		(K)KKELEEI	(K)K K E L E E I\V\Q/P I/I S K(L)		135.12	414.2486	1653.978	-0.006	-3.6	6.23	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
24242	dirMS_041712_NAR_120mM_minus.8478.8478.3	3	3.89	1	4.66E+05		(R)QREVTL	(R)Q R\E V T|L/G Q|V A K(L)		100.85	410.2375	1228.701	-0.0029	-2.3	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
24243	dirMS_041712_NAR_30mM_minus2.11967.11967.2	2	3.89	0	2.68E+05		(K)NGQDL	(K)N G Q/D/L G V/A/F/K(I)		118.93	524.7749	1048.542	0.0003	0.3	5.84	91324.5	5.75	HUMAN	Q00839	Heterogeneous nuclear ribonucleoprotein U
24244	dirMS_041712_NAR_30mM_minus2.4564.4564.2	2	3.89	0	8.69E+05		(K)QASEGP	(K)Q A/S E G\P L/K(G)		75.78	415.2235	829.441	-0.0017	-2	6	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
24245	dirMS_041712_NAR_30mM_minus2.8630.8630.2	2	3.89	0	6.17E+04		(R)LDPGTIS	(R)L/D P/G T I S/R(G)		101.43	429.7348	858.468	-0.0056	-6.6	5.84	18709.2	5.1	HUMAN	A8MXE0	Prolyl 4-hydroxylase subunit alpha-2 (Fragment)
24246	dirMS_041712_NAR_30mM_minus2.9820.9820.2	2	3.89	1	8.20E+05		(K)AIYKGP	(K)A I Y/K G P G S E\A/G|P(-)		107.48	573.7932	1146.579	0.0002	0.1	6.04	30492.9	5.26	HUMAN	P21964	Catechol O-methyltransferase
24247	dirMS_041712_NAR_50mM_minus2.10551.10551.3	3	3.89	1	3.78E+04	S1508s	(R)LAAGYG	(R)L A A G Y/G D G s L R I F S V S R(T)	s:N-acetylglucosamine (S)	127.67	658.0062	1768.934	203.07	-4.8	8.75	191043	6.61	HUMAN	F8VUX9	WD repeat-containing protein 90
24248	dirMS_041712_NAR_50mM_minus2.12045.12045.3	3	3.89	0	1.60E+05		(K)EMNPAL	(K)E M N/P A/L/G\I D C L H K(G)	C:Carbamidomethylation	136.77	499.9082	1497.719	-0.0088	-5.9	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
24249	dirMS_041712_NAR_60mM_minus.10548.10548.3	3	3.89	1	1.71E+04		(R)YAAVTQ	(R)Y/A/A\V/T/Q F E A T D A R R(A)		118.3	533.5999	1598.792	-0.007	-4.4	6.07	54259.7	5.17	HUMAN	A6NEC2	Puromycin-sensitive aminopeptidase-like protein
24250	dirMS_041712_NAR_60mM_minus.19214.19214.3	3	3.89	1	4.87E+04		(K)TFVNITP	(K)T F|V N|I T/P A E V G V L V G K D R(S)		170.42	639.0293	1915.065	0.0086	4.5	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
24251	dirMS_041712_NAR_60mM_minus.9708.9708.3	3	3.89	1	5.70E+04		(R)RQQEQ	(R)R\Q\Q/E\Q Q\V/P I L E K(F)		113.73	499.2763	1495.823	-0.0084	-5.6	6.14	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
24252	dirMS_041712_NAR_120mM_plus.21740.21740.4	4	3.89	2	3.25E+05		(K)LDLWNF	(K)L D L W N F L/D I P R S/R L V K(Y)		167.42	497.041	1985.133	0.0091	4.6	8.75	48129.1	7.85	HUMAN	C9J586	Rho guanine nucleotide exchange factor 3
24253	dirMS_041712_NAR_120mM_plus.4533.4533.3	3	3.89	0	2.66E+05	M76m M7	(R)LTNSm	(R)L/T/N S/m M m H/G R(N)	m:Oxidized methionine	72.88	403.8446	1177.527	31.9918	1.6	9.75	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
24254	dirMS_041712_NAR_20mM_plus.11602.11602.3	3	3.89	0	9.59E+04		(R)AQAALA	(R)A Q\A A L A V/N/I S A/A/R(G)		153.17	419.2429	1255.712	0.0024	1.9	9.79	58479.6	6.23	HUMAN	P40227	T-complex protein 1 subunit zeta
24255	dirMS_041712_NAR_20mM_plus.12017.12017.2	2	3.89	0	4.82E+04	T466t	(R)AQELtL	(R)A Q E|L/t/L Q T\P A K(R)	t:N-acetylglucosamine (T)	156.15	701.8644	1199.663	203.0585	-14.9	6.05	59229.3	9.65	HUMAN	Q6B0I6	Lysine-specific demethylase 4D
24256	dirMS_041712_NAR_20mM_plus.16858.16858.2	2	3.89	0	1.40E+05		(R)ELLIIGG	(R)E L|L|I I|G G V A A R(D)		186.82	556.3437	1111.683	-0.0032	-2.9	6.1	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
24257	dirMS_041712_NAR_20mM_plus.19253.19253.2	2	3.89	0	1.45E+05		(K)TGTATV	(K)T G T A T|V L S T/P H S H R(E)		204.43	732.889	1464.755	0.0154	10.5	9.47	280111.7	5.03	HUMAN	A6NMY3	Alstrom syndrome protein 1
24258	dirMS_041712_NAR_20mM_plus.8731.8731.2	2	3.89	0	1.10E+05	M118m	(R)mVVPA	(R)m V V/P A A/L K(V)	m:Oxidized methionine	130.37	422.7485	828.501	15.9886	-7.5	8.5	23633.9	11.02	HUMAN	P40429	60S ribosomal protein L13a
24259	dirMS_041712_NAR_20mM_plus.9987.9987.2	2	3.89	0	6.91E+04		(R)ALGQNF	(R)A L\G/Q/N|P T N A E V\L K(V)		140.02	677.8702	1354.733	0.0006	0.5	6.05	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
24260	dirMS_041712_NAR_30mM_plus2.21734.21734.2	2	3.89	0	1.76E+04		(K)NGFLLD	(K)N G F|L/L/D G F\P R(T)		169.18	568.3022	1135.59	0.0077	6.7	5.84	21283.1	6.45	HUMAN	F8VY04	Adenylate kinase 2, mitochondrial
24261	dirMS_041712_NAR_30mM_plus2.7020.7020.2	2	3.89	0	4.30E+05		(R)GPGPLQ	(R)G P|G|P L Q E/R(S)		90.62	427.2296	853.453	-0.0007	-0.8	6	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
24262	dirMS_041712_NAR_40mM_plus2.7859.7859.2	2	3.89	0	1.40E+05		(K)FCLDNG	(K)F/C\L D/N/G A K(S)	C:Carbamidomethylation	106.55	462.7191	924.424	0.0065	7.1	5.84	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
24263	dirMS_041712_NAR_50mM_plus2.8007.8007.3	3	3.89	0	9.70E+03		(K)STAGDT	(K)S T/A G D T H/L/G G E D F D N R(M)		108.98	564.5793	1691.726	-0.0022	-1.3	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
24264	dirMS_041712_NAR_60mM_plus.10358.10358.2	2	3.89	0	1.68E+06		(R)AVLLVG	(R)A V/L L V G L C D S G K(T)	C:Carbamidomethylation	111.5	616.3425	1231.671	0.0062	5.1	5.88	10093.6	10.36	HUMAN	C9J5Z8	Signal recognition particle receptor subunit beta (Fragment)
24265	dirMS_041712_NAR_60mM_plus.15672.15672.3	3	3.89	0	1.71E+05		(R)ILHGLGF	(R)I L H G L G F\T|P/A/M Q R(K)		138.35	480.9305	1440.778	-0.0011	-0.7	9.75	27043.5	6.34	HUMAN	C9JHK9	ATP-binding cassette sub-family F member 2 (Fragment)
24266	dirMS_041712_NAR_60mM_plus.18729.18729.3	3	3.89	1	1.45E+05		(K)SKDSLVI	(K)S K D S L V/D\I/I G I/C K(S)	C:Carbamidomethylation	155.25	483.2704	1447.783	0.0142	9.8	5.68	35399.1	5.17	HUMAN	I3L4R8	Replication protein A 70 kDa DNA-binding subunit (Fragment)
24267	dirMS_041712_NAR_60mM_plus.6257.6257.3	3	3.89	1	5.10E+05		(K)SVQATT	(K)S V|Q/A/T T E N/K E L K(T)		91.72	449.9085	1347.711	-0.0005	-0.4	5.86	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
24268	dirMS_041712_NAR_60mM_plus.7716.7716.2	2	3.89	1	7.47E+05		(R)VITEEEK	(R)V I/T E E/E/K N F K(A)		97.92	618.8282	1236.647	0.0021	1.7	4.79	18901.8	11.65	HUMAN	F5H1S2	60S ribosomal protein L13
24269	dirMS_041712_NAR_120mM_minus.10445.10445.2	2	3.88	0	1.45E+05		(K)HGLYLPT	(K)H/G|L/Y L/P T/R(V)		111.18	478.7694	956.531	0.0003	0.3	8.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
24270	dirMS_041712_NAR_120mM_minus.8458.8458.3	3	3.88	1	6.17E+04		(R)QREVTL	(R)Q R E V\T\L/G Q/V A/K(L)		99.07	410.2375	1228.701	-0.0029	-2.3	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
24271	dirMS_041712_NAR_30mM_minus2.6281.6281.2	2	3.88	0	9.00E+04		(R)EAEEVYI	(R)E\A/E/E/V/Y R(N)		88.33	448.2136	895.416	0.0043	4.8	4.25	54793.4	10.51	HUMAN	B7Z4Q3	Putative RNA-binding protein Luc7-like 2
24272	dirMS_041712_NAR_30mM_minus2.8120.8120.2	2	3.88	1	2.20E+05		(K)TYEDIDK	(K)T Y E/D I D K R(G)		99.18	520.2591	1039.506	0.0055	5.3	4.56	41379.7	7.83	HUMAN	G5E9V5	28S ribosomal protein S22, mitochondrial
24273	dirMS_041712_NAR_30mM_minus2.8176.8176.2	2	3.88	0	1.84E+04		(R)LSEHTQI	(R)L/S|E/H T Q R(Y)		99	435.7203	870.443	-0.0095	-10.9	6.75	384118.5	5.99	HUMAN	A4UGR9	Xin actin-binding repeat-containing protein 2
24274	dirMS_041712_NAR_50mM_minus2.13382.13382.3	3	3.88	0	1.45E+05	M170m	(K)SAIPHPL	(K)S A\I/P H/P L I m G V I R(E)	m:Oxidized methionine	144.12	473.9405	1403.819	15.9878	-5	9.49	44513	5.59	HUMAN	B4DIH5	COP9 signalosome complex subunit 2
24275	dirMS_041712_NAR_50mM_minus2.15488.15488.3	3	3.88	0	2.99E+05	M118m	(R)AGKPVI	(R)A G K P V\I/C\A T|Q/M/L E/S m I K(K)	C:Carbamidomethylation m:Oxid	155.8	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
24276	dirMS_041712_NAR_50mM_minus2.16171.16171.3	3	3.88	0	1.54E+05		(K)VVDELN	(K)V V|D/E L N L L H T E L A K(Q)		160.45	531.9638	1593.885	-0.0078	-4.9	4.65	16381.6	5.83	HUMAN	F8VWV2	DCC-interacting protein 13-beta (Fragment)
24277	dirMS_041712_NAR_50mM_minus2.7706.7706.3	3	3.88	1	1.66E+04	M26m	(K)LAEQAE	(K)L/A|E Q A/E R Y D D\M/A A C m K(S)	C:Carbamidomethylation m:Oxid	111.05	639.9511	1901.819	16.0197	12.9	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
24278	dirMS_041712_NAR_60mM_minus.11073.11073.3	3	3.88	1	1.26E+05		(K)TRLQLQ	(K)T R L Q L Q G E/L Q A R(G)		121.12	471.6068	1412.797	0.009	6.4	9.26	32565.3	9.76	HUMAN	Q6PIV7	Solute carrier family 25 member 34
24279	dirMS_041712_NAR_60mM_minus.11875.11875.3	3	3.88	0	1.69E+05	M184m	(K)TDLVTm	(K)T D/L/V T m N P S\V I Q R(A)	m:Oxidized methionine	125.47	497.2558	1473.773	15.9799	-10.1	5.5	40534.1	9.48	HUMAN	C6G488	Alpha-2,8-sialyltransferase 8B
24280	dirMS_041712_NAR_60mM_minus.16985.16985.3	3	3.88	0	1.00E+05		(R)LLANQQ	(R)L L|A/N Q Q/V F H I/S C F R(C)	C:Carbamidomethylation	154.67	578.3012	1732.895	-0.0061	-3.5	9.75	67446.5	5.63	HUMAN	F8VQE1	LIM domain and actin-binding protein 1
24281	dirMS_041712_NAR_60mM_minus.19672.19672.3	3	3.88	1	3.08E+05		(R)ARDDLI	(R)A R D D L\I|T D\L/L N E A\K(Q)		176.97	529.6145	1586.838	-0.0095	-6	4.23	23653.1	9.28	HUMAN	C9J8H1	V-type proton ATPase subunit E 1 (Fragment)
24282	dirMS_041712_NAR_60mM_minus.8284.8284.3	3	3.88	1	1.04E+04		(R)SSPVPP	(R)S S/P V/P P V P E R\R(G)		106.18	407.5617	1220.675	-0.004	-3.3	9.32	96735.1	9.2	HUMAN	J3KPS2	Protein FAM83H (Fragment)
24283	dirMS_041712_NAR_120mM_plus.11997.11997.3	3	3.88	2	2.21E+05		(R)AEELQE	(R)A E E L Q/E A/E R F S R K(A)		115.28	531.6047	1592.803	-0.0032	-2	4.95	114162.3	5.15	HUMAN	Q5JVD1	Centriolin
24284	dirMS_041712_NAR_120mM_plus.16975.16975.3	3	3.88	1	1.33E+06		(K)LKVPEW	(K)L\K V/P E|W/V/D T V K(L)		141.93	438.5868	1313.746	-0.0005	-0.4	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
24285	dirMS_041712_NAR_20mM_plus.10959.10959.2	2	3.88	0	6.08E+04		(K)LSELEPG	(K)L S E L/E|P G T G/D L R(F)		147.47	643.8371	1286.659	0.0083	6.4	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
24286	dirMS_041712_NAR_20mM_plus.14096.14096.3	3	3.88	1	4.03E+05		(-)XNGGGG	(-)X N G G G G S A T A R G/G E Y R(L)		168.7	508.2519	1522.736	0.0055	3.6	8.75	88719.7	9.24	HUMAN	H0Y5T9	Bromodomain-containing protein 2 (Fragment)
24287	dirMS_041712_NAR_20mM_plus.14133.14133.2	2	3.88	0	9.68E+04		(R)ELAVQIY	(R)E L/A V/Q/I Y E/E/A R(K)		169.83	660.839	1320.679	-0.0087	-6.6	4.25	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
24288	dirMS_041712_NAR_30mM_plus2.12639.12639.2	2	3.88	0	5.57E+05		(R)TIGISVD	(R)T/I/G\I/S V/D/P R(R)		118.58	479.2725	957.536	0.0014	1.4	5.5	14749.1	12.2	HUMAN	J3QSB4	60S ribosomal protein L13 (Fragment)
24289	dirMS_041712_NAR_30mM_plus2.16265.16265.2	2	3.88	0	6.89E+05		(R)ICCDLD	(R)I/C|C/D/L D V L A S K(K)	C:Carbamidomethylation	137.33	647.3131	1293.618	0.0012	0.9	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
24290	dirMS_041712_NAR_30mM_plus2.9325.9325.2	2	3.88	0	2.28E+05		(R)LASYLDF	(R)L/A/S Y L/D R(V)		103.22	419.2286	837.447	0.0034	4.1	5.83	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
24291	dirMS_041712_NAR_50mM_plus2.11584.11584.3	3	3.88	1	8.20E+04	M72m	(R)TEmENE	(R)T\E/m/E N E|F V/L I K K(D)	m:Oxidized methionine	128.73	499.5943	1480.772	15.9968	1.2	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
24292	dirMS_041712_NAR_50mM_plus2.12679.12679.3	3	3.88	1	5.35E+05		(K)FSIEDLK	(K)F/S/I/E/D L K A Q/P K(Q)		134.4	425.8966	1275.694	-0.0191	-15	6.07	13579.2	9.99	HUMAN	E9PPQ6	Thymocyte nuclear protein 1 (Fragment)
24293	dirMS_041712_NAR_50mM_plus2.21874.21874.3	3	3.88	1	3.60E+03		(K)TFKDEEL	(K)T F K D/E/E L F P L/Q V V M K(K)		187.17	608.6505	1823.961	-0.0242	-13.3	4.68	137427.9	7.13	HUMAN	Q2M389	WASH complex subunit 7
24294	dirMS_041712_NAR_50mM_plus2.7926.7926.3	3	3.88	1	2.07E+05	M227m M2	(R)mQKEIT	(R)m/Q K E I\T A L\A|P S/T m K(I)	m:Oxidized methionine	108.78	527.6045	1548.812	31.9865	-2.1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
24295	dirMS_041712_NAR_60mM_plus.17648.17648.3	3	3.88	0	3.72E+05		(R)SLESLHS	(R)S L/E\S L/H S F V A A A T K(E)		149.9	487.5963	1460.774	0	0	6.47	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
24296	dirMS_041712_NAR_60mM_plus.7993.7993.3	3	3.88	1	9.32E+04	K240k	(K)IEMDkR	(K)I E/M/D k R Q L/R(A)	k:Ubiquitin-K	99.77	434.9004	1188.652	114.0349	-6.2	8.75	42602.6	9.24	HUMAN	D6RF47	Protein Wnt
24297	dirMS_041712_NAR_120mM_minus.18201.18201.4	4	3.87	1	1.95E+05		(K)YYITIIDA	(K)Y Y\I T I/I/D A/P G H R D F I K(N)		154.23	481.2594	1922.017	-0.0013	-0.7	6.75	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
24298	dirMS_041712_NAR_120mM_minus.20092.20092.3	3	3.87	0	3.02E+05		(K)VHLVGII	(K)V H\L V G\I|D/I/F/T G K(K)		166.22	433.5866	1298.747	-0.0015	-1.1	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
24299	dirMS_041712_NAR_120mM_minus.7655.7655.3	3	3.87	1	1.50E+05		(R)RIVAVT	(R)R I V A\V|T G\A E A Q K(A)		96.17	414.9088	1242.717	-0.0046	-3.7	8.75	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
24300	dirMS_041712_NAR_120mM_minus.9827.9827.4	4	3.87	1	8.39E+04		(R)VVMLTM	(R)V V M/L T M/E E R/V T S P/R(I)		107.88	412.714	1647.856	-0.0215	-13	6.11	293114.8	9.56	HUMAN	Q6WRI0	Immunoglobulin superfamily member 10
24301	dirMS_041712_NAR_20mM_minus.10376.10376.2	2	3.87	0	4.24E+04		(K)AVLSLYA	(K)A V|L S L/Y/A S/G R(T)		152.4	518.7929	1036.579	0	0	8.79	14579.3	5.13	HUMAN	K7EM38	Actin, cytoplasmic 2, N-terminally processed (Fragment)
24302	dirMS_041712_NAR_30mM_minus2.11470.11470.2	2	3.87	0	2.19E+05		(K)ATAVMI	(K)A T\A|V/M/P D G Q F K(D)		115.47	582.7922	1164.572	0.0054	4.6	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1

24303	dirMS_041712_NAR_30mM_minus2.16597.16597.2	2	3.87	0	2.57E+05	M2243m	(K)mSIYQA	(K)m S|I/Y Q A M W K(G)	m:Oxidized methionine	144.07	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
24304	dirMS_041712_NAR_40mM_minus2.11450.11450.3	3	3.87	0	1.96E+05		(K)LVTSIGD	(K)L V|T S\I/G D/V V N H D/P V V G D R(L)		150.4	631.3335	1891.987	-0.0013	-0.7	4.41	27786.2	5.93	HUMAN	H0Y4Z6	Phosphorylase (Fragment)
24305	dirMS_041712_NAR_40mM_minus2.12344.12344.3	3	3.87	1	1.79E+04		(K)VVEEAP	(K)V V/E/E/A P S I F L D A E T R R(A)		155.72	611.3244	1831.955	0.0038	2.1	4.41	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
24306	dirMS_041712_NAR_40mM_minus2.12407.12407.3	3	3.87	1	1.79E+04		(K)VVEEAP	(K)V V|E/E A\P S I F L D A E T R R(A)		155.72	611.3244	1831.955	0.0038	2.1	4.41	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
24307	dirMS_041712_NAR_40mM_minus2.7999.7999.3	3	3.87	0	1.24E+05	M147m	(K)LQmEA	(K)L Q/m E A/P H|I I/V G T/P G R(V)	m:Oxidized methionine	127.3	545.627	1618.873	15.9931	-1.1	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
24308	dirMS_041712_NAR_50mM_minus2.10471.10471.3	3	3.87	0	1.28E+05	M391m T3	(K)AmDItG	(K)A/m D\I/t G Y S/D P\Y V K(V)	m:Oxidized methionine t:Pho	127.72	519.2182	1459.677	95.9627	0.9	4.21	58008.6	8.96	HUMAN	Q5T7P8	Synaptotagmin-6
24309	dirMS_041712_NAR_50mM_minus2.12215.12215.3	3	3.87	1	2.11E+04		(K)IGSLIDV	(K)I G S L/I/D/V N Q S K D P E/G L R(V)		137.88	614.3277	1840.976	-0.0078	-4.2	4.56	13012.7	6.91	HUMAN	A6NEC0	Protein mago nashi homolog 2
24310	dirMS_041712_NAR_50mM_minus2.8815.8815.3	3	3.87	1	7.72E+04		(R)SATKVT	(R)S A T K V T A D V/I/N A A E/K(L)		118.25	506.6094	1517.817	-0.0033	-2.2	5.79	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
24311	dirMS_041712_NAR_60mM_minus.11778.11778.2	2	3.87	1	3.16E+05		(K)TIDDLE	(K)T I|D D/L/E D K L K(C)		126.35	595.3185	1189.631	-0.0013	-1.1	4.22	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
24312	dirMS_041712_NAR_60mM_minus.13485.13485.3	3	3.87	1	1.67E+05		(R)GAGGQ	(R)G A G G Q G K L D V T|I/L/S P S R(K)		135.4	552.6388	1655.908	-0.0057	-3.4	8.75	258215.9	5.48	HUMAN	E7EN95	Filamin-B
24313	dirMS_041712_NAR_60mM_minus.13680.13680.3	3	3.87	0	1.10E+05	T164t	(R)tEIPATTI	(R)t\E I/P A T T L A/T/K(T)	t:N-acetylglucosamine (T)	136.02	450.254	1145.641	203.1062	19.9	5.66	113769.5	9.69	HUMAN	B4DSV9	Target of Nesh-SH3
24314	dirMS_041712_NAR_60mM_minus.5042.5042.3	3	3.87	1	3.90E+04	M277m M	(K)LGREEP	(K)L G R E E|P A\m|S/m/D A N G K(I)	m:Oxidized methionine	82.83	546.5777	1605.736	31.9826	-4.4	4.68	99900.1	5.04	HUMAN	B4DZI8	Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b
24315	dirMS_041712_NAR_60mM_minus.6299.6299.2	2	3.87	1	8.32E+03		(K)IIAPPER	(K)I I|A/P P E R K(Y)		93.55	462.287	923.567	-0.0006	-0.6	8.75	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
24316	dirMS_041712_NAR_60mM_minus.7934.7934.3	3	3.87	0	8.63E+04		(K)QVQMA	(K)Q/V Q M A/A/T/H/I\A R(K)		104.13	409.2199	1225.647	-0.0019	-1.5	9.75	35345.8	9.26	HUMAN	Q00403	Transcription initiation factor IIB
24317	dirMS_041712_NAR_60mM_minus.8100.8100.3	3	3.87	1	8.45E+04		(K)VDATAE	(K)V D/A/T A E T/D L/A K/R(F)		105.18	430.5619	1289.67	0.0016	1.2	4.56	73273.4	4.96	HUMAN	P13667	Protein disulfide-isomerase A4
24318	dirMS_041712_NAR_120mM_plus.5930.5930.3	3	3.87	1	3.09E+05		(K)VTEGQ	(K)V/T/E/G Q Q E/R L E R(Q)		83.33	448.8979	1344.687	-0.0075	-5.6	4.79	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
24319	dirMS_041712_NAR_20mM_plus.13234.13234.2	2	3.87	0	6.37E+04		(R)IGGGID	(R)I G G G/I/D V/P/V P R(H)		163.3	540.3131	1079.621	-0.0018	-1.7	5.84	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
24320	dirMS_041712_NAR_20mM_plus.13792.13792.2	2	3.87	0	6.76E+03	K305k	(R)SNLAEk	(R)S N L/A E k V R(L)	k:Ubiquitin-K	167.37	515.7856	916.521	114.0429	-0.1	8.46	134915.9	5.4	HUMAN	Q6AWC2	Protein WWC2
24321	dirMS_041712_NAR_20mM_plus.15843.15843.2	2	3.87	1	1.19E+05		(K)LDLPRE	(K)L/D L/P R E A F E A A S\R(E)		180.08	737.8794	1474.765	-0.0133	-9	4.68	21283.1	6.72	HUMAN	Q6AHZ8	Beta-ureidopropionase
24322	dirMS_041712_NAR_30mM_plus2.12777.12777.2	2	3.87	0	5.63E+05		(R)CNNVLY	(R)C N/N\V/L/Y I R(G)	C:Carbamidomethylation	120.8	526.2726	1051.535	0.0026	2.5	8.75	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F
24323	dirMS_041712_NAR_30mM_plus2.15656.15656.2	2	3.87	0	2.83E+05		(R)MAGAIA	(R)M\A/G A/I\A Q G L/I/R(A)		134.38	550.816	1100.624	0.0002	0.2	9.5	4449.1	11.42	HUMAN	F8WEI0	Pyrroline-5-carboxylate reductase 3
24324	dirMS_041712_NAR_30mM_plus2.17602.17602.3	3	3.87	0	7.33E+05		(R)ASLEAAI	(R)A S L E A A I|A/D/A/E Q R(G)		144.93	448.8963	1344.675	-0.001	-0.8	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
24325	dirMS_041712_NAR_30mM_plus2.5842.5842.2	2	3.87	0	3.59E+04	M119m	(K)VTmQN	(K)V/T/m/Q N L/N D R(L)	m:Oxidized methionine	84.63	553.7615	1090.531	15.9848	-9.2	5.81	51902.9	5.09	HUMAN	P02533	Keratin, type I cytoskeletal 14
24326	dirMS_041712_NAR_40mM_plus2.10373.10373.2	2	3.87	0	2.39E+04		(R)CNNVLY	(R)C N/N\V|L/Y/I R(G)	C:Carbamidomethylation	125.85	526.2705	1051.535	-0.0016	-1.5	8.75	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F
24327	dirMS_041712_NAR_40mM_plus2.6403.6403.2	2	3.87	0	1.22E+04		(R)IYVSANS	(R)I Y|V/S/A N S G A R(I)		96.83	519.2719	1037.537	-0.0009	-0.9	8.75	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
24328	dirMS_041712_NAR_40mM_plus2.9063.9063.2	2	3.87	0	5.32E+05		(K)SSFFSDR	(K)S S/F/F/S D\R(G)		116.18	423.1935	845.379	0.0009	1.1	5.55	15031.5	6.72	HUMAN	B4DLA0	ATP-dependent RNA helicase DDX3X
24329	dirMS_041712_NAR_50mM_plus2.12350.12350.3	3	3.87	0	3.32E+05		(R)VRPCVV	(R)V R P C V V Y\G/G\A D\I/G Q\Q I/R(D)	C:Carbamidomethylation	133.12	629.9955	1887.986	-0.0138	-7.3	8.71	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
24330	dirMS_041712_NAR_50mM_plus2.13886.13886.3	3	3.87	0	6.88E+05		(K)EGKPTIV	(K)E G K/P T I|V E|E D D/P E L F K(Q)		140.68	615.9744	1845.912	-0.003	-1.6	4.08	29841.1	9.04	HUMAN	O75937	DnaJ homolog subfamily C member 8
24331	dirMS_041712_NAR_50mM_plus2.18963.18963.3	3	3.87	0	3.08E+05		(K)LAKPLSS	(K)L A K\P L S S L/T/P L I M A A K(E)		167.87	552.004	1653.997	0.0003	0.2	10	24711.4	5.19	HUMAN	H7C1X3	PAK-2p34 (Fragment)
24332	dirMS_041712_NAR_50mM_plus2.7916.7916.3	3	3.87	0	2.07E+05		(K)INVPELP	(K)I N V P|E L P\T/P D E D N K(L)		108.78	527.6045	1580.78	0.0187	11.8	3.91	77604	5.92	HUMAN	A1A528	Centromere/kinetochore protein zw10 homolog
24333	dirMS_041712_NAR_50mM_plus2.8227.8227.3	3	3.87	0	1.26E+05		(K)QLAVAE	(K)Q L A V\A E/G K/P P E/A P K(G)		109.72	478.9337	1434.795	-0.0086	-6	6.14	24364.9	9.64	HUMAN	H0YIP0	Methionine--tRNA ligase, cytoplasmic (Fragment)
24334	dirMS_041712_NAR_60mM_plus.12393.12393.3	3	3.87	1	6.87E+05		(K)YGQISE	(K)Y G/Q I/S E V V V/V K D R(E)		121.35	497.9427	1491.817	-0.003	-2	6.07	28815.3	9.52	HUMAN	B4E2X2	Cold-inducible RNA-binding protein
24335	dirMS_041712_NAR_60mM_plus.21988.21988.3	3	3.87	1	2.98E+05		(R)KEGGLG	(R)K E G G L G\P L N I|P L L/A D V T R(R)		187.33	621.6926	1863.07	-0.0066	-3.5	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
24336	dirMS_041712_NAR_60mM_plus.8803.8803.3	3	3.87	1	5.73E+05		(K)ELKSPDE	(K)E L|K S P D/E/G/F E G K(S)		104.43	445.8862	1335.643	0.0014	1	4.41	84557.3	6.5	HUMAN	Q04609	Glutamate carboxypeptidase 2
24337	dirMS_041712_NAR_120mM_minus.16226.16226.4	4	3.86	1	1.16E+05	K177k	(K)RIEFkHG	(K)R\I E F k/H G/G\N Y V P A P K(E)	k:Ubiquitin-K	141.63	457.499	1712.923	114.0511	4.5	9.7	38247.2	5.48	HUMAN	C9JF58	Protein OSCP1
24338	dirMS_041712_NAR_120mM_minus.17981.17981.3	3	3.86	0	6.88E+04		(R)GQNPAE	(R)G Q N P A E G S F S T/L G R(L)		153.5	474.2316	1420.681	-0.0013	-0.9	6	78489.2	9.8	HUMAN	Q9Y252	E3 ubiquitin-protein ligase RNF6
24339	dirMS_041712_NAR_120mM_minus.20076.20076.3	3	3.86	0	2.72E+05		(K)VHLVGI	(K)V H\L V\G I/D/I/F T G K(K)		166.13	433.5866	1298.747	-0.0015	-1.1	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
24340	dirMS_041712_NAR_30mM_minus2.7294.7294.2	2	3.86	0	5.49E+05		(R)QIDNPD	(R)Q I\D N/P D/Y/K(G)		94.5	496.7354	992.468	-0.0048	-4.9	4.21	28545.1	4.5	HUMAN	K7EJB9	Calreticulin (Fragment)
24341	dirMS_041712_NAR_40mM_minus2.12367.12367.3	3	3.86	0	7.12E+04		(R)VYALPE	(R)V Y|A L P/E D L V/E V K/P K(M)		156.23	533.9726	1599.899	0.004	2.5	4.68	69862.6	5.58	HUMAN	B4DGB4	Plastin-3
24342	dirMS_041712_NAR_50mM_minus2.10102.10102.3	3	3.86	1	9.80E+04		(R)VGEPVA	(R)V/G\E P V/A L/S E E/E R L K(L)		125.42	519.2824	1555.833	0	0	4.49	8516.9	5.1	HUMAN	E9PIL8	Splicing factor 3B subunit 2 (Fragment)
24343	dirMS_041712_NAR_50mM_minus2.13875.13875.3	3	3.86	1	1.99E+05		(R)YLYTLV	(R)Y L|Y T L/V/I T D/K E/K(A)		147.38	495.9437	1485.82	-0.0034	-2.3	6.07	7621.9	10.1	HUMAN	J3KT73	60S ribosomal protein L38
24344	dirMS_041712_NAR_60mM_minus.11872.11872.3	3	3.86	1	1.25E+05		(K)ESNGPV	(K)E S N G/P V K V/W/G S I K(G)		126.37	467.5875	1400.753	-0.0053	-3.8	8.69	16163.7	5.7	HUMAN	P00441	Superoxide dismutase [Cu-Zn]
24345	dirMS_041712_NAR_120mM_plus.23534.23534.3	3	3.86	0	3.27E+05		(R)GEPWL	(R)G E P W\L P P P A/S F/G P L R(T)		178.6	540.9492	1620.853	-0.0202	-12.5	6	23836.8	11.9	HUMAN	G5E945	Myelin-associated oligodendrocyte basic protein
24346	dirMS_041712_NAR_120mM_plus.5313.5313.3	3	3.86	1	1.54E+05		(R)NDDDEE	(R)N/D/D D/E E/E/A A\R E/R(R)		81.02	483.5401	1448.588	0.0173	12	3.95	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
24347	dirMS_041712_NAR_120mM_plus.5638.5638.2	2	3.86	0	1.20E+05		(R)HVVFSG	(R)H\V|V/F/S G S G R(A)		82.4	473.2482	945.49	-0.001	-1	9.75	17802.1	10.98	HUMAN	Q8N5L8	Ribonuclease P protein subunit p25-like protein
24348	dirMS_041712_NAR_20mM_plus.16862.16862.3	3	3.86	0	3.42E+05		(K)VQIAVA	(K)V Q I A|V\A\N A Q/E L L/Q R(M)		187.55	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
24349	dirMS_041712_NAR_20mM_plus.6419.6419.2	2	3.86	0	2.42E+04		(R)SQSAAV	(R)S Q\S A A/V/T/P S S T T S S T R(A)		107.12	784.3802	1567.756	-0.0027	-1.7	9.47	42437.8	4.97	HUMAN	Q16186	Proteasomal ubiquitin receptor ADRM1
24350	dirMS_041712_NAR_20mM_plus.7927.7927.2	2	3.86	0	6.85E+03		(R)INISEGN	(R)I N|I|S E G N C P E/R(I)	C:Carbamidomethylation	124.18	644.7995	1288.595	-0.0033	-2.6	4.53	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
24351	dirMS_041712_NAR_30mM_plus2.21129.21129.2	2	3.86	0	2.71E+05		(R)FDAMP	(R)F D/A|M/P F T L R(A)		166.28	549.276	1097.545	-0.0001	-0.1	5.84	42088	5.39	HUMAN	F8VTY8	Proliferation-associated protein 2G4
24352	dirMS_041712_NAR_40mM_plus2.15190.15190.3	3	3.86	0	3.88E+04		(R)LSDVLK	(R)L S/D V/L K P L\T D A Q\V/E A M/K(L)		155.97	620.0038	1857.999	-0.0022	-1.2	4.56	142001.7	5.82	HUMAN	Q92797	Symplekin
24353	dirMS_041712_NAR_40mM_plus2.6548.6548.2	2	3.86	0	2.94E+04		(K)AGFAGD	(K)A G/F|A/G D|D/A P R(A)		97.9	488.728	976.448	0.0004	0.4	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
24354	dirMS_041712_NAR_50mM_plus2.10457.10457.3	3	3.86	1	6.51E+04		(R)YLTTAVI	(R)Y/L/T T A V I T N K D/V/R(K)		122.27	498.6121	1493.832	-0.0105	-7	8.59	41755.9	6.13	HUMAN	E5RGA2	Eukaryotic translation initiation factor 3 subunit E
24355	dirMS_041712_NAR_50mM_plus2.19615.19615.3	3	3.86	1	9.25E+04		(K)TFVNITP	(K)T F/V/N I/T P A E V/G V L V G K D R(S)		171.23	639.0247	1915.065	-0.0052	-2.7	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
24356	dirMS_041712_NAR_50mM_plus2.20335.20335.3	3	3.86	1	1.87E+04		(K)SSVLEN	(K)S S/V/L/E N F V G R D F L P\R(G)		176.38	579.3128	1735.913	0.0113	6.5	5.79	73288.1	8.96	HUMAN	E5RHK8	Dynamin-3
24357	dirMS_041712_NAR_50mM_plus2.6504.6504.3	3	3.86	0	1.31E+05		(K)LVEAGC	(K)L V/E A G/C V A N N/A V I R(K)	C:Carbamidomethylation	98.88	495.9283	1485.784	-0.0139	-9.3	6	107488.2	5.67	HUMAN	E7ES94	Calcium-transporting ATPase type 2C member 2
24358	dirMS_041712_NAR_50mM_plus2.8737.8737.3	3	3.86	0	7.40E+05		(R)AALAHS	(R)A A L A H\S|E E\V/T/A/S/Q V A A T K(T)		113.43	595.312	1783.919	0.003	1.7	5.4	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
24359	dirMS_041712_NAR_50mM_plus2.8958.8958.3	3	3.86	0	1.77E+05		(K)IGSCTQ	(K)I G\S C T Q Q D/V/E L H/V Q K(I)	C:Carbamidomethylation	113.98	581.2895	1741.854	0.0002	0.1	5.32	20139.7	9.34	HUMAN	C9J7S3	Aspartate--tRNA ligase, cytoplasmic (Fragment)
24360	dirMS_041712_NAR_60mM_plus.6194.6194.3	3	3.86	0	2.39E+05	M480m	(R)AAHSEG	(R)A A H S E G N\T T/A/G L/D m/R(E)	m:Oxidized methionine	91.13	516.2346	1530.697	15.9927	-1.4	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
24361	dirMS_041712_NAR_60mM_plus.7047.7047.2	2	3.86	1	4.51E+05		(K)IVSGKD	(K)I/V/S\G K\D Y/N V\T A N\S K(L)		95.18	748.3906	1495.775	-0.0012	-0.8	8.5	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
24362	dirMS_041712_NAR_60mM_plus.7825.7825.3	3	3.86	1	3.89E+05		(K)FEDKTV	(K)F/E D K T V/A/Y/T E Q/K(M)		98.93	486.9076	1458.711	-0.0029	-2	4.68	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
24363	dirMS_041712_NAR_120mM_minus.15946.15946.4	4	3.85	0	3.20E+05		(K)EVVHTV	(K)E V V H T V S L H E I D\V I/N S R(T)		140.75	487.5112	1947.029	-0.0064	-3.3	5.27	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
24364	dirMS_041712_NAR_120mM_minus.20051.20051.3	3	3.85	1	2.47E+05		(R)AKFEEL	(R)A K F E E\L\N|M/D L/F R(S)		164.85	504.9216	1512.752	-0.0013	-0.8	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
24365	dirMS_041712_NAR_120mM_minus.8942.8942.3	3	3.85	1	3.33E+05	K421k	(K)IKHQTEE	(K)I K H Q T/E/E E k K(H)	k:Ubiquitin-K	103.18	461.9056	1269.68	114.0225	-14.8	6.76	121954.4	5.87	HUMAN	Q9ULE4	Protein FAM184B
24366	dirMS_041712_NAR_30mM_minus2.20049.20049.2	2	3.85	1	3.20E+05		(K)DVLNEN	(K)D V|L N E N L/Q R K(R)		169.93	614.8388	1228.664	0.0059	4.8	6.07	230080	9.51	HUMAN	Q5HYC2	Uncharacterized protein KIAA2026
24367	dirMS_041712_NAR_40mM_minus2.9326.9326.2	2	3.85	1	1.28E+04	K36k	(R)LKGMH	(R)L K G/M H T V N S k(W)	k:Ubiquitin-K	138.63	614.8224	1114.604	114.0338	-7.4	10	17607.6	8	HUMAN	F8WDD3	Protein eyes shut homolog
24368	dirMS_041712_NAR_50mM_minus2.13729.13729.3	3	3.85	0	4.47E+04		(R)QVSASE	(R)Q V/S A S E L H T S G/I/L/G/P E T L R(D)		146.6	665.688	1995.051	-0.0011	-0.6	5.4	558007.1	5.44	HUMAN	P58107	Epiplakin
24369	dirMS_041712_NAR_60mM_minus.10777.10777.3	3	3.85	1	1.68E+05	N805n	(K)LEDCRn	(K)L/E D/C\R\n M I A E L R(I)	C:Carbamidomethylation n:N-ac	120.02	574.9362	1519.736	203.0585	-12.1	4.68	130734.2	6.02	HUMAN	Q92574	Hamartin
24370	dirMS_041712_NAR_60mM_minus.17214.17214.3	3	3.85	0	5.90E+03		(K)SGPLFN	(K)S G P\L/F/N F D V H/D D/V R(L)		156.05	539.9245	1617.766	-0.0066	-4.1	4.41	30693	5.41	HUMAN	B0S8I6	Protein FAM50A (Fragment)
24371	dirMS_041712_NAR_60mM_minus.8515.8515.3	3	3.85	1	5.17E+04		(K)SAVGFE	(K)S A/V/G F E Y Q/G K T E K(H)		107.35	481.9071	1443.711	-0.0047	-3.2	5.86	25153.2	6.6	HUMAN	H7C314	Src substrate cortactin (Fragment)
24372	dirMS_041712_NAR_120mM_plus.25628.25628.3	3	3.85	1	4.23E+05		(R)GVMLA	(R)G V/M L/A/V D/A V I A E/L/K K(Q)		193.13	519.6402	1556.908	-0.002	-1.3	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
24373	dirMS_041712_NAR_120mM_plus.6737.6737.2	2	3.85	0	9.17E+04		(K)EMQPT	(K)E M/Q/P T H/P I R(L)		88.62	554.7822	1108.557	0.0003	0.3	6.85	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
24374	dirMS_041712_NAR_20mM_plus.12516.12516.2	2	3.85	0	5.86E+04		(R)LGTLSP	(R)L G T\L/S/P A/F S T R(V)		159	575.3192	1149.626	0.0049	4.2	9.75	102679.8	6.75	HUMAN	Q7KZF4	Staphylococcal nuclease domain-containing protein 1
24375	dirMS_041712_NAR_20mM_plus.15863.15863.2	2	3.85	0	1.48E+05		(K)VGINYQ	(K)V G I N\Y/Q/P P T V V/P G G D L/A K(V)		179.68	912.9952	1824.985	-0.0023	-1.3	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
24376	dirMS_041712_NAR_20mM_plus.18497.18497.2	2	3.85	0	1.64E+05	M332m	(R)IVSQLLT	(R)I V\S/Q L/L/T/L m D G L K(Q)	m:Oxidized methionine	199.23	723.9145	1430.829	15.993	-1.3	5.84	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
24377	dirMS_041712_NAR_20mM_plus.18718.18718.3	3	3.85	0	1.06E+05	M80m	(R)APLPDL	(R)A P L P D L\Y|P F/G T m\R(G)	m:Oxidized methionine	200.35	498.5865	1477.751	15.9941	-0.5	5.88	81122.9	9.03	HUMAN	H3BLZ8	Probable ATP-dependent RNA helicase DDX17
24378	dirMS_041712_NAR_20mM_plus.9082.9082.2	2	3.85	0	2.61E+05		(R)VLTVIN	(R)V L/T V I/N Q/T Q K(E)		133.12	572.3399	1143.673	-0.0007	-0.6	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
24379	dirMS_041712_NAR_30mM_plus2.12666.12666.2	2	3.85	0	9.03E+04		(R)NLGLYV	(R)N/L|G/L Y/V/K(T)		118.83	403.7418	806.477	-0.0007	-0.9	8.59	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
24380	dirMS_041712_NAR_30mM_plus2.13510.13510.2	2	3.85	0	1.00E+06		(K)ELSDIAL	(K)E L/S/D/I/A L R(I)		123.72	458.7641	916.51	0.0111	12.1	4.37	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
24381	dirMS_041712_NAR_30mM_plus2.15866.15866.2	2	3.85	0	3.45E+04		(K)TLAAEM	(K)T L/A A/E/M Q E L/R(V)		135.77	581.307	1161.593	0.0135	11.6	4.53	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
24382	dirMS_041712_NAR_40mM_plus2.14151.14151.3	3	3.85	0	1.64E+05	M1m	(-)mPASM	(-)m P/A/S/M F S I D N/I L A A R P R(C)	m:Oxidized methionine	149.7	635.9975	1889.972	16.0055	5.6	9.35	28491.5	9.34	HUMAN	P56915	Homeobox protein goosecoid
24383	dirMS_041712_NAR_40mM_plus2.5754.5754.2	2	3.85	0	8.99E+03		(R)TYDETY	(R)T Y|D\E T Y Q R(Y)		91.52	538.2401	1075.469	0.0038	3.6	4.37	40616.6	9.46	HUMAN	H0YHI8	Protein phosphatase 1 regulatory subunit 12A (Fragment)
24384	dirMS_041712_NAR_50mM_plus2.12220.12220.3	3	3.85	0	1.79E+05		(R)GPVPAK	(R)G P|V/P/A K/P T V L F E/K(M)		132.2	461.6038	1382.804	-0.0074	-5.3	8.59	110755.6	7.92	HUMAN	B4DH53	MAP1S light chain
24385	dirMS_041712_NAR_50mM_plus2.20932.20932.3	3	3.85	1	2.05E+05		(R)LLLQQL	(R)L L\L/Q/Q L\E A/T L E T G K R(F)		178.87	571.6722	1712.991	0.0115	6.7	6.14	113203.2	6.21	HUMAN	Q14CX7	N-alpha-acetyltransferase 25, NatB auxiliary subunit
24386	dirMS_041712_NAR_50mM_plus2.22284.22284.3	3	3.85	0	7.77E+05		(R)GGHPPA	(R)G G H P P A I Q S L\I/N/L/L/A D N R(Y)		191.52	629.3448	1886.024	-0.0044	-2.3	6.74	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
24387	dirMS_041712_NAR_50mM_plus2.8272.8272.3	3	3.85	1	7.95E+04		(R)DTGEKL	(R)D T/G E K L T V|A/E/N E A E T K(L)		109.95	578.9478	1734.839	-0.0104	-6	4.25	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
24388	dirMS_041712_NAR_60mM_plus.13396.13396.3	3	3.85	1	9.05E+05		(R)VIDRELY	(R)V/I/D R E\L Y Q/Q L Q R(G)		126.18	520.952	1560.849	-0.0078	-5	6.04	533778	5.74	HUMAN	Q15149	Plectin
24389	dirMS_041712_NAR_60mM_plus.20291.20291.3	3	3.85	1	6.73E+04		(R)KEGLLG	(R)K E G L L\G|L/Q N L L K(S)		166.17	442.6086	1325.815	-0.0039	-2.9	8.59	164028.5	9.06	HUMAN	B7ZLX3	CLASP1 protein
24390	dirMS_041712_NAR_120mM_minus.10648.10648.2	2	3.84	1	2.31E+05		(R)VKYETEL	(R)V/K/Y E T E L/A M/R(Q)		112.72	620.3232	1239.64	-0.0011	-0.9	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
24391	dirMS_041712_NAR_120mM_minus.11287.11287.3	3	3.84	1	7.89E+05		(R)RFDDAV	(R)R F D D\A\V/V\Q S D/M K(H)		115.33	470.8939	1410.668	-0.001	-0.7	4.43	20069.4	6.74	HUMAN	E9PK54	Heat shock cognate 71 kDa protein (Fragment)
24392	dirMS_041712_NAR_120mM_minus.13729.13729.3	3	3.84	1	1.12E+05		(R)KYEMFA	(R)K Y E M F\A/Q T\L/Q/Q S R(G)		129.37	543.9428	1629.805	0.0085	5.2	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
24393	dirMS_041712_NAR_120mM_minus.14341.14341.4	4	3.84	1	1.15E+05		(R)ETNLDS	(R)E T N L D S L/P/L V/D T H S K R(T)		132.23	456.992	1824.945	0.0012	0.6	5.38	53707.8	5.06	HUMAN	P08670	Vimentin
24394	dirMS_041712_NAR_120mM_minus.6733.6733.2	2	3.84	1	7.21E+04		(K)GSGTAE	(K)G S|G T/A/E/V E L K K(G)		91.03	559.8072	1118.605	0.0019	1.7	6.14	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
24395	dirMS_041712_NAR_120mM_minus.7203.7203.2	2	3.84	1	1.12E+05		(R)LSKEDIE	(R)L/S/K/E/D I/E R(M)		93.87	495.2658	989.526	-0.0019	-1.9	4.68	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
24396	dirMS_041712_NAR_20mM_minus.10211.10211.2	2	3.84	0	8.40E+04		(K)ALDFIAS	(K)A L/D\F I A/S K(G)		152	432.7455	864.482	0.0012	1.4	5.88	107710.1	5.38	HUMAN	B7TY16	Actinin alpha 1 isoform 3
24397	dirMS_041712_NAR_40mM_minus2.8138.8138.3	3	3.84	2	1.68E+05	M134m	(K)EPVTKA	(K)E P V T/K|A E m L E/S V I K N Y K(R)	m:Oxidized methionine	128.68	665.6822	1979.052	15.9803	-7.3	6.32	34644.3	4.54	HUMAN	E5RH97	Melanoma-associated antigen 9 (Fragment)
24398	dirMS_041712_NAR_40mM_minus2.8304.8304.3	3	3.84	0	1.94E+05	M35m	(K)AASDIA	(K)A A/S D I/A/m\T E/L P/P T/H P I R(L)	m:Oxidized methionine	128.9	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
24399	dirMS_041712_NAR_50mM_minus2.13238.13238.3	3	3.84	0	1.42E+04	M84m	(K)YPIEHGI	(K)Y P I/E H G I I\T N W|D D/m E K(I)	m:Oxidized methionine	144.15	659.6398	1960.911	15.9939	-0.5	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
24400	dirMS_041712_NAR_50mM_minus2.14479.14479.3	3	3.84	0	4.07E+05		(R)QIFHPE	(R)Q I F H/P E Q L/I/T/G K(E)		149.77	470.9286	1410.774	-0.0027	-1.9	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
24401	dirMS_041712_NAR_50mM_minus2.15101.15101.3	3	3.84	0	1.83E+05		(K)TLSPTGT	(K)T L S P/T G T A\Q P/S/W G V D P K(E)		154.87	581.2998	1741.876	0.0093	5.3	5.5	116940.4	6.04	HUMAN	Q9BXX0	EMILIN-2
24402	dirMS_041712_NAR_50mM_minus2.16865.16865.3	3	3.84	0	2.56E+05		(K)ALVSHN	(K)A L V S H\N G S\L I|N\V/G S L L Q R(A)		164.02	626.6879	1878.056	-0.0064	-3.4	9.8	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
24403	dirMS_041712_NAR_50mM_minus2.17120.17120.2	2	3.84	0	1.54E+05	K657k	(K)VTVVNS	(K)V T/V V/N S I k P S S P/T E G K(R)	k:Ubiquitin-K	166.55	878.9837	1642.901	114.0591	9.2	8.56	76902.6	9.63	HUMAN	O95447	Lebercilin-like protein
24404	dirMS_041712_NAR_50mM_minus2.7358.7358.3	3	3.84	0	6.43E+03		(R)IEAITSS	(R)I E A I T S S G Q M/G S F I R(L)		108.53	532.9391	1596.805	-0.0023	-1.4	6	50734.3	6.89	HUMAN	B3KMG0	Nucleoporin GLE1
24405	dirMS_041712_NAR_60mM_minus.13198.13198.3	3	3.84	2	2.81E+05	M1m	(-)mKSVIPS	(-)m/K/S V I P S D G P\S V A C V\K K(A)	C:Carbamidomethylation m:Oxid	133.93	606.9793	1802.95	15.973	-12	9.7	8203.2	4.52	HUMAN	C9JB55	Serotransferrin (Fragment)
24406	dirMS_041712_NAR_60mM_minus.17999.17999.3	3	3.84	1	3.70E+05		(K)NLRDID	(K)N L R D I D\E|V/S/S L L/R(T)		160.93	510.6099	1529.828	-0.013	-8.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
24407	dirMS_041712_NAR_60mM_minus.5246.5246.3	3	3.84	0	1.35E+05	S349s	(K)AAMYDI	(K)A A\M Y D I/I/s S P S/K(D)	s:N-acetylglucosamine (S)	84.4	495.9133	1282.635	203.0906	7.5	5.88	318099.5	8.39	HUMAN	Q6KC79	Nipped-B-like protein
24408	dirMS_041712_NAR_60mM_minus.6752.6752.3	3	3.84	1	1.12E+05	M281m	(R)SRAEAE	(R)S R A E\A E S m/Y/Q I K(Y)	m:Oxidized methionine	96.7	476.895	1412.684	15.9866	-5.8	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
24409	dirMS_041712_NAR_120mM_plus.10785.10785.3	3	3.84	2	3.57E+05		(K)SKGCGV	(K)S K/G C G V V/K F\E\S/P E V A E R(A)	C:Carbamidomethylation	109.5	626.9844	1878.938	0.0008	0.4	5.95	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
24410	dirMS_041712_NAR_120mM_plus.13135.13135.2	2	3.84	0	2.97E+05		(R)HLVAGG	(R)H/L|V A G G G A G A V S/R(T)		122.32	576.3101	1151.628	-0.0151	-13.1	9.75	17934.5	10.31	HUMAN	H7C4Z4	Calcium-binding mitochondrial carrier protein SCaMC-2 (Fragment)
24411	dirMS_041712_NAR_120mM_plus.4518.4518.3	3	3.84	0	2.28E+04		(R)THSQGG	(R)T H S Q G G|Y G S Q G/Y K(Y)		73.05	457.2092	1369.613	-0.0001	-0.1	8.2	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit

24412	dirMS_041712_NAR_20mM_plus.12405.12405.2	2	3.84	0	5.73E+04		(K)LLQLVE	(K)L L Q|L/V E D/R(G)		157.63	493.2863	985.568	-0.0023	-2.4	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
24413	dirMS_041712_NAR_20mM_plus.5978.5978.3	3	3.84	0	1.02E+06	M295m M	(R)mGQmA	(R)m G Q m A m\G\G A m/G I/N N R(G)	m:Oxidized methionine	100.27	534.8861	1538.67	63.9743	-3.4	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
24414	dirMS_041712_NAR_20mM_plus.7696.7696.2	2	3.84	0	2.07E+05	M328m	(K)ALmDEV	(K)A L|m D/E V/V K(A)	m:Oxidized methionine	122.63	460.741	904.481	15.9939	-1.1	4.37	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
24415	dirMS_041712_NAR_20mM_plus.7915.7915.2	2	3.84	0	3.59E+05	M239m	(K)EVDEQm	(K)E V/D E Q/m L N/V/Q N K(N)	m:Oxidized methionine	124.95	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
24416	dirMS_041712_NAR_20mM_plus.9654.9654.2	2	3.84	0	6.07E+04	M465m	(K)VLQDm	(K)V L Q D/m/G L\P T G A E G R(D)	m:Oxidized methionine	138.02	730.3568	1443.726	15.9803	-10	4.37	96205.6	9.06	HUMAN	G5E9M5	Interleukin enhancer binding factor 3, 90kDa, isoform CRA_b
24417	dirMS_041712_NAR_20mM_plus.9857.9857.2	2	3.84	1	6.91E+04		(R)AQTQG	(R)A/Q T Q G P V/K A E T\P K(A)		140.02	677.8702	1354.733	0.0006	0.5	8.64	149260.3	11.04	HUMAN	E9PDE0	Uncharacterized protein KIAA1683
24418	dirMS_041712_NAR_30mM_plus2.16407.16407.3	3	3.84	0	5.50E+05		(R)GLCAIA	(R)G L C A I\A/Q/A/E/S L R(Y)	C:Carbamidomethylation	138.52	430.2276	1288.668	0.0005	0.3	6	18529.2	9.98	HUMAN	E9PL45	40S ribosomal protein S3
24419	dirMS_041712_NAR_30mM_plus2.19080.19080.2	2	3.84	0	1.24E+04		(R)LSNIFVI	(R)L/S/N\I F V/I G K(G)		153.3	495.8019	990.598	-0.0017	-1.7	8.75	29825.4	10.37	HUMAN	P62701	40S ribosomal protein S4, X isoform
24420	dirMS_041712_NAR_40mM_plus2.8936.8936.3	3	3.84	1	1.79E+03	T105t	(R)DHWVF	(R)D H W V F G/G G/t K L/T V L G(-)	t:N-acetylglucosamine (T)	113.93	597.3016	1586.833	203.0577	-12.1	6.74	12361.3	4.91	HUMAN	P06317	Ig lambda chain V-VI region SUT
24421	dirMS_041712_NAR_50mM_plus2.11894.11894.3	3	3.84	0	2.19E+05		(K)LIHPDE	(K)L I H/P D E D\I/S/L E E R(R)		130.8	522.5972	1565.781	-0.0035	-2.3	4.17	53035.1	9.47	HUMAN	E1P660	Zinc finger protein 207
24422	dirMS_041712_NAR_50mM_plus2.17347.17347.3	3	3.84	0	2.34E+05		(K)LLDAYT	(K)L/L/D/A Y T Q I S D L K(R)		159.02	460.5906	1379.742	0.0156	11.3	4.21	76115.6	7.42	HUMAN	H0YG46	M-phase phosphoprotein 9 (Fragment)
24423	dirMS_041712_NAR_50mM_plus2.6526.6526.3	3	3.84	1	3.51E+05		(R)IVDGKV	(R)I V\D/G K V V S E T N D T K(V)		100.28	502.2651	1504.785	-0.0046	-3	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
24424	dirMS_041712_NAR_50mM_plus2.8807.8807.3	3	3.84	0	2.04E+05		(K)VVQVSA	(K)V V/Q V|S A/G D S H/T A A L T D D G R(V)		113.45	633.6509	1898.92	0.0179	9.4	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
24425	dirMS_041712_NAR_60mM_plus.11007.11007.3	3	3.84	1	1.12E+06		(K)AEDKEW	(K)A E/D|K\E W M/P V T K(L)		115.58	445.2196	1333.646	-0.0014	-1.1	4.68	23145.8	11.25	HUMAN	E9PMM9	40S ribosomal protein S2 (Fragment)
24426	dirMS_041712_NAR_60mM_plus.12424.12424.3	3	3.84	1	9.17E+05	T176t	(K)AVEtLLD	(K)A V E t L L/D L/I M K R(M)	t:N-acetylglucosamine (T)	121.42	535.6249	1401.813	203.0467	-20.3	6.12	24835.6	5.36	HUMAN	O00194	Ras-related protein Rab-27B
24427	dirMS_041712_NAR_60mM_plus.13591.13591.3	3	3.84	1	5.96E+05	S219s	(K)GGYTQs	(K)G G Y/T\Q s V|K E I L K(R)	s:Phosphorylated S	128.43	468.2401	1322.731	79.9743	5.7	8.5	146897.2	7.22	HUMAN	E9PH70	Kinase D-interacting substrate of 220 kDa (Fragment)
24428	dirMS_041712_NAR_60mM_plus.13675.13704.3	3	3.84	0	4.98E+05		(R)IHQIEYA	(R)I H Q\I\E Y/A/M/E A V K(Q)		128.4	477.9163	1431.73	0.0043	3	5.4	18685.5	9.45	HUMAN	B4DEV8	Proteasome subunit alpha type
24429	dirMS_041712_NAR_60mM_plus.17818.17818.3	3	3.84	1	3.65E+04		(R)GKFLEM	(R)G K F L E\M/C\N D L/L/A/R(V)	C:Carbamidomethylation	151.67	522.9381	1566.777	0.0231	14.7	6.07	95185.1	5.11	HUMAN	P34932	Heat shock 70 kDa protein 4
24430	dirMS_041712_NAR_60mM_plus.19871.19871.3	3	3.84	0	3.29E+04		(K)SFLIWV	(K)S F\L I W/V/N E E D/H T R(V)		163.53	549.2699	1645.797	-0.0017	-1.1	4.65	29478.9	6.26	HUMAN	E9PCP8	Creatine kinase U-type, mitochondrial
24431	dirMS_041712_NAR_60mM_plus.20579.20579.3	3	3.84	1	2.04E+05		(R)AQFEGI	(R)A Q/F E/G I V T D L I R/R(T)		167.4	506.6178	1517.843	-0.0046	-3	6.12	18505.2	10.14	HUMAN	H0YBG6	Stress-70 protein, mitochondrial (Fragment)
24432	dirMS_041712_NAR_60mM_plus.5078.5078.3	3	3.84	0	2.84E+05	T113t	(R)LIAAAtS	(R)L/I A A A t S V C K(C)	C:Carbamidomethylation t:N-ace	84.13	412.8904	1033.571	203.0856	5	8.75	17058.7	9.47	HUMAN	Q5JV82	Cyclin C
24433	dirMS_041712_NAR_60mM_plus.5142.5142.3	3	3.84	0	8.43E+04		(R)NLDNG	(R)N L D N G G F/Y I S/P R(I)		85.22	451.5555	1352.659	-0.0074	-5.5	5.83	31969.9	5.03	HUMAN	E9PAP0	Tyrosine-protein kinase Lck (Fragment)
24434	dirMS_041712_NAR_120mM_minus.10942.10942.4	4	3.83	2	2.32E+05		(K)QERAAA	(K)Q E R A A A A A/A/A A A K N G S S G/K(K)		113.65	433.2296	1729.894	0.0026	1.5	9.99	18943.6	9.77	HUMAN	H0YAD2	Paired mesoderm homeobox protein 2B (Fragment)
24435	dirMS_041712_NAR_120mM_minus.12401.12401.4	4	3.83	1	1.56E+05		(R)IPFIRPA	(R)I P/F I R P A D Q/Y K D/P Q S K(K)		121.97	476.5062	1903.007	-0.0043	-2.2	8.5	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
24436	dirMS_041712_NAR_120mM_minus.13004.13004.3	3	3.83	0	1.97E+05		(K)GQVTW	(K)G Q V T W/F G Y\E S P/R(S)		125.03	476.2347	1426.675	0.0146	10.2	6	51264.7	5.37	HUMAN	E9PBR4	RUN domain-containing protein 3B
24437	dirMS_041712_NAR_120mM_minus.19165.19165.3	3	3.83	1	2.16E+05		(R)LDFSITK	(R)L D/F/S I T|K D P A A E A\R(M)		160.47	511.9289	1533.791	-0.0186	-12.1	4.56	50034.3	6.1	HUMAN	B7Z4L4	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1
24438	dirMS_041712_NAR_120mM_minus.7604.7604.3	3	3.83	1	5.53E+04	M281m	(R)SRAEAE	(R)S R A E\A\E\S|m/Y Q I K(Y)	m:Oxidized methionine	95.73	476.8951	1412.684	15.9869	-5.6	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
24439	dirMS_041712_NAR_20mM_minus.11334.11334.2	2	3.83	0	3.30E+05	M1m N6n	(-)mPLFPnL	(-)m P|L F|P n L/P R(L)	m:Oxidized methionine n:N-	160.05	652.3395	1084.597	219.0745	0.2	9.5	39133.5	4.5	HUMAN	Q8TD91-2	Isoform 2 of Melanoma-associated antigen C3
24440	dirMS_041712_NAR_20mM_minus.7824.7824.2	2	3.83	0	7.81E+04	M406m	(R)EYQELm	(R)E Y/Q|E/L m N V/K(L)	m:Oxidized methionine	128.13	585.2788	1153.556	15.9945	-0.3	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
24441	dirMS_041712_NAR_20mM_minus.7855.7855.2	2	3.83	0	8.48E+04	S634s M63	(K)SVGVHs	(K)S V G V/H s V/m K(H)	s:N-acetylglucosamine (S) m:	128.45	581.7886	943.503	219.067	-6.3	8.49	98251.3	9.33	HUMAN	F5H493	DNA excision repair protein ERCC-6
24442	dirMS_041712_NAR_20mM_minus.9743.9743.2	2	3.83	0	2.50E+05	M33m	(K)VAGmD	(K)V A/G m/D V/E L T V E/E R(N)	m:Oxidized methionine	147.53	732.355	1447.71	15.993	-1.3	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
24443	dirMS_041712_NAR_50mM_minus2.11165.11165.3	3	3.83	0	3.49E+05		(K)QADLYI	(K)Q A D L Y I/S/E G L H/P R(I)		131.38	500.2598	1498.765	0	0	5.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
24444	dirMS_041712_NAR_50mM_minus2.6097.6097.3	3	3.83	1	8.51E+04		(K)IQDKEG	(K)I Q D K E G I/P/P D/Q Q R(L)		97	508.597	1523.781	-0.0048	-3.1	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
24445	dirMS_041712_NAR_50mM_minus2.8187.8187.3	3	3.83	1	2.04E+05		(K)GILAAD	(K)G I\L\A/A/D E S/T G S I A/K R(L)		114.43	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
24446	dirMS_041712_NAR_60mM_minus.14764.14764.3	3	3.83	1	3.59E+05	T390t	(R)LKAAHt	(R)L K/A A H t Y/V S\E E L R(A)	t:Phosphorylated T	142.55	532.935	1516.812	79.9786	7.7	6.75	57893	6.01	HUMAN	Q96QU6	1-aminocyclopropane-1-carboxylate synthase-like protein 1
24447	dirMS_041712_NAR_60mM_minus.16457.16457.3	3	3.83	1	1.28E+05		(K)WVAIQS	(K)W V|A/I/Q S V S A/W P E K/R(G)		151.82	552.9674	1656.886	0.002	1.2	8.75	6412.4	9.52	HUMAN	J3KSS4	Cytosolic non-specific dipeptidase (Fragment)
24448	dirMS_041712_NAR_60mM_minus.9013.9013.3	3	3.83	1	1.10E+05	M754m	(K)TCVFEK	(K)T C|V/F E K E N D/P S/V m R(S)	C:Carbamidomethylation m:Oxid	110.13	576.5915	1711.778	15.9821	-7.4	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
24449	dirMS_041712_NAR_120mM_plus.4088.4088.3	3	3.83	1	9.51E+06	M310m	(R)TKTEISE	(R)T\K\T E I|S/E/m N R(N)	m:Oxidized methionine	69.42	408.8687	1208.594	15.9976	2.2	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
24450	dirMS_041712_NAR_20mM_plus.16134.16134.3	3	3.83	0	1.70E+05		(K)DAGTIA	(K)D A G T I A/G L/N V/L R(I)		183.65	400.5627	1199.674	-0.0007	-0.6	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
24451	dirMS_041712_NAR_20mM_plus.16554.16554.2	2	3.83	1	6.63E+04	M416m	(R)TTEPST	(R)T T\E P/S T K S M/m E V E R(K)	m:Oxidized methionine	185.55	821.3739	1625.751	15.9896	-3.2	4.78	62626.3	8.69	HUMAN	Q76KD6	Speriolin
24452	dirMS_041712_NAR_30mM_plus2.18345.18345.2	2	3.83	0	6.04E+04		(K)NLGTAL	(K)N L/G|T/A L/A E L R(T)		150	529.3028	1057.6	-0.0017	-1.6	6	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
24453	dirMS_041712_NAR_30mM_plus2.18988.18988.2	2	3.83	0	3.69E+05		(K)AVVMDI	(K)A V|V/M/D|L L R(Q)		153.42	458.7641	916.528	-0.0075	-8.2	5.88	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
24454	dirMS_041712_NAR_30mM_plus2.20607.20607.2	2	3.83	0	1.10E+05		(K)SVVTSIF	(K)S V|V/T S I F G V K(N)		162.73	518.799	1036.604	-0.013	-12.5	8.47	132902.3	5.82	HUMAN	J3KR24	Isoleucine--tRNA ligase, cytoplasmic
24455	dirMS_041712_NAR_40mM_plus2.11157.11157.3	3	3.83	1	9.36E+04		(R)VLVFVM	(R)V L|V/F V M G K E G/V H G G G L N K(K)		131.92	614.3443	1841.01	0.0081	4.4	8.57	9912.2	9.69	HUMAN	C9J712	Profilin-2
24456	dirMS_041712_NAR_50mM_plus2.10557.10557.3	3	3.83	0	5.38E+05		(K)MIVDPV	(K)M I V\D/P V E P H/G E M/K(F)		123.13	494.5783	1481.713	0.0076	5.2	4.65	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
24457	dirMS_041712_NAR_50mM_plus2.12391.12391.3	3	3.83	1	2.51E+05		(R)LQEHLR	(R)L Q E H L R\L|C Q/L R(R)	C:Carbamidomethylation	133.3	489.2747	1465.806	0.0039	2.7	9.61	272689.3	5.79	HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
24458	dirMS_041712_NAR_50mM_plus2.19105.19105.3	3	3.83	0	5.24E+05		(R)GFGFITF	(R)G F G F/I/T F/T N P E H A S V A M R(A)		168.9	661.3258	1981.959	0.004	2	6.75	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
24459	dirMS_041712_NAR_60mM_plus.16122.16122.3	3	3.83	1	1.12E+06		(K)TDKTLV	(K)T/D K T L\V|L/L/M G K(E)		141.08	406.908	1218.713	-0.0032	-2.6	8.26	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
24460	dirMS_041712_NAR_60mM_plus.7695.7695.3	3	3.83	1	7.88E+05		(K)TPKGPS	(K)T P/K G P S S V E D/I/K(A)		98.27	419.894	1257.669	-0.0011	-0.8	5.73	32745.6	4.64	HUMAN	P06748	Nucleophosmin
24461	dirMS_041712_NAR_60mM_plus.7942.7942.3	3	3.83	1	2.00E+05		(R)YLAEVA	(R)Y/L/A E V/A C G D D R K(Q)	C:Carbamidomethylation	99.72	466.2245	1396.652	0.0064	4.6	4.56	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
24462	dirMS_041712_NAR_120mM_minus.13883.13883.2	2	3.82	1	4.52E+05		(R)MRLEAT	(R)M R L/E A\T|Q L E G/V\A/R(R)		130.48	737.385	1473.784	-0.0215	-14.6	5.9	403267.9	7.39	HUMAN	Q96T58	Msx2-interacting protein
24463	dirMS_041712_NAR_120mM_minus.18827.18827.3	3	3.82	2	1.33E+04		(R)KIEEIKD	(R)K\I E E I\K/D F/L L/T A R(R)		158.12	525.9767	1575.911	0.0051	3.2	6.18	2559	9.99	HUMAN	J3KSP2	60S ribosomal protein L38 (Fragment)
24464	dirMS_041712_NAR_120mM_minus.8496.8600.3	3	3.82	1	4.66E+05		(R)QREVTL	(R)Q R E\V\T\L/G Q V/A K(L)		100.85	410.2375	1228.701	-0.0029	-2.3	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
24465	dirMS_041712_NAR_20mM_minus.12706.12706.2	2	3.82	0	1.72E+05	M179m M	(K)mFVLDE	(K)m F\V|L\D E A D/E m L S R(G)	m:Oxidized methionine	176.52	794.3534	1555.713	31.9864	-2.1	3.91	41517.9	5.45	HUMAN	E7EQG2	Eukaryotic initiation factor 4A-II
24466	dirMS_041712_NAR_50mM_minus2.6203.6203.3	3	3.82	0	4.44E+05	M437m	(R)LESGMC	(R)L E/S/G M Q N m S I H/T K(T)	m:Oxidized methionine	97.77	497.9018	1475.698	15.9927	-1.5	6.75	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
24467	dirMS_041712_NAR_60mM_minus.13845.13845.3	3	3.82	0	2.23E+05		(R)VQIEHIS	(R)V/Q/I/E/H I S S L I/K(L)		137.73	422.9181	1266.742	-0.0019	-1.5	6.72	47748.2	6.08	HUMAN	O00231	26S proteasome non-ATPase regulatory subunit 11
24468	dirMS_041712_NAR_120mM_plus.11122.11122.3	3	3.82	1	2.57E+04		(R)RLEESD	(R)R L E\E\S D\V|L/Q/E A R(R)		112.85	482.2449	1444.739	-0.0189	-13.1	4.41	51697.1	8.8	HUMAN	O43615	Mitochondrial import inner membrane translocase subunit TIM44
24469	dirMS_041712_NAR_120mM_plus.8653.8653.3	3	3.82	0	1.23E+06		(R)RPELEDS	(R)R P\E\L\E|D/S/T L R(Y)		98.38	405.8796	1215.633	-0.0085	-7	4.68	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
24470	dirMS_041712_NAR_120mM_plus.8929.8929.2	2	3.82	0	2.03E+05		(R)FACHSA	(R)F/A/C/H|S A S L T V\R(N)	C:Carbamidomethylation	100.43	624.8103	1248.615	-0.002	-1.6	9.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
24471	dirMS_041712_NAR_20mM_plus.10510.10510.2	2	3.82	0	1.10E+05		(R)AVLLGPI	(R)A V\L/L/G\P P G A G K(G)		144.87	490.2992	979.593	-0.0024	-2.4	8.8	4460.2	8.14	HUMAN	F8VPP1	Adenylate kinase 2, mitochondrial
24472	dirMS_041712_NAR_20mM_plus.12625.12625.2	2	3.82	0	1.23E+05		(R)GVEICIA	(R)G V\E/I/C I/A/T/P G R(L)	C:Carbamidomethylation	159.2	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
24473	dirMS_041712_NAR_20mM_plus.16629.16629.3	3	3.82	0	6.48E+04	M137m M	(R)IIGATDS	(R)I I G A\T D S S G E/L/m F L m/K(W)	m:Oxidized methionine	185.8	582.2872	1712.86	31.9873	-1.5	4.37	19439.5	4.97	HUMAN	B5MD17	Chromobox protein homolog 1 (Fragment)
24474	dirMS_041712_NAR_30mM_plus2.12840.12840.2	2	3.82	0	6.70E+04		(R)YLDGLT	(R)Y L|D/G L T A E R(T)		120.43	519.2668	1037.526	0.0001	0.1	4.37	65717	8.32	HUMAN	P35908	Keratin, type II cytoskeletal 2 epidermal
24475	dirMS_041712_NAR_30mM_plus2.4861.4861.2	2	3.82	0	5.46E+05		(K)QASEGP	(K)Q/A S E G P/L K(G)		77.43	415.225	829.441	0.0013	1.6	6	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
24476	dirMS_041712_NAR_30mM_plus2.5391.5391.2	2	3.82	0	2.58E+04		(R)VSMEEC	(R)V/S|M/E E Q R(Q)		82.07	439.7064	878.404	0.0019	2.1	4.53	21119.9	4.34	HUMAN	H0Y3Y9	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
24477	dirMS_041712_NAR_50mM_plus2.12373.12373.3	3	3.82	0	2.46E+05		(K)AQIHDL	(K)A Q I H D L\V|L|V G/G S T R(I)		133.28	489.2747	1465.812	-0.0026	-1.8	6.79	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
24478	dirMS_041712_NAR_50mM_plus2.13614.13614.3	3	3.82	0	1.68E+06		(R)VLVVHD	(R)V/L|V V/H D G F E G L A K(G)		139.98	461.9229	1383.763	-0.0089	-6.5	5.32	18719.9	6.91	HUMAN	F8VP00	6-phosphofructokinase, muscle type (Fragment)
24479	dirMS_041712_NAR_60mM_plus.18749.18749.3	3	3.82	2	3.20E+05	S203s	(K)LIYKDLV	(K)L/I/Y/K D L V s V R K(N)	s:N-acetylglucosamine (S)	155.15	512.9699	1333.82	203.0749	-2.9	9.7	28275.1	6.85	HUMAN	E9PM77	Uncharacterized protein C11orf70
24480	dirMS_041712_NAR_60mM_plus.18862.18862.3	3	3.82	2	2.88E+04	T53t	(K)LESTRTT	(K)L E S T R T T|V/R t G L D L K(A)	t:Phosphorylated T	156.05	590.6485	1689.949	79.9816	8.6	8.75	15919.3	9.57	HUMAN	C9J3I4	Protein-tyrosine sulfotransferase 1 (Fragment)
24481	dirMS_041712_NAR_60mM_plus.19072.19072.3	3	3.82	0	5.07E+03		(R)HNIAYF	(R)H N I\A Y\F\P Q|I\V/S V/A A R(M)		158.1	562.6339	1685.912	-0.0251	-14.9	8.75	19693.7	9.29	HUMAN	K7EKW4	Isochorismatase domain-containing protein 2, mitochondrial (Fragment)
24482	dirMS_041712_NAR_60mM_plus.6131.6131.3	3	3.82	0	2.28E+05	M480m	(R)AAHSEG	(R)A A H S E G N T T/A/G/L/D/m R(E)	m:Oxidized methionine	91.07	516.2346	1530.697	15.9927	-1.4	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
24483	dirMS_041712_NAR_120mM_minus.6587.6587.3	3	3.81	1	1.45E+05		(K)VTEGQC	(K)V/T/E/G Q Q E/R L E R(Q)		90.35	448.9032	1344.687	0.0084	6.3	4.79	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
24484	dirMS_041712_NAR_30mM_minus2.7005.7005.2	2	3.81	0	2.54E+05	M169m	(R)MQSFG	(R)M Q/S F/G m K(T)	m:Oxidized methionine	92.28	422.689	828.374	15.9965	1.8	8.5	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
24485	dirMS_041712_NAR_40mM_minus2.11038.11038.3	3	3.81	0	8.53E+04		(K)SPAPPLL	(K)S P A/P/P L L H/V A A L G Q K(Q)		148.18	500.2927	1498.874	-0.0105	-7	8.49	17549.1	10.39	HUMAN	E5RFJ3	DBIRD complex subunit KIAA1967 (Fragment)
24486	dirMS_041712_NAR_50mM_minus2.10169.10169.3	3	3.81	0	1.71E+05	T704t	(K)tELISVSE	(K)t E L I S/V S E V H P/S R(L)	t:N-acetylglucosamine (T)	125.28	552.9403	1453.765	203.0418	-22.7	5.37	87903.7	5.74	HUMAN	P42224	Signal transducer and activator of transcription 1-alpha/beta
24487	dirMS_041712_NAR_50mM_minus2.15192.15192.3	3	3.81	2	3.39E+05		(R)LYLESTR	(R)L Y L E S T R G K E V T S K(L)		153.88	537.6375	1610.875	0.0231	14.4	8.5	37856.9	9.23	HUMAN	H0Y884	Probable tubulin polyglutamylase TTLL1 (Fragment)
24488	dirMS_041712_NAR_50mM_minus2.6855.6855.3	3	3.81	1	2.44E+04		(K)TLKMWI	(K)T L K M W F L E E/S N/E/T E/K(I)		105.68	628.9794	1884.905	0.0189	10	4.49	362095.2	5.94	HUMAN	Q96RL7	Vacuolar protein sorting-associated protein 13A
24489	dirMS_041712_NAR_50mM_minus2.8213.8213.3	3	3.81	2	2.34E+05		(K)KDVDAA	(K)K D/V/D A A Y M N K/V E L Q A K(V)		115.43	608.3087	1822.937	-0.0252	-13.8	6.12	36053	5.02	HUMAN	B4DXK4	Keratin, type II cytoskeletal 72
24490	dirMS_041712_NAR_60mM_minus.17602.17602.3	3	3.81	1	1.75E+04	S502s	(K)ILIRFsDY	(K)I\L|I R F s D Y/V/E V A K(A)	s:N-acetylglucosamine (S)	158.4	585.9955	1552.873	203.0986	10.9	6.07	62722.2	9.38	HUMAN	Q96KR7	Phosphatase and actin regulator 3
24491	dirMS_041712_NAR_120mM_plus.5261.5261.4	4	3.81	0	3.55E+03	Y1166y	(R)SGDEVH	(R)S G D E V/H y H V T A/G P/R(W)	y:Phosphorylated Y	80.45	401.9251	1524.719	79.9596	-4.2	5.94	251216.7	5.27	HUMAN	Q6UVK1	Chondroitin sulfate proteoglycan 4
24492	dirMS_041712_NAR_20mM_plus.10891.10891.3	3	3.81	0	1.01E+05		(K)ALIAAQ	(K)A L\I\A A Q|Y\S G A Q V/R(V)		147.88	449.9174	1347.738	-0.0003	-0.2	8.79	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
24493	dirMS_041712_NAR_20mM_plus.11029.11029.2	2	3.81	1	1.57E+05		(K)CTFGRG	(K)C T F G R G D/T G L\G/H S R(D)	C:Carbamidomethylation	149	760.8538	1520.702	-0.002	-1.3	9.61	40893.1	7.96	HUMAN	E7EME6	Cytochrome P450 4B1
24494	dirMS_041712_NAR_20mM_plus.16840.16840.2	2	3.81	0	1.51E+05		(R)ELLIIGG	(R)E L|L I/I/G G V A A R(D)		186.73	556.3437	1111.683	-0.0032	-2.9	6.1	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
24495	dirMS_041712_NAR_20mM_plus.7602.7602.2	2	3.81	0	2.49E+05		(K)VLTPTQ	(K)V L/T|P T Q V K(N)		121.73	443.2734	885.54	-0.0009	-1	8.72	21170.5	7.02	HUMAN	P30086	Phosphatidylethanolamine-binding protein 1
24496	dirMS_041712_NAR_30mM_plus2.17459.17459.2	2	3.81	0	4.48E+05	N102n	(K)ILVnMG	(K)I L/V n M/G D R(T)	n:N-acetylglucosamine (N)	144.83	560.7925	917.487	203.0904	9.9	5.84	21829.6	9.15	HUMAN	Q8N1E2	Lysozyme g-like protein 1
24497	dirMS_041712_NAR_30mM_plus2.21590.21590.2	2	3.81	0	2.58E+05		(R)EADDIVI	(R)E A D D/I/V N/W L/K(K)		167.68	601.81	1202.605	0.0075	6.3	4.03	26363.4	4.91	HUMAN	I3L312	Protein disulfide-isomerase (Fragment)
24498	dirMS_041712_NAR_30mM_plus2.6174.6174.2	2	3.81	0	1.55E+05	M516m M	(K)NEQmm	(K)N E/Q m/m\E Q/K(E)	m:Oxidized methionine	86.67	535.2159	1037.439	31.9855	-4.1	4.53	68443	5.97	HUMAN	P32455	Interferon-induced guanylate-binding protein 1
24499	dirMS_041712_NAR_40mM_plus2.11071.11071.3	3	3.81	0	1.02E+05		(R)SSLGVGI	(R)S\S L G/V G I G S M A A|D/S I E V S R(K)		131.07	612.652	1835.917	0.0247	13.5	4.37	161421.4	6.91	HUMAN	Q86VH2	Kinesin-like protein KIF27
24500	dirMS_041712_NAR_40mM_plus2.15054.15054.3	3	3.81	2	9.08E+03		(K)VSNKGL	(K)V S N K\G L P S S I E K T I/S K(A)		154.95	563.3222	1687.959	-0.0068	-4	9.7	36453.4	7.26	HUMAN	P01861	Ig gamma-4 chain C region
24501	dirMS_041712_NAR_50mM_plus2.10374.10374.3	3	3.81	0	1.38E+05	M277m	(R)GLGHQ	(R)G L G H Q V\A T D\A/L V/A m E K(A)	m:Oxidized methionine	120.62	552.6181	1639.847	15.9925	-1.4	5.32	55722.8	6.78	HUMAN	Q9Y3I0	tRNA-splicing ligase RtcB homolog
24502	dirMS_041712_NAR_50mM_plus2.13572.13572.3	3	3.81	1	2.68E+05		(R)FVNVVP	(R)F V N V/V/P T/F G K K(K)		139.53	412.5763	1235.715	-0.0003	-0.3	10	10904.6	11.56	HUMAN	E9PR30	40S ribosomal protein S30
24503	dirMS_041712_NAR_50mM_plus2.21337.21337.3	3	3.81	1	1.60E+05		(R)EVIRND	(R)E V I R N D G V|L\L|L Q A/L T R(S)		182.28	604.0209	1810.055	-0.0064	-3.5	6.17	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
24504	dirMS_041712_NAR_50mM_plus2.21532.21532.3	3	3.81	1	1.51E+05		(K)AKNEILD	(K)A K N E I L D E V\I/S/L S/Q\V T P K(H)		183.83	662.036	1984.096	-0.0027	-1.3	4.68	118312	7.77	HUMAN	E5KLJ5	Dynamin-like 120 kDa protein, mitochondrial
24505	dirMS_041712_NAR_50mM_plus2.6793.6793.3	3	3.81	1	1.83E+05		(K)AIEQLKE	(K)A I/E\Q L K E Q/A A T/G K(Q)		100.22	462.9247	1386.759	0.0008	0.6	6.18	58392.6	9.36	HUMAN	B4DF96	Eukaryotic translation initiation factor 2A
24506	dirMS_041712_NAR_50mM_plus2.9762.9762.2	2	3.81	1	9.29E+04	K550k	(K)IREAkAF	(K)I R/E|A k\A F L P S(-)	k:Ubiquitin-K	118.83	623.3474	1131.652	114.0355	-6	8.75	62994.9	4.92	HUMAN	Q2M329	Coiled-coil domain-containing protein 96
24507	dirMS_041712_NAR_60mM_plus.10260.10260.3	3	3.81	0	3.50E+05		(K)VGAHA	(K)V G A H A G E Y G A|E/A/L E/R(M)		111.77	510.5819	1529.734	-0.0031	-2.1	4.75	15314.3	8.9	HUMAN	P69905	Hemoglobin subunit alpha
24508	dirMS_041712_NAR_60mM_plus.13285.13285.3	3	3.81	1	2.29E+05		(R)QGPEGL	(R)Q G/P E G L E V S F R G/R(C)		126.7	477.9163	1431.734	0.0004	0.3	6.14	26587.6	6	HUMAN	E9PN81	Ribonuclease H2 subunit C
24509	dirMS_041712_NAR_60mM_plus.20860.20860.3	3	3.81	1	1.40E+05		(K)TFVNITP	(K)T F/V N I T/P A E V/G V L V G K D R(S)		170.55	639.0248	1915.065	-0.0049	-2.6	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
24510	dirMS_041712_NAR_120mM_minus.14597.14597.3	3	3.8	1	2.59E+05		(K)LDKSQI	(K)L D/K/S Q I H\D\I\V\L\V/G G S T R(I)		133.85	613.3393	1838.013	-0.0097	-5.3	6.75	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
24511	dirMS_041712_NAR_120mM_minus.6346.6346.3	3	3.8	0	1.48E+05	M480m	(R)AAHSEG	(R)A A H S E G N T|T/A/G L/D m R(E)	m:Oxidized methionine	89.12	516.2356	1530.697	15.9957	0.5	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
24512	dirMS_041712_NAR_120mM_minus.9309.9309.3	3	3.8	1	1.47E+05		(R)EQAEEE	(R)E Q/A/E E/E/R Y F R(A)		104.9	452.8778	1356.618	0.001	0.7	4.5	12248.6	9.34	HUMAN	Q9UII2	ATPase inhibitor, mitochondrial
24513	dirMS_041712_NAR_20mM_minus.10962.10962.2	2	3.8	0	7.01E+04		(R)LAVEAL	(R)L A|V/E A L V/R(T)		157.07	435.7738	870.541	-0.0004	-0.5	6	65558.6	9.87	HUMAN	G3V1S7	Hyaluronan synthase 1
24514	dirMS_041712_NAR_30mM_minus2.13838.13838.2	2	3.8	0	1.44E+05		(K)LAEYVAI	(K)L A|E/Y V A R(N)		128.45	411.2348	821.452	0.0107	13.1	6	59649.4	5.05	HUMAN	F5H5X1	Splicing factor, suppressor of white-apricot homolog (Fragment)
24515	dirMS_041712_NAR_30mM_minus2.14005.14006.2	2	3.8	0	2.85E+05	N269n	(K)nAAVMI	(K)n A A/V M\D Q G P\A G D R(T)	n:N-acetylglucosamine (N)	129.45	752.8364	1301.59	203.0752	-2.7	4.21	41119.8	9.05	HUMAN	Q8NHK3	Killer cell immunoglobulin-like receptor 2DL5B
24516	dirMS_041712_NAR_40mM_minus2.6262.6262.3	3	3.8	1	2.98E+03		(R)SSPKSEII	(R)S S P/K S E I/E V I S E P P E E K(V)		102.53	628.9779	1884.944	-0.0245	-13	4.32	27727.8	5.88	HUMAN	E9PDX4	SLIT-ROBO Rho GTPase-activating protein 2
24517	dirMS_041712_NAR_50mM_minus2.12865.12865.3	3	3.8	1	3.16E+05	S47s	(R)SSSSSSR	(R)S S S S S S R S|I/L s/S S I L(-)	s:Phosphorylated S	140.7	526.5884	1497.776	79.9752	5.6	9.47	5432	12.3	HUMAN	E9PLC2	Putative protein TPRXL (Fragment)
24518	dirMS_041712_NAR_50mM_minus2.15942.15942.3	3	3.8	1	1.14E+05	K916k	(R)VAAKN	(R)V/A A\K N G H S Q I I/k(L)	k:Ubiquitin-K	159.03	460.5908	1265.732	114.0254	-12.7	10	137809.7	5.94	HUMAN	E9PDW0	Ankyrin repeat domain-containing protein 50
24519	dirMS_041712_NAR_60mM_minus.10371.10371.3	3	3.8	0	1.40E+05	M693m	(R)LLNTAAI	(R)L/L/N T A A F G/L A E m R(S)	m:Oxidized methionine	117.98	474.9156	1406.746	15.9862	-6.1	6	84457.9	6.98	HUMAN	K7EMM9	Contactin-associated protein 1
24520	dirMS_041712_NAR_60mM_minus.10429.10429.3	3	3.8	1	1.71E+04		(R)YAAVTQ	(R)Y/A/A/V/T/Q F E A T D A R R(A)		118.3	533.5999	1598.792	-0.007	-4.4	6.07	54259.7	5.17	HUMAN	A6NEC2	Puromycin-sensitive aminopeptidase-like protein

24521	dirMS_041712_NAR_60mM_minus.11157.11157.3	3	3.8	1	6.58E+04		(K)IDKTDYN	(K)I D K T D\Y\M|V/G/S/Y G P R(A)		122.35	534.591	1601.763	-0.0044	-2.7	5.96	21671	5.37	HUMAN	J3KTF8	Rho GDP-dissociation inhibitor 1 (Fragment)
24522	dirMS_041712_NAR_60mM_minus.8886.8886.3	3	3.8	0	4.32E+03		(R)TLHSDD	(R)T L H S D D E G T\V/L/D/D/S R(A)		109.43	553.919	1659.746	-0.0032	-1.9	4.03	23307.1	5.11	HUMAN	E9PMH2	Peptidyl-prolyl cis-trans isomerase (Fragment)
24523	dirMS_041712_NAR_120mM_plus.4388.4388.3	3	3.8	1	2.58E+05		(R)AAEEED	(R)A A|E E E D E/A D/P K R(Q)		72.2	453.8721	1359.602	-0.0005	-0.4	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
24524	dirMS_041712_NAR_120mM_plus.7808.7808.3	3	3.8	1	1.27E+05	S2s	(-)MsLGGA	(-)M s L G G\A S E\R S/V P A T/K(I)	s:N-acetylglucosamine (S)	94.02	565.2917	1490.763	203.0974	10.6	8.5	62319.4	5.18	HUMAN	Q8IYJ1	Copine-9
24525	dirMS_041712_NAR_30mM_plus2.19883.19883.2	2	3.8	1	4.21E+05		(K)EKLEATI	(K)E K L E A\T I\N\E|L|V(-)		158.18	629.8458	1258.689	-0.0046	-3.6	4.25	9680	5.77	HUMAN	B1ALW1	Thioredoxin
24526	dirMS_041712_NAR_30mM_plus2.19960.19960.2	2	3.8	0	1.19E+05		(K)SLNNQF	(K)S L/N N/Q F A S F I/D K(V)		158.18	692.3489	1383.69	0.0002	0.2	5.55	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
24527	dirMS_041712_NAR_30mM_plus2.5410.5410.2	2	3.8	0	4.56E+05		(K)VSSFEEK	(K)V/S/S F E/E K(M)		81.8	413.203	825.399	-0.0002	-0.2	4.53	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
24528	dirMS_041712_NAR_40mM_plus2.10362.10362.3	3	3.8	0	3.00E+04		(K)QAAASA	(K)Q A/A A S A T/Q T I A A\A/Q/H\A/A S T P K(A)		125.83	665.6807	1995.025	0.0022	1.1	8.76	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
24529	dirMS_041712_NAR_40mM_plus2.5931.5931.2	2	3.8	0	2.43E+04		(K)GEGQLG	(K)G E/G Q L G P A E R(A)		92.77	507.2532	1013.501	-0.0019	-1.9	4.53	96306.4	6.41	HUMAN	P13639	Elongation factor 2
24530	dirMS_041712_NAR_40mM_plus2.6732.6732.2	2	3.8	0	9.58E+04	M189m	(K)LTGmAF	(K)L/T|G m A/F/R(V)	m:Oxidized methionine	99.87	406.2085	795.418	15.9916	-4.1	9.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
24531	dirMS_041712_NAR_40mM_plus2.7251.7251.2	2	3.8	0	1.06E+05		(R)SGYFDEI	(R)S G|Y/F D E/R(Y)		102.97	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
24532	dirMS_041712_NAR_40mM_plus2.7257.7257.2	2	3.8	0	6.89E+03		(K)QGGGG	(K)Q G/G G/G G G G S V/P G I/E R(M)		102.55	642.8175	1284.629	-0.0014	-1.1	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
24533	dirMS_041712_NAR_40mM_plus2.9784.9784.2	2	3.8	0	1.72E+05		(K)ELNYFAI	(K)E L/N/Y/F A K(A)		121.2	442.7291	884.451	-0.0003	-0.4	6.1	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
24534	dirMS_041712_NAR_60mM_plus.5491.5491.3	3	3.8	0	5.20E+04	M111m	(R)MEELHN	(R)M E/E L/H N Q\E m Q K(R)	m:Oxidized methionine	86.12	478.2118	1416.625	15.9962	0.9	4.75	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
24535	dirMS_041712_NAR_120mM_minus.13921.13921.3	3	3.79	1	3.18E+05		(R)EMDRET	(R)E M/D R E T L|I/D V A R(T)		129.7	483.2462	1447.721	0.0031	2.1	4.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
24536	dirMS_041712_NAR_20mM_minus.7027.7027.2	2	3.79	0	2.13E+05	M33m	(R)IDEmPE	(R)I/D|E\m/P E A A V K(S)	m:Oxidized methionine	117.98	559.7733	1102.545	15.9944	-0.4	4.14	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
24537	dirMS_041712_NAR_30mM_minus2.11307.11334.2	2	3.79	0	7.99E+05		(R)TFSSIPV	(R)T F|S/S I/P V\S R(I)		115.13	497.265	993.536	-0.0136	-13.7	9.41	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
24538	dirMS_041712_NAR_30mM_minus2.11908.11908.2	2	3.79	0	2.93E+05		(R)AFPGPL	(R)A/F/P G P L A K(D)		117.87	400.7352	800.467	-0.0034	-4.2	8.8	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
24539	dirMS_041712_NAR_30mM_minus2.12253.12253.2	2	3.79	0	2.84E+05		(K)STLTDSL	(K)S T|L/T D S L V C\K(A)	C:Carbamidomethylation	120.08	562.2838	1123.566	-0.006	-5.4	5.55	96306.4	6.41	HUMAN	P13639	Elongation factor 2
24540	dirMS_041712_NAR_30mM_minus2.14437.14437.2	2	3.79	0	2.19E+06	M320m	(K)YmACCL	(K)Y m|A/C/C L L\Y R(G)	C:Carbamidomethylation m:Oxid	131.17	633.2775	1249.553	15.9951	0.1	8.59	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
24541	dirMS_041712_NAR_30mM_minus2.7535.7535.2	2	3.79	0	2.56E+05		(K)QYQDAI	(K)Q Y Q/D/A I R(A)		95.52	447.2217	893.448	-0.0114	-12.8	5.83	69832.2	8.82	HUMAN	H0Y517	Coiled-coil and C2 domain-containing protein 1B (Fragment)
24542	dirMS_041712_NAR_40mM_minus2.8054.8054.3	3	3.79	1	3.06E+05		(R)DGKLVS	(R)D G K L V S E/S\S D V L P K(-)		128.17	491.9311	1473.78	-0.0008	-0.5	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
24543	dirMS_041712_NAR_40mM_minus2.8317.8317.3	3	3.79	0	8.43E+03		(R)MLTGPV	(R)M L T G P V Y/S Q/S T A L T H K(Q)		129.58	578.6359	1733.889	0.0041	2.3	8.37	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
24544	dirMS_041712_NAR_50mM_minus2.11147.11147.3	3	3.79	1	3.80E+05	T698t	(K)LLTCKDI	(K)L L/T C K D D A E A V/t A L N R(F)	C:Carbamidomethylation t:Phosp	130.85	623.9684	1789.911	79.9794	7	4.56	129589.3	5.69	HUMAN	J3KN75	TBC1 domain family member 8B
24545	dirMS_041712_NAR_60mM_minus.13426.13426.3	3	3.79	1	3.04E+05		(K)FSIEDLK	(K)F/S/I E D L K A Q/P/K(Q)		135.1	425.9025	1275.694	-0.0014	-1.1	6.07	13579.2	9.99	HUMAN	E9PPQ6	Thymocyte nuclear protein 1 (Fragment)
24546	dirMS_041712_NAR_60mM_minus.8519.8519.3	3	3.79	1	1.02E+05		(K)ELKSPDE	(K)E L/K S P D/E/G F E G K(S)		107.42	445.8849	1335.643	-0.0025	-1.9	4.41	84557.3	6.5	HUMAN	Q04609	Glutamate carboxypeptidase 2
24547	dirMS_041712_NAR_120mM_plus.13162.13162.3	3	3.79	1	8.67E+05	K266k	(R)IHFSRED	(R)I/H/F S R\E D Q A G k(T)	k:Ubiquitin-K	122.27	467.9029	1287.644	114.0501	5.1	6.75	36961.9	6.1	HUMAN	H0YF88	Protein NLRC5 (Fragment)
24548	dirMS_041712_NAR_120mM_plus.17564.17564.4	4	3.79	1	2.88E+05		(K)SKNILFV	(K)S K N I L F/V/I/T K/P\D V/Y K(S)		145.25	442.0115	1765.026	-0.0017	-0.9	9.53	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
24549	dirMS_041712_NAR_120mM_plus.22758.22758.4	4	3.79	2	5.39E+04	K32k	(R)RTREELV	(R)R T R E/E L V S Q G/I M\P P L/k(S)	k:Ubiquitin-K	173.47	492.7685	1854.027	114.0256	-8.8	8.75	8810.1	11.28	HUMAN	B0QY74	MKL/myocardin-like protein 1 (Fragment)
24550	dirMS_041712_NAR_20mM_plus.10422.10422.3	3	3.79	0	2.60E+05		(R)AQIFAN	(R)A Q I F A N/T/V/D/N A R(I)		145.25	440.5608	1319.67	-0.0024	-1.8	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
24551	dirMS_041712_NAR_20mM_plus.12239.12239.2	2	3.79	0	1.17E+05		(K)VNQIGS	(K)V N|Q I/G S\V T E S I/Q A/C K(L)	C:Carbamidomethylation	157.67	817.4114	1633.821	-0.0059	-3.6	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
24552	dirMS_041712_NAR_20mM_plus.7582.7582.2	2	3.79	0	1.52E+05	M328m	(K)ALmDEV	(K)A/L/m/D E\V V K(A)	m:Oxidized methionine	122.15	460.741	904.481	15.9939	-1.1	4.37	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
24553	dirMS_041712_NAR_40mM_plus2.10979.10979.3	3	3.79	2	9.57E+04		(R)VLDASW	(R)V L D A S W Y S P/G T R E A R K(E)		130.82	612.652	1835.94	0.0016	0.9	8.56	14293	7.03	HUMAN	B1AH48	Thiosulfate sulfurtransferase (Fragment)
24554	dirMS_041712_NAR_40mM_plus2.5046.5046.2	2	3.79	0	1.24E+05		(R)GGAGV	(R)G G A/G V/G/S/M T K(I)		84.1	432.7157	864.424	-0.0003	-0.3	8.75	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
24555	dirMS_041712_NAR_40mM_plus2.5636.5636.2	2	3.79	0	1.07E+05		(K)APGFGD	(K)A/P G F/G D/N R(K)		90.47	417.1996	833.39	0.0019	2.3	5.88	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
24556	dirMS_041712_NAR_50mM_plus2.10476.10476.3	3	3.79	1	5.08E+05		(K)MITKVQ	(K)M I/T K V\Q D F Q E D/K(E)		123.07	494.5783	1481.73	-0.0101	-6.8	4.56	27633.2	8.89	HUMAN	A8MTS8	Phytanoyl-CoA dioxygenase, peroxisomal
24557	dirMS_041712_NAR_50mM_plus2.19949.19949.3	3	3.79	1	5.08E+05		(R)LFLDRDI	(R)L F/L/D R D L M T\L/P I Q\N K(L)		173.67	606.3362	1816.999	-0.0049	-2.7	5.96	18188.9	10.98	HUMAN	K7EKP7	Ferrochelatase, mitochondrial (Fragment)
24558	dirMS_041712_NAR_50mM_plus2.7267.7267.3	3	3.79	0	1.11E+05		(K)TNPPLIC	(K)T N/P P L/I Q/E K P A K(T)		104	445.9257	1335.763	-0.0005	-0.4	8.26	102841.5	6.73	HUMAN	D3DQV9	Eukaryotic translation initiation factor 4 gamma 2 (Fragment)
24559	dirMS_041712_NAR_60mM_plus.12924.12924.3	3	3.79	0	5.27E+05	K135k	(K)LYHNLQ	(K)L Y/H N L Q E Y A k/R(Y)	k:Ubiquitin-K	124.07	516.9402	1434.749	114.0572	9.2	8.5	42782	7.95	HUMAN	Q6ICH7	Aspartate beta-hydroxylase domain-containing protein 2
24560	dirMS_041712_NAR_60mM_plus.16433.16433.3	3	3.79	0	6.32E+05		(R)ETHSAL	(R)E T H S A\L G|P A|L Q|A A F K(L)		142.2	514.2744	1540.812	-0.0032	-2.1	6.85	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
24561	dirMS_041712_NAR_120mM_minus.17129.17129.4	4	3.78	1	2.93E+05		(R)ELDTVTI	(R)E L D T V/T/L E/D I K/E H V/K(Q)		148.33	442.9877	1768.933	-0.0038	-2.1	4.5	61090.6	8.58	HUMAN	O43242	26S proteasome non-ATPase regulatory subunit 3
24562	dirMS_041712_NAR_20mM_minus.11891.11891.3	3	3.78	1	3.43E+05	S410s	(K)VGGTsD	(K)V G G T s D/V E V N E K K(D)	s:N-acetylglucosamine (S)	167.15	522.2561	1361.691	203.063	-10.4	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
24563	dirMS_041712_NAR_20mM_minus.7566.7566.2	2	3.78	0	8.14E+05	M239m	(K)EVDEQm	(K)E V/D E Q m L N V\Q/N K(N)	m:Oxidized methionine	124.17	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
24564	dirMS_041712_NAR_30mM_minus2.9580.9580.2	2	3.78	0	1.74E+05		(K)QTTCWI	(K)Q T/T|C/W/D|G V/R(N)	C:Carbamidomethylation	106.35	561.7582	1122.5	0.0095	8.4	5.84	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1
24565	dirMS_041712_NAR_50mM_minus2.13108.13108.3	3	3.78	0	3.52E+06	M84m	(K)YPIEHGI	(K)Y/P\I E H G I I/T/N/W/D D m E K(I)	m:Oxidized methionine	141.82	659.6398	1960.911	15.9939	-0.5	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
24566	dirMS_041712_NAR_50mM_minus2.17603.17603.3	3	3.78	1	1.24E+05		(K)NAAGAL	(K)N A/A|G/A L D/L L K E L K(N)		168.68	452.601	1355.789	-0.0008	-0.6	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
24567	dirMS_041712_NAR_60mM_minus.11050.11050.3	3	3.78	2	1.71E+05		(R)IIEGSPAI	(R)I I E G/S P A D R C G K L/K(V)	C:Carbamidomethylation	121.48	515.2815	1543.826	0.0039	2.5	8.59	123793.4	5.45	HUMAN	H7C4U7	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1 (Fragment)
24568	dirMS_041712_NAR_120mM_plus.10847.10847.3	3	3.78	1	7.48E+04		(K)KYEFGES	(K)K Y E F G\E/S D/L/R(S)		109.63	415.205	1243.595	0.0051	4.1	4.68	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
24569	dirMS_041712_NAR_20mM_plus.10771.10771.2	2	3.78	0	6.30E+04		(K)DVNAAL	(K)D V\N\A/A I A\T\I/K(T)		147.08	508.292	1015.578	-0.0015	-1.5	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
24570	dirMS_041712_NAR_20mM_plus.11354.11354.2	2	3.78	0	1.79E+05		(K)VGLQVV	(K)V/G/L Q|V V A V K(A)		150.78	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
24571	dirMS_041712_NAR_20mM_plus.12291.12291.3	3	3.78	0	1.55E+05	M586m	(K)NGSVVA	(K)N G S V V A m T G D/G\V N D A V A L K(A)	m:Oxidized methionine	158.23	611.9768	1817.906	16.0097	8	4.21	98683.3	6.01	HUMAN	E7ERC6	Calcium-transporting ATPase type 2C member 1
24572	dirMS_041712_NAR_20mM_plus.17796.17796.2	2	3.78	0	1.48E+05		(R)TVQSLEI	(R)T V/Q|S L E/I\D L D S M R(N)		194.77	753.8776	1506.747	0.0011	0.7	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
24573	dirMS_041712_NAR_20mM_plus.18345.18345.2	2	3.78	0	2.38E+04		(K)VLALAAI	(K)V L|A\L/A A E S D P N V R(T)		197.58	677.8702	1354.733	0.0006	0.5	4.37	186221.6	5.56	HUMAN	G5E9G7	Neurexin 2, isoform CRA_a
24574	dirMS_041712_NAR_20mM_plus.18430.18430.2	2	3.78	0	1.95E+05		(R)AAVEEG	(R)A A V\E E G I|V|L/G/G G C A L L R(C)	C:Carbamidomethylation	197.9	842.9549	1684.905	-0.0025	-1.5	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
24575	dirMS_041712_NAR_20mM_plus.19261.19261.2	2	3.78	1	1.45E+05		(R)MEQNG	(R)M E/Q N G R A T G F L L K(E)		204.43	732.889	1464.763	0.008	5.4	8.5	86404.1	9.33	HUMAN	E1B6W6	Colony stimulating factor 3 receptor (Granulocyte), isoform CRA_a
24576	dirMS_041712_NAR_30mM_plus2.10675.10696.3	3	3.78	0	2.74E+05		(K)WCELIP	(K)W/C E L I P G A E F/R(C)	C:Carbamidomethylation	109.65	459.901	1377.662	0.0265	19.2	4.53	17708.4	4.6	HUMAN	H7BZW7	Cell division cycle protein 123 homolog (Fragment)
24577	dirMS_041712_NAR_30mM_plus2.5491.5491.2	2	3.78	0	3.55E+04		(K)SAAQAA	(K)S A/A Q|A/A A Q T/N S N A A/G K(Q)		83.37	730.8568	1460.709	-0.0025	-1.7	8.47	45021.6	8.74	HUMAN	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein
24578	dirMS_041712_NAR_40mM_plus2.5550.5550.2	2	3.78	0	1.07E+05		(R)NQGGY	(R)N Q/G\G Y/G/G/S S S S S S Y G S G R(R)		90.3	847.8525	1694.7	-0.0024	-1.4	8.59	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
24579	dirMS_041712_NAR_50mM_plus2.19282.19282.3	3	3.78	1	2.29E+05		(K)DGKTLN	(K)D G K T L N\D\E/L/E\I/I E G M K(F)		169.8	602.3071	1804.9	0.007	3.9	4.18	23782.2	9.5	HUMAN	E7EXB4	60 kDa heat shock protein, mitochondrial (Fragment)
24580	dirMS_041712_NAR_50mM_plus2.7990.7990.3	3	3.78	1	1.75E+04		(R)VLVNDA	(R)V L/V N\D/A Q K V T/E\G Q Q E R(L)		108.38	605.3151	1813.94	-0.0095	-5.2	4.68	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
24581	dirMS_041712_NAR_60mM_plus.14057.14057.3	3	3.78	0	1.49E+05		(K)LAQANG	(K)L A/Q A N G W/G V M V/S\H R(S)		130.15	509.2606	1525.769	-0.002	-1.3	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
24582	dirMS_041712_NAR_60mM_plus.20269.20269.3	3	3.78	1	4.02E+05		(K)NAAGAL	(K)N/A|A/G A L/D L L/K E L/K(N)		166.9	452.6004	1355.789	-0.0026	-2	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
24583	dirMS_041712_NAR_120mM_minus.12164.12164.4	4	3.77	0	3.12E+05		(R)QATINIG	(R)Q A T I N\I/G T I/G H V A H G K(S)		120.33	404.977	1616.887	-0.0005	-0.3	8.76	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
24584	dirMS_041712_NAR_120mM_minus.7412.7412.3	3	3.77	1	7.95E+04		(K)SNKDGG	(K)S N K D G G N Q E|V/E I A R(C)		94.58	506.2424	1516.735	-0.0224	-14.8	4.68	10305.6	6.94	HUMAN	H7C330	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
24585	dirMS_041712_NAR_120mM_minus.7452.7452.3	3	3.77	0	1.37E+05		(R)EVRPDT	(R)E V R P D T Q/Y/T|G R(K)		94.9	441.2234	1321.65	0.0061	4.6	6.17	34187.3	9.64	HUMAN	C9K060	Uncharacterized methyltransferase WBSCR22
24586	dirMS_041712_NAR_20mM_minus.11140.11140.2	2	3.77	0	2.96E+05	M1m N6n	(-)mPLFPnL	(-)m P|L/F/P n L P R(L)	m:Oxidized methionine n:N-	159.48	652.3395	1084.597	219.0745	0.2	9.5	39133.5	4.5	HUMAN	Q8TD91-2	Isoform 2 of Melanoma-associated antigen C3
24587	dirMS_041712_NAR_20mM_minus.7567.7567.2	2	3.77	0	8.14E+05	M239m	(K)EVDEQm	(K)E V/D E Q m\L/N V|Q N K(N)	m:Oxidized methionine	124.17	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
24588	dirMS_041712_NAR_30mM_minus2.11192.11192.2	2	3.77	0	3.89E+05		(R)NTDEM	(R)N T|D\E/M/V/E L R(I)		115.05	553.7611	1106.515	0.0003	0.2	4.14	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
24589	dirMS_041712_NAR_30mM_minus2.13331.13331.2	2	3.77	0	2.45E+05		(K)QYGNEV	(K)Q Y/G/N/E V F/L/A K(L)		126.23	584.7961	1168.6	-0.0148	-12.6	6	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
24590	dirMS_041712_NAR_30mM_minus2.16211.16211.2	2	3.77	0	1.37E+05	M256m	(R)SLDmDS	(R)S/L/D m D S I I|A E/V K(A)	m:Oxidized methionine	141.78	668.8368	1320.671	15.9948	-0.1	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
24591	dirMS_041712_NAR_30mM_minus2.5486.5486.2	2	3.77	0	3.32E+05		(R)TDTGEP	(R)T D|T/G/E\P M G R(G)		83.03	482.2145	963.42	0.0017	1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
24592	dirMS_041712_NAR_30mM_minus2.7387.7387.2	2	3.77	0	3.01E+05	M514m M	(K)NEEmm	(K)N E|E m/m E Q/K(E)	m:Oxidized methionine	94.68	535.7092	1038.423	31.9881	-1.6	4.25	67721.3	5.54	HUMAN	P32456	Interferon-induced guanylate-binding protein 2
24593	dirMS_041712_NAR_30mM_minus2.9034.9034.2	2	3.77	0	2.45E+05		(R)ELAEAV	(R)E L/A/E/A V/A/G G R(V)		103.72	486.7596	972.511	0.001	1.1	4.53	30204.9	6.02	HUMAN	K7EPL2	SUMO-activating enzyme subunit 2 (Fragment)
24594	dirMS_041712_NAR_40mM_minus2.14565.14565.3	3	3.77	2	1.59E+05	S17727s	(K)DRVVIDI	(K)D R V|V I D N/V G T K s E L I I K(D)	s:Phosphorylated S	170.63	660.3663	1899.091	79.9934	13.7	6.12	4024332	6.06	HUMAN	K7ENY1	Titin
24595	dirMS_041712_NAR_40mM_minus2.8179.8179.3	3	3.77	1	4.65E+04		(R)DVVICPI	(R)D V|V I\C|P D A/S L E D A K K(E)	C:Carbamidomethylation	128.47	553.9467	1659.826	-0.0003	-0.2	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
24596	dirMS_041712_NAR_50mM_minus2.13313.13313.3	3	3.77	0	1.98E+04	M212m S2	(R)VLmSVA	(R)V L\m S V A P s A/L Q L R(V)	m:Oxidized methionine s:Ph	143.18	494.2621	1384.798	95.9737	8.4	9.72	39783.5	10.85	HUMAN	O60683-2	Isoform 2 of Peroxisome biogenesis factor 10
24597	dirMS_041712_NAR_50mM_minus2.14069.14069.3	3	3.77	0	6.70E+04		(R)EALAEA	(R)E A\L/A/E/A A L E S P R P A L V R(S)		148.12	598.3345	1792.992	-0.0026	-1.5	4.79	22148.2	5.87	HUMAN	B3KY21	Na(+)/H(+) exchange regulatory cofactor NHE-RF1
24598	dirMS_041712_NAR_50mM_minus2.15720.15720.3	3	3.77	1	4.29E+04		(K)ILDKLEL	(K)I/L/D K L E\L/S L/I/H S R(G)		158.82	512.97	1536.911	-0.0154	-10	6.75	92139.8	5.51	HUMAN	Q5TG85	Chromodomain helicase DNA binding protein 5
24599	dirMS_041712_NAR_50mM_minus2.9078.9078.3	3	3.77	1	1.03E+04		(R)ILNEKVN	(R)I/L|N E K V N T/P T/T T V Y R(C)		119.65	583.6518	1748.954	-0.0133	-7.6	8.59	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
24600	dirMS_041712_NAR_60mM_minus.10201.10201.3	3	3.77	0	1.86E+05	M502m	(R)SGGmEF	(R)S G/G/m E R|P F V L A R(A)	m:Oxidized methionine	116.5	445.9007	1319.689	15.9987	2.8	9.32	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
24601	dirMS_041712_NAR_60mM_minus.18285.18285.3	3	3.77	1	1.41E+05		(R)IRVESLL	(R)I R V E S L\L|V\T A I S K(A)		162.7	476.9628	1428.878	-0.0046	-3.2	8.75	91730	7.16	HUMAN	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15
24602	dirMS_041712_NAR_120mM_plus.11302.11302.3	3	3.77	0	2.30E+05	M109m	(K)NmSVHI	(K)N/m S V H L/S/P C F R(D)	C:Carbamidomethylation m:Oxid	112.17	455.2145	1347.63	15.9993	3.2	9.75	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
24603	dirMS_041712_NAR_120mM_plus.6630.6630.2	2	3.77	1	5.24E+05		(R)DKHSGT	(R)D K H S G T/E S Q A K(H)		87.48	594.2868	1187.565	0.0012	1	6.75	91170.5	6.62	HUMAN	E9PMT0	Tyrosine-protein phosphatase non-receptor type 22
24604	dirMS_041712_NAR_120mM_plus.8886.8886.2	2	3.77	0	5.69E+05		(R)NGVMP	(R)N G V|M/P S H F S R(G)		99.85	566.274	1131.536	0.0043	3.8	9.75	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
24605	dirMS_041712_NAR_120mM_plus.9500.9500.4	4	3.77	2	6.82E+04		(K)LRYQYLE	(K)L R Y Q Y L E E L/V S S R E R(A)		103.02	486.008	1941.019	-0.0087	-4.5	6.23	13954.8	10.16	HUMAN	O60519	cAMP-responsive element-binding protein-like 2
24606	dirMS_041712_NAR_20mM_plus.10578.10578.2	2	3.77	0	2.04E+05		(K)NAGVEG	(K)N A|G/V|E G S L I V E K(I)		146.07	608.3304	1215.658	-0.0044	-3.6	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
24607	dirMS_041712_NAR_20mM_plus.15999.15999.2	2	3.77	0	3.37E+05		(R)GNPTVE	(R)G N/P T/V E V D L F T S K(G)		180.87	703.861	1406.716	-0.0015	-1	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
24608	dirMS_041712_NAR_30mM_plus2.11748.11748.2	2	3.77	0	9.40E+05		(K)YGDGIQ	(K)Y/G\D G I/Q/L/T/R(S)		114.05	511.766	1022.527	-0.0018	-1.8	5.83	334221.3	6.44	HUMAN	P15924	Desmoplakin
24609	dirMS_041712_NAR_30mM_plus2.12526.12526.2	2	3.77	0	2.56E+05		(R)NCSSFLI	(R)N/C|S S F L I K(R)	C:Carbamidomethylation	118.62	484.7469	968.487	-0.0005	-0.5	8.75	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
24610	dirMS_041712_NAR_30mM_plus2.17136.17136.3	3	3.77	0	6.88E+05		(R)EFVSISSI	(R)E F V S I S S P A H V A/T(-)		143.18	448.8963	1344.679	-0.0051	-3.8	5.24	100943.3	6.1	HUMAN	P22681	E3 ubiquitin-protein ligase CBL
24611	dirMS_041712_NAR_30mM_plus2.20061.20061.2	2	3.77	0	5.01E+05		(K)ETLIITPP	(K)E T/L/I I T P P S C K(S)	C:Carbamidomethylation	158.35	629.8458	1258.671	0.0132	10.5	6.1	279771.8	9.54	HUMAN	Q8NDH2	Coiled-coil domain-containing protein 168
24612	dirMS_041712_NAR_30mM_plus2.6858.6858.2	2	3.77	0	1.33E+05		(K)AVELAAI	(K)A V|E L|A/A/N T K(G)		90.63	458.7641	916.51	0.0111	12.1	6.05	63448.4	7.29	HUMAN	B4E022	Transketolase
24613	dirMS_041712_NAR_40mM_plus2.10278.10278.2	2	3.77	0	1.32E+05		(R)QINLSNI	(R)Q I/N L/S/N I R(A)		125.02	479.2747	957.548	-0.0055	-5.7	9.75	102679.8	6.75	HUMAN	Q7KZF4	Staphylococcal nuclease domain-containing protein 1
24614	dirMS_041712_NAR_40mM_plus2.12241.12241.2	2	3.77	1	1.10E+04		(K)KQEGTP	(K)K Q E G T/P/E G\L|Y L(-)		138.2	617.8179	1234.631	-0.0029	-2.3	4.53	41280.4	4.9	HUMAN	B4DR63	26S protease regulatory subunit 4
24615	dirMS_041712_NAR_40mM_plus2.12379.12379.3	3	3.77	1	1.78E+05		(K)IINADSE	(K)I I/N/A D S E/D P K/Y I I N V K(Q)		139.03	611.3255	1831.98	-0.0181	-9.9	4.56	14693.3	4.69	HUMAN	C9JLS9	26S protease regulatory subunit 7 (Fragment)
24616	dirMS_041712_NAR_40mM_plus2.16035.16035.3	3	3.77	1	2.13E+05	S77s	(K)RACQDV	(K)R\A C Q D V\s/V I I H/T(-)	C:Carbamidomethylation s:Phosp	160.63	493.5656	1398.716	79.9664	0.1	6.74	9384.8	8.06	HUMAN	E9PRN7	3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 1 (Fragment)
24617	dirMS_041712_NAR_40mM_plus2.4150.4150.2	2	3.77	0	1.38E+05	M299m M	(K)NmmAA	(K)N m\m A/A/C D/P R(H)	C:Carbamidomethylation m:Oxid	68.97	549.2114	1065.427	31.9881	-1.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
24618	dirMS_041712_NAR_40mM_plus2.6970.6970.2	2	3.77	0	2.31E+03		(R)TALAMG	(R)T A|L/A/M G\A D\R(G)		102.3	453.2358	905.451	0.0134	14.8	5.5	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
24619	dirMS_041712_NAR_40mM_plus2.7647.7647.2	2	3.77	0	8.63E+04		(R)FGQGG	(R)F G Q G/G/A/G/P V/G G Q G P R(G)		105.47	671.3368	1341.666	0.0005	0.4	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
24620	dirMS_041712_NAR_50mM_plus2.10839.10839.3	3	3.77	2	1.83E+04	T790t M79	(R)GVGWtI	(R)G V G\W t P P G S/Y K V E m A R/R(A)	t:Phosphorylated T m:Oxidiz	124.33	662.9865	1890.964	95.9806	9.8	9.99	97074.2	9.45	HUMAN	B1ANW7	Nebulin-related anchoring protein
24621	dirMS_041712_NAR_50mM_plus2.14119.14119.3	3	3.77	1	1.41E+05		(K)VAAIRGI	(K)V A|A/I R G E\V T A A D L\F N S R(V)		142.43	597.3178	1789.956	-0.0167	-9.3	6.04	266161	5.68	HUMAN	E9PPU0	Epiplakin
24622	dirMS_041712_NAR_50mM_plus2.15242.15242.3	3	3.77	0	2.34E+05		(R)LASTLVI	(R)L A/S T/L V H L G E Y Q/A/A/V D G A/R(K)		148.03	657.6802	1971.029	-0.0034	-1.7	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
24623	dirMS_041712_NAR_50mM_plus2.15521.15521.3	3	3.77	0	2.60E+05		(K)ANLLNN	(K)A N|L/L/N N E A H A I T M Q V T K(S)		149.67	623.3237	1867.969	-0.0129	-6.9	6.79	74483	8.6	HUMAN	P46063	ATP-dependent DNA helicase Q1
24624	dirMS_041712_NAR_50mM_plus2.8284.8284.3	3	3.77	1	6.01E+04		(R)LTPREISI	(R)L T/P R|E I S E/V V R(E)		110.05	433.5865	1298.743	0.0023	1.7	6.14	19939.5	4.45	HUMAN	Q9NP86	Calcium-binding protein 5
24625	dirMS_041712_NAR_60mM_plus.16787.16787.3	3	3.77	0	2.39E+05		(R)YQEALH	(R)Y/Q/E A L/H L G S/Q L L R(E)		144.33	509.946	1527.828	-0.0044	-2.9	6.75	47748.2	6.08	HUMAN	O00231	26S proteasome non-ATPase regulatory subunit 11
24626	dirMS_041712_NAR_60mM_plus.17552.17552.3	3	3.77	1	8.36E+05		(R)DKLNNL	(R)D K L N N\L V/L/F D K(A)		148.42	440.2499	1318.737	-0.0014	-1	5.96	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
24627	dirMS_041712_NAR_60mM_plus.18991.18991.3	3	3.77	0	1.66E+05		(R)NHPGLL	(R)N H/P G L L\L|M/D/T T F R(D)		156.77	505.6001	1514.778	0.0073	4.8	6.74	130372.9	6.37	HUMAN	P11498	Pyruvate carboxylase, mitochondrial
24628	dirMS_041712_NAR_60mM_plus.19271.19271.3	3	3.77	0	1.09E+05		(R)ALGISSV	(R)A L G|I S/S V F L Q/G L R(S)		158.23	454.2724	1360.795	0.0079	5.8	9.79	46221.1	5.41	HUMAN	Q13515	Phakinin
24629	dirMS_041712_NAR_60mM_plus.8760.8760.3	3	3.77	1	1.65E+05	M23m K26	(K)LKKTEm	(K)L K|K/T E m Q E\k(N)	m:Oxidized methionine k:Ub	104.38	422.2223	1134.619	130.0336	-3.3	8.5	5112.7	5.02	HUMAN	Q5T4B6	HCG1780554

24630	dirMS_041712_NAR_120mM_minus.15214.15214.4	4	3.76	2	1.02E+05		(R)ALKDEEI	(R)A L K\D E/E K M E\L Q E/I Q/L/K(E)		136.97	487.0126	1945.031	-0.0025	-1.3	4.58	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
24631	dirMS_041712_NAR_120mM_minus.6530.6530.2	2	3.76	1	2.24E+05		(R)KLLEGEE	(R)K\L/L/E/G E E S/R(I)		89.75	530.7845	1060.563	-0.0016	-1.5	4.79	49709.6	5.19	HUMAN	B0YJC4	Vimentin
24632	dirMS_041712_NAR_30mM_minus2.11176.11176.2	2	3.76	0	3.89E+05		(R)NTDEM	(R)N/T|D E\M/V/E/L/R(I)		115.05	553.7611	1106.515	0.0003	0.2	4.14	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
24633	dirMS_041712_NAR_50mM_minus2.10195.10195.3	3	3.76	2	1.37E+05		(R)HPGVPS	(R)H P G V P/S/V E K/S R E L R(L)		126.83	530.9592	1590.871	-0.008	-5	8.75	100418.1	9.65	HUMAN	Q9Y283-2	Isoform 2 of Inversin
24634	dirMS_041712_NAR_50mM_minus2.15189.15189.3	3	3.76	1	1.33E+05		(K)VSEQGL	(K)V/S E Q\G\L I E I/L K K(V)		154.37	452.9385	1356.81	-0.0087	-6.4	6.11	12899.6	6.59	HUMAN	K7EL31	Programmed cell death protein 5
24635	dirMS_041712_NAR_50mM_minus2.7148.7148.3	3	3.76	0	6.97E+04	T1246t M1	(R)SPQtLAF	(R)S P|Q/t/L A P V/G E D A m K(T)	t:N-acetylglucosamine (T) m:	107.35	554.9379	1443.715	219.0843	6	4.37	142001.7	5.82	HUMAN	Q92797	Symplekin
24636	dirMS_041712_NAR_50mM_minus2.9708.9708.3	3	3.76	0	1.89E+05	M329m	(K)SNmGHI	(K)S N m\G\H P E P A/S G L/A A/L A K(V)	m:Oxidized methionine	122.73	556.279	1650.827	15.9956	0.4	6.47	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
24637	dirMS_041712_NAR_60mM_minus.10053.10053.3	3	3.76	1	3.39E+05		(K)GQYDVA	(K)G Q/Y D V A V/K M I K(E)		115.77	417.9007	1251.677	0.011	8.8	8.5	78750.9	9.01	HUMAN	P51813	Cytoplasmic tyrosine-protein kinase BMX
24638	dirMS_041712_NAR_60mM_minus.10514.10514.3	3	3.76	1	1.64E+06		(K)TLQEVT	(K)T L/Q E/V/T E M D S V K/R(Y)		119.37	512.5957	1535.773	-0.0008	-0.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
24639	dirMS_041712_NAR_60mM_minus.7407.7407.3	3	3.76	0	1.48E+05		(K)TIEAEAA	(K)T\I/E A/E/A A/H G/T V T R(H)		100.25	452.5678	1355.691	-0.0025	-1.9	5.37	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
24640	dirMS_041712_NAR_60mM_minus.7571.7571.3	3	3.76	0	1.62E+05	S9s	(-)MGTCW	(-)M G|T/C W G D I\s E N V R(V)	C:Carbamidomethylation s:N-ace	102.03	576.5915	1524.657	203.103	13.7	4.37	47571.8	6.71	HUMAN	Q05BQ5-3	Isoform 3 of MBT domain-containing protein 1
24641	dirMS_041712_NAR_120mM_plus.10784.10784.2	2	3.76	1	3.17E+05		(R)EKLEME	(R)E/K/L/E/M E/M E A A R(H)		109.58	668.8148	1336.623	-0.0012	-0.9	4.49	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)
24642	dirMS_041712_NAR_120mM_plus.11832.11832.4	4	3.76	2	3.85E+05	T30t	(R)tFLVGER	(R)t F L V/G E R V T/L A A E/P K A K(D)	t:Phosphorylated T	114.12	478.2542	1830.048	79.9466	-10.3	8.26	24239	7.03	HUMAN	E7EMT2	Uncharacterized protein
24643	dirMS_041712_NAR_120mM_plus.4387.4387.3	3	3.76	0	6.50E+05	M76m M7	(R)LTNSmM	(R)L/T/N S m M m/H/G R(N)	m:Oxidized methionine	71.3	403.8446	1177.527	31.9918	1.6	9.75	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
24644	dirMS_041712_NAR_120mM_plus.5683.5683.3	3	3.76	1	3.17E+04		(R)DGYGGS	(R)D G Y/G G S R D\S Y S S S R(S)		82.67	498.5477	1493.625	0.0034	2.3	5.96	28019.3	10.03	HUMAN	B3KRG5	RNA-binding motif protein, X chromosome, N-terminally processed
24645	dirMS_041712_NAR_120mM_plus.6064.6064.3	3	3.76	0	1.40E+05	S188s S19	(K)LsCsDVH	(K)L s/C s D V H/F\N V/K(M)	C:Carbamidomethylation s:Phos	85.22	489.1935	1305.626	159.9403	5.2	6.74	35022.9	9.43	HUMAN	Q9Y585	Olfactory receptor 1A2
24646	dirMS_041712_NAR_120mM_plus.7338.7338.3	3	3.76	1	4.31E+05		(R)SSFREED	(R)S/S/F R E E/D/N\T Y|R(C)		91.53	468.5449	1403.619	0.0015	1.1	4.68	95051	6.63	HUMAN	B3KXW5	AP-1 complex subunit gamma-1
24647	dirMS_041712_NAR_20mM_plus.10700.10700.2	2	3.76	0	8.63E+04		(R)FLEQQN	(R)F L\E/Q Q/N Q V\L Q|T K(W)		146.73	738.3942	1475.785	-0.0041	-2.8	6	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
24648	dirMS_041712_NAR_20mM_plus.11123.11123.2	2	3.76	0	9.54E+04	M188m	(K)VVEILAD	(K)V V|E/I/L/A D m T A/R(D)	m:Oxidized methionine	148.77	617.3237	1217.656	15.9843	-8.6	4.37	68200.1	8.69	HUMAN	Q13322	Growth factor receptor-bound protein 10
24649	dirMS_041712_NAR_20mM_plus.15215.15215.3	3	3.76	0	1.08E+05		(K)DVLSVA	(K)D V L/S V A F/S S D/N R(Q)		176.4	437.2168	1309.638	-0.0024	-1.9	4.21	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
24650	dirMS_041712_NAR_30mM_plus2.13026.13026.2	2	3.76	0	9.44E+05		(K)FSVSPV	(K)F/S/V/S/P/V V R(V)		122.38	445.759	890.509	0.0013	1.5	9.75	96306.4	6.41	HUMAN	P13639	Elongation factor 2
24651	dirMS_041712_NAR_30mM_plus2.15443.15443.2	2	3.76	0	2.52E+05	T890t	(K)LLVQtGS	(K)L L|V Q t G\S R(D)	t:Phosphorylated T	133.05	477.2409	873.515	79.9593	-7.4	9.75	162082.3	6.42	HUMAN	Q13635	Protein patched homolog 1
24652	dirMS_041712_NAR_30mM_plus2.17689.17689.2	2	3.76	1	9.72E+05	M188m	(R)mAVERE	(R)m/A|V/E R E L E K(V)	m:Oxidized methionine	146.38	560.7925	1104.572	16.006	9.9	4.78	56155.2	8.78	HUMAN	B4DWR9	Peptidylprolyl isomerase domain and WD repeat-containing protein 1
24653	dirMS_041712_NAR_30mM_plus2.19343.19343.2	2	3.76	0	4.62E+05		(R)LDFNLIR	(R)L/D|F/N|L I R(V)		155.87	445.759	890.509	0.0013	1.5	5.84	18956.4	6.97	HUMAN	C9JLK0	Phosphoribosylaminoimidazolecarboxamide formyltransferase (Fragment)
24654	dirMS_041712_NAR_30mM_plus2.9757.9757.2	2	3.76	0	6.72E+05		(R)GGGQII	(R)G G G\Q/I|I/P T A R(R)		104.35	485.2772	969.548	-0.0005	-0.5	9.75	15036.9	7.16	HUMAN	K7EJ74	116 kDa U5 small nuclear ribonucleoprotein component (Fragment)
24655	dirMS_041712_NAR_40mM_plus2.17853.17853.3	3	3.76	0	1.58E+05		(R)LPVPPL	(R)L P V|P/P L Q Q S L D H Y L K(A)		171.4	583.3378	1747.974	0.0247	14.1	6.74	18575.3	9.69	HUMAN	A6PVN3	Carnitine O-acetyltransferase
24656	dirMS_041712_NAR_40mM_plus2.18677.18677.3	3	3.76	1	9.82E+03		(K)IYVAAN	(K)I Y V A/A N S G A R I G M/A E E I K(H)		175.73	631.6626	1892.99	-0.0166	-8.8	6.14	97883.4	6.02	HUMAN	F6QQI9	Acetyl-CoA carboxylase 2
24657	dirMS_041712_NAR_50mM_plus2.7066.7066.3	3	3.76	0	1.15E+04	Y19y M21	(R)DLVEGP	(R)D L/V E G P Q y L m/P P K(K)	y:Phosphorylated Y m:Oxidiz	102.95	528.2459	1486.761	95.9621	0.6	4.37	47165.4	8.29	HUMAN	J3KQ32	Obg-like ATPase 1
24658	dirMS_041712_NAR_60mM_plus.16265.16265.3	3	3.76	0	1.40E+05		(R)EHALLA	(R)E H A L L/A/Y T L G V K(Q)		141.87	438.9179	1314.742	-0.0025	-1.9	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
24659	dirMS_041712_NAR_60mM_plus.20792.20792.3	3	3.76	1	3.33E+05		(R)KVESLW	(R)K V E S L\W|P I F R(I)		169.8	425.5789	1274.726	-0.0034	-2.7	8.75	14138.1	9.89	HUMAN	C9JNV2	Protein BUD31 homolog
24660	dirMS_041712_NAR_120mM_minus.8281.8281.3	3	3.75	0	2.35E+04	T294t	(R)EIEEVLt	(R)E I|E\E V L t/P E M L M R(W)	t:N-acetylglucosamine (T)	99.42	598.2869	1589.791	203.0548	-13.7	4.09	48712.2	7.36	HUMAN	P29622	Kallistatin
24661	dirMS_041712_NAR_30mM_minus2.13919.13919.2	2	3.75	0	2.31E+05		(R)IYFLEER	(R)I Y|F/L\E E/R(M)		129.37	485.2556	969.504	-0.0001	-0.1	4.53	277018.3	5.35	HUMAN	E9PJ64	Myomegalin
24662	dirMS_041712_NAR_30mM_minus2.17576.17576.2	2	3.75	0	1.23E+05		(R)TTEMAL	(R)T/T|E M A L/E S L K(Q)		150.5	561.7944	1122.571	0.0104	9.3	4.53	198019.2	5.45	HUMAN	E7ER66	Centrosomal protein of 152 kDa
24663	dirMS_041712_NAR_30mM_minus2.4310.4310.2	2	3.75	0	3.76E+03	M33m	(R)TAYGPN	(R)T A/Y/G P/N G\m N K(M)	m:Oxidized methionine	72.02	534.7431	1052.483	15.996	1	8.26	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
24664	dirMS_041712_NAR_30mM_minus2.6506.6506.2	2	3.75	0	1.63E+05		(R)QGEAEF	(R)Q G\E|A/E/F N/R(I)		89.93	475.7203	950.433	0.0007	0.7	4.53	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
24665	dirMS_041712_NAR_40mM_minus2.14715.14715.3	3	3.75	0	1.13E+06		(K)ISSIQSIV	(K)I S\S I/Q/S I/V/P A L E I A/N A H R(K)		172.05	640.3618	1919.071	0	0	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
24666	dirMS_041712_NAR_50mM_minus2.11402.11402.3	3	3.75	0	6.00E+04		(R)GPVPAK	(R)G P\V|P A\K P/T V L F E K(M)		133.48	461.6052	1382.804	-0.0032	-2.3	8.59	110755.6	7.92	HUMAN	B4DH53	MAP1S light chain
24667	dirMS_041712_NAR_60mM_minus.14741.14741.3	3	3.75	1	4.11E+05		(R)IKIGDPL	(R)I K I G D|P\L\L\E/D/T R(M)		142.35	457.2595	1369.769	-0.0046	-3.4	4.56	47309.6	5.42	HUMAN	B4DXY7	4-trimethylaminobutyraldehyde dehydrogenase
24668	dirMS_041712_NAR_60mM_minus.15626.15626.3	3	3.75	1	1.88E+05		(R)ISYLYNV	(R)I S Y L Y N|V/L/L S R R(T)		146.65	499.6192	1496.858	-0.0153	-10.2	9.99	87540.7	9.25	HUMAN	Q5T1A1	DC-STAMP domain-containing protein 2
24669	dirMS_041712_NAR_60mM_minus.17147.17147.3	3	3.75	1	4.89E+04		(R)STVRDI	(R)S T V R D I\D|P\Q/N D|L T F L/R(I)		155.6	630.6628	1889.972	0.0023	1.2	4.43	16537.8	6.59	HUMAN	B1AKR6	Dynein light chain roadblock-type 1
24670	dirMS_041712_NAR_60mM_minus.6596.6643.3	3	3.75	0	1.29E+05		(K)LAELYGE	(K)L A E/L/Y\G E I E S E R(T)		95.48	470.2283	1408.696	-0.0251	-17.8	4.09	88641.6	4.98	HUMAN	Q13634	Cadherin-18
24671	dirMS_041712_NAR_120mM_plus.10904.10904.3	3	3.75	0	3.88E+05	S143s	(K)GGVVVD	(K)G/G V V V D E/L G C s R(Q)	C:Carbamidomethylation s:N-ace	110.13	484.2258	1247.605	203.058	-14.7	4.37	38445	8.74	HUMAN	Q92858	Protein atonal homolog 1
24672	dirMS_041712_NAR_120mM_plus.11202.11202.3	3	3.75	1	9.59E+05		(K)TSKLNV	(K)T|S K/L N V V E T S/R(L)		112.13	411.8988	1233.68	0.0021	1.7	8.41	111104.3	8.79	HUMAN	Q8NAT2	Tudor domain-containing protein 5
24673	dirMS_041712_NAR_120mM_plus.3563.3563.3	3	3.75	1	3.84E+06	M76m T78	(R)mEtRDP	(R)m E t/R D/P/E/R(K)	m:Oxidized methionine t:N-a	59.57	418.1852	1033.473	219.0679	-5.1	4.68	12703.1	11.31	HUMAN	H0YEY5	Plakophilin-3 (Fragment)
24674	dirMS_041712_NAR_120mM_plus.8108.8108.2	2	3.75	0	4.29E+05		(K)AGEVFI	(K)A/G E|V/F I/H K(D)		96.3	450.7531	900.494	0.0051	5.7	6.79	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
24675	dirMS_041712_NAR_20mM_plus.10342.10342.2	2	3.75	0	1.88E+05	M592m M5	(R)mGPAm	(R)m G P A m G P A L/G/A G I E R(M)	m:Oxidized methionine	144.65	730.3568	1427.713	31.993	2.1	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
24676	dirMS_041712_NAR_20mM_plus.10654.10654.2	2	3.75	0	4.16E+04		(K)LLSNDE	(K)L L|S\N D/E V T I/K(Y)		146.08	566.3156	1131.626	-0.0017	-1.5	4.37	20421.7	4.86	HUMAN	C9JJP5	Protein TFG (Fragment)
24677	dirMS_041712_NAR_20mM_plus.12014.12014.2	2	3.75	0	5.20E+04		(K)VVLVLA	(K)V V/L V/L A/G R(Y)		156.4	413.778	826.551	-0.0022	-2.6	9.72	4480.4	11.2	HUMAN	K7ERY7	60S ribosomal protein L27
24678	dirMS_041712_NAR_20mM_plus.14369.14369.2	2	3.75	0	1.13E+05		(R)FIDTTLA	(R)F I/D\T T/L A\I\T S R(F)		171.23	619.3413	1237.679	-0.0034	-2.7	5.84	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
24679	dirMS_041712_NAR_20mM_plus.15997.15997.2	2	3.75	0	1.15E+05		(R)GTPLISP	(R)G T|P L/I/S P L/I K(W)		181.3	519.8306	1038.656	-0.0018	-1.8	8.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
24680	dirMS_041712_NAR_20mM_plus.18488.18488.3	3	3.75	0	1.05E+04		(R)AAVEEG	(R)A A V E E G I V/L/G/G G C A L L R(C)	C:Carbamidomethylation	198.63	562.3058	1684.905	-0.0022	-1.3	4.53	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
24681	dirMS_041712_NAR_20mM_plus.6434.6434.3	3	3.75	0	8.39E+04	M38m	(R)SPPPGm	(R)S P/P P G m/G L/N Q N R(G)	m:Oxidized methionine	107.48	428.5446	1267.621	15.9981	2.5	9.47	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
24682	dirMS_041712_NAR_20mM_plus.8254.8254.2	2	3.75	0	3.33E+05	M176m	(K)VLEGmE	(K)V/L|E|G m E V/V R(K)	m:Oxidized methionine	126.95	524.278	1031.555	15.9933	-1.5	4.53	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
24683	dirMS_041712_NAR_30mM_plus2.15887.15887.2	2	3.75	0	4.22E+05		(R)MGPNIY	(R)M G\P/N I/Y E/L/R(T)		136.4	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
24684	dirMS_041712_NAR_30mM_plus2.7485.7485.2	2	3.75	0	7.39E+05		(K)MQLDNI	(K)M/Q|L D N/P S K(V)		93.82	466.7319	932.451	0.0059	6.4	5.59	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
24685	dirMS_041712_NAR_40mM_plus2.17630.17630.3	3	3.75	0	5.36E+04		(K)ASVITQ	(K)A S|V/I/T Q V F/H V P L E E R(K)		170.05	575.6528	1724.933	0.0109	6.3	5.4	24511.6	6.62	HUMAN	C9J5E5	Vigilin (Fragment)
24686	dirMS_041712_NAR_120mM_minus.10538.10538.3	3	3.74	1	3.05E+05		(K)ISNPVY	(K)I/S N/P V Y R M Q H K(I)		111.85	458.2485	1372.715	0.0155	11.3	9.99	139305.8	8.55	HUMAN	Q13201	Multimerin-1
24687	dirMS_041712_NAR_120mM_minus.11247.11247.3	3	3.74	0	1.74E+05		(R)GFCLPP	(R)G F C/L/P P H C S R(G)	C:Carbamidomethylation	114.25	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
24688	dirMS_041712_NAR_120mM_minus.20324.20324.3	3	3.74	0	1.02E+05	M195m	(R)LHFFmP	(R)L H F F m|P G|F A/P L T\S R(G)	m:Oxidized methionine	166.12	546.2809	1620.835	15.9926	-1.4	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
24689	dirMS_041712_NAR_120mM_minus.8081.8081.3	3	3.74	1	1.45E+05	T156t S161	(R)LEDtIRQ	(R)L E/D t I/R Q T s\L/R(E)	t:Phosphorylated T s:Phosph	97.53	497.8941	1331.728	159.94	4.9	6.07	39907.3	6.36	HUMAN	E7ET36	Transferrin receptor protein 2
24690	dirMS_041712_NAR_20mM_minus.12115.12115.2	2	3.74	0	1.57E+05	M73m	(R)AVLVDLI	(R)A V L\V D L/E|P G T m D S V R(S)	m:Oxidized methionine	171.02	809.4088	1601.82	15.99	-3	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
24691	dirMS_041712_NAR_30mM_minus2.12255.12255.2	2	3.74	0	4.11E+04		(K)QALSGF	(K)Q A|L/S/G F G Y R(L)		119.07	499.7499	998.505	-0.0129	-12.9	8.75	21925.1	5.16	HUMAN	O75340	Programmed cell death protein 6
24692	dirMS_041712_NAR_40mM_minus2.9421.9421.3	3	3.74	1	4.72E+04		(K)AGTEEA	(K)A G\T/E/E/A I/V Y S D I D L K K(L)		138.08	584.64	1751.906	-0.0007	-0.4	4.32	31006.8	6.85	HUMAN	Q9NQR4	Omega-amidase NIT2
24693	dirMS_041712_NAR_50mM_minus2.11543.11543.3	3	3.74	1	9.69E+04	N97n	(K)LYALDV	(K)L Y A/L D/V/R V n S L(-)	n:N-acetylglucosamine (N)	134.38	489.2711	1262.71	203.0884	6.2	5.83	11201.5	4.95	HUMAN	E9PQF9	Pre-mRNA cleavage complex 2 protein Pcf11 (Fragment)
24694	dirMS_041712_NAR_50mM_minus2.17578.17578.3	3	3.74	1	2.59E+04		(K)VYFPEQ	(K)V/Y/F P E Q I H D/V V R A T K(Y)		169.05	601.3217	1801.959	-0.009	-5	6.72	50279.8	6.77	HUMAN	F5H7K4	Neutral cholesterol ester hydrolase 1
24695	dirMS_041712_NAR_50mM_minus2.6882.6882.3	3	3.74	0	2.02E+04		(K)TNPPLI	(K)T N|P/P L I Q E K P A K(T)		105.67	445.926	1335.763	0.0004	0.3	8.26	102841.5	6.73	HUMAN	D3DQV9	Eukaryotic translation initiation factor 4 gamma 2 (Fragment)
24696	dirMS_041712_NAR_50mM_minus2.9951.9951.3	3	3.74	1	1.23E+05		(K)NQLTSN	(K)N\Q/L/T S N/P E N/T V F D A K R(L)		124.82	611.9745	1833.909	0	0	6.07	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
24697	dirMS_041712_NAR_60mM_minus.12714.12714.3	3	3.74	1	1.44E+05		(K)GLLGEFL	(K)G L/L G E F L R/T H K(Y)		131.23	424.2501	1270.727	0.0091	7.2	8.76	10110.6	9.6	HUMAN	A2A3L9	Gastricsin (Fragment)
24698	dirMS_041712_NAR_60mM_minus.17076.17076.3	3	3.74	2	2.04E+04		(K)HKESDL	(K)H/K E S/D L/R D V K(K)		155.58	409.5576	1226.649	0.0095	7.7	6.76	25568.2	6.34	HUMAN	G3V375	MAP3K12-binding inhibitory protein 1 (Fragment)
24699	dirMS_041712_NAR_60mM_minus.8778.8778.3	3	3.74	1	1.45E+05		(R)SRAEAE	(R)S R A E\A\E/S|M Y Q/I K(Y)		108.83	471.5706	1412.684	0.0134	9.5	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
24700	dirMS_041712_NAR_60mM_minus.8888.8888.3	3	3.74	1	2.77E+05	M298m	(R)VAmTAE	(R)V A m T\A E A\C S/R Q\H R(L)	C:Carbamidomethylation m:Oxid	110.18	511.5711	1516.711	15.988	-4.5	9.57	57627.1	8.44	HUMAN	Q12933	TNF receptor-associated factor 2
24701	dirMS_041712_NAR_120mM_plus.10208.10208.2	2	3.74	0	5.91E+05		(R)VHIEIGP	(R)V/H|I E\I G P D/G R(V)		105.8	546.7931	1092.58	-0.0007	-0.6	5.32	47371.6	5.93	HUMAN	E9PCY7	Heterogeneous nuclear ribonucleoprotein H
24702	dirMS_041712_NAR_120mM_plus.11084.11084.3	3	3.74	1	7.04E+05		(K)VIADNV	(K)V/I/A D N\V K D W S K(V)		110.95	425.5621	1274.674	-0.0022	-1.7	5.93	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
24703	dirMS_041712_NAR_120mM_plus.12151.12151.3	3	3.74	0	1.65E+04		(R)QIEQLL	(R)Q I E\Q/L L D P/S R(G)		117.08	400.2199	1198.643	0.0025	2.1	4.37	27441.6	9.49	HUMAN	C9JE72	IQ domain-containing protein E (Fragment)
24704	dirMS_041712_NAR_120mM_plus.16130.16130.4	4	3.74	1	1.12E+06		(R)ALEHFT	(R)A L E/H/F T D L Y D/I/K R(A)		138.4	405.9647	1620.838	-0.0011	-0.7	5.38	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
24705	dirMS_041712_NAR_120mM_plus.7055.7055.3	3	3.74	1	5.15E+05		(R)NTEEEG	(R)N T/E E E/G L K Y/K(S)		90.52	404.2038	1210.595	0.0018	1.5	4.79	83344.9	10.18	HUMAN	E9PK09	Bcl-2-associated transcription factor 1 (Fragment)
24706	dirMS_041712_NAR_120mM_plus.7794.7794.3	3	3.74	0	4.72E+05		(R)SGSMDF	(R)S G S|M/D/P S G A H P S V R(Q)		94.15	462.218	1384.627	0.0121	8.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
24707	dirMS_041712_NAR_20mM_plus.15178.15178.2	2	3.74	0	2.17E+05		(K)GLAITFV	(K)G L A I T F/V|S D E/N D A/K(I)		175.3	740.3693	1479.733	-0.0012	-0.8	4.03	40918.8	9.33	HUMAN	B4DP52	HCG2005638, isoform CRA_c
24708	dirMS_041712_NAR_20mM_plus.15904.15904.2	2	3.74	0	3.83E+05	M81m	(K)SFYPEEV	(K)S F/Y/P E/E V/S S m V L T/K(M)	m:Oxidized methionine	180.6	816.8988	1616.788	16.0027	4.8	4.53	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
24709	dirMS_041712_NAR_20mM_plus.9569.9569.2	2	3.74	0	4.68E+05		(R)ISVYYNE	(R)I/S/V Y/Y N E A/T G G K(Y)		138.13	651.3211	1301.637	-0.0023	-1.8	6	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
24710	dirMS_041712_NAR_30mM_plus2.4425.4425.2	2	3.74	0	1.88E+05		(R)MGQTM	(R)M G/Q/T/M E\R(I)		72.68	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
24711	dirMS_041712_NAR_30mM_plus2.6119.6119.2	2	3.74	1	1.06E+06		(K)SRDDVP	(K)S R|D D/V|P K(L)		86.58	408.7194	816.421	0.0105	12.9	5.68	34430.2	7.86	HUMAN	E9PFG0	Alcohol dehydrogenase class 4 mu/sigma chain
24712	dirMS_041712_NAR_40mM_plus2.12409.12409.3	3	3.74	0	3.63E+04		(R)VLTEDE	(R)V L|T/E\D E M G H/P E I G D A I A R(L)		138.75	651.6493	1952.938	-0.0049	-2.5	4.17	40874	5.06	HUMAN	E9PCI9	Farnesyl pyrophosphate synthase
24713	dirMS_041712_NAR_40mM_plus2.19421.19421.3	3	3.74	1	1.47E+05		(R)TEGLSVL	(R)T E|G L/S V L S Q A/M/A V I K E K(I)		181.78	602.0005	1803.988	-0.0015	-0.8	5.81	31604.9	6.88	HUMAN	G3V4T5	Eukaryotic translation initiation factor 2 subunit 1 (Fragment)
24714	dirMS_041712_NAR_40mM_plus2.19490.19490.3	3	3.74	1	1.50E+05	T1832t	(K)TEAGVQ	(K)T E|A G V Q/K Q W t A/L I/R(S)	t:N-acetylglucosamine (T)	181.87	602.0005	1600.881	203.1064	15	8.41	226980	6.78	HUMAN	Q9P2D3	HEAT repeat-containing protein 5B
24715	dirMS_041712_NAR_40mM_plus2.5650.5650.2	2	3.74	0	1.12E+05		(R)FSSSSGY	(R)F/S/S S/S G Y|G G G S S R(V)		90.98	618.2686	1235.529	0.0012	1	8.75	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
24716	dirMS_041712_NAR_40mM_plus2.7041.7041.2	2	3.74	0	8.74E+03	M1m S4s	(-)mVFsR(R	(-)m/V/F s R(R)	m:Oxidized methionine s:N-a	101.73	429.7019	639.328	219.0682	-7.1	9.5	103463.7	5.03	HUMAN	Q9Y5I3	Protocadherin alpha-1
24717	dirMS_041712_NAR_40mM_plus2.9705.9705.2	2	3.74	0	5.26E+04		(R)NGYGFII	(R)N G/Y/G F/I N R(N)		120.1	470.7291	940.463	-0.0126	-13.4	8.75	23597.5	10.26	HUMAN	C9J5V9	Nuclease-sensitive element-binding protein 1 (Fragment)
24718	dirMS_041712_NAR_50mM_plus2.7768.7768.3	3	3.74	1	2.73E+04		(K)AMKEA	(K)A M|K E A V S A/A S E D D\I F R(R)		108.18	580.6104	1739.827	-0.0102	-5.9	4.32	249906.7	6.48	HUMAN	E9PDI6	Voltage-dependent L-type calcium channel subunit alpha-1C
24719	dirMS_041712_NAR_60mM_plus.15518.15518.2	2	3.74	1	4.90E+05		(K)VKEGM	(K)V/K/E|G M\N I\V/E A M\E R(F)		137.75	753.3758	1505.745	-0.0007	-0.5	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
24720	dirMS_041712_NAR_60mM_plus.19810.19810.3	3	3.74	1	1.46E+05		(R)SELELTL	(R)S E|L|E L T L/G K L E Q V/R(S)		163.83	538.9738	1614.906	0.0007	0.5	4.78	533778	5.74	HUMAN	Q15149	Plectin
24721	dirMS_041712_NAR_60mM_plus.20237.20237.3	3	3.74	1	3.71E+04		(R)NFSWRS	(R)N F S W R/S\I/L T E H/K(R)		164.65	506.6046	1517.786	0.0133	8.8	8.76	27306	9.89	HUMAN	B1APK8	Zinc finger protein 678 (Fragment)
24722	dirMS_041712_NAR_60mM_plus.4737.4737.3	3	3.74	1	3.12E+05		(K)AGADEE	(K)A/G|A D/E E/R A E T A R(L)		79.38	425.868	1275.592	-0.0029	-2.3	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
24723	dirMS_041712_NAR_60mM_plus.5194.5194.3	3	3.74	1	3.33E+05		(R)DSQAG	(R)D S/Q A G D S/A S R/A G/G R(V)		85.17	445.5416	1334.604	0.0059	4.4	5.96	16963.8	9.76	HUMAN	H0Y724	Cytohesin-4 (Fragment)
24724	dirMS_041712_NAR_60mM_plus.5223.5223.3	3	3.74	1	9.39E+03	K497k M50	(R)kTEAIRm	(R)k T E/A I R/m E R(E)	k:Ubiquitin-K m:Oxidized me	84.68	421.8837	1133.61	130.027	-8.6	8.75	205899	5.42	HUMAN	O60333	Kinesin-like protein KIF1B
24725	dirMS_041712_NAR_20mM_minus.9665.9665.2	2	3.73	1	2.79E+05		(R)IKVEPAS	(R)I K/V/E P A S/E K(D)		146.27	500.7862	1000.567	-0.0022	-2.2	6.14	57285.5	8.99	HUMAN	P41162	ETS translocation variant 3
24726	dirMS_041712_NAR_40mM_minus2.7847.7847.3	3	3.73	1	1.59E+05	M119m	(K)KEALLA	(K)K E A/L L A G/m V D S V/P/K(G)	m:Oxidized methionine	125.2	491.9311	1457.803	15.9755	-13.2	6.07	127738.5	8.67	HUMAN	P48552	Nuclear receptor-interacting protein 1
24727	dirMS_041712_NAR_50mM_minus2.10352.10352.3	3	3.73	0	7.23E+04		(R)LTSPIVS	(R)L T|S/P I V/S T H L D T R(N)		127.37	480.6	1439.785	0.0002	0.1	6.74	58760.2	5.26	HUMAN	Q6ZTN6	Ankyrin repeat domain-containing protein 13D
24728	dirMS_041712_NAR_50mM_minus2.11389.11389.3	3	3.73	1	1.29E+05		(K)NQVALN	(K)N Q|V/A L/N/P Q N\T V F D A K R(L)		132.68	605.6545	1814.951	-0.0018	-1	8.75	70336.2	5.48	HUMAN	P08107	Heat shock 70 kDa protein 1A/1B
24729	dirMS_041712_NAR_50mM_minus2.15592.15592.3	3	3.73	0	1.59E+05		(K)ICDQW	(K)I/C/D/Q W/D A L/G/S L T H S R(R)	C:Carbamidomethylation	156.43	586.9489	1758.823	0.0094	5.3	5.21	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
24730	dirMS_041712_NAR_50mM_minus2.16133.16133.3	3	3.73	2	1.48E+05		(K)VVYTVK	(K)V/V/Y/T V K\Q S A E D\V K K(T)		160.42	531.9638	1593.885	-0.0078	-4.9	8.4	207834.9	4.84	HUMAN	G3XAI2	Laminin subunit beta-1
24731	dirMS_041712_NAR_50mM_minus2.17071.17071.3	3	3.73	0	6.09E+03	M370m	(K)TAVVPA	(K)T A V|V P A S H m S S/L N/V V\K(M)	m:Oxidized methionine	165.92	552.6273	1639.884	15.9837	-6.7	8.44	138869.6	7.84	HUMAN	C9JU50	DNA-binding protein RFX7
24732	dirMS_041712_NAR_50mM_minus2.18331.18331.3	3	3.73	1	8.07E+05		(R)KAIIIFVP	(R)K A I I I F\V/P V P Q L K(S)		173.98	489.3206	1465.95	-0.0032	-2.2	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
24733	dirMS_041712_NAR_60mM_minus.10752.10752.3	3	3.73	0	1.41E+04		(R)ESVDHL	(R)E\S V/D H L/T I/P S|R(C)		119.45	418.5551	1253.648	0.0023	1.8	5.32	132902.3	5.82	HUMAN	J3KR24	Isoleucine--tRNA ligase, cytoplasmic
24734	dirMS_041712_NAR_60mM_minus.12770.12770.3	3	3.73	1	2.28E+05	K56k	(R)IkQSELS	(R)I k Q S E L S/A K/M R(E)	k:Ubiquitin-K	130.92	468.9273	1290.72	114.0475	3.3	9.99	9222.5	5.33	HUMAN	K7EJI9	Truncated apolipoprotein C-I
24735	dirMS_041712_NAR_60mM_minus.15165.15165.3	3	3.73	1	5.19E+05	S24s	(K)VYQKTT	(K)V Y Q K T T|F/S s R(M)	s:N-acetylglucosamine (S)	144.68	473.9047	1216.632	203.0675	-8.4	9.99	7160.2	10.34	HUMAN	F8VY05	Coiled-coil domain-containing protein 38 (Fragment)
24736	dirMS_041712_NAR_120mM_plus.5983.5983.2	2	3.73	1	2.29E+06		(K)IREEYPD	(K)I R/E/E Y|P D|R(I)		84.93	539.2694	1077.532	-0.0008	-0.8	4.68	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
24737	dirMS_041712_NAR_120mM_plus.6196.6196.3	3	3.73	1	2.28E+05	S108s	(K)EAsDKT	(K)E A/s D K T T/A P G P(-)	s:N-acetylglucosamine (S)	85.37	426.2066	1073.511	203.0943	11.7	4.37	11143.9	4.65	HUMAN	H0YH61	Mucin-19 (Fragment)
24738	dirMS_041712_NAR_120mM_plus.8946.8946.2	2	3.73	0	2.03E+05		(R)FACHSA	(R)F/A C/H/S A/S/L T\V\R(N)	C:Carbamidomethylation	100.43	624.8103	1248.615	-0.002	-1.6	9.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)

24739	dirMS_041712_NAR_20mM_plus.10674.10674.2	2	3.73	0	4.28E+04	M414m	(K)mDATAN	(K)m D A\T\A N/D\V/P S P Y E V R(G)	m:Oxidized methionine	146.12	840.8792	1664.758	15.9927	-1.3	4.03	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
24740	dirMS_041712_NAR_20mM_plus.12805.12805.3	3	3.73	0	4.15E+05		(K)VVETELQ	(K)V V E T\E L Q/E G/A T K(Q)		161.6	435.2319	1303.674	0.0072	5.5	4.26	332628.7	5	HUMAN	Q8NFC6	Biorientation of chromosomes in cell division protein 1-like 1
24741	dirMS_041712_NAR_20mM_plus.17132.17132.2	2	3.73	0	1.19E+05		(K)FATEAAI	(K)F A/T\E/A A/I/T I/L R(I)		188.97	603.3442	1205.689	-0.0077	-6.4	6	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
24742	dirMS_041712_NAR_20mM_plus.7870.7870.2	2	3.73	0	8.65E+04	M21m	(K)ATAVmP	(K)A T A V/m/P D G Q F K(D)	m:Oxidized methionine	124.45	590.7861	1164.572	15.9932	-1.5	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
24743	dirMS_041712_NAR_20mM_plus.8627.8627.2	2	3.73	1	2.94E+04		(R)IDAEEKQ	(R)I D A/E E K Q|E\L R(A)		130.13	615.823	1230.632	0.0063	5.1	4.41	60731.3	4.68	HUMAN	Q9H175	Cysteine/serine-rich nuclear protein 2
24744	dirMS_041712_NAR_30mM_plus2.10017.10017.2	2	3.73	0	2.90E+05		(R)VQESAD	(R)V/Q\E\S A\D E L/Q/K(M)		106.02	573.7938	1146.564	0.0166	14.5	4.14	17163.6	6.74	HUMAN	C9J1Z8	ADP-ribosylation factor 5 (Fragment)
24745	dirMS_041712_NAR_30mM_plus2.18911.18911.2	2	3.73	0	5.51E+05		(R)GLFIIDD	(R)G L/F|I/I D D K(G)		151.88	460.7596	920.509	0.0032	3.4	4.21	18498.6	5.82	HUMAN	H7C3T4	Peroxiredoxin-4 (Fragment)
24746	dirMS_041712_NAR_30mM_plus2.4875.4875.2	2	3.73	0	3.07E+05	M71m	(K)ETmQSL	(K)E T/m Q/S L/N/D R(L)	m:Oxidized methionine	77.37	555.2469	1093.494	15.9923	-2.4	4.37	48845.9	4.72	HUMAN	C4AM86	Keratin, type I cuticular Ha5
24747	dirMS_041712_NAR_30mM_plus2.6597.6597.2	2	3.73	0	2.14E+05		(K)ALDEME	(K)A/L/D/E M E/K(Q)		89.15	418.1994	835.387	0.0049	5.9	4.14	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
24748	dirMS_041712_NAR_40mM_plus2.15556.15556.3	3	3.73	0	9.34E+05		(R)DVQIGD	(R)D V Q/I/G D I V T V/G E C R P L S K(T)	C:Carbamidomethylation	157.35	662.6815	1986.033	-0.0025	-1.3	4.56	18601.6	10.52	HUMAN	P62280	40S ribosomal protein S11
24749	dirMS_041712_NAR_40mM_plus2.8974.8974.3	3	3.73	1	4.93E+04		(K)VPEPCQ	(K)V/P E P C/Q P K V P E P/C H P K(V)	C:Carbamidomethylation	115.07	633.6448	1898.925	-0.0053	-2.8	6.73	10343.8	9.76	HUMAN	P22528	Cornifin-B
24750	dirMS_041712_NAR_50mM_plus2.17307.17307.3	3	3.73	2	2.35E+05		(R)LKGDDLG	(R)L K G D D/L G Q/K V L F R(D)		158.85	496.9634	1488.853	0.0224	15	8.59	51648.4	5.55	HUMAN	B7XGB9	Protein phosphatase 1M
24751	dirMS_041712_NAR_50mM_plus2.20336.20336.3	3	3.73	1	3.99E+05	T378t	(R)SIYSQtEK	(R)S/I Y/S Q t E K L V/A G K(S)	t:N-acetylglucosamine (T)	176.32	542.9621	1423.779	203.0926	8.1	8.22	52187	9.34	HUMAN	P04279	Semenogelin-1
24752	dirMS_041712_NAR_50mM_plus2.6481.6481.3	3	3.73	1	1.31E+05	M365m	(R)IVEQDTm	(R)I/V|E Q D T m/P P K G V R(H)	m:Oxidized methionine	98.88	495.9283	1469.778	15.9923	-1.8	6.07	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
24753	dirMS_041712_NAR_50mM_plus2.8145.8145.3	3	3.73	0	1.12E+04		(K)ASSEGGT	(K)A S/S/E/G G T A A/G A G L D S L H K(N)		109.45	543.6023	1628.787	0.0049	3	5.32	41747.8	9.36	HUMAN	O15143	Actin-related protein 2/3 complex subunit 1B
24754	dirMS_041712_NAR_60mM_plus.18600.18600.3	3	3.73	1	3.72E+06		(K)VFSIISSE	(K)V F/S/I I S S E K E L/K(N)		155.8	460.5914	1379.778	-0.0184	-13.3	6.11	21205.4	6.66	HUMAN	E7EWK7	Nuclear valosin-containing protein-like (Fragment)
24755	dirMS_041712_NAR_60mM_plus.20251.20251.3	3	3.73	1	8.29E+03		(R)VYEFLDK	(R)V Y/E/F/L/D K L D\V V/R(S)		165.92	499.2786	1495.815	0.0057	3.8	4.56	41296.9	9.52	HUMAN	B4DT72	26S proteasome non-ATPase regulatory subunit 3
24756	dirMS_041712_NAR_120mM_minus.10597.10597.3	3	3.72	1	2.05E+04		(K)LEEKEW	(K)L E E/K E W/L F K(D)		111.65	407.8893	1221.651	0.0019	1.6	4.79	299790.8	6.71	HUMAN	Q6UB99	Ankyrin repeat domain-containing protein 11
24757	dirMS_041712_NAR_120mM_minus.15838.15838.4	4	3.72	1	1.10E+05		(K)QLEAIDQ	(K)Q L E A I/D Q/L H/L E Y A K/R(A)		140.1	457.499	1826.976	-0.0018	-1	5.45	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
24758	dirMS_041712_NAR_120mM_minus.4367.4367.2	2	3.72	0	3.95E+05		(K)HYAMQ	(K)H/Y|A M Q E\A K(Q)		72.92	489.2307	977.451	0.0032	3.3	6.75	39309.6	4.32	HUMAN	F8WCY5	Reticulocalbin-2
24759	dirMS_041712_NAR_120mM_minus.7749.7749.3	3	3.72	0	9.84E+04		(R)LTGASD	(R)L T G A S D K P G E V/S K(L)		96.62	430.2279	1288.674	-0.0052	-4	6.07	45227.6	6.28	HUMAN	O75936	Gamma-butyrobetaine dioxygenase
24760	dirMS_041712_NAR_20mM_minus.12252.12252.3	3	3.72	0	9.42E+04		(K)LVSIGAE	(K)L V S I G/A E E\I/V D/G N A K(M)		171.42	505.6069	1514.806	0.0001	0.1	4.14	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
24761	dirMS_041712_NAR_20mM_minus.8843.8843.2	2	3.72	1	1.42E+05		(K)IKEYCPQ	(K)I K/E\Y/C P/Q V F R(N)	C:Carbamidomethylation	137.93	670.3403	1339.683	-0.0094	-7	8.59	45223.7	6.03	HUMAN	Q8TBX8-3	Isoform 3 of Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma
24762	dirMS_041712_NAR_20mM_minus.9467.9467.2	2	3.72	1	1.36E+04	M903m	(K)DCmRRL	(K)D C m/R R/L\F Y N F D K(N)	C:Carbamidomethylation m:Oxid	144.63	840.8764	1664.767	15.9783	-9.9	8.59	139608.9	6.7	HUMAN	B4DF41	DNA mismatch repair protein Msh6
24763	dirMS_041712_NAR_40mM_minus2.15430.15430.3	3	3.72	1	3.01E+05		(R)GGPNIIT	(R)G G P\N I/I/T L A D/I V/K D P V S R(T)		178.45	622.3523	1865.049	-0.0067	-3.6	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
24764	dirMS_041712_NAR_40mM_minus2.9530.9530.3	3	3.72	0	1.67E+05	M84m	(K)YPIEHGI	(K)Y/P I E H G I I|T N/W/D D m E K(I)	m:Oxidized methionine	138.73	659.6395	1960.911	15.993	-1	4.31	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
24765	dirMS_041712_NAR_50mM_minus2.11544.11544.3	3	3.72	1	9.69E+04		(K)IEEGGYK	(K)I E E G G Y K|R L/C L K(E)	C:Carbamidomethylation	134.38	489.2711	1465.783	0.0156	10.6	8.5	50792.4	6.34	HUMAN	E7EM93	Peroxisomal NADH pyrophosphatase NUDT12
24766	dirMS_041712_NAR_50mM_minus2.11871.11871.3	3	3.72	1	1.60E+05	M264m	(K)TmTDVV	(K)T m T D V V G/N P E/E E R R(A)	m:Oxidized methionine	135.73	550.2563	1632.765	15.9897	-3.1	4.41	37190.7	6.16	HUMAN	F8VRQ4	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1
24767	dirMS_041712_NAR_50mM_minus2.13019.13019.3	3	3.72	2	1.55E+05	S523s	(K)AAEIASS	(K)A A E I A/S S D s A N V S S R G G K K(F)	s:Phosphorylated S	141.72	638.9739	1834.925	79.9818	8.1	8.63	124129.4	6.7	HUMAN	P42338	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit beta isoform
24768	dirMS_041712_NAR_50mM_minus2.14505.14505.3	3	3.72	0	6.18E+04		(K)VALLLLD	(K)V/A\L\L/L L/D Q G A S P H/A A A K(N)		150.53	558.9883	1674.954	-0.0034	-2	6.71	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
24769	dirMS_041712_NAR_60mM_minus.11012.11012.3	3	3.72	0	9.73E+03	N363n M3	(K)GHnDW	(K)G H n D W V/m D V A/I S N N K(K)	n:N-acetylglucosamine (N) m	121.62	640.2914	1699.786	219.074	-0.2	5.21	53875.2	7.03	HUMAN	Q6ZMY6	WD repeat-containing protein 88
24770	dirMS_041712_NAR_60mM_minus.7163.7163.3	3	3.72	0	1.73E+05		(R)VTGPNS	(R)V T\G|P N S\S S/G I Q A/R(K)		99.07	425.2172	1273.65	-0.0125	-9.8	9.72	91877.7	6.48	HUMAN	B4DLN2	FYN-binding protein
24771	dirMS_041712_NAR_60mM_minus.7911.7911.3	3	3.72	1	1.19E+05		(K)FEDKTVA	(K)F/E/D K T V/A Y T E/Q K(M)		104.37	486.908	1458.711	-0.0017	-1.1	4.68	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
24772	dirMS_041712_NAR_120mM_plus.10725.10725.3	3	3.72	0	8.92E+05		(K)RPLFGSP	(K)R P L/F G S/P S P/A E K(T)		108.87	429.2327	1285.69	-0.0064	-5	8.75	81396	9.01	HUMAN	A1L443	Protein FAM22F
24773	dirMS_041712_NAR_120mM_plus.11745.11745.3	3	3.72	1	1.48E+05		(K)RGVFNV	(K)R G V\F\N\V/Q M E/P K(V)		114.45	435.5647	1304.678	0.0016	1.2	8.75	36396.8	5.02	HUMAN	P05198	Eukaryotic translation initiation factor 2 subunit 1
24774	dirMS_041712_NAR_20mM_plus.15617.15617.2	2	3.72	0	6.27E+04		(K)VFLENVI	(K)V/F|L/E N V I R(D)		179.5	495.2908	989.578	-0.0035	-3.6	5.97	11367.1	11.36	HUMAN	P62805	Histone H4
24775	dirMS_041712_NAR_30mM_plus2.13557.13557.2	2	3.72	1	3.04E+05	K136k	(K)DVNTRE	(K)D V/N|T R E P k(L)	k:Ubiquitin-K	124.8	536.7755	958.495	114.0485	5.2	6.07	18317.8	6.19	HUMAN	B7Z3E2	Serine/threonine-protein phosphatase 6 catalytic subunit
24776	dirMS_041712_NAR_30mM_plus2.21622.21622.2	2	3.72	0	1.91E+05		(R)TTNFAG	(R)T T/N F|A G I L S Q G/L|R(I)		169.22	689.3749	1377.748	-0.006	-4.3	9.41	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
24777	dirMS_041712_NAR_40mM_plus2.6669.6669.2	2	3.72	0	5.19E+05		(R)FFSDCK(	(R)F/F/S/D/C K(I)	C:Carbamidomethylation	99.88	402.1734	803.339	0.0003	0.3	5.84	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
24778	dirMS_041712_NAR_40mM_plus2.6869.6869.2	2	3.72	0	5.56E+03		(R)LSVAAQ	(R)L S V/A/A Q E A A/R(L)		100.35	508.2775	1015.553	-0.0054	-5.3	6	533778	5.74	HUMAN	Q15149	Plectin
24779	dirMS_041712_NAR_40mM_plus2.8006.8006.3	3	3.72	0	3.12E+04		(R)SSQSSSQ	(R)S S Q S S S Q/Q/F/S G I G R(S)		107.58	485.8998	1455.682	0.0026	1.8	9.47	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
24780	dirMS_041712_NAR_40mM_plus2.8888.8888.2	2	3.72	0	1.19E+05		(R)GYSFTTT	(R)G Y/S/F/T T/T A E/R(E)		114.9	566.7672	1132.527	0.0002	0.2	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
24781	dirMS_041712_NAR_50mM_plus2.10455.10455.3	3	3.72	0	4.83E+04		(R)AASIFGG	(R)A A\S I/F G G A K/P V D/T A A R(E)		123.57	511.2769	1531.823	-0.0066	-4.3	8.79	64861.3	5.86	HUMAN	B4DS13	Eukaryotic translation initiation factor 4B
24782	dirMS_041712_NAR_50mM_plus2.10472.10472.3	3	3.72	1	2.19E+05		(K)SVEAAA	(K)S V|E A A/A E L/S A K D/L K(E)		122.85	477.9286	1431.769	0.0023	1.6	4.68	12131.5	11.14	HUMAN	F5GXR3	Parathymosin
24783	dirMS_041712_NAR_50mM_plus2.12359.12359.3	3	3.72	0	1.16E+05		(K)GPLLYCA	(K)G P L/L/Y C A R/P P Q D L K(I)	C:Carbamidomethylation	132.63	543.2913	1627.863	-0.0031	-1.9	8.59	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
24784	dirMS_041712_NAR_50mM_plus2.6581.6581.3	3	3.72	1	9.00E+04	M797m	(K)KmLEEE	(K)K\m/L E E E V/L N L K(T)	m:Oxidized methionine	99.67	454.5791	1345.74	15.9832	-8.6	4.79	116622.2	8.24	HUMAN	Q8IVF6	Ankyrin repeat domain-containing protein 18A
24785	dirMS_041712_NAR_50mM_plus2.9047.9047.3	3	3.72	1	7.98E+04	T220t M22	(R)GLLRtW	(R)G L L R t/W P\P D A m Y R(L)	t:N-acetylglucosamine (T) m:	114.3	598.962	1575.81	219.0614	-7.2	8.75	68223	9.61	HUMAN	E7EP55	Protein LOC100652824
24786	dirMS_041712_NAR_60mM_plus.16995.16995.3	3	3.72	0	1.22E+05	S623s	(R)SVGHSIs	(R)S V G H S I s/I E/C/K(G)	C:Carbamidomethylation s:N-ace	145.77	473.9034	1216.599	203.0966	12.1	6.47	336378.7	9.73	HUMAN	Q9NR48	Histone-lysine N-methyltransferase ASH1L
24787	dirMS_041712_NAR_60mM_plus.18023.18023.3	3	3.72	0	1.55E+05		(K)ILLQPTS	(K)I L L Q P T S S/I/S T T K(T)		151.32	463.6084	1388.8	0.0111	8	8.75	192522.7	5.74	HUMAN	Q9P1Z9	Uncharacterized protein C9orf174
24788	dirMS_041712_NAR_60mM_plus.5410.5410.3	3	3.72	0	4.17E+05	M21m	(R)SGSmDP	(R)S G\S m D P S/G A H/P S V R(Q)	m:Oxidized methionine	86.32	467.5464	1384.627	15.9973	1.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
24789	dirMS_041712_NAR_60mM_plus.8547.8547.3	3	3.72	0	2.30E+05		(K)LSAEDAG	(K)L S/A E D A G V F I\S/R(M)		103.22	422.2223	1264.653	-0.0008	-0.7	4.37	162336.6	7.14	HUMAN	P29475	Nitric oxide synthase, brain
24790	dirMS_041712_NAR_60mM_plus.9190.9190.3	3	3.72	0	1.44E+05		(R)AFVVGIC	(R)A F V/V G/I C D L/A R(L)	C:Carbamidomethylation	106.87	407.5532	1220.646	-0.0006	-0.5	5.88	82447.3	7.94	HUMAN	Q15027	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 1
24791	dirMS_041712_NAR_120mM_minus.12552.12552.3	3	3.71	1	1.83E+05		(R)NKQEVM	(R)N K Q E\V\M/I/S D L E E R(L)		122.7	530.9318	1590.779	0.0016	1	4.41	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
24792	dirMS_041712_NAR_120mM_minus.5234.5234.3	3	3.71	1	9.83E+04	M50m	(K)QmNDE	(K)Q m N|D E K\T A/A/D\Y K(I)	m:Oxidized methionine	81.57	477.2144	1413.632	15.9972	1.6	4.56	9786.1	5.52	HUMAN	E9PS38	Protein NEDD8-MDP1
24793	dirMS_041712_NAR_20mM_minus.10466.10466.3	3	3.71	1	2.05E+05	T221t M22	(K)ItLFmKY	(K)I t L F m/K Y S S Y R(E)	t:Phosphorylated T m:Oxidiz	152.88	502.2275	1408.729	95.9386	-15	9.7	311253.2	6.01	HUMAN	Q14571	Inositol 1,4,5-trisphosphate receptor type 2
24794	dirMS_041712_NAR_20mM_minus.11804.11804.3	3	3.71	0	1.52E+05		(R)QASPNI	(R)Q A S|P N I V/I A L S G N K(A)		165.68	471.2674	1411.79	-0.0027	-1.9	8.75	22348.8	9.3	HUMAN	B4DJA5	Ras-related protein Rab-5A
24795	dirMS_041712_NAR_30mM_minus2.15725.15725.2	2	3.71	1	4.68E+04		(K)VQKNIEE	(K)V Q|K N/I/E/E V R(S)		139.15	557.811	1114.622	-0.0068	-6.1	6.11	46949.5	9.33	HUMAN	P0CB48	Putative upstream-binding factor 1-like protein 6
24796	dirMS_041712_NAR_30mM_minus2.16313.16313.2	2	3.71	0	1.84E+05		(K)GFVEIQT	(K)G F|V E I Q T\P K(I)		141.08	509.7867	1018.557	0.0094	9.2	6	57534.6	6.11	HUMAN	P14868	Aspartate--tRNA ligase, cytoplasmic
24797	dirMS_041712_NAR_30mM_minus2.19396.19396.2	2	3.71	0	1.27E+04		(K)EGLLLW	(K)E G L/L/L W/C Q R(K)	C:Carbamidomethylation	161.12	587.8058	1174.604	0.0006	0.5	6.1	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
24798	dirMS_041712_NAR_50mM_minus2.10725.10725.3	3	3.71	2	4.36E+05	T363t	(K)IAQMRV	(K)I/A Q/M R W E L M M K t K(E)	t:N-acetylglucosamine (T)	130.17	623.6418	1665.864	203.0471	-17.3	9.99	47661.7	5.55	HUMAN	F8W806	WD repeat-containing protein 52
24799	dirMS_041712_NAR_50mM_minus2.9717.9717.3	3	3.71	1	7.03E+03		(K)KVEEAEP	(K)K V E E A E|P E E/F V/V E K(V)		123.65	554.6146	1661.827	0.0024	1.4	4.2	11857.8	9.63	HUMAN	B8ZZ43	Chromobox homolog 3 (HP1 gamma homolog, Drosophila), isoform CRA_b
24800	dirMS_041712_NAR_60mM_minus.13358.13358.3	3	3.71	1	2.62E+04		(R)TVENIKD	(R)T/V/E N I\K D/P L F R(F)		134.57	444.5792	1331.732	-0.0087	-6.6	5.74	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
24801	dirMS_041712_NAR_120mM_plus.19682.19682.4	4	3.71	0	4.26E+05		(R)DLKPQN	(R)D\L K P Q N I L V T S S/G/Q I/K(L)		156.22	436.0076	1740.985	0.0231	13.3	8.59	37280	6.02	HUMAN	Q00534	Cyclin-dependent kinase 6
24802	dirMS_041712_NAR_120mM_plus.23118.23118.4	4	3.71	1	3.68E+06		(K)GLAPDLP	(K)G L A P D L/P E D/L Y H/L I K K(A)		174.17	456.259	1822.011	0.0033	1.8	5.38	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
24803	dirMS_041712_NAR_120mM_plus.8819.8819.2	2	3.71	0	7.90E+05		(K)HFVALST	(K)H F|V\A\L S T N/T T K(V)		99.17	609.8311	1218.648	0.0072	5.9	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
24804	dirMS_041712_NAR_20mM_plus.16975.16975.3	3	3.71	0	2.28E+05	S923s	(R)NSIPVsP	(R)N S/I P V s P V R|P\K P/I E K(S)	s:Phosphorylated S	188.85	580.9864	1660.975	79.9702	2.2	9.99	109977.8	9.06	HUMAN	B7Z9C6	SH3 and PX domain-containing protein 2A
24805	dirMS_041712_NAR_30mM_plus2.13024.13024.2	2	3.71	0	7.26E+05		(K)NLLETLK	(K)N/L L E/T L K(E)		121.2	415.7543	830.498	0.0031	3.8	6	46769.6	6.37	HUMAN	H9KVD6	Lysine-specific demethylase 7 (Fragment)
24806	dirMS_041712_NAR_30mM_plus2.20916.20916.2	2	3.71	0	1.27E+05	M153m	(K)VVTYGm	(K)V V T|Y\G/m/A N L L T G P K(R)	m:Oxidized methionine	163.65	740.3971	1463.793	15.9943	-0.4	8.56	28454.5	6.24	HUMAN	B0AZP7	Synaptic vesicle membrane protein VAT-1 homolog
24807	dirMS_041712_NAR_30mM_plus2.4275.4275.2	2	3.71	0	8.31E+05	M299m M3	(K)NmmAA	(K)N m|m\A A C D/P R(H)	C:Carbamidomethylation m:Oxid	69.98	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
24808	dirMS_041712_NAR_30mM_plus2.4818.4818.2	2	3.71	0	7.71E+05	M571m	(R)mGANSL	(R)m/G\A/N/S L E R(M)	m:Oxidized methionine	76.48	447.2119	877.42	15.9969	2.2	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
24809	dirMS_041712_NAR_40mM_plus2.10347.10347.3	3	3.71	2	3.00E+04	S288s	(R)sQEQEV	(R)s Q E Q E\V/L E/R G G R F T R(S)	s:N-acetylglucosamine (S)	125.83	665.6807	1791.91	203.1179	19.3	5.95	147759.4	6.33	HUMAN	E7EQT4	Apoptotic chromatin condensation inducer in the nucleus
24810	dirMS_041712_NAR_40mM_plus2.15746.15746.3	3	3.71	1	5.12E+04		(R)IILPPEKE	(R)I I/L/P/P E K E L A M/P G E D L K(F)		158.48	631.6874	1893.04	0.0075	4	4.41	49883	7.3	HUMAN	P49411	Elongation factor Tu, mitochondrial
24811	dirMS_041712_NAR_50mM_plus2.10801.10801.3	3	3.71	0	7.19E+04		(K)ATVMDV	(K)A/T|V M D V/K P V D/Y R(E)		123.92	465.2419	1393.714	-0.0033	-2.3	6	35399.1	5.17	HUMAN	I3L4R8	Replication protein A 70 kDa DNA-binding subunit (Fragment)
24812	dirMS_041712_NAR_50mM_plus2.12065.12065.3	3	3.71	0	1.54E+05		(R)ISLGMPV	(R)I/S L G M P V/G/P N A H K(V)		131.02	440.9073	1320.709	-0.0019	-1.5	8.76	98282.7	5.49	HUMAN	E9PPJ0	Splicing factor 3B subunit 2
24813	dirMS_041712_NAR_50mM_plus2.12668.12668.3	3	3.71	1	7.18E+04		(-)MRREFC	(-)M R R E F/C W D/A/Y S K(A)	C:Carbamidomethylation	134.17	550.256	1648.736	0.0176	10.6	8.34	10364.5	9.57	HUMAN	C9JDS5	WD repeat-containing and planar cell polarity effector protein fritz homolog (Fragment)
24814	dirMS_041712_NAR_50mM_plus2.21449.21449.3	3	3.71	0	2.09E+04		(K)NHEIVPG	(K)N H E I V\P G S L/I/A S I A/S L K(H)		184.53	583.67	1748.991	0.0049	2.8	6.75	54906.6	5.26	HUMAN	D6RDI3	Serine/threonine-protein kinase RIO2
24815	dirMS_041712_NAR_50mM_plus2.7815.7815.3	3	3.71	1	6.95E+04	M227m M2	(R)mQKEITA	(R)m Q/K E I\T A L|A/P S T m K(I)	m:Oxidized methionine	106.93	527.6045	1548.812	31.9865	-2.1	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
24816	dirMS_041712_NAR_50mM_plus2.9003.9003.3	3	3.71	1	1.56E+05		(R)YLMEED	(R)Y/L|M/E E D E/D A Y K/K(Q)		114.85	511.8989	1533.678	0.0044	2.9	4.18	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
24817	dirMS_041712_NAR_60mM_plus.7389.7389.3	3	3.71	1	1.93E+06		(R)SEEKISD	(R)S/E/E K/I S D/S E G F K(A)		96.8	452.5501	1355.632	0.0032	2.4	4.41	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
24818	dirMS_041712_NAR_60mM_plus.7583.7583.3	3	3.71	0	2.93E+05		(K)NCPHVV	(K)N C/P H V|V/V/G T/P G R(I)	C:Carbamidomethylation	97.75	431.5519	1292.653	-0.0117	-9	9.75	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
24819	dirMS_041712_NAR_20mM_minus.12603.12603.2	2	3.7	0	2.31E+05	M185m	(K)LAVNmV	(K)L A/V/N m\V/P F P R(L)	m:Oxidized methionine	173.62	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
24820	dirMS_041712_NAR_20mM_minus.7570.7570.2	2	3.7	0	8.26E+05	M239m	(K)EVDEQm	(K)E V\D/E Q m L/N|V/Q|N\K(N)	m:Oxidized methionine	124.23	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
24821	dirMS_041712_NAR_30mM_minus2.15707.15707.2	2	3.7	0	2.22E+04		(R)NFDGLE	(R)N F/D G L/E E I D R(A)		139.02	604.2858	1207.559	0.0054	4.4	3.91	60342.9	9.25	HUMAN	F8WAJ2	Nuclear receptor coactivator 2
24822	dirMS_041712_NAR_40mM_minus2.13450.13450.3	3	3.7	0	1.46E+05		(K)VAIVKPG	(K)V A I/V K/P G V|P M/E I V L N K(E)		163.22	569.6777	1707.024	-0.0052	-3	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
24823	dirMS_041712_NAR_40mM_minus2.7790.7790.3	3	3.7	1	1.59E+05		(R)DGKLVS	(R)D G K L V\S E S S/D V L/P K(-)		125.2	491.9311	1473.78	-0.0008	-0.5	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
24824	dirMS_041712_NAR_50mM_minus2.15136.15136.3	3	3.7	1	2.04E+05		(K)GADFLV	(K)G A/D F/L/V/T/E/V E N G G S L\G S K K(G)		154.93	636.662	1907.971	0.0005	0.3	4.68	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
24825	dirMS_041712_NAR_50mM_minus2.16527.16527.3	3	3.7	0	7.04E+03	M75m T77	(R)FLILDRPA	(R)F L I L D R P A E/m/P t K(C)	m:Oxidized methionine t:N-a	162.83	583.963	1530.835	219.0396	-19.8	6.07	40363.2	4.86	HUMAN	E5RG96	von Willebrand factor D and EGF domain-containing protein
24826	dirMS_041712_NAR_60mM_minus.12107.12107.3	3	3.7	1	3.77E+05		(K)AAAGKA	(K)A A|A G K A E L/E|L E/L/G R(I)		127.53	476.6071	1427.785	0.0215	15	4.79	533778	5.74	HUMAN	Q15149	Plectin
24827	dirMS_041712_NAR_60mM_minus.12914.12914.3	3	3.7	1	1.64E+05		(R)TPSDVKE	(R)T P\S D V K E L V/L/D N S R(S)		131.63	524.9451	1572.823	-0.002	-1.3	4.55	20111	4.47	HUMAN	H0YN26	Acidic leucine-rich nuclear phosphoprotein 32 family member A
24828	dirMS_041712_NAR_60mM_minus.15042.15042.3	3	3.7	1	1.53E+05		(K)KVEEVV	(K)K\V E E V\V|Y/D/L S I/R(G)		143.53	483.9327	1449.795	-0.0112	-7.7	4.68	25685.9	6.4	HUMAN	E9PGT1	Translin
24829	dirMS_041712_NAR_60mM_minus.16065.16065.3	3	3.7	1	1.98E+05		(K)EIIDPVLD	(K)E I I/D P V L D/R I R(K)		150.17	446.9287	1338.774	-0.0024	-1.8	4.56	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
24830	dirMS_041712_NAR_60mM_minus.6271.6271.3	3	3.7	0	6.62E+04	M385m	(R)AQLmNC	(R)A Q|L m/N C H V/S/A G T R(H)	C:Carbamidomethylation m:Oxid	93.73	487.5623	1444.678	15.994	-0.6	9.8	57941.9	5.52	HUMAN	Q96RE7	Nucleus accumbens-associated protein 1
24831	dirMS_041712_NAR_60mM_minus.8040.8040.3	3	3.7	1	1.34E+05	K32k	(K)NPSSLFS	(K)N P S S L\F S K E A P k(R)	k:Ubiquitin-K	104.88	473.5815	1304.685	114.0455	1.8	8.59	92049.9	9.16	HUMAN	G3V529	ATP-dependent RNA helicase DDX24
24832	dirMS_041712_NAR_120mM_plus.11584.11584.2	2	3.7	1	4.43E+05		(R)GKIGLDF	(R)G K|I/G L D/F C/K(Y)	C:Carbamidomethylation	113.02	519.2706	1037.545	-0.0109	-10.5	8.59	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
24833	dirMS_041712_NAR_120mM_plus.8143.8143.3	3	3.7	0	1.60E+06		(-)XEVEAAL	(-)X E\V E A/A/L Y Y/K(D)		96.27	400.2199	1198.635	0.0097	8.1	4.53	21103.9	10.38	HUMAN	H7C3H5	WD repeat-containing protein 27 (Fragment)
24834	dirMS_041712_NAR_20mM_plus.11600.11600.2	2	3.7	0	8.93E+04		(R)AQAALA	(R)A Q A A/L|A\V N I S A A R(G)		153.17	628.3565	1255.712	-0.006	-4.8	9.79	58479.6	6.23	HUMAN	P40227	T-complex protein 1 subunit zeta
24835	dirMS_041712_NAR_20mM_plus.9956.9998.2	2	3.7	0	1.46E+05		(R)VLLPTGN	(R)V L|L|P T G N Q R(A)		140.57	499.2863	997.579	-0.0136	-13.6	9.72	99570.4	9.54	HUMAN	P53814	Smoothelin
24836	dirMS_041712_NAR_30mM_plus2.12536.12536.2	2	3.7	0	9.70E+05		(R)TIGISVD	(R)T I|G\I S V D/P R(R)		118.55	479.2725	957.536	0.0014	1.4	5.5	14749.1	12.2	HUMAN	J3QSB4	60S ribosomal protein L13 (Fragment)
24837	dirMS_041712_NAR_30mM_plus2.19896.19896.2	2	3.7	0	5.50E+05		(-)MDELQL	(-)M D\E|L/Q/L F R(G)		157.03	526.2726	1051.524	0.0138	13.2	4.37	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
24838	dirMS_041712_NAR_30mM_plus2.22775.22775.2	2	3.7	0	2.69E+05		(R)ELSDFIS	(R)E L/S D/F I/S Y L Q R(E)		177.22	685.8507	1370.695	-0.0009	-0.7	4.37	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
24839	dirMS_041712_NAR_30mM_plus2.5433.5433.2	2	3.7	0	1.84E+05		(R)TDTGEP	(R)T/D|T/G E P M G R(G)		82.82	482.2128	963.42	-0.0017	-1.8	4.37	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
24840	dirMS_041712_NAR_30mM_plus2.9705.9705.2	2	3.7	0	1.46E+05		(R)LGVAEA	(R)L G/V/A E A G G/R(R)		103.75	415.225	829.453	-0.0099	-12	6	48714.9	10.42	HUMAN	B0S7Q4	Chromosome 6 open reading frame 136 (Fragment)
24841	dirMS_041712_NAR_40mM_plus2.11188.11188.3	3	3.7	0	1.63E+05	S185s	(R)SsHSPGP	(R)S s H S/P G P V V A P(-)	s:N-acetylglucosamine (S)	131.92	413.2151	1034.526	203.1042	20.1	6.46	21671	5.37	HUMAN	J3KTF8	Rho GDP-dissociation inhibitor 1 (Fragment)
24842	dirMS_041712_NAR_50mM_plus2.10653.10653.3	3	3.7	1	2.12E+05		(K)AQALRD	(K)A Q|A/L R D N S T\M/G Y M M A/K(K)		123.72	596.6125	1787.824	-0.0008	-0.4	8.63	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
24843	dirMS_041712_NAR_50mM_plus2.11063.11063.3	3	3.7	2	2.37E+05	M469m	(R)QRSVSQ	(R)Q R/S V S Q E R L E D S V L m K(Y)	m:Oxidized methionine	125.5	640.9957	1904.986	15.9867	-4.3	6.18	126416.4	8.89	HUMAN	E7ESW5	Rho GTPase-activating protein 21 (Fragment)
24844	dirMS_041712_NAR_50mM_plus2.13070.13070.3	3	3.7	0	2.93E+05		(K)VSHVSTG	(K)V S H V S T G G G\A/S L|E/L L E/G K(V)		136.75	580.9801	1740.913	0.0131	7.5	5.4	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
24845	dirMS_041712_NAR_50mM_plus2.19238.19238.3	3	3.7	0	3.59E+05		(-)MKPLVV	(-)M K/P L V V F\V/L/G G P G A/G K(G)		169.73	523.9715	1569.919	-0.0186	-11.8	10	22450.2	5.44	HUMAN	P30085	UMP-CMP kinase
24846	dirMS_041712_NAR_50mM_plus2.8906.8906.3	3	3.7	1	6.36E+04		(K)ATFIKVP	(K)A T/F/I K V/P\Q N Q N G K(S)		113.77	482.2676	1444.791	-0.0024	-1.7	10	32503.1	5.29	HUMAN	H7BY16	Nucleolin (Fragment)
24847	dirMS_041712_NAR_50mM_plus2.9763.9763.3	3	3.7	0	2.98E+04		(K)GAVDGG	(K)G A V/D\G G L S I/P H S T K(R)		119.98	446.9057	1338.701	0.0013	1	6.74	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5

24848	dirMS_041712_NAR_60mM_plus.10062.10062.3	3	3.7	1	3.71E+05	S1153s	(K)VGRVsIY	(K)V G/R V s I Y D\S/K(R)	s:N-acetylglucosamine (S)	110.05	442.9125	1123.611	203.1123	24.9	8.56	142137.5	9.17	HUMAN	E7ENU4	Double-stranded RNA-specific adenosine deaminase
24849	dirMS_041712_NAR_60mM_plus.10827.10827.2	2	3.7	0	3.85E+05		(R)AHSSM\	(R)A H|S S M/V G V N L P Q K(A)		114.47	684.3577	1367.71	-0.0019	-1.4	8.8	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
24850	dirMS_041712_NAR_60mM_plus.17152.17152.3	3	3.7	1	4.68E+05		(R)GPIKFN\	(R)G P/I K F N V\W/D/T A G Q E K(F)		146.57	563.9572	1689.86	-0.0024	-1.4	6.07	26394.9	6.5	HUMAN	B5MDF5	GTP-binding nuclear protein Ran
24851	dirMS_041712_NAR_60mM_plus.5405.5405.3	3	3.7	0	2.28E+04	M74m T75	(K)NmtHQ\	(K)N m/t H Q V Q A E/R(D)	m:Oxidized methionine t:N-a	84.53	478.2118	1213.574	219.0466	-19.3	6.75	98458.4	5.67	HUMAN	Q96GX5	Serine/threonine-protein kinase greatwall
24852	dirMS_041712_NAR_60mM_plus.5699.5699.3	3	3.7	2	1.13E+05	S422s	(K)ESSVKT\	(K)E S S/V K T/V\R s T S/K(V)	s:Phosphorylated S	88.37	463.5601	1308.712	79.954	-8.9	10	113840.7	9.67	HUMAN	B4E3L9	Bromodomain-containing protein 1
24853	dirMS_041712_NAR_60mM_plus.7268.7268.2	2	3.7	0	5.06E+05		(R)IGKPAPI	(R)I G K/P A P D|F K(A)		95.78	486.7793	972.551	0	0	8.59	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
24854	dirMS_041712_NAR_60mM_plus.8083.8083.3	3	3.7	1	1.27E+06	N8n	(K)VLVDnPI	(K)V/L/V D n/P/K/N R(M)	n:N-acetylglucosamine (N)	100.88	419.894	1054.6	203.0671	-9.8	8.72	24092.5	8.08	HUMAN	J3QS11	Integrin beta-4 (Fragment)
24855	dirMS_041712_NAR_60mM_plus.8905.8905.3	3	3.7	1	7.11E+05		(R)QLQLAC	(R)Q L\Q/L\A/Q/E A/A Q K R(L)		104.87	461.9268	1383.77	-0.0044	-3.2	8.75	533778	5.74	HUMAN	Q15149	Plectin
24856	dirMS_041712_NAR_120mM_minus.13715.13715.3	3	3.69	0	4.19E+04	S936s	(K)NLFsDTE	(K)N L F s/D T E|T E Y R(C)	s:N-acetylglucosamine (S)	129.23	526.5672	1374.617	203.0698	-6	4.14	117616.3	9.59	HUMAN	A2A341	Synaptonemal complex protein 2 (Fragment)
24857	dirMS_041712_NAR_120mM_minus.6783.6783.3	3	3.69	1	2.31E+05		(R)TKTEISEI	(R)T K T E I/S/E/M/N/R(N)		91.52	403.5363	1208.594	0.0004	0.3	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
24858	dirMS_041712_NAR_120mM_minus.7326.7326.3	3	3.69	1	1.18E+05		(R)LQATER'	(R)L Q A T E\R T M V/R(E)		94.07	402.2156	1204.647	-0.0144	-12	9.6	71722.8	9.49	HUMAN	D4QA03	C-terminal-620AA lysine-specific demethylase 2A
24859	dirMS_041712_NAR_20mM_minus.14488.14488.3	3	3.69	0	2.19E+05		(K)LAAELSA	(K)L A\A\E\L S A T L/E\Q A/A/A T A R(V)		198.9	562.9713	1686.902	-0.0027	-1.6	4.53	558007.1	5.44	HUMAN	P58107	Epiplakin
24860	dirMS_041712_NAR_20mM_minus.9043.9043.2	2	3.69	0	6.54E+04	M68m M7	(R)NLAmG\	(R)N L/A|m/G V\N L T S m S K(I)	m:Oxidized methionine	139.73	699.34	1365.687	31.9862	-2.6	8.75	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
24861	dirMS_041712_NAR_30mM_minus2.8374.8374.2	2	3.69	0	3.16E+05		(K)ELQSTFK	(K)E L Q/S/T F/K(-)		100.22	426.7259	852.446	-0.0016	-1.9	6.1	26810.9	5.15	HUMAN	Q96C19	EF-hand domain-containing protein D2
24862	dirMS_041712_NAR_50mM_minus2.10563.10563.3	3	3.69	0	1.77E+05		(R)VEAFELY	(R)V E A/F E|L Y Q L E L K(D)		128.57	494.6068	1481.789	0.0172	11.6	4.25	112199	5.71	HUMAN	O75665-3	Isoform 3 of Oral-facial-digital syndrome 1 protein
24863	dirMS_041712_NAR_50mM_minus2.5724.5724.3	3	3.69	0	2.41E+05		(K)ATCAPQ	(K)A T/C/A|P Q\H G A\P G\P G\P A D A S K(V)	C:Carbamidomethylation	93.82	597.279	1789.829	-0.0062	-3.4	6.79	83264.1	6.04	HUMAN	E9PHF0	Filamin-A
24864	dirMS_041712_NAR_50mM_minus2.8588.8588.3	3	3.69	1	2.14E+05		(R)VAIEPG/	(R)V/A/I/E|P G A P R E N D E F C K(M)	C:Carbamidomethylation	117.37	611.2923	1831.864	-0.002	-1.1	4.41	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
24865	dirMS_041712_NAR_60mM_minus.6958.6958.3	3	3.69	1	6.14E+04		(R)DSGRGD	(R)D S G R G\D S V|S/D S/G S D A\L R(S)		97.03	560.916	1680.742	-0.0085	-5.1	4.14	50974.6	5.31	HUMAN	B5ME91	Programmed cell death protein 4
24866	dirMS_041712_NAR_120mM_plus.5566.5566.3	3	3.69	1	3.76E+05		(K)TCEESSF	(K)T|C/E E/S S F/C K R(Q)	C:Carbamidomethylation	82.18	435.1877	1303.541	0.008	6.1	5.81	10576.1	11.44	HUMAN	E9PRF8	Neutral alpha-glucosidase AB
24867	dirMS_041712_NAR_120mM_plus.8954.8954.3	3	3.69	1	2.48E+05		(R)LRECELS	(R)L R E C E\L\S/P G V N\R(D)	C:Carbamidomethylation	100.87	477.2447	1429.722	-0.0021	-1.5	6.14	57188.9	5.97	HUMAN	H7C3A1	Serrate RNA effector molecule homolog (Fragment)
24868	dirMS_041712_NAR_20mM_plus.11222.11222.2	2	3.69	1	4.63E+04	N473n	(K)STGKnLI	(K)S T|G K|n\L D S\V Q K(L)	n:N-acetylglucosamine (N)	150.08	690.3592	1176.622	203.0892	7.1	8.31	90363.7	9.71	HUMAN	Q14241	Transcription elongation factor B polypeptide 3
24869	dirMS_041712_NAR_20mM_plus.11737.11737.2	2	3.69	0	6.09E+03	M402m	(R)mAFGA1	(R)m A|F/G A T L/D V\K(T)	m:Oxidized methionine	153.78	534.7743	1052.545	15.9968	1.8	5.59	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
24870	dirMS_041712_NAR_20mM_plus.14932.14932.2	2	3.69	1	9.93E+04		(R)FTTKVCS	(R)F T T K V/C/S V T/K(C)	C:Carbamidomethylation	173.5	585.8066	1170.619	-0.0128	-10.9	10	53325.9	8.4	HUMAN	B7Z3P4	Dimethylaniline monooxygenase [N-oxide-forming] 1
24871	dirMS_041712_NAR_20mM_plus.15806.15806.2	2	3.69	0	1.10E+05		(R)GTPLISP	(R)G T|P L I S/P L I K(W)		180.75	519.8306	1038.656	-0.0018	-1.8	8.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
24872	dirMS_041712_NAR_30mM_plus2.11226.11226.2	2	3.69	0	3.50E+05		(K)LIECGW	(K)L I|E C G W K(D)	C:Carbamidomethylation	111.65	453.2369	905.455	0.0116	12.8	6	6239.3	9.99	HUMAN	E5RHT9	Enhancer of yellow 2 transcription factor homolog
24873	dirMS_041712_NAR_30mM_plus2.15888.15888.2	2	3.69	0	4.22E+05		(R)MGPNIY	(R)M/G/P N/I/Y E L R(T)		136.4	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
24874	dirMS_041712_NAR_30mM_plus2.18443.18464.2	2	3.69	0	1.64E+04		(K)VVNSILA	(K)V/V|N/S I L A F R(E)		149.52	509.8031	1018.604	-0.0055	-5.4	9.72	56564.1	6.56	HUMAN	B4DNW0	Aminoacylase-1
24875	dirMS_041712_NAR_30mM_plus2.21873.21873.2	2	3.69	0	8.58E+04		(K)GLVQAL	(K)G L V Q A\L|G/L/S/N F N S R(Q)		169.67	738.3989	1475.796	-0.006	-4.1	9.75	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
24876	dirMS_041712_NAR_30mM_plus2.4031.4031.2	2	3.69	0	5.76E+05	M299m M	(K)NmmAA	(K)N/m|m A A C D|P R(H)	C:Carbamidomethylation m:Oxid	67.82	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
24877	dirMS_041712_NAR_30mM_plus2.5890.5890.2	2	3.69	0	2.07E+05		(K)LDDYQE	(K)L/D/D Y Q/E R(M)		85.12	469.719	938.421	0.0093	9.9	4.03	20235.4	6.77	HUMAN	E9PLA9	Caprin-1 (Fragment)
24878	dirMS_041712_NAR_40mM_plus2.12689.12689.2	2	3.69	0	1.93E+04		(K)ICSWNV	(K)I C|S\W N V/D/G L R(A)	C:Carbamidomethylation	141.22	610.297	1219.589	-0.0021	-1.7	5.84	19395.5	5.38	HUMAN	G3V359	DNA-(apurinic or apyrimidinic site) lyase (Fragment)
24879	dirMS_041712_NAR_40mM_plus2.17924.17924.3	3	3.69	0	4.94E+04		(K)DMTVPI	(K)D M|T/V/P I L V/S K P P V F T G K(D)		173.25	610.3443	1829.024	-0.0058	-3.2	8.59	53885.5	9	HUMAN	P11182	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial
24880	dirMS_041712_NAR_40mM_plus2.7745.7745.2	2	3.69	0	1.60E+05		(R)MSFSSLI	(R)M S F S S L K(R)		104.95	400.2001	799.402	-0.0089	-11.2	8.5	69917.2	6.12	HUMAN	P35240	Merlin
24881	dirMS_041712_NAR_40mM_plus2.8305.8305.2	2	3.69	0	6.85E+03		(K)VGQMQ	(K)V/G Q M/Q/I L/R(Q)		108.97	472.7655	944.535	-0.0109	-11.5	9.72	117805.4	8.78	HUMAN	E7EQI7	WASH complex subunit strumpellin
24882	dirMS_041712_NAR_40mM_plus2.8659.8659.2	2	3.69	0	1.31E+05		(K)DFSTTTK	(K)D/F/S T T T K(L)		111.85	400.2001	799.383	0.0097	12.1	5.84	31652.5	9.88	HUMAN	Q8N3J9	Zinc finger protein 664
24883	dirMS_041712_NAR_50mM_plus2.13554.13554.3	3	3.69	1	3.68E+05		(R)SLIANLA	(R)S L/I/A/N L\A/A/A N C Y K/K(E)	C:Carbamidomethylation	139	512.9444	1536.82	-0.0016	-1.1	9.7	36978.6	6.33	HUMAN	B7Z800	Adenosine kinase
24884	dirMS_041712_NAR_50mM_plus2.19283.19283.3	3	3.69	2	2.29E+05	N139n	(R)ESKSnA/	(R)E S/K S/n A A/T P T K G P E\G K(V)	n:N-acetylglucosamine (N)	169.8	602.3071	1601.813	203.0938	8	8.59	129794.7	9.88	HUMAN	H7BZ90	Histone-lysine N-methyltransferase, H3 lysine-79-specific (Fragment)
24885	dirMS_041712_NAR_50mM_plus2.20222.20222.3	3	3.69	0	2.34E+05		(K)GHVDIL/	(K)G H V D I L A|P T/V/Q/E L A|A L E K(E)		174.63	635.3536	1904.049	-0.0025	-1.3	4.65	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
24886	dirMS_041712_NAR_50mM_plus2.21332.21332.3	3	3.69	1	5.25E+05	M145m	(R)GVmLA\	(R)G V/m L\A V D A V|I A E L K K(Q)	m:Oxidized methionine	182.27	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
24887	dirMS_041712_NAR_50mM_plus2.8883.8883.3	3	3.69	0	1.80E+05		(K)TPVEPE\	(K)T\P V E/P E/V/A/I H R(I)		113.98	416.5627	1247.674	-0.0007	-0.6	5.37	5429.1	9.6	HUMAN	E5RIP1	40S ribosomal protein S20
24888	dirMS_041712_NAR_20mM_minus.10059.10059.2	2	3.68	0	1.24E+05		(R)YALYDA'	(R)Y/A/L|Y/D A T Y E/T K(E)		150.82	669.3156	1337.626	-0.0021	-1.5	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
24889	dirMS_041712_NAR_30mM_minus2.19304.19304.2	2	3.68	1	1.33E+05		(K)SKLEFSI\	(K)S K L E F S I Y P/A|P(-)		159.2	626.334	1251.662	-0.0012	-1	5.72	21962.5	5.85	HUMAN	C9JJQ8	Tubulin alpha-4A chain (Fragment)
24890	dirMS_041712_NAR_40mM_minus2.11599.11599.3	3	3.68	1	1.06E+05		(R)IINEPTA.	(R)I I/N E P T A/A A I A Y G L D/K K(V)		152.32	596.6671	1787.99	-0.0034	-1.9	6.07	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
24891	dirMS_041712_NAR_50mM_minus2.17117.17117.3	3	3.68	1	7.74E+04		(R)YDEIVKE	(R)Y/D|E I V K/E V/S/A Y I K(K)		166.15	519.6148	1556.821	0.0092	5.9	4.68	50811.6	9.32	HUMAN	Q05639	Elongation factor 1-alpha 2
24892	dirMS_041712_NAR_60mM_minus.12298.12298.3	3	3.68	1	7.93E+05		(K)AVIFCLS.	(K)A V/I F/C L S A D K K(C)	C:Carbamidomethylation	127.92	417.9007	1251.677	0.011	8.8	8.64	15739.2	9.3	HUMAN	F6RFD5	Destrin
24893	dirMS_041712_NAR_60mM_minus.12900.12900.3	3	3.68	1	1.59E+05		(R)TPSDVKI	(R)T P/S D V K E L|V\L/D/N S R(S)		131.57	524.9451	1572.823	-0.002	-1.3	4.55	20111	4.47	HUMAN	H0YN26	Acidic leucine-rich nuclear phosphoprotein 32 family member A
24894	dirMS_041712_NAR_60mM_minus.15422.15422.3	3	3.68	0	3.11E+04		(R)LGGLRPI	(R)L G G L R P E\S P/E/S L T S V S R(T)		144.78	595.6552	1784.95	0.0009	0.5	6.14	9248	8.73	HUMAN	H0YG79	Coiled-coil domain-containing protein 86 (Fragment)
24895	dirMS_041712_NAR_60mM_minus.7323.7323.3	3	3.68	0	2.04E+05	S326s	(K)IVAsNLV	(K)I/V A s N L/V\T G/L P K(Q)	s:Phosphorylated S	100.47	431.2376	1211.736	79.9624	-3	8.75	62245.9	5.34	HUMAN	Q8WWZ8	Oncoprotein-induced transcript 3 protein
24896	dirMS_041712_NAR_20mM_plus.10469.10469.3	3	3.68	0	5.88E+04		(K)EVDEQN	(K)E V D E\Q M L/N/V Q N K(N)		144.9	482.9	1446.689	-0.0039	-2.7	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
24897	dirMS_041712_NAR_20mM_plus.11574.11574.2	2	3.68	0	1.35E+05		(R)YALYDA'	(R)Y/A\L|Y D A/T Y E T K(E)		151.8	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
24898	dirMS_041712_NAR_20mM_plus.12038.12038.3	3	3.68	0	3.25E+03		(K)SVEVQG	(K)S V E V/Q G E T E\T I I A/T K(T)		156.2	535.6108	1604.838	-0.0199	-12.4	4.25	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
24899	dirMS_041712_NAR_20mM_plus.13071.13071.2	2	3.68	0	2.38E+05	M316m	(R)ISEQFTA	(R)I/S\E Q F/T/A m F R(R)	m:Oxidized methionine	161.82	623.3012	1229.598	15.9968	1.5	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
24900	dirMS_041712_NAR_20mM_plus.13621.13621.2	2	3.68	0	2.82E+05	S29s	(R)DLSsSFR	(R)D L/S/s S F R(D)	s:N-acetylglucosamine (S)	165.27	507.7439	811.394	203.0861	6.6	5.84	94409.4	6.9	HUMAN	Q8N3F8	MICAL-like protein 1
24901	dirMS_041712_NAR_20mM_plus.14438.14438.2	2	3.68	0	6.21E+04		(K)GAVEIIF	(K)G A|V/E/I I F K(G)		170.95	438.7639	876.519	0.0016	1.8	6	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
24902	dirMS_041712_NAR_20mM_plus.14718.14718.2	2	3.68	0	1.05E+05		(K)FANPFP/	(K)F A|N/P F/P A/A V\R(G)		173.67	545.2958	1089.584	0.0003	0.3	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
24903	dirMS_041712_NAR_20mM_plus.16829.16829.2	2	3.68	0	1.62E+05		(R)ELLIIGG\	(R)E L L/I/I/G/G V A A/R(D)		186.67	556.3437	1111.683	-0.0032	-2.9	6.1	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
24904	dirMS_041712_NAR_20mM_plus.19172.19172.2	2	3.68	0	2.10E+05		(K)ILTFDQL	(K)I L/T F D Q L/A L D S/P K(G)		203.3	730.9063	1460.8	0.0058	4	4.21	14643	11.93	HUMAN	F8VUA6	60S ribosomal protein L18 (Fragment)
24905	dirMS_041712_NAR_30mM_plus2.21945.21945.2	2	3.68	0	1.56E+05		(R)QSSFALI	(R)Q/S\S F/A L L/G D/L T K(A)		170.63	640.3472	1279.689	-0.0021	-1.7	5.84	46579.3	4.96	HUMAN	E5RI07	Transportin-1
24906	dirMS_041712_NAR_30mM_plus2.5867.5867.2	2	3.68	0	1.76E+05		(R)ISAGCLS	(R)I S/A G C/L S/R(L)	C:Carbamidomethylation	85.28	432.2218	863.44	-0.004	-4.7	9.75	19893.2	10.13	HUMAN	F5H2G5	Nuclear receptor-interacting protein 2 (Fragment)
24907	dirMS_041712_NAR_30mM_plus2.5904.5904.2	2	3.68	0	1.64E+05		(K)TSEVNC'	(K)T S|E|V/N C Y R(C)	C:Carbamidomethylation	84.77	514.7261	1028.447	-0.0016	-1.6	5.66	18946.7	9.13	HUMAN	B4DP17	Cellular nucleic acid-binding protein
24908	dirMS_041712_NAR_50mM_plus2.13138.13138.3	3	3.68	0	7.93E+05		(R)VLHVSEI	(R)V L H V\S E N\P V|P L T V R(V)		137.38	520.6339	1559.89	-0.0033	-2.1	6.72	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
24909	dirMS_041712_NAR_50mM_plus2.13939.13939.3	3	3.68	0	1.30E+06		(K)DLAGCIH	(K)D L|A G C I/H G L S N/V K(L)	C:Carbamidomethylation	140.57	461.9061	1383.705	-0.0012	-0.8	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
24910	dirMS_041712_NAR_60mM_plus.11053.11053.3	3	3.68	1	9.67E+05		(R)KTEELEE	(R)K T E E\L\E E/E S F/P E R(S)		115.75	541.5897	1622.754	0.0001	0.1	4.2	108720.9	10.17	HUMAN	Q9Y2W1	Thyroid hormone receptor-associated protein 3
24911	dirMS_041712_NAR_60mM_plus.15237.15237.3	3	3.68	1	1.21E+05		(K)ANLIKEA	(K)A N/L/I K E\A E/E/M/C S K(F)	C:Carbamidomethylation	136.23	508.2453	1522.724	-0.0026	-1.7	4.79	102525.8	7.33	HUMAN	Q9BXJ9	N-alpha-acetyltransferase 15, NatA auxiliary subunit
24912	dirMS_041712_NAR_60mM_plus.16455.16455.2	2	3.68	0	6.27E+05		(R)EHALLA'	(R)E H|A\L\L|A|Y/T L G V K(Q)		143.55	657.8735	1314.742	-0.0019	-1.4	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
24913	dirMS_041712_NAR_120mM_minus.4924.4924.3	3	3.67	0	1.16E+06	M46m M4	(R)HQGVm	(R)H Q G\V\m/V G\m/G Q K(D)	m:Oxidized methionine	77.48	401.8604	1171.571	31.9956	4.8	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
24914	dirMS_041712_NAR_20mM_minus.7696.7696.2	2	3.67	0	4.88E+05	M239m	(K)EVDEQn	(K)E V/D E Q/m L/N V Q/N K(N)	m:Oxidized methionine	125.43	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
24915	dirMS_041712_NAR_20mM_minus.7702.7702.3	3	3.67	0	5.43E+05	M239m	(K)EVDEQn	(K)E V D E Q/m L/N V Q N K(N)	m:Oxidized methionine	125.52	488.2327	1446.689	15.9942	-0.5	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
24916	dirMS_041712_NAR_30mM_minus2.12535.12535.2	2	3.67	0	2.78E+05		(R)GGAEQF	(R)G G A E Q/F|M E E/T E R(S)		122.52	692.2961	1383.584	0.0004	0.3	4.09	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
24917	dirMS_041712_NAR_30mM_minus2.13201.13201.2	2	3.67	2	3.55E+05		(K)KSFKSPE	(K)K S/F/K S P/E P/R(L)		124.82	538.2931	1075.59	-0.0105	-9.8	9.99	31183.3	5.86	HUMAN	P21583	Kit ligand
24918	dirMS_041712_NAR_30mM_minus2.15175.15175.2	2	3.67	0	3.39E+06		(K)EGSVGL!	(K)E\G/S|V G L S V Q/R(S)		134.75	516.281	1031.548	0.0067	6.5	6.1	61513.2	9.46	HUMAN	J3KQS2	Cell division cycle 7-related protein kinase
24919	dirMS_041712_NAR_30mM_minus2.7197.7197.2	2	3.67	0	4.07E+05		(R)ASYISSA	(R)A/S|Y/I S S A R(L)		94.2	427.7216	854.437	-0.0007	-0.9	8.79	59288.4	7.16	HUMAN	Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)
24920	dirMS_041712_NAR_40mM_minus2.5291.5291.2	2	3.67	0	1.64E+05		(R)FLEQQN	(R)F/L/E/Q Q\N K(I)		88.28	453.7371	906.468	-0.001	-1.1	6	49709.6	5.19	HUMAN	B0YJC4	Vimentin
24921	dirMS_041712_NAR_40mM_minus2.8180.8180.3	3	3.67	1	4.65E+04		(R)DVVICPI	(R)D V/V\I/C/P D A S L E D A K K(E)	C:Carbamidomethylation	128.47	553.9467	1659.826	-0.0003	-0.2	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
24922	dirMS_041712_NAR_40mM_minus2.8326.8326.3	3	3.67	0	3.89E+03	S564s M56	(R)LIVSLAL!	(R)L I|V S L A L s/V G T Q m K(T)	s:N-acetylglucosamine (S) m:	129.42	560.3204	1459.855	219.0914	10.2	8.75	137427.9	7.13	HUMAN	Q2M389	WASH complex subunit 7
24923	dirMS_041712_NAR_50mM_minus2.15047.15047.3	3	3.67	1	2.35E+05		(K)LALDIEI/	(K)L A L D I/E\I A/T Y R K(L)		154.05	469.2729	1405.805	-0.0008	-0.6	6.07	49564	5.84	HUMAN	E9PAX3	Glial fibrillary acidic protein
24924	dirMS_041712_NAR_50mM_minus2.15387.15387.3	3	3.67	1	2.25E+04		(K)CEFQDA	(K)C E/F Q D\A/Y V/L L/S E K K(I)	C:Carbamidomethylation	156.05	577.2917	1729.847	0.014	8.1	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
24925	dirMS_041712_NAR_60mM_minus.15516.15516.3	3	3.67	2	3.72E+05	M937m	(K)DmFADI	(K)D m/F A/D R\L S K/S I I/K(H)	m:Oxidized methionine	146.35	513.947	1523.825	16.0014	4.2	8.59	213075.9	5.23	HUMAN	Q9UKA4	A-kinase anchor protein 11
24926	dirMS_041712_NAR_60mM_minus.5339.5339.3	3	3.67	1	5.73E+04		(K)IECDDK(	(K)I/E|C D D K/G D G S C D V/R(Y)	C:Carbamidomethylation	85.25	542.5547	1625.653	-0.0035	-2.1	4.04	283472.4	5.71	HUMAN	P21333	Filamin-A
24927	dirMS_041712_NAR_60mM_minus.6756.6756.3	3	3.67	2	4.23E+04	K696k	(R)VVAAMI	(R)V V|A A M/N R/M D Q K k(H)	k:Ubiquitin-K	96	502.2642	1390.729	114.0487	3.8	9.99	81388.8	5.94	HUMAN	Q2YD98	UV-stimulated scaffold protein A
24928	dirMS_041712_NAR_60mM_minus.7120.7120.3	3	3.67	1	2.74E+05		(R)IVDGKV'	(R)I/V|D G K/V V S E T\N D T K(V)		97.95	502.2642	1504.785	-0.0073	-4.8	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
24929	dirMS_041712_NAR_60mM_minus.8459.8459.3	3	3.67	0	4.60E+05	M148m	(R)AHSSm\	(R)A H S S m|V G\V N L/P Q K(A)	m:Oxidized methionine	106.77	461.9064	1367.71	15.9947	-0.2	8.8	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
24930	dirMS_041712_NAR_60mM_minus.8546.8546.3	3	3.67	1	3.27E+04	S79s	(R)VALYKs\	(R)V A|L Y/K s V P T R(L)	s:Phosphorylated S	107.65	405.2193	1133.668	79.9756	7.7	9.99	30714	10.53	HUMAN	B1AKM6	Phosphatidylserine decarboxylase
24931	dirMS_041712_NAR_120mM_plus.12410.12502.2	2	3.67	0	8.66E+05		(R)HGSLGF	(R)H/G|S\L G F\L\P R(K)		118.47	492.2735	983.542	-0.0024	-2.4	9.75	20053	10.46	HUMAN	F8WCR1	60S ribosomal protein L3
24932	dirMS_041712_NAR_120mM_plus.4020.4020.3	3	3.67	0	3.37E+05		(R)FAGHSE.	(R)F A G H S E A/G G/G S G D R(R)		67.78	435.5253	1304.561	-0.0001	-0.1	5.32	64356.2	9.96	HUMAN	O96013	Serine/threonine-protein kinase PAK 4
24933	dirMS_041712_NAR_120mM_plus.5705.5705.3	3	3.67	0	1.64E+05	T1530t	(R)YFtQEDI	(R)Y/F t Q|E D I\N Q G K(V)	t:Phosphorylated T	83.07	474.8734	1342.627	79.9783	8.4	4.37	226496	5.48	HUMAN	A2RRR8	Extracellular matrix protein FRAS1
24934	dirMS_041712_NAR_20mM_plus.10980.10980.2	2	3.67	0	2.60E+04		(R)IVLQIDN	(R)I V L|Q I/D N A R(L)		148.23	521.3056	1041.605	-0.0012	-1.1	5.84	20842.9	5.32	HUMAN	C9JM50	Keratin, type I cytoskeletal 19 (Fragment)
24935	dirMS_041712_NAR_20mM_plus.7557.7557.2	2	3.67	0	2.30E+04		(R)TVGIVGI	(R)T V/G\I/V G N Q P K(V)		121	506.7922	1012.579	-0.0014	-1.4	8.41	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
24936	dirMS_041712_NAR_30mM_plus2.16557.16557.2	2	3.67	0	3.41E+05		(R)LWDLTT	(R)L W|D/L/T/T G/T T T R(R)		139.88	632.8304	1264.653	0.0003	0.3	5.84	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
24937	dirMS_041712_NAR_30mM_plus2.21637.21637.3	3	3.67	0	1.67E+05		(K)GLVQAL	(K)G L V Q A L/G/L\S/N F/N S R(Q)		169.37	492.6036	1475.796	-0.0003	-0.2	9.75	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
24938	dirMS_041712_NAR_30mM_plus2.5650.5650.2	2	3.67	0	6.39E+04		(R)SCMAAT	(R)S\C M/A A T\L/R(I)	C:Carbamidomethylation	83.72	455.2133	909.428	-0.0088	-9.6	9.47	68619.5	9.37	HUMAN	E9PIN3	Nuclear RNA export factor 1 (Fragment)
24939	dirMS_041712_NAR_30mM_plus2.6051.6051.2	2	3.67	0	1.61E+05		(K)SPEYPE(	(K)S P E|Y P E/G/R(D)		85.98	467.7183	934.427	0.0028	3	4.53	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
24940	dirMS_041712_NAR_40mM_plus2.12191.12191.3	3	3.67	1	2.10E+05		(R)VVDALG	(R)V V/D A\L G N A I D G K G P I G S K(T)		137.27	570.9838	1710.939	-0.0016	-1	5.93	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
24941	dirMS_041712_NAR_40mM_plus2.12479.12479.3	3	3.67	2	1.29E+05	S306s	(R)LSQLEEE	(R)L/S Q/L E E E R A F/L R s K(T)	s:N-acetylglucosamine (S)	139.77	637.0002	1705.923	203.0629	-8.6	6.23	61619.8	5.42	HUMAN	E7EQ67	Protein FAM184A
24942	dirMS_041712_NAR_40mM_plus2.9259.9259.2	2	3.67	0	5.45E+05		(K)SSFFSDR	(K)S S F/F/S D R(G)		116.45	423.1935	845.379	0.0009	1.1	5.55	15031.5	6.72	HUMAN	B4DLA0	ATP-dependent RNA helicase DDX3X
24943	dirMS_041712_NAR_50mM_plus2.12598.12598.3	3	3.67	0	2.22E+05		(K)LQELPD/	(K)L Q E/L/P D A V/P H G E M P R(H)		134.13	563.6145	1688.843	-0.0135	-8	4.65	78390.7	9.27	HUMAN	B1AHB1	DNA replication licensing factor MCM5
24944	dirMS_041712_NAR_50mM_plus2.12684.12684.3	3	3.67	1	9.32E+04		(R)YMVADI	(R)Y M/V/A D/K F T E L Q/K(A)		135.1	491.5877	1472.745	0.0032	2.2	6.07	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
24945	dirMS_041712_NAR_50mM_plus2.13372.13372.3	3	3.67	0	4.70E+05		(K)QLTEED(	(K)Q L/T E/E D G V/H S V I E E N I/K(C)		138.32	647.3311	1939.961	0.018	9.3	4.25	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
24946	dirMS_041712_NAR_50mM_plus2.17987.17987.3	3	3.67	0	4.88E+04		(R)ATAAFIL	(R)A T/A A/F/I/L/A N E H N V A L F/K(H)		162.67	610.6671	1829.991	-0.0041	-2.2	6.79	125399.7	4.93	HUMAN	H0Y8C6	Importin-5 (Fragment)
24947	dirMS_041712_NAR_50mM_plus2.18060.18060.3	3	3.67	1	3.42E+05		(R)WAAGS'	(R)W/A A G S V T D L A F K V A S R(E)		162.77	560.3031	1678.891	0.0036	2.2	8.75	42147.8	5.3	HUMAN	H0YH91	Histone deacetylase 7 (Fragment)
24948	dirMS_041712_NAR_60mM_plus.13694.13694.3	3	3.67	1	6.42E+05		(K)ITDHFM	(K)I T D H\F M R/L P K(A)		128.72	419.894	1257.677	-0.0098	-7.8	8.76	112534.8	6.03	HUMAN	Q86W56	Poly(ADP-ribose) glycohydrolase
24949	dirMS_041712_NAR_60mM_plus.8572.8572.2	2	3.67	0	4.27E+05		(R)FACHSA:	(R)F/A/C/H S A/S L T V R(N)	C:Carbamidomethylation	102.73	624.8118	1248.615	0.001	0.8	9.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
24950	dirMS_041712_NAR_120mM_minus.12423.12423.4	4	3.66	2	5.21E+05		(K)LLGCQSI	(K)L/L G C Q S I E K F R\S H/G D R(E)	C:Carbamidomethylation	121.03	476.5062	1902.96	0.0427	22.4	8.75	254376.5	6.2	HUMAN	Q8WYP5	Protein ELYS
24951	dirMS_041712_NAR_120mM_minus.4687.4687.2	2	3.66	0	1.38E+06	M46m M4	(R)HQGVm	(R)H Q/G|V m V/G m G Q K(D)	m:Oxidized methionine	75.45	602.2834	1171.571	31.9885	-1.1	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
24952	dirMS_041712_NAR_120mM_minus.9887.9887.3	3	3.66	1	3.03E+05		(K)AYPLAD,	(K)A Y/P L A D A/H L T K K(L)		108.43	443.2499	1327.737	-0.0017	-1.3	8.55	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
24953	dirMS_041712_NAR_30mM_minus2.15907.15907.2	2	3.66	0	9.08E+03		(R)ALQASA	(R)A L Q|A/S A/L/N A W/R(G)		140.85	600.8272	1200.648	-0.0013	-1	9.79	36636.9	7.84	HUMAN	A8MVZ9	Fructose-bisphosphate aldolase
24954	dirMS_041712_NAR_30mM_minus2.8060.8060.2	2	3.66	0	1.48E+05		(R)NYLSQP	(R)N/Y|L|S Q/P R(L)		98.7	439.2266	877.453	-0.0067	-7.7	8.75	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
24955	dirMS_041712_NAR_60mM_minus.16507.16756.3	3	3.66	1	7.78E+06	M25m	(R)KAHQm!	(R)K\A H Q m S/L/E/G F T R(Y)	m:Oxidized methionine	151.55	474.2315	1404.705	15.9747	-14.2	8.76	9196.3	5.85	HUMAN	F5GZK3	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase zeta-1 (Fragment)
24956	dirMS_041712_NAR_60mM_minus.16772.16772.3	3	3.66	1	3.13E+05		(R)LKLPAV\	(R)L K L P A\V V/T/A D/L R(L)		153.9	432.6056	1295.805	-0.0023	-1.8	8.75	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta

24957	dirMS_041712_NAR_60mM_minus.6696.6696.3	3	3.66	1	5.48E+03		(K)SSADKIG	(K)S S A D/K/I G E V/S S P K(A)		95.88	435.5549	1304.669	-0.0191	-14.6	5.79	128765.8	9.47	HUMAN	P35251	Replication factor C subunit 1
24958	dirMS_041712_NAR_120mM_plus.5449.5449.3	3	3.66	0	3.85E+04	S203s	(R)LsGLAD	(R)L\s G L A/D Q M V A R(G)	s:Phosphorylated S	81.43	414.1962	1160.609	79.9648	-1.2	5.84	37759.9	4.49	HUMAN	O95400	CD2 antigen cytoplasmic tail-binding protein 2
24959	dirMS_041712_NAR_20mM_plus.14281.14281.3	3	3.66	2	7.24E+03		(K)ACATQK	(K)A C A T Q K/Q G Q P E K\G/K(A)	C:Carbamidomethylation	169.75	510.9348	1530.769	0.0205	13.4	9.7	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
24960	dirMS_041712_NAR_20mM_plus.17673.17673.3	3	3.66	0	1.12E+04		(R)IINEPTA	(R)I I\N E P T A A A\I/A/Y/G/L D R(T)		193.42	563.3055	1687.901	0.0006	0.3	4.37	25598.3	6.45	HUMAN	E7EP11	Heat shock 70 kDa protein 1A/1B
24961	dirMS_041712_NAR_20mM_plus.8263.8263.2	2	3.66	0	1.06E+05		(K)TAVCDIF	(K)T/A V\C D/I\P/P R(G)	C:Carbamidomethylation	127.63	514.7664	1028.519	0.0062	6	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
24962	dirMS_041712_NAR_30mM_plus2.16383.16383.3	3	3.66	0	5.59E+05		(R)GLCAIA	(R)G L\C A I A/Q/A/E S L R(Y)	C:Carbamidomethylation	138.5	430.2276	1288.668	0.0005	0.3	6	18529.2	9.98	HUMAN	E9PL45	40S ribosomal protein S3
24963	dirMS_041712_NAR_30mM_plus2.6068.6068.2	2	3.66	0	1.88E+05	M1m	(-)mATANF	(-)m A T/A N F\G\K(I)	m:Oxidized methionine	86.4	428.1992	839.408	15.9831	-13.8	8.5	32919.6	6.41	HUMAN	D6R9M0	Kinesin-like protein KIF2A (Fragment)
24964	dirMS_041712_NAR_30mM_plus2.9502.9502.2	2	3.66	0	2.55E+05		(R)LAAVDV	(R)L A/A/V/D V\S A R(A)		103.58	451.2545	901.51	-0.0084	-9.4	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin
24965	dirMS_041712_NAR_50mM_plus2.12923.12923.3	3	3.66	1	1.58E+05		(K)LVKELEG	(K)L V\K E/L E/G V I T K(A)		136.27	410.2529	1228.751	-0.007	-5.7	6.14	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
24966	dirMS_041712_NAR_50mM_plus2.9137.9137.3	3	3.66	0	7.57E+05	N427n	(K)GFNVNE	(K)G F N V N E L\L/V/D n/K(A)	n:N-acetylglucosamine (N)	115.63	522.2726	1361.706	203.0973	11.5	4.37	288508.2	6.01	HUMAN	Q8WWQ8	Stabilin-2
24967	dirMS_041712_NAR_60mM_plus.11580.11580.3	3	3.66	1	2.85E+06		(K)TAVCDIF	(K)T A|V C D I/P P R G L K(M)	C:Carbamidomethylation	117.63	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
24968	dirMS_041712_NAR_60mM_plus.12147.12147.3	3	3.66	0	2.92E+05		(R)QADFEA	(R)Q A D F E/A/H N I L R(E)		120.55	438.558	1313.66	-0.0002	-0.2	5.32	66612.6	7.28	HUMAN	F8W720	GMP synthase [glutamine-hydrolyzing]
24969	dirMS_041712_NAR_60mM_plus.18067.18067.3	3	3.66	2	2.19E+04	M242m	(R)RGSVTD	(R)R G S V T D/I|P G T A m V R\G G D(-)	m:Oxidized methionine	152.08	568.9563	1688.838	16.0159	12.3	6.14	27812.5	5.9	HUMAN	Q86YJ6-5	Isoform SOLAT of Threonine synthase-like 2
24970	dirMS_041712_NAR_60mM_plus.18913.18913.3	3	3.66	1	1.98E+05		(R)ANTFVA	(R)A N T/F/V A/E/L K G L D/P A R(V)		155.85	534.6306	1601.865	0.0127	7.9	6.12	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
24971	dirMS_041712_NAR_60mM_plus.19120.19120.3	3	3.66	2	5.14E+05	M1m	(-)mKEGRLI	(-)m K E G R L/E/E S V A/L R(I)	m:Oxidized methionine	157.07	511.9392	1517.81	15.9926	-1.5	5.99	17425.9	5.37	HUMAN	E9PK68	Serine/threonine-protein phosphatase (Fragment)
24972	dirMS_041712_NAR_60mM_plus.19686.19686.3	3	3.66	1	4.49E+04		(K)SLLGKD	(K)S L/L/G K D V L F L K(D)		161.07	411.5915	1232.761	-0.0013	-1.1	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
24973	dirMS_041712_NAR_120mM_minus.12905.12905.4	4	3.65	2	6.71E+04	N380n	(R)GKFNTS	(R)G K F N T S D V S A I/E/K n/K(E)	n:N-acetylglucosamine (N)	124.18	460.9843	1637.849	203.066	-7.2	8.5	107509.8	6.66	HUMAN	E7ENR4	Hexokinase-1
24974	dirMS_041712_NAR_120mM_minus.5202.5202.3	3	3.65	0	5.75E+04		(K)LDFLPDI	(K)L D F L P\D/M/M\V E G/R(L)		81.4	474.8965	1422.676	-0.0006	-0.4	4.03	56130	9.21	HUMAN	E9PC62	CUGBP Elav-like family member 2
24975	dirMS_041712_NAR_120mM_minus.8540.8540.3	3	3.65	1	2.97E+04	M160m S1	(K)VTYmEA	(K)V T Y/m E/A s/A K I R(M)	m:Oxidized methionine s:Ph	101.15	455.5425	1268.667	95.9462	-11	8.56	24423.3	5.74	HUMAN	B7Z5Z2	Ras-related protein R-Ras2
24976	dirMS_041712_NAR_20mM_minus.11667.11667.2	2	3.65	0	1.22E+04	T1437t M1	(K)EVVVtLn	(K)E V|V V/t L m K(K)	t:Phosphorylated T m:Oxidiz	164.05	507.7443	918.533	95.9485	-12.6	6.1	424721.6	6.38	HUMAN	Q709C8	Vacuolar protein sorting-associated protein 13C
24977	dirMS_041712_NAR_30mM_minus2.11423.11423.2	2	3.65	0	5.79E+04		(-)XSAISAD	(-)X/S|A I/S A D/L G R(Q)		115.77	501.7874	1002.558	0.0097	9.7	5.84	10095.1	5.55	HUMAN	H7C4I4	Sugar phosphate exchanger 3 (Fragment)
24978	dirMS_041712_NAR_30mM_minus2.13102.13102.2	2	3.65	0	6.50E+04		(K)ITDFGLS	(K)I/T/D F G\L S K(E)		124.75	440.7465	880.477	0.0083	9.4	5.84	73570.2	8.28	HUMAN	B7Z3B5	Ribosomal protein S6 kinase alpha-2
24979	dirMS_041712_NAR_30mM_minus2.14164.14189.2	2	3.65	0	2.63E+05		(R)ISMLYM	(R)I S M L Y/M/A K(L)		130.72	478.7508	956.494	0	-0.1	8.59	72152.1	5.27	HUMAN	A0MZ66	Shootin-1
24980	dirMS_041712_NAR_30mM_minus2.15621.15621.2	2	3.65	0	1.06E+04		(K)FGFAIGS	(K)F G F A/I|G S Q T T K(K)		137.17	578.811	1156.6	0.015	13	8.75	18924.5	6.86	HUMAN	Q8WW12	PEST proteolytic signal-containing nuclear protein
24981	dirMS_041712_NAR_30mM_minus2.7837.7837.2	2	3.65	0	3.24E+05		(R)ISESAAS	(R)I S\E/S A A S G/A/R(F)		96.1	474.7377	948.475	-0.0064	-6.7	6	102603.5	4.86	HUMAN	Q9Y5F6	Protocadherin gamma-C5
24982	dirMS_041712_NAR_40mM_minus2.15190.15190.3	3	3.65	0	1.34E+05		(R)NEVSFVI	(R)N E|V/S/F V I/H/N L P\V L A K(M)		175.17	560.6529	1679.948	-0.0038	-2.2	6.75	35663.7	5.91	HUMAN	B4DWK0	Selenide, water dikinase 1
24983	dirMS_041712_NAR_40mM_minus2.15850.15850.3	3	3.65	0	3.22E+05		(R)DLLDTVI	(R)D L|L/D T V L/P H L Y N E T K(V)		185.38	590.9795	1770.927	-0.0033	-1.9	4.54	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
24984	dirMS_041712_NAR_40mM_minus2.9905.9905.2	2	3.65	1	5.19E+04		(R)RTPDYFI	(R)R T/P D\Y\F|L(-)		140.98	456.2336	911.462	-0.0022	-2.4	5.83	6212.9	6.77	HUMAN	H0YBN9	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform (Fragment)
24985	dirMS_041712_NAR_50mM_minus2.10270.10270.3	3	3.65	1	2.02E+05	S358s	(K)DLsDLTA	(K)D L/s D L T/A Q A K\S R(D)	s:Phosphorylated S	127.1	462.2268	1304.68	79.9854	13.8	5.96	80823.8	5.78	HUMAN	H0YJE3	Centrosomal protein of 128 kDa (Fragment)
24986	dirMS_041712_NAR_50mM_minus2.12218.12218.3	3	3.65	0	1.53E+05		(R)QVPVST	(R)Q/V/P V S T\T V V\S T S Q A G/K(L)		137.92	530.2953	1588.854	0.0173	10.9	8.75	139455.1	9.44	HUMAN	Q6P4R8	Nuclear factor related to kappa-B-binding protein
24987	dirMS_041712_NAR_50mM_minus2.12990.12990.3	3	3.65	1	1.60E+05		(K)GGELVY	(K)G G E|L V/Y/T D S E A R D V/F E/K(A)		141.68	638.9739	1914.908	-0.0008	-0.4	4.18	533778	5.74	HUMAN	Q15149	Plectin
24988	dirMS_041712_NAR_50mM_minus2.13226.13226.3	3	3.65	2	2.03E+05	S581s	(K)GEAGGF	(K)G E A|G G P P s/T R E/A E L K L R(L)	s:Phosphorylated S	143.65	616.6435	1767.935	79.9812	8	6.23	103225.4	5.81	HUMAN	E9PJP2	Protein SOGA3
24989	dirMS_041712_NAR_60mM_minus.8301.8301.3	3	3.65	0	6.53E+03	S100s	(R)TVDNLLI	(R)T V D\N L L/E\V/s A/R(H)	s:Phosphorylated S	106.3	432.8748	1216.653	79.9567	-7.5	4.37	20289.2	5.07	HUMAN	Q16082	Heat shock protein beta-2
24990	dirMS_041712_NAR_60mM_minus.9435.9435.3	3	3.65	0	1.04E+05	M409m	(K)VLAmSG	(K)V L/A/m S G D|P N/Y L H R(M)	m:Oxidized methionine	112.23	496.9147	1472.732	15.9981	2.1	6.71	57818.1	5.5	HUMAN	E9PH38	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
24991	dirMS_041712_NAR_120mM_plus.21828.21828.3	3	3.65	2	1.65E+05		(R)RLTPTE	(R)R L T P T E\V K D Y\L A\A\I A(-)		167.68	554.3112	1660.927	-0.0078	-4.7	6.07	18720.9	5.74	HUMAN	C9JCK5	Proteasome subunit alpha type-2
24992	dirMS_041712_NAR_120mM_plus.24473.24473.4	4	3.65	2	2.44E+04		(R)IAIYELLF	(R)I/A\I/Y E\L L F/K E G V M V/A K K(D)		184.15	488.7863	1952.129	-0.0055	-2.8	8.43	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
24993	dirMS_041712_NAR_120mM_plus.6071.6071.3	3	3.65	1	3.76E+04		(R)YDSNSG	(R)Y/D|S N S G/G E R E I Q R(T)		85.05	504.2287	1510.688	-0.0165	-10.9	4.68	41280.4	4.9	HUMAN	B4DR63	26S protease regulatory subunit 4
24994	dirMS_041712_NAR_20mM_plus.12758.12758.2	2	3.65	0	1.21E+05	M55m	(R)LLTAAPL	(R)L L/T A A|P/L S m E Q R(R)	m:Oxidized methionine	160.13	673.3693	1329.719	16.0118	12.6	6	62389.8	6.55	HUMAN	O75051-2	Isoform 2 of Plexin-A2
24995	dirMS_041712_NAR_20mM_plus.13604.13604.2	2	3.65	0	1.37E+05		(K)TVTELGI	(K)T/V\T E L G N Q/L E G K(W)		165.9	644.8389	1288.674	-0.0038	-2.9	4.53	73350	6.3	HUMAN	B4DXA9	Zinc finger protein 398
24996	dirMS_041712_NAR_20mM_plus.17177.17177.2	2	3.65	0	1.09E+05		(K)FATEAAI	(K)F A/T\E/A A/I T I L R(I)		189.05	603.3442	1205.689	-0.0077	-6.4	6	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
24997	dirMS_041712_NAR_20mM_plus.9561.9561.2	2	3.65	0	1.69E+04		(K)TIAPALV	(K)T I|A/P A L/V S K(K)		137.23	450.2814	899.556	-0.0005	-0.6	8.41	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
24998	dirMS_041712_NAR_30mM_plus2.14854.14889.2	2	3.65	0	6.47E+05		(-)MTLDDF	(-)M/T|L/D D/F R(I)		130.87	449.2114	897.414	0.002	2.3	4.21	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
24999	dirMS_041712_NAR_30mM_plus2.15735.15735.2	2	3.65	0	3.97E+05		(R)NILFGA	(R)N I/L/F G/A V R(G)		134.25	445.2649	889.525	-0.0029	-3.2	9.75	22103.9	9.92	HUMAN	C9JSU7	STE20-related kinase adapter protein beta (Fragment)
25000	dirMS_041712_NAR_30mM_plus2.4079.4079.2	2	3.65	0	8.97E+05	T860t	(K)TDQQGI	(K)T/D Q Q G/D t|P R(Q)	t:Phosphorylated T	68.33	549.2125	1017.46	79.9581	-7.5	4.21	102170	8.79	HUMAN	A8MVN1	Diacylglycerol kinase zeta
25001	dirMS_041712_NAR_40mM_plus2.16022.16022.3	3	3.65	2	1.82E+05	N647n	(K)QRLVVL	(K)Q R L/V/V/L/V/K D n G E P P R(S)	n:N-acetylglucosamine (N)	161.12	641.701	1719.986	203.102	11.8	8.75	85381.1	5	HUMAN	Q9NRJ7	Protocadherin beta-16
25002	dirMS_041712_NAR_40mM_plus2.6113.6113.2	2	3.65	0	5.46E+04		(K)EAVYSDI	(K)E A/V Y/S D K(L)		94.97	406.1921	811.383	-0.0063	-7.8	4.37	61685.6	7.77	HUMAN	B3KTB2	Ephrin type-B receptor 1
25003	dirMS_041712_NAR_40mM_plus2.6692.6692.2	2	3.65	0	8.62E+04	M189m	(K)LTGmAF	(K)L T|G m A F R(V)	m:Oxidized methionine	99.75	406.2085	795.418	15.9916	-4.1	9.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
25004	dirMS_041712_NAR_50mM_plus2.11905.11905.3	3	3.65	1	4.38E+05	M327m	(R)VAGGPC	(R)V/A/G\G P Q m I Q L/S L D G K R(L)	m:Oxidized methionine	131	562.6377	1669.905	15.9931	-1	8.72	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
25005	dirMS_041712_NAR_50mM_plus2.8085.8085.3	3	3.65	1	2.94E+04		(-)MEMGK	(-)M E/M G K W I/H L/E L/R(N)		109.3	514.9321	1542.792	-0.0102	-6.6	6.51	14919.8	4.98	HUMAN	O95626	Acidic leucine-rich nuclear phosphoprotein 32 family member D
25006	dirMS_041712_NAR_60mM_plus.14160.14160.3	3	3.65	1	7.89E+05		(K)WKDSDE	(K)W K D S D\E|A|D\L V/L A K(E)		130.77	497.2559	1489.753	-0.0002	-0.1	4.23	20982.2	5.23	HUMAN	Q13185	Chromobox protein homolog 3
25007	dirMS_041712_NAR_60mM_plus.18027.18027.3	3	3.65	0	2.19E+04		(K)ACQSIYF	(K)A C/Q S I/Y P L H D V F V R(K)	C:Carbamidomethylation	152.08	568.9563	1704.853	0.0017	1	6.79	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
25008	dirMS_041712_NAR_60mM_plus.19305.19305.3	3	3.65	1	4.76E+05		(K)WNLDEL	(K)W/N/L D E L/P K F E K(N)		158.7	473.5847	1418.731	0.0081	5.7	4.68	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
25009	dirMS_041712_NAR_120mM_minus.7059.7059.4	4	3.64	2	1.75E+05		(K)KDPPSA	(K)K\D P P/S\A A L\S G E G A T P\R K(E)		92.37	421.2327	1681.887	0.0222	13.2	8.59	92840.4	6.73	HUMAN	B4DI49	Period circadian protein homolog 1
25010	dirMS_041712_NAR_30mM_minus2.16517.16517.2	2	3.64	0	4.08E+05		(R)DFFLAN	(R)D F/F|L A N A S R(A)		142.48	520.763	1040.516	0.0028	2.6	5.84	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
25011	dirMS_041712_NAR_30mM_minus2.6921.6921.2	2	3.64	0	2.07E+05	K462k	(R)VTCkEEI	(R)V/T|C k/E E K(V)	C:Carbamidomethylation k:Ubiq	91.93	504.238	893.44	114.029	-13.8	6.11	98062.5	5.57	HUMAN	B4E2Z2	DNA mismatch repair protein Msh2
25012	dirMS_041712_NAR_50mM_minus2.10649.10649.3	3	3.64	0	7.88E+04		(R)ITNAQN	(R)I T/N A Q/N I T/V/I V Q K(M)		128.58	481.2838	1441.837	-0.0005	-0.3	8.75	120678.4	5.56	HUMAN	H0YKX4	AP-4 complex subunit epsilon-1
25013	dirMS_041712_NAR_50mM_minus2.13626.13626.3	3	3.64	0	3.00E+04		(K)TGEEIFG	(K)T/G E E/I/F G T I/G M R P N A K(N)		146.93	574.2947	1720.869	0.0009	0.5	5.81	38222.2	5.77	HUMAN	E9PKG1	Protein arginine N-methyltransferase 1
25014	dirMS_041712_NAR_50mM_minus2.15281.15281.3	3	3.64	0	4.23E+05	M118m	(R)AGKPVI	(R)A G K P V I\C A T Q/M/L/E S m I K(K)	C:Carbamidomethylation m:Oxid	155.28	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
25015	dirMS_041712_NAR_50mM_minus2.16154.16154.3	3	3.64	1	5.46E+05	Y29y	(K)AGVIySG	(K)A G V/I y/S G R|K A Q E H G T G R(T)	y:Phosphorylated Y	159.35	622.978	1786.931	79.9887	12	9.99	10147.3	10.94	HUMAN	F5H4J8	Serine/threonine-protein kinase MARK2 (Fragment)
25016	dirMS_041712_NAR_50mM_minus2.7674.7674.3	3	3.64	1	3.75E+04		(K)NSDEAD	(K)N S/D E A D L V/P A K E A N V K(C)		110.73	567.289	1699.85	0.0027	1.6	4.32	19439.5	4.97	HUMAN	B5MD17	Chromobox protein homolog 1 (Fragment)
25017	dirMS_041712_NAR_60mM_minus.13050.13050.3	3	3.64	1	5.71E+04	S214s	(R)LLDQLsF	(R)L L/D Q L s R A/S E\V E R(Q)	s:N-acetylglucosamine (S)	133.1	573.6304	1515.813	203.0641	-8.9	4.68	65296	4.93	HUMAN	Q6ZP65	Bicaudal D-related protein 1
25018	dirMS_041712_NAR_60mM_minus.18203.18203.3	3	3.64	1	1.21E+05		(R)QQQYKF	(R)Q Q Q Y\K F\L/P/S E L R(D)		162.82	512.9419	1536.817	-0.0058	-3.7	8.59	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
25019	dirMS_041712_NAR_60mM_minus.19160.19160.3	3	3.64	1	7.64E+05		(R)LDLAGR	(R)L D|L A G R\D L T D/Y L M K(I)		168.88	541.9507	1623.841	-0.0035	-2.2	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
25020	dirMS_041712_NAR_120mM_plus.6631.6653.2	2	3.64	0	2.24E+05		(K)MYEEHL	(K)M/Y/E E H L K(R)		88.32	475.2263	949.445	0.0005	0.6	5.38	8374.4	4.57	HUMAN	G3V279	Enhancer of rudimentary homolog
25021	dirMS_041712_NAR_120mM_plus.7560.7560.2	2	3.64	1	1.19E+06		(R)AQYDEL	(R)A Q|Y|D/E L A R K(N)		93.32	547.2874	1093.564	0.0039	3.5	6.11	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
25022	dirMS_041712_NAR_20mM_plus.13194.13194.2	2	3.64	0	2.58E+05	M148m	(R)DLTDYL	(R)D L|T/D Y/L/m K(I)	m:Oxidized methionine	164.18	507.7439	998.486	15.9942	-0.7	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
25023	dirMS_041712_NAR_20mM_plus.14452.14452.2	2	3.64	1	6.84E+04	M1250m K	(R)VEQmTF	(R)V E Q/m/T R A k A N/A E K(L)	m:Oxidized methionine k:Ub	171.18	803.415	1475.764	130.0592	13.3	8.56	226041.3	5.67	HUMAN	Q9Y2K3	Myosin-15
25024	dirMS_041712_NAR_20mM_plus.14555.14555.2	2	3.64	0	2.24E+05		(K)AEVILGS	(K)A E V I/L G S/I I K(K)		172.28	521.8283	1042.651	-0.0013	-1.3	6.05	43759.5	9.53	HUMAN	B7Z8E5	Voltage-gated potassium channel subunit beta-1
25025	dirMS_041712_NAR_20mM_plus.14748.14748.3	3	3.64	0	1.11E+05	T148t M15	(R)ItITGmY	(R)I t I T G|m/Y A A G K(A)	t:N-acetylglucosamine (T) m:	172.75	448.8957	1125.597	219.0753	0.7	8.59	54725.6	9.21	HUMAN	B4DKL4	Lipolysis-stimulated lipoprotein receptor
25026	dirMS_041712_NAR_20mM_plus.7068.7068.2	2	3.64	1	1.24E+05	S41s	(K)ETSsVKR	(K)E T/S|s V K/R(N)	s:Phosphorylated S	116.03	443.7115	806.437	79.9791	14.4	8.85	20471.3	4.53	HUMAN	Q8TCZ2-3	Isoform 3 of CD99 antigen-like protein 2
25027	dirMS_041712_NAR_30mM_plus2.21052.21052.2	2	3.64	0	2.22E+05		(R)GVVQEL	(R)G V V|Q/E L Q Q/A I S/K(L)		165.42	650.3632	1299.727	-0.0076	-5.8	6	22489.6	5.38	HUMAN	E9PI39	Elongation factor 1-delta (Fragment)
25028	dirMS_041712_NAR_30mM_plus2.4083.4083.2	2	3.64	0	9.13E+05	M299m M	(K)NmmAA	(K)N m|m A A C D/P R(H)	C:Carbamidomethylation m:Oxid	68.37	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
25029	dirMS_041712_NAR_40mM_plus2.12788.12788.2	2	3.64	0	2.97E+04		(R)FGLNVS	(R)F G L/N\V/S\S I/S R(K)		141.92	540.2954	1079.584	-0.0009	-0.8	9.75	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
25030	dirMS_041712_NAR_50mM_plus2.16229.16229.3	3	3.64	0	2.89E+05		(K)ACQSIYF	(K)A C|Q/S I/Y/P/L H D V F V R(K)	C:Carbamidomethylation	154.4	568.9562	1704.853	0.0014	0.8	6.79	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
25031	dirMS_041712_NAR_50mM_plus2.5366.5366.3	3	3.64	1	1.12E+04		(R)GLPAPG	(R)G L P\A/P G P S P A D K K(R)		88.47	412.2315	1234.679	0.0009	0.8	8.59	53139.8	6.18	HUMAN	P42768	Wiskott-Aldrich syndrome protein
25032	dirMS_041712_NAR_50mM_plus2.7487.7487.3	3	3.64	1	4.97E+04		(K)VQSLEG	(K)V/Q|S L E/G E K L S/P K(S)		105.45	438.9176	1314.726	0.0119	9	6.11	271827.6	4.73	HUMAN	P46821	Microtubule-associated protein 1B
25033	dirMS_041712_NAR_60mM_plus.10054.10054.3	3	3.64	0	1.94E+06		(K)TPVEPE	(K)T P V E P E V/A I H R(I)		109.87	416.5628	1247.674	-0.0004	-0.3	5.37	5429.1	9.6	HUMAN	E5RIP1	40S ribosomal protein S20
25034	dirMS_041712_NAR_60mM_plus.11285.11285.2	2	3.64	0	2.12E+06		(K)GIVEFAS	(K)G I/V|E/F/A S K/P A A R(K)		116.18	623.3504	1245.695	-0.0015	-1.2	8.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
25035	dirMS_041712_NAR_60mM_plus.7248.7248.3	3	3.64	0	2.03E+05	K133k	(K)DkMSQI	(K)D k/M S Q/M A/S V/P/E R(E)	k:Ubiquitin-K	96.03	498.2381	1378.645	114.0544	7.7	6.07	41588.3	4.97	HUMAN	Q53QW1	Uncharacterized protein C2orf57
25036	dirMS_041712_NAR_120mM_minus.12254.12254.2	2	3.63	0	9.16E+04		(K)HLSVND	(K)H/L|S V N/D|L P V G R(S)		120.85	603.8309	1206.659	-0.0044	-3.7	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
25037	dirMS_041712_NAR_120mM_minus.16871.16871.3	3	3.63	0	4.35E+05		(K)HLEINPD	(K)H/L\E/I N P\D H/S/I/I E T L/R(Q)		146.67	596.3176	1786.945	-0.0064	-3.6	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
25038	dirMS_041712_NAR_120mM_minus.6164.6164.3	3	3.63	0	1.54E+05		(K)IAGHPL	(K)I/A/G H/P L\A Q N E R(C)		87.88	402.5466	1205.639	-0.0133	-11	6.75	18455.6	6.76	HUMAN	F8W8K5	Sorting nexin-12
25039	dirMS_041712_NAR_20mM_minus.11153.11153.2	2	3.63	0	1.10E+05	M316m	(R)ISEQFTA	(R)I/S E Q|F T/A m F R(R)	m:Oxidized methionine	159.05	623.3005	1229.598	15.9954	0.4	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
25040	dirMS_041712_NAR_20mM_minus.7283.7283.2	2	3.63	0	1.32E+05	M374m	(R)mAPTPII	(R)m|A|P T/P I P T R(S)	m:Oxidized methionine	121.02	500.2679	983.534	15.9943	-0.7	9.5	76925.9	4.46	HUMAN	A8MV58	Drebrin
25041	dirMS_041712_NAR_20mM_minus.8419.8419.2	2	3.63	0	1.07E+05		(K)VTADVII	(K)V T|A D|V/I N A/A E K(L)		132.58	565.8065	1130.605	0.0005	0.5	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
25042	dirMS_041712_NAR_30mM_minus2.11761.11761.2	2	3.63	0	5.66E+05		(R)NLQDAI	(R)N L/Q/D A/M/Q V C/R(N)	C:Carbamidomethylation	117.25	617.7907	1234.567	0.0074	6	5.84	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
25043	dirMS_041712_NAR_30mM_minus2.14484.14484.2	2	3.63	1	1.61E+05	M308m	(K)LmKEISS	(K)L m K E I S/S/T/K(K)	m:Oxidized methionine	132.15	526.7803	1036.571	15.9826	-11.7	8.59	68675.9	8.39	HUMAN	O00186	Syntaxin-binding protein 3
25044	dirMS_041712_NAR_30mM_minus2.17926.17926.3	3	3.63	0	6.94E+04	S393s	(K)LQNQPC	(K)L Q N\Q P G/s G P/T I R(K)	s:N-acetylglucosamine (S)	152.48	490.9238	1267.675	203.0815	1.5	9.75	45370.5	4.75	HUMAN	Q92783-2	Isoform 2 of Signal transducing adapter molecule 1
25045	dirMS_041712_NAR_30mM_minus2.7555.7555.2	2	3.63	0	2.90E+05		(K)AEYLCR	(K)A E/Y/L|C/R(I)	C:Carbamidomethylation	95.65	406.1957	811.377	0.0074	9.1	6.04	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
25046	dirMS_041712_NAR_30mM_minus2.9262.9262.2	2	3.63	1	2.07E+05		(K)VINVETI	(K)V I/N/V E T N R G(-)		106.03	501.2667	1001.537	-0.0113	-11.3	5.97	15548.7	9.16	HUMAN	H0Y8N5	Peptidylprolyl isomerase domain and WD repeat-containing protein 1 (Fragment)
25047	dirMS_041712_NAR_40mM_minus2.13236.13236.3	3	3.63	2	1.24E+05	N647n	(K)QRLVVL	(K)Q R L|V\V L/V K D n G E/P P\R(S)	n:N-acetylglucosamine (N)	161.83	641.7007	1719.986	203.1011	11.3	8.75	85381.1	5	HUMAN	Q9NRJ7	Protocadherin beta-16
25048	dirMS_041712_NAR_50mM_minus2.11669.11669.3	3	3.63	1	2.41E+04		(R)ESDVPLI	(R)E S D V/P L K\T E\E F/E V/T K(T)		133.62	584.3049	1750.874	0.0256	14.6	4.25	18909	6.21	HUMAN	Q969H8	UPF0556 protein C19orf10
25049	dirMS_041712_NAR_50mM_minus2.13344.13344.3	3	3.63	1	1.09E+05		(K)LSTVKTI	(K)L S/T V K T M S E G T/L\A K(C)		143.48	489.2711	1465.793	0.0057	3.9	8.59	95116.5	7.83	HUMAN	E9PAJ6	Probable ribonuclease ZC3H12B
25050	dirMS_041712_NAR_50mM_minus2.17924.17924.3	3	3.63	0	2.16E+05		(R)LGFHLPI	(R)L G F H L P L E|V/A/Y/Q R(G)		170.27	514.953	1542.843	0.0017	1.1	6.75	533778	5.74	HUMAN	Q15149	Plectin
25051	dirMS_041712_NAR_50mM_minus2.5445.5638.3	3	3.63	0	5.21E+06	M522m T5	(K)VADmts	(K)V A D\m/t s V L D P N K(M)	m:Oxidized methionine t:Ph	91.68	489.1898	1289.641	175.9143	-9.1	4.21	279771.8	9.54	HUMAN	Q8NDH2	Coiled-coil domain-containing protein 168
25052	dirMS_041712_NAR_50mM_minus2.9962.9962.3	3	3.63	0	1.54E+05	M392m	(K)EmNPAL	(K)E m N/P A/L G I D C L H K(G)	C:Carbamidomethylation m:Oxid	125.47	505.2416	1497.719	15.9914	-2.3	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
25053	dirMS_041712_NAR_60mM_minus.11127.11127.3	3	3.63	1	7.95E+05		(K)IDFLTKQ	(K)I D/F L T K/Q/M/E K(I)		122.48	418.226	1252.661	0.0029	2.3	6.07	9535	8.01	HUMAN	H3BMQ1	Prefoldin subunit 5
25054	dirMS_041712_NAR_60mM_minus.11763.11763.3	3	3.63	0	2.42E+05	M42m	(K)GVGISVI	(K)G V/G I S V L/E m S/H R(S)	m:Oxidized methionine	125.82	434.2267	1284.673	15.9927	-1.7	6.75	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
25055	dirMS_041712_NAR_120mM_plus.5148.5148.3	3	3.63	1	3.12E+05	M163m	(K)IYEDGDI	(K)I/Y/E D G/D D D m K R(T)	m:Oxidized methionine	79.73	458.195	1356.574	15.9968	1.4	4.03	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
25056	dirMS_041712_NAR_20mM_plus.10171.10171.2	2	3.63	0	1.47E+05		(K)GEATVSI	(K)G E\A\T|V/S/F D D/P P S A K(A)		142.15	710.8324	1420.659	-0.0015	-1.1	4.03	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
25057	dirMS_041712_NAR_20mM_plus.11346.11346.2	2	3.63	0	5.10E+03		(R)TSGSVYI	(R)T/S|G S/V/Y I T L K(K)		150.4	534.8004	1068.594	0	0	8.26	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
25058	dirMS_041712_NAR_20mM_plus.14027.14027.2	2	3.63	0	1.34E+05		(R)GGIVDE	(R)G G I\V/D E G/A/L/L/R(A)		167.83	550.3066	1099.611	-0.0047	-4.3	4.37	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
25059	dirMS_041712_NAR_20mM_plus.16421.16421.3	3	3.63	0	5.15E+04	M178m	(R)LmTDTII	(R)L m T D T I\N E|P/I/L L C R(F)	C:Carbamidomethylation m:Oxid	184.57	568.9602	1688.871	15.9951	0.1	4.37	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
25060	dirMS_041712_NAR_20mM_plus.16916.16916.2	2	3.63	0	1.07E+05		(R)ELLIIGG	(R)E L L I/I/G/G V A A R(D)		187.43	556.3437	1111.683	-0.0032	-2.9	6.1	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
25061	dirMS_041712_NAR_20mM_plus.6796.6796.2	2	3.63	0	4.30E+05	M132m	(R)DmVGIA	(R)D m V/G/I|A/Q T/G S G K(T)	m:Oxidized methionine	112.67	590.2864	1163.573	15.993	-1.6	5.84	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
25062	dirMS_041712_NAR_30mM_plus2.21063.21063.2	2	3.63	0	1.64E+05		(R)QTLMW	(R)Q T/L/M/W/S A T W P K(E)		165.23	674.8389	1348.672	-0.0013	-1	8.75	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
25063	dirMS_041712_NAR_30mM_plus2.5830.5830.2	2	3.63	0	2.44E+04		(R)SAENPP	(R)S A\E\N/P|P S G S V\R(K)		84.53	550.7692	1100.533	-0.002	-1.8	5.72	32364.3	9.76	HUMAN	Q15014	Mortality factor 4-like protein 2
25064	dirMS_041712_NAR_30mM_plus2.8141.8141.2	2	3.63	0	4.69E+05		(R)FAQIVQ	(R)F/A/Q\I V/Q K(G)		97.13	417.2466	833.488	-0.002	-2.4	8.75	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
25065	dirMS_041712_NAR_40mM_plus2.13640.13640.3	3	3.63	1	1.31E+04		(K)DMELPT	(K)D M/E\L/P T/E K E V A L V K(D)		146.4	534.6192	1601.845	-0.0024	-1.5	4.41	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein

25066	dirMS_041712_NAR_40mM_plus2.9736.9736.2	2	3.63	0	1.65E+05		(R)RPCTLSE	(R)R P C T L\S\E|L/E(-)	C:Carbamidomethylation	120.03	552.7699	1104.535	-0.0029	-2.6	4.85	61333.4	5.7	HUMAN	P13674	Prolyl 4-hydroxylase subunit alpha-1
25067	dirMS_041712_NAR_50mM_plus2.11365.11365.3	3	3.63	1	2.80E+06	M72m	(R)TEmENE	(R)T E/m E N E/F/V L\I/K K(D)	m:Oxidized methionine	127.98	499.5943	1480.772	15.9968	1.2	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
25068	dirMS_041712_NAR_50mM_plus2.19677.19677.3	3	3.63	1	1.38E+05		(R)VAAKLE	(R)V A A K L E V A/P I|S/D I I A I K(S)		171.43	584.3568	1751.068	-0.0119	-6.8	6.04	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
25069	dirMS_041712_NAR_50mM_plus2.21267.21267.3	3	3.63	1	5.65E+05	M145m	(R)GVmLA	(R)G V/m L/A V D A V/I/A/E L K K(Q)	m:Oxidized methionine	181.98	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
25070	dirMS_041712_NAR_50mM_plus2.6549.6549.3	3	3.63	0	3.80E+05	S76s	(R)IsELGAG	(R)I/s/E L G A G N G G V V/T K(V)	s:N-acetylglucosamine (S)	100.3	502.2651	1301.706	203.0748	-3	6	44708.6	6.12	HUMAN	P36507	Dual specificity mitogen-activated protein kinase kinase 2
25071	dirMS_041712_NAR_50mM_plus2.7170.7170.3	3	3.63	1	7.50E+04		(K)DISTNYY	(K)D I|S T/N Y/Y A/S Q K K(T)		103.52	473.2382	1417.696	0.0043	3	8.43	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
25072	dirMS_041712_NAR_50mM_plus2.8765.8765.3	3	3.63	0	2.01E+05		(K)VVQVSA	(K)V V/Q V/S A/G D S/H T A A L T D D G R(V)		113.43	633.6509	1898.92	0.0179	9.4	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
25073	dirMS_041712_NAR_60mM_plus.20018.20018.3	3	3.63	0	1.60E+05		(K)LILPHVD	(K)L I/L/P/H V D I Q L K(Y)		164.48	430.2695	1288.799	-0.0048	-3.7	6.74	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
25074	dirMS_041712_NAR_60mM_plus.5592.5592.2	2	3.63	0	4.83E+04		(K)ADSQLQ	(K)A D S/Q L Q/P H G G D L T K(A)		87.62	733.8625	1466.723	-0.0057	-3.9	5.21	134614.7	8.76	HUMAN	P51826	AF4/FMR2 family member 3
25075	dirMS_041712_NAR_60mM_plus.7388.7388.3	3	3.63	1	1.93E+06		(R)SEEKISD	(R)S/E\E K I/S D S E G F/K(A)		96.8	452.5501	1355.632	0.0032	2.4	4.41	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
25076	dirMS_041712_NAR_120mM_minus.10389.10389.3	3	3.62	1	6.08E+05	M142m	(K)VKEGMN	(K)V K E G M N\I|V/E/A m E R(F)	m:Oxidized methionine	110.1	507.9186	1505.745	15.9962	0.8	4.79	18240.4	7.96	HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
25077	dirMS_041712_NAR_120mM_minus.11291.11291.3	3	3.62	2	2.09E+04		(K)FSCAFRE	(K)F S C A F/R|E K A K(E)	C:Carbamidomethylation	116.38	415.2091	1243.625	-0.0125	-10	9.99	139212.9	7.06	HUMAN	E2QRD4	Protein MMS22-like
25078	dirMS_041712_NAR_120mM_minus.8481.8481.2	2	3.62	0	2.25E+05		(R)HSVGVV	(R)H/S/V/G V\V I G R(S)		100.23	462.2742	923.542	-0.001	-1.1	9.75	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
25079	dirMS_041712_NAR_20mM_minus.8417.8417.2	2	3.62	0	1.10E+05		(R)GYSFTTT	(R)G Y/S\F/T T T A E R(E)		133.33	566.771	1132.527	0.0078	6.9	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
25080	dirMS_041712_NAR_30mM_minus2.16058.16058.2	2	3.62	1	1.07E+05	M89m	(K)AFSIGKn	(K)A F|S I G K m S T\A K(R)	m:Oxidized methionine	141.43	578.811	1140.608	16.0066	10.1	10	17799.4	9.3	HUMAN	C9J5L1	U2 snRNP-associated SURP motif-containing protein (Fragment)
25081	dirMS_041712_NAR_30mM_minus2.16370.16370.2	2	3.62	0	1.35E+05		(K)STFVNIL	(K)S T|F V/N I L K(Q)		142.7	461.2712	921.54	-0.0053	-5.7	8.47	23232.7	5.07	HUMAN	D6RCP9	Deoxycytidine kinase
25082	dirMS_041712_NAR_30mM_minus2.7084.7084.2	2	3.62	0	1.24E+05		(K)CATITPD	(K)C A/T\I/T/P D/E K(R)	C:Carbamidomethylation	93.68	517.7448	1034.482	0	0	4.37	17833.3	8.73	HUMAN	C9J4N6	Isocitrate dehydrogenase [NADP] cytoplasmic (Fragment)
25083	dirMS_041712_NAR_30mM_minus2.7831.7831.2	2	3.62	0	5.43E+05		(R)AAMGP	(R)A A/M|G/P G I S/R(M)		96.53	430.2325	859.445	0.0123	14.3	9.79	22167.3	10.15	HUMAN	E7ENQ8	Phosphoglucomutase-2
25084	dirMS_041712_NAR_30mM_minus2.9943.9943.2	2	3.62	1	6.63E+05	K137k	(K)TSNNGG	(K)T S N N/G G G L G K k(M)	k:Ubiquitin-K	107.68	573.7932	1032.543	114.0359	-6.2	10	50196.6	5.04	HUMAN	F8WAA1	SAM domain-containing protein SAMSN-1
25085	dirMS_041712_NAR_40mM_minus2.12681.12681.3	3	3.62	0	2.55E+03	K614k	(K)ETLPISST	(K)E/T/L/P I S S T P S\k/S V L P R(T)	k:Ubiquitin-K	157.08	609.3307	1711.959	114.0187	-13.3	8.85	84737.7	8.33	HUMAN	Q08050	Forkhead box protein M1
25086	dirMS_041712_NAR_50mM_minus2.11682.11682.3	3	3.62	0	1.03E+05		(K)AQIHDL	(K)A Q I H D L V\L/V G G S T R(I)		134.6	489.2711	1465.812	-0.0134	-9.1	6.79	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
25087	dirMS_041712_NAR_50mM_minus2.16173.16173.3	3	3.62	1	1.58E+05		(K)ISMPEVI	(K)I/S/M P/E V D/L/N L\K G P K(M)		160.03	514.2852	1540.84	0.0007	0.5	6.07	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
25088	dirMS_041712_NAR_60mM_minus.17661.17661.3	3	3.62	0	1.17E+05		(R)GGHVVE	(R)G G H V V\E G\L\A|G/E/L\E/Q L R(A)		158.32	555.2959	1663.876	-0.0031	-1.8	4.75	106088.3	5.78	HUMAN	P10275	Androgen receptor
25089	dirMS_041712_NAR_60mM_minus.17765.17765.3	3	3.62	1	3.73E+05		(K)YGKLEV	(K)Y G K L E V|A N|L\L L Q K(S)		159.58	496.9631	1488.878	-0.0037	-2.5	8.5	482683.6	6.07	HUMAN	Q12955	Ankyrin-3
25090	dirMS_041712_NAR_60mM_minus.17841.17841.3	3	3.62	1	2.05E+05	M148m	(R)LDLAGR	(R)L/D|L/A G R D L T D Y/L m K(I)	m:Oxidized methionine	159.53	547.2829	1623.841	15.9931	-1.1	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
25091	dirMS_041712_NAR_60mM_minus.18626.18626.3	3	3.62	0	1.40E+04		(R)SLLAAA	(R)S L L/A/A A P G P/T G A Q L N S R(Q)		166.75	541.9639	1623.881	-0.0041	-2.6	9.47	27747.5	12.09	HUMAN	Q8N5S0	Hypothetical gene supported by BC031673
25092	dirMS_041712_NAR_60mM_minus.9477.9477.3	3	3.62	1	8.00E+04		(R)NVMEE	(R)N V/M E E G K D/F Q/P S R(S)		112.28	512.9085	1536.711	-0.0002	-0.1	4.68	99900.1	5.04	HUMAN	B4DZI8	Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b
25093	dirMS_041712_NAR_120mM_plus.10083.10083.4	4	3.62	0	9.82E+05		(K)NLPLAD	(K)N L/P L A D Q G S S H H I T V K(I)		106.7	429.9809	1716.903	-0.001	-0.6	6.92	334221.3	6.44	HUMAN	P15924	Desmoplakin
25094	dirMS_041712_NAR_20mM_plus.19229.19229.2	2	3.62	0	8.69E+04		(R)ASVILAG	(R)A S V I|L/A/G L G F T P K(M)		204.32	637.3763	1273.751	-0.0061	-4.8	8.8	80142.6	5.95	HUMAN	Q9NUQ8	ATP-binding cassette sub-family F member 3
25095	dirMS_041712_NAR_20mM_plus.5851.5851.2	2	3.62	0	7.42E+04	M283m	(R)DYDDm	(R)D Y|D/D m S P R(R)	m:Oxidized methionine	97.63	507.6952	998.388	15.9947	-0.2	3.93	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
25096	dirMS_041712_NAR_20mM_plus.7007.7007.2	2	3.62	0	1.45E+05	M35m	(R)VEFmD	(R)V E|F/m D D T S R(S)	m:Oxidized methionine	115.45	558.2383	1099.473	15.9969	1.8	4.03	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
25097	dirMS_041712_NAR_20mM_plus.8226.8226.3	3	3.62	0	2.30E+05	M346m M3	(K)mGGmE	(K)m G G m E/G P/F/G/G/G m E N m G R(F)	m:Oxidized methionine	126.3	593.558	1714.68	63.979	-0.4	4.53	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
25098	dirMS_041712_NAR_30mM_plus2.11394.11394.3	3	3.62	0	4.09E+05	M304m	(R)MGQM	(R)M G Q M A M G/G A/m/G I/N N R(G)	m:Oxidized methionine	113.05	518.8921	1538.67	15.9923	-1.7	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
25099	dirMS_041712_NAR_40mM_plus2.5654.5654.2	2	3.62	0	1.12E+05		(R)FSSSSGY	(R)F/S S S/S/G Y G G G S S R(V)		90.98	618.2686	1235.529	0.0012	1	8.75	62291.5	5.13	HUMAN	P35527	Keratin, type I cytoskeletal 9
25100	dirMS_041712_NAR_40mM_plus2.5693.5693.2	2	3.62	0	1.19E+05		(R)NQGGY	(R)N Q/G G/Y G G S S S S S/S Y\G S G R(R)		90.62	847.8525	1694.7	-0.0024	-1.4	8.59	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
25101	dirMS_041712_NAR_40mM_plus2.6361.6361.2	2	3.62	0	1.57E+05		(K)SLESINSI	(K)S L|E/S I/N S R(L)		96.65	453.2358	905.469	-0.0044	-4.8	5.72	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
25102	dirMS_041712_NAR_50mM_plus2.12183.12183.3	3	3.62	1	4.14E+05		(K)LSAEKVE	(K)L S/A E/K V E I\A T/L T R(E)		132.12	477.6113	1430.821	-0.002	-1.4	6.14	26661.1	7.81	HUMAN	H0YL69	Proteasome subunit alpha type (Fragment)
25103	dirMS_041712_NAR_50mM_plus2.15236.15236.3	3	3.62	1	2.05E+05		(R)QVFGEA	(R)Q V/F G E A T K Q/P G I T F I A A K(F)		147.35	636.0141	1906.043	-0.0155	-8.1	8.59	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
25104	dirMS_041712_NAR_50mM_plus2.16244.16244.3	3	3.62	1	5.06E+04		(R)FKAHPD	(R)F K A/H P D Q L V L I F A G K(I)		154.05	561.9883	1683.958	-0.0077	-4.6	8.6	24188.4	6.44	HUMAN	C9IYQ4	Ubiquilin-3 (Fragment)
25105	dirMS_041712_NAR_50mM_plus2.8342.8342.3	3	3.62	0	9.46E+04		(K)ATAGDT	(K)A T|A G D T H L G G E/D/F D N R(L)		110.23	559.2487	1675.731	0.0009	0.5	4.22	58502.6	6.09	HUMAN	B4DXY3	Heat shock 70 kDa protein 1-like
25106	dirMS_041712_NAR_60mM_plus.17447.17447.3	3	3.62	1	8.46E+05		(R)DKLNNL	(R)D K L N\N\L|V/L/F/D K(A)		148.4	440.2499	1318.737	-0.0014	-1	5.96	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
25107	dirMS_041712_NAR_60mM_plus.5580.5580.3	3	3.62	1	1.74E+04		(R)YYGGGS	(R)Y Y/G/G G S E G G R A P K(R)		86.15	433.5425	1298.612	0.0006	0.4	8.5	64759.2	8.88	HUMAN	P14866	Heterogeneous nuclear ribonucleoprotein L
25108	dirMS_041712_NAR_60mM_plus.9790.9790.3	3	3.62	1	7.09E+05		(R)TPGKEA	(R)T P G K E A V/A|M/E/S Y A K(A)		109.58	494.5808	1481.73	-0.0026	-1.8	5.81	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
25109	dirMS_041712_NAR_120mM_minus.18260.18260.4	4	3.61	1	3.15E+05		(K)ILGSGIS	(K)I L G S/G\I\S/S S S V L/H G M V F K K(E)		154.12	487.5223	1947.073	-0.0058	-3	10	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
25110	dirMS_041712_NAR_120mM_minus.7066.7066.2	2	3.61	0	4.18E+05		(K)HNAAFC	(K)H/N|A A/F\C/Y K(L)	C:Carbamidomethylation	92.42	505.7282	1010.451	-0.0021	-2.1	8.6	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
25111	dirMS_041712_NAR_20mM_minus.10370.10370.2	2	3.61	1	1.34E+04		(R)DPHTLR	(R)D P/H T\L R A H E R(L)		152.57	616.3225	1231.629	0.0087	7	6.92	80206.2	6.91	HUMAN	Q9H9D4	Zinc finger protein 408
25112	dirMS_041712_NAR_20mM_minus.14530.14530.2	2	3.61	1	7.32E+04		(K)EILKIDG	(K)E I L\K|I/D G S N T V D|H K(N)		199.67	784.9166	1568.828	-0.0019	-1.2	5.38	131273.2	8.93	HUMAN	H7C5E4	5'-3' exoribonuclease 1 (Fragment)
25113	dirMS_041712_NAR_30mM_minus2.16183.16183.2	2	3.61	0	1.14E+05		(R)GLGLDD	(R)G L/G\L D/D/A L E/P R(Q)		142.1	578.299	1155.6	-0.0097	-8.4	4.03	51326.8	5.49	HUMAN	Q9Y230	RuvB-like 2
25114	dirMS_041712_NAR_30mM_minus2.16797.16797.2	2	3.61	0	1.92E+04		(K)FANPFP	(K)F A|N\P/F/P A A\V R(G)		144.35	545.2937	1089.584	-0.0039	-3.5	9.75	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
25115	dirMS_041712_NAR_30mM_minus2.6487.6487.2	2	3.61	0	6.49E+04		(R)EGGAEE	(R)E G G\A/E/E S\A I/R(V)		89.65	509.7452	1018.48	0.0031	3.1	4.25	108105.4	6.57	HUMAN	E7EP00	Protein transport protein Sec24C
25116	dirMS_041712_NAR_30mM_minus2.6795.6795.2	2	3.61	0	6.28E+05		(K)EIEVGG	(K)E I/E/V/G G G/R(K)		92.03	408.72	816.421	0.0117	14.4	4.53	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
25117	dirMS_041712_NAR_40mM_minus2.14441.14441.3	3	3.61	1	1.19E+05		(K)GTVPDD	(K)G T V|P D D A V E A/L A D S L G K K(E)		170.15	595.9791	1785.923	-0.0001	-0.1	4.23	81397.3	4.99	HUMAN	B7Z468	Calpastatin
25118	dirMS_041712_NAR_50mM_minus2.17507.17507.3	3	3.61	0	2.35E+05		(R)DVCTELI	(R)D V|C/T E\L L P L I/K P Q G R(V)	C:Carbamidomethylation	168.53	580.3212	1738.952	-0.003	-1.7	6.07	30659.7	9.02	HUMAN	P16152	Carbonyl reductase [NADPH] 1
25119	dirMS_041712_NAR_50mM_minus2.9579.9579.3	3	3.61	0	1.73E+05	M329m	(K)SNmGHI	(K)S N\m G H/P E/P\A/S G L A/A L A K(V)	m:Oxidized methionine	122.73	556.279	1650.827	15.9956	0.4	6.47	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
25120	dirMS_041712_NAR_60mM_minus.20211.20211.3	3	3.61	1	5.17E+05		(R)KEGGLG	(R)K E G G L G P L N I/P L L/A D V T R(R)		186.13	621.6933	1863.07	-0.0045	-2.4	6.07	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
25121	dirMS_041712_NAR_60mM_minus.8761.8761.3	3	3.61	1	5.81E+03		(K)AQAEVE	(K)A Q|A E V E/G L G K G V/A R(L)		108.32	462.2579	1384.754	0.0048	3.5	6.19	533778	5.74	HUMAN	Q15149	Plectin
25122	dirMS_041712_NAR_120mM_plus.12169.12169.4	4	3.61	2	6.61E+04		(K)NDTVAG	(K)N\D T V A G Q/G E R|D H L I T K R(D)		116.2	478.2542	1909.984	0.0111	5.8	6.76	15599.4	6.48	HUMAN	H7BZG1	Integrin alpha-V light chain (Fragment)
25123	dirMS_041712_NAR_20mM_plus.12900.12900.3	3	3.61	1	5.22E+05		(K)EENKQV	(K)E E N K Q V A/L/G\T S K(L)		161.82	435.2319	1303.685	-0.0041	-3.1	6.24	12945.6	9.79	HUMAN	H0YAR3	DNA topoisomerase I, mitochondrial (Fragment)
25124	dirMS_041712_NAR_20mM_plus.14169.14169.3	3	3.61	0	7.24E+03		(R)VPTANV	(R)V P T A N V\S\V\V/D L T C R(L)	C:Carbamidomethylation	169.75	510.9348	1530.795	-0.0046	-3	5.81	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
25125	dirMS_041712_NAR_20mM_plus.9138.9138.2	2	3.61	0	3.16E+04	M239m	(K)EITALAP	(K)E I\T A/L|A/P\S T m K(I)	m:Oxidized methionine	133.95	589.309	1161.618	15.9923	-2.2	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
25126	dirMS_041712_NAR_30mM_plus2.10256.10256.2	2	3.61	1	3.23E+05	T270t	(K)tNLAPKS	(K)t N/L A P K S/T(-)	t:Phosphorylated T	106.95	456.2155	831.457	79.9667	0.4	8.41	31778.8	9.23	HUMAN	A2A2L5	Chromosome 20 open reading frame 43 (Fragment)
25127	dirMS_041712_NAR_30mM_plus2.11897.11897.2	2	3.61	0	1.45E+06		(R)NTDEM	(R)N T|D/E/M/V E L R(I)		114.92	553.7615	1106.515	0.0011	1	4.14	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
25128	dirMS_041712_NAR_30mM_plus2.15990.15990.2	2	3.61	0	3.44E+05		(K)GVLFYGI	(K)G V L/F/Y/G/P P G C G K(T)	C:Carbamidomethylation	136.78	626.3175	1251.619	0.0087	6.9	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
25129	dirMS_041712_NAR_30mM_plus2.17360.17360.2	2	3.61	0	7.45E+05		(R)IMNTFS	(R)I M/N T/F S V V P S P K(V)		144.9	660.3537	1319.703	-0.0027	-2	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
25130	dirMS_041712_NAR_30mM_plus2.21515.21515.2	2	3.61	0	8.15E+03		(R)VNQAIW	(R)V N/Q/A I W L/L/C T G A R(E)	C:Carbamidomethylation	167.72	751.3976	1501.794	-0.0065	-4.3	9.72	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
25131	dirMS_041712_NAR_40mM_plus2.10701.10701.3	3	3.61	1	4.10E+05		(R)DGKLVS	(R)D G/K L\V\S E/S/S/D V L/P K(-)		128.58	491.9315	1473.78	0.0004	0.3	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
25132	dirMS_041712_NAR_40mM_plus2.11486.11486.3	3	3.61	1	3.78E+04		(R)IPTALQE	(R)I P T A L Q E G R I V Q/R(-)		133.68	494.2917	1480.859	0.0011	0.7	9.6	63359.4	5.46	HUMAN	F2Z2Q7	Protein AKNAD1
25133	dirMS_041712_NAR_50mM_plus2.8109.8109.3	3	3.61	1	1.12E+04	S74s	(K)GGIsNV	(K)G G I s N V W|F|D R F/K(I)	s:N-acetylglucosamine (S)	109.45	543.6023	1425.727	203.065	-8.8	8.75	26601.2	7.98	HUMAN	Q5VWZ2	Lysophospholipase-like protein 1
25134	dirMS_041712_NAR_50mM_plus2.8551.8551.3	3	3.61	0	4.72E+04		(K)ISNPTEF	(K)I S/N|P T E/F Q N/H E K(Q)		112.13	481.9059	1443.686	0.0169	11.7	5.4	42522	9.96	HUMAN	E7ERR5	Nucleolar and spindle-associated protein 1
25135	dirMS_041712_NAR_50mM_plus2.9535.9535.3	3	3.61	0	2.45E+05		(R)LVKPGN	(R)L V/K/P G N Q N T Q\V/T E A W N K(V)		117.08	643.0046	1927.003	-0.004	-2.1	8.59	31751.6	6.33	HUMAN	F8VR77	Proliferation-associated protein 2G4
25136	dirMS_041712_NAR_60mM_plus.15696.15696.3	3	3.61	1	2.14E+05	K92k	(K)LDSLGkE	(K)L D/S L/G k E/K N K(D)	k:Ubiquitin-K	138.32	415.8936	1131.637	114.0294	-10.8	8.5	67997.7	6.93	HUMAN	B4DN07	Rho GTPase-activating protein 6
25137	dirMS_041712_NAR_60mM_plus.20128.20128.3	3	3.61	1	1.54E+05		(R)ELIKVLEI	(R)E L I K V L E E\A/N Q A|I/N/P K(L)		165.17	603.6768	1809.012	0.0042	2.3	4.79	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
25138	dirMS_041712_NAR_20mM_minus.11731.11731.2	2	3.6	0	3.31E+05		(R)GALQNI	(R)G A L Q/N\I|I\P A S T G A A K(A)		165.32	706.3976	1411.79	-0.0024	-1.7	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
25139	dirMS_041712_NAR_30mM_minus2.8602.8602.2	2	3.6	0	4.19E+05		(R)YLFVDR	(R)Y/L\F V D R(A)		101.45	406.7193	812.43	0.0012	1.5	5.83	21781.4	5.48	HUMAN	E7ERA5	Myosin-10 (Fragment)
25140	dirMS_041712_NAR_40mM_minus2.15671.15671.3	3	3.6	1	3.98E+05	M145m	(R)GVmLA	(R)G V/m/L/A V D A V I A E L K/K(Q)	m:Oxidized methionine	181.67	524.9715	1556.908	15.9919	-1.9	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
25141	dirMS_041712_NAR_40mM_minus2.7693.7693.3	3	3.6	0	7.75E+04	M778m	(R)mLTGPV	(R)m L/T G P V Y/S Q S T A L/T\H K(Q)	m:Oxidized methionine	123.6	583.9659	1733.889	15.9941	-0.5	8.37	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
25142	dirMS_041712_NAR_50mM_minus2.12744.12744.3	3	3.6	0	1.44E+05		(K)ASLASLP	(K)A S L A\S L/P/P L/H V A K(L)		141.3	435.2622	1303.773	-0.0012	-0.9	8.8	141626	5.5	HUMAN	A8MY36	Dynactin subunit 1
25143	dirMS_041712_NAR_50mM_minus2.13516.13516.3	3	3.6	1	2.38E+05		(K)ITDIIGKE	(K)I/T/D I/I G K E E/G I/G P E/N L R(G)		145.2	618.665	1853.997	-0.0163	-8.8	4.41	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
25144	dirMS_041712_NAR_50mM_minus2.14618.14618.3	3	3.6	2	1.63E+04		(K)LPGRSPS	(K)L P G R S P S T I/S L K E S K(S)		151.28	533.9773	1599.906	0.0109	6.8	9.99	555035.4	6.1	HUMAN	Q9Y6V0	Protein piccolo
25145	dirMS_041712_NAR_50mM_minus2.17112.17112.3	3	3.6	1	5.84E+04	M477m	(R)VKRQDS	(R)V K R Q/D S m E A/L Q M D R(S)	m:Oxidized methionine	165.27	574.9529	1706.831	16.0129	10.4	6.09	79067.9	8.7	HUMAN	A8MTK4	TRAF3-interacting protein 1
25146	dirMS_041712_NAR_50mM_minus2.17736.17736.3	3	3.6	0	4.27E+05	M203m	(R)DTGIFLD	(R)D T G I/F L D/L m H/L K(K)	m:Oxidized methionine	170.33	473.5826	1402.74	15.9933	-1.1	5.21	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
25147	dirMS_041712_NAR_50mM_minus2.7561.7561.3	3	3.6	1	6.20E+05	M289m	(R)VVDLM	(R)V V|D L M/A/H m A S K E(-)	m:Oxidized methionine	110.2	449.5526	1330.649	15.9939	-0.8	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
25148	dirMS_041712_NAR_60mM_minus.11978.11978.3	3	3.6	1	1.07E+05		(K)LAEQAE	(K)L/A|E Q A E R Y D D M A A A M/K(A)		126.75	604.9459	1812.825	-0.0023	-1.3	4.32	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
25149	dirMS_041712_NAR_60mM_minus.12610.12610.3	3	3.6	0	1.65E+05		(K)LAQANG	(K)L/A Q\A/N/G W\G V/M\V/S H R(S)		130	509.2631	1525.769	0.0055	3.6	9.75	47510.4	7.04	HUMAN	P06733	Alpha-enolase
25150	dirMS_041712_NAR_20mM_plus.12207.12207.2	2	3.6	0	5.25E+04		(R)LGGEVS	(R)L G G E/V S/C L V A/G T K(C)	C:Carbamidomethylation	157	645.8383	1290.672	-0.0029	-2.2	6	30619.5	9.34	HUMAN	H0YKF0	Electron transfer flavoprotein subunit alpha, mitochondrial (Fragment)
25151	dirMS_041712_NAR_20mM_plus.13758.13758.2	2	3.6	0	5.96E+04		(K)ASAELAI	(K)A S A E\L\A\L|G E N S E V|L/K(S)		166.92	765.8991	1530.801	-0.0101	-6.6	4.25	47916.2	9.44	HUMAN	P00505	Aspartate aminotransferase, mitochondrial
25152	dirMS_041712_NAR_20mM_plus.14344.14344.3	3	3.6	0	7.24E+03		(R)VPTANV	(R)V P T A N V S\V\V/D|L/T C R(L)	C:Carbamidomethylation	169.75	510.9348	1530.795	-0.0046	-3	5.81	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
25153	dirMS_041712_NAR_20mM_plus.14489.14489.3	3	3.6	0	1.24E+05	M174m	(K)AmGAA	(K)A m G A A Q\V\V\V/T|D L/S A T R(L)	m:Oxidized methionine	171.43	535.9457	1589.832	15.991	-2.5	5.88	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
25154	dirMS_041712_NAR_30mM_plus2.8656.8656.2	2	3.6	0	1.02E+05		(R)YNYIEGT	(R)Y/N|Y I E G T K(M)		99.03	494.2448	987.478	0.0041	4.2	6	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
25155	dirMS_041712_NAR_40mM_plus2.12821.12821.3	3	3.6	1	1.03E+04		(R)LADPVP	(R)L A/D P V/P S G G S S\S P R F L P R(G)		142	613.999	1839.971	0.0113	6.1	9.6	101883.9	10.46	HUMAN	Q96DN6	Methyl-CpG-binding domain protein 6
25156	dirMS_041712_NAR_40mM_plus2.9395.9395.2	2	3.6	0	6.70E+04		(K)SLLSSPT	(K)S L|L S/S/P T K(D)		118.4	416.7466	832.477	0.0085	10.2	8.47	39475.1	5.72	HUMAN	I3NI36	A-kinase anchor protein 1, mitochondrial (Fragment)
25157	dirMS_041712_NAR_50mM_plus2.18230.18230.3	3	3.6	1	1.11E+06		(K)GPVREG	(K)G P V R E G D V L|T/L L/E S E\R(E)		163.57	590.6519	1769.939	0.0019	1.1	4.41	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
25158	dirMS_041712_NAR_50mM_plus2.19700.19700.3	3	3.6	0	3.68E+04		(R)QLPAMT	(R)Q L|P/A/M T A L Q T L H L R(S)		171.93	531.635	1592.894	-0.0037	-2.3	9.75	78827.3	5.92	HUMAN	J3KS54	Protein flightless-1 homolog
25159	dirMS_041712_NAR_50mM_plus2.21050.21050.3	3	3.6	1	1.56E+05		(R)GGGNQ	(R)G G G/N Q V/S L L N V V M D L K K(C)		179.7	591.3291	1771.974	-0.0007	-0.4	8.59	218583	5.58	HUMAN	F5GWX5	Chromodomain-helicase-DNA-binding protein 4
25160	dirMS_041712_NAR_50mM_plus2.7083.7083.3	3	3.6	1	6.35E+04	M53m	(K)LTDCVV	(K)L/T D C V/V m R D/P/A S K(R)	C:Carbamidomethylation m:Oxid	102.43	503.2495	1491.729	16.0045	6.4	5.96	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
25161	dirMS_041712_NAR_60mM_plus.14717.14717.3	3	3.6	1	7.04E+04		(K)FSIEDLK	(K)F/S I/E/D L K A Q P K(Q)		134.43	425.898	1275.694	-0.0149	-11.7	6.07	13579.2	9.99	HUMAN	E9PPQ6	Thymocyte nuclear protein 1 (Fragment)
25162	dirMS_041712_NAR_60mM_plus.17028.17028.3	3	3.6	0	3.51E+05		(K)EGHVEV	(K)E/G H V E V\V/S E L L/Q R(E)		146.07	498.9326	1494.791	-0.0078	-5.2	4.75	48586.6	9.32	HUMAN	D6RCB2	Ankyrin-3
25163	dirMS_041712_NAR_60mM_plus.17232.17232.3	3	3.6	0	2.06E+04		(K)EGHVEV	(K)E G H V E V\V/S/E/L L Q/R(E)		148.32	498.9326	1494.791	-0.0078	-5.2	4.75	48586.6	9.32	HUMAN	D6RCB2	Ankyrin-3
25164	dirMS_041712_NAR_60mM_plus.5355.5355.2	2	3.6	1	8.14E+04		(K)CDSSPD	(K)C D|S/S/P D/S A E D V R K(V)	C:Carbamidomethylation	85.72	733.3133	1465.622	-0.003	-2.1	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
25165	dirMS_041712_NAR_60mM_plus.7445.7445.3	3	3.6	1	1.00E+06		(K)GGETIK	(K)G G\E/T I/K Q L Q/E R(A)		97.45	420.23	1258.675	0.0005	0.4	6.14	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
25166	dirMS_041712_NAR_20mM_minus.7501.7501.3	3	3.59	0	7.57E+05		(K)TGTEAE	(K)T G T E A/E A A D S\G A V G A R(R)		123.5	488.2327	1462.677	0.0067	4.6	4.14	9966.3	5.56	HUMAN	F2Z2A2	Major facilitator superfamily domain-containing protein 9
25167	dirMS_041712_NAR_40mM_minus2.12262.12262.2	2	3.59	1	2.00E+05	M170m	(R)DQKEmI	(R)D Q/K/E m L\E V/S G I(-)	m:Oxidized methionine	156.63	632.8108	1248.614	16.0003	4.3	4.14	19926	9.56	HUMAN	C9JJ63	Transmembrane protein 176A
25168	dirMS_041712_NAR_40mM_minus2.14196.14196.3	3	3.59	0	1.23E+05	S651s	(K)VPsELGL	(K)V P s\E L G L G E E/F T I Q V K(K)	s:N-acetylglucosamine (S)	168.55	650.3366	1745.932	203.0633	-8.3	4.26	83768.8	4.96	HUMAN	Q8IZE3	Protein-associating with the carboxyl-terminal domain of ezrin
25169	dirMS_041712_NAR_50mM_minus2.11015.11015.3	3	3.59	1	8.29E+04		(K)LIPDSIGI	(K)L I P/D S I G K/D I E K(A)		130.92	443.2546	1327.747	0.0025	1.9	4.56	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
25170	dirMS_041712_NAR_60mM_minus.10072.10072.3	3	3.59	0	3.39E+05		(K)LTPLSHE	(K)L T/P L/S H E/V/I S R(Q)		115.77	417.9007	1251.706	-0.018	-14.4	6.75	51099.4	8.43	HUMAN	F8W810	Uncharacterized protein
25171	dirMS_041712_NAR_60mM_minus.10453.10453.3	3	3.59	1	9.41E+03	K1065k	(K)SSHEkSN	(K)S S H/E k\S N/K/S L E D K(S)	k:Ubiquitin-K	118.07	534.9257	1488.729	114.0337	-5.8	6.48	247515.6	5.33	HUMAN	H0Y6I0	Golgin subfamily A member 4 (Fragment)
25172	dirMS_041712_NAR_60mM_minus.14082.14082.3	3	3.59	1	1.20E+05		(R)SILKIDD	(R)S I/L K I D D V/V/N T R(-)		138.5	458.2637	1372.78	-0.0029	-2.1	5.68	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
25173	dirMS_041712_NAR_60mM_minus.5124.5124.3	3	3.59	0	8.40E+04	T27815t	(K)AYAtITN	(K)A Y A t I/T/N N C T/K(T)	C:Carbamidomethylation t:N-ace	83.85	487.236	1256.594	203.0995	13.8	8.63	4024332	6.06	HUMAN	K7ENY1	Titin
25174	dirMS_041712_NAR_120mM_plus.10029.10029.3	3	3.59	0	8.62E+04	S162s	(K)IsQAPQ	(K)I s/Q A P/Q V S I S/R(S)	s:Phosphorylated S	105.42	422.551	1185.659	79.9798	10.7	9.75	58558.3	5.14	HUMAN	Q96QS3	Homeobox protein ARX

25175	dirMS_041712_NAR_120mM_plus.15347.15347.4	4	3.59	2	4.85E+05		(K)LLVGVD	(K)L L V/G/V D E K L N/P E D I K K(H)		133.67	453.2599	1810.032	-0.0143	-7.9	4.79	121749.9	6.97	HUMAN	P53396	ATP-citrate synthase
25176	dirMS_041712_NAR_120mM_plus.6733.6733.3	3	3.59	1	2.82E+05		(R)CREMDE	(R)C/R E M D\E/Q/I/R(L)	C:Carbamidomethylation	88.48	412.8549	1236.546	0.0042	3.4	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
25177	dirMS_041712_NAR_120mM_plus.6770.6770.2	2	3.59	0	1.87E+05		(K)SFLKPGE	(K)S F/L/K P/G E/K(T)		89.02	453.2599	905.509	0.0034	3.8	8.31	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
25178	dirMS_041712_NAR_20mM_plus.13554.13554.2	2	3.59	0	2.03E+05		(R)GDLGIEI	(R)G D|L/G\I E/I P A E/K(V)		166.5	571.3075	1141.61	-0.0022	-1.9	4.14	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
25179	dirMS_041712_NAR_20mM_plus.19039.19039.3	3	3.59	0	6.34E+04		(K)DTSYLFI	(K)D T S Y L F I/T/G P D V V K(S)		201.93	518.9378	1554.805	-0.0062	-4	4.21	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
25180	dirMS_041712_NAR_20mM_plus.8530.8530.2	2	3.59	0	3.02E+05		(K)DVNQQI	(K)D V/N Q Q E/F|V/R(A)		129.47	567.7865	1134.554	0.0119	10.5	4.37	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
25181	dirMS_041712_NAR_30mM_plus2.11704.11704.3	3	3.59	0	3.53E+05		(R)GGGGNI	(R)G G\G G\N F G/P/G/P/G S N F/R(G)		114.45	459.8807	1377.629	-0.0019	-1.4	9.75	37486.1	9.03	HUMAN	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1
25182	dirMS_041712_NAR_30mM_plus2.19385.19385.2	2	3.59	0	4.56E+04		(R)FFFDVG	(R)F F|F D V/G S/N K(Y)		155.13	530.7617	1060.51	0.0063	5.9	5.84	35024.2	6.07	HUMAN	Q00577	Transcriptional activator protein Pur-alpha
25183	dirMS_041712_NAR_30mM_plus2.5298.5298.2	2	3.59	0	5.47E+05		(K)VSSFEEK	(K)V/S|S F E E/K(M)		81.57	413.203	825.399	-0.0002	-0.2	4.53	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
25184	dirMS_041712_NAR_30mM_plus2.9390.9390.2	2	3.59	0	4.65E+05		(K)ATFDAIS	(K)A T|F D A/I S K(T)		103	426.7266	852.446	-0.0002	-0.3	5.88	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
25185	dirMS_041712_NAR_40mM_plus2.10876.10876.3	3	3.59	1	1.50E+04		(R)DVVICPI	(R)D V|V/I/C/P D A S L E D A K K(E)	C:Carbamidomethylation	130.32	553.9465	1659.826	-0.0009	-0.5	4.23	18080.7	7.92	HUMAN	K7ELW0	Protein DJ-1
25186	dirMS_041712_NAR_40mM_plus2.9085.9085.2	2	3.59	0	1.94E+05		(K)LQQWYI	(K)L/Q/Q W/Y\R(E)		115.2	447.2352	893.463	0.0003	0.3	8.75	12797.5	10.58	HUMAN	K7EIL4	Glucose-6-phosphate isomerase (Fragment)
25187	dirMS_041712_NAR_40mM_plus2.9824.9824.2	2	3.59	0	2.75E+05		(K)SCNCLLL	(K)S/C|N C L L/L K(V)	C:Carbamidomethylation	121.03	504.2542	1007.501	-0.0001	-0.1	8.47	47510.4	7.04	HUMAN	P06733	Alpha-enolase
25188	dirMS_041712_NAR_50mM_plus2.10504.10504.3	3	3.59	0	4.00E+04		(R)TSAYTLI	(R)T S/A Y T/L I A P N I N R(R)		122.55	478.5966	1433.775	0.0005	0.4	8.41	36963.8	10.04	HUMAN	Q96J88	Epithelial-stromal interaction protein 1
25189	dirMS_041712_NAR_50mM_plus2.12699.12699.3	3	3.59	1	3.83E+05		(K)LPGGELI	(K)L/P/G G E L/N P G E D\E/V E G L K R(L)		134.28	636.9936	1908.966	0.0001	0.1	4.25	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
25190	dirMS_041712_NAR_50mM_plus2.14232.14232.3	3	3.59	1	6.66E+05		(R)MSMKE	(R)M S M K E V\D E Q|M\L/N/V Q N K(N)		142.87	641.9706	1923.897	0	0	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
25191	dirMS_041712_NAR_50mM_plus2.16097.16097.3	3	3.59	0	4.14E+04		(K)ACQSIYF	(K)A C/Q S I/Y P L/H D V F V R(K)	C:Carbamidomethylation	153.83	568.9562	1704.853	0.0014	0.8	6.79	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
25192	dirMS_041712_NAR_50mM_plus2.21822.21822.3	3	3.59	1	2.08E+05		(R)KVPELM	(R)K V P E L\M/E|M F L/P A T K(N)		185.52	545.2925	1633.869	-0.0063	-3.8	6.14	95051	6.63	HUMAN	B3KXW5	AP-1 complex subunit gamma-1
25193	dirMS_041712_NAR_50mM_plus2.8074.8074.3	3	3.59	1	2.94E+04		(K)ELQAAG	(K)E L/Q/A/A G K/S P E/D L E R(L)		109.3	514.9321	1542.776	0.0059	3.8	4.41	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
25194	dirMS_041712_NAR_50mM_plus2.9536.9536.3	3	3.59	2	1.71E+05	M1m	(-)mIDDSTF	(-)m I/D/D S T R V/P L G K S K(D)	m:Oxidized methionine	117.6	521.6042	1546.826	15.9723	-14.5	8.35	26772.6	8.92	HUMAN	Q4JDL3-6	Isoform 6 of Tyrosine-protein phosphatase non-receptor type 20
25195	dirMS_041712_NAR_60mM_plus.19087.19087.3	3	3.59	0	1.51E+05		(R)NHPGLL	(R)N H/P G L/L\L/M D T T F R(D)		156.87	505.6001	1514.778	0.0073	4.8	6.74	130372.9	6.37	HUMAN	P11498	Pyruvate carboxylase, mitochondrial
25196	dirMS_041712_NAR_60mM_plus.6160.6160.3	3	3.59	0	4.30E+05		(R)LGQSSN	(R)L/G|Q S S\M L/G E Q G A R(I)		91.62	445.2196	1333.653	-0.0086	-6.5	6	133450	7.41	HUMAN	Q13751	Laminin subunit beta-3
25197	dirMS_041712_NAR_60mM_plus.7771.7771.2	2	3.59	1	2.95E+05		(R)LKSTCIY	(R)L/K|S/T C/I Y G/G A P K(G)	C:Carbamidomethylation	98.9	647.8427	1294.682	-0.0043	-3.3	9.7	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
25198	dirMS_041712_NAR_60mM_plus.9708.9708.3	3	3.59	1	7.62E+04		(K)EAALSTA	(K)E A/A/L/S T A/L/S E K R(T)		108.7	425.898	1275.69	-0.0109	-8.5	6.24	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
25199	dirMS_041712_NAR_20mM_minus.13194.13194.2	2	3.58	0	1.40E+05		(K)VGINYQ	(K)V G I N Y\Q/P P/T V V/P G G D L A K(V)		183.15	912.9938	1824.985	-0.0051	-2.8	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
25200	dirMS_041712_NAR_20mM_minus.14552.14552.3	3	3.58	0	1.76E+04		(K)LAVEALS	(K)L A V E A/L S S L/D/G D L A G\R(Y)		199.98	529.6163	1586.838	-0.0041	-2.6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
25201	dirMS_041712_NAR_20mM_minus.7581.7581.3	3	3.58	0	1.03E+06	M239m	(K)EVDEQn	(K)E V D E/Q m L|N V Q N K(N)	m:Oxidized methionine	124.38	488.2327	1446.689	15.9942	-0.5	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
25202	dirMS_041712_NAR_20mM_minus.8707.8707.2	2	3.58	0	1.91E+04	M149m	(K)ITLDNAY	(K)I T|L/D N A Y m E K(C)	m:Oxidized methionine	136.55	607.2934	1197.582	15.9975	2.1	4.37	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
25203	dirMS_041712_NAR_30mM_minus2.11838.11838.2	2	3.58	0	8.06E+05		(K)SADDTY	(K)S A D/D T Y/L Q/L/K(K)		118.07	577.2825	1153.574	-0.0158	-13.7	4.21	144991.9	9.19	HUMAN	E9PKC0	Pleckstrin homology domain-containing family A member 7
25204	dirMS_041712_NAR_30mM_minus2.14714.14714.2	2	3.58	0	2.04E+04		(R)LWVDEA	(R)L W|V/D/E A V R(A)		133.2	494.2641	987.526	-0.0049	-4.9	4.37	266161	5.68	HUMAN	E9PPU0	Epiplakin
25205	dirMS_041712_NAR_30mM_minus2.8921.8921.2	2	3.58	0	2.07E+05		(K)QAEILQE	(K)Q A/E/I/L Q E/S R(M)		102.72	537.2824	1073.559	-0.001	-1	4.53	15962.5	9.61	HUMAN	B4DT30	Tubulin-specific chaperone A
25206	dirMS_041712_NAR_40mM_minus2.13366.13366.3	3	3.58	1	1.01E+04	M148m	(R)LDLAGR	(R)L D L/A G R\D L\T D/Y L m K(I)	m:Oxidized methionine	161.87	547.2822	1623.841	15.991	-2.4	4.43	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
25207	dirMS_041712_NAR_50mM_minus2.12883.12883.3	3	3.58	0	1.53E+05		(K)ASLASLP	(K)A S L A\S L/P/P L H V/A K(L)		141.37	435.2622	1303.773	-0.0012	-0.9	8.8	141626	5.5	HUMAN	A8MY36	Dynactin subunit 1
25208	dirMS_041712_NAR_50mM_minus2.12929.12929.3	3	3.58	1	5.01E+05		(K)VLAGDK	(K)V L|A G D K N F\I/T A E E L R(R)		142.53	559.3044	1675.901	-0.0027	-1.6	4.68	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
25209	dirMS_041712_NAR_50mM_minus2.15027.15027.3	3	3.58	0	8.32E+04	K348k	(R)ISkPGAV	(R)I S k P G A V S T P\V/K(H)	k:Ubiquitin-K	153.6	433.2554	1183.705	114.0471	3.3	10	197797.8	6.21	HUMAN	G3V1L9	Tight junction protein 1 (Zona occludens 1), isoform CRA_a
25210	dirMS_041712_NAR_50mM_minus2.9002.9002.3	3	3.58	2	4.90E+04	S470s	(K)KEPsVEE	(K)K E P s|V/E|E K L Q K(L)	s:N-acetylglucosamine (S)	119.6	506.6094	1314.726	203.0873	5.2	6.23	74986.2	6.56	HUMAN	I3L080	Hepatoma-derived growth factor-related protein 2
25211	dirMS_041712_NAR_60mM_minus.7277.7277.2	2	3.58	0	1.12E+05		(K)STTTGHI	(K)S/T/T T G H L\I Y/K(C)		99.65	560.8028	1120.6	-0.0014	-1.2	8.34	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
25212	dirMS_041712_NAR_120mM_plus.18725.18725.4	4	3.58	1	2.48E+05	K2172k	(K)IFQSFDS	(K)I F Q S/F/D S G K L L T S k(E)	k:Ubiquitin-K	151.23	421.9839	1570.848	114.0662	13.8	8.59	356242.3	8.87	HUMAN	E9PJL5	Uncharacterized protein C12orf55
25213	dirMS_041712_NAR_120mM_plus.6183.6183.3	3	3.58	0	2.12E+05	T200t	(K)ADVLEG	(K)A D/V L E\G/t/A E/R(L)	t:N-acetylglucosamine (T)	85.42	421.8744	1060.527	203.0817	1.9	4.14	89133	5.76	HUMAN	Q32MK0	Myosin light chain kinase 3
25214	dirMS_041712_NAR_120mM_plus.7028.7028.3	3	3.58	1	9.66E+04		(K)SNKDGG	(K)S N K D G G N Q\E/V/E I A R(C)		89.93	506.2499	1516.735	0.0001	0.1	4.68	10305.6	6.94	HUMAN	H7C330	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
25215	dirMS_041712_NAR_20mM_plus.13270.13270.2	2	3.58	0	5.69E+04		(R)ILGADTS	(R)I L/G A D\T S V\D L/E E/T G R(V)		163.27	788.3928	1575.786	-0.0077	-4.9	3.91	15338.4	5.51	HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
25216	dirMS_041712_NAR_20mM_plus.16191.16191.2	2	3.58	0	6.43E+04		(R)LSNIFVI	(R)L/S N I F V/I G K(G)		183.62	495.8022	990.598	-0.0011	-1.1	8.75	29825.4	10.37	HUMAN	P62701	40S ribosomal protein S4, X isoform
25217	dirMS_041712_NAR_20mM_plus.18369.18369.3	3	3.58	0	1.87E+04		(R)LEQPDP	(R)L E Q P D P G A\V/A A|A A I L R(A)		197.85	531.2985	1591.88	0.0007	0.4	4.37	59288.4	7.16	HUMAN	Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)
25218	dirMS_041712_NAR_30mM_plus2.10910.10910.2	2	3.58	1	5.02E+05		(K)VVVLGD	(K)V V|V L G D K\D K(S)		110.63	486.7894	972.572	-0.0009	-0.9	5.93	104112.2	9.8	HUMAN	Q9UNA0	A disintegrin and metalloproteinase with thrombospondin motifs 5
25219	dirMS_041712_NAR_30mM_plus2.13531.13531.2	2	3.58	0	5.55E+05		(K)VGLQVV	(K)V/G/L|Q V\V/A\V K(A)		124.08	456.7974	912.588	-0.0002	-0.2	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
25220	dirMS_041712_NAR_30mM_plus2.4745.4745.2	2	3.58	0	3.04E+05		(R)MDDYCI	(R)M/D/D Y/C R(R)	C:Carbamidomethylation	75.88	430.1579	859.307	0.0012	1.4	4.21	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
25221	dirMS_041712_NAR_30mM_plus2.6683.6683.2	2	3.58	0	1.41E+05	M514m M!	(K)NEEmm	(K)N E|E m/m\E Q/K(E)	m:Oxidized methionine	89.23	535.7086	1038.423	31.9869	-2.8	4.25	67721.3	5.54	HUMAN	P32456	Interferon-induced guanylate-binding protein 2
25222	dirMS_041712_NAR_40mM_plus2.9701.9701.2	2	3.58	0	1.34E+05	M14m	(R)NTFmVS	(R)N/T|F m/V S K(R)	m:Oxidized methionine	120.45	421.7119	826.413	16.0038	10.5	8.75	13026	9.97	HUMAN	A8MXJ9	Protein tweety homolog 3 (Fragment)
25223	dirMS_041712_NAR_50mM_plus2.12747.12747.3	3	3.58	1	4.26E+05		(R)ELAVQIY	(R)E L/A V Q/I/Y E E|A R K(F)		135.2	483.5916	1448.774	-0.0141	-9.7	4.79	73386.6	8.73	HUMAN	B4DXX7	ATP-dependent RNA helicase DDX3Y
25224	dirMS_041712_NAR_50mM_plus2.17258.17258.3	3	3.58	1	3.37E+05		(R)VSFELFA	(R)V S F/E L F/A D K V P K(T)		158.8	460.5906	1379.757	0.0003	0.2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
25225	dirMS_041712_NAR_50mM_plus2.4847.4847.3	3	3.58	1	2.29E+05		(R)AAEDDE	(R)A/A\E D/D E D D D/V D T K K(Q)		80.78	522.5519	1565.645	-0.0038	-2.4	3.76	14366.2	3.71	HUMAN	B8ZZA1	Thymosin alpha-1
25226	dirMS_041712_NAR_50mM_plus2.4998.4998.3	3	3.58	0	8.39E+04	S638s M63	(R)DGLPAH	(R)D G L P A/H I G s m A/Q R(A)	s:Phosphorylated S m:Oxidiz	83.28	483.5541	1352.674	95.9738	8.7	6.74	287505.9	6.45	HUMAN	F5GXR6	Unconventional myosin-XVIIIb
25227	dirMS_041712_NAR_60mM_plus.10926.10926.3	3	3.58	0	1.18E+06	M223m	(K)TVmGIA	(K)T|V m G I A S G Q E/E A/K(S)	m:Oxidized methionine	115.43	446.2162	1320.646	15.9877	-5.4	4.53	35425.3	9.05	HUMAN	Q9Y5P0	Olfactory receptor 51B4
25228	dirMS_041712_NAR_60mM_plus.12718.12718.3	3	3.58	1	1.86E+05		(K)YFVEAG	(K)Y/F|V E A G A M A V/R/R(V)		123.17	457.2397	1369.705	0	0	8.75	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
25229	dirMS_041712_NAR_60mM_plus.15962.15962.3	3	3.58	0	2.82E+05		(K)NFDLRP	(K)N F/D|L R P G V/I V R(-)		140.05	429.248	1285.738	-0.0081	-6.3	9.6	33192.3	6.77	HUMAN	B4DN45	S-adenosylmethionine synthase
25230	dirMS_041712_NAR_60mM_plus.19411.19411.3	3	3.58	1	2.02E+05		(R)AGEAGK	(R)A G/E A\G K L\E/E\V/M/Q\E L R(A)		159.67	553.9525	1659.837	0.0059	3.6	4.49	54918.3	5.61	HUMAN	Q9BR76	Coronin-1B
25231	dirMS_041712_NAR_60mM_plus.5659.5659.3	3	3.58	0	3.20E+04		(R)AEAEAG	(R)A E A\E A/G S P R P D/P R(E)		87.72	451.5555	1352.655	-0.0034	-2.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
25232	dirMS_041712_NAR_120mM_minus.8685.8685.3	3	3.57	0	2.90E+05	N186n	(K)LGAAAG	(K)L/G/A/A A/G F n Y K(K)	n:N-acetylglucosamine (N)	101.85	405.54	1011.526	203.0796	0.2	8.59	22710.7	6.11	HUMAN	H7BZH6	Quinone oxidoreductase PIG3 (Fragment)
25233	dirMS_041712_NAR_20mM_minus.10388.10388.3	3	3.57	1	2.05E+05	M60m S62	(R)LKTAmS	(R)L K T\A/m S/s E T P/T S R(Q)	m:Oxidized methionine s:Pho	152.88	502.2275	1408.71	95.9579	-2.2	8.75	81199.3	9.38	HUMAN	P22079	Lactoperoxidase
25234	dirMS_041712_NAR_20mM_minus.10840.10840.2	2	3.57	0	3.55E+05		(R)ELCAGP	(R)E L C A G P/A\C N E V\E/R(A)	C:Carbamidomethylation	155.48	752.8365	1504.652	0.0138	9.2	4.25	208752.1	6	HUMAN	Q8IZJ3	C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8
25235	dirMS_041712_NAR_20mM_minus.8229.8229.2	2	3.57	0	1.66E+05	M161m	(K)LLIEmEC	(K)L L|I/E m E/Q R(L)	m:Oxidized methionine	132.15	524.2783	1031.555	15.9939	-0.9	4.53	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
25236	dirMS_041712_NAR_30mM_minus2.5608.5608.2	2	3.57	0	8.84E+04		(K)DSYVGD	(K)D S|Y|V/G/D E A Q S K(R)		84.25	599.7632	1198.522	-0.0031	-2.6	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
25237	dirMS_041712_NAR_30mM_minus2.9525.9525.2	2	3.57	0	5.82E+04		(R)NSGPVV	(R)N S G/P V V E/K(L)		104.68	415.2235	829.441	-0.0017	-2	6	54177	6.47	HUMAN	P03956	Interstitial collagenase
25238	dirMS_041712_NAR_40mM_minus2.9786.9786.2	2	3.57	0	2.01E+06		(R)VAPEEH	(R)V A/P E E H|P V L L T E A/P L/N/P K(A)		140.27	977.5343	1954.064	-0.0031	-1.6	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
25239	dirMS_041712_NAR_50mM_minus2.11668.11668.3	3	3.57	0	9.18E+04	T761t M76	(K)tLmVVQ	(K)t/L m V V Q V/S P V E/K(N)	t:N-acetylglucosamine (T) m:	134.77	516.9426	1329.745	219.0686	-3.7	5.66	95130.6	6.63	HUMAN	B7Z484	Kinesin-like protein KIFC3
25240	dirMS_041712_NAR_50mM_minus2.14860.14860.3	3	3.57	1	4.06E+05		(K)GCLELIK	(K)G C/L E L I K E/T G V/P I A G R(H)	C:Carbamidomethylation	151.85	571.6494	1712.936	-0.0027	-1.6	6.14	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
25241	dirMS_041712_NAR_50mM_minus2.15618.15618.3	3	3.57	1	5.23E+05		(K)SIYGEKF	(K)S I/Y G E K F E|D E N F/I L K(H)		157.8	611.3086	1831.911	0	0	4.41	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
25242	dirMS_041712_NAR_50mM_minus2.17131.17131.3	3	3.57	1	1.05E+04	M297m	(K)FLVESKK	(K)F L/V E S K K m\S I/S/N P K(T)	m:Oxidized methionine	165.95	541.9562	1607.882	15.9715	-14.4	9.7	113037.3	7.4	HUMAN	Q63HQ2	Pikachurin
25243	dirMS_041712_NAR_50mM_minus2.5701.5701.3	3	3.57	1	5.51E+04		(K)TAGPIAS	(K)T A|G P/I A S A Q\K Q P A G K(V)		93.67	475.5972	1424.786	-0.0086	-6	10	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
25244	dirMS_041712_NAR_60mM_minus.10603.10603.3	3	3.57	1	6.53E+05		(K)TAVCDIF	(K)T A/V/C D/I/P P R G L K(M)	C:Carbamidomethylation	118.72	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
25245	dirMS_041712_NAR_60mM_minus.11996.11996.3	3	3.57	1	4.11E+04	S257s	(R)ITTTKKG	(R)I/T/T T K/K G S I T/s V Q(-)	s:Phosphorylated S	126.87	481.9183	1363.779	79.9612	-3.5	10	27217.7	6.92	HUMAN	F8W0P7	ATP synthase subunit beta, mitochondrial (Fragment)
25246	dirMS_041712_NAR_120mM_plus.11110.11110.3	3	3.57	1	1.75E+05	M406m	(R)QLREYQ	(R)Q/L R E Y Q/E/L m N V K(L)	m:Oxidized methionine	112.53	522.9357	1550.8	15.993	-1.2	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
25247	dirMS_041712_NAR_120mM_plus.12652.12652.4	4	3.57	1	1.01E+06	S317s M31	(K)IFSEPGS	(K)I/F S E P G S L s m A T V A\K L R(E)	s:Phosphorylated S m:Oxidiz	118.87	476.4875	1806.978	95.9499	-5.9	8.75	38952.5	9.45	HUMAN	Q5TC63	Growth hormone-regulated TBC protein 1
25248	dirMS_041712_NAR_120mM_plus.3700.3700.3	3	3.57	1	1.98E+06	M139m	(R)QREmEE	(R)Q R E m E/E/Q/M R(R)	m:Oxidized methionine	61.3	418.1852	1236.546	15.9951	0.1	4.79	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
25249	dirMS_041712_NAR_120mM_plus.5630.5630.3	3	3.57	0	9.60E+04		(K)IAGHPLA	(K)I/A G H/P L/A Q N E R(C)		82.47	402.5461	1205.639	-0.0148	-12.3	6.75	18455.6	6.76	HUMAN	F8W8K5	Sorting nexin-12
25250	dirMS_041712_NAR_120mM_plus.5634.5634.3	3	3.57	0	2.35E+05	M1m	(-)mFSPDQ	(-)m F/S P D Q E N H P S K(A)	m:Oxidized methionine	82.2	478.2139	1416.621	16.0059	7.7	5.3	47084.2	9.01	HUMAN	Q96FA3	E3 ubiquitin-protein ligase pellino homolog 1
25251	dirMS_041712_NAR_120mM_plus.5845.5845.2	2	3.57	1	1.65E+05		(R)KGESGQ	(R)K|G E S G Q S\W/P R(L)		83.37	566.274	1131.554	-0.0134	-11.9	8.75	14686.6	4.13	HUMAN	B4DDC6	Prostaglandin E synthase 3
25252	dirMS_041712_NAR_120mM_plus.9096.9096.3	3	3.57	0	1.02E+06		(K)HTGPNS	(K)H T G P N S P D|T A|N/D/G F V R(L)		100.28	562.26	1684.767	-0.0019	-1.2	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
25253	dirMS_041712_NAR_20mM_plus.10719.10719.3	3	3.57	0	2.82E+04		(K)SQLLAPI	(K)S Q L L A/P\P|P/P S A P P G N K(T)		146.3	524.2902	1570.859	-0.0027	-1.7	8.47	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
25254	dirMS_041712_NAR_20mM_plus.11234.11234.2	2	3.57	0	1.12E+04		(R)TSGSVYI	(R)T/S\G S V/Y I T L/K(K)		149.97	534.8004	1068.594	0	0	8.26	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
25255	dirMS_041712_NAR_20mM_plus.16301.16301.2	2	3.57	0	1.08E+05		(R)LLDAQLA	(R)L L D/A Q L/A T\G/G/I V/D|P R(L)		184.4	769.9362	1538.854	0.0114	7.4	4.21	533778	5.74	HUMAN	Q15149	Plectin
25256	dirMS_041712_NAR_20mM_plus.16575.16575.2	2	3.57	1	5.77E+04		(-)MYSSSSC	(-)M Y S\S S S/C K L P S L S P/V A R(S)	C:Carbamidomethylation	185.8	935.4704	1869.92	0.0138	7.4	9.99	48845.9	4.72	HUMAN	C4AM86	Keratin, type I cuticular Ha5
25257	dirMS_041712_NAR_20mM_plus.18824.18824.3	3	3.57	0	1.27E+05		(K)IYVDDGI	(K)I Y V D D G\L|I/S L Q V K(Q)		200.65	488.2764	1462.815	-0.0005	-0.4	4.21	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
25258	dirMS_041712_NAR_20mM_plus.9342.9342.2	2	3.57	1	3.43E+04		(R)DAPAGD	(R)D A P|A G D/A G R W L R(V)		135.58	642.8265	1284.644	0.0014	1.1	5.96	18031.8	6.85	HUMAN	E9PPN4	Endonuclease 8-like 2 (Fragment)
25259	dirMS_041712_NAR_30mM_plus2.21457.21457.2	2	3.57	0	1.52E+05	K2757k	(K)LDSFINK	(K)L D/S F I/N\k(F)	k:Ubiquitin-K	168.22	475.7563	836.451	114.0541	11.7	5.84	570870.9	5.18	HUMAN	P21817	Ryanodine receptor 1
25260	dirMS_041712_NAR_30mM_plus2.22475.22475.2	2	3.57	0	1.02E+05		(R)SLDMDS	(R)S L/D\M/D S I/I A E|V K(A)		173.67	660.8437	1320.671	0.0086	6.5	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
25261	dirMS_041712_NAR_30mM_plus2.5670.5670.2	2	3.57	0	6.92E+04	S131s	(K)YAGESsK	(K)Y A|G/E S\s K(E)	s:N-acetylglucosamine (S)	83.82	472.7087	741.341	203.0688	-11.2	6	140159.9	7.9	HUMAN	J3KRP9	Protein TANC2 (Fragment)
25262	dirMS_041712_NAR_30mM_plus2.9100.9240.2	2	3.57	0	2.82E+05		(-)LGLLVER	(-)L G|L L V/E/R(Q)		101.7	400.2546	799.504	-0.0017	-2.1	6	18320	10.32	HUMAN	B1AVV1	Novel protein (Fragment)
25263	dirMS_041712_NAR_40mM_plus2.10855.10855.3	3	3.57	1	3.82E+05		(R)DGKLVS	(R)D G\K L/V\S E|S/S D V L/P K(-)		128.75	491.9315	1473.78	0.0004	0.3	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
25264	dirMS_041712_NAR_40mM_plus2.9808.9808.2	2	3.57	0	9.48E+04		(R)GYFSEEN	(R)G Y|F/S E E M N R(V)		121.53	566.7355	1132.473	-0.0091	-8	4.53	533778	5.74	HUMAN	Q15149	Plectin
25265	dirMS_041712_NAR_50mM_plus2.14081.14081.3	3	3.57	1	1.41E+05	K3651k	(K)LKAkPVS	(K)L K/A/k P V S S L N E C T T/K(D)	C:Carbamidomethylation k:Ubiqu	142.43	597.3178	1675.905	114.0341	-4.9	9.7	419509.2	6.23	HUMAN	Q9NRC6	Spectrin beta chain, non-erythrocytic 5
25266	dirMS_041712_NAR_50mM_plus2.20716.20716.3	3	3.57	0	1.04E+05	S1059s	(R)LQWVAS	(R)L Q|W V A s S W/S/E\V W I R(S)	s:N-acetylglucosamine (S)	177.52	650.6675	1746.896	203.0917	6.3	6	123189.4	9.65	HUMAN	Q8TE60-2	Isoform 2 of A disintegrin and metalloproteinase with thrombospondin motifs 18
25267	dirMS_041712_NAR_50mM_plus2.7289.7289.3	3	3.57	0	1.11E+05		(K)TNPPLIC	(K)T N/P/P L I Q E K P A K(T)		104	445.9257	1335.763	-0.0005	-0.4	8.26	102841.5	6.73	HUMAN	D3DQV9	Eukaryotic translation initiation factor 4 gamma 2 (Fragment)
25268	dirMS_041712_NAR_50mM_plus2.7485.7485.3	3	3.57	1	5.04E+04		(K)ALAAAG	(K)A L|A\A/A G Y D V/E K N N S R(I)		105.45	526.9339	1578.787	0.0001	0.1	6.11	21864.9	11.03	HUMAN	P10412	Histone H1.4
25269	dirMS_041712_NAR_50mM_plus2.9744.9744.3	3	3.57	0	8.80E+04		(R)AVIEHNI	(R)A V/I E/H N L L/S A S K(L)		119.05	427.9124	1281.716	0.0065	5.1	6.79	40481.5	6.48	HUMAN	B3KST5	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis), isoform CRA_a
25270	dirMS_041712_NAR_60mM_plus.11708.11708.3	3	3.57	0	1.04E+06		(R)SIFQHIQ	(R)S I/F Q H/I/Q/S A Q S Q R(S)		118	510.6056	1529.782	0.0203	13.3	9.49	108720.9	10.17	HUMAN	Q9Y2W1	Thyroid hormone receptor-associated protein 3
25271	dirMS_041712_NAR_60mM_plus.12015.12015.3	3	3.57	0	5.62E+05	K756k	(K)LSADTYE	(K)L S A D T Y E D/L/k A K(L)	k:Ubiquitin-K	119.98	489.9162	1353.69	114.0444	1	4.56	87755.5	6.26	HUMAN	Q8IY22	C-Maf-inducing protein
25272	dirMS_041712_NAR_60mM_plus.12775.12775.3	3	3.57	0	3.02E+05		(R)ILHLLGQ	(R)I L H\L L/G Q|E G/P K(T)		123.6	402.2397	1204.705	-0.0003	-0.2	6.75	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
25273	dirMS_041712_NAR_60mM_plus.14684.14684.3	3	3.57	1	6.97E+05		(R)RAPEPSA	(R)R A P E/P S A G/T F Q E M R(A)		133.05	526.2613	1576.754	0.0157	10	6.14	166366.2	5.8	HUMAN	Q8TER5	Rho guanine nucleotide exchange factor 40
25274	dirMS_041712_NAR_60mM_plus.6040.6040.3	3	3.57	1	1.91E+04	S416s	(K)EsQGQP	(K)E s Q G Q P P G A/P/P R S F(-)	s:N-acetylglucosamine (S)	89.98	553.2578	1454.702	203.0566	-13.7	6.1	47791	7.19	HUMAN	K7EJF0	Centrosomal protein of 89 kDa
25275	dirMS_041712_NAR_60mM_plus.6205.6205.3	3	3.57	1	1.20E+05	M605m Y6	(R)RmENLV	(R)R m/E/N L V A y A R(K)	m:Oxidized methionine y:Ph	91.78	440.2075	1222.636	95.9718	8	8.75	267066	9.36	HUMAN	Q09472	Histone acetyltransferase p300
25276	dirMS_041712_NAR_60mM_plus.7999.7999.3	3	3.57	1	5.90E+05		(R)NGNLEG	(R)N G/N L\E G E A\R K T K(V)		99.57	439.5631	1316.692	-0.017	-12.9	8.59	207827.7	8.91	HUMAN	Q9UI33	Sodium channel protein type 11 subunit alpha
25277	dirMS_041712_NAR_120mM_minus.7636.7636.3	3	3.56	1	3.52E+05		(K)IQDKEGI	(K)I Q D/K E G I|P/P D Q Q R(L)		96.85	508.5981	1523.781	-0.0015	-1	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
25278	dirMS_041712_NAR_120mM_minus.8511.8511.3	3	3.56	1	4.85E+04	K366k	(K)LTASKNC	(K)L T|A S K N C L E k(L)	C:Carbamidomethylation k:Ubiqu	100.2	426.5498	1163.609	114.026	-13.3	8.59	73377.3	7.24	HUMAN	E9PK39	Leucine-rich repeat serine/threonine-protein kinase 1
25279	dirMS_041712_NAR_20mM_minus.7710.7710.3	3	3.56	0	5.26E+05		(K)TANLAEA	(K)T A N L A E A\N A\S E E D K(I)		125.55	488.2327	1462.666	0.0179	12.3	4	33767.9	5.76	HUMAN	H3BUN0	E3 ubiquitin-protein ligase RBBP6 (Fragment)
25280	dirMS_041712_NAR_30mM_minus2.11842.11842.2	2	3.56	0	4.48E+05		(K)NELLMA	(K)N/E/L/L M A Q R(S)		117.72	487.762	974.509	0.0079	8.2	6	187857.6	8.4	HUMAN	Q15058	Kinesin-like protein KIF14
25281	dirMS_041712_NAR_30mM_minus2.18347.18347.2	2	3.56	0	1.27E+05		(K)GLGILSL	(K)G L|G/I|L S/L K(Q)		154.3	400.7655	800.524	-0.0003	-0.4	8.75	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
25282	dirMS_041712_NAR_50mM_minus2.8932.8932.3	3	3.56	1	7.72E+04		(R)SATKVTA	(R)S A T K/V T A D|V/I N A A E K(L)		118.25	506.6094	1517.817	-0.0033	-2.2	5.79	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
25283	dirMS_041712_NAR_50mM_minus2.9290.9290.3	3	3.56	0	1.99E+05		(K)VGQEIEV	(K)V/G Q E I E V R/P G I V/S K(D)		120.43	504.2902	1510.859	-0.0027	-1.8	6.11	51679.1	9.11	HUMAN	P41091	Eukaryotic translation initiation factor 2 subunit 3

25284	dirMS_041712_NAR_60mM_minus.14369.14369.3	3	3.56	1	7.76E+04	M73m	(K)HHmGTI	(K)H H\m G T R Y/I/E V Y\K(A)	m:Oxidized methionine	140.25	517.2624	1533.763	16.0096	9.4	8.51	10593.8	9.22	HUMAN	E5RI26	Epithelial-splicing regulatory protein 1 (Fragment)
25285	dirMS_041712_NAR_60mM_minus.15352.15352.3	3	3.56	0	1.17E+05		(R)QIFHPE	(R)Q I/F H/P E Q L I/T G K(E)		145.13	470.9285	1410.774	-0.003	-2.1	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
25286	dirMS_041712_NAR_60mM_minus.17305.17305.3	3	3.56	1	1.08E+05		(R)CRVDLP	(R)C R V D\L|P L/A\V L/S K(M)	C:Carbamidomethylation	156.02	457.5982	1370.782	-0.0024	-1.7	8.75	7765.6	8.23	HUMAN	H3BSA6	dCTP pyrophosphatase 1
25287	dirMS_041712_NAR_120mM_plus.12865.12865.4	4	3.56	2	1.97E+04	S383s	(K)sMLEKFI	(K)s M L E K F K L/V N\A/R(T)	s:N-acetylglucosamine (S)	120.03	410.4735	1435.809	203.0632	-9.9	9.99	236508.3	9.06	HUMAN	E7EUA9	Neuron navigator 3
25288	dirMS_041712_NAR_120mM_plus.5545.5545.2	2	3.56	0	8.44E+05	T289t	(R)tIQDSNY	(R)t I Q D S|N/Y\G\G|K(I)	t:N-acetylglucosamine (T)	82.2	643.2993	1082.511	203.08	0.5	5.5	37461.8	9.56	HUMAN	F8WD55	Transient receptor potential cation channel subfamily M member 8
25289	dirMS_041712_NAR_120mM_plus.5701.5701.3	3	3.56	0	1.38E+04		(R)LLGSASS	(R)L/L G S/A S S E D I W R(N)		81.93	445.2267	1333.675	-0.0091	-6.8	4.37	23478.5	8.69	HUMAN	B0QYI5	EF-hand calcium binding domain 6
25290	dirMS_041712_NAR_120mM_plus.6860.6860.3	3	3.56	0	4.61E+04		(K)TINCSCP	(K)T I/N C S/C P A/G E K(G)	C:Carbamidomethylation	90.67	412.8549	1236.535	0.0154	12.5	5.66	162169.4	6.9	HUMAN	Q8NFW1	Collagen alpha-1(XXII) chain
25291	dirMS_041712_NAR_120mM_plus.6986.6986.3	3	3.56	0	7.24E+03	N108n	(K)GYGFVS	(K)G Y G F/V/S F|Y n/K(L)	n:N-acetylglucosamine (N)	89.1	462.218	1181.563	203.0769	-1.8	8.5	14673.3	7.99	HUMAN	E7ETJ9	Nucleolysin TIAR (Fragment)
25292	dirMS_041712_NAR_20mM_plus.11260.11260.2	2	3.56	0	1.12E+04		(R)TSGSVYI	(R)T S|G S|V/Y I T L K(K)		149.97	534.8004	1068.594	0	0	8.26	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
25293	dirMS_041712_NAR_20mM_plus.13354.13354.2	2	3.56	0	3.84E+04		(K)IFVGGLS	(K)I/F|V G G\L S/P D/T/P E E K(I)		165.3	744.8731	1488.758	-0.0191	-12.8	4.14	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
25294	dirMS_041712_NAR_20mM_plus.14182.14182.2	2	3.56	0	8.54E+04		(K)GVVDSD	(K)G V\V/D/S D D/L P L N V\S R(E)		170.25	743.3789	1485.754	-0.0038	-2.6	3.93	92752.5	4.76	HUMAN	P14625	Endoplasmin
25295	dirMS_041712_NAR_20mM_plus.14699.14699.2	2	3.56	0	6.58E+04		(R)GITAFIV	(R)G I/T/A/F I V E/K(G)		172.87	489.2861	977.567	-0.0017	-1.7	6	16060.3	9.43	HUMAN	H0YKV0	Isovaleryl-CoA dehydrogenase, mitochondrial (Fragment)
25296	dirMS_041712_NAR_20mM_plus.6497.6497.2	2	3.56	0	1.46E+05		(R)GAGSIA	(R)G A/G\S\I A/G A\S A S P K(E)		108.42	537.277	1073.559	-0.0118	-11	8.75	334221.3	6.44	HUMAN	P15924	Desmoplakin
25297	dirMS_041712_NAR_30mM_plus2.15589.15589.2	2	3.56	0	3.31E+05		(R)YNFFTG	(R)Y N|F/F T G C P K(A)	C:Carbamidomethylation	133.95	567.2595	1133.508	0.0033	2.9	8.59	46550.7	7.81	HUMAN	B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a
25298	dirMS_041712_NAR_30mM_plus2.15706.15706.2	2	3.56	0	5.84E+05		(R)YPVNSV	(R)Y/P/V/N S/V N I L K(A)		134.93	573.8278	1146.652	-0.0034	-3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
25299	dirMS_041712_NAR_30mM_plus2.16958.16958.2	2	3.56	0	3.28E+05		(K)GCSFLPD	(K)G C|S\F/L/P D P Y/Q K(Q)	C:Carbamidomethylation	141.17	656.306	1311.604	0.0009	0.7	5.83	63688.6	5.11	HUMAN	B1AVU8	Prosaposin
25300	dirMS_041712_NAR_30mM_plus2.21499.21499.2	2	3.56	0	1.41E+05		(R)IITLAGP	(R)I/I|T/L/A/G/P T N A I\F K(A)		167.95	679.9016	1358.804	-0.0083	-6.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
25301	dirMS_041712_NAR_40mM_plus2.18396.18396.3	3	3.56	1	2.56E+04		(R)IAEVGG	(R)I A E\V/G/G V/P Y L L/P L V N Q K K(V)		174.58	646.716	1938.142	-0.0088	-4.5	8.5	18803.3	5.55	HUMAN	E9PIP1	Ester hydrolase C11orf54 (Fragment)
25302	dirMS_041712_NAR_40mM_plus2.7171.7171.2	2	3.56	0	7.19E+04	K127k	(K)YFHPk(E	(K)Y/F|H P\k(E)	k:Ubiquitin-K	101	403.2039	691.356	114.0443	1.7	8.6	49990.8	5.14	HUMAN	Q9Y366	Intraflagellar transport protein 52 homolog
25303	dirMS_041712_NAR_40mM_plus2.9923.9923.3	3	3.56	0	5.27E+04	M376m	(K)mAPVPL	(K)m/A/P/V/P L D D S N R P A S L T K(D)	m:Oxidized methionine	122.05	609.9795	1811.932	15.9919	-1.6	5.71	53030.7	11.3	HUMAN	E9PJA7	Bcl-2-associated transcription factor 1
25304	dirMS_041712_NAR_50mM_plus2.14215.14215.3	3	3.56	1	2.91E+05		(K)ALDDMI	(K)A/L|D D/M I/S T L K K(I)		143.27	412.2315	1234.671	0.0088	7.1	6	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
25305	dirMS_041712_NAR_50mM_plus2.17977.17977.3	3	3.56	0	2.49E+05		(R)VTMLFL	(R)V T/M L/F/L G L H N V R(Q)		162.78	467.267	1399.788	-0.0014	-1	9.73	21721.5	5.37	HUMAN	H7BZ35	Aspartate--tRNA ligase, cytoplasmic (Fragment)
25306	dirMS_041712_NAR_50mM_plus2.21103.21103.3	3	3.56	1	3.21E+05	M145m	(R)GVmLA	(R)G V/m L A\V/D A/V I A E L K K(Q)	m:Oxidized methionine	180.98	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
25307	dirMS_041712_NAR_50mM_plus2.21737.21737.3	3	3.56	1	1.20E+05		(K)ESLCQA	(K)E S/L/C/Q A A L G L I L K E K(A)	C:Carbamidomethylation	185.33	558.3196	1672.93	0.014	8.4	6.24	66923.1	6.88	HUMAN	E9PG35	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (Fragment)
25308	dirMS_041712_NAR_60mM_plus.10090.10090.3	3	3.56	1	3.71E+05		(K)TAVCDI	(K)T A|V/C D I/P P R G L K(M)	C:Carbamidomethylation	110.05	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
25309	dirMS_041712_NAR_60mM_plus.13332.13332.3	3	3.56	1	4.51E+06		(R)VVDLM	(R)V V|D L M A H/M A S K E(-)		126.87	444.2219	1330.649	0.0018	1.3	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
25310	dirMS_041712_NAR_60mM_plus.17814.17814.3	3	3.56	1	8.63E+04		(R)VFIGNL	(R)V F/I/G N L N T L V V K K(S)		150.35	482.3003	1444.889	-0.0023	-1.6	10	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
25311	dirMS_041712_NAR_60mM_plus.17941.17941.3	3	3.56	1	3.58E+05		(K)CEFQDA	(K)C E/F/Q D\A Y V/L L/S E/K K(I)	C:Carbamidomethylation	150.55	577.288	1729.847	0.0029	1.7	4.68	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
25312	dirMS_041712_NAR_120mM_minus.15571.15571.4	4	3.55	2	3.13E+05		(R)EDLRLPE	(R)E D L R L P E/G D L G K E I E/Q K(Y)		138.63	493.0108	1969.024	-0.0023	-1.2	4.36	16346.3	4.85	HUMAN	I3L397	Eukaryotic translation initiation factor 5A-1 (Fragment)
25313	dirMS_041712_NAR_120mM_minus.5470.5470.3	3	3.55	0	7.84E+04		(R)TGIYSST	(R)T G/I/Y S/S/T/S C H K(T)	C:Carbamidomethylation	83.18	414.1973	1240.563	0.0147	11.8	8.28	38077.6	8.9	HUMAN	P09668	Pro-cathepsin H
25314	dirMS_041712_NAR_120mM_minus.5773.5773.3	3	3.55	0	4.34E+04	T969t	(R)LQEGPt	(R)L Q\E G P/t/S|C S G R(V)	C:Carbamidomethylation t:Phosp	85.02	424.5104	1191.542	79.9744	6.3	6	129266.2	5.86	HUMAN	C9JHR8	Scavenger receptor cysteine-rich type 1 protein M130
25315	dirMS_041712_NAR_20mM_minus.13041.13041.2	2	3.55	0	8.44E+05	M73m	(R)AILVDLE	(R)A I\L\V D L/E/P G T m D S V R(S)	m:Oxidized methionine	182.52	816.4184	1615.836	15.9935	-0.8	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
25316	dirMS_041712_NAR_30mM_minus2.16120.16120.2	2	3.55	0	2.24E+04		(K)SEGGFIV	(K)S E|G G/F I W|A C K(N)	C:Carbamidomethylation	141.03	577.7702	1154.53	0.0032	2.8	5.72	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
25317	dirMS_041712_NAR_30mM_minus2.19102.19102.2	2	3.55	1	3.10E+04	M139m	(K)KFmGTE	(K)K F m/G/T E L N G K(T)	m:Oxidized methionine	158.87	570.7897	1124.577	15.9953	0.3	8.59	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
25318	dirMS_041712_NAR_50mM_minus2.11947.11947.3	3	3.55	0	9.95E+03	T165t	(R)IMNLICD	(R)I M N L\I|C\D P D L/t K(V)	C:Carbamidomethylation t:N-ace	136.35	545.9296	1432.717	203.0568	-13.8	4.21	24489.1	10.1	HUMAN	F8VVC7	11-cis retinol dehydrogenase
25319	dirMS_041712_NAR_50mM_minus2.12675.12675.3	3	3.55	1	3.47E+05	T215t	(K)KNMLFS	(K)K\N M L F S G T/N I\t S G K(A)	t:Phosphorylated T	140.6	526.5884	1497.773	79.9777	7.2	10	115515.8	5.42	HUMAN	Q93084	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3
25320	dirMS_041712_NAR_50mM_minus2.17372.17372.3	3	3.55	0	2.01E+05		(R)LLLDGA	(R)L L L D/G A P L I A/I H K(A)		168.32	458.6218	1373.852	-0.0007	-0.5	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
25321	dirMS_041712_NAR_50mM_minus2.8328.8328.3	3	3.55	1	3.36E+05	M1172m M	(K)EMQQm	(K)E/M Q/Q m V K L E/A E m D R(R)	m:Oxidized methionine	116.27	590.5989	1737.797	31.9853	-2.6	4.41	136983.7	6.37	HUMAN	E2QRH8	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-4
25322	dirMS_041712_NAR_60mM_minus.15536.15536.3	3	3.55	1	5.92E+05	M81m	(K)EVNKFQ	(K)E V/N K F Q/m/A/Y/S/N/L L R(A)	m:Oxidized methionine	146.73	576.9619	1712.879	15.9923	-1.5	8.69	14683.8	10.19	HUMAN	P37108	Signal recognition particle 14 kDa protein
25323	dirMS_041712_NAR_60mM_minus.16000.16000.3	3	3.55	1	5.46E+03		(K)AKEIGA	(K)A K E I G A\D\L V/L/Q/I\S/K(E)		147.67	495.6258	1484.868	-0.0054	-3.7	6.11	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
25324	dirMS_041712_NAR_60mM_minus.7180.7180.3	3	3.55	0	7.47E+04		(R)VETQFQ	(R)V E|T Q F/Q N/G H/Y D K(C)		98.7	489.232	1465.671	0.0108	7.4	5.32	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
25325	dirMS_041712_NAR_60mM_minus.7813.7813.3	3	3.55	0	2.41E+04		(R)NIIHGSD	(R)N I\I H G S D\S V/E/S A E K(E)		103.25	495.9133	1485.718	0.0074	5	4.65	17319.6	5.83	HUMAN	P15531	Nucleoside diphosphate kinase A
25326	dirMS_041712_NAR_60mM_minus.7918.7918.3	3	3.55	0	4.20E+04		(R)HPQQLQ	(R)H P Q Q\L Q/H V D|E/R(K)		103.87	462.9072	1386.687	0.0198	14.3	5.99	44456.4	6.1	HUMAN	Q8WTW4	Nitrogen permease regulator 2-like protein
25327	dirMS_041712_NAR_60mM_minus.8988.8988.3	3	3.55	1	3.60E+05	M232m M	(R)MSmKE	(R)M S m K E V\D|E Q/m L/N|V Q N K(N)	m:Oxidized methionine	110.3	652.6318	1923.897	31.9836	-3.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
25328	dirMS_041712_NAR_60mM_minus.9410.9410.3	3	3.55	1	4.92E+04		(R)STTQEL	(R)S T/T Q E/L M/E D D R V K(R)		112.2	517.9146	1551.732	-0.0027	-1.7	4.32	266161	5.68	HUMAN	E9PPU0	Epiplakin
25329	dirMS_041712_NAR_120mM_plus.4473.4473.3	3	3.55	1	3.13E+05		(R)AAEEED	(R)A A/E E E/D E A D/P K R(Q)		72.47	453.8721	1359.602	-0.0005	-0.4	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
25330	dirMS_041712_NAR_120mM_plus.8178.8178.2	2	3.55	0	6.59E+05		(R)YAHVVL	(R)Y A/H/V/V L R(K)		96.78	429.2529	857.499	-0.0007	-0.8	8.75	17718.4	10.99	HUMAN	P62269	40S ribosomal protein S18
25331	dirMS_041712_NAR_120mM_plus.9338.9338.4	4	3.55	1	3.37E+05	M1m	(-)mSEHQK	(-)m S E/H Q K E Q T/L D/T P S L R(T)	m:Oxidized methionine	102.05	479.7354	1899.923	15.9969	1	5.43	50599	5.91	HUMAN	Q92556-3	Isoform 3 of Engulfment and cell motility protein 1
25332	dirMS_041712_NAR_30mM_plus2.12544.12544.2	2	3.55	0	2.50E+05		(R)NCSSFLI	(R)N/C|S/S F L I K(R)	C:Carbamidomethylation	118.65	484.7469	968.487	-0.0005	-0.5	8.75	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
25333	dirMS_041712_NAR_50mM_plus2.13974.13974.3	3	3.55	1	4.41E+04	K118k	(R)EDVYQR	(R)E D/V/Y Q R I V/W L Q E k(V)	k:Ubiquitin-K	142.8	607.3177	1705.891	114.0478	2.7	4.68	20804.1	5.4	HUMAN	K7EKB6	Thimet oligopeptidase (Fragment)
25334	dirMS_041712_NAR_50mM_plus2.14073.14073.3	3	3.55	1	4.18E+05		(K)TSIAIDTI	(K)T/S I/A\I/D T I/I N Q/K R(F)		142.57	491.6191	1472.843	-0.0004	-0.3	8.41	48851.3	9.2	HUMAN	K7EK63	ATP synthase subunit alpha, mitochondrial
25335	dirMS_041712_NAR_50mM_plus2.7107.7107.3	3	3.55	2	5.08E+04	Y21y T28t	(R)yGQNGD	(R)y G Q N/G D/F|t R A L K T V/N K(I)	y:Phosphorylated Y t:Phosph	102.73	657.9666	1811.94	159.9454	6.4	9.7	68448.8	9.63	HUMAN	G5E9Z8	Signal recognition particle 72 kDa protein
25336	dirMS_041712_NAR_60mM_plus.10033.10033.3	3	3.55	0	1.29E+06		(K)GISVHIS	(K)G I|S V/H I S N A E/P K(H)		110.1	417.8951	1251.669	0.0016	1.3	6.75	33803.8	6.12	HUMAN	B1AKP7	TAR DNA binding protein
25337	dirMS_041712_NAR_60mM_plus.14205.14205.3	3	3.55	1	2.55E+04		(R)FASEND	(R)F/A/S E N D L/P E W K E R(G)		129.5	540.9287	1620.765	0.0063	3.9	4.41	19157.5	10.04	HUMAN	C9JDM3	Ran-specific GTPase-activating protein (Fragment)
25338	dirMS_041712_NAR_60mM_plus.14522.14522.3	3	3.55	0	2.01E+05		(-)XGETLGI	(-)X G|E T L G\I I G/L G R(V)		132.28	400.2383	1198.715	-0.0151	-12.6	6	16136.2	8.39	HUMAN	H0Y9M9	C-terminal-binding protein 1 (Fragment)
25339	dirMS_041712_NAR_60mM_plus.17406.17406.3	3	3.55	1	8.46E+05		(R)DKLNNL	(R)D K L N N\L/V L F/D K(A)		148.4	440.2499	1318.737	-0.0014	-1	5.96	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
25340	dirMS_041712_NAR_60mM_plus.17650.17650.3	3	3.55	1	2.77E+05	S86s	(K)AFLWKT	(K)A F/L W K T V G s W/K(T)	s:Phosphorylated S	149.8	468.2401	1322.726	79.9802	9.9	10	28277.1	9.99	HUMAN	H7C2X8	cAMP-regulated phosphoprotein 21 (Fragment)
25341	dirMS_041712_NAR_60mM_plus.19747.19747.3	3	3.55	0	3.30E+05		(R)NSVSNF	(R)N S|V/S N F L H/S L/E R(G)		162.65	468.2401	1402.707	-0.0016	-1.1	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
25342	dirMS_041712_NAR_60mM_plus.6159.6159.3	3	3.55	1	4.61E+05	M22m	(K)EmDEED	(K)E/m/D E/E/D K A\F K(Q)	m:Oxidized methionine	91.48	419.8479	1241.535	15.9937	-1	4.18	7066.2	10	HUMAN	Q9Y2S6	Translation machinery-associated protein 7
25343	dirMS_041712_NAR_120mM_minus.11204.11204.2	2	3.54	1	4.01E+05		(R)LASYLDI	(R)L A\S/Y L D|R V R(S)		114.93	546.811	1092.616	-0.0013	-1.2	8.75	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
25344	dirMS_041712_NAR_120mM_minus.13139.13139.3	3	3.54	1	1.94E+05		(K)LYSIVCG	(K)L Y S I\V/C G\K S T\P E K(E)	C:Carbamidomethylation	125.57	494.6008	1481.767	0.021	14.2	8.5	47111.1	6.28	HUMAN	F5H061	Tumor necrosis factor receptor superfamily member 1A, membrane form
25345	dirMS_041712_NAR_120mM_minus.17468.17468.3	3	3.54	0	9.21E+04	T487t	(K)GNHFQD	(K)G N/H F Q D/G/T I t K(T)	t:N-acetylglucosamine (T)	149.38	474.2316	1217.591	203.0893	7	6.74	75261.9	5.96	HUMAN	Q99467	CD180 antigen
25346	dirMS_041712_NAR_120mM_minus.20189.20189.3	3	3.54	0	3.83E+05		(K)VHLVGID	(K)V H L V\G\I|D\I|F T G K(K)		166.43	433.5866	1298.747	-0.0015	-1.1	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
25347	dirMS_041712_NAR_20mM_minus.13412.13412.3	3	3.54	0	4.55E+05		(K)LRPQVF	(K)L R P\Q V F S/P G D\Y I C R(K)	C:Carbamidomethylation	185.83	569.9577	1707.863	-0.005	-2.9	8.75	76560.3	5.88	HUMAN	Q16280	Cyclic nucleotide-gated olfactory channel
25348	dirMS_041712_NAR_20mM_minus.13545.13545.2	2	3.54	0	1.26E+05		(R)QAQEYE	(R)Q A Q|E/Y/E A L L N I K(V)		186.72	710.3754	1419.748	-0.0043	-3	4.53	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
25349	dirMS_041712_NAR_30mM_minus2.16810.16810.2	2	3.54	0	2.88E+05	M2243m	(K)mSIYQA	(K)m S|I|Y Q/A M/W K(G)	m:Oxidized methionine	145.07	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
25350	dirMS_041712_NAR_30mM_minus2.18919.18919.2	2	3.54	0	6.82E+04		(K)APDFVF	(K)A/P/D|F/V/F\Y A/P R(L)		157.32	591.8008	1182.594	0.0001	0.1	5.88	71218.8	6.3	HUMAN	A7YIJ8	Radixin
25351	dirMS_041712_NAR_30mM_minus2.18942.18942.2	2	3.54	1	5.71E+04		(K)LVEAIEK	(K)L/V/E|A I E K K(G)		157.08	465.2877	929.567	0.0015	1.6	6.14	14934	4.9	HUMAN	H0YB27	Phosphatidylinositol 3-kinase regulatory subunit alpha (Fragment)
25352	dirMS_041712_NAR_30mM_minus2.19311.19311.2	2	3.54	0	2.12E+05		(R)LTIAILR	(R)L T|I/A I L R(H)		159.48	400.2731	799.54	-0.0011	-1.3	9.75	87498	6.43	HUMAN	C9J266	E3 ubiquitin-protein ligase RNF123
25353	dirMS_041712_NAR_40mM_minus2.12137.12137.3	3	3.54	0	2.91E+05		(R)LQQELD	(R)L Q\Q/E L D D L T V/D L/D/H Q R(Q)		154.27	646.6596	1937.956	0.0079	4.1	4.03	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
25354	dirMS_041712_NAR_60mM_minus.16400.16400.3	3	3.54	2	1.17E+05		(K)ISDVKSR	(K)I S|D V/K S R V Q/D L W R(G)		150.6	534.6361	1601.876	0.0179	11.2	8.75	282124	6.12	HUMAN	Q7Z2Y8	Interferon-induced very large GTPase 1
25355	dirMS_041712_NAR_60mM_minus.5127.5127.3	3	3.54	0	4.68E+03	S237s	(K)NsLFEFV	(K)N/s/L F E F V S/E H R(L)	s:N-acetylglucosamine (S)	83.28	523.2497	1364.659	203.0752	-2.7	5.4	36157	10.84	HUMAN	C9JAQ0	Protein SSUH2 homolog
25356	dirMS_041712_NAR_60mM_minus.8881.8881.3	3	3.54	1	3.60E+05	M357m	(K)TDSDMF	(K)T D/S D M R L m\Q/G D E I/C L R(Y)	C:Carbamidomethylation m:Oxid	110.3	652.6318	1939.867	16.0138	9.7	4.22	124345.8	6.24	HUMAN	Q92900-2	Isoform 2 of Regulator of nonsense transcripts 1
25357	dirMS_041712_NAR_120mM_plus.14200.14200.4	4	3.54	2	1.80E+06	S13s	(-)XAEQQSI	(-)X A\E Q Q S K A\V F G R s V S T G K(L)	s:Phosphorylated S	127.23	494.0077	1893.019	79.9901	12.1	9.99	21418.7	5.32	HUMAN	K7EIU2	Serine/threonine-protein kinase ULK2 (Fragment)
25358	dirMS_041712_NAR_120mM_plus.4362.4362.3	3	3.54	1	2.01E+05		(K)IKTDNGI	(K)I K T D N G P/G Y C/S K(A)	C:Carbamidomethylation	71.1	447.2112	1339.631	-0.012	-9	8.5	115965.7	9.46	HUMAN	P10266	HERV-K_5q33.3 provirus ancestral Pol protein
25359	dirMS_041712_NAR_120mM_plus.9183.9183.3	3	3.54	1	1.06E+06		(R)EQAEEE	(R)E\Q/A/E E E/R Y F R(A)		101.13	452.8785	1356.618	0.0031	2.3	4.5	12248.6	9.34	HUMAN	Q9UII2	ATPase inhibitor, mitochondrial
25360	dirMS_041712_NAR_20mM_plus.15343.15343.3	3	3.54	0	3.85E+04	M73m	(R)AILVDLE	(R)A I\L\V D L E/P/G T\m D S V R(S)	m:Oxidized methionine	177.93	544.6139	1615.836	15.9912	-2.3	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
25361	dirMS_041712_NAR_20mM_plus.15982.15982.2	2	3.54	0	1.17E+05		(R)GTPLISP	(R)G T/P L/I/S P L I K(W)		181.27	519.8306	1038.656	-0.0018	-1.8	8.75	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
25362	dirMS_041712_NAR_20mM_plus.7463.7463.2	2	3.54	0	1.21E+05		(K)AQYEDI	(K)A Q|Y\E/D I/A N R(S)		120.45	540.2601	1079.512	0.0013	1.2	4.37	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
25363	dirMS_041712_NAR_20mM_plus.8623.8623.2	2	3.54	0	7.78E+03		(R)ELSEQL	(R)E L/S E Q/L G Q\A E/R(A)		129.77	630.3137	1259.623	-0.0025	-2	4.25	266161	5.68	HUMAN	E9PPU0	Epiplakin
25364	dirMS_041712_NAR_30mM_plus2.21085.21085.2	2	3.54	0	1.43E+04		(R)EMVLEII	(R)E M V|L/E/I I R(E)		163.6	501.7877	1002.565	0.0029	2.9	4.53	61981.6	8.97	HUMAN	Q96I24	Far upstream element-binding protein 3
25365	dirMS_041712_NAR_30mM_plus2.21777.21777.2	2	3.54	0	1.49E+05		(K)ANFLQN	(K)A N/F L/Q N M I/E D R(T)		170.22	675.8282	1350.647	0.0021	1.5	4.37	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
25366	dirMS_041712_NAR_30mM_plus2.22569.22569.2	2	3.54	0	1.91E+04		(R)FLTWIL	(R)F L|T/W I\L N R(Y)		175.12	531.8078	1062.61	-0.0012	-1.1	9.75	35548.6	4.91	HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
25367	dirMS_041712_NAR_30mM_plus2.8497.8497.2	2	3.54	0	4.21E+05		(R)AVNYFS	(R)A V|N/Y\F S K(V)		98.73	414.7159	828.425	-0.0005	-0.6	8.63	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
25368	dirMS_041712_NAR_30mM_plus2.9119.9451.2	2	3.54	0	5.53E+05		(R)MQSFGI	(R)M/Q|S F/G M/K(T)		102.12	414.6908	828.374	0.0001	0.1	8.5	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
25369	dirMS_041712_NAR_40mM_plus2.11526.11526.2	2	3.54	0	1.27E+05		(R)FPGQLN	(R)F/P|G/Q L N A/D/L R(K)		134.2	565.7995	1130.595	-0.0036	-3.1	5.84	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
25370	dirMS_041712_NAR_60mM_plus.16724.16724.3	3	3.54	1	4.68E+04		(K)VGEVIVT	(K)V/G|E\V/I V T K D D A M L L K(G)		144.18	544.3059	1630.908	-0.0053	-3.2	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
25371	dirMS_041712_NAR_60mM_plus.18894.18894.3	3	3.54	0	5.48E+05		(K)GISDLAC	(K)G I/S D L A/Q H/Y L M R(A)		155.78	468.5804	1403.71	0.0167	11.9	6.74	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
25372	dirMS_041712_NAR_60mM_plus.6364.6364.3	3	3.54	0	1.27E+05		(R)ASVPSV	(R)A/S|V P/S V Q I Q G Q R(I)		92.5	423.898	1269.691	-0.0115	-9.1	9.79	47091.3	10.55	HUMAN	B4DKZ7	Transcriptional repressor p66-alpha
25373	dirMS_041712_NAR_120mM_minus.17522.17522.4	4	3.53	1	5.43E+05		(R)GFGHIG	(R)G F G H I G I\A V|P D/V Y S A C K R(F)	C:Carbamidomethylation	150.4	487.502	1946.991	-0.0044	-2.2	8.6	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
25374	dirMS_041712_NAR_120mM_minus.5622.5622.3	3	3.53	0	1.10E+05	K340k	(K)VEDQPE	(K)V/E/D Q P E k V/M A K(Q)	k:Ubiquitin-K	84.03	463.2365	1273.646	114.0493	4.6	4.68	51675.5	6.46	HUMAN	F8W8J7	NGFI-A-binding protein 1
25375	dirMS_041712_NAR_120mM_minus.8725.8725.2	2	3.53	0	1.04E+06	K41k	(K)LMkHEK	(K)L/M k/H\E K(L)	k:Ubiquitin-K	102.27	450.238	785.434	114.0349	-8.9	8.6	31950	4.83	HUMAN	B5MDL5	Mitogen-activated protein kinase 12
25376	dirMS_041712_NAR_120mM_minus.9653.9653.3	3	3.53	1	1.97E+05		(K)IRSLQEC	(K)I/R S L\Q E\Q A|D|A A/E E R(A)		106.9	539.2683	1615.803	-0.0131	-8.1	4.41	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
25377	dirMS_041712_NAR_20mM_minus.14153.14153.2	2	3.53	0	7.07E+03		(R)YLTVAA	(R)Y L/T/V/A A V F R(G)		195.1	520.3009	1039.593	0.001	1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
25378	dirMS_041712_NAR_20mM_minus.9087.9087.2	2	3.53	0	1.78E+04	M239m	(K)EITALAP	(K)E I T|A/L A/P S T/m\K(I)	m:Oxidized methionine	139.97	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
25379	dirMS_041712_NAR_20mM_minus.9164.9164.2	2	3.53	0	1.98E+04		(K)LVSESSD	(K)L V|S E S S D V/L/P K(-)		140.43	587.321	1173.636	-0.0014	-1.2	4.37	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
25380	dirMS_041712_NAR_30mM_minus2.14647.14647.2	2	3.53	0	2.77E+05		(R)IILLAEG	(R)I I|L L A E/G R(L)		132.68	442.7816	884.556	-0.0005	-0.5	6	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
25381	dirMS_041712_NAR_30mM_minus2.18333.18333.2	2	3.53	0	2.00E+05	K411k	(R)LTTTSLN	(R)L T/T/T S L N k(H)	k:Ubiquitin-K	154.47	496.277	877.499	114.0478	4.9	8.75	70441.2	9.69	HUMAN	Q969P6	DNA topoisomerase I, mitochondrial
25382	dirMS_041712_NAR_30mM_minus2.4992.4992.2	2	3.53	0	1.22E+05		(R)ENDEFC	(R)E/N|D E F/C K(M)	C:Carbamidomethylation	80.23	471.188	941.367	0.0018	1.9	4.14	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
25383	dirMS_041712_NAR_30mM_minus2.5782.5782.2	2	3.53	0	9.22E+04	M57m	(K)EmGTPD	(K)E m G T/P/D/V/R(I)	m:Oxidized methionine	85.88	460.7171	904.419	16.0076	13.8	4.37	15175.4	10.46	HUMAN	B7Z4C8	60S ribosomal protein L31
25384	dirMS_041712_NAR_30mM_minus2.6937.6937.2	2	3.53	0	8.10E+04		(R)SAEEGEI	(R)S A|E|E/G E/L A/E/S K(S)		92.15	575.2682	1149.527	0.0021	1.9	4.09	182819.3	4.77	HUMAN	Q9C0C2	182 kDa tankyrase-1-binding protein
25385	dirMS_041712_NAR_30mM_minus2.7139.7139.2	2	3.53	0	1.16E+05		(K)MQAVQ	(K)M Q|A|V/Q E A T/R(L)		94	517.257	1033.509	-0.0028	-2.7	5.75	533778	5.74	HUMAN	Q15149	Plectin
25386	dirMS_041712_NAR_30mM_minus2.8028.8028.2	2	3.53	0	2.04E+04		(R)TSTSQA	(R)T S|T/S Q A/V F R(L)		98.32	498.7592	996.511	0.0002	0.2	9.41	20139.7	9.34	HUMAN	C9J7S3	Aspartate--tRNA ligase, cytoplasmic (Fragment)
25387	dirMS_041712_NAR_40mM_minus2.11488.11488.3	3	3.53	2	1.30E+04		(R)NGDRYF	(R)N G/D R Y F K G/I V Y\A V S S D R(F)		151.05	649.6701	1946.972	0.0238	12.2	8.5	13189.7	10.18	HUMAN	E7EU50	Neuronal migration protein doublecortin (Fragment)
25388	dirMS_041712_NAR_50mM_minus2.11650.11650.3	3	3.53	0	1.02E+05		(K)AQIHDL	(K)A Q I H D L V|L|V G/G S T R(I)		134.53	489.2711	1465.812	-0.0134	-9.1	6.79	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
25389	dirMS_041712_NAR_50mM_minus2.17256.17256.3	3	3.53	0	6.09E+03	M459m	(K)IYYRPAL	(K)I Y Y R P A L/m T/A I D G R(H)	m:Oxidized methionine	165.92	552.6273	1639.863	16.0049	6	8.59	63996.6	6.98	HUMAN	H0Y2W3	Protein FAM35A (Fragment)
25390	dirMS_041712_NAR_50mM_minus2.17367.17367.3	3	3.53	0	2.29E+05		(K)VAHALA	(K)V A H A L\A\E\G\L/G\V I/A C I G E K(L)	C:Carbamidomethylation	168.25	603.3247	1807.974	-0.0139	-7.7	5.4	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
25391	dirMS_041712_NAR_50mM_minus2.7241.7241.3	3	3.53	1	5.55E+04	M754m	(K)TCVFEKE	(K)T C/V/F E K E N D/P S V m R(S)	C:Carbamidomethylation m:Oxid	108.07	576.5935	1711.778	15.9881	-3.9	4.68	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
25392	dirMS_041712_NAR_60mM_minus.10843.10843.3	3	3.53	0	7.56E+04		(R)TIVITSHI	(R)T I/V/I/T S H/P G Q I V K(H)		120.03	464.9423	1392.821	-0.0086	-6.2	8.44	27999.4	5.61	HUMAN	B7Z5C0	DnaJ homolog subfamily A member 1

25393	dirMS_041712_NAR_120mM_plus.10535.10535.3	3	3.53	1	6.74E+05		(R)FYKNEG	(R)F Y/K N\E G/G/T W S/V E K(V)		109	515.5841	1544.738	-0.0002	-0.2	6.14	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
25394	dirMS_041712_NAR_120mM_plus.11902.11902.3	3	3.53	1	1.87E+04	M1m T8t	(-)mSSHKTI	(-)m S|S H|K T F t I\K(R)	m:Oxidized methionine t:Pho	116.32	425.869	1179.619	95.9734	9.5	10	6292.4	12.41	HUMAN	Q96EH5	60S ribosomal protein L39-like
25395	dirMS_041712_NAR_120mM_plus.13679.13679.3	3	3.53	1	1.33E+05		(R)KYEMFA	(R)K Y E M F A\Q\T/L/Q Q/S/R(G)		124.65	543.9369	1629.805	-0.0092	-5.6	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
25396	dirMS_041712_NAR_120mM_plus.9622.9622.3	3	3.53	1	7.40E+04		(R)TFKEICA	(R)T\F K E I C/A V/S R(I)	C:Carbamidomethylation	102.52	404.2141	1210.625	0.0029	2.4	8.41	25558.6	9.3	HUMAN	B1APE1	General transcription factor IIB (Fragment)
25397	dirMS_041712_NAR_20mM_plus.11374.11374.2	2	3.53	0	1.91E+05		(R)YALYDA	(R)Y A\L/Y D A T Y E/T K(E)		150.8	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
25398	dirMS_041712_NAR_20mM_plus.8706.8706.3	3	3.53	0	1.41E+05	M224m	(K)GGKPEP	(K)G G K P E P P A m P Q P\V P T/A(-)	m:Oxidized methionine	130.62	530.6038	1573.804	15.9926	-1.5	6	25541.5	9.92	HUMAN	E9PL09	40S ribosomal protein S3
25399	dirMS_041712_NAR_30mM_plus2.14461.14461.3	3	3.53	0	1.03E+04		(K)VNQIGS	(K)V N\Q I\G S V T|E/S I/Q A C K(L)	C:Carbamidomethylation	127.72	545.28	1633.821	0.0041	2.5	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
25400	dirMS_041712_NAR_30mM_plus2.15795.15795.2	2	3.53	0	5.03E+05		(R)LVPHPTI	(R)L V/P H/P T/R(A)		135.4	410.2436	819.484	-0.0036	-4.4	9.75	38149	6.38	HUMAN	Q8WUA8	Tsukushin
25401	dirMS_041712_NAR_30mM_plus2.19871.19871.2	2	3.53	1	2.55E+05		(K)LTLDQLI	(K)L T|L/D Q L K M R(C)		157.35	559.3295	1117.64	0.0119	10.7	8.75	98559.7	8.5	HUMAN	Q99665	Interleukin-12 receptor subunit beta-2
25402	dirMS_041712_NAR_30mM_plus2.20695.20695.2	2	3.53	0	1.01E+05		(K)NLQEEIL	(K)N L|Q/E/E I D A L/E\S R(V)		162.52	708.8513	1416.697	-0.0012	-0.8	4	15712.4	4.48	HUMAN	E9PQY2	Prefoldin subunit 4
25403	dirMS_041712_NAR_30mM_plus2.6558.6558.2	2	3.53	0	8.62E+04		(K)SLDEME	(K)S L/D E M E/K(Q)		87.63	426.1971	851.381	0.0054	6.4	4.14	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
25404	dirMS_041712_NAR_30mM_plus2.7174.7174.2	2	3.53	0	2.12E+04		(R)FYQQVT	(R)F/Y/Q Q V T K(D)		91.88	457.2405	913.478	-0.0041	-4.5	8.59	253486.5	5.51	HUMAN	J3KNL6	Protein transport protein Sec16A
25405	dirMS_041712_NAR_40mM_plus2.5071.5071.2	2	3.53	0	2.46E+05	Y236y	(K)GyVDDP	(K)G y V D/D|P R(N)	y:Phosphorylated Y	84.87	451.1811	821.379	79.9761	10.9	4.21	31653.2	8.92	HUMAN	H7C386	ADP-ribose pyrophosphatase, mitochondrial (Fragment)
25406	dirMS_041712_NAR_40mM_plus2.6444.6444.2	2	3.53	0	1.39E+05		(K)SLESINSI	(K)S L|E/S I N S R(L)		96.85	453.2358	905.469	-0.0044	-4.8	5.72	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
25407	dirMS_041712_NAR_50mM_plus2.13597.13597.3	3	3.53	1	5.62E+05		(K)SLYDEV	(K)S L Y/D/E V A A/Q G E V V R K(L)		139.82	555.2908	1663.865	-0.0071	-4.3	4.68	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
25408	dirMS_041712_NAR_50mM_plus2.14086.14086.3	3	3.53	0	1.76E+06	M457m	(R)mGPLGL	(R)m G|P L/G L D/H/M A S S I E R(M)	m:Oxidized methionine	142.73	543.9304	1613.777	15.9992	2.6	5.3	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
25409	dirMS_041712_NAR_50mM_plus2.18880.18880.3	3	3.53	0	2.77E+05		(K)LAKPLSS	(K)L A K|P L S S L T|P L I/M A A K(E)		167.55	552.004	1653.997	0.0003	0.2	10	24711.4	5.19	HUMAN	H7C1X3	PAK-2p34 (Fragment)
25410	dirMS_041712_NAR_50mM_plus2.19952.19952.3	3	3.53	0	3.74E+05		(K)NGGLGI	(K)N G G/L G H M N\I|A|L/L/S/D L T K(Q)		173.03	585.311	1753.927	-0.0081	-4.6	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
25411	dirMS_041712_NAR_50mM_plus2.21643.21643.3	3	3.53	1	1.07E+04	T145t	(R)YTTILtPI	(R)Y/T/T/I L t P K T I I K(S)	t:N-acetylglucosamine (T)	183.92	532.3178	1391.851	203.088	5.4	9.7	36389.9	9.05	HUMAN	Q8NGJ2	Olfactory receptor 52H1
25412	dirMS_041712_NAR_50mM_plus2.9404.9404.3	3	3.53	1	8.96E+04	T282t	(R)VSTGtKI	(R)V S/T/G t K F A\L K(L)	t:N-acetylglucosamine (T)	116.7	418.9081	1051.615	203.0951	12.6	10	36151	6.2	HUMAN	P0C025	Nucleoside diphosphate-linked moiety X motif 17
25413	dirMS_041712_NAR_60mM_plus.14073.14073.3	3	3.53	0	1.87E+06		(K)GIHPTIIS	(K)G I H P T\I/I|S E/S F Q K(A)		130.65	486.2646	1456.78	-0.0002	-0.1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
25414	dirMS_041712_NAR_60mM_plus.17205.17205.3	3	3.53	0	1.53E+04		(K)EGHVEV	(K)E G H V E V|V S E/L L/Q R(E)		148.27	498.9326	1494.791	-0.0078	-5.2	4.75	48586.6	9.32	HUMAN	D6RCB2	Ankyrin-3
25415	dirMS_041712_NAR_60mM_plus.18021.18021.3	3	3.53	1	8.54E+04	S1417s	(K)KEEDVS	(K)K E E D V S Y|L/s G Q/L/S E\K(E)	s:N-acetylglucosamine (S)	151.25	638.979	1711.839	203.084	2.4	4.41	378557.2	4.96	HUMAN	E7EP74	Golgin subfamily B member 1
25416	dirMS_041712_NAR_120mM_minus.10514.10514.2	2	3.52	1	2.92E+05	K33k	(K)IMREkAI	(K)I/M/R E k/A/K(E)	k:Ubiquitin-K	111.28	495.2884	875.513	114.0564	13.6	9.99	13533.5	9.82	HUMAN	H7C3D8	COX assembly mitochondrial protein homolog (Fragment)
25417	dirMS_041712_NAR_20mM_minus.10303.10303.3	3	3.52	0	3.90E+03		(R)ELIQEYG	(R)E L\I Q E/Y G A Q S G G L E K(L)		152.13	541.2755	1621.807	0.0052	3.2	4.25	266161	5.68	HUMAN	E9PPU0	Epiplakin
25418	dirMS_041712_NAR_20mM_minus.13164.13164.2	2	3.52	0	2.52E+05		(R)GNPTVE	(R)G N/P T\V/E V D L F T S K(G)		183.18	703.8605	1406.716	-0.0025	-1.8	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
25419	dirMS_041712_NAR_30mM_minus2.19368.19368.2	2	3.52	0	5.23E+05		(R)LFDQAF	(R)L F/D Q/A/F G L|P R(L)		161.92	582.315	1163.621	0.002	1.7	5.84	20576.9	9.84	HUMAN	F8WE04	Heat shock protein beta-1
25420	dirMS_041712_NAR_40mM_minus2.11617.11617.3	3	3.52	1	1.06E+05	T136t	(R)ILHKLCQ	(R)I L/H K L C Q G/L G L/N L t K(F)	C:Carbamidomethylation t:Phosp	152.32	596.6671	1707.994	79.9929	14.9	10	63108.1	9.01	HUMAN	Q96RQ9	L-amino-acid oxidase
25421	dirMS_041712_NAR_40mM_minus2.12123.12123.3	3	3.52	0	2.87E+05		(R)LQQELD	(R)L/Q/Q/E L D D L T V D L D/H Q R(Q)		154.23	646.6596	1937.956	0.0079	4.1	4.03	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
25422	dirMS_041712_NAR_50mM_minus2.14425.14425.3	3	3.52	1	8.33E+04		(R)LSQELEY	(R)L/S Q E/L E/Y L/T/E D V K/R(L)		149.87	574.9724	1722.891	0.0118	6.8	4.41	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
25423	dirMS_041712_NAR_60mM_minus.10896.10896.3	3	3.52	1	5.49E+05	M112m	(R)EmDRET	(R)E m/D/R E T|L\I/D|V A R(T)	m:Oxidized methionine	121.17	488.5781	1447.721	15.9988	2.6	4.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
25424	dirMS_041712_NAR_60mM_minus.11971.11971.3	3	3.52	1	2.41E+05	N456n	(R)LRADnTI	(R)L R A\D/n/T L V/A V/K(S)	n:N-acetylglucosamine (N)	126.9	468.2618	1199.711	203.0602	-13.7	8.75	77484.4	6.25	HUMAN	E7ENM8	Tyrosine-protein kinase Fes/Fps
25425	dirMS_041712_NAR_60mM_minus.13704.13704.3	3	3.52	2	2.78E+05	N64n	(R)ILAKSnE	(R)I L A\K S n/E/D L K K(K)	n:N-acetylglucosamine (N)	136.02	487.934	1258.737	203.0509	-19.5	8.5	62156.9	9.16	HUMAN	Q8ND07	Coiled-coil domain-containing protein 176
25426	dirMS_041712_NAR_60mM_minus.13789.13789.3	3	3.52	1	2.42E+05	K2263k	(K)AASAAQ	(K)A A S\A/A/Q R E L V A Q G k(V)	k:Ubiquitin-K	136.62	505.2679	1399.765	114.0239	-12.5	8.79	260187.7	6.1	HUMAN	Q5TCU6	Talin 1
25427	dirMS_041712_NAR_60mM_minus.8766.8766.3	3	3.52	1	3.21E+04		(R)FVKQDC	(R)F/V/K Q D\Q/V C I A R(L)	C:Carbamidomethylation	109.12	455.2427	1363.715	-0.0015	-1.1	8.75	53458.1	5.47	HUMAN	H3BR35	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A (Fragment)
25428	dirMS_041712_NAR_120mM_plus.4800.4800.3	3	3.52	0	4.66E+03	M76m M7	(R)LTNSmN	(R)L/T/N S/m\M m H\G R(N)	m:Oxidized methionine	77.6	403.8446	1177.527	31.9918	1.6	9.75	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
25429	dirMS_041712_NAR_120mM_plus.7967.7967.2	2	3.52	0	2.60E+05		(K)FHSQLM	(K)F/H|S Q L/M/R(L)		95.58	459.7341	918.461	-0.0005	-0.6	9.75	10225.7	7.97	HUMAN	P49458	Signal recognition particle 9 kDa protein
25430	dirMS_041712_NAR_20mM_plus.11178.11178.2	2	3.52	0	6.82E+03		(R)TIYAGN	(R)T I/Y|A G N A L/C T V K(C)	C:Carbamidomethylation	149.13	655.8428	1310.677	0.001	0.8	8.26	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
25431	dirMS_041712_NAR_20mM_plus.12571.12571.2	2	3.52	1	1.31E+05		(K)LDKTLQI	(K)L D|K\T L Q R(F)		158.85	437.2558	873.515	-0.0109	-12.5	8.75	42217.6	6.36	HUMAN	A2RU49	Hydroxylysine kinase
25432	dirMS_041712_NAR_20mM_plus.18865.18865.3	3	3.52	0	1.01E+05		(R)AAVPSG	(R)A A V|P S G A S/T G I Y E A L E L R(D)		201.5	602.3183	1804.944	-0.0036	-2	4.53	43048.9	4.99	HUMAN	B7Z2X9	Enolase
25433	dirMS_041712_NAR_20mM_plus.7778.7778.2	2	3.52	0	6.78E+04		(R)AQYDEL	(R)A Q|Y/D/E L A/R(K)		123.52	483.2393	965.469	0.0026	2.7	4.37	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
25434	dirMS_041712_NAR_40mM_plus2.11301.11301.3	3	3.52	0	3.11E+04		(K)LQALAN	(K)L Q|A\L A\N E Q A A/A A H E L E K(M)		132.83	602.981	1806.935	-0.006	-3.3	4.75	156557.7	5.52	HUMAN	Q86UP2	Kinectin
25435	dirMS_041712_NAR_40mM_plus2.12844.12844.2	2	3.52	0	2.97E+04		(R)FGLNVS	(R)F/G L N V/S S I/S R(K)		141.92	540.2954	1079.584	-0.0009	-0.8	9.75	24161.9	5.27	HUMAN	F8VZQ9	SAP domain-containing ribonucleoprotein
25436	dirMS_041712_NAR_40mM_plus2.16564.16564.3	3	3.52	1	1.42E+05	S589s M59	(K)LLsmAYS	(K)L\L s m/A\Y S/A V/G K L S S R(M)	s:N-acetylglucosamine (S) m:	164	601.3202	1582.862	219.0839	5.3	9.99	225629.8	9.3	HUMAN	J3KN16	Protein KIAA0368
25437	dirMS_041712_NAR_40mM_plus2.6855.6855.2	2	3.52	0	5.95E+04		(K)CCTESLV	(K)C C/T|E/S/L V N R(R)	C:Carbamidomethylation	100.58	569.7569	1138.498	0.0086	7.5	6	57751.3	6.9	HUMAN	B7WNR0	Serum albumin
25438	dirMS_041712_NAR_50mM_plus2.13827.13827.3	3	3.52	1	5.97E+05		(K)GGELVY	(K)G G E\L|V/Y/T D S E A R D V F E K(A)		141.28	638.9735	1914.908	-0.002	-1.1	4.18	533778	5.74	HUMAN	Q15149	Plectin
25439	dirMS_041712_NAR_50mM_plus2.16137.16137.3	3	3.52	0	2.73E+04	S205s	(R)GVDLHE	(R)G V/D L H E Q/s Q Q N K(S)	s:N-acetylglucosamine (S)	152.35	529.2635	1382.666	203.1101	19.4	5.32	23934.6	8.71	HUMAN	P61020	Ras-related protein Rab-5B
25440	dirMS_041712_NAR_60mM_plus.11451.11451.3	3	3.52	0	4.84E+05		(K)NFYVEH	(K)N F/Y/V E/H/P E V A R(L)		117.65	454.2286	1360.664	0.0068	5	5.4	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
25441	dirMS_041712_NAR_60mM_plus.13062.13062.2	2	3.52	0	6.28E+05	N255n	(K)LNNSSP	(K)L N N S S P/n S S G G|V K(E)	n:N-acetylglucosamine (N)	125.17	732.3483	1260.618	203.0715	-5.4	8.75	45094.4	6.38	HUMAN	B4DNK7	RNA polymerase II elongation factor ELL2
25442	dirMS_041712_NAR_60mM_plus.18505.18505.3	3	3.52	1	1.01E+06		(R)VSFELFA	(R)V S\F/E L F/A D K V/P K(T)		155.47	460.5914	1379.757	0.0027	2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
25443	dirMS_041712_NAR_60mM_plus.19851.19851.3	3	3.52	0	1.43E+05	S2s M10m	(-)XsPLLLAS	(-)X/s P L L L A S/G m A R(D)	s:N-acetylglucosamine (S) m:	163.97	483.2704	1228.708	219.0884	9.8	9.75	2139.5	5.96	HUMAN	H0YJJ7	Creatine kinase B-type (Fragment)
25444	dirMS_041712_NAR_60mM_plus.6405.6405.3	3	3.52	0	2.18E+05	M26m K33	(K)DYmILS	(K)D Y/m I L S G/P/Q\k(T)	m:Oxidized methionine k:Ub	92.18	427.8711	1151.576	130.0222	-12.2	5.83	40421.8	9.26	HUMAN	P34972	Cannabinoid receptor 2
25445	dirMS_041712_NAR_120mM_minus.12968.12968.3	3	3.51	1	1.43E+05		(R)VGDLYSI	(R)V/G D\L Y/S D L R D G/R(N)		124.9	455.898	1365.676	0.0037	2.7	4.43	13611	6.13	HUMAN	E9PJZ2	Spectrin beta chain, non-erythrocytic 2 (Fragment)
25446	dirMS_041712_NAR_120mM_minus.13473.13473.3	3	3.51	0	7.83E+04		(K)LSLGTYA	(K)L S\L/G/T Y A/S L/H G/R(I)		128.13	425.5623	1274.685	-0.0128	-10.1	8.75	67446.5	5.63	HUMAN	F8VQE1	LIM domain and actin-binding protein 1
25447	dirMS_041712_NAR_120mM_minus.18312.18312.3	3	3.51	0	8.75E+04		(R)DGLAFN	(R)D G\L A|F/N A L I H R(H)		154.33	409.5584	1226.664	-0.0034	-2.8	6.74	146974	5.55	HUMAN	C9JRP8	Spectrin beta chain, non-erythrocytic 4
25448	dirMS_041712_NAR_120mM_minus.5448.5448.2	2	3.51	0	4.20E+04		(R)VGEFCH	(R)V/G\E/F/C H N R(G)	C:Carbamidomethylation	83.02	509.7318	1018.452	0.004	3.9	6.72	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
25449	dirMS_041712_NAR_120mM_minus.8038.8038.3	3	3.51	0	2.04E+05		(K)HEQNID	(K)H E Q\N\I D|C/G G G Y V/K(L)	C:Carbamidomethylation	97.95	492.8901	1476.654	0.0021	1.5	5.32	48311.8	4.29	HUMAN	P27797	Calreticulin
25450	dirMS_041712_NAR_120mM_minus.9884.9884.3	3	3.51	1	6.41E+05		(R)AREQAE	(R)A R E Q A E\A E\V/A/S/L N\R(R)		107.8	515.2649	1543.782	-0.0022	-1.4	4.79	11017	4.8	HUMAN	D6R904	Tropomyosin alpha-3 chain
25451	dirMS_041712_NAR_20mM_minus.10951.10951.2	2	3.51	0	1.58E+05		(K)IDIIPNP	(K)I D/I\I/P N P Q E R(T)		157.38	597.8271	1194.648	-0.0008	-0.7	4.37	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
25452	dirMS_041712_NAR_20mM_minus.11661.11661.2	2	3.51	0	1.66E+05		(R)VEVTEFI	(R)V E|V/T E F E D/I/K(S)		164.77	604.8043	1208.604	-0.0032	-2.6	4	30992.3	4.14	HUMAN	B2REB8	Protein SET
25453	dirMS_041712_NAR_30mM_minus2.9637.9637.2	2	3.51	0	2.74E+05		(K)ILEMWK	(K)I L/E M W K(D)		106.38	410.2222	819.443	-0.0062	-7.6	6	18937	10.12	HUMAN	B7Z1I7	Nik-related protein kinase
25454	dirMS_041712_NAR_50mM_minus2.17925.17925.3	3	3.51	1	1.70E+05	T94t	(R)LGQEAt	(R)L G Q/E/A t/G/I V R A I R(D)	t:N-acetylglucosamine (T)	171.33	529.6358	1383.807	203.0862	4.3	9.6	91839.6	9.22	HUMAN	B4E3P0	ATP-citrate synthase
25455	dirMS_041712_NAR_50mM_minus2.18791.18791.3	3	3.51	1	2.02E+06		(R)LIALLEVI	(R)L/I A|L L/E/V L/S Q K R(M)		183.65	461.6289	1382.873	-0.0008	-0.6	8.75	280326.9	5.48	HUMAN	O75369	Filamin-B
25456	dirMS_041712_NAR_50mM_minus2.8293.8293.3	3	3.51	0	4.48E+04	M96m	(R)DSDAFS	(R)D S D A\F S T/L m P S S\V K(A)	m:Oxidized methionine	114.83	500.9062	1484.694	16.0103	10.3	4.21	11629.9	10.21	HUMAN	Q9BRY0-2	Isoform 2 of Zinc transporter ZIP3
25457	dirMS_041712_NAR_50mM_minus2.9852.9852.3	3	3.51	0	8.02E+04	K865k	(K)NDNLQI	(K)N D N L\Q/k/I/I K(L)	k:Ubiquitin-K	123.92	400.5678	1085.631	114.0575	12.2	8.59	166548.7	5.26	HUMAN	A2RUR9	Coiled-coil domain-containing protein 144A
25458	dirMS_041712_NAR_60mM_minus.15421.15421.3	3	3.51	1	3.11E+04		(R)VEKIPGC	(R)V E/K I\P\G G\I|I/E D S C V L\R(G)	C:Carbamidomethylation	144.78	595.6552	1784.958	-0.0064	-3.6	4.68	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
25459	dirMS_041712_NAR_60mM_minus.18322.18322.3	3	3.51	1	1.37E+05		(R)SELELTL	(R)S E|L/E L/T/L/G K L E Q V R(S)		163.05	538.9724	1614.906	-0.0035	-2.1	4.78	533778	5.74	HUMAN	Q15149	Plectin
25460	dirMS_041712_NAR_60mM_minus.6144.6144.3	3	3.51	0	1.96E+05	M171m	(K)DImPFS	(K)D/I\m P F S A\Q\V G D E/R(M)	m:Oxidized methionine	92.5	494.235	1464.679	16.0117	11.3	4.03	45440.8	9.83	HUMAN	H7C3W7	Taste receptor type 1 member 1 (Fragment)
25461	dirMS_041712_NAR_120mM_plus.10091.10091.4	4	3.51	0	2.44E+05		(R)GHAAFT	(R)G H A A F T\S D P K/P T I\E V/S/G K(K)		105.2	461.2368	1841.939	-0.0138	-7.5	6.75	15844.7	6.65	HUMAN	E5RI06	Glutathione reductase, mitochondrial (Fragment)
25462	dirMS_041712_NAR_120mM_plus.15632.15632.4	4	3.51	2	7.26E+05		(R)KTVGVE	(R)K T V G V\E|P/A A D G K G V V V V I K(R)		135.47	467.2783	1866.106	-0.0145	-7.8	8.5	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
25463	dirMS_041712_NAR_120mM_plus.17144.17144.3	3	3.51	2	7.18E+05		(R)NLKASLI	(R)N L/K/A/S L E N S\L R E V E/A R(Y)		143.33	610.332	1828.988	-0.0061	-3.3	6.23	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
25464	dirMS_041712_NAR_120mM_plus.4781.4781.3	3	3.51	0	3.19E+04	M76m M7	(R)LTNSmN	(R)L/T|N\S m M m H G R(N)	m:Oxidized methionine	76.82	403.8446	1177.527	31.9918	1.6	9.75	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
25465	dirMS_041712_NAR_20mM_plus.10239.10239.2	2	3.51	0	1.15E+05	M189m M	(K)SLAmEm	(K)S L|A/m/E m V L T/G D R(I)	m:Oxidized methionine	143.35	677.8247	1322.644	31.9978	5.9	4.37	31843.3	8.87	HUMAN	P30084	Enoyl-CoA hydratase, mitochondrial
25466	dirMS_041712_NAR_20mM_plus.17510.17510.2	2	3.51	0	3.36E+04		(R)YLTVAA	(R)Y L\T\V/A\A V F R(G)		192.65	520.3009	1039.593	0.001	1	8.75	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
25467	dirMS_041712_NAR_20mM_plus.7874.7874.3	3	3.51	0	3.11E+05	M239m	(K)EVDEQn	(K)E V/D E Q m/L/N V Q N K(N)	m:Oxidized methionine	124.8	488.2328	1446.689	15.9945	-0.3	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
25468	dirMS_041712_NAR_30mM_plus2.16436.16436.3	3	3.51	0	4.29E+05		(K)LLDLVQ	(K)L L\D\L V|Q/Q S C N Y K(Q)	C:Carbamidomethylation	139.03	494.2566	1480.746	0.0088	5.9	5.83	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
25469	dirMS_041712_NAR_30mM_plus2.4684.4684.2	2	3.51	0	7.73E+05		(R)FQANEE	(R)F Q/A N E/E/R(L)		75.32	447.2119	893.411	0.0054	6	4.53	85622.3	5.85	HUMAN	Q96RT6	Protein cTAGE-2
25470	dirMS_041712_NAR_40mM_plus2.15512.15512.3	3	3.51	0	1.01E+04		(R)LQVIVCS	(R)L/Q V|I/V C S A T L H S F D/V K(K)	C:Carbamidomethylation	158.6	606.3237	1816.963	-0.006	-3.3	6.74	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
25471	dirMS_041712_NAR_40mM_plus2.6538.6538.2	2	3.51	0	1.70E+05	M154m	(R)mGYMD	(R)m G Y/M D|P R(E)	m:Oxidized methionine	97.13	443.1854	869.364	15.9991	4.7	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
25472	dirMS_041712_NAR_40mM_plus2.8598.8648.2	2	3.51	0	1.49E+05		(K)DFSTTTI	(K)D/F/S T T T K(L)		111.7	400.2001	799.383	0.0097	12.1	5.84	31652.5	9.88	HUMAN	Q8N3J9	Zinc finger protein 664
25473	dirMS_041712_NAR_40mM_plus2.8992.8992.2	2	3.51	0	3.51E+04		(K)QGYVIYI	(K)Q G/Y/V I/Y/R(I)		115.2	449.7407	898.478	-0.004	-4.5	8.59	20608.6	11.48	HUMAN	E7ENU7	Ribosomal protein L15 (Fragment)
25474	dirMS_041712_NAR_50mM_plus2.19882.19882.2	2	3.51	1	3.80E+05		(R)KAIIIFVP	(R)K\A\I I/I F V|P V|P Q L K(S)		173.13	733.4779	1465.95	-0.002	-1.3	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
25475	dirMS_041712_NAR_50mM_plus2.9147.9147.3	3	3.51	1	1.75E+04		(K)EYDELAI	(K)E Y D E L A/E T Q G K L E E K(L)		115.38	594.6247	1781.844	0.0156	8.7	4.14	95734.8	5.9	HUMAN	F6S0T5	Lysine-specific histone demethylase 1A
25476	dirMS_041712_NAR_60mM_plus.14434.14434.3	3	3.51	0	2.46E+05		(R)VNAIEH	(R)V N/A\I E H/V I I/P R(I)		132	420.9182	1260.742	-0.0022	-1.8	6.72	21920.7	5.63	HUMAN	G3V2S6	V-type proton ATPase subunit D
25477	dirMS_041712_NAR_60mM_plus.18148.18148.3	3	3.51	1	1.35E+05		(K)IGLKDVI	(K)I G L K D|V I T/L W/R(H)		151.77	438.6094	1313.794	0.0197	15	8.75	38487.9	10.15	HUMAN	A6NHP6	NPIP-like protein LOC729602
25478	dirMS_041712_NAR_60mM_plus.20274.20274.3	3	3.51	1	3.04E+04	T781t	(K)AEIMKTI	(K)A E I/M K T/L E/V\L/t K(N)	t:N-acetylglucosamine (T)	166.2	526.9566	1375.786	203.0687	-6.7	6.18	113994.6	9.34	HUMAN	Q5T8P6	RNA-binding protein 26
25479	dirMS_041712_NAR_60mM_plus.20753.20753.3	3	3.51	0	6.50E+05		(R)LSPEAAI	(R)L S P E A/A I K\P|N F T V R(D)		168.73	514.9568	1542.864	-0.008	-5.2	8.75	84398.3	4.65	HUMAN	B7Z2U6	Cadherin-12
25480	dirMS_041712_NAR_120mM_minus.15394.15394.4	4	3.5	1	2.25E+05	S3853s	(K)RsSFAEV	(K)R s S F A\E V V/G L T E L K(L)	s:N-acetylglucosamine (S)	137.72	435.4914	1535.843	203.101	12.4	6.14	492083.9	4.69	HUMAN	E9PQ73	Protocadherin Fat 3
25481	dirMS_041712_NAR_120mM_minus.9119.9119.3	3	3.5	0	5.32E+05		(K)HFVALST	(K)H F\V A\L/S T N T T K(V)		103.52	406.8876	1218.648	0.0005	0.4	8.76	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
25482	dirMS_041712_NAR_20mM_minus.13290.13290.2	2	3.5	0	1.40E+05		(K)VGINYQ	(K)V G I N Y Q|P P T V\V|P G G D L A K(V)		183.15	912.9938	1824.985	-0.0051	-2.8	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
25483	dirMS_041712_NAR_20mM_minus.13605.13605.3	3	3.5	0	1.70E+05		(R)ETTDTD	(R)E T T D T D T\A/D Q V I/A S F/K(V)		186.45	581.2735	1741.813	-0.0067	-3.9	3.84	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
25484	dirMS_041712_NAR_30mM_minus2.15052.15052.2	2	3.5	2	3.28E+05		(K)KSSTSVI	(K)K S S T S/V R D/G G K(R)		135.13	561.2964	1121.591	-0.0054	-4.8	9.99	24297.4	9.87	HUMAN	B4DXK0	Protein DBF4 homolog A
25485	dirMS_041712_NAR_30mM_minus2.15382.15382.2	2	3.5	0	2.04E+05		(K)TNLPIFK	(K)T N|L P I/F K(L)		136.4	416.7494	832.493	-0.0012	-1.4	8.41	18819.1	8.89	HUMAN	O60493	Sorting nexin-3
25486	dirMS_041712_NAR_30mM_minus2.18081.18081.2	2	3.5	0	2.69E+03		(R)VVLFEM	(R)V V/L/F E M E A R(K)		151.45	547.289	1093.571	-0.0003	-0.3	4.53	27142.4	5.34	HUMAN	E5RG68	Copine-3 (Fragment)
25487	dirMS_041712_NAR_40mM_minus2.15423.15423.3	3	3.5	1	3.20E+05		(R)GGPNIIT	(R)G G/P N/I|I/T L A D I V K D P V S R(T)		178.37	622.3523	1865.049	-0.0067	-3.6	5.96	45481.2	7.85	HUMAN	E7EU96	Casein kinase II subunit alpha
25488	dirMS_041712_NAR_40mM_minus2.16054.16054.3	3	3.5	0	1.19E+04	M166m	(K)VLDFEHI	(K)V L|D F E H F L P m L/Q/T V/A K(N)	m:Oxidized methionine	188.75	635.3376	1888.004	15.9945	-0.2	5.32	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
25489	dirMS_041712_NAR_50mM_minus2.14341.14341.3	3	3.5	0	1.26E+05		(K)QGPLHG	(K)Q G/P L H G M L I/N/T/P Y V T K(D)		149.4	590.3118	1768.941	-0.0206	-11.6	8.6	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
25490	dirMS_041712_NAR_50mM_minus2.16627.16627.3	3	3.5	1	7.04E+03		(R)GVGFDI	(R)G V G F/D\R T L G G L/E M E L R(L)		162.83	583.963	1749.895	-0.0208	-11.9	4.68	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
25491	dirMS_041712_NAR_50mM_minus2.17349.17349.3	3	3.5	0	1.23E+05		(K)VHLVGII	(K)V H L V G|I/D I\F T G K(K)		167.63	433.5856	1298.747	-0.0045	-3.4	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
25492	dirMS_041712_NAR_50mM_minus2.6684.6684.3	3	3.5	0	6.16E+03		(K)IGASLAI	(K)I G/A S/L A D V D P M Q L D S S V R(F)		104.6	625.3125	1873.932	-0.0095	-5	3.93	159920.6	5.94	HUMAN	Q6PL18	ATPase family AAA domain-containing protein 2
25493	dirMS_041712_NAR_50mM_minus2.7090.7090.3	3	3.5	0	1.07E+05		(R)VGQAVI	(R)V/G Q/A\V/D\V V G Q A G K P K(T)		107.38	484.9436	1452.817	-0.0007	-0.5	8.56	86346.5	5.05	HUMAN	E7EW34	26S proteasome non-ATPase regulatory subunit 2
25494	dirMS_041712_NAR_50mM_minus2.8577.8577.3	3	3.5	1	8.87E+04		(R)YESLTDI	(R)Y E/S L T D/P S K/L D S G K(E)		116.3	513.9233	1539.754	0.0017	1.1	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
25495	dirMS_041712_NAR_60mM_minus.14350.14350.4	4	3.5	0	2.69E+05		(R)IHTGERI	(R)I H T\G E R P Y V C M E\C G/K(S)	C:Carbamidomethylation	139.93	459.9648	1836.819	0.0184	10	6.75	76491.3	9.55	HUMAN	Q6P9A3	Zinc finger protein 549
25496	dirMS_041712_NAR_60mM_minus.14720.14720.3	3	3.5	1	3.13E+05		(K)DLVKEAI	(K)D L V K E A/I/N S Y I R(G)		141.6	474.2636	1420.78	-0.0032	-2.3	6.07	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
25497	dirMS_041712_NAR_60mM_minus.9998.9998.3	3	3.5	1	1.14E+05	M181m	(R)VVGAm	(R)V/V/G A m Q L Y S V D/R K(V)	m:Oxidized methionine	115.35	494.5906	1465.783	15.9741	-14.1	8.56	144109.9	6.01	HUMAN	J3KR87	Clathrin heavy chain 2
25498	dirMS_041712_NAR_120mM_plus.10572.10572.3	3	3.5	0	1.23E+06		(R)GLHQSII	(R)G L/H Q S\I/E/E F/R(A)		109.27	405.8796	1215.612	0.0126	10.4	5.4	81007.1	6.31	HUMAN	E9PMV1	Plectin (Fragment)
25499	dirMS_041712_NAR_120mM_plus.5376.5376.3	3	3.5	1	7.24E+05	M117m	(K)EmQLRC	(K)E m/Q/L/R Q E E E/R(R)	m:Oxidized methionine	80.92	455.2145	1347.632	15.9968	1.4	4.49	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
25500	dirMS_041712_NAR_20mM_plus.10365.10365.3	3	3.5	2	1.35E+05	S88s	(R)EKLLSGS	(R)E K L/L S/G S|E S S s K/K(R)	s:Phosphorylated S	144.65	487.2418	1379.738	79.9732	4.7	8.59	12410.1	10.23	HUMAN	G3XAI9	Protein FAM133B
25501	dirMS_041712_NAR_20mM_plus.14604.14604.3	3	3.5	1	1.54E+05	S267s	(K)sKAFSV	(K)s K/A F S V V I Q A S K(S)	s:Phosphorylated S	172.37	448.8957	1264.726	79.9466	-14.7	10	43221.8	9.66	HUMAN	Q16533	snRNA-activating protein complex subunit 1

25502	dirMS_041712_NAR_20mM_plus.14649.14649.2	2	3.5	0	3.89E+04	M185m	(K)LAVNm\	(K)L/A\V/N m|V/P F P R(L)	m:Oxidized methionine	172.75	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
25503	dirMS_041712_NAR_20mM_plus.15463.15463.2	2	3.5	1	2.23E+03	T8t	(-)XAILACK	(-)X A/I L A C/K/t P/K(K)	C:Carbamidomethylation t:Phosp	177.25	597.8227	1114.665	79.9728	5.5	10	29589.1	9.54	HUMAN	H0YEX9	Junctional adhesion molecule B (Fragment)
25504	dirMS_041712_NAR_20mM_plus.16302.16302.3	3	3.5	0	7.24E+04		(K)VTLVQTI	(K)V T L V Q T/L E/I Q R(Q)		184.12	433.9257	1299.763	-0.0005	-0.4	5.97	533778	5.74	HUMAN	Q15149	Plectin
25505	dirMS_041712_NAR_20mM_plus.18339.18339.2	2	3.5	0	2.71E+04		(K)SSGPTSL	(K)S S G P T S L\F\A V|T|V A/P P G A R(Q)		197.6	857.9559	1714.912	-0.0077	-4.5	9.47	91324.5	5.75	HUMAN	Q00839	Heterogeneous nuclear ribonucleoprotein U
25506	dirMS_041712_NAR_20mM_plus.7234.7234.2	2	3.5	0	3.80E+05	M532m M5	(R)mVPAG	(R)m V|P A G m G A G L E R(M)	m:Oxidized methionine	117.6	610.7907	1188.586	31.9877	-1.7	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
25507	dirMS_041712_NAR_30mM_plus2.14922.14922.2	2	3.5	0	5.32E+05		(K)LAVEAVI	(K)L A/V/E/A V/L R(L)		130.53	435.7729	870.541	-0.0022	-2.5	6	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
25508	dirMS_041712_NAR_30mM_plus2.21117.21117.2	2	3.5	0	1.02E+05		(K)VFSIGPV	(K)V F/S I G/P V F R(A)		164.3	511.2941	1021.583	-0.002	-2	9.72	57534.6	6.11	HUMAN	P14868	Aspartate--tRNA ligase, cytoplasmic
25509	dirMS_041712_NAR_30mM_plus2.6283.6283.2	2	3.5	0	2.56E+05		(K)SAVLQE	(K)S A|V/L/Q E/A R(I)		87.2	437.2414	873.479	-0.0033	-3.8	5.72	28218.2	9.35	HUMAN	F6X838	Coatomer subunit gamma-2
25510	dirMS_041712_NAR_30mM_plus2.7613.7613.2	2	3.5	1	1.97E+05		(R)LDKTES	(R)L/D/K T E/S K(I)		93.9	410.7181	820.441	-0.0122	-14.8	6.07	239401.5	5.45	HUMAN	O75923	Dysferlin
25511	dirMS_041712_NAR_40mM_plus2.8498.8498.2	2	3.5	1	3.51E+04	M577m	(K)QRIDEFE	(K)Q R I D E/F E|S/m(-)	m:Oxidized methionine	111.23	585.7575	1154.515	15.9931	-1.6	4.14	67933	6.08	HUMAN	P26038	Moesin
25512	dirMS_041712_NAR_40mM_plus2.9407.9407.2	2	3.5	0	9.68E+04		(R)ISVYYNE	(R)I S|V/Y/Y N E A T G/G K(Y)		118.55	651.3206	1301.637	-0.0033	-2.5	6	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
25513	dirMS_041712_NAR_50mM_plus2.10590.10590.3	3	3.5	1	4.20E+05		(K)IDKQINN	(K)I/D K Q I N N/L/I T/K(V)		123.78	433.922	1299.763	-0.0116	-8.9	8.59	61684.2	8.36	HUMAN	Q6PEW3	ATP10D protein
25514	dirMS_041712_NAR_50mM_plus2.11805.11805.3	3	3.5	1	3.79E+05		(K)IGRIEDV	(K)I G R I E\D V T P I/P/S/D S T R(R)		130.28	585.9784	1755.924	-0.0029	-1.7	4.56	16443.6	10.45	HUMAN	P62263	40S ribosomal protein S14
25515	dirMS_041712_NAR_50mM_plus2.6295.6295.3	3	3.5	1	1.09E+05		(R)VVSSIEC	(R)V V/S/S I/E/Q K T E/G A E K(K)		96.73	502.2651	1504.785	-0.0046	-3	4.79	8491.4	6.28	HUMAN	E5RIR4	14-3-3 protein zeta/delta (Fragment)
25516	dirMS_041712_NAR_60mM_plus.20104.20104.3	3	3.5	1	9.67E+04		(K)AKIGLIQ	(K)A K I G L I Q/F/C L S/A/P K(T)	C:Carbamidomethylation	164.8	515.9646	1545.882	-0.0029	-1.9	10	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
25517	dirMS_041712_NAR_60mM_plus.20835.20835.3	3	3.5	1	2.58E+05		(K)CKIPALD	(K)C K\I|P A/L/D L/L I K(L)	C:Carbamidomethylation	169.68	428.5975	1283.776	0.0024	1.9	8.59	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
25518	dirMS_041712_NAR_60mM_plus.7378.7378.3	3	3.5	0	4.65E+05		(K)DVQML	(K)D V/Q M L/Q D A I\S K(M)		96.47	416.5533	1247.63	0.0153	12.3	4.21	11829.2	4.96	HUMAN	K7EIU0	Hsp90 co-chaperone Cdc37 (Fragment)
25519	dirMS_041712_NAR_60mM_plus.7595.7595.3	3	3.5	1	2.43E+05		(R)DNSTM	(R)D N S T/M/G Y M/A A K K(H)		98.1	439.5393	1316.597	0.006	4.6	8.5	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
25520	dirMS_041712_NAR_120mM_minus.21381.21381.3	3	3.49	0	7.96E+05		(R)LHFFMP	(R)L H F F M|P G\F A/P\L T S R(G)		182.15	540.9497	1620.835	-0.001	-0.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
25521	dirMS_041712_NAR_20mM_minus.11342.11342.3	3	3.49	2	9.23E+04	S151s T152	(R)LRDIstVI	(R)L R D I s/t V K S L/F A K(R)	s:Phosphorylated S t:Phosph	160.65	546.6118	1477.874	159.9472	8.9	9.99	20473	11.6	HUMAN	P20800	Endothelin-2
25522	dirMS_041712_NAR_20mM_minus.13433.13433.3	3	3.49	0	1.02E+05	M223m	(K)VLNNmE	(K)V L N N m E\I/G T S/L/F D E E G A K(I)	m:Oxidized methionine	185.08	661.6505	1966.943	15.9943	-0.3	4	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
25523	dirMS_041712_NAR_20mM_minus.8112.8112.2	2	3.49	1	8.15E+04		(R)MLPPEC	(R)M L P/P E/Q R K(R)		130.8	499.7804	998.545	0.0084	8.4	8.5	31470.2	9.55	HUMAN	A6PVU7	Cingulin (Fragment)
25524	dirMS_041712_NAR_20mM_minus.9072.9072.2	2	3.49	1	3.02E+05	M617m S6	(R)AEAMm	(R)A E A M/m R S/s I E|R(G)	m:Oxidized methionine s:N-a	139.95	750.3397	1280.609	219.0636	-7.2	6.19	106220	5.51	HUMAN	H7C563	Dynein heavy chain 1, axonemal (Fragment)
25525	dirMS_041712_NAR_30mM_minus2.13845.13845.2	2	3.49	0	6.05E+05	S1333s	(R)ITPsQVK	(R)I/T/P s/Q V K(M)	s:N-acetylglucosamine (S)	128.57	488.273	772.456	203.0824	3.1	8.75	163852.7	5.43	HUMAN	C9JJN9	Vacuolar protein sorting-associated protein 8 homolog
25526	dirMS_041712_NAR_30mM_minus2.14379.14379.2	2	3.49	0	2.83E+05		(R)FCSNLCI	(R)F/C/S\N/L/C L/P K(Q)	C:Carbamidomethylation	132.45	569.7687	1138.538	-0.0082	-7.2	8.75	26149.4	9.29	HUMAN	B1APE2	General transcription factor IIB (Fragment)
25527	dirMS_041712_NAR_30mM_minus2.9654.9654.2	2	3.49	0	1.20E+05		(K)LAFGCQ	(K)L/A|F/G/C Q R(S)	C:Carbamidomethylation	107.05	426.2191	851.419	0.0117	13.7	9.75	18347.7	6.44	HUMAN	F8VUG8	Prickle-like protein 1 (Fragment)
25528	dirMS_041712_NAR_50mM_minus2.10440.10440.3	3	3.49	0	2.53E+05		(R)TFIAIKPI	(R)T F/I A I K/P D G V Q R(G)		126.9	448.923	1344.763	-0.009	-6.7	8.41	6640.6	8.25	HUMAN	C9K028	Nucleoside diphosphate kinase A (Fragment)
25529	dirMS_041712_NAR_50mM_minus2.11247.11247.3	3	3.49	1	1.21E+05		(R)TVSKVD	(R)T/V S K/V D D F\L/A N E A K(G)		132.27	512.9329	1536.79	-0.0063	-4.1	4.55	52385	7.18	HUMAN	B4DQJ8	6-phosphogluconate dehydrogenase, decarboxylating
25530	dirMS_041712_NAR_50mM_minus2.18131.18131.3	3	3.49	2	8.78E+04		(R)NKGESA	(R)N/K G/E/S A G R D S L/L A G S A R(F)		171.98	563.634	1688.867	0.02	11.8	8.75	20091.2	10.08	HUMAN	C9JUY1	AF4/FMR2 family member 3 (Fragment)
25531	dirMS_041712_NAR_50mM_minus2.5726.5726.3	3	3.49	0	3.05E+04		(K)CHVVNG	(K)C H/V V N G Q/G P A C/R(A)	C:Carbamidomethylation	93.88	452.2119	1354.61	0.0108	8	9.75	78834.1	10.03	HUMAN	Q5T6C5	Ataxin-7-like protein 2
25532	dirMS_041712_NAR_60mM_minus.11225.11225.3	3	3.49	1	6.58E+04		(K)IDKTDY	(K)I D K T D Y M|V/G S Y G P R(A)		122.35	534.591	1601.763	-0.0044	-2.7	5.96	21671	5.37	HUMAN	J3KTF8	Rho GDP-dissociation inhibitor 1 (Fragment)
25533	dirMS_041712_NAR_60mM_minus.16243.16243.3	3	3.49	0	2.80E+05		(R)HDPTSEI	(R)H D P T S E N|I/L Q L V K(A)		150.53	498.6051	1493.796	0.0049	3.3	5.32	13564.4	5.9	HUMAN	F8VZ98	Serine/threonine-protein kinase D1 (Fragment)
25534	dirMS_041712_NAR_60mM_minus.18600.18600.3	3	3.49	1	1.76E+05	T231t	(R)VVFNLN	(R)V V|F N L N T Y K/t/K(E)	t:N-acetylglucosamine (T)	165.17	510.6099	1326.742	203.0735	-3.8	9.7	89473.4	5.06	HUMAN	E7EMF1	Integrin alpha-2
25535	dirMS_041712_NAR_60mM_minus.18631.18631.3	3	3.49	0	2.58E+05		(R)DFLLKPE	(R)D F L L/K/P E L L R(A)		165.43	415.25	1243.741	-0.0054	-4.4	6.07	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
25536	dirMS_041712_NAR_60mM_minus.5636.5636.3	3	3.49	1	4.86E+03		(K)QQTLEA	(K)Q Q T L/E A/E/E A K R(R)		87.05	434.8904	1302.665	-0.0082	-6.3	4.79	76925.9	4.46	HUMAN	A8MV58	Drebrin
25537	dirMS_041712_NAR_60mM_minus.9853.9854.3	3	3.49	2	3.02E+05	S5055s	(R)VKAsVEI	(R)V K/A/s V/E/H I S R I L K(G)	s:Phosphorylated S	114.55	520.6207	1479.901	79.947	-12.4	9.99	619633.9	5.43	HUMAN	A6NGQ3	Obscurin
25538	dirMS_041712_NAR_20mM_plus.10716.10716.2	2	3.49	0	8.63E+04		(R)FLEQQN	(R)F L\E|Q Q N Q V|L/Q/T K(W)		146.73	738.3942	1475.785	-0.0041	-2.8	6	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
25539	dirMS_041712_NAR_20mM_plus.16928.16928.2	2	3.49	0	1.32E+05		(K)FATEAAI	(K)F A\T E/A|A/I/T I L R(I)		188.33	603.3442	1205.689	-0.0077	-6.4	6	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
25540	dirMS_041712_NAR_20mM_plus.9896.9896.3	3	3.49	1	6.34E+04	K1487k	(R)ISGGKEN	(R)I S G G K E/N T A S S/k(Q)	k:Ubiquitin-K	138.75	431.5577	1178.601	114.0574	11.2	8.59	455998.5	4.95	HUMAN	Q99996	A-kinase anchor protein 9
25541	dirMS_041712_NAR_30mM_plus2.22531.22531.2	2	3.49	0	6.10E+04		(R)LEGLTDE	(R)L E|G\L/T/D E\I\N F L R(Q)		174.63	710.3766	1419.748	-0.0019	-1.3	4.14	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
25542	dirMS_041712_NAR_30mM_plus2.4455.4455.2	2	3.49	0	3.06E+05		(K)EDAANN	(K)E D A A/N N Y A/R(G)		72.7	512.2281	1023.449	-0.0001	-0.1	4.37	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
25543	dirMS_041712_NAR_40mM_plus2.5917.5917.2	2	3.49	1	5.71E+03	M159m Y1	(R)mEFIKyL	(R)m/E F/I K y L K(S)	m:Oxidized methionine y:Ph	92.85	584.273	1071.591	95.948	-11.3	8.26	21176.7	5.03	HUMAN	Q9H7X7	Rab-like protein 5
25544	dirMS_041712_NAR_50mM_plus2.10207.10207.3	3	3.49	0	3.95E+05		(R)NSNLVG	(R)N S|N/L/V/G A A/H E E L Q Q S R(I)		120.72	584.9601	1752.862	0.0034	1.9	5.4	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
25545	dirMS_041712_NAR_50mM_plus2.11457.11482.3	3	3.49	0	4.29E+05		(R)VEAFELY	(R)V E A F E|L/Y Q L E L K(D)		127.87	494.6071	1481.789	0.0181	12.2	4.25	112199	5.71	HUMAN	O75665-3	Isoform 3 of Oral-facial-digital syndrome 1 protein
25546	dirMS_041712_NAR_50mM_plus2.13924.13924.3	3	3.49	1	4.11E+05		(R)SILKIDD	(R)S I/L K I D D V/V/N T R(-)		140.93	458.2605	1372.78	-0.0125	-9.1	5.68	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
25547	dirMS_041712_NAR_50mM_plus2.18155.18155.3	3	3.49	0	2.93E+04		(K)AFLTGVI	(K)A F|L/T/G\V D P I L G/H Q L S A R(E)		163.97	598.9953	1794.986	-0.0147	-8.2	6.79	109305.5	6.58	HUMAN	Q6P9B9	Integrator complex subunit 5
25548	dirMS_041712_NAR_60mM_plus.18427.18427.3	3	3.49	1	1.11E+05		(K)REVFSYL	(K)R E V F S Y/L V H/V A\K(C)		154.03	483.2704	1447.806	-0.009	-6.2	8.6	261905	6.07	HUMAN	Q9P212	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase epsilon-1
25549	dirMS_041712_NAR_120mM_minus.16924.16924.3	3	3.48	0	1.66E+04	M1m T4t	(-)mAAtAA	(-)m/A A t A A E A V/A S/G\S G E P/R(E)	m:Oxidized methionine t:Ph	147.3	557.9061	1575.743	95.9606	-0.4	4.53	3563.8	3.83	HUMAN	E9PNR8	Hypoxia-inducible factor 1-alpha inhibitor
25550	dirMS_041712_NAR_120mM_minus.6090.6090.3	3	3.48	1	5.64E+05		(K)TCEESSF	(K)T/C|E E/S S F/C K R(Q)	C:Carbamidomethylation	86.8	435.1849	1303.541	-0.0004	-0.3	5.81	10576.1	11.44	HUMAN	E9PRF8	Neutral alpha-glucosidase AB
25551	dirMS_041712_NAR_120mM_minus.7139.7199.3	3	3.48	1	3.75E+05	M71m	(R)VNEARE	(R)V/N E/A R E E/L m R(M)	m:Oxidized methionine	92.97	421.542	1246.621	15.9906	-3.4	4.79	16201.6	6.74	HUMAN	B7ZB63	ADP-ribosylation factor 3
25552	dirMS_041712_NAR_20mM_minus.10174.10174.3	3	3.48	0	3.04E+04		(K)IEDLSQC	(K)I/E D L S Q\Q/A/Q/L A A A E K(F)		151.12	538.9478	1614.833	-0.0045	-2.8	4.14	206102.3	9.72	HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
25553	dirMS_041712_NAR_20mM_minus.8403.8403.2	2	3.48	1	1.06E+05		(R)LQRAQV	(R)L Q R/A Q V S E R(E)		133.62	543.7973	1086.601	-0.0141	-13	9.6	25048.3	6.85	HUMAN	J3QQT3	Interleukin-34
25554	dirMS_041712_NAR_30mM_minus2.11520.11520.2	2	3.48	0	8.84E+05		(K)CGDLVF	(K)C G/D|L/V/F|A K(M)	C:Carbamidomethylation	117	455.2306	909.45	0.0041	4.5	5.84	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
25555	dirMS_041712_NAR_30mM_minus2.12234.12234.2	2	3.48	0	4.11E+04		(K)QALSGF	(K)Q A/L/S/G F/G Y/R(L)		119.07	499.7499	998.505	-0.0129	-12.9	8.75	21925.1	5.16	HUMAN	O75340	Programmed cell death protein 6
25556	dirMS_041712_NAR_30mM_minus2.9736.9964.2	2	3.48	0	1.04E+06		(K)SILYDER	(K)S I|L/Y D/E/R(S)		108.5	448.2316	895.452	0.004	4.4	4.37	26012.2	6.92	HUMAN	P25787	Proteasome subunit alpha type-2
25557	dirMS_041712_NAR_50mM_minus2.10278.10278.3	3	3.48	2	1.71E+05	S263s	(K)VVLREs	(K)V V L R E s/C|F/Y R K(L)	C:Carbamidomethylation s:N-ace	127.75	553.9474	1456.773	203.0547	-14.9	9.99	35012	4.7	HUMAN	H0YFJ7	Cell division cycle and apoptosis regulator protein 1 (Fragment)
25558	dirMS_041712_NAR_50mM_minus2.17086.17086.3	3	3.48	0	5.84E+04		(R)FGNQAD	(R)F/G N Q A D H F L G S L|A/F A K(L)		165.27	574.9529	1722.86	-0.0157	-9.1	6.74	44411.4	9.19	HUMAN	Q9H488	GDP-fucose protein O-fucosyltransferase 1
25559	dirMS_041712_NAR_50mM_minus2.6737.6737.3	3	3.48	0	4.47E+04	M361m	(R)ISNRPAF	(R)I/S/N R P A F\m P S E/G K(M)	m:Oxidized methionine	104.93	483.9086	1433.721	15.9907	-2.9	8.75	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
25560	dirMS_041712_NAR_50mM_minus2.8506.8506.3	3	3.48	1	1.32E+05		(K)NKNMG	(K)N K N/M/G Q E V L N L T K(E)		115.58	496.9372	1488.784	0.0132	8.8	8.59	138620.2	8.63	HUMAN	Q7Z7B0	Filamin-A-interacting protein 1
25561	dirMS_041712_NAR_120mM_plus.21701.21701.4	4	3.48	2	3.09E+05		(R)SAKDDF	(R)S/A K D D F T S I I G/K C Q V P K(D)	C:Carbamidomethylation	167.22	474.2499	1893.974	0.0039	2.1	8.22	271875.5	5.65	HUMAN	A2RRP1	Neuroblastoma-amplified sequence
25562	dirMS_041712_NAR_20mM_plus.13186.13186.2	2	3.48	1	8.86E+04	K109k	(R)RNPLLLF	(R)R N P\L/L/L\P V D k(I)	k:Ubiquitin-K	163.27	639.8734	1164.71	114.0296	-10.4	8.75	150311.9	6.33	HUMAN	B7ZKT6	SOS2 protein
25563	dirMS_041712_NAR_20mM_plus.13424.13424.2	2	3.48	0	1.40E+05	M273m	(K)mISDAIP	(K)m I/S/D A I/P E\L K(A)	m:Oxidized methionine	165.03	566.7967	1116.597	15.9892	-5	4.37	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
25564	dirMS_041712_NAR_20mM_plus.13472.13472.3	3	3.48	1	4.82E+03	S44s	(R)WPSAAs	(R)W P S A/A/s V K S S S S D T G S R(S)	s:N-acetylglucosamine (S)	165.2	638.3035	1709.809	203.087	4	8.75	104197.2	8.76	HUMAN	Q5U651	Ras-interacting protein 1
25565	dirMS_041712_NAR_20mM_plus.18010.18010.3	3	3.48	0	1.85E+05	M4826m	(R)LPPYSSC	(R)L P P Y S S\Q L/V m A E R(L)	m:Oxidized methionine	195.08	502.9236	1490.767	15.9891	-3.9	6	539122.1	5.69	HUMAN	Q15751	Probable E3 ubiquitin-protein ligase HERC1
25566	dirMS_041712_NAR_20mM_plus.18058.18058.2	2	3.48	0	1.79E+05		(K)VANVSL	(K)V A|N\V/S/L L|A L Y K(G)		195.43	595.8558	1190.714	-0.01	-8.4	8.56	15978.4	10.84	HUMAN	P62266	40S ribosomal protein S23
25567	dirMS_041712_NAR_20mM_plus.7700.7700.2	2	3.48	0	5.13E+04		(K)LAAIGEA	(K)L A|A/I/G E A T R(L)		123.13	451.2557	901.51	-0.006	-6.7	6	533778	5.74	HUMAN	Q15149	Plectin
25568	dirMS_041712_NAR_30mM_plus2.12651.12651.2	2	3.48	0	3.18E+05		(R)IFYDMK	(R)I/F/Y D\M K(V)		119.3	408.702	816.396	0.0007	0.8	5.83	15739.2	9.3	HUMAN	F6RFD5	Destrin
25569	dirMS_041712_NAR_30mM_plus2.13027.13027.2	2	3.48	0	6.18E+05	T722t	(R)STLPtGI	(R)S T/L/P t G I Q V K(E)	t:Phosphorylated T	121.23	562.2876	1043.61	79.9584	-7.1	8.47	509686.6	4.85	HUMAN	Q14517	Protocadherin Fat 1
25570	dirMS_041712_NAR_30mM_plus2.14412.14412.2	2	3.48	0	4.22E+05	S468s	(K)LGSTTV	(K)L G|S T T V G s K(S)	s:N-acetylglucosamine (S)	129.12	526.7806	849.468	203.0863	6.6	8.75	89514.5	9.61	HUMAN	Q9P0L2	Serine/threonine-protein kinase MARK1
25571	dirMS_041712_NAR_30mM_plus2.16324.16342.2	2	3.48	1	3.78E+05		(R)VMLYPS	(R)V M|L|Y P S R I(-)		138.08	489.7759	978.544	0.0004	0.4	8.72	12594.5	11.24	HUMAN	P18077	60S ribosomal protein L35a
25572	dirMS_041712_NAR_30mM_plus2.19282.19282.2	2	3.48	0	4.27E+04		(K)FIIPNVV	(K)F/I|I P N V V K(Y)		154.68	465.2943	929.582	-0.0005	-0.6	8.75	17529.3	9.3	HUMAN	F5GXY2	L-lactate dehydrogenase A chain (Fragment)
25573	dirMS_041712_NAR_30mM_plus2.19815.19815.2	2	3.48	0	7.30E+04		(K)ALAGCD	(K)A/L|A/G C D/F L T I S/P/K(L)	C:Carbamidomethylation	157.48	696.8591	1392.719	-0.0082	-5.9	5.88	35556.4	9.3	HUMAN	F2Z393	Transaldolase
25574	dirMS_041712_NAR_30mM_plus2.21947.21947.2	2	3.48	1	1.54E+05		(R)VIRADSF	(R)V I/R\A D S F\S K(I)		171.07	511.7906	1022.563	0.011	10.8	8.72	47521.9	6.47	HUMAN	Q8N5Z0	Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial
25575	dirMS_041712_NAR_30mM_plus2.22648.22648.3	3	3.48	0	1.19E+06		(R)LEGLTDE	(R)L E\G L T D/E I/N F L R(Q)		175.42	473.9205	1419.748	-0.0009	-0.6	4.14	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
25576	dirMS_041712_NAR_30mM_plus2.4891.4891.2	2	3.48	0	1.89E+05		(K)NCSETQ	(K)N\C|S E T\Q/Y E S K(V)	C:Carbamidomethylation	76.98	623.256	1245.505	-0.0005	-0.4	4.53	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
25577	dirMS_041712_NAR_30mM_plus2.5372.5372.2	2	3.48	0	1.71E+05		(R)CQYVTE	(R)C Q\Y V|T/E K(V)	C:Carbamidomethylation	82.42	464.213	927.424	-0.0053	-5.7	6	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
25578	dirMS_041712_NAR_40mM_plus2.16219.16219.3	3	3.48	2	1.28E+05	S426s	(K)KsTLASV	(K)K s T L A S V N/I Q A|L/P D K G Q K(L)	s:Phosphorylated S	161.82	660.0113	1898.071	79.9488	-8.9	9.7	130841	9.05	HUMAN	Q9UNY4	Transcription termination factor 2
25579	dirMS_041712_NAR_40mM_plus2.18326.18326.3	3	3.48	1	7.03E+03		(R)VLEALLP	(R)V L/E/A L L P L K/G L E E R(V)		173.77	527.3177	1579.942	-0.0032	-2	4.79	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
25580	dirMS_041712_NAR_50mM_plus2.12692.12692.3	3	3.48	0	3.35E+05		(K)LQELPD	(K)L Q E L P D/A V/P H G E M P R(H)		134.28	563.6145	1688.843	-0.0135	-8	4.65	78390.7	9.27	HUMAN	B1AHB1	DNA replication licensing factor MCM5
25581	dirMS_041712_NAR_50mM_plus2.15332.15332.3	3	3.48	0	9.75E+05		(R)QVLIASH	(R)Q V/L I/A S H L/P/S Y E L R(H)		149.48	542.6394	1625.901	0.0027	1.6	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
25582	dirMS_041712_NAR_60mM_plus.11920.11920.3	3	3.48	1	1.87E+05	T324t	(R)GLDPKt	(R)G L D/P K t C F/R(K)	C:Carbamidomethylation t:N-ace	119.52	432.8835	1093.546	203.0901	8.2	8.75	75780.8	9.09	HUMAN	Q5H9K5	Zinc finger matrin-type protein 1
25583	dirMS_041712_NAR_60mM_plus.12756.12756.3	3	3.48	1	9.60E+05	M232m	(R)MSmKE	(R)M S m\K E V\D E\Q|M/L/N V Q N K(N)	m:Oxidized methionine	123.5	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
25584	dirMS_041712_NAR_60mM_plus.16545.16545.3	3	3.48	0	1.92E+05		(R)LSQYQE	(R)L/S Q/Y/Q/E P L H L P G V R(V)		143.7	546.297	1636.881	-0.0041	-2.5	6.75	80685.1	7.31	HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
25585	dirMS_041712_NAR_60mM_plus.18190.18190.3	3	3.48	0	2.09E+05	K964k	(K)LLTkSVA	(K)L L|T k S V/A E T P V H/K(Q)	k:Ubiquitin-K	153.08	512.9699	1422.832	114.0637	13.5	8.6	212850	9.41	HUMAN	Q7Z2Z1	Treslin
25586	dirMS_041712_NAR_60mM_plus.20690.20690.3	3	3.48	1	1.68E+04	T155t	(K)YLHLLQI	(K)Y L H/L L Q I V E T/E/K t V A K(Q)	t:Phosphorylated T	168.58	655.6825	1885.079	79.9536	-6.5	6.75	144413.1	6.93	HUMAN	F8VPA5	Ras-specific guanine nucleotide-releasing factor 1
25587	dirMS_041712_NAR_20mM_minus.10687.10687.2	2	3.47	0	4.95E+04	M750m	(R)HLSAmL	(R)H L S\A|m L S S T A R(A)	m:Oxidized methionine	155.37	595.3105	1173.604	16.0093	12.1	9.75	89402.9	6.64	HUMAN	B4DVB0	Oxysterol-binding protein
25588	dirMS_041712_NAR_20mM_minus.12483.12483.3	3	3.47	0	2.53E+05	M256m	(R)SLDmDS	(R)S L D m D S/I/I A E V K(A)	m:Oxidized methionine	172.38	446.227	1320.671	15.9949	0	4.03	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
25589	dirMS_041712_NAR_20mM_minus.13111.13111.2	2	3.47	0	4.41E+04	S1104s	(R)NSSPGE	(R)N S S/P/G/E A s L L E K(E)	s:N-acetylglucosamine (S)	181.85	717.8609	1231.617	203.0981	13	4.53	132527	6.68	HUMAN	Q76FK4	Nucleolar protein 8
25590	dirMS_041712_NAR_20mM_minus.9149.9149.2	2	3.47	0	1.90E+05	M239m	(K)EITALAP	(K)E I\T/A L/A/P S T m K(I)	m:Oxidized methionine	141.92	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
25591	dirMS_041712_NAR_30mM_minus2.15714.15714.2	2	3.47	0	3.38E+05		(K)EGALDL	(K)E G A/L/D/L S/G L R(A)		138.85	515.7847	1030.553	0.0094	9.1	4.37	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
25592	dirMS_041712_NAR_30mM_minus2.5628.5628.2	2	3.47	0	8.95E+04		(-)MESKPSI	(-)M E|S/K/P S R(I)		84.85	417.7114	834.414	0.0017	2	8.5	11342.1	10.24	HUMAN	C9J159	E3 ubiquitin-protein ligase MARCH7 (Fragment)
25593	dirMS_041712_NAR_40mM_minus2.14353.14353.3	3	3.47	0	1.23E+05		(R)GTEDITS	(R)G T E/D I\T S/P H/G I/P L D/L L D R(V)		168.55	650.3366	1948.997	-0.0022	-1.1	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
25594	dirMS_041712_NAR_50mM_minus2.11679.11679.3	3	3.47	2	2.08E+05	T159t	(K)RStPEEE	(K)R S t P E\E/E G R\S/A P/E K(I)	t:N-acetylglucosamine (T)	134.82	592.6214	1572.761	203.0884	5.1	4.95	24895.1	11.03	HUMAN	A8MQB3	Uncharacterized protein C17orf51
25595	dirMS_041712_NAR_50mM_minus2.14342.14342.3	3	3.47	0	1.26E+05		(K)QGPLHG	(K)Q/G P L\H G M L I/N T P Y V/T K(D)		149.4	590.3118	1768.941	-0.0206	-11.6	8.6	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
25596	dirMS_041712_NAR_50mM_minus2.15172.15172.3	3	3.47	1	1.70E+05	S9s	(K)HsRIYLP	(K)H s R I Y/L/P/P E A S S Q R(R)	s:N-acetylglucosamine (S)	154.33	615.3184	1640.85	203.0903	5.9	8.75	17629.8	9.87	HUMAN	C9J2Q8	Mis18-binding protein 1 (Fragment)
25597	dirMS_041712_NAR_50mM_minus2.16355.16355.3	3	3.47	0	1.86E+04	S124s	(K)VLDLLDF	(K)V L|D/L L D P A s G/D\L V I R(E)	s:N-acetylglucosamine (S)	161.05	600.3221	1595.9	203.0514	-15.5	3.93	66591.2	9.24	HUMAN	B7Z265	Kinesin family member 22, isoform CRA_b
25598	dirMS_041712_NAR_50mM_minus2.8414.8414.3	3	3.47	1	2.25E+05		(R)AGTGVD	(R)A G/T G/V/D N V/D L E/A A\T R K(G)		116.48	539.6119	1616.824	-0.0027	-1.7	4.56	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
25599	dirMS_041712_NAR_60mM_minus.13111.13111.3	3	3.47	1	7.34E+04		(R)ETFELVG	(R)E T F/E L V G R L D K(Q)		134.12	436.2401	1306.7	0.0056	4.3	4.68	75085.3	9.61	HUMAN	O75820	Zinc finger protein 189
25600	dirMS_041712_NAR_60mM_minus.15939.15939.3	3	3.47	1	1.98E+04		(K)AKEIGAD	(K)A K E I G A D\L\V/L/Q I S/K(E)		147.5	495.6258	1484.868	-0.0054	-3.7	6.11	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
25601	dirMS_041712_NAR_120mM_plus.10876.10876.2	2	3.47	1	2.27E+06		(R)LASYLDF	(R)L A/S Y L D/R V/R(S)		109.83	546.8117	1092.616	0.0001	0.1	8.75	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
25602	dirMS_041712_NAR_120mM_plus.18126.18126.4	4	3.47	1	1.10E+06	S1349s	(R)LDSRAEI	(R)L D\S R A E\E G s V Q A I T E G/K(V)	s:N-acetylglucosamine (S)	148.73	499.002	1789.893	203.0935	7.1	4.41	170594	7.76	HUMAN	Q9NRJ4	Tubby-related protein 4
25603	dirMS_041712_NAR_120mM_plus.21288.21288.4	4	3.47	0	1.36E+05		(K)ALEHAF	(K)A/L E/H A F\Q/L E H\I M D L T R(L)		164.42	481.7493	1923.975	0.0008	0.4	5.27	535136.6	6.01	HUMAN	Q14204	Cytoplasmic dynein 1 heavy chain 1
25604	dirMS_041712_NAR_120mM_plus.5096.5096.3	3	3.47	1	2.96E+05	M163m	(K)IYEDGDI	(K)I/Y/E/D G D D D m K R(T)	m:Oxidized methionine	79.67	458.195	1356.574	15.9968	1.4	4.03	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
25605	dirMS_041712_NAR_20mM_plus.13019.13019.2	2	3.47	0	3.89E+04		(K)ILSDTYT	(K)I L S/D/T Y T V E K(V)		162.18	584.808	1168.61	-0.0009	-0.7	4.37	16797.2	7.93	HUMAN	G3V2T6	Uncharacterized protein
25606	dirMS_041712_NAR_30mM_plus2.15779.15779.2	2	3.47	0	2.13E+05		(K)LLPPYLR	(K)L L/P/P/Y L R(V)		135.47	436.2709	871.54	-0.0055	-6.3	8.75	55805.4	6.7	HUMAN	P43490	Nicotinamide phosphoribosyltransferase
25607	dirMS_041712_NAR_30mM_plus2.17229.17229.2	2	3.47	0	2.77E+05		(K)SQLLSYII	(K)S Q|L/L/S Y I D R(L)		142.78	547.7952	1094.584	-0.0009	-0.8	5.55	81934.1	6.08	HUMAN	P33993	DNA replication licensing factor MCM7
25608	dirMS_041712_NAR_30mM_plus2.18300.18300.2	2	3.47	1	1.96E+05	S318s	(R)AKsPNG	(R)A K s P/N G S S S|V N W P P(-)	s:Phosphorylated S	148.67	754.3298	1427.691	79.961	-3.6	8.8	36153	10.03	HUMAN	Q8NDV7-3	Isoform 3 of Trinucleotide repeat-containing gene 6A protein
25609	dirMS_041712_NAR_30mM_plus2.22430.22430.2	2	3.47	0	1.74E+06		(K)LVNFFLK	(K)L V/N F/F L/K(Y)		172.6	440.7682	880.529	0	0	8.75	19849	4.4	HUMAN	C9JCG3	Coiled-coil domain-containing protein 164 (Fragment)
25610	dirMS_041712_NAR_30mM_plus2.7124.7124.2	2	3.47	0	2.31E+05		(R)AQVIYTI	(R)A Q|V\I/Y/T R(N)		91.63	425.7397	850.478	-0.006	-7.1	8.79	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25

25611	dirMS_041712_NAR_30mM_plus2.9063.9063.2	2	3.47	0	5.36E+05		(K)QADVNL	(K)Q A D\V/N/L/V/N A K(L)		100.82	536.2922	1071.579	-0.0022	-2	5.84	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
25612	dirMS_041712_NAR_40mM_plus2.13182.13182.3	3	3.47	0	3.53E+04		(R)VVLSVSS	(R)V V/L/S V/S S G G Q H T V L L V\K(D)		143.85	575.0089	1723.011	0.0009	0.5	8.73	45424.7	7.24	HUMAN	P18754	Regulator of chromosome condensation
25613	dirMS_041712_NAR_40mM_plus2.14192.14192.3	3	3.47	1	1.32E+05		(K)NVMKN	(K)N/V/M K N I M A G L Q Q T/N S E K(I)		150.7	635.9975	1905.952	0.0259	13.6	8.59	428018	5.66	HUMAN	E9PDN5	Dystrophin
25614	dirMS_041712_NAR_40mM_plus2.18282.18282.3	3	3.47	0	1.86E+05	K272k	(K)FDTSISFI	(K)F D T/S I S F P P V N/L E I I k(K)	k:Ubiquitin-K	173.83	645.3466	1819.984	114.0412	-0.9	4.37	89953.6	5.71	HUMAN	P16383	GC-rich sequence DNA-binding factor 2
25615	dirMS_041712_NAR_50mM_plus2.11051.11051.3	3	3.47	1	4.11E+04	M278m	(K)DmESPT	(K)D m|E/S\P T K L/D V T L A K(D)	m:Oxidized methionine	125.45	521.9356	1547.799	15.9937	-0.8	4.56	85679.3	7.65	HUMAN	B9ZVR1	Microtubule-associated protein
25616	dirMS_041712_NAR_50mM_plus2.6800.6800.3	3	3.47	0	2.76E+04	M89m	(R)SSTTSm	(R)S S|T T S m T S V/P K P L K(F)	m:Oxidized methionine	100.47	493.935	1463.777	16.013	12.2	10	24799.7	5.16	HUMAN	C9JPC0	26S proteasome non-ATPase regulatory subunit 2 (Fragment)
25617	dirMS_041712_NAR_50mM_plus2.7001.7001.3	3	3.47	1	1.69E+05	M643m K6	(R)DGmRQ	(R)D G m R Q S S|L k/K(D)	m:Oxidized methionine k:Ub	101.85	427.222	1149.604	130.047	7.1	9.99	232072.6	5.71	HUMAN	B2RTQ9	FANCM protein
25618	dirMS_041712_NAR_50mM_plus2.9745.9745.3	3	3.47	1	1.22E+05		(K)VVNSILA	(K)V V N\S/I L A F R\E K(E)		118.35	425.9225	1275.742	0.011	8.6	8.72	56564.1	6.56	HUMAN	B4DNW0	Aminoacylase-1
25619	dirMS_041712_NAR_60mM_plus.13231.13231.3	3	3.47	0	7.77E+05	M1m	(-)mVNHFI	(-)m V/N/H F I/A E F K(R)	m:Oxidized methionine	125.95	417.8778	1235.624	15.9947	-0.2	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
25620	dirMS_041712_NAR_60mM_plus.15851.15851.3	3	3.47	0	4.48E+05		(R)VWYVSN	(R)V/W|Y V/S N I/D G T H I A K(T)		139.77	534.9464	1602.828	-0.0028	-1.8	6.71	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
25621	dirMS_041712_NAR_60mM_plus.21070.21070.3	3	3.47	2	1.07E+05		(K)VKIEGEP	(K)V K I/E G/E P/E F R\L I\K(E)		173.7	519.9722	1557.9	0.0021	1.4	6.2	91050.4	7.05	HUMAN	B1ALD8	Periostin
25622	dirMS_041712_NAR_120mM_minus.15229.15229.3	3	3.46	1	1.28E+05		(R)RLTPLQL	(R)R L T\P\L\Q/L|E/I Q R(V)		136.62	456.2732	1366.816	-0.0115	-8.4	9.6	67732.1	4.71	HUMAN	G3V119	DBIRD complex subunit KIAA1967
25623	dirMS_041712_NAR_120mM_minus.6102.6102.3	3	3.46	2	1.20E+05		(K)KAKNEN	(K)K A/K/N E N S/P D T\Q R(S)		87.68	463.2365	1387.692	0.0025	1.8	8.59	79741.9	9.67	HUMAN	Q9HCS5	Band 4.1-like protein 4A
25624	dirMS_041712_NAR_120mM_minus.7057.7057.3	3	3.46	1	3.74E+05		(K)DSYVGD	(K)D S/Y/V G D E/A Q S K R(G)		92.47	452.2134	1354.623	0.0023	1.7	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
25625	dirMS_041712_NAR_120mM_minus.7197.7197.3	3	3.46	1	5.50E+05		(R)SKEQAE	(R)S K E Q A E/L/E|A A R(Q)		93.17	411.2157	1231.628	0.0048	3.9	4.78	533778	5.74	HUMAN	Q15149	Plectin
25626	dirMS_041712_NAR_20mM_minus.11994.11994.2	2	3.46	0	4.18E+05	M313m	(R)TVQSLEI	(R)T V/Q S/L E I D L/D S/m R(N)	m:Oxidized methionine	169.78	761.8733	1506.747	15.9925	-1.6	4.03	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
25627	dirMS_041712_NAR_30mM_minus2.4885.4885.2	2	3.46	0	1.15E+05		(R)ENDEFC	(R)E N/D|E F/C/K(M)	C:Carbamidomethylation	80.18	471.188	941.367	0.0018	1.9	4.14	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
25628	dirMS_041712_NAR_30mM_minus2.5860.5860.2	2	3.46	1	1.36E+05		(K)GRLQEA	(K)G R|L/Q E/A K(L)		86.08	401.2385	801.458	0.012	15	8.75	25375.4	5.15	HUMAN	H0YEX1	Cytoplasmic dynein 2 heavy chain 1 (Fragment)
25629	dirMS_041712_NAR_30mM_minus2.8465.8465.2	2	3.46	0	9.27E+04		(K)IFCISPQI	(K)I F/C I/S/P Q R(I)	C:Carbamidomethylation	100.43	510.7635	1020.53	-0.0098	-9.6	9.75	139207	8.74	HUMAN	Q4VNC0	Probable cation-transporting ATPase 13A5
25630	dirMS_041712_NAR_40mM_minus2.13593.13593.3	3	3.46	0	9.78E+03	M134m T1	(R)AAPLLLP	(R)A A P/L/L L P P P P A A m E t G K(D)	m:Oxidized methionine t:N-a	163.33	631.6641	1673.93	219.0483	-13.8	6.05	58563.8	10.1	HUMAN	Q8TDR2	Serine/threonine-protein kinase 35
25631	dirMS_041712_NAR_50mM_minus2.13288.13288.3	3	3.46	1	2.32E+04		(R)TQVELLE	(R)T Q/V E/L L E/A/P T P A L K R(T)		143.82	555.9883	1665.953	-0.003	-1.8	5.81	18460.6	5.48	HUMAN	C9IYM4	Glycogen [starch] synthase, muscle (Fragment)
25632	dirMS_041712_NAR_50mM_minus2.15426.15426.3	3	3.46	1	1.05E+05		(K)YAVLYQ	(K)Y A/V L Y Q/P L F D/K R(F)		155.65	504.9453	1512.821	0.0004	0.3	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
25633	dirMS_041712_NAR_120mM_plus.10743.10743.3	3	3.46	0	4.73E+05	S1470s	(R)LPLSWA	(R)L P L/S/W A L G s/R(S)	s:N-acetylglucosamine (S)	109	434.9023	1099.626	203.0665	-9.9	9.75	204372.7	5.9	HUMAN	P16144-3	Isoform Beta-4B of Integrin beta-4
25634	dirMS_041712_NAR_20mM_plus.11271.11271.2	2	3.46	0	1.45E+05		(R)YALYDAT	(R)Y A\L/Y D|A T Y E T/K(E)		150.35	669.3157	1337.626	-0.0019	-1.4	4.37	22956	8.8	HUMAN	E9PK25	Cofilin-1
25635	dirMS_041712_NAR_20mM_plus.14710.14710.2	2	3.46	2	1.17E+05	M95m	(R)ETmFHK	(R)E T/m/F H K E R/F/K(I)	m:Oxidized methionine	172.88	684.8399	1352.678	15.9946	-0.3	8.69	68871.3	7.87	HUMAN	B4DF52	Protein kinase C theta type
25636	dirMS_041712_NAR_20mM_plus.17322.17322.3	3	3.46	0	1.90E+04	S189s	(R)ALSLsCP	(R)A L S L/s C P V P H/L H R(W)	C:Carbamidomethylation s:N-ace	190.05	563.9558	1486.795	203.0581	-12.6	9.81	26651.2	9.48	HUMAN	E9PBC3	Uncharacterized protein C5orf34 (Fragment)
25637	dirMS_041712_NAR_20mM_plus.8695.8695.3	3	3.46	0	1.41E+05	M224m	(K)GGKPEP	(K)G G K P E P P A\m P Q\P V\P/T\A(-)	m:Oxidized methionine	130.62	530.6038	1573.804	15.9926	-1.5	6	25541.5	9.92	HUMAN	E9PL09	40S ribosomal protein S3
25638	dirMS_041712_NAR_30mM_plus2.4215.4215.2	2	3.46	0	2.89E+05	M367m M3	(R)FGSGmN	(R)F G/S/G\m N m G/R(I)	m:Oxidized methionine	69.77	494.7017	956.408	31.9884	-1.4	9.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
25639	dirMS_041712_NAR_40mM_plus2.5248.5248.2	2	3.46	0	1.31E+05		(R)QQEEMI	(R)Q\Q/E/E|M M/R(R)		86.35	476.2049	951.402	0.0003	0.3	4.53	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
25640	dirMS_041712_NAR_40mM_plus2.9313.9313.2	2	3.46	0	4.56E+05		(R)DPYGFG	(R)D P Y/G/F/G D/S R(D)		116.57	507.2256	1013.432	0.0116	11.5	4.21	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
25641	dirMS_041712_NAR_50mM_plus2.20355.20355.3	3	3.46	0	9.85E+04		(R)DYLHLPI	(R)D Y L H L\P P E\I\V/P A/T L R(R)		174.38	578.658	1733.959	0.001	0.6	5.32	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
25642	dirMS_041712_NAR_50mM_plus2.21870.21870.3	3	3.46	0	1.62E+04		(K)GHYTEG	(K)G H Y T E G A E|L\V|D/S/V L D V V R(K)		185.95	653.6688	1958.982	0.0101	5.1	4.31	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
25643	dirMS_041712_NAR_50mM_plus2.7343.7343.3	3	3.46	1	7.78E+03		(K)SGVISGG	(K)S G/V I/S\G/G A/S D L K A K(A)		104.25	430.5716	1289.706	-0.0057	-4.4	8.31	59390.2	9.41	HUMAN	G8JLG1	Structural maintenance of chromosomes protein 1A
25644	dirMS_041712_NAR_60mM_plus.15357.15357.3	3	3.46	1	5.97E+05		(R)FVNVVP	(R)F V\N\V|V/P T F G K K(K)		137.58	412.5761	1235.715	-0.0009	-0.7	10	10904.6	11.56	HUMAN	E9PR30	40S ribosomal protein S30
25645	dirMS_041712_NAR_60mM_plus.8206.8206.3	3	3.46	0	2.68E+06	M3128m	(K)SSNNSm	(K)S S N/N S m L|L/V F K(T)	m:Oxidized methionine	101.47	419.2169	1239.64	15.996	0.8	8.47	407515.3	5.14	HUMAN	O60494	Cubilin
25646	dirMS_041712_NAR_120mM_minus.7078.7078.4	4	3.45	1	6.56E+04	K97k	(R)EQWPQ	(R)E\Q W/P Q C/P T I k E/I R D(-)	C:Carbamidomethylation k:Ubiqu	93.12	479.2322	1799.874	114.0325	-5.5	4.87	11987.6	9.52	HUMAN	E9PJ67	Cathepsin B heavy chain (Fragment)
25647	dirMS_041712_NAR_120mM_minus.7637.7637.3	3	3.45	1	3.52E+05		(K)IQDKEGI	(K)I Q D K E G|I/P/P D Q Q R(L)		96.85	508.5981	1523.781	-0.0015	-1	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
25648	dirMS_041712_NAR_20mM_minus.10440.10440.2	2	3.45	1	6.73E+04	S17s	(K)LSSLLCK	(K)L S|S L/L C K F s P D G K(Y)	C:Carbamidomethylation s:N-ace	153.2	827.9072	1451.756	203.0508	-17.2	8.59	35067.7	6.66	HUMAN	Q5T0D5	WD repeat domain 8 (Fragment)
25649	dirMS_041712_NAR_20mM_minus.10503.10503.2	2	3.45	1	4.33E+03		(K)KGETPTV	(K)K\G E T P T/V D G\T/W K(T)		153.68	659.8282	1318.664	-0.0146	-11.1	6.07	39438.5	10.1	HUMAN	Q9H9L3	Interferon-stimulated 20 kDa exonuclease-like 2
25650	dirMS_041712_NAR_20mM_minus.13034.13034.2	2	3.45	0	3.73E+05	M35m	(K)NDIAINE	(K)N/D I\A|I/N\E L m K(R)	m:Oxidized methionine	181.53	588.7948	1160.598	15.9843	-9	4.37	28354	7.11	HUMAN	B4DXI8	26S proteasome non-ATPase regulatory subunit 7
25651	dirMS_041712_NAR_20mM_minus.14567.14567.3	3	3.45	0	3.53E+03		(R)APVPAS	(R)A P\V P\A S E L L\A/S G V/L\S R(A)		200.08	522.9653	1566.885	-0.0036	-2.3	6.05	533778	5.74	HUMAN	Q15149	Plectin
25652	dirMS_041712_NAR_20mM_minus.7409.7409.2	2	3.45	0	1.55E+05	M21m	(K)ATAVmF	(K)A T A|V|m|P D G Q F K(D)	m:Oxidized methionine	122.23	590.7864	1164.572	15.9938	-1	5.88	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
25653	dirMS_041712_NAR_20mM_minus.9813.9813.2	2	3.45	1	2.14E+03		(R)KDLGAS	(R)K D L G/A S E A I G S G/S/K(A)		148.4	660.3291	1319.68	-0.0292	-22.1	6.07	385966.4	5.72	HUMAN	F8WAI1	Immunoglobulin-like and fibronectin type III domain-containing protein 1
25654	dirMS_041712_NAR_30mM_minus2.11335.11335.2	2	3.45	0	7.83E+05		(R)SSGLISH	(R)S S G L I\S/H H R(V)		115.15	497.265	993.523	0.0003	0.3	9.51	39581.9	10.07	HUMAN	Q6AZW8	Zinc finger protein 660
25655	dirMS_041712_NAR_30mM_minus2.13057.13057.2	2	3.45	1	2.29E+05		(K)LFSNKAK	(K)L/F S/N K A/K(L)		124.93	404.2383	807.472	-0.003	-3.7	10	25871.8	9.96	HUMAN	Q6NZ36-3	Isoform 3 of Fanconi anemia-associated protein of 20 kDa
25656	dirMS_041712_NAR_30mM_minus2.18867.18867.2	2	3.45	0	9.16E+04		(K)NYLIDFK	(K)N Y|L/I D F K(H)		157.13	456.7503	912.482	0.0108	11.8	5.83	49548.2	9.34	HUMAN	B7Z9D5	Testis-expressed sequence 10 protein
25657	dirMS_041712_NAR_30mM_minus2.7164.7164.2	2	3.45	0	1.96E+05	M88m	(K)DVDEAY	(K)D V|D|E/A Y m N K(V)	m:Oxidized methionine	92.77	550.7326	1084.462	15.9964	1.3	4.03	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
25658	dirMS_041712_NAR_30mM_minus2.9947.9947.2	2	3.45	0	1.27E+05		(R)FTTYEVF	(R)F/T/T Y E/V/R(M)		108.35	458.2372	915.457	0.0101	11	6	19901.3	7.97	HUMAN	Q9UMY4	Sorting nexin-12
25659	dirMS_041712_NAR_50mM_minus2.11169.11169.3	3	3.45	1	1.10E+05		(K)QIDLSTV	(K)Q\I D L/S/T V/D L K K(L)		131.23	420.5783	1259.72	-0.0002	-0.2	5.96	21156.2	9.41	HUMAN	P55145	Mesencephalic astrocyte-derived neurotrophic factor
25660	dirMS_041712_NAR_50mM_minus2.16742.16742.3	3	3.45	1	2.13E+05		(K)SLLGKDV	(K)S L/L G/K D V\L F/L/K(D)		164.12	411.5911	1232.761	-0.0025	-2.1	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
25661	dirMS_041712_NAR_50mM_minus2.17446.17446.3	3	3.45	0	2.53E+05		(R)LLLDGAI	(R)L L|L D G A/P L/I A I H K(A)		168.48	458.6218	1373.852	-0.0007	-0.5	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
25662	dirMS_041712_NAR_50mM_minus2.8605.8605.3	3	3.45	1	7.13E+04	M73m	(K)LDKPDV	(K)L D/K P/D V V N W/m C Y R K(T)	C:Carbamidomethylation m:Oxid	116.82	613.9753	1823.893	16.0182	12.7	8.5	49919.3	5.71	HUMAN	P04180	Phosphatidylcholine-sterol acyltransferase
25663	dirMS_041712_NAR_60mM_minus.10668.10668.3	3	3.45	0	9.91E+05		(K)FHVTPLF	(K)F/H V T P L F G/N V K(K)		120.27	420.2346	1258.694	-0.005	-4	8.76	74874.4	8.54	HUMAN	Q6PIW4	Fidgetin-like protein 1
25664	dirMS_041712_NAR_60mM_minus.11153.11153.3	3	3.45	0	7.43E+04		(R)QGTMA	(R)Q G T M/A L\P A/L\L T R(L)		122.25	424.5804	1271.714	0.0126	9.9	9.75	55117.9	9.82	HUMAN	H3BQ65	Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase B
25665	dirMS_041712_NAR_60mM_minus.15996.15996.3	3	3.45	1	6.43E+05		(R)IGSIYKK	(R)I G/S I Y\K K/A/V Y R(R)		149.2	433.2572	1297.763	-0.0056	-4.3	10	132627.1	6.27	HUMAN	Q6MZM0	Hephaestin-like protein 1
25666	dirMS_041712_NAR_120mM_plus.18133.18133.2	2	3.45	1	3.64E+04	M1145m K	(R)KmIALTT	(R)K|m I|A L\T T\k(E)	m:Oxidized methionine k:Ub	149.15	518.3018	905.549	130.0475	9.3	10	150953.3	8.03	HUMAN	E7EPI0	Inhibitor of Bruton tyrosine kinase
25667	dirMS_041712_NAR_120mM_plus.7904.7904.4	4	3.45	1	7.66E+04	N202n	(R)LATVVnI	(R)L A T V V n D E\R F V S/K(A)	n:N-acetylglucosamine (N)	95.02	420.9801	1477.801	203.0977	10.9	6.07	100477.2	5.87	HUMAN	F5H315	Pre-mRNA-splicing factor SYF1
25668	dirMS_041712_NAR_20mM_plus.10452.10452.3	3	3.45	2	5.88E+04		(R)QACRTP	(R)Q A C R/T P\S R D E A R(V)	C:Carbamidomethylation	144.9	482.9	1446.687	-0.0012	-0.8	9.51	66457	6.51	HUMAN	A8MT19	Putative rhophilin-2-like protein RHPN2P1
25669	dirMS_041712_NAR_20mM_plus.14446.14446.2	2	3.45	0	6.63E+04		(R)ELAQQV	(R)E L/A Q Q/V|Q Q V A D D Y|G K(C)		170.78	846.4161	1691.824	0.0014	0.8	4.03	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
25670	dirMS_041712_NAR_20mM_plus.15857.15857.3	3	3.45	0	8.77E+03		(K)IEQGEEF	(K)I E\Q\G E E P W/I/L E K(G)		179.37	490.9251	1470.747	0.0133	9	4.09	12044.2	4.44	HUMAN	B1AL40	Zinc finger protein 248 (Fragment)
25671	dirMS_041712_NAR_20mM_plus.16596.16596.3	3	3.45	0	9.70E+04	M50m	(R)DSLLQD	(R)D S/L\L Q D G E|F/S m D L R(T)	m:Oxidized methionine	185.67	547.9201	1625.748	15.9982	2	3.84	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
25672	dirMS_041712_NAR_20mM_plus.18242.18242.3	3	3.45	0	1.06E+05		(R)LTGQLFI	(R)L T G Q L F|L/G G S I V K(G)		197.02	444.9339	1332.789	-0.0014	-1.1	8.75	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
25673	dirMS_041712_NAR_20mM_plus.8397.8397.2	2	3.45	0	2.72E+04	M254m M2	(R)LIDDmV	(R)L I|D D m V/A Q/A m K(S)	m:Oxidized methionine	128.07	633.8075	1234.617	31.9907	0.7	4.21	46943.7	6.54	HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic
25674	dirMS_041712_NAR_20mM_plus.9683.9683.2	2	3.45	0	2.38E+05	M697m	(K)AENFEFI	(K)A E\N F E F F F|A m S G K(V)	m:Oxidized methionine	137.57	770.8494	1524.683	16.0087	9	4.53	139557.9	9.73	HUMAN	Q8TE60	A disintegrin and metalloproteinase with thrombospondin motifs 18
25675	dirMS_041712_NAR_30mM_plus2.19707.19707.2	2	3.45	1	2.71E+05		(R)ERPITKL	(R)E/R/P I T/K L/N F(-)		157.28	559.3295	1117.636	0.0153	13.7	8.85	124041.8	6.82	HUMAN	Q9Y4D1	Disheveled-associated activator of morphogenesis 1
25676	dirMS_041712_NAR_30mM_plus2.22073.22073.2	2	3.45	0	1.56E+05		(R)QSSFALL	(R)Q S\S F/A L L/G/D/L T/K(A)		170.63	640.3472	1279.689	-0.0021	-1.7	5.84	46579.3	4.96	HUMAN	E5RI07	Transportin-1
25677	dirMS_041712_NAR_30mM_plus2.8469.8469.2	2	3.45	0	5.13E+05		(R)FSELTAE	(R)F/S|E\L/T A E K(L)		98.87	462.7408	924.467	0.007	7.6	4.53	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
25678	dirMS_041712_NAR_40mM_plus2.10382.10382.3	3	3.45	0	3.10E+04		(R)VTNENS	(R)V T\N E N S N C E/M/R(K)	C:Carbamidomethylation	125.88	451.8617	1353.552	0.0184	13.6	4.53	41346.1	9.93	HUMAN	O95389	WNT1-inducible-signaling pathway protein 3
25679	dirMS_041712_NAR_50mM_plus2.10416.10416.3	3	3.45	1	2.66E+05	S627s	(R)sQGAEG	(R)s Q/G A/E G L L A R I H H/G D R(G)	s:N-acetylglucosamine (S)	121.93	640.6519	1716.889	203.0523	-14.1	6.66	82685	10.04	HUMAN	C9JS30	Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adapter 1
25680	dirMS_041712_NAR_50mM_plus2.10822.10822.3	3	3.45	1	2.00E+05	S381s T38	(R)LsNtDGL	(R)L s N/t D G L P R/V Q L S\S P R(Q)	s:Phosphorylated S t:Phosph	123.87	633.9707	1739.94	159.9577	13.2	9.6	105657.6	6	HUMAN	H3BMX2	Alpha-mannosidase 2C1
25681	dirMS_041712_NAR_50mM_plus2.12548.12548.3	3	3.45	1	6.41E+04	M264m	(K)TmTDVV	(K)T m T D\V V G/N P E/E E R R(A)	m:Oxidized methionine	132.8	550.256	1632.765	15.9888	-3.7	4.41	37190.7	6.16	HUMAN	F8VRQ4	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1
25682	dirMS_041712_NAR_60mM_plus.15258.15258.3	3	3.45	1	1.76E+05		(R)VEVTEFE	(R)V E/V/T E F E D I/K S G Y R(I)		136.78	557.9447	1671.822	-0.0029	-1.7	4.41	30992.3	4.14	HUMAN	B2REB8	Protein SET
25683	dirMS_041712_NAR_120mM_minus.12123.12123.3	3	3.44	1	2.45E+05		(R)MQKEIT	(R)M Q K E I T A/L/A/P S T M/K(I)		119.85	516.9425	1548.812	0.0005	0.3	8.35	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
25684	dirMS_041712_NAR_120mM_minus.16340.16340.3	3	3.44	2	1.19E+05		(K)KQGGLG	(K)K\Q/G G L G P M N\I/P L V\S D P K R(T)		143.52	636.3552	1907.053	-0.0021	-1.1	9.99	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
25685	dirMS_041712_NAR_120mM_minus.17227.17227.4	4	3.44	2	5.35E+05		(R)YEEIVKE	(R)Y E/E I/V K E V S/T Y/I K K(I)		148.72	432.9911	1728.942	0.0007	0.4	6.23	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
25686	dirMS_041712_NAR_120mM_minus.18525.18525.4	4	3.44	1	3.54E+05		(K)FQIPPNA	(K)F Q\I P/P/N A E L K Y E L/H L K(S)		156.78	485.7686	1940.064	-0.0114	-5.9	6.75	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
25687	dirMS_041712_NAR_120mM_minus.4643.4643.2	2	3.44	0	5.45E+05		(R)HSDGNL	(R)H/S/D/G N L\C V K(V)	C:Carbamidomethylation	74.2	515.2423	1029.478	-0.0009	-0.9	6.74	7781.8	6.82	HUMAN	E9PE20	Signal recognition particle 9 kDa protein
25688	dirMS_041712_NAR_120mM_minus.7754.7754.3	3	3.44	0	1.88E+05	M110m	(K)LSEVQAS	(K)L S/E V Q A S E A E m R(L)	m:Oxidized methionine	95.92	455.8866	1349.637	16.0087	10.1	4.25	130627.1	8.75	HUMAN	Q8IY37	Probable ATP-dependent RNA helicase DHX37
25689	dirMS_041712_NAR_20mM_minus.13299.13299.2	2	3.44	0	2.25E+05		(R)GVVDSE	(R)G V V D S E/D I|P L N L\S R(E)		183.05	757.3944	1513.786	-0.0041	-2.7	4.03	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
25690	dirMS_041712_NAR_30mM_minus2.15598.15598.2	2	3.44	0	1.84E+04		(R)IGSGFDN	(R)I/G/S G F D N I\D\I K(S)		138.72	589.8069	1178.605	0.0013	1.1	4.21	20631.5	6.98	HUMAN	D6RAX2	C-terminal-binding protein 1 (Fragment)
25691	dirMS_041712_NAR_30mM_minus2.5181.5181.2	2	3.44	0	3.98E+04		(R)LGPWAG	(R)L G P W A G/G\C S/K(M)	C:Carbamidomethylation	81.58	516.7465	1032.493	-0.0074	-7.2	8.75	47009	9.87	HUMAN	F5H1F5	Vasoactive intestinal polypeptide receptor 1
25692	dirMS_041712_NAR_30mM_minus2.5465.5465.2	2	3.44	0	2.75E+05		(R)SNAEDT	(R)S/N/A/E/D T L R(S)		84.07	453.2209	905.432	0.0022	2.5	4.37	533778	5.74	HUMAN	Q15149	Plectin
25693	dirMS_041712_NAR_30mM_minus2.6885.6885.2	2	3.44	0	1.20E+05		(K)APTSSSQ	(K)A/P|T S S S Q R(S)		91.97	417.2093	833.411	0.0002	0.2	9.79	109137.3	4.87	HUMAN	K7EJ81	116 kDa U5 small nuclear ribonucleoprotein component
25694	dirMS_041712_NAR_30mM_minus2.8590.8590.2	2	3.44	0	2.61E+05		(R)YEGEFAQ	(R)Y E|G E F\A Q G/K(F)		100.97	514.7436	1028.468	0.0116	11.3	4.53	16292.8	8	HUMAN	Q8NDC4	MORN repeat-containing protein 4
25695	dirMS_041712_NAR_40mM_minus2.11765.11765.3	3	3.44	1	5.91E+04		(K)EAFSLFD	(K)E A F/S/L/F\D K D G D G/T I T T K(E)		152.78	615.6437	1844.891	0.0253	13.7	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
25696	dirMS_041712_NAR_40mM_minus2.13063.13063.3	3	3.44	0	4.09E+05		(K)FTISDHP	(K)F T|I S D H/P Q P I D|P L L K(N)		159.7	574.3124	1720.927	-0.0042	-2.4	5.21	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
25697	dirMS_041712_NAR_40mM_minus2.7709.7709.3	3	3.44	0	6.54E+04		(K)EVVKPV	(K)E V V K P V P I/T S/P A V/S K(V)		123.68	517.6416	1550.915	-0.005	-3.2	8.69	65142.1	9.24	HUMAN	Q96HC4	PDZ and LIM domain protein 5
25698	dirMS_041712_NAR_50mM_minus2.12488.12488.3	3	3.44	0	2.27E+05		(R)TTTGDV	(R)T T|T G D\V Q V L/G L V/H T Q K(L)		138.78	566.3109	1696.923	-0.0047	-2.8	6.41	281330.5	5.64	HUMAN	P11717	Cation-independent mannose-6-phosphate receptor
25699	dirMS_041712_NAR_50mM_minus2.14282.14282.3	3	3.44	0	1.31E+05		(K)EGHVEV	(K)E G H V E\V\V/S E L\L Q R(E)		149.75	498.9399	1494.791	0.0141	9.4	4.75	48586.6	9.32	HUMAN	D6RCB2	Ankyrin-3
25700	dirMS_041712_NAR_50mM_minus2.14882.14882.3	3	3.44	0	3.07E+04		(K)GQYFGE	(K)G Q|Y/F G E L/A L/V T N K P R(A)		152.52	564.9709	1692.907	-0.0086	-5.1	8.59	10305.6	6.94	HUMAN	H7C330	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
25701	dirMS_041712_NAR_50mM_minus2.6123.6123.3	3	3.44	0	1.34E+04		(K)TQAYQD	(K)T Q|A/Y Q D Q K/P G T S G L R(K)		97.55	550.6108	1649.824	-0.0063	-3.8	8.25	61733.3	6.3	HUMAN	P36871	Phosphoglucomutase-1
25702	dirMS_041712_NAR_50mM_minus2.8439.8439.3	3	3.44	1	1.03E+05		(K)KSDCSLF	(K)K S D C S L F M F G/S H\N K(K)	C:Carbamidomethylation	116.1	553.2484	1657.746	-0.0155	-9.3	8.6	24386.3	9.7	HUMAN	Q5VXM9	Brix domain containing 1 (Fragment)
25703	dirMS_041712_NAR_60mM_minus.10024.10024.3	3	3.44	1	1.15E+05		(R)YESLTDF	(R)Y/E|S L/T D P S K L D S G K(E)		115.58	513.9233	1539.754	0.0017	1.1	4.56	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
25704	dirMS_041712_NAR_60mM_minus.10695.10695.3	3	3.44	1	5.79E+04		(R)LAEVEA	(R)L/A/E V E A/A L E/K Q R(Q)		119.55	452.9148	1356.748	-0.0183	-13.5	4.79	533778	5.74	HUMAN	Q15149	Plectin
25705	dirMS_041712_NAR_60mM_minus.15892.15892.3	3	3.44	1	3.78E+05		(K)KANLQID	(K)K A N L Q I D\Q/I/N/T/D L N L E R(S)		148.08	666.6911	1998.061	-0.0027	-1.3	4.56	227783.5	5.5	HUMAN	P35579	Myosin-9
25706	dirMS_041712_NAR_60mM_minus.16264.16264.3	3	3.44	0	2.78E+05		(R)HDPTSEI	(R)H D\P T S E\N\I/L Q|L V/K(A)		150.57	498.6051	1493.796	0.0049	3.3	5.32	13564.4	5.9	HUMAN	F8VZ98	Serine/threonine-protein kinase D1 (Fragment)
25707	dirMS_041712_NAR_60mM_minus.18924.18924.3	3	3.44	0	2.39E+05		(R)CRPDQL	(R)C R P D Q\L T\G\L|S\L L/P L S E K(A)	C:Carbamidomethylation	168	643.0129	1927.032	-0.0076	-3.9	6.07	533778	5.74	HUMAN	Q15149	Plectin
25708	dirMS_041712_NAR_60mM_minus.7678.7678.3	3	3.44	1	5.65E+05		(R)YLAEVA	(R)Y L/A E|V/A A G D D/K K(G)		102.07	427.222	1279.653	-0.0014	-1.1	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
25709	dirMS_041712_NAR_120mM_plus.10694.10694.3	3	3.44	0	4.24E+05		(K)GSYVSIH	(K)G S Y/V/S I/H/S S G F R(D)		109.6	432.8823	1296.633	-0.0008	-0.6	8.75	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
25710	dirMS_041712_NAR_120mM_plus.11663.11663.4	4	3.44	1	8.30E+05		(R)KVSQPIE	(R)K\V S Q/P\I/E/G H A A S F A Q F K(M)		113.77	461.9971	1844.965	0.0012	0.7	8.6	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
25711	dirMS_041712_NAR_120mM_plus.14686.14686.4	4	3.44	2	1.37E+06		(R)YLYTLVI	(R)Y L Y/T L V/I T D K E K A E K(L)		130.85	454.2533	1813.995	-0.0032	-1.8	6.18	7621.9	10.1	HUMAN	J3KT73	60S ribosomal protein L38
25712	dirMS_041712_NAR_120mM_plus.18513.18513.4	4	3.44	0	4.36E+04		(R)LGWDPK	(R)L G W D P K/P G E G/H/L/D A L L R(G)		150.98	469.253	1873.992	-0.0017	-0.9	5.38	95141.7	5.22	HUMAN	B7Z463	Puromycin-sensitive aminopeptidase
25713	dirMS_041712_NAR_120mM_plus.7468.7468.2	2	3.44	0	1.55E+05		(R)LYVHEA	(R)L Y/V/H E A V/K(A)		93.12	479.7757	958.536	0.0085	8.8	6.75	533778	5.74	HUMAN	Q15149	Plectin
25714	dirMS_041712_NAR_20mM_plus.12202.12202.2	2	3.44	0	9.14E+03		(R)SIFASPE	(R)S I/F A S/P E S V T G K(V)		157.07	611.8175	1222.631	-0.0037	-3	5.72	26881.8	6.79	HUMAN	O75940	Survival of motor neuron-related-splicing factor 30
25715	dirMS_041712_NAR_20mM_plus.18037.18037.2	2	3.44	0	8.59E+04	M848m	(R)SLSELLG	(R)S L|S E L/L G P Y G m K(F)	m:Oxidized methionine	195.4	655.8428	1294.671	16.0072	9.4	5.72	130100	6.18	HUMAN	Q9Y2A7	Nck-associated protein 1
25716	dirMS_041712_NAR_20mM_plus.18229.18229.2	2	3.44	0	5.11E+04		(K)FIIPQIVK	(K)F\I/I/P Q I V K(Y)		197.13	479.3081	957.613	-0.0042	-4.4	8.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
25717	dirMS_041712_NAR_20mM_plus.6424.6424.3	3	3.44	1	5.31E+04		(K)LAHAMN	(K)L A H/A M M/E A F/R K(T)		107.1	435.561	1304.66	0.0082	6.3	8.76	28784.6	6.53	HUMAN	Q7Z2X4	PTB-containing, cubilin and LRP1-interacting protein
25718	dirMS_041712_NAR_20mM_plus.8798.8798.2	2	3.44	0	3.05E+03		(R)DVAYQY	(R)D V/A|Y Q Y/V K(K)		131.12	493.2543	985.499	0.0024	2.4	5.83	14130.9	9.56	HUMAN	C9K0U8	Single-stranded DNA-binding protein (Fragment)
25719	dirMS_041712_NAR_30mM_plus2.21342.21342.2	2	3.44	0	1.94E+04		(R)SEIDLFN	(R)S E/I/D\L F/N I/R(K)		166.08	553.8012	1106.584	0.0111	10	4.37	24754.5	4.77	HUMAN	D6RBE9	Annexin

25720	dirMS_041712_NAR_30mM_plus2.7217.7217.2	2	3.44	0	3.73E+04		(K)SLESINSI	(K)S L|E/S I/N S/R(L)		92.13	453.2369	905.469	-0.0022	-2.4	5.72	12826.8	9.82	HUMAN	E5RI99	60S ribosomal protein L30 (Fragment)
25721	dirMS_041712_NAR_40mM_plus2.10119.10119.3	3	3.44	0	5.15E+04		(K)EVVKPV	(K)E V V K P V\P I/T/S/P A V S K(V)		123.87	517.6421	1550.915	-0.0035	-2.2	8.69	65142.1	9.24	HUMAN	Q96HC4	PDZ and LIM domain protein 5
25722	dirMS_041712_NAR_40mM_plus2.5694.5694.2	2	3.44	0	1.02E+05		(K)APGFGD	(K)A/P/G/F G D/N R(K)		90.75	417.1996	833.39	0.0019	2.3	5.88	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
25723	dirMS_041712_NAR_50mM_plus2.15791.15791.3	3	3.44	0	1.18E+05		(K)GQYFGE	(K)G Q|Y|F G E L A L V T N K P R(A)		151.15	564.9788	1692.907	0.0151	8.9	8.59	10305.6	6.94	HUMAN	H7C330	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
25724	dirMS_041712_NAR_50mM_plus2.17416.17416.3	3	3.44	0	1.06E+06		(R)LPLEILEF	(R)L P L E I L/E F/V Q E|A M K(G)		159.73	553.9791	1659.903	0.0201	12.1	4.25	139420.2	5.9	HUMAN	Q9NQ66	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1
25725	dirMS_041712_NAR_50mM_plus2.17579.17579.3	3	3.44	0	7.51E+05	M910m	(K)IVVGAL	(K)I V V G A L Q M A/E I L m Q\K(L)	m:Oxidized methionine	160.43	553.9791	1643.922	16.0005	3.3	6	222369.5	9.18	HUMAN	Q14669	E3 ubiquitin-protein ligase TRIP12
25726	dirMS_041712_NAR_50mM_plus2.19410.19410.3	3	3.44	1	2.25E+05		(K)DGKTLN	(K)D G K T L N D E\L/E/I|I E G M K(F)		169.82	602.3071	1804.9	0.007	3.9	4.18	23782.2	9.5	HUMAN	E7EXB4	60 kDa heat shock protein, mitochondrial (Fragment)
25727	dirMS_041712_NAR_50mM_plus2.9366.9366.3	3	3.44	1	4.29E+05	Y38y	(R)CCITAAF	(R)C\C|I T A A P Y R G I S\C y R(G)	C:Carbamidomethylation y:Phos	116.6	643.2708	1847.835	79.9629	-1.8	9.99	55154.3	5.57	HUMAN	O43790	Keratin, type II cuticular Hb6
25728	dirMS_041712_NAR_60mM_plus.10833.10833.3	3	3.44	1	1.66E+06	M2m S10s	(-)XmEEKEI	(-)X m E E K E/L Q/A s/K(N)	m:Oxidized methionine s:Ph	114.45	467.8876	1305.672	95.9764	10.8	4.79	15880	4.92	HUMAN	H0YB14	Dedicator of cytokinesis protein 5 (Fragment)
25729	dirMS_041712_NAR_60mM_plus.5426.5426.3	3	3.44	1	1.58E+05	S117s	(R)QEILKLE	(R)Q E/I L K/L E N/s G G K(K)	s:N-acetylglucosamine (S)	85.63	506.9426	1315.722	203.0916	8.1	6.14	60279.9	5.91	HUMAN	A8MPP8	Meckel syndrome type 1 protein
25730	dirMS_041712_NAR_60mM_plus.9249.9249.3	3	3.44	0	4.62E+05	T1436t	(R)VYQtNY	(R)V/Y/Q t/N Y F A S K(C)	t:N-acetylglucosamine (T)	106.78	475.2309	1220.595	203.0835	2.9	8.47	215927.6	7.38	HUMAN	F5H3G6	Receptor-type tyrosine-protein phosphatase beta
25731	dirMS_041712_NAR_120mM_minus.18299.18299.3	3	3.43	1	2.92E+05		(K)IESQAAF	(K)I E S Q A A R\L|L S L E\G R(T)		154.38	514.9655	1542.86	0.0221	14.3	6.14	19841.3	6.19	HUMAN	C9JNZ9	Zinc finger protein 746
25732	dirMS_041712_NAR_120mM_minus.20401.20401.4	4	3.43	2	2.11E+05		(K)NTLGSD	(K)N T/L G S D L P R I K T E I E A L K(N)		167.5	500.2804	1998.123	-0.0232	-11.6	6.18	69970.5	9.38	HUMAN	F5H0Y0	Maternal embryonic leucine zipper kinase
25733	dirMS_041712_NAR_120mM_minus.7290.7290.3	3	3.43	1	9.18E+04	T182t	(R)LEtLLEEI	(R)L E/t L/L/E E/R/E S K(A)	t:Phosphorylated T	93.77	476.2347	1346.716	79.9734	4.9	4.49	102247.6	9.19	HUMAN	A2AVK2	Glutamate [NMDA] receptor subunit zeta-1
25734	dirMS_041712_NAR_30mM_minus2.11707.11707.2	2	3.43	0	8.84E+05		(K)CGDLVF	(K)C G\D|L/V/F A K(M)	C:Carbamidomethylation	117	455.2306	909.45	0.0041	4.5	5.84	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
25735	dirMS_041712_NAR_30mM_minus2.16350.16350.2	2	3.43	0	1.23E+05		(K)LSTGCTC	(K)L S|T G C T G\T/L V A E K(H)	C:Carbamidomethylation	142.05	668.8368	1336.678	-0.0114	-8.5	6	40040.2	9.87	HUMAN	B4E2J3	Serine protease 23
25736	dirMS_041712_NAR_30mM_minus2.5905.5905.2	2	3.43	1	7.36E+03	S488s	(K)NGVKFT	(K)N/G/V\K F T N s/K(L)	s:Phosphorylated S	85.85	537.7506	994.532	79.9623	-3.7	10	98062.5	5.57	HUMAN	B4E2Z2	DNA mismatch repair protein Msh2
25737	dirMS_041712_NAR_30mM_minus2.8112.8112.2	2	3.43	0	1.83E+05		(K)GSGTAE	(K)G S|G T/A/E V E/L K(K)		98.32	495.7528	990.51	-0.0119	-12	4.53	30947.9	6.47	HUMAN	H3BQ34	Pyruvate kinase
25738	dirMS_041712_NAR_30mM_minus2.8721.8721.2	2	3.43	0	2.68E+05	K93k	(R)kEAGLG	(R)k/E/A G/L/G R(R)	k:Ubiquitin-K	101.58	422.7411	730.421	114.0543	13.5	8.75	154176.6	6.37	HUMAN	Q6TFL3	Coiled-coil domain-containing protein 171
25739	dirMS_041712_NAR_40mM_minus2.13303.13303.3	3	3.43	0	1.89E+05	K89k	(R)VSVQLE	(R)V/S V Q L/E A\S P A F L A V P V\E k(E)	k:Ubiquitin-K	161.73	666.6932	1884.048	114.0174	-12.8	4.53	22472.4	5.82	HUMAN	H0YGH6	Alpha-2-macroglobulin (Fragment)
25740	dirMS_041712_NAR_40mM_minus2.14947.14947.3	3	3.43	0	9.28E+05		(K)ISSIQSIV	(K)I S\S I Q S I V/P A|L E/I A N A H R(K)		172.32	640.3618	1919.071	0	0	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
25741	dirMS_041712_NAR_50mM_minus2.12807.12807.3	3	3.43	1	1.12E+04	K164k	(K)NQAIRQ	(K)N/Q A I R Q P E V Q A A P k(E)	k:Ubiquitin-K	140.88	555.3037	1549.844	114.052	5.5	8.75	33581.2	11.07	HUMAN	I3L0U5	Coiled-coil domain-containing protein 137 (Fragment)
25742	dirMS_041712_NAR_50mM_minus2.13308.13308.3	3	3.43	1	2.32E+04		(R)TQVELLE	(R)T Q|V E/L L E A/P T/P A/L K R(T)		143.82	555.9883	1665.953	-0.003	-1.8	5.81	18460.6	5.48	HUMAN	C9IYM4	Glycogen [starch] synthase, muscle (Fragment)
25743	dirMS_041712_NAR_50mM_minus2.14280.14280.3	3	3.43	0	1.26E+04		(K)LLAQEA	(K)L L\A Q E A W/A Q G/T A M V G V R(E)		149.32	600.9885	1800.943	0.0084	4.7	6	413303.4	5.14	HUMAN	F8W8T3	Obscurin
25744	dirMS_041712_NAR_50mM_minus2.17506.17506.3	3	3.43	0	1.01E+06	M195m	(R)LHFFmP	(R)L H F\F m/P G|F/A/P L T S R(G)	m:Oxidized methionine	167.35	546.2872	1620.835	16.0115	10.1	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
25745	dirMS_041712_NAR_50mM_minus2.17828.17828.3	3	3.43	0	3.27E+04		(K)TTLLNYII	(K)T T L L/N/Y I L T\E/Q H S K(R)		170.32	554.3024	1660.891	0.0022	1.3	6.41	42238.2	4.88	HUMAN	B4DNG9	COBW domain-containing protein 3
25746	dirMS_041712_NAR_60mM_minus.12614.12614.3	3	3.43	1	5.64E+03		(K)NQVALN	(K)N Q\V/A\L N/P Q N T V F D A K R(L)		130.18	605.6583	1814.951	0.0096	5.3	8.75	70336.2	5.48	HUMAN	P08107	Heat shock 70 kDa protein 1A/1B
25747	dirMS_041712_NAR_60mM_minus.17106.17106.3	3	3.43	2	1.20E+05	Y354y	(R)ATyERG	(R)A T\y E R/G V/K/V/R(L)	y:Phosphorylated Y	155.85	420.2191	1178.664	79.9787	9.8	9.99	55160.8	6.02	HUMAN	Q8IV08	Phospholipase D3
25748	dirMS_041712_NAR_60mM_minus.8782.8782.3	3	3.43	1	3.21E+04	K258k	(K)FkEKTAE	(K)F/k E|K T A E Q L R(V)	k:Ubiquitin-K	109.12	455.2427	1249.69	114.0236	-14.1	8.59	63271.6	8.84	HUMAN	H0YB50	Zinc fingers and homeoboxes protein 1 (Fragment)
25749	dirMS_041712_NAR_120mM_plus.21178.21178.4	4	3.43	2	2.79E+05		(R)SDHPKS	(R)S D/H P K S T G E P T R E I\E L K(S)		164.12	481.7493	1923.977	-0.0017	-0.9	5.51	125928	5.71	HUMAN	Q8IWB9	Testis-expressed sequence 2 protein
25750	dirMS_041712_NAR_120mM_plus.8641.8641.3	3	3.43	1	1.57E+05		(R)RTEEGP	(R)R T E E G|P T L/S/Y G R(D)		99.07	455.8929	1365.676	-0.0116	-8.5	6.14	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
25751	dirMS_041712_NAR_20mM_plus.12740.12740.2	2	3.43	1	1.01E+04		(R)QMDRA	(R)Q M D/R/A E|H K(G)		160.45	507.7439	1014.479	0.002	2	6.75	126097.4	5.65	HUMAN	Q8IX03	Protein KIBRA
25752	dirMS_041712_NAR_20mM_plus.7190.7190.2	2	3.43	0	9.96E+04	M46m M4	(R)EGTGTE	(R)E G T/G T/E\m P\m I/G D R(V)	m:Oxidized methionine	117.32	713.3007	1393.609	31.9855	-3	4.14	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
25753	dirMS_041712_NAR_20mM_plus.8259.8259.2	2	3.43	0	5.19E+04		(R)AVVIVDI	(R)A V/V|I V D/D/R(G)		127.05	443.7527	886.499	-0.0011	-1.3	4.21	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
25754	dirMS_041712_NAR_30mM_plus2.17163.17163.2	2	3.43	0	2.74E+05		(R)ISWYLR(	(R)I/S/W Y/L/R(D)		142.77	419.2286	837.462	-0.0118	-14.1	8.75	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
25755	dirMS_041712_NAR_30mM_plus2.20828.20828.2	2	3.43	0	7.80E+04		(K)NLQEEIL	(K)N L Q E E/I D/A/L/E S R(V)		163.13	708.8513	1416.697	-0.0012	-0.8	4	15712.4	4.48	HUMAN	E9PQY2	Prefoldin subunit 4
25756	dirMS_041712_NAR_30mM_plus2.4471.4471.2	2	3.43	0	3.69E+05		(R)SYTSGPC	(R)S Y/T/S G P G S R(I)		72.98	456.2155	911.422	0.002	2.2	8.46	19288.4	10.19	HUMAN	F8VQY3	Keratin, type II cytoskeletal 8 (Fragment)
25757	dirMS_041712_NAR_40mM_plus2.8161.8161.2	2	3.43	0	4.70E+04		(R)LASYLDF	(R)L/A/S Y L D/R(V)		108.52	419.2273	837.447	0.0008	1	5.83	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
25758	dirMS_041712_NAR_50mM_plus2.11240.11240.3	3	3.43	2	4.55E+04		(R)QFLMN	(R)Q F L/M N W K A\S/K D A K(K)		126.6	522.9433	1566.81	0.0056	3.6	9.7	35878.9	9.15	HUMAN	G3V118	Protein phosphatase 1 regulatory subunit 42
25759	dirMS_041712_NAR_50mM_plus2.16807.16807.3	3	3.43	1	1.14E+05	N239n	(R)IQnGSYK	(R)I/Q n G S/Y K/S I H A M A K(D)	n:N-acetylglucosamine (N)	155.92	584.2981	1547.8	203.0799	0.3	9.7	169758	6.18	HUMAN	E7EVG2	Protein polybromo-1 (Fragment)
25760	dirMS_041712_NAR_50mM_plus2.17075.17076.3	3	3.43	1	1.01E+06		(R)VTTVTEI	(R)V T/T V T/E I G K D V/I/G L R(I)		156.87	534.308	1600.927	-0.0174	-10.9	6.04	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
25761	dirMS_041712_NAR_50mM_plus2.19664.19664.3	3	3.43	1	9.25E+04		(K)TFVNITP	(K)T F/V/N/I/T/P A E V/G V L V G K D R(S)		171.23	639.0247	1915.065	-0.0052	-2.7	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
25762	dirMS_041712_NAR_50mM_plus2.19786.19786.3	3	3.43	0	2.50E+05		(K)LFLFHTS	(K)L F L F/H T S L/P I A E A/P G K(L)		172.83	580.9943	1740.968	0	0	6.75	108105.4	6.57	HUMAN	E7EP00	Protein transport protein Sec24C
25763	dirMS_041712_NAR_60mM_plus.10093.10093.3	3	3.43	1	1.28E+05		(K)DSQICEL	(K)D S Q/I/C E L\K Y D/K(Q)	C:Carbamidomethylation	109.98	466.8941	1398.657	0.0108	7.7	4.56	21156.2	9.41	HUMAN	P55145	Mesencephalic astrocyte-derived neurotrophic factor
25764	dirMS_041712_NAR_60mM_plus.15665.15665.3	3	3.43	1	5.06E+04	T586t	(K)SPNHVK	(K)S P/N H V K|I t D F\G L A R(L)	t:Phosphorylated T	138.55	545.6107	1554.839	79.9788	7.7	8.49	109737	5.35	HUMAN	B4DTR1	Receptor tyrosine-protein kinase erbB-2
25765	dirMS_041712_NAR_60mM_plus.18695.18695.3	3	3.43	1	2.31E+03		(K)YGYEIPV	(K)Y/G Y E/I/P V D/M L C K R(I)	C:Carbamidomethylation	154.42	548.6028	1643.792	0.0018	1.1	6.07	19157.6	5.18	HUMAN	B4DQR4	Proteasome subunit alpha type-6
25766	dirMS_041712_NAR_60mM_plus.5539.5539.3	3	3.43	0	1.90E+06	M21m	(R)SGSmDF	(R)S G\S/m/D P S G A/H/P S V R(Q)	m:Oxidized methionine	87.5	467.5464	1384.627	15.9973	1.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
25767	dirMS_041712_NAR_120mM_minus.9606.9606.2	2	3.42	0	3.20E+04		(K)HVVFIAC	(K)H V|V F I/A Q R(R)		107.08	485.2837	969.563	-0.0027	-2.8	9.75	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
25768	dirMS_041712_NAR_20mM_minus.10638.10638.2	2	3.42	0	7.23E+04	M78m	(K)TLVLLm	(K)T L|V/L/L m G K(E)	m:Oxidized methionine	154.37	445.7725	874.543	15.9947	-0.3	8.41	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
25769	dirMS_041712_NAR_20mM_minus.11930.11930.3	3	3.42	0	2.54E+04		(R)NFLCSLE	(R)N F L C S L/E/S N P S V R(E)	C:Carbamidomethylation	168.1	508.2517	1522.732	0.0087	5.7	6	45781.9	6.88	HUMAN	P14902	Indoleamine 2,3-dioxygenase 1
25770	dirMS_041712_NAR_30mM_minus2.5003.5003.2	2	3.42	0	9.07E+05		(K)TNAANL	(K)T N/A A N L S|D A R(Y)		80.17	516.7465	1032.507	-0.0211	-20.5	5.5	198040.3	9.37	HUMAN	Q86VF7	Nebulin-related-anchoring protein
25771	dirMS_041712_NAR_30mM_minus2.5836.5836.2	2	3.42	0	2.25E+05		(R)DALSAS	(R)D/A/L S A S V V K(V)		85.98	445.2523	889.499	-0.0016	-1.8	5.84	24622.5	9.12	HUMAN	Q13103	Secreted phosphoprotein 24
25772	dirMS_041712_NAR_40mM_minus2.13330.13330.3	3	3.42	1	1.01E+04	M10m K20	(R)LKFmSSI	(R)L K F/m S S P S L S D L G k(R)	m:Oxidized methionine k:Ub	161.87	547.2822	1509.798	130.0339	-2.4	8.59	64834.7	9.77	HUMAN	B1AHC3	Protein PRR5-ARHGAP8
25773	dirMS_041712_NAR_50mM_minus2.10168.10168.3	3	3.42	2	5.01E+04	T230t	(K)HKtMLE	(K)H K t M L E A R/N G S G/T I K(A)	t:Phosphorylated T	125.95	574.9529	1642.869	79.9748	4.9	9.99	42751.4	10.35	HUMAN	Q9H6B1	Zinc finger protein 385D
25774	dirMS_041712_NAR_50mM_minus2.15983.15983.3	3	3.42	0	6.82E+03		(K)SAIPHPL	(K)S A I/P H/P L I M/G V\I R(E)		158.98	468.6077	1403.819	-0.0106	-7.6	9.49	44513	5.59	HUMAN	B4DIH5	COP9 signalosome complex subunit 2
25775	dirMS_041712_NAR_50mM_minus2.5714.5714.3	3	3.42	1	5.51E+04		(K)TAGPIAS	(K)T A/G P/I A S A Q K Q P A G K(V)		93.67	475.5972	1424.786	-0.0086	-6	10	75259.2	9.59	HUMAN	B5MEG9	Microtubule-associated protein 4 (Fragment)
25776	dirMS_041712_NAR_50mM_minus2.6132.6132.3	3	3.42	1	5.69E+04	M322m	(K)AAGSGE	(K)A A/G/S/G E L G V T m/K G P K(G)	m:Oxidized methionine	97.78	473.5826	1402.736	15.9974	1.7	8.64	258215.9	5.48	HUMAN	E7EN95	Filamin-B
25777	dirMS_041712_NAR_60mM_minus.13072.13072.3	3	3.42	2	3.15E+05	M449m K4	(R)KmLEAL	(R)K m/L E A L S W K D k(V)	m:Oxidized methionine k:Ub	133.25	493.5966	1348.729	130.0459	5.5	8.5	90000.9	6.58	HUMAN	Q8IYT2	FtsJ methyltransferase domain-containing protein 1
25778	dirMS_041712_NAR_120mM_plus.8898.8898.4	4	3.42	1	2.33E+04		(K)AEGHRV	(K)A E G\H R V L I F T Q/M T/R(M)		100.25	415.4731	1658.88	-0.0089	-5.4	9.65	345203	5.69	HUMAN	Q6ZRS2	Helicase SRCAP
25779	dirMS_041712_NAR_20mM_plus.12397.12397.2	2	3.42	0	8.61E+04	M78m	(K)TLVLLm	(K)T L/V L/L/m G/K(E)	m:Oxidized methionine	157.57	445.7707	874.543	15.9911	-4.3	8.41	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
25780	dirMS_041712_NAR_20mM_plus.12704.12704.2	2	3.42	0	2.75E+04		(K)YDGIILP	(K)Y/D/G I/I/L/P G K(-)		160.08	488.2764	975.551	-0.0054	-5.6	5.83	20480.2	9.91	HUMAN	P62913	60S ribosomal protein L11
25781	dirMS_041712_NAR_20mM_plus.13428.13428.2	2	3.42	0	1.22E+05		(K)IFVGGLS	(K)I F\V/G\G L|S|P D T P E E K(I)		164.67	744.8731	1488.758	-0.0191	-12.8	4.14	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
25782	dirMS_041712_NAR_20mM_plus.19188.19188.2	2	3.42	0	9.26E+04		(R)DLLFQAI	(R)D L|L|F/Q A L/G R(T)		203.47	516.7952	1032.584	-0.0005	-0.5	5.84	66742	6.4	HUMAN	Q9NSD9	Phenylalanine--tRNA ligase beta subunit
25783	dirMS_041712_NAR_20mM_plus.7342.7342.3	3	3.42	0	2.14E+05		(K)TGQAPG	(K)T G Q A|P G\Y|S Y/T A A N K(N)		119.53	476.8963	1428.675	-0.001	-0.7	8.16	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
25784	dirMS_041712_NAR_20mM_plus.8126.8126.2	2	3.42	0	2.02E+05		(R)FGQGG	(R)F G Q|G/G A/G P V|G G Q G P R(G)		125.25	671.3361	1341.666	-0.0009	-0.7	9.75	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
25785	dirMS_041712_NAR_20mM_plus.8947.8947.3	3	3.42	1	1.55E+04		(K)LEAAGP	(K)L E A A/G P G E P G T K A K(K)		131.57	442.5729	1325.706	-0.0018	-1.4	6.14	27412	9.84	HUMAN	Q9HBU1	Homeobox protein BarH-like 1
25786	dirMS_041712_NAR_20mM_plus.9872.9872.2	2	3.42	2	1.32E+05	S69s	(K)DKsGAP	(K)D K s G/A/P/P V R S(-)	s:N-acetylglucosamine (S)	139.6	608.8139	1013.537	203.0831	3.1	8.75	7710.9	10.27	HUMAN	C9JIY9	Nucleoporin NUP53 (Fragment)
25787	dirMS_041712_NAR_30mM_plus2.13664.13685.2	2	3.42	0	9.40E+05		(K)DLSELGS	(K)D L|S E/L/G S V R(T)		125.37	488.2554	975.511	-0.007	-7.2	4.37	533778	5.74	HUMAN	Q15149	Plectin
25788	dirMS_041712_NAR_30mM_plus2.16137.16137.2	2	3.42	0	3.11E+05		(R)MGPNIY	(R)M/G/P/N I/Y E/L/R(T)		136.67	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
25789	dirMS_041712_NAR_30mM_plus2.7066.7066.2	2	3.42	0	1.56E+05		(R)IAAISM	(R)I A|A I S/M A\S/K(I)		91	446.2501	891.497	-0.0039	-4.4	8.75	130097.9	9.74	HUMAN	Q12986	Transcriptional repressor NF-X1
25790	dirMS_041712_NAR_30mM_plus2.7868.7868.2	2	3.42	0	1.00E+05		(R)GTQGAE	(R)G T/Q/G A E E V L/R(A)		94.8	530.2783	1059.543	0.0064	6	4.53	533778	5.74	HUMAN	Q15149	Plectin
25791	dirMS_041712_NAR_30mM_plus2.8913.8913.2	2	3.42	0	1.12E+05		(R)AIYQAT	(R)A I/Y/Q/A\T Y R(D)		100.07	493.2607	985.51	0.004	4	8.63	17952.8	6.73	HUMAN	E9PAV2	Proteasome subunit beta type-5
25792	dirMS_041712_NAR_40mM_plus2.10588.10588.3	3	3.42	1	7.94E+04	S71s	(R)AAAAAL	(R)A A/A/A/A L S Q Q Q s L Q E R L R(L)	s:Phosphorylated S	127.48	640.9931	1840.999	79.966	-0.2	9.64	99930.3	8.46	HUMAN	J3KMW8	Cactin
25793	dirMS_041712_NAR_40mM_plus2.11058.11058.3	3	3.42	0	1.70E+04		(R)MLTGPV	(R)M L/T G/P V/Y/S\Q S/T A L T H K(Q)		130.95	578.6331	1733.889	-0.0043	-2.5	8.37	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
25794	dirMS_041712_NAR_40mM_plus2.14958.14958.3	3	3.42	0	1.08E+05		(R)TPSIQPS	(R)T P\S I Q/P S L L/P H A A/P F A K(S)		154.65	592.3321	1774.985	-0.0033	-1.9	8.44	14289.1	10.11	HUMAN	H0YF36	Nuclear pore complex protein Nup214 (Fragment)
25795	dirMS_041712_NAR_40mM_plus2.7545.7545.3	3	3.42	0	1.52E+04		(R)EATNPP	(R)E A T/N P/P V I/Q E E K P\K(K)		104.03	527.286	1579.833	0.0108	6.9	4.79	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
25796	dirMS_041712_NAR_40mM_plus2.9119.9119.2	2	3.42	0	8.01E+04		(K)IQDFMR	(K)I/Q/D F/M R(Q)		115.7	405.2041	809.397	0.0035	4.3	5.84	63566.6	6.3	HUMAN	P07686	Beta-hexosaminidase subunit beta
25797	dirMS_041712_NAR_50mM_plus2.10705.10705.3	3	3.42	0	4.20E+05		(K)TSEVDL	(K)T/S/E V/D L A K P L\V K(F)		123.78	433.922	1299.752	-0.0004	-0.3	5.73	17178.3	5.63	HUMAN	C9IZF9	Programmed cell death 6-interacting protein (Fragment)
25798	dirMS_041712_NAR_50mM_plus2.10945.10945.3	3	3.42	1	2.48E+05		(K)YGQISE	(K)Y/G Q/I S/E V V/V/V K D R(E)		125.47	497.9426	1491.817	-0.0033	-2.2	6.07	28815.3	9.52	HUMAN	B4E2X2	Cold-inducible RNA-binding protein
25799	dirMS_041712_NAR_50mM_plus2.11850.11850.3	3	3.42	2	1.27E+05	Y137y	(K)IyVEIER	(K)I y/V E I E R A R L T/K(T)	y:Phosphorylated Y	130.32	524.2855	1490.869	79.973	4.3	8.59	53302.9	7.71	HUMAN	O00232	26S proteasome non-ATPase regulatory subunit 12
25800	dirMS_041712_NAR_50mM_plus2.18869.18869.3	3	3.42	2	1.55E+05		(K)LNSKWN	(K)L N S K/W N/I L/C E/K I K(G)	C:Carbamidomethylation	167.52	549.3076	1645.909	-0.0012	-0.7	9.7	43106	9.19	HUMAN	Q9Y234	Lipoyltransferase 1, mitochondrial
25801	dirMS_041712_NAR_50mM_plus2.19823.19823.3	3	3.42	0	3.74E+05		(K)NGGLGH	(K)N G\G\L G H M N\I A|L L/S D L T\K(Q)		173.03	585.311	1753.927	-0.0081	-4.6	6.74	26123.4	7.07	HUMAN	E9PH29	Thioredoxin-dependent peroxide reductase, mitochondrial
25802	dirMS_041712_NAR_50mM_plus2.7174.7174.3	3	3.42	2	1.29E+04		(R)LAGSAL	(R)L A G S A/L/T D K H S D K S(-)		103.17	477.252	1429.728	0.0133	9.3	6.75	162818.7	5.43	HUMAN	E9PMR6	Rho guanine nucleotide exchange factor 12
25803	dirMS_041712_NAR_50mM_plus2.8793.8793.3	3	3.42	0	2.04E+05		(K)VVQVSA	(K)V V/Q\V/S A/G D S H T/A A L T D D G R(V)		113.45	633.6509	1898.92	0.0179	9.4	4.41	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
25804	dirMS_041712_NAR_60mM_plus.18167.18167.3	3	3.42	2	3.17E+05	S356s	(R)KYNLQE	(R)K Y N L Q/E|V/V K/s P K(D)	s:Phosphorylated S	151.48	504.9258	1432.816	79.947	-12.8	9.53	49061.4	9.37	HUMAN	J3KQB0	THUMP domain-containing protein 1
25805	dirMS_041712_NAR_20mM_minus.13107.13107.3	3	3.41	0	3.94E+05		(K)TITLEVEI	(K)T I\T L E V/E|P\S D T I E N V K(A)		183.03	596.6453	1787.927	-0.006	-3.3	4	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
25806	dirMS_041712_NAR_30mM_minus2.7357.7357.2	2	3.41	1	2.41E+05		(K)VAVRGG	(K)V|A|V/R G G D K(K)		94.85	401.2385	801.458	0.012	15	8.72	12359.5	9.52	HUMAN	C9JCJ9	Obg-like ATPase 1 (Fragment)
25807	dirMS_041712_NAR_30mM_minus2.9094.9094.2	2	3.41	1	5.25E+04		(R)NGVLGD	(R)N G/V L G D S R D K(E)		104.73	530.7694	1060.538	-0.0066	-6.3	5.96	69553.6	9.28	HUMAN	Q9Y289	Sodium-dependent multivitamin transporter
25808	dirMS_041712_NAR_50mM_minus2.15054.15054.3	3	3.41	1	1.43E+05		(R)LLLEFTD	(R)L L|L E F T D T/S Y E E K R(Y)		153.77	581.9591	1743.88	-0.0172	-9.9	4.41	27015.5	5.37	HUMAN	P21266	Glutathione S-transferase Mu 3
25809	dirMS_041712_NAR_50mM_minus2.17936.17936.3	3	3.41	1	2.31E+05		(K)LALFQAI	(K)L A|L F Q A I/G K E V/V D R(A)		170.53	520.3043	1558.895	0.0032	2	6.07	266161	5.68	HUMAN	E9PPU0	Epiplakin
25810	dirMS_041712_NAR_60mM_minus.13326.13326.3	3	3.41	1	5.38E+05		(R)KLVIIEGI	(R)K L V I\I\E/G D L/E R(T)		135.08	428.9221	1284.752	-0.0004	-0.3	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
25811	dirMS_041712_NAR_60mM_minus.8701.8701.3	3	3.41	1	1.14E+05		(K)YAGKDG	(K)Y A/G/K D/G Y\N Y T L S K(T)		109.12	493.9126	1479.711	0.0118	8	8.38	11854.4	6.57	HUMAN	P31949	Protein S100-A11
25812	dirMS_041712_NAR_60mM_minus.9614.9614.3	3	3.41	1	5.37E+05		(R)IITEGFE	(R)I I/T E G F/E/A A K/E K(A)		113.88	445.91	1335.716	0	0	4.79	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
25813	dirMS_041712_NAR_120mM_plus.19176.19176.3	3	3.41	1	6.13E+05		(R)HGVQEL	(R)H G/V/Q E\L E\I E|L/Q/S Q L S K\K(A)		153.85	656.0237	1966.06	-0.0038	-2	5.5	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
25814	dirMS_041712_NAR_20mM_plus.14395.14395.3	3	3.41	0	3.00E+04	M61m	(R)IIPGFmC	(R)I I/P G F m C Q/G G D F T R(H)	C:Carbamidomethylation m:Oxid	170.67	538.9176	1598.745	15.9929	-1.3	5.84	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
25815	dirMS_041712_NAR_20mM_plus.19195.19195.2	2	3.41	0	8.61E+04		(R)ASVILAG	(R)A S V I\L|A G\L G/F T/P K(M)		203.95	637.3763	1273.751	-0.0061	-4.8	8.8	80142.6	5.95	HUMAN	Q9NUQ8	ATP-binding cassette sub-family F member 3
25816	dirMS_041712_NAR_20mM_plus.6390.6390.2	2	3.41	0	1.60E+05		(K)DSYVGD	(K)D S Y|V/G D E A Q S K(R)		107.17	599.7645	1198.522	-0.0005	-0.4	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
25817	dirMS_041712_NAR_20mM_plus.8705.8705.2	2	3.41	0	1.87E+05	M224m	(K)GGKPEP	(K)G G K/P E\P P A/m\P Q\P V|P T\A(-)	m:Oxidized methionine	130.62	795.402	1573.804	15.9924	-1.6	6	25541.5	9.92	HUMAN	E9PL09	40S ribosomal protein S3
25818	dirMS_041712_NAR_40mM_plus2.19760.19760.3	3	3.41	0	3.68E+05		(R)DLLDTVI	(R)D L|L D T V L/P H\L Y N E T K(V)		185.23	590.9774	1770.927	-0.0096	-5.4	4.54	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
25819	dirMS_041712_NAR_50mM_plus2.11233.11233.3	3	3.41	0	2.13E+05		(K)NAQLNI	(K)N/A\Q L/N I E/L E A/A H H(-)		127	487.2488	1459.729	0.003	2.1	5.23	13452	8.89	HUMAN	F5H246	Protein NAMPTL
25820	dirMS_041712_NAR_50mM_plus2.20782.20782.3	3	3.41	1	8.31E+03		(R)VTRLPLL	(R)V T\R L P\L L|M/D T L/C L K(T)	C:Carbamidomethylation	178.12	558.3196	1672.949	-0.0046	-2.7	8.72	20868.8	9.29	HUMAN	B0QZD4	Rho guanine exchange factor (GEF) 16 (Fragment)
25821	dirMS_041712_NAR_50mM_plus2.7929.7929.3	3	3.41	0	2.22E+04	S149s M15	(K)NEGVIEF	(K)N E G/V/I E F V s Y S D m K(R)	s:N-acetylglucosamine (S) m:	108.25	612.9457	1617.747	219.076	1	4.14	56791.5	11.56	HUMAN	Q08170	Serine/arginine-rich splicing factor 4
25822	dirMS_041712_NAR_60mM_plus.11498.11498.3	3	3.41	1	3.18E+05		(K)TAVCDIF	(K)T/A/V/C D I/P P R G L K(M)	C:Carbamidomethylation	118.8	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
25823	dirMS_041712_NAR_60mM_plus.19310.19310.3	3	3.41	1	2.50E+04		(K)RSIQFVD	(K)R S I Q F\V\D W|C P\T G F/K(V)	C:Carbamidomethylation	159.1	580.9558	1740.853	0.0002	0.1	8.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
25824	dirMS_041712_NAR_60mM_plus.21323.21323.3	3	3.41	1	5.45E+05		(R)SKALGSI	(R)S K A L G S D H C P I T L\Y\L A|L(-)	C:Carbamidomethylation	175.57	620.326	1858.973	-0.0097	-5.2	6.46	5634.5	9.82	HUMAN	G3V574	DNA-(apurinic or apyrimidinic site) lyase
25825	dirMS_041712_NAR_60mM_plus.7655.7655.3	3	3.41	0	3.87E+04	S811s	(K)FLGGSQ	(K)F L/G G S Q V S P s/R(A)	s:N-acetylglucosamine (S)	98.18	446.56	1134.59	203.0752	-3.1	9.75	106109	6.7	HUMAN	F5H6H8	Zinc finger protein GLI1
25826	dirMS_041712_NAR_60mM_plus.9900.9900.3	3	3.41	1	2.90E+05		(K)SEEQLKE	(K)S E/E Q L K E/E/G I E Y K(V)		109.28	527.9264	1581.764	0.0004	0.2	4.32	43928.7	6.58	HUMAN	B4DHG0	Dihydrolipoyl dehydrogenase, mitochondrial
25827	dirMS_041712_NAR_120mM_minus.13560.13560.3	3	3.4	0	6.88E+05	K412k	(R)LDFELGK	(R)L/D F E/L/G k M I K(Q)	k:Ubiquitin-K	128.02	436.5665	1193.66	114.0251	-13.6	6.07	62671	9.21	HUMAN	E9PC91	Polycystic kidney disease 2-like 2 protein
25828	dirMS_041712_NAR_120mM_minus.15880.15880.4	4	3.4	1	3.85E+05		(R)ALEHFTI	(R)A L/E H/F T D L Y D I/K R(A)		140.32	405.9646	1620.838	-0.0015	-0.9	5.38	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1

25829	dirMS_041712_NAR_120mM_minus.17489.17489.4	4	3.4	2	8.56E+03	T892t	(R)ItRWLSD	(R)I t R W L/S D F V A A Q E K K(F)	t:N-acetylglucosamine (T)	150.65	499.5124	1791.975	203.0526	-13.4	8.59	163805	6.67	HUMAN	A2PYH4	Probable ATP-dependent DNA helicase HFM1
25830	dirMS_041712_NAR_120mM_minus.19324.19324.3	3	3.4	1	3.72E+05	K266k	(R)IEELNKE	(R)I E\E L N K\E|V/k A S R(D)	k:Ubiquitin-K	161.42	510.614	1415.785	114.0422	-0.5	6.23	104369.4	5.94	HUMAN	Q7Z3E2	Uncharacterized protein C10orf118
25831	dirMS_041712_NAR_120mM_minus.6932.6932.2	2	3.4	1	1.64E+05		(K)STLPDAD	(K)S/T L P D A D\R E|R(E)		92.07	580.2866	1159.57	-0.0043	-3.7	4.56	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
25832	dirMS_041712_NAR_20mM_minus.14002.14002.3	3	3.4	0	9.84E+04		(R)LLAEETA	(R)L L A E E T A A T I S A I E A M K(N)		192.37	587.9823	1761.93	0.0021	1.2	4.25	204795.5	5.16	HUMAN	H0Y2S9	Myosin phosphatase Rho-interacting protein (Fragment)
25833	dirMS_041712_NAR_20mM_minus.7655.7655.2	2	3.4	0	6.65E+05	M239m	(K)EVDEQm	(K)E V/D E Q/m L/N V|Q\N K(N)	m:Oxidized methionine	125.12	731.843	1446.689	15.9894	-3.8	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
25834	dirMS_041712_NAR_20mM_minus.7829.7829.2	2	3.4	0	7.81E+04	M406m	(R)EYQELm	(R)E Y/Q E/L m N V K(L)	m:Oxidized methionine	128.13	585.2788	1153.556	15.9945	-0.3	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
25835	dirMS_041712_NAR_20mM_minus.8340.8340.2	2	3.4	0	1.40E+05		(K)DVGSLA	(K)D V|G S L|A/S V Q R(Y)		132.47	516.2772	1031.548	-0.0009	-0.8	5.84	266161	5.68	HUMAN	E9PPU0	Epiplakin
25836	dirMS_041712_NAR_30mM_minus2.12850.12850.2	2	3.4	0	1.49E+05		(R)YTSLMLI	(R)Y/T/S L\M L R(D)		123.27	442.2405	883.471	0.0031	3.5	8.75	66876.9	6.17	HUMAN	O75083	WD repeat-containing protein 1
25837	dirMS_041712_NAR_30mM_minus2.16625.16625.2	2	3.4	0	2.63E+04		(R)SSGLTAV	(R)S S|G\L\T/A V/W/V A\R(N)		144.03	573.8112	1146.627	-0.0115	-10	9.47	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
25838	dirMS_041712_NAR_30mM_minus2.6252.6252.2	2	3.4	0	4.16E+05		(K)YAEAVTI	(K)Y/A|E\A/V T/R(A)		87.57	405.2098	809.415	-0.0029	-3.5	6	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
25839	dirMS_041712_NAR_30mM_minus2.7502.7502.2	2	3.4	0	3.25E+05	M121m K1	(K)MmSkEF	(K)M/m/S k E R(L)	m:Oxidized methionine k:Ub	95.22	456.2018	781.37	130.0268	-12.1	8.5	25730.2	6.1	HUMAN	C9JBY0	Bromodomain-containing protein 9 (Fragment)
25840	dirMS_041712_NAR_50mM_minus2.13412.13412.3	3	3.4	0	3.28E+05		(K)LQMEAP	(K)L Q|M E/A P H I/I V G T P G R(V)		144.97	540.2947	1618.873	-0.0038	-2.4	6.75	20859.5	4.85	HUMAN	J3KS25	Eukaryotic initiation factor 4A-I (Fragment)
25841	dirMS_041712_NAR_50mM_minus2.15668.15668.3	3	3.4	1	1.13E+05	T392t	(R)LtFPVRD	(R)L t F P V R D/G V V L E P/F R(L)	t:N-acetylglucosamine (T)	157.72	650.0294	1744.975	203.0992	10.2	6.07	94636	6.69	HUMAN	E7EWM3	Zinc finger MIZ domain-containing protein 2
25842	dirMS_041712_NAR_50mM_minus2.17747.17747.3	3	3.4	1	1.00E+04		(K)QLKLDPS	(K)Q L K L D P S|I/F E S L Q K(E)		169.85	549.3073	1645.916	-0.0086	-5.2	6.07	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
25843	dirMS_041712_NAR_60mM_minus.12628.12628.3	3	3.4	1	2.63E+05		(R)EMDRET	(R)E M D/R E T L/I/D/V A R(T)		129.77	483.2454	1447.721	0.0007	0.5	4.32	55323	6.02	HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
25844	dirMS_041712_NAR_60mM_minus.15077.15077.3	3	3.4	1	3.39E+05		(K)AKLEQLF	(K)A/K L E Q L\F/Q|D/E V/A K(A)		144.37	506.9421	1518.816	-0.0045	-3	4.68	23903	4.94	HUMAN	H0YDN1	Plectin (Fragment)
25845	dirMS_041712_NAR_60mM_minus.18127.18127.3	3	3.4	2	3.59E+04	S702s	(K)KGFKAH	(K)K G F K/A H F|F s|V/L E G A G D R(H)	s:Phosphorylated S	162.35	649.3238	1865.966	79.9912	12.8	8.6	94364.4	9.09	HUMAN	P13497-6	Isoform BMP1-7 of Bone morphogenetic protein 1
25846	dirMS_041712_NAR_60mM_minus.6079.6079.3	3	3.4	1	2.29E+05		(K)LEEAEKA	(K)L E|E A E K/A A D E\S E R(G)		92.53	492.8981	1476.681	-0.0015	-1	4.14	31923.6	4.85	HUMAN	B7Z596	Tropomyosin alpha-1 chain
25847	dirMS_041712_NAR_60mM_minus.7239.7239.3	3	3.4	1	3.04E+05		(R)ELFESST	(R)E L/F/E/S S T/N N\N K D T K(Q)		98.72	542.9247	1626.761	-0.001	-0.6	4.68	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
25848	dirMS_041712_NAR_120mM_plus.23549.23549.3	3	3.4	0	3.94E+05		(R)LHFFMP	(R)L H F F M\P\G\F/A|P\L/T S R(G)		178.68	540.9492	1620.835	-0.0025	-1.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
25849	dirMS_041712_NAR_20mM_plus.17137.17137.3	3	3.4	0	1.02E+04		(R)EGGSIPV	(R)E G G S I P V/T L/T F Q E A/T/G K(N)		189.33	578.9671	1734.891	-0.0041	-2.4	4.53	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
25850	dirMS_041712_NAR_20mM_plus.8842.8842.3	3	3.4	0	1.37E+05	T192t M19	(K)tQYIFNN	(K)t Q Y I/F/N/N m V L K(L)	t:N-acetylglucosamine (T) m:	130.65	530.6038	1370.714	219.0832	5.6	8.26	131822.8	7.28	HUMAN	Q16706	Alpha-mannosidase 2
25851	dirMS_041712_NAR_30mM_plus2.19124.19124.2	2	3.4	0	1.13E+05		(K)IYVISLAE	(K)I Y|V/I/S/L A E P R(L)		152.97	580.8349	1160.667	-0.0049	-4.2	6	20139.7	9.34	HUMAN	C9J7S3	Aspartate--tRNA ligase, cytoplasmic (Fragment)
25852	dirMS_041712_NAR_30mM_plus2.20313.20313.2	2	3.4	2	1.76E+05	T189t	(R)QRQALS	(R)Q/R|Q A L S t E T G K G\K(D)	t:Phosphorylated T	160.97	742.362	1403.76	79.9566	-6.6	9.99	30230.5	9.74	HUMAN	G3V2K8	WD repeat-containing protein 25
25853	dirMS_041712_NAR_30mM_plus2.4813.4813.2	2	3.4	0	8.11E+05		(R)MGQTM	(R)M/G|Q/T/M E R(I)		76.78	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
25854	dirMS_041712_NAR_30mM_plus2.8623.8623.2	2	3.4	0	1.74E+05		(R)ELNITAA	(R)E L/N\I/T/A/A\K(E)		98.63	430.2487	859.488	0.0018	2.1	6.1	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
25855	dirMS_041712_NAR_40mM_plus2.10061.10061.3	3	3.4	0	6.65E+04	T78t	(R)WTAAPt	(R)W/T A A P t/Q A P A P S R(V)	t:Phosphorylated T	123.88	478.5511	1353.691	79.9478	-12.9	9.75	9940.4	11.03	HUMAN	F8WDZ4	B-cell CLL/lymphoma 7 protein family member B
25856	dirMS_041712_NAR_40mM_plus2.12223.12223.2	2	3.4	0	4.91E+04		(R)YIELLTR	(R)Y I/E/L L T R(S)		138	454.2649	907.525	-0.0022	-2.4	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
25857	dirMS_041712_NAR_40mM_plus2.18036.18036.3	3	3.4	0	9.77E+04	M159m	(R)SVAAIHP	(R)S V|A/A I H P S L E I/P m L I P K(E)	m:Oxidized methionine	172.8	611.3472	1816.04	15.9869	-4.4	6.47	31606.3	6.72	HUMAN	B4E329	Phosphoribosyl pyrophosphate synthase-associated protein 2
25858	dirMS_041712_NAR_50mM_plus2.17117.17117.3	3	3.4	0	2.97E+05		(R)AVTPLRP	(R)A V/T/P L R P G E L L F R(S)		158.08	490.2879	1468.863	-0.0143	-9.7	9.64	21357.6	9.92	HUMAN	B0QZ88	SET and MYND domain containing 3
25859	dirMS_041712_NAR_50mM_plus2.7998.7998.3	3	3.4	0	8.23E+03		(K)LNLEHIA	(K)L N L E/H I/A T S S A/V S K(E)		108.18	490.5973	1469.796	-0.0185	-12.6	6.75	92504.1	5.32	HUMAN	Q96QK1	Vacuolar protein sorting-associated protein 35
25860	dirMS_041712_NAR_60mM_plus.16409.16409.3	3	3.4	0	6.30E+05		(R)ETHSALG	(R)E T H S A L G\P/A/L/Q A A F K(L)		142.15	514.2744	1540.812	-0.0032	-2.1	6.85	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
25861	dirMS_041712_NAR_60mM_plus.19041.19041.3	3	3.4	1	5.74E+05	K79k	(R)STANVLE	(R)S T/A N V L E E T T/V K k(E)	k:Ubiquitin-K	156.97	511.9392	1419.769	114.0341	-5.8	5.86	91592.8	5.08	HUMAN	H0YCN2	Remodeling and spacing factor 1 (Fragment)
25862	dirMS_041712_NAR_60mM_plus.4743.4743.3	3	3.4	1	6.64E+04		(R)AAEEED	(R)A/A\E/E E/D/E A D/P K R(Q)		78.85	453.872	1359.602	-0.0008	-0.6	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
25863	dirMS_041712_NAR_120mM_minus.11111.11111.3	3	3.39	0	6.08E+05		(R)ISNRPAF	(R)I/S/N\R P A\F\M/P S E G K(M)		113.93	478.5776	1433.721	-0.0023	-1.6	8.75	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
25864	dirMS_041712_NAR_120mM_minus.12823.12823.3	3	3.39	0	2.84E+05	M251m	(K)TFHSmA	(K)T F/H S m A Y G H I G R(K)	m:Oxidized methionine	122.98	464.8871	1376.653	15.9939	-0.7	8.47	46199.4	9.14	HUMAN	Q5JVB6	F-box only protein 18
25865	dirMS_041712_NAR_120mM_minus.5762.5762.3	3	3.39	1	3.11E+05	T264t	(R)tFEKIEEV	(R)t/F E K/I E E V S A R(L)	t:Phosphorylated T	85.25	463.5589	1308.679	79.9827	11.8	4.78	98854	5.37	HUMAN	B4DTU4	DNA ligase
25866	dirMS_041712_NAR_20mM_minus.13216.13216.3	3	3.39	0	7.44E+04		(R)GNPTVE	(R)G N/P T/V E V D/L F/T S K(G)		183.13	469.5754	1406.716	-0.0045	-3.2	4.37	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
25867	dirMS_041712_NAR_20mM_minus.9047.9047.2	2	3.39	0	1.50E+05	K509k	(R)QSFALEQ	(R)Q S/F A L E/Q L k(A)	k:Ubiquitin-K	140.22	589.3094	1063.578	114.0333	-8.2	6	106708.1	6.11	HUMAN	Q6NX52	ARHGEF1 protein
25868	dirMS_041712_NAR_30mM_minus2.5795.5795.2	2	3.39	0	6.55E+04		(K)TSETLSQ	(K)T/S\E/T/L S Q A G Q\K(A)		85.58	575.2877	1149.575	-0.0065	-5.6	5.66	25978.5	4.91	HUMAN	C9J502	Prostate leucine zipper variant 2
25869	dirMS_041712_NAR_40mM_minus2.12878.12878.3	3	3.39	1	8.25E+03		(R)LDQEVA	(R)L/D/Q/E V A/E\V D K N I E L\L K(K)		159.83	619.3351	1856.001	-0.0104	-5.6	4.18	41088.1	5.18	HUMAN	F5H442	Tumor susceptibility gene 101 protein
25870	dirMS_041712_NAR_40mM_minus2.6667.6681.2	2	3.39	0	3.88E+05		(K)LAADDF	(K)L/A|A\D D/F R(T)		107.55	404.2037	807.399	0.0006	0.7	4.21	48845.9	4.72	HUMAN	C4AM86	Keratin, type I cuticular Ha5
25871	dirMS_041712_NAR_50mM_minus2.15117.15117.3	3	3.39	0	1.19E+05		(K)LYRPPPV	(K)L Y R P P P V/L D A/L/G R(V)		153.45	489.617	1466.848	-0.0114	-7.7	8.75	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
25872	dirMS_041712_NAR_50mM_minus2.6850.6850.3	3	3.39	0	8.00E+03	M233m	(K)SAAmLG	(K)S A A\m L/G N S E D/H T A L S R(A)	m:Oxidized methionine	105.48	559.2593	1659.776	15.9878	-4.2	5.3	46211	6.76	HUMAN	B4DEK4	Sorting nexin-2
25873	dirMS_041712_NAR_50mM_minus2.7968.7968.3	3	3.39	0	4.48E+03	M172m	(R)mVQVH	(R)m V|Q V/H E L/S/C E G I S/K(S)	C:Carbamidomethylation m:Oxid	112.05	544.9272	1616.777	15.99	-3	5.38	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
25874	dirMS_041712_NAR_60mM_minus.14205.14205.2	2	3.39	1	1.05E+06	S984s	(K)TCSRAN	(K)T C S R/A N E L D/P D/s L R(W)	C:Carbamidomethylation s:N-ace	139.38	918.9231	1633.76	203.0791	-0.2	4.55	234283.8	5.68	HUMAN	Q8WYB5	Histone acetyltransferase KAT6B
25875	dirMS_041712_NAR_60mM_minus.15509.15509.3	3	3.39	1	1.72E+05		(R)GRLPLLA	(R)G R/L\P L\L/A/V C D Y K(Q)	C:Carbamidomethylation	146.87	468.9273	1404.767	0.0006	0.4	8.59	533778	5.74	HUMAN	Q15149	Plectin
25876	dirMS_041712_NAR_60mM_minus.18485.18485.3	3	3.39	0	2.38E+05		(K)SQLDIIIH	(K)S Q|L D I/I I H S L K(K)		164.08	422.9181	1266.742	-0.0019	-1.5	6.46	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
25877	dirMS_041712_NAR_120mM_plus.18103.18103.4	4	3.39	1	1.10E+06	S30s	(R)ICLALEsI	(R)I C/L A L E s I/I S E E E R K(T)	C:Carbamidomethylation s:N-ace	148.73	499.002	1789.936	203.0497	-14.9	4.49	21765.5	9.84	HUMAN	H0YAL6	Serine/threonine-protein kinase PLK4 (Fragment)
25878	dirMS_041712_NAR_120mM_plus.20509.20509.4	4	3.39	1	4.67E+04	T1066t T10	(R)LQSIQET	(R)L Q S I Q E T L R/G/t Q t A L/R(Q)	t:Phosphorylated T	160.95	494.4975	1815.008	159.9599	13.8	9.6	204795.5	5.16	HUMAN	H0Y2S9	Myosin phosphatase Rho-interacting protein (Fragment)
25879	dirMS_041712_NAR_120mM_plus.5383.5383.3	3	3.39	0	1.63E+05	S805s T80	(K)QMTEAI	(K)Q M T/E A I G P s t I R(D)	s:Phosphorylated S t:Phosph	81.03	488.5349	1303.668	159.9227	-6.8	6	99610.3	5.34	HUMAN	Q14764	Major vault protein
25880	dirMS_041712_NAR_120mM_plus.5654.5654.2	2	3.39	0	1.20E+05		(R)HVVFSG	(R)H/V|V F\S G S G R(A)		82.4	473.2482	945.49	-0.001	-1	9.75	17802.1	10.98	HUMAN	Q8N5L8	Ribonuclease P protein subunit p25-like protein
25881	dirMS_041712_NAR_20mM_plus.10792.10792.2	2	3.39	0	1.13E+04		(K)YEELQIT	(K)Y E/E|L/Q I T A/G R(H)		145.52	590.304	1179.6	0.0003	0.3	4.53	60351.2	8.36	HUMAN	P04259	Keratin, type II cytoskeletal 6B
25882	dirMS_041712_NAR_20mM_plus.18125.18125.3	3	3.39	1	1.55E+04		(K)NPESPKV	(K)N P E S P K/V L A Q/L/Q/A/V\R(E)		196.63	550.644	1649.933	-0.0159	-9.6	8.75	419509.2	6.23	HUMAN	Q9NRC6	Spectrin beta chain, non-erythrocytic 5
25883	dirMS_041712_NAR_20mM_plus.7833.7833.2	2	3.39	0	6.78E+04		(R)AQYDEL	(R)A/Q|Y/D E L A R(K)		123.52	483.2393	965.469	0.0026	2.7	4.37	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
25884	dirMS_041712_NAR_30mM_plus2.10429.10429.2	2	3.39	0	2.93E+05		(R)DPYGFG	(R)D/P|Y/G/F G D S R(D)		108.67	507.2274	1013.432	0.0152	15	4.21	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
25885	dirMS_041712_NAR_30mM_plus2.11406.11406.3	3	3.39	1	5.28E+04	M70m S74	(R)GQGVSS	(R)G Q G V S S|N/m R E I s/K(E)	m:Oxidized methionine s:Pho	113.02	496.8957	1392.69	95.9826	14.3	8.75	26870.9	9.32	HUMAN	C9IYI1	Dermokine
25886	dirMS_041712_NAR_30mM_plus2.19432.19432.2	2	3.39	0	3.48E+05		(-)MDELQL	(-)M/D|E/L/Q L/F/R(G)		156.53	526.2726	1051.524	0.0138	13.2	4.37	18601	5.1	HUMAN	C9IZA5	Transitional endoplasmic reticulum ATPase (Fragment)
25887	dirMS_041712_NAR_30mM_plus2.21600.21600.2	2	3.39	0	1.49E+05		(R)VFIGNLN	(R)V F|I/G|N L N T L V V K(K)		167.43	658.8983	1316.794	-0.0043	-3.3	8.72	15791.7	9.22	HUMAN	B4DSU6	Heterogeneous nuclear ribonucleoproteins C1/C2
25888	dirMS_041712_NAR_40mM_plus2.5194.5194.2	2	3.39	0	1.76E+05		(R)QQEEMI	(R)Q Q E/E/M/M/R(R)		86.23	476.2049	951.402	0.0003	0.3	4.53	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
25889	dirMS_041712_NAR_50mM_plus2.12043.12043.3	3	3.39	1	5.81E+05	M34m M3	(R)LQLERQ	(R)L Q|L E/R Q L I m Q/S E m R(E)	m:Oxidized methionine	131.57	602.9721	1774.93	31.9715	-10.1	6.14	17201	9.58	HUMAN	Q9HBL7	Plasminogen receptor (KT)
25890	dirMS_041712_NAR_50mM_plus2.12791.12791.3	3	3.39	1	5.22E+05		(K)FSIEDLK	(K)F/S/I/E/D L K A Q P K(Q)		134.42	425.8966	1275.694	-0.0191	-15	6.07	13579.2	9.99	HUMAN	E9PPQ6	Thymocyte nuclear protein 1 (Fragment)
25891	dirMS_041712_NAR_50mM_plus2.18152.18152.3	3	3.39	0	3.10E+05		(K)LQLQELS	(K)L Q L Q E L S D|T W Q A\H L A R(G)		163.75	637.018	1908.993	0.0468	24.5	5.32	91887.5	5.25	HUMAN	Q96CN4	EVI5-like protein
25892	dirMS_041712_NAR_50mM_plus2.19881.19881.3	3	3.39	0	8.05E+05		(K)LNEHFLN	(K)L N E H F L/N T/T/D/F L D T I K(S)		173.27	640.9957	1920.97	0.0024	1.2	4.54	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
25893	dirMS_041712_NAR_60mM_plus.10367.10367.2	2	3.39	0	9.30E+05		(R)SSGPYGG	(R)S/S/G/P Y/G G G G Q Y/F A/K\P\R(N)		112.17	814.8941	1628.782	-0.0007	-0.4	9.7	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
25894	dirMS_041712_NAR_60mM_plus.14575.14575.3	3	3.39	1	2.23E+05	T34t M36m	(K)VQISSM	(K)V Q I/S S M V/L t K m K(E)	t:Phosphorylated T m:Oxidiz	131.48	487.578	1364.764	95.9554	-4	10	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
25895	dirMS_041712_NAR_60mM_plus.16634.16634.3	3	3.39	1	1.05E+06		(K)IQGANA	(K)I Q/G A N A P L/V N K K(V)		144.17	418.2478	1252.737	-0.0083	-6.7	10	16953.3	5.37	HUMAN	C9JG62	Thioredoxin domain-containing protein 3 (Fragment)
25896	dirMS_041712_NAR_60mM_plus.17709.17709.3	3	3.39	1	4.67E+05	Y294y	(K)LQLTDFV	(K)L/Q L T D F V S/K A y G K(N)	y:Phosphorylated Y	149.37	517.2632	1469.8	79.9752	5.7	8.5	40506.8	6.21	HUMAN	Q6NXP6	NADP-dependent oxidoreductase domain-containing protein 1
25897	dirMS_041712_NAR_60mM_plus.18379.18379.3	3	3.39	0	2.42E+05	S731s	(K)FVsHGG	(K)F/V s H G G I Q A/F L T K(V)	s:N-acetylglucosamine (S)	153	536.6218	1404.763	203.0874	5	8.76	178358.9	8.27	HUMAN	E9PGK7	Transient receptor potential cation channel subfamily M member 2
25898	dirMS_041712_NAR_60mM_plus.19490.19490.3	3	3.39	1	1.28E+05		(K)SLLGKDV	(K)S L/L G K/D V L F L/K(D)		160.98	411.5915	1232.761	-0.0013	-1.1	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
25899	dirMS_041712_NAR_60mM_plus.20733.20733.3	3	3.39	0	7.00E+05		(R)LGFHLPL	(R)L G F H L/P L\E|V/A/Y Q R(G)		168.67	514.9568	1542.843	0.0131	8.5	6.75	533778	5.74	HUMAN	Q15149	Plectin
25900	dirMS_041712_NAR_60mM_plus.21214.21214.3	3	3.39	1	1.11E+05		(K)KIPGIYV	(K)K I P G I Y\V\L/S|L E/I G K(T)		174.77	510.646	1529.93	-0.0067	-4.4	8.5	16316.9	9.1	HUMAN	E9PK48	Palmitoyl-protein thioesterase 1
25901	dirMS_041712_NAR_120mM_minus.12525.12525.3	3	3.38	1	3.39E+05	M316m	(R)ISEQFTA	(R)I/S|E Q F T/A m F R R(K)	m:Oxidized methionine	122.32	467.9028	1385.699	15.9944	-0.4	9.6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
25902	dirMS_041712_NAR_120mM_minus.9357.9357.3	3	3.38	0	1.55E+06		(K)EFHLNES	(K)E F H L N\E S G D/P S S/K(S)		106.1	482.8881	1446.65	0.0002	0.1	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
25903	dirMS_041712_NAR_30mM_minus2.13833.13833.2	2	3.38	0	4.06E+05		(K)LSSLPFQ	(K)L/S\S L/P F Q K(I)		127.9	460.2646	919.525	-0.0028	-3.1	8.75	12272.7	5.08	HUMAN	H3BRV9	Nuclear transport factor 2 (Fragment)
25904	dirMS_041712_NAR_30mM_minus2.18993.18993.2	2	3.38	0	4.54E+05		(R)ISEQFTA	(R)I S E Q/F T A/M F R(R)		157.42	615.3038	1229.598	0.002	1.6	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
25905	dirMS_041712_NAR_30mM_minus2.4541.4541.2	2	3.38	0	9.19E+05		(K)QASEGP	(K)Q A/S E G P L/K(G)		75.55	415.2235	829.441	-0.0017	-2	6	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
25906	dirMS_041712_NAR_40mM_minus2.11099.11099.3	3	3.38	1	3.79E+03	S8s	(-)MAADTQ	(-)M A/A D T Q V s/E T L K R/F A G K(V)	s:Phosphorylated S	148.77	644.9839	1852.959	79.9786	6.3	8.35	295149.3	7.4	HUMAN	Q92616	Translational activator GCN1
25907	dirMS_041712_NAR_40mM_minus2.5374.5374.2	2	3.38	1	4.64E+04		(R)ARGDSE	(R)A R G D\S\E A|L\D\E\E\S(-)		88.97	639.774	1278.544	-0.0037	-2.9	3.83	74986.2	6.56	HUMAN	I3L080	Hepatoma-derived growth factor-related protein 2
25908	dirMS_041712_NAR_40mM_minus2.5512.5512.2	2	3.38	1	1.58E+05		(R)SKQAEE	(R)S K Q A E\E E|F(-)		91.33	484.2235	967.437	0.003	3.1	4.25	71231.7	9.22	HUMAN	E7ERI3	Threonine--tRNA ligase, cytoplasmic
25909	dirMS_041712_NAR_40mM_minus2.9623.9623.3	3	3.38	0	3.21E+04	M433m M	(R)LILGLmm	(R)L I|L G L m/m P P A H Y D/A K(Q)	m:Oxidized methionine	139.13	567.9619	1669.88	31.9907	0.5	6.74	75617.5	5.46	HUMAN	A6NN80	Annexin
25910	dirMS_041712_NAR_50mM_minus2.15056.15056.3	3	3.38	1	1.57E+05	K298k M29	(R)LEVkmE	(R)L E V k m E/I/G L P D E K G R(L)	k:Ubiquitin-K m:Oxidized me	154	615.3184	1713.92	130.0203	-9.5	4.87	71924.9	6.25	HUMAN	B4DFA2	Vesicle-fusing ATPase
25911	dirMS_041712_NAR_50mM_minus2.6674.6674.3	3	3.38	1	6.32E+04		(R)AVASQP	(R)A V|A/S Q/P D S V/D A A E R A\E K(F)		105	581.9591	1743.851	0.012	6.9	4.32	81955.5	5.78	HUMAN	E9PHT6	Pantothenate kinase 4
25912	dirMS_041712_NAR_60mM_minus.11513.11513.3	3	3.38	1	9.32E+04	T131t	(K)AYEItYV	(K)A Y/E/I t Y V R L K(F)	t:Phosphorylated T	123.83	445.9007	1255.705	79.983	12.5	8.54	178274.3	6.2	HUMAN	Q5JTC4	Laminin subunit gamma-3
25913	dirMS_041712_NAR_60mM_minus.19741.19741.3	3	3.38	1	9.65E+05		(K)EIIDLVLD	(K)E I I/D/L V L D R I R(K)		179.3	452.2739	1354.805	0.0019	1.4	4.56	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
25914	dirMS_041712_NAR_60mM_minus.5138.5138.3	3	3.38	0	8.71E+04	K904k	(R)AALAPA	(R)A A/L A P A k E/S P/R(K)	k:Ubiquitin-K	83.97	408.8971	1110.627	114.0502	5.9	8.79	152529.5	8.95	HUMAN	E7ETY2	Treacle protein
25915	dirMS_041712_NAR_60mM_minus.7560.7560.3	3	3.38	1	1.59E+05	Y40y T47t	(K)TSTQEyA	(K)T S|T/Q/E y A A K I I N t K(K)	y:Phosphorylated Y t:Phosph	102.02	576.5915	1567.833	159.9273	-3.1	8.17	21044.3	9.93	HUMAN	B4DVQ3	Calcium/calmodulin-dependent protein kinase type II subunit gamma
25916	dirMS_041712_NAR_120mM_plus.10319.10319.3	3	3.38	1	1.43E+05		(R)RGVVGP	(R)R G V V G|P/E|L Y G R(L)		107.48	401.5586	1202.664	-0.0028	-2.3	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
25917	dirMS_041712_NAR_120mM_plus.14473.14473.2	2	3.38	0	5.59E+05		(R)HFDQFW	(R)H/F\D/Q F W S A/A\K(T)		128.88	618.7928	1236.58	-0.0013	-1.1	6.74	160853.1	6.11	HUMAN	F8VU51	YLP motif-containing protein 1
25918	dirMS_041712_NAR_120mM_plus.15053.15053.4	4	3.38	0	6.98E+05		(K)SIVIRPLE	(K)S I/V I R P L E P Q/P A/P H L A R(E)		132.4	474.2836	1894.102	0.0104	5.5	9.34	109137.3	4.87	HUMAN	K7EJ81	116 kDa U5 small nuclear ribonucleoprotein component
25919	dirMS_041712_NAR_120mM_plus.18628.18628.4	4	3.38	1	1.57E+06		(K)FQIPPNA	(K)F Q\I/P P\N\A E L K Y E L H L K(S)		150.52	485.7703	1940.064	-0.0046	-2.4	6.75	52088.9	5.35	HUMAN	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4
25920	dirMS_041712_NAR_120mM_plus.21048.21048.4	4	3.38	1	3.11E+05		(-)XSAFGDR	(-)X S A F G D R/P E K R D N N W R(Y)		163.53	491.0027	1960.974	0.0153	7.8	8.74	54333.1	6.51	HUMAN	H0Y5S1	Protein transport protein Sec16A (Fragment)
25921	dirMS_041712_NAR_120mM_plus.5208.5208.3	3	3.38	1	3.17E+05	M163m	(K)IYEDGDD	(K)I/Y/E D G D D D m K/R(T)	m:Oxidized methionine	79.92	458.195	1356.574	15.9968	1.4	4.03	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
25922	dirMS_041712_NAR_20mM_plus.18477.18477.2	2	3.38	1	1.33E+05		(K)DIGFIKLI	(K)D I/G/F I K L D(-)		198.15	460.7578	920.509	-0.0004	-0.5	4.53	6904.9	11.35	HUMAN	P62273	40S ribosomal protein S29
25923	dirMS_041712_NAR_20mM_plus.7430.7430.2	2	3.38	0	7.99E+04		(R)GTSFDA	(R)G T S F/D A/A/A|T S G/G S A S S E K(A)		119.65	815.8661	1630.719	0.0058	3.6	4.37	24273.5	8.98	HUMAN	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial
25924	dirMS_041712_NAR_40mM_plus2.15012.15012.3	3	3.38	1	6.60E+04		(K)RATTGD	(K)R A T/T G D A/S E S A L L/K(F)		154.73	473.9204	1419.744	0.0028	2	6.07	57870.7	9.3	HUMAN	E9PRA5	Sodium/potassium-transporting ATPase subunit alpha-4
25925	dirMS_041712_NAR_40mM_plus2.7001.7001.2	2	3.38	0	5.07E+04		(K)ATDFVA	(K)A T|D/F/V A D R(A)		101.15	447.7259	894.432	0.013	14.5	4.21	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
25926	dirMS_041712_NAR_50mM_plus2.10178.10178.3	3	3.38	0	6.39E+04		(R)TIVITSHI	(R)T\I|V I/T S H/P G Q I V K(H)		120.92	464.946	1392.821	0.0025	1.8	8.44	27999.4	5.61	HUMAN	B7Z5C0	DnaJ homolog subfamily A member 1
25927	dirMS_041712_NAR_50mM_plus2.10274.10274.3	3	3.38	1	3.17E+04		(R)ELQSMA	(R)E L Q/S/M/A D Q E Q V/S P A A I K K(T)		121.53	658.3369	1973.001	-0.0047	-2.4	4.68	36208.1	7.21	HUMAN	B4DMU0	Pyrroline-5-carboxylate reductase
25928	dirMS_041712_NAR_50mM_plus2.16228.16228.3	3	3.38	0	2.89E+05		(K)ACQSIYP	(K)A C Q/S\I/Y/P/L/H D V F V R(K)	C:Carbamidomethylation	154.4	568.9562	1704.853	0.0014	0.8	6.79	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
25929	dirMS_041712_NAR_50mM_plus2.17286.17286.3	3	3.38	2	3.07E+05	T426t	(R)KHQItYL	(R)K\H/Q I t Y\L/I/H Q A K E R(E)	t:Phosphorylated T	158.4	615.664	1764.987	79.9907	13.2	9.7	48959.2	5.41	HUMAN	A6NG79	Proline-rich protein PRCC
25930	dirMS_041712_NAR_50mM_plus2.7255.7255.3	3	3.38	1	7.50E+04		(K)DISTNYY	(K)D I S T/N Y Y A S/Q K K(T)		103.52	473.2382	1417.696	0.0043	3	8.43	17045.4	4.25	HUMAN	H0YIV0	Endoplasmin (Fragment)
25931	dirMS_041712_NAR_60mM_plus.20518.20518.3	3	3.38	1	2.96E+04	S70s	(K)SRTVSsE	(K)S R/T\V/S s E/Q P P G L K(A)	s:N-acetylglucosamine (S)	166.83	530.2831	1385.738	203.0964	10.7	8.46	66208.1	9.51	HUMAN	H7BXK8	Ankyrin repeat domain-containing protein 36C
25932	dirMS_041712_NAR_120mM_minus.11409.11409.3	3	3.37	0	2.71E+05	T146t S150	(R)LQtVALs	(R)L Q t V A\L/s Q\Q I R(Q)	t:Phosphorylated T s:Phosph	116.42	472.8961	1256.732	159.9416	6.3	9.75	127738.5	8.67	HUMAN	P48552	Nuclear receptor-interacting protein 1
25933	dirMS_041712_NAR_120mM_minus.12862.12862.3	3	3.37	1	1.89E+05		(K)KTSCEFT	(K)K T S\C E\F/T|G/D I L R(T)	C:Carbamidomethylation	124.6	476.2347	1426.699	-0.0099	-7	6.07	21230	6.36	HUMAN	H0YC04	V-type proton ATPase subunit B, brain isoform (Fragment)
25934	dirMS_041712_NAR_120mM_minus.14340.14340.4	4	3.37	0	1.15E+05		(K)LYTGPGI	(K)L/Y T G P G L A/I H C M Q V H K(E)	C:Carbamidomethylation	132.23	456.992	1824.925	0.0214	11.7	8.6	53035.1	9.47	HUMAN	E1P660	Zinc finger protein 207
25935	dirMS_041712_NAR_120mM_minus.14787.14787.3	3	3.37	1	3.45E+04		(R)VFDKDG	(R)V F D K D G N G\Y/I/S/A/A E/L R(H)		134.25	585.629	1754.871	0.0017	0.9	4.56	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
25936	dirMS_041712_NAR_120mM_minus.17249.17249.4	4	3.37	2	6.24E+05		(R)KVESLQI	(R)K\V E S L Q E E I/A/F L K K(L)		148.93	416.2415	1661.947	-0.0031	-1.9	6.23	49709.6	5.19	HUMAN	B0YJC4	Vimentin
25937	dirMS_041712_NAR_120mM_minus.8688.8688.3	3	3.37	1	1.37E+05		(R)LRDTEEM	(R)L R D T\E E/M/L/S K(K)		102.05	407.877	1221.614	0.0021	1.7	4.68	24949.7	4.76	HUMAN	Q9H444	Charged multivesicular body protein 4b

25938	dirMS_041712_NAR_20mM_minus.11215.11215.2	2	3.37	0	6.06E+04		(R)LVVPAS	(R)L V|V/P A/S Q C G S L I G K(G)	C:Carbamidomethylation	159.67	714.8954	1428.788	-0.0044	-3.1	8.75	32621	8.75	HUMAN	B4DLC0	Poly(rC)-binding protein 2
25939	dirMS_041712_NAR_20mM_minus.7459.7459.3	3	3.37	0	5.40E+05	M239m	(K)EVDEQn	(K)E V D E Q\m L N V/Q N K(N)	m:Oxidized methionine	123.17	488.2327	1446.689	15.9942	-0.5	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
25940	dirMS_041712_NAR_20mM_minus.9915.9915.2	2	3.37	1	1.62E+05		(R)IIEDPAR	(R)I I E D/P/A R S A G(-)		148.75	514.7668	1028.537	-0.0108	-10.5	4.37	13472.8	5.33	HUMAN	K7ELI8	Echinoderm microtubule-associated protein-like 2 (Fragment)
25941	dirMS_041712_NAR_30mM_minus2.16901.16901.2	2	3.37	0	1.20E+05		(R)NPSAAF	(R)N P\S A/A/F F C/V A R(L)	C:Carbamidomethylation	145.43	620.3013	1239.594	0.0014	1.1	9.75	18626.5	5.64	HUMAN	B8ZZK2	Gamma-glutamylcyclotransferase
25942	dirMS_041712_NAR_30mM_minus2.6969.6969.2	2	3.37	0	1.47E+05		(K)ISTVVSS	(K)I/S\T\V V/S S K(E)		92.48	410.7405	820.477	-0.0037	-4.6	8.75	13286.2	9.99	HUMAN	H0YLA2	Signal recognition particle 14 kDa protein
25943	dirMS_041712_NAR_30mM_minus2.7568.7568.2	2	3.37	1	1.28E+05		(R)SNRDQI	(R)S/N/R D Q/I K(N)		95.32	430.7364	860.458	0.0071	8.2	8.46	49127.1	9.11	HUMAN	Q9BS91	Probable UDP-sugar transporter protein SLC35A5
25944	dirMS_041712_NAR_40mM_minus2.11535.11535.3	3	3.37	1	9.99E+03		(R)EKGATV	(R)E K G A T V F A N V A E L I H N T R(F)		152.05	657.3545	1970.045	0.0035	1.8	6.86	24407.9	9.96	HUMAN	Q6XR72-3	Isoform 3 of Zinc transporter 10
25945	dirMS_041712_NAR_40mM_minus2.9358.9358.3	3	3.37	1	2.47E+05		(K)DIFYIEN	(K)D/I F|Y I/E N Q K E Y E/N K(K)		136.73	611.627	1832.87	-0.0037	-2	4.41	44573	5.28	HUMAN	Q9H814	Phosphorylated adapter RNA export protein
25946	dirMS_041712_NAR_50mM_minus2.8505.8505.3	3	3.37	0	1.32E+05		(R)VAELVG	(R)V A E L V G V E/E G F L A R(C)		115.58	496.9372	1488.806	-0.0086	-5.8	4.25	292466.7	7.12	HUMAN	O75417	DNA polymerase theta
25947	dirMS_041712_NAR_60mM_minus.13013.13013.3	3	3.37	0	6.59E+05		(K)GIHPTIIS	(K)G I H\P T\I\I/S E S F Q K(A)		132.77	486.2642	1456.78	-0.0014	-1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
25948	dirMS_041712_NAR_60mM_minus.14142.14142.3	3	3.37	0	3.54E+05		(K)DCGATV	(K)D C G A T W V/V L/G H S E/R(R)	C:Carbamidomethylation	138.02	529.5838	1586.738	-0.0012	-0.7	5.32	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
25949	dirMS_041712_NAR_60mM_minus.18582.18582.2	2	3.37	0	1.90E+05	M195m	(R)LHFFmP	(R)L H F|F/m\P G F A/P L T\S R(G)	m:Oxidized methionine	165.65	818.9168	1620.835	15.9908	-2.5	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
25950	dirMS_041712_NAR_60mM_minus.19665.19665.3	3	3.37	0	3.13E+05		(K)LAVEALS	(K)L A V E/A L S/S L D G D L A G R(Y)		176.95	529.6145	1586.838	-0.0095	-6	4.03	24286.7	4.89	HUMAN	G3V4N7	Creatine kinase B-type (Fragment)
25951	dirMS_041712_NAR_60mM_minus.7629.7629.3	3	3.37	1	5.65E+05		(R)YLAEVA	(R)Y L/A E V A/A G D/D/K K(G)		102.07	427.222	1279.653	-0.0014	-1.1	4.56	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
25952	dirMS_041712_NAR_120mM_plus.6534.6534.2	2	3.37	1	2.84E+05		(R)SIAKEGF	(R)S I|A/K E G F E K(I)		87.12	504.7715	1008.536	-0.0003	-0.3	5.86	17213.7	10.05	HUMAN	B7Z712	60 kDa heat shock protein, mitochondrial
25953	dirMS_041712_NAR_20mM_plus.12437.12437.3	3	3.37	0	5.48E+05	M213m	(R)VGAIGS	(R)V G A I G S A G m S H/C W R(S)	C:Carbamidomethylation m:Oxid	158.63	502.2264	1488.684	15.9812	-9.1	9.73	27281	5.35	HUMAN	H7C5J7	Protein C3orf52 (Fragment)
25954	dirMS_041712_NAR_20mM_plus.12616.12616.2	2	3.37	0	2.33E+05		(R)DGPLLA	(R)D G P L|L A A|L/K(A)		159.18	449.2728	897.54	-0.0021	-2.3	5.84	638399.7	5.46	HUMAN	Q9NU22	Midasin
25955	dirMS_041712_NAR_20mM_plus.14050.14050.2	2	3.37	1	7.46E+04	K1185k	(R)SFEEAIP.	(R)S F|E E A I P/A R k(L)	k:Ubiquitin-K	168.57	631.3387	1147.611	114.0595	13.2	5.87	482399.6	5.8	HUMAN	H0Y7V4	Dynein heavy chain 8, axonemal
25956	dirMS_041712_NAR_20mM_plus.8143.8143.2	2	3.37	0	5.46E+04		(K)AQLEPV.	(K)A/Q|L|E/P V A S P A K(K)		126.35	555.8092	1110.615	-0.0042	-3.8	6.05	533778	5.74	HUMAN	Q15149	Plectin
25957	dirMS_041712_NAR_20mM_plus.8809.8809.2	2	3.37	0	1.32E+04	T48t	(K)NIVDtEA	(K)N I|V/D t/E\A K(M)	t:N-acetylglucosamine (T)	130.8	546.7755	889.462	203.0812	1.7	4.37	205056.4	5.48	HUMAN	K7EKI8	Periplakin
25958	dirMS_041712_NAR_30mM_plus2.13040.13040.2	2	3.37	0	5.68E+05		(K)NQAVNI	(K)N Q|A/V N/F L R(M)		121.65	481.2676	961.521	0.0065	6.8	9.75	22166.1	7.91	HUMAN	Q7LBR1	Charged multivesicular body protein 1b
25959	dirMS_041712_NAR_30mM_plus2.6893.6893.2	2	3.37	0	2.76E+05		(K)AEYLCR	(K)A E|Y/L/C/R(I)	C:Carbamidomethylation	90.83	406.1945	811.377	0.005	6.2	6.04	52378.2	6.32	HUMAN	C9IZE4	26S proteasome non-ATPase regulatory subunit 6
25960	dirMS_041712_NAR_40mM_plus2.12465.12465.2	2	3.37	0	1.03E+05		(R)VLQALE	(R)V L/Q/A L E/G L K(M)		138.83	485.8002	970.593	0	0	5.97	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
25961	dirMS_041712_NAR_40mM_plus2.13691.13691.3	3	3.37	1	1.35E+05		(R)IPEGPID	(R)I P E/G\P I D Q G P A I G|R V/R(V)		147.8	558.9886	1674.929	0.0227	13.5	6.07	66971	7.42	HUMAN	Q9BYC5	Alpha-(1,6)-fucosyltransferase
25962	dirMS_041712_NAR_40mM_plus2.6141.6141.2	2	3.37	1	1.40E+04		(R)TGSSGA	(R)T G S|S/G A K E M K(L)		95	498.2392	995.483	-0.0115	-11.6	8.26	81194.7	6.61	HUMAN	C9JDD6	Microtubule-associated protein tau
25963	dirMS_041712_NAR_40mM_plus2.7948.7948.2	2	3.37	0	1.43E+05		(R)ELNITAA	(R)E L|N I/T/A A K(E)		106.88	430.2474	859.488	-0.0008	-1	6.1	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
25964	dirMS_041712_NAR_40mM_plus2.9283.9283.2	2	3.37	1	6.98E+05		(K)KELSLPR	(K)K E L/S/L/P R(R)		117.95	421.7572	842.509	-0.0023	-2.7	8.75	7665.7	10.89	HUMAN	H7C146	Microtubule-associated serine/threonine-protein kinase 4 (Fragment)
25965	dirMS_041712_NAR_50mM_plus2.12869.12869.3	3	3.37	2	1.51E+06		(R)GKAVGF	(R)G K A\V G P A S I L K E/V E D K(E)		136.45	547.6436	1640.922	-0.0055	-3.4	6.18	37860.2	10.33	HUMAN	O95218	Zinc finger Ran-binding domain-containing protein 2
25966	dirMS_041712_NAR_50mM_plus2.15261.15261.3	3	3.37	0	2.34E+05		(R)LASTLVH	(R)L/A|S T/L V/H L G E Y\Q A A\V D G A R(K)		148.03	657.6802	1971.029	-0.0034	-1.7	5.32	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
25967	dirMS_041712_NAR_50mM_plus2.6169.6169.3	3	3.37	0	6.16E+04		(K)VDCTAH	(K)V/D|C T A H S D V C/S/A Q G V/R(G)	C:Carbamidomethylation	96.33	587.9271	1761.764	0.0025	1.4	5.21	41053.3	5.58	HUMAN	Q86UY0	TXNDC5 protein
25968	dirMS_041712_NAR_50mM_plus2.8410.8410.3	3	3.37	2	5.68E+04		(K)IHDQMT	(K)I H D Q M T V|I/D K G K K(R)		110.75	504.9436	1512.82	-0.004	-2.7	8.51	4097.8	9.78	HUMAN	H3BQR9	Adenosine deaminase-like protein
25969	dirMS_041712_NAR_50mM_plus2.9402.9402.3	3	3.37	0	5.81E+04		(R)YMPQNI	(R)Y M/P Q N P H I/I A T K(T)		116.63	471.5817	1412.736	-0.0049	-3.5	8.6	47279.6	4.92	HUMAN	E9PC52	Histone-binding protein RBBP7
25970	dirMS_041712_NAR_60mM_plus.13677.13677.3	3	3.37	2	3.54E+05		(K)VNELKQ	(K)V/N E L K Q F K/E\H R(K)		128.42	476.5985	1427.775	0.0056	3.9	8.57	317778.9	5.51	HUMAN	Q02224	Centromere-associated protein E
25971	dirMS_041712_NAR_60mM_plus.16018.16018.3	3	3.37	1	1.12E+06		(K)TDKTLVI	(K)T D K T L V/L/L/M G K(E)		141.08	406.908	1218.713	-0.0032	-2.6	8.26	11504.1	9.57	HUMAN	K7EJ44	Profilin 1, isoform CRA_b
25972	dirMS_041712_NAR_60mM_plus.20581.20581.3	3	3.37	1	2.02E+05		(K)RSLEAYF	(K)R S\L E A/Y F A V/Q P/R P S S E K(I)		168	655.6825	1965.019	0.0141	7.2	8.59	42981.8	9.5	HUMAN	Q01851	POU domain, class 4, transcription factor 1
25973	dirMS_041712_NAR_60mM_plus.5377.5377.3	3	3.37	0	3.49E+05	M21m	(R)SGSmDF	(R)S G/S m D/P S G A H/P S\V/R(Q)	m:Oxidized methionine	86.2	467.5464	1384.627	15.9973	1.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
25974	dirMS_041712_NAR_120mM_minus.12225.12225.4	4	3.36	1	3.84E+05	M155m K1	(R)DLPLLIEI	(R)D L P L L I/E N m k/K A/L R(L)	m:Oxidized methionine k:Ub	120.6	446.7554	1653.972	130.0277	-5.7	8.59	19285.1	7.92	HUMAN	Q8TD06	Anterior gradient protein 3 homolog
25975	dirMS_041712_NAR_120mM_minus.4469.4469.4	4	3.36	1	1.37E+05	K352k	(R)EDKENIF	(R)E D\K/E N/I/P E D S\S M V S k(R)	k:Ubiquitin-K	73.37	456.2146	1707.774	114.0624	10.7	4.18	42913.8	5.13	HUMAN	O94768	Serine/threonine-protein kinase 17B
25976	dirMS_041712_NAR_30mM_minus2.14352.14352.2	2	3.36	0	5.06E+05		(R)SEQFINL	(R)S E|Q/F/I N/L R(E)		130.87	503.7677	1006.532	-0.0035	-3.5	5.72	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
25977	dirMS_041712_NAR_30mM_minus2.6550.6550.2	2	3.36	0	1.90E+05		(K)EIEVGG	(K)E I/E V/G G G R(K)		90.53	408.72	816.421	0.0117	14.4	4.53	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
25978	dirMS_041712_NAR_40mM_minus2.13361.13361.3	3	3.36	0	3.95E+05	S413s	(R)GGFPsG	(R)G G F P s G G G G\G G G Q Q/R(A)	s:N-acetylglucosamine (S)	162.57	493.5654	1275.583	203.0992	13.4	9.75	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
25979	dirMS_041712_NAR_50mM_minus2.6688.6688.3	3	3.36	1	2.52E+05		(R)ASVDTK	(R)A S/V/D T K E A E\G A|P Q V/E A G K(R)		104.8	596.2904	1786.882	-0.0251	-14	4.41	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
25980	dirMS_041712_NAR_50mM_minus2.9437.9437.3	3	3.36	1	1.88E+04	S11s	(-)XGECPSP	(-)X/G E C P S P G R/G s A A K(R)	C:Carbamidomethylation s:N-ace	122.27	530.5989	1386.679	203.1027	14.7	8.75	18627.7	11.08	HUMAN	H0YIZ3	Paired mesoderm homeobox protein 2 (Fragment)
25981	dirMS_041712_NAR_60mM_minus.11514.11514.3	3	3.36	0	9.32E+04	M974m	(R)EEVSSLV	(R)E E V S S L/V I/N A m K(E)	m:Oxidized methionine	123.83	445.9007	1319.688	16	3.8	4.53	512542.6	5.52	HUMAN	K7EK91	Dynein heavy chain 17, axonemal
25982	dirMS_041712_NAR_60mM_minus.12627.12627.2	2	3.36	0	4.80E+05		(R)LLAMPP	(R)L L A M/P P N E T C T/V K(G)	C:Carbamidomethylation	130.53	737.3855	1473.744	0.0197	13.4	6	45536.8	9.03	HUMAN	B7Z1K2	HBS1-like protein
25983	dirMS_041712_NAR_60mM_minus.18311.18311.3	3	3.36	1	1.08E+05		(R)GMLREI	(R)G M/L R E D A\V/L E|Y L K(I)		162.97	512.9419	1536.809	0.0021	1.4	4.68	67933	6.08	HUMAN	P26038	Moesin
25984	dirMS_041712_NAR_60mM_minus.9806.9806.3	3	3.36	1	2.83E+05		(R)TNAENE	(R)T/N/A/E N E F V/T I K\K(D)		114.3	465.2487	1393.732	-0.0006	-0.4	5.81	66208.7	8.32	HUMAN	P04264	Keratin, type II cytoskeletal 1
25985	dirMS_041712_NAR_120mM_plus.13598.13598.3	3	3.36	1	1.33E+05		(R)KYEMFA	(R)K Y E\M F\A Q/T|L/Q Q S R(G)		124.65	543.9369	1629.805	-0.0092	-5.6	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
25986	dirMS_041712_NAR_120mM_plus.15615.15615.4	4	3.36	2	7.33E+05		(R)KTVGVE	(R)K\T V G V E/P A A D G K/G V V V V I K(R)		135.43	467.2783	1866.106	-0.0145	-7.8	8.5	7945.1	11.03	HUMAN	C9JB50	60S ribosomal protein L28
25987	dirMS_041712_NAR_120mM_plus.4427.4427.3	3	3.36	1	3.08E+05		(K)AGADEE	(K)A/G|A D/E/E R A E T A R(L)		71.55	425.869	1275.592	0.0001	0.1	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
25988	dirMS_041712_NAR_120mM_plus.6853.6853.3	3	3.36	0	7.47E+04	S23s	(K)sPPGQV	(K)s\P P/G/Q V/T E A V K(V)	s:N-acetylglucosamine (S)	88.78	439.2268	1112.595	203.0712	-6.2	5.72	29786.8	6.51	HUMAN	E9PCX2	Aldose reductase
25989	dirMS_041712_NAR_120mM_plus.6882.6882.3	3	3.36	0	6.23E+04	T227t M23	(R)YtVTVEG	(R)Y t/V T/V E G m I/K(L)	t:Phosphorylated T m:Oxidiz	90.72	412.8549	1140.597	95.9532	-6.5	6	49673.3	8.49	HUMAN	B4DY26	TGF-beta receptor type-1
25990	dirMS_041712_NAR_120mM_plus.8034.8034.2	2	3.36	0	1.80E+05		(R)HSEIQQI	(R)H/S|E I/Q Q L E R(S)		95.23	570.2961	1139.58	0.0046	4	5.4	34011.4	9.72	HUMAN	A8MXY0	Syntaxin 4A (Placental), isoform CRA_c
25991	dirMS_041712_NAR_20mM_plus.12012.12012.2	2	3.36	0	4.00E+04		(R)ETPIGLV	(R)E T|P I G L V/P/K(E)		155.55	477.2872	953.567	0.0005	0.5	6.1	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
25992	dirMS_041712_NAR_20mM_plus.12402.12402.2	2	3.36	0	6.77E+05		(K)YSEQTEI	(K)Y S E Q T E/F/G I T|S D K(L)		158.58	752.8363	1504.68	-0.0149	-9.9	4.14	61388.9	5.43	HUMAN	B3KRB7	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta, isoform CRA_a
25993	dirMS_041712_NAR_20mM_plus.15726.15726.2	2	3.36	0	4.98E+03		(R)SSFYVN	(R)S S/F\Y/V N G L/T L G/G Q K(C)		180.83	735.8818	1470.759	-0.0024	-1.6	8.31	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
25994	dirMS_041712_NAR_20mM_plus.18340.18340.2	2	3.36	0	5.11E+04		(K)FIIPQIVI	(K)F I|I/P Q I V K(Y)		197.13	479.3081	957.613	-0.0042	-4.4	8.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
25995	dirMS_041712_NAR_20mM_plus.7745.7745.2	2	3.36	0	3.70E+04		(R)VAIEPG	(R)V A/I/E/P G A P R(E)		123.08	455.26	909.515	-0.0025	-2.8	5.97	36856.1	8.55	HUMAN	H0YLA4	Sorbitol dehydrogenase
25996	dirMS_041712_NAR_20mM_plus.8662.8662.3	3	3.36	1	1.01E+05	S190s	(R)RKsTQA	(R)R K s T/Q A G/D D L M R(C)	s:N-acetylglucosamine (S)	129.4	527.5924	1377.69	203.0723	-4.5	8.75	34433.6	6.7	HUMAN	B7Z1Q2	Growth arrest-specific protein 7
25997	dirMS_041712_NAR_30mM_plus2.11219.11219.3	3	3.36	0	2.68E+05	M300m	(R)MGQM	(R)M G Q M A m G G A/M/G I/N N R(G)	m:Oxidized methionine	112.58	518.8921	1538.67	15.9923	-1.7	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
25998	dirMS_041712_NAR_30mM_plus2.12234.12234.2	2	3.36	0	3.30E+05		(R)LPLETAY	(R)L/P/L/E T A Y R(R)		117.17	481.7661	962.531	-0.0056	-5.9	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
25999	dirMS_041712_NAR_30mM_plus2.20409.20409.3	3	3.36	2	5.86E+04	K276k	(K)LIFRESD	(K)L I F R E S D N D R/k(V)	k:Ubiquitin-K	160.6	502.9201	1392.723	114.0227	-13.4	6.12	48389.2	6.58	HUMAN	Q14642	Type I inositol 1,4,5-trisphosphate 5-phosphatase
26000	dirMS_041712_NAR_30mM_plus2.21593.21593.2	2	3.36	0	1.14E+05		(K)EVLAELE	(K)E V/L\A/E L\E/A L E R(R)		168.53	636.3523	1271.684	0.0132	10.4	4.09	56522.6	6.66	HUMAN	B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
26001	dirMS_041712_NAR_40mM_plus2.11908.11908.2	2	3.36	0	3.87E+04		(R)QITVND	(R)Q I\T/V/N D/L/P V/G R(S)		136.42	606.3387	1211.674	-0.0041	-3.4	5.84	22062.7	5.66	HUMAN	P32119	Peroxiredoxin-2
26002	dirMS_041712_NAR_40mM_plus2.14098.14098.3	3	3.36	0	8.85E+04		(R)ITYPLPE	(R)I T/Y P L P E S L/V G N/P V R(F)		149.18	552.3142	1654.916	0.0118	7.1	6	395275	5.54	HUMAN	J3KQ66	Reelin
26003	dirMS_041712_NAR_40mM_plus2.4445.4445.2	2	3.36	0	1.71E+05		(R)SYTSGP	(R)S Y\T/S/G/P G S/R(I)		73.85	456.2136	911.422	-0.0018	-2	8.46	19288.4	10.19	HUMAN	F8VQY3	Keratin, type II cytoskeletal 8 (Fragment)
26004	dirMS_041712_NAR_50mM_plus2.15689.15689.3	3	3.36	1	5.78E+05		(R)QLDFNS	(R)Q L/D F/N S S/K D V/A/V M Q L R(S)		150.95	617.6485	1850.943	-0.012	-6.5	5.96	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
26005	dirMS_041712_NAR_50mM_plus2.20057.20057.3	3	3.36	0	5.36E+05		(R)QARPTY	(R)Q/A R P T\Y\A/T/A/M L/Q S L L K(-)		174.55	597.9962	1791.979	-0.0045	-2.5	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
26006	dirMS_041712_NAR_50mM_plus2.21262.21262.3	3	3.36	0	9.64E+03		(R)SLVEIIEH	(R)S L/V E/I I E H G L\V D/E Q Q K(V)		181.1	612.9957	1836.97	0.0024	1.3	4.4	146569.5	6.65	HUMAN	O75533	Splicing factor 3B subunit 1
26007	dirMS_041712_NAR_50mM_plus2.21325.21325.3	3	3.36	1	1.61E+05		(R)EVIRND	(R)E V I R N D G V/L/L/L\Q|A L/T R(S)		182.25	604.0209	1810.055	-0.0064	-3.5	6.17	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
26008	dirMS_041712_NAR_60mM_plus.10049.10049.3	3	3.36	0	3.52E+05		(R)YSVAEEI	(R)Y S V A/E E M E S/G/S F V A/N V A K(D)		110.8	639.9721	1917.89	0.0119	6.2	4.25	91002.4	5.2	HUMAN	Q9Y5F3	Protocadherin beta-1
26009	dirMS_041712_NAR_60mM_plus.15708.15708.3	3	3.36	0	1.08E+05		(R)HLEIIYAI	(R)H L E I\I|Y|A/I/N Q R(H)		137.72	457.2595	1369.759	0.0053	3.9	6.75	97378.8	6.4	HUMAN	P11216	Glycogen phosphorylase, brain form
26010	dirMS_041712_NAR_60mM_plus.19756.19756.3	3	3.36	1	1.15E+05		(R)SLVQEM	(R)S L/V Q E M V/G S F G K R(D)		163.55	479.9219	1437.752	-0.0007	-0.5	8.46	71929.1	5.1	HUMAN	C9JAQ9	U5 small nuclear ribonucleoprotein 200 kDa helicase
26011	dirMS_041712_NAR_120mM_minus.5326.5326.4	4	3.35	1	1.12E+05	M1m N7n	(-)mQKVLS	(-)m Q K V L S n G/Q T E/E V R(S)	m:Oxidized methionine n:N-	82.45	460.2337	1618.822	219.0912	9.2	5.9	21321.2	9.56	HUMAN	E7EUF7	Receptor expression-enhancing protein 1 (Fragment)
26012	dirMS_041712_NAR_20mM_minus.10465.10465.2	2	3.35	0	2.17E+05	M443m M	(K)SNmEID	(K)S N m/E I D m T Y Q L K(V)	m:Oxidized methionine	152.92	752.8365	1472.676	31.9897	-0.1	4.37	134347.5	5.59	HUMAN	E9PF63	Rho-associated protein kinase 2
26013	dirMS_041712_NAR_20mM_minus.13507.13507.2	2	3.35	0	2.68E+05		(R)ALTVPEI	(R)A L T|V|P E L T Q Q M/F D S K(N)		186.27	854.4348	1707.862	0.0001	0.1	4.37	50305.5	4.78	HUMAN	Q13885	Tubulin beta-2A chain
26014	dirMS_041712_NAR_20mM_minus.8143.8143.2	2	3.35	0	3.12E+05	M239m	(K)EITALAP	(K)E I T A|L/A/P S T m K(I)	m:Oxidized methionine	131.35	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
26015	dirMS_041712_NAR_20mM_minus.8256.8256.2	2	3.35	0	8.90E+04	T61t	(R)VtCLESG	(R)V t\C/L/E S|G L R(V)	C:Carbamidomethylation t:N-ace	132.15	619.3164	1034.53	203.0956	13.1	5.97	22319.8	9.48	HUMAN	F8WAZ6	Mitochondrial-processing peptidase subunit beta
26016	dirMS_041712_NAR_20mM_minus.9445.9445.2	2	3.35	0	1.36E+04	M414m	(K)mDATAI	(K)m D A T A N D V/P S P Y E V/R(G)	m:Oxidized methionine	144.63	840.8764	1664.758	15.9871	-4.7	4.03	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
26017	dirMS_041712_NAR_30mM_minus2.18624.18624.2	2	3.35	0	2.21E+05		(R)LDFNLIR	(R)L/D/F N/L/I R(V)		157	445.759	890.509	0.0013	1.5	5.84	18956.4	6.97	HUMAN	C9JLK0	Phosphoribosylaminoimidazolecarboxamide formyltransferase (Fragment)
26018	dirMS_041712_NAR_30mM_minus2.6237.6237.2	2	3.35	0	3.39E+05		(R)IQEAFGI	(R)I Q/E A/F G|N K(L)		88.75	453.7335	906.468	-0.0082	-9.1	6	35176	9.89	HUMAN	Q0VAA5	PI-PLC X domain-containing protein 2
26019	dirMS_041712_NAR_40mM_minus2.15365.15365.3	3	3.35	2	3.13E+05	T121t	(K)EPVIAQ	(K)E P V I|A Q K Q K/H t G A V R(A)	t:N-acetylglucosamine (T)	177.87	622.3523	1661.945	203.0978	9.9	10	39291.8	6.3	HUMAN	B4DGE3	Protein transport protein Sec31B
26020	dirMS_041712_NAR_50mM_minus2.18512.18512.3	3	3.35	1	1.45E+06		(R)VISGVLC	(R)V I/S G V L Q L/G N I V F K K(E)		177.02	539.0018	1614.994	-0.0033	-2	10	227783.5	5.5	HUMAN	P35579	Myosin-9
26021	dirMS_041712_NAR_60mM_minus.10247.10247.3	3	3.35	1	5.47E+04		(K)GWQDV	(K)G W/Q D V T/A/T S A Y K K(T)		117.88	485.5809	1454.727	0.0007	0.5	8.5	25978.5	4.91	HUMAN	C9J502	Prostate leucine zipper variant 2
26022	dirMS_041712_NAR_60mM_minus.12783.12783.3	3	3.35	0	7.19E+04	M762m	(K)mHGGG	(K)m H G G G P T V/T/A/G L P L/P/K(A)	m:Oxidized methionine	131.53	516.9421	1532.825	15.9864	-5.5	8.52	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
26023	dirMS_041712_NAR_60mM_minus.8506.8506.3	3	3.35	0	3.90E+05	S81s	(R)FSVPSG	(R)F S V P S G S S P G S|Q s/D A E P R(E)	s:N-acetylglucosamine (S)	107.05	665.636	1791.814	203.0791	-0.2	4.37	281787.5	5.31	HUMAN	E9PF99	Centrosomal protein of 192 kDa
26024	dirMS_041712_NAR_120mM_plus.14725.14725.3	3	3.35	1	1.06E+06		(R)QLREYQ	(R)Q L R E Y\Q/E L M/N V K(L)		129.78	517.6042	1550.8	-0.0015	-1	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
26025	dirMS_041712_NAR_120mM_plus.6179.6179.4	4	3.35	2	2.82E+05	N241n	(K)ACKFnEI	(K)A C K F n/E D/L H K Q G S(-)	C:Carbamidomethylation n:N-ac	86.28	434.951	1533.711	203.0707	-5	6.8	28906.1	6.4	HUMAN	E7ERD3	HLA class II histocompatibility antigen, DP beta 1 chain
26026	dirMS_041712_NAR_120mM_plus.8179.8179.3	3	3.35	1	3.26E+05		(K)LERGNLI	(K)L/E R G N/L M G G W K(Y)		96.3	420.8864	1260.652	-0.0071	-5.6	8.75	12429.1	8.04	HUMAN	J3KST0	Cerebellin-2
26027	dirMS_041712_NAR_120mM_plus.8716.8716.3	3	3.35	1	4.46E+05		(R)RTEEGP	(R)R T E E G|P/T|L S Y G R(D)		98.62	455.8929	1365.676	-0.0116	-8.5	6.14	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
26028	dirMS_041712_NAR_20mM_plus.10377.10377.2	2	3.35	0	1.17E+05	N486n	(K)VQDNHI	(K)V/Q|D N H L S/P n K(W)	n:N-acetylglucosamine (N)	144.27	677.8247	1151.58	203.0618	-13	6.71	96731.7	8.74	HUMAN	Q14721	Potassium voltage-gated channel subfamily B member 1
26029	dirMS_041712_NAR_20mM_plus.11729.11729.2	2	3.35	0	1.18E+05		(R)ANTFVA	(R)A N|T/F V A E L K(G)		153.17	496.7735	992.541	-0.0014	-1.4	6.05	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
26030	dirMS_041712_NAR_20mM_plus.14528.14528.3	3	3.35	0	1.51E+05		(R)LQEAGII	(R)L Q E A G I L/S/A/E E L Q R(L)		171.78	519.6131	1556.828	-0.0031	-2	4.25	533778	5.74	HUMAN	Q15149	Plectin
26031	dirMS_041712_NAR_20mM_plus.18165.18165.2	2	3.35	2	7.51E+04	M765m K7	(R)VLQKAK	(R)V L/Q K A K E W E m k(K)	m:Oxidized methionine k:Ub	196.97	760.3973	1389.756	130.0314	-4.2	8.47	87514.2	6.38	HUMAN	Q8TED9	Actin filament-associated protein 1-like 1
26032	dirMS_041712_NAR_20mM_plus.18885.18885.3	3	3.35	0	1.16E+05	K269k	(R)TMGINL	(R)T M G I N L L F Q A I/k(F)	k:Ubiquitin-K	200.73	488.2764	1348.766	114.0489	4.1	8.41	34345.2	9.55	HUMAN	H7C5E2	B-cell receptor-associated protein 29 (Fragment)
26033	dirMS_041712_NAR_20mM_plus.6647.6647.2	2	3.35	0	7.77E+04	M357m	(K)AELDDTI	(K)A E|L|D/D T P m R(G)	m:Oxidized methionine	110.62	532.24	1047.478	15.9952	0.3	4.03	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
26034	dirMS_041712_NAR_20mM_plus.9892.9892.2	2	3.35	0	1.11E+05		(K)GEATVSI	(K)G E\A T V S F D D|P P S A K(A)		140	710.8324	1420.659	-0.0015	-1.1	4.03	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
26035	dirMS_041712_NAR_30mM_plus2.20327.20327.2	2	3.35	0	1.71E+05		(K)NIEDVIA	(K)N/I|E D V|I/A Q G I G K(L)		160.45	628.8445	1256.685	-0.0028	-2.2	4.37	9098.8	4.38	HUMAN	H0YDD8	60S acidic ribosomal protein P2 (Fragment)
26036	dirMS_041712_NAR_40mM_plus2.12087.12087.2	2	3.35	0	1.26E+04		(R)VWQVTI	(R)V/W|Q|V\T I G T/R(-)		137.38	530.2982	1059.595	-0.0054	-5.1	9.72	30149.5	5.96	HUMAN	D6RAC2	Guanine nucleotide-binding protein subunit beta-2-like 1
26037	dirMS_041712_NAR_40mM_plus2.17856.17856.3	3	3.35	1	5.20E+05		(R)GLLPGLI	(R)G L|L/P\G L L/P\A/P A D K L T P K(G)		170.65	567.6811	1701.031	-0.0022	-1.3	8.59	153084.9	5.55	HUMAN	Q6P2E9	Enhancer of mRNA-decapping protein 4
26038	dirMS_041712_NAR_40mM_plus2.7500.7500.2	2	3.35	0	1.95E+05		(R)SGYFDEI	(R)S G/Y/F D/E R(Y)		104.17	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
26039	dirMS_041712_NAR_50mM_plus2.11042.11042.3	3	3.35	1	1.34E+05		(R)LGGEVS	(R)L/G/G E V/S C L V A G T K C D K(V)	C:Carbamidomethylation	125.42	565.2794	1693.825	-0.0011	-0.7	6.07	30619.5	9.34	HUMAN	H0YKF0	Electron transfer flavoprotein subunit alpha, mitochondrial (Fragment)
26040	dirMS_041712_NAR_50mM_plus2.20987.20987.3	3	3.35	1	7.13E+03	S473s	(K)YASsLLK	(K)Y A S s L/L K H G/F L R(H)	s:N-acetylglucosamine (S)	180.82	532.2964	1391.779	203.0953	10	9.99	75584.8	7.92	HUMAN	O14640	Segment polarity protein dishevelled homolog DVL-1
26041	dirMS_041712_NAR_50mM_plus2.21216.21216.3	3	3.35	1	9.07E+03		(K)ALFEEVF	(K)A L/F E E/V/P E L L T E A E K K(E)		182.25	615.9987	1845.984	-0.0029	-1.6	4.32	65036	6.27	HUMAN	E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase
26042	dirMS_041712_NAR_60mM_plus.19117.19117.3	3	3.35	1	1.23E+05	S2870s S28	(R)sAAQPS	(R)s A A Q P S T s P A E/V/Q S L/K K(A)	s:Phosphorylated S	157.33	630.2949	1728.913	159.9575	13.1	8.31	378557.2	4.96	HUMAN	E7EP74	Golgin subfamily B member 1
26043	dirMS_041712_NAR_60mM_plus.5821.5821.3	3	3.35	0	2.06E+04		(R)AVTNHS	(R)A/V|T N H/S V/Y C S T K(G)	C:Carbamidomethylation	88.8	456.2187	1366.642	-0.0004	-0.3	8.64	15120.3	9.29	HUMAN	J3KRZ4	L-xylulose reductase (Fragment)
26044	dirMS_041712_NAR_60mM_plus.6010.6010.3	3	3.35	1	1.28E+05		(K)AQQELE	(K)A Q/Q E/L/E E Q T/R R(A)		89.27	463.233	1387.692	-0.008	-5.8	4.79	67933	6.08	HUMAN	P26038	Moesin
26045	dirMS_041712_NAR_60mM_plus.9363.9363.3	3	3.35	0	4.74E+04		(R)IEYDTFG	(R)I E Y D\T F\G E L/K(V)		108	405.5315	1214.594	-0.014	-11.5	4.14	54807.2	9.02	HUMAN	P07954	Fumarate hydratase, mitochondrial
26046	dirMS_041712_NAR_120mM_minus.18591.18591.3	3	3.34	1	9.58E+03	M616m	(R)LLVLmS	(R)L L/V L m S/S P Y K G E/G R(G)	m:Oxidized methionine	156.62	522.6151	1549.841	15.9901	-3.1	8.59	195341	6.24	HUMAN	A6NES4	HEAT repeat-containing protein 7B1

26047	dirMS_041712_NAR_120mM_minus.5723.5723.2	2	3.34	1	9.25E+04		(R)DRDGQ	(R)D R|D G Q H S W V|P R(G)		84.4	676.8296	1352.645	0.0065	4.8	6.75	73400.1	10.94 HUMAN	Q99501	GAS2-like protein 1
26048	dirMS_041712_NAR_120mM_minus.5939.5939.3	3	3.34	1	1.96E+05	M1m	(-)mPAHRD	(-)m/P A H R D/P D|V Q/G H R(L)	m:Oxidized methionine	86.45	511.2386	1515.723	15.9779	-11.1	6.69	48937.1	11.92 HUMAN	F5H450	Frizzled-10
26049	dirMS_041712_NAR_30mM_minus2.10771.10771.2	2	3.34	1	3.18E+05	T435t	(K)MRVEA	(K)M R|V E A/V G/C t R(R)	C:Carbamidomethylation t:N-ace	111.98	691.3271	1178.577	203.0701	-6.7	9.35	306910.7	5.96 HUMAN	H7BY31	Obscurin
26050	dirMS_041712_NAR_30mM_minus2.16396.16396.2	2	3.34	0	1.29E+04		(K)QITMEE	(K)Q I/T M/E/E L V R(S)		142.57	559.8008	1118.587	0.0069	6.2	4.53	533778	5.74 HUMAN	Q15149	Plectin
26051	dirMS_041712_NAR_30mM_minus2.5713.5713.2	2	3.34	0	1.31E+05		(K)VHFSGE	(K)V H F\S G E\S K(E)		85.4	445.7185	890.437	-0.0069	-7.8	6.72	47152.3	9.23 HUMAN	B4DZU0	Serine/threonine-protein kinase Nek2
26052	dirMS_041712_NAR_50mM_minus2.15531.15531.3	3	3.34	0	2.72E+05	M118m	(R)AGKPVI	(R)A G K P V I C A\T/Q/M/L/E S m I K(K)	C:Carbamidomethylation m:Oxid	155.9	631.6612	1876.969	15.9997	2.5	8.64	18466.1	5.78 HUMAN	H3BSU3	Pyruvate kinase (Fragment)
26053	dirMS_041712_NAR_50mM_minus2.8662.8662.3	3	3.34	0	8.70E+04		(-)XLFLLPS	(-)X L|F L L P S P G D/E E N C K(H)	C:Carbamidomethylation	117.43	577.9535	1731.862	-0.0163	-9.4	4.14	48866.2	9.1 HUMAN	H7BYF9	XK-related protein 6 (Fragment)
26054	dirMS_041712_NAR_60mM_minus.11036.11036.3	3	3.34	0	2.33E+05		(R)DAQQS	(R)D A/Q Q S S\S P/A A D N L R(E)		121.02	487.236	1459.677	0.0163	11.1	4.21	62343.6	5.47 HUMAN	B7Z7P0	Ubiquitin conjugation factor E4 A
26055	dirMS_041712_NAR_60mM_minus.13944.13944.3	3	3.34	0	1.94E+05		(K)ADFCIIH	(K)A D F/C I I/H Y A/G K(V)	C:Carbamidomethylation	137.33	432.2132	1294.625	0.0002	0.1	6.79	233493.8	5.45 HUMAN	F8VTL3	Myosin-10
26056	dirMS_041712_NAR_60mM_minus.8398.8398.3	3	3.34	1	3.90E+05	K872k	(R)TVECRD	(R)T V E C R D P/S G Q/A S A T C N k(A)	C:Carbamidomethylation k:Ubiqu	107.05	665.636	1880.823	114.0709	14	5.74	98740.7	5.79 HUMAN	Q9UP79	A disintegrin and metalloproteinase with thrombospondin motifs 8
26057	dirMS_041712_NAR_120mM_plus.6883.6883.3	3	3.34	1	6.23E+04	S42s	(R)sTLESTIS	(R)s T L E/S T I S R/Y(-)	s:Phosphorylated S	90.72	412.8549	1156.584	79.9657	-0.5	5.72	6148.1	9.3 HUMAN	H3BTM4	Uncharacterized protein
26058	dirMS_041712_NAR_120mM_plus.8591.8591.2	2	3.34	0	6.90E+05		(K)HFVALS	(K)H F|V|A L S T N T T K(V)		98.9	609.8311	1218.648	0.0072	5.9	8.76	63374.2	8.64 HUMAN	P06744	Glucose-6-phosphate isomerase
26059	dirMS_041712_NAR_20mM_plus.14183.14183.2	2	3.34	1	2.39E+03	S309s	(K)LIGKKsQ	(K)L I|G\K K s Q(-)	s:N-acetylglucosamine (S)	169.48	488.7934	773.488	203.0916	12.5	10	35385.2	7.88 HUMAN	Q8NGP9	Olfactory receptor 5AR1
26060	dirMS_041712_NAR_20mM_plus.18300.18300.2	2	3.34	0	4.35E+04		(R)GILLFGP	(R)G I L L/F/G P P G/T G K(S)		197.1	578.8387	1156.672	-0.0023	-2	8.75	32617.4	7.2 HUMAN	I3L4J1	Uncharacterized protein (Fragment)
26061	dirMS_041712_NAR_20mM_plus.18852.18852.3	3	3.34	2	7.06E+04		(K)MKTFFE	(K)M K T/F F\E K S/L I D I K(N)		201.58	533.9719	1599.882	0.0197	12.3	8.25	282124	6.12 HUMAN	Q7Z2Y8	Interferon-induced very large GTPase 1
26062	dirMS_041712_NAR_30mM_plus2.10282.10282.2	2	3.34	0	2.31E+05		(R)LNQDQ	(R)L N Q|D Q L/D A V/S K(Y)		107.4	615.819	1230.632	-0.0017	-1.4	4.21	20235.4	6.77 HUMAN	E9PLA9	Caprin-1 (Fragment)
26063	dirMS_041712_NAR_30mM_plus2.13408.13408.2	2	3.34	0	8.79E+05		(K)NSGVL	(K)N S|G V/L/M V/V K(C)		123	473.7749	946.539	0.0035	3.7	8.75	9148.5	9.4 HUMAN	C9JES7	COX assembly mitochondrial protein homolog
26064	dirMS_041712_NAR_30mM_plus2.16516.16516.2	2	3.34	0	2.13E+05		(K)QLQEM	(K)Q L|Q E/M L/G L S K(V)		140.12	573.8112	1146.619	-0.0036	-3.1	6	83880.6	7.33 HUMAN	F5H365	Protein transport protein Sec23A
26065	dirMS_041712_NAR_30mM_plus2.21763.21763.2	2	3.34	0	1.02E+05		(R)IITLAGP	(R)I I T/L A/G/P T N A I F K(A)		168.57	679.9016	1358.804	-0.0083	-6.1	8.75	32621	8.75 HUMAN	B4DLC0	Poly(rC)-binding protein 2
26066	dirMS_041712_NAR_30mM_plus2.4936.4936.2	2	3.34	0	6.90E+05		(R)MGQTM	(R)M/G|Q|T M/E R(I)		77.4	426.6906	852.37	0.0037	4.3	5.75	77799.7	9.09 HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
26067	dirMS_041712_NAR_30mM_plus2.5640.5640.2	2	3.34	0	3.85E+04		(K)GSSNSY	(K)G S/S N/S/Y A I K(K)		83.67	463.7311	926.458	-0.0029	-3.1	8.59	23047.2	9.95 HUMAN	P46782	40S ribosomal protein S5
26068	dirMS_041712_NAR_40mM_plus2.15323.15323.3	3	3.34	0	1.08E+05		(R)IETMLG	(R)I E T|M L G D V A V/A V H P K(D)		156.37	527.286	1579.851	-0.0078	-4.9	5.32	141718.6	7.8 HUMAN	B0V043	Valine--tRNA ligase
26069	dirMS_041712_NAR_40mM_plus2.7599.7599.2	2	3.34	0	1.68E+05		(R)SGYFDE	(R)S/G Y/F D|E R(Y)		104.45	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91 HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
26070	dirMS_041712_NAR_50mM_plus2.11551.11551.3	3	3.34	0	2.85E+05		(K)ITKPGSI	(K)I T/K P G S I D S N N Q\L/F/A P G G R(L)		128.32	658.0091	1972.025	-0.0119	-6	8.75	176357.7	5.25 HUMAN	D3DNT2	Eukaryotic translation initiation factor 4 gamma 1
26071	dirMS_041712_NAR_50mM_plus2.17413.17413.3	3	3.34	1	3.34E+05	T318t	(R)IYNVVG	(R)I Y/N V V G t I R G S|V/E P D R(Y)	t:N-acetylglucosamine (T)	159.43	660.0107	1774.945	203.0729	-3.3	6.07	80333.4	8.55 HUMAN	J3KNJ3	N-acetylated-alpha-linked acidic dipeptidase 2
26072	dirMS_041712_NAR_50mM_plus2.5826.5826.3	3	3.34	0	3.07E+04	T44t M51m	(K)SAtQVS	(K)S/A/t Q V S A I H m/D S K(V)	t:N-acetylglucosamine (T) m:	94.12	531.9144	1374.668	219.0605	-8.7	6.46	13747.4	5.92 HUMAN	Q8WU43	Uncharacterized protein C2orf15
26073	dirMS_041712_NAR_60mM_plus.13723.13723.2	2	3.34	1	3.36E+05		(K)GIIDPTK	(K)G I I/D/P T K V V R(T)		128.75	549.3331	1097.668	-0.0088	-8	8.75	61224.7	5.7 HUMAN	P10809	60 kDa heat shock protein, mitochondrial
26074	dirMS_041712_NAR_60mM_plus.5822.5822.3	3	3.34	0	1.32E+05		(-)XYPAPA	(-)X Y P A P A C G E/V D R(R)	C:Carbamidomethylation	88.53	449.8794	1347.636	-0.0125	-9.3	4.37	8704	5.05 HUMAN	H0YC92	Sodium/glucose cotransporter 4 (Fragment)
26075	dirMS_041712_NAR_120mM_minus.13397.13397.4	4	3.33	2	1.00E+06	M440m	(R)IEEQKLL	(R)I E E Q\K L L R m\Q/F E Q/R(E)	m:Oxidized methionine	127.45	466.7525	1847.98	16.0085	7.3	6.23	69155	5.06 HUMAN	H7BXY5	Nexilin (Fragment)
26076	dirMS_041712_NAR_20mM_minus.10289.10289.2	2	3.33	0	9.30E+04		(R)NTGIICT	(R)N T/G I|I/C T I\G P A S R(S)	C:Carbamidomethylation	152.63	680.3561	1359.705	0	0	9.75	30947.9	6.47 HUMAN	H3BQ34	Pyruvate kinase
26077	dirMS_041712_NAR_20mM_minus.14449.14449.3	3	3.33	0	5.82E+04		(R)LTGQLF	(R)L T G Q L F\L/G G S I V K(G)		198.63	444.9343	1332.789	-0.0002	-0.2	8.75	45924.5	5.29 HUMAN	B4E1F3	Selenium-binding protein 1
26078	dirMS_041712_NAR_30mM_minus2.12483.12483.2	2	3.33	0	2.19E+05		(K)NIILGGV	(K)N/I|I/L G G V K(A)		121.63	407.263	813.519	-0.0005	-0.7	8.75	118930.9	5.49 HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
26079	dirMS_041712_NAR_30mM_minus2.5729.5729.2	2	3.33	0	1.60E+05	Y728y S73	(R)GySLSA	(R)G y S/L/S A P s/R(I)	y:Phosphorylated Y s:Phosph	85.28	549.2137	937.474	159.9464	12.5	8.75	154801.1	6.72 HUMAN	B5MEF5	Sushi, nidogen and EGF-like domain-containing protein 1
26080	dirMS_041712_NAR_30mM_minus2.7371.7371.2	2	3.33	0	5.59E+04		(R)AQQFYR	(R)A/Q/Q/F Y/R(D)		94.57	406.7069	812.405	0.0016	1.9	8.79	272689.3	5.79 HUMAN	O15020	Spectrin beta chain, non-erythrocytic 2
26081	dirMS_041712_NAR_50mM_minus2.12741.12741.3	3	3.33	1	1.18E+04		(R)RLQGQL	(R)R L Q G\Q L E Q G D/D T\A A/E R(L)		140.88	596.2904	1786.868	-0.0112	-6.3	4.32	68118.7	8.68 HUMAN	H0YGW7	ATP-binding cassette sub-family F member 1 (Fragment)
26082	dirMS_041712_NAR_50mM_minus2.5930.5930.3	3	3.33	1	7.79E+04	S174s	(K)TESDFs	(K)T E/S D/F s N L D S E K H K(K)	s:Phosphorylated S	95.88	572.9159	1636.745	79.9882	12.8	4.75	26757.5	8.58 HUMAN	B5ME25	Methyltransferase-like protein 8 (Fragment)
26083	dirMS_041712_NAR_60mM_minus.10045.10045.3	3	3.33	0	2.74E+04		(K)VNSEGK	(K)V N S E G K P S L/L L K(L)		115.45	428.9126	1284.752	-0.0289	-22.5	8.56	36313.6	8.76 HUMAN	P47870-3	Isoform 3 of Gamma-aminobutyric acid receptor subunit beta-2
26084	dirMS_041712_NAR_60mM_minus.10826.10826.3	3	3.33	0	2.47E+05		(K)FYEEVH	(K)F Y|E E V/H D\L E|R(K)		119.73	446.2105	1336.617	0.0001	0.1	4.4	18209.2	5.03 HUMAN	A8MXH2	Nucleosome assembly protein 1-like 4 (Fragment)
26085	dirMS_041712_NAR_60mM_minus.12225.12225.3	3	3.33	2	2.56E+05		(R)LISDSVE	(R)L I/S D S V E/R D R D R(D)		127.93	487.5978	1460.745	0.0337	23	4.68	71145.8	6.04 HUMAN	F8W781	Zinc finger CCCH domain-containing protein 13
26086	dirMS_041712_NAR_60mM_minus.14429.14429.3	3	3.33	1	2.19E+05		(R)KTTLQV	(R)K T T L Q/V D T L\N/A\E/L/A A E R(S)		140.22	625.0044	1873.003	-0.0039	-2.1	4.68	233493.8	5.45 HUMAN	F8VTL3	Myosin-10
26087	dirMS_041712_NAR_60mM_minus.8898.8898.3	3	3.33	1	1.72E+04		(K)SHDLKV	(K)S/H D L K V S/A H P K(E)		109.98	406.8868	1218.659	-0.0131	-10.7	8.36	26240.1	6.53 HUMAN	H3BQ21	Signal-regulatory protein beta-1 isoform 3 (Fragment)
26088	dirMS_041712_NAR_120mM_plus.4749.4749.3	3	3.33	0	3.08E+05		(K)ISRPGD	(K)I/S R P G D S/D D S R(S)		75.27	402.1896	1204.555	-0.001	-0.8	4.43	64759.2	8.88 HUMAN	P14866	Heterogeneous nuclear ribonucleoprotein L
26089	dirMS_041712_NAR_20mM_plus.13757.13757.2	2	3.33	0	5.96E+04		(K)ASAELA	(K)A S A E L|A/L/G E N S E V L K(S)		166.92	765.8991	1530.801	-0.0101	-6.6	4.25	47916.2	9.44 HUMAN	P00505	Aspartate aminotransferase, mitochondrial
26090	dirMS_041712_NAR_20mM_plus.15231.15231.2	2	3.33	1	5.88E+04	S46s	(K)GISPIKD	(K)G I/S|P I/K D\s K(C)	s:N-acetylglucosamine (S)	176.1	574.312	944.541	203.0756	-3.3	8.59	6775.1	9.82 HUMAN	G3V3K0	Retinol dehydrogenase 11
26091	dirMS_041712_NAR_20mM_plus.15986.15986.2	2	3.33	0	1.93E+05		(K)DAGTIA	(K)D/A G T\I A/G L/N V\L R(I)		182.17	600.3422	1199.674	0.0029	2.4	5.84	17973	5.16 HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
26092	dirMS_041712_NAR_20mM_plus.16246.16246.3	3	3.33	0	1.70E+05		(K)DAGTIA	(K)D A G T I/A/G\L/N V L/R(I)		183.65	400.5627	1199.674	-0.0007	-0.6	5.84	17973	5.16 HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
26093	dirMS_041712_NAR_20mM_plus.19338.19338.2	2	3.33	0	1.55E+05		(R)TGAIVD	(R)T G A I/V D|V|P V G E E L L/G R(V)		204.58	812.9497	1624.891	0.0017	1	4.14	15338.4	5.51 HUMAN	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment)
26094	dirMS_041712_NAR_30mM_plus2.10708.10742.2	2	3.33	0	3.12E+05		(K)QLIVGV	(K)Q L|I/V G V/N/K(M)		110.95	435.7729	870.541	-0.0022	-2.5	8.75	50482.3	9.31 HUMAN	P68104	Elongation factor 1-alpha 1
26095	dirMS_041712_NAR_30mM_plus2.15924.15924.2	2	3.33	0	9.00E+05		(R)MGAGM	(R)M/G\A\G/M/G/F G L E R(M)		137.02	563.2636	1125.518	0.002	1.7	5.75	77799.7	9.09 HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
26096	dirMS_041712_NAR_30mM_plus2.20337.20337.3	3	3.33	0	5.86E+04	S196s	(R)sQWCPL	(R)s Q W C/P L P I F R(S)	C:Carbamidomethylation s:N-ace	160.6	502.9201	1303.662	203.0842	3.2	9.47	24390.7	8.05 HUMAN	Q07812-2	Isoform Beta of Apoptosis regulator BAX
26097	dirMS_041712_NAR_30mM_plus2.4135.4135.2	2	3.33	0	1.25E+06	M299m M3	(K)NmmAA	(K)N m\m/A\A C D|P R(H)	C:Carbamidomethylation m:Oxid	69.17	549.2125	1065.427	31.9903	0.4	5.84	50199.4	4.75 HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
26098	dirMS_041712_NAR_30mM_plus2.4629.4629.2	2	3.33	0	2.77E+05		(R)SYTSGP	(R)S Y/T S G/P G S R(I)		74.18	456.2155	911.422	0.002	2.2	8.46	19288.4	10.19 HUMAN	F8VQY3	Keratin, type II cytoskeletal 8 (Fragment)
26099	dirMS_041712_NAR_40mM_plus2.11009.11009.3	3	3.33	0	1.18E+05	N106n	(R)LVFTDV	(R)L V|F T/D V A n A I H A(-)	n:N-acetylglucosamine (N)	130.05	491.9315	1270.679	203.1009	14.6	5.08	12480.2	9.59 HUMAN	C9IYC4	Uncharacterized protein C3orf18
26100	dirMS_041712_NAR_40mM_plus2.13416.13416.3	3	3.33	1	2.43E+05		(K)ISEGNSY	(K)I S/E/G N S Y\L L S E\N/L S R A R(I)		145.88	637.0002	1908.977	0.0087	4.5	6.14	52951.8	9.63 HUMAN	Q86VV4	Ran-binding protein 3-like
26101	dirMS_041712_NAR_40mM_plus2.14527.14527.3	3	3.33	1	5.08E+03		(R)SRAFSES	(R)S R A F S E S H I S L/A P/Q S T R(A)		153.03	625.3155	1873.951	-0.0196	-10.4	9.34	167136.6	6.2 HUMAN	Q9ULL8	Protein Shroom4
26102	dirMS_041712_NAR_40mM_plus2.6368.6368.2	2	3.33	1	2.65E+04		(R)YSGGNY	(R)Y/S/G G N Y R D\N Y D/N(-)		96.45	719.2857	1437.567	-0.0024	-1.7	4.21	17170.1	8.86 HUMAN	P98179	Putative RNA-binding protein 3
26103	dirMS_041712_NAR_50mM_plus2.19091.19091.3	3	3.33	0	2.48E+05		(K)LAKPLSS	(K)L A/K P L S S L/T|P L I M A A K(E)		168.28	552.004	1653.997	0.0003	0.2	10	24711.4	5.19 HUMAN	H7C1X3	PAK-2p34 (Fragment)
26104	dirMS_041712_NAR_50mM_plus2.20410.20410.3	3	3.33	1	6.44E+05		(K)SYLNMD	(K)S Y|L N/M D A I M E A I K K(T)		177.13	542.9473	1626.823	0.0044	2.7	5.79	80685.1	7.31 HUMAN	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial
26105	dirMS_041712_NAR_50mM_plus2.6319.6319.3	3	3.33	0	2.09E+05	M70m	(K)EAPPmE	(K)E A/P/P m E K P E V/V/K(T)	m:Oxidized methionine	97.97	457.2387	1353.708	15.9933	-1.2	4.79	14798.1	10.35 HUMAN	K7EJ78	40S ribosomal protein S15 (Fragment)
26106	dirMS_041712_NAR_60mM_plus.17250.17250.3	3	3.33	0	2.53E+04		(K)EGHVEV	(K)E/G\H V E\V V/S E/L L Q R(E)		148.35	498.9326	1494.791	-0.0078	-5.2	4.75	48586.6	9.32 HUMAN	D6RCB2	Ankyrin-3
26107	dirMS_041712_NAR_60mM_plus.19531.19531.3	3	3.33	1	5.37E+05		(R)TRIEGLL	(R)T R I E G\L\L A/A F/P K(L)		160.08	439.262	1315.773	-0.0018	-1.4	8.41	62195.8	5.63 HUMAN	B0YIW6	Archain 1, isoform CRA_a
26108	dirMS_041712_NAR_60mM_plus.19827.19827.3	3	3.33	2	1.09E+05		(K)LAKEFLK	(K)L A K E/F L K E Q A W/K(I)		163.82	497.6187	1490.837	0.005	3.3	8.5	144424.4	5.18 HUMAN	Q6ZT07	TBC1 domain family member 9
26109	dirMS_041712_NAR_120mM_minus.10243.10243.3	3	3.32	1	1.95E+05	K151k	(K)KPYVSK	(K)K\P/Y V S/K Q C/G k(S)	C:Carbamidomethylation k:Ubiqu	109.92	436.8918	1194.63	114.0309	-9.2	10	35620.1	9.93 HUMAN	A8MUZ8	Putative zinc finger protein 705G
26110	dirMS_041712_NAR_120mM_minus.12743.12743.4	4	3.32	0	4.92E+04	K1352k	(R)ISQLIQP	(R)I S Q L I Q/P Q Q/D/N\L k(A)	k:Ubiquitin-K	122.28	410.4736	1524.838	114.0345	-5.1	5.84	296711.5	5.69 HUMAN	Q9C0D2	Centrosomal protein KIAA1731
26111	dirMS_041712_NAR_120mM_minus.18801.18801.4	4	3.32	0	1.06E+05	S79s	(R)LPsEQES	(R)L P s E/Q E S I T/V\I L T A K(V)	s:N-acetylglucosamine (S)	157.9	458.7498	1628.911	203.0668	-6.8	4.53	10051	5.49 HUMAN	F8W8F0	Ubiquitin-conjugating enzyme E2 E2
26112	dirMS_041712_NAR_120mM_minus.9481.9481.3	3	3.32	1	9.19E+04		(K)LNRYNY	(K)L/N R Y|N Y|I E G T K(M)		106.13	457.5734	1370.706	-0.0006	-0.5	8.5	53219.8	5.66 HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
26113	dirMS_041712_NAR_20mM_minus.10683.10683.2	2	3.32	1	3.77E+05		(K)TLMSKA	(K)T L M S K A/A\L|T\H K(F)		155.6	600.8502	1200.677	0.0162	13.5	10	118849.2	6.23 HUMAN	F8VWZ8	Rho GTPase-activating protein 29
26114	dirMS_041712_NAR_20mM_minus.9216.9216.2	2	3.32	0	1.90E+05	M239m	(K)EITALAP	(K)E I T A/L/A/P S T m K(I)	m:Oxidized methionine	141.92	589.3094	1161.618	15.9931	-1.5	6.1	32616.5	5.18 HUMAN	A6NL76	Actin, alpha skeletal muscle
26115	dirMS_041712_NAR_30mM_minus2.16181.16181.2	2	3.32	1	1.21E+05	N49n	(R)InDISQR	(R)I/n D|I|S/Q R R(F)	n:N-acetylglucosamine (N)	141.47	602.816	1001.549	203.0761	-2.8	9.6	23466.9	10.09 HUMAN	J3QLH9	F-box/WD repeat-containing protein 10
26116	dirMS_041712_NAR_30mM_minus2.16439.16439.2	2	3.32	1	4.44E+04	M1m	(-)mGLSLP	(-)m G/L S L P K E K(G)	m:Oxidized methionine	142.18	509.7867	1002.565	16.0009	5.9	8.35	84064.3	7.87 HUMAN	Q9H1D0	Transient receptor potential cation channel subfamily V member 6
26117	dirMS_041712_NAR_30mM_minus2.16844.16844.2	2	3.32	0	6.13E+05		(K)MIFVGI	(K)M/I|F/V G I/K(K)		145.8	404.2383	807.48	-0.0104	-12.9	8.5	11447.2	9.81 HUMAN	C9JFR7	Cytochrome c (Fragment)
26118	dirMS_041712_NAR_30mM_minus2.18918.18918.2	2	3.32	0	2.07E+05		(R)AIGIGAY	(R)A I|G/I/G A Y L V R(L)		157.58	516.8122	1032.62	-0.0029	-2.8	8.79	9731	5.19 HUMAN	E9PEW7	Acetyl-CoA carboxylase 2
26119	dirMS_041712_NAR_50mM_minus2.11179.11179.3	3	3.32	1	1.86E+05		(R)DNKQA	(R)D N K Q A G V|F/E P T I V K(V)		132.05	515.9485	1545.827	0.0038	2.5	6.07	44227.3	7.81 HUMAN	E7EQR6	T-complex protein 1 subunit alpha
26120	dirMS_041712_NAR_50mM_minus2.12426.12426.3	3	3.32	0	6.17E+03	K380k	(K)KPLPPV	(K)K P/L P P V Q S/D k K(I)	k:Ubiquitin-K	138.4	450.9284	1236.731	114.0396	-2.5	9.7	111104.3	8.79 HUMAN	Q8NAT2	Tudor domain-containing protein 5
26121	dirMS_041712_NAR_50mM_minus2.15675.15675.3	3	3.32	0	1.29E+05		(K)FTISDHP	(K)F T|I S D H\P Q/P I D\P/L L K(N)		157.77	574.3122	1720.927	-0.0048	-2.8	5.21	138084.9	5.52 HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
26122	dirMS_041712_NAR_50mM_minus2.6732.6732.3	3	3.32	1	8.76E+04	M22m M2	(K)LAEQAE	(K)L/A/E/Q/A E R Y D D m A\A C m K(S)	C:Carbamidomethylation m:Oxid	104.8	645.2741	1901.819	31.9887	-0.6	4.32	5919.6	4.73 HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
26123	dirMS_041712_NAR_60mM_minus.16684.16684.3	3	3.32	1	1.80E+05		(K)VSEQGL	(K)V/S/E/Q G L I E I L K K(V)		152.83	452.9408	1356.81	-0.0018	-1.4	6.11	12899.6	6.59 HUMAN	K7EL31	Programmed cell death protein 5
26124	dirMS_041712_NAR_60mM_minus.17953.17953.3	3	3.32	1	2.73E+05		(K)LEALKD	(K)L E A L K D\L/A/S L S R(D)		161.65	439.2618	1315.758	0.0129	9.8	6.07	18679.9	4.7 HUMAN	C9IZR8	Engulfment and cell motility protein 1 (Fragment)
26125	dirMS_041712_NAR_60mM_minus.18061.18061.3	3	3.32	0	9.48E+04		(R)NSVSNF	(R)N S/V/S N F L H S L E/R(G)		162.5	468.2409	1402.707	0.0008	0.6	6.75	267260.7	5.95 HUMAN	Q13085	Acetyl-CoA carboxylase 1
26126	dirMS_041712_NAR_60mM_minus.18248.18248.3	3	3.32	1	1.13E+04		(K)IVLHNT	(K)I V L H N T F G F K/F/N/L/T(-)		163.17	550.9705	1650.9	-0.0033	-2	8.76	8607.6	6.9 HUMAN	H0Y9M6	Protein sel-1 homolog 3 (Fragment)
26127	dirMS_041712_NAR_60mM_minus.18708.18708.3	3	3.32	0	1.19E+05		(K)KPGGFD	(K)K\P G G F D\I/S\L/F/Y R(D)		165.55	467.2495	1399.737	-0.0029	-2.1	8.59	64302.5	6.4 HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
26128	dirMS_041712_NAR_60mM_minus.5209.5209.3	3	3.32	0	9.70E+04	K904k	(R)AALAPA	(R)A/A/L A P A k E/S P R(K)	k:Ubiquitin-K	84.08	408.8971	1110.627	114.0502	5.9	8.79	152529.5	8.95 HUMAN	E7ETY2	Treacle protein
26129	dirMS_041712_NAR_60mM_minus.6633.6633.3	3	3.32	0	1.19E+05	N259n	(R)NTTnTS	(R)N|T T n T S/V T A E R(L)	n:N-acetylglucosamine (N)	95.23	466.2187	1193.576	203.0659	-9.7	6	104323.4	5.34 HUMAN	C9JCH2	Receptor-type tyrosine-protein phosphatase H
26130	dirMS_041712_NAR_60mM_minus.8356.8356.3	3	3.32	0	2.81E+05	K115k	(K)IYTNQE	(K)I Y T N/Q E k/T/R(T)	k:Ubiquitin-K	106.87	422.8919	1152.601	114.0604	13.8	8.59	24985	6.11 HUMAN	H3BNM8	Putative U6 snRNA phosphodiesterase
26131	dirMS_041712_NAR_120mM_plus.10765.10765.2	2	3.32	1	2.27E+06		(R)LASYLD	(R)L A S Y/L D/R V/R(S)		109.83	546.8117	1092.616	0.0001	0.1	8.75	43773.3	5.26 HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
26132	dirMS_041712_NAR_120mM_plus.5746.5746.3	3	3.32	0	2.56E+05	S442s	(R)EDsAPP	(R)E D s A/P P S S/V/A R(S)	s:N-acetylglucosamine (S)	82.62	440.2048	1115.533	203.0671	-9.3	4.37	60449.7	9.6 HUMAN	B4DY13	Nucleolar GTP-binding protein 1
26133	dirMS_041712_NAR_120mM_plus.6438.6438.2	2	3.32	0	1.01E+05	M419m	(R)mGAGL	(R)m G\A G L/G|H/G M D/R(V)	m:Oxidized methionine	86.92	559.2491	1101.493	15.9981	2.9	6.49	77799.7	9.09 HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
26134	dirMS_041712_NAR_20mM_plus.11751.11751.3	3	3.32	1	1.37E+04		(R)QSTSQH	(R)Q S T S Q H I P/K L P P K(T)		153.73	487.6115	1460.822	-0.002	-1.4	10	151824.4	6.41 HUMAN	G5E9C8	Son of sevenless homolog 1
26135	dirMS_041712_NAR_20mM_plus.14706.14706.2	2	3.32	0	8.06E+04		(K)NLYIISV	(K)N L|Y/I I/S\V K(G)		173.1	475.2896	949.572	0.0002	0.2	8.59	12270.4	11.49 HUMAN	B9ZVP7	60S ribosomal protein L23
26136	dirMS_041712_NAR_20mM_plus.17245.17245.2	2	3.32	0	1.97E+05		(K)VLAQNS	(K)V L/A Q N/S G F D L Q E T L V K(I)		190.7	881.4709	1761.938	-0.0036	-2.1	4.37	55323	6.02 HUMAN	B4DPJ8	T-complex protein 1 subunit zeta
26137	dirMS_041712_NAR_30mM_plus2.13643.13643.2	2	3.32	0	1.08E+05		(R)SGPNIY	(R)S G/P N|I|Y E L R(S)		124.67	524.7749	1048.542	0.0003	0.3	5.72	7939	9.59 HUMAN	C9J7B1	Protein NipSnap homolog 2 (Fragment)
26138	dirMS_041712_NAR_30mM_plus2.4955.4955.2	2	3.32	1	1.89E+05		(R)NTKGG	(R)N T\K G G D/A P/A/A G E|D A(-)		77.23	637.286	1273.565	-0.0008	-0.6	4.03	13798.9	10.17 HUMAN	P62851	40S ribosomal protein S25
26139	dirMS_041712_NAR_30mM_plus2.8056.8056.2	2	3.32	0	2.92E+05	M441m	(R)MGLVm	(R)M/G L/V m/D/R(M)	m:Oxidized methionine	96.67	419.2004	821.401	15.9927	-2.6	5.59	77799.7	9.09 HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
26140	dirMS_041712_NAR_40mM_plus2.6499.6499.2	2	3.32	0	6.23E+04	M188m	(R)SPNGP	(R)S\P|N G P m S K(E)	m:Oxidized methionine	97.82	417.1996	817.387	16.0047	11.7	8.47	71105.4	6.94 HUMAN	F8W9S8	Lethal(3)malignant brain tumor-like protein 4
26141	dirMS_041712_NAR_40mM_plus2.6796.6796.2	2	3.32	0	1.97E+04		(K)TPGPGA	(K)T/P/G/P/G A/Q S A L R(A)		100.07	527.7842	1054.564	-0.0029	-2.7	9.41	14466.4	9.92 HUMAN	E5RH77	40S ribosomal protein S14
26142	dirMS_041712_NAR_40mM_plus2.8212.8212.2	2	3.32	0	1.93E+05		(K)SFYMQ	(K)S F/Y/M Q R(C)		108.45	416.1954	831.382	0.0017	2.1	8.46	35548.6	4.91 HUMAN	B4DN60	Asparagine--tRNA ligase, cytoplasmic
26143	dirMS_041712_NAR_50mM_plus2.13163.13163.3	3	3.32	1	1.58E+06		(K)LIADVA	(K)L I/A D/V A P S/A I R E N D I K(S)		136.75	575.6533	1724.954	-0.0088	-5.1	4.56	18388.8	6.85 HUMAN	F5H1Y3	Flap endonuclease 1 (Fragment)
26144	dirMS_041712_NAR_50mM_plus2.14331.14331.3	3	3.32	1	4.62E+05	M17m	(K)GAEEm	(K)G A|E/E/m E/T\V I P V D V/M R R(A)	m:Oxidized methionine	143.47	616.6377	1831.904	15.9945	-0.2	4.41	18080.7	7.92 HUMAN	K7ELW0	Protein DJ-1
26145	dirMS_041712_NAR_50mM_plus2.14456.14456.3	3	3.32	0	1.21E+05		(K)SPYQEF	(K)S/P Y Q E/F T\D H L V/K(T)		144.07	488.5772	1463.717	0.0005	0.4	5.3	25381.9	10.49 HUMAN	E9PQD7	40S ribosomal protein S2
26146	dirMS_041712_NAR_50mM_plus2.7210.7210.3	3	3.32	2	1.11E+05		(K)SKLSEIV	(K)S K/L S E I/V R E F K(S)		104	445.9257	1335.763	-0.0005	-0.4	8.31	117947.2	8.04 HUMAN	F6TQG2	Probable global transcription activator SNF2L1 (Fragment)
26147	dirMS_041712_NAR_60mM_plus.10632.10632.3	3	3.32	0	1.36E+06	S1540s	(R)THAPSA	(R)T/H A P S A\L/s P P/R(K)	s:N-acetylglucosamine (S)	112.93	446.2368	1133.606	203.0897	7.7	9.44	316110	9.16 HUMAN	H9KVB4	Trinucleotide repeat-containing gene 18 protein
26148	dirMS_041712_NAR_60mM_plus.15546.15546.2	2	3.32	1	4.90E+05		(K)VKEGM	(K)V K|E G M/N\I V E\A M E R(F)		137.75	753.3758	1505.745	-0.0007	-0.5	4.79	18240.4	7.96 HUMAN	P62937	Peptidyl-prolyl cis-trans isomerase A
26149	dirMS_041712_NAR_120mM_minus.17655.17655.2	2	3.31	1	2.80E+05		(R)QAGRYL	(R)Q A G R/Y L P/E F R(E)		150.83	618.8211	1236.648	-0.0135	-10.9	8.75	25655.1	5.22 HUMAN	H0Y5R6	Uroporphyrinogen decarboxylase (Fragment)
26150	dirMS_041712_NAR_120mM_minus.17782.17782.4	4	3.31	1	2.71E+05		(K)SKNILFV	(K)S K N\I L\F|V/I/T K/P\D V Y K(S)		151.3	442.0108	1765.026	-0.0045	-2.5	9.53	206102.3	9.72 HUMAN	E9PAV3	Nascent polypeptide-associated complex subunit alpha
26151	dirMS_041712_NAR_120mM_minus.5513.5513.3	3	3.31	0	2.91E+05	M46m M4	(R)HQGVm	(R)H Q G V\m|V|G m G Q/K(D)	m:Oxidized methionine	83.3	401.8604	1171.571	31.9956	4.8	8.76	32616.5	5.18 HUMAN	A6NL76	Actin, alpha skeletal muscle
26152	dirMS_041712_NAR_120mM_minus.8290.8290.4	4	3.31	1	8.15E+04	T579t M58	(R)LYSGTA	(R)L Y S G T A R Y H t\Q m L/R(V)	t:Phosphorylated T m:Oxidiz	99.17	448.9645	1696.859	95.9774	9	9.99	116661.1	7.47 HUMAN	C4PFH9	Potassium voltage-gated channel subfamily H member 2
26153	dirMS_041712_NAR_20mM_minus.13414.13414.3	3	3.31	1	9.81E+04	T1051t	(R)LVTRtD	(R)L V T R/t D G M/V A P Q S W V S R(V)	t:Phosphorylated T	185.03	661.6505	1902.985	79.9515	-7.5	9.6	166309.4	5.64 HUMAN	A6NIZ6	Putative Polycomb group protein ASXL1
26154	dirMS_041712_NAR_20mM_minus.7619.7619.3	3	3.31	0	9.90E+05	M239m	(K)EVDEQ	(K)E V D E Q/m L/N/V Q/N K(N)	m:Oxidized methionine	124.8	488.2327	1446.689	15.9942	-0.5	4.14	40069.4	4.83 HUMAN	E7EWR1	Tubulin beta chain
26155	dirMS_041712_NAR_30mM_minus2.14292.14292.2	2	3.31	0	4.31E+05		(R)RPLDPV	(R)R P|L D P/V K(V)		130.53	412.7522	824.499	-0.0017	-2.1	8.75	59001.4	5.76 HUMAN	Q6ZU67	BEN domain-containing protein 4

26156	dirMS_041712_NAR_30mM_minus2.8042.8042.2	2	3.31	0	2.04E+04		(R)TSTSQA	(R)T S/T/S/Q A V F R(L)		98.32	498.7592	996.511	0.0002	0.2	9.41	20139.7	9.34	HUMAN	C9J7S3	Aspartate--tRNA ligase, cytoplasmic (Fragment)
26157	dirMS_041712_NAR_40mM_minus2.11697.11697.3	3	3.31	1	5.36E+03	S163s	(R)LAAsVS	(R)L/A/A\s V/S G S F T L M R D E R(A)	s:Phosphorylated S	151.75	607.293	1739.874	79.99	13	6.07	50264.3	10.16	HUMAN	O60422	One cut domain family member 3
26158	dirMS_041712_NAR_40mM_minus2.12842.12842.3	3	3.31	1	2.01E+05		(K)DVLFLK	(K)D V/L/F L K D/C V/G P E V E K(A)	C:Carbamidomethylation	158.43	583.3021	1747.893	-0.0018	-1	4.32	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
26159	dirMS_041712_NAR_50mM_minus2.10615.10615.3	3	3.31	1	2.79E+05	K761k	(R)KTHSSP	(R)K T/H S/S P A L S Q G H V T G S/k(T)	k:Ubiquitin-K	128.3	612.6486	1721.893	114.0383	-2.5	10	85343.5	5.05	HUMAN	Q9BQI7	PH and SEC7 domain-containing protein 2
26160	dirMS_041712_NAR_50mM_minus2.15698.15698.3	3	3.31	0	3.40E+05		(K)LYGPTNI	(K)L Y/G P/T N F/S/P I I N H V A R(F)		158.15	600.3221	1798.96	-0.0081	-4.5	8.75	60985.3	5.6	HUMAN	O75131	Copine-3
26161	dirMS_041712_NAR_50mM_minus2.8193.8193.3	3	3.31	1	2.09E+05		(K)GILAAD	(K)G I L A/A/D E S T G S I A K\R(L)		114.5	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
26162	dirMS_041712_NAR_60mM_minus.13726.13726.3	3	3.31	1	7.02E+04		(R)ALEEALE	(R)A L|E/E/A L/E A K E/E F E R(Q)		136.33	555.2761	1663.817	-0.0036	-2.2	4.2	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
26163	dirMS_041712_NAR_60mM_minus.18077.18077.3	3	3.31	1	1.38E+05		(K)TVTAM	(K)T V T A M D/V/V|Y A L K/R(Q)		161.93	489.6057	1466.804	-0.001	-0.7	8.25	11367.1	11.36	HUMAN	P62805	Histone H4
26164	dirMS_041712_NAR_60mM_minus.8756.8756.3	3	3.31	1	2.25E+05	S167s	(R)QNEGSK	(R)Q N E G S/K T s E E A L/V T V Q R(L)	s:Phosphorylated S	109.53	652.6318	1875.941	79.9402	-13.4	4.79	67432.6	7.9	HUMAN	E7EUY8	WD repeat-containing protein 20
26165	dirMS_041712_NAR_60mM_minus.9310.9310.3	3	3.31	1	2.96E+05	T410t	(R)tWRSVP	(R)t W/R S/V/P E K(K)	t:N-acetylglucosamine (T)	111.73	402.5435	1002.537	203.0792	-0.1	8.41	79464.8	5.81	HUMAN	E9PHA1	Neuroendocrine convertase 1
26166	dirMS_041712_NAR_120mM_plus.14582.14582.4	4	3.31	2	8.39E+05		(R)YLYTLVI	(R)Y L Y/T L V I/T D K/E K A E K(L)		130.45	454.2533	1813.995	-0.0032	-1.8	6.18	7621.9	10.1	HUMAN	J3KT73	60S ribosomal protein L38
26167	dirMS_041712_NAR_120mM_plus.14713.14713.3	3	3.31	1	9.61E+05		(K)LDKSQI	(K)L D K S Q I H D\I|V\L|V/G G S T R(I)		130.72	613.3369	1838.013	-0.0169	-9.2	6.75	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
26168	dirMS_041712_NAR_120mM_plus.5854.5854.3	3	3.31	1	1.17E+05	T1075t	(R)NADSRt	(R)N/A/D S R t E F G/K(Y)	t:Phosphorylated T	83.63	402.1676	1124.533	79.9552	-9.3	6.07	169823.9	7.73	HUMAN	Q8IVE3	Pleckstrin homology domain-containing family H member 2
26169	dirMS_041712_NAR_120mM_plus.5996.5996.3	3	3.31	0	7.67E+04		(K)LLHSEN	(K)L/L H S\E N/Y V T K(R)		84.85	401.882	1203.637	-0.0054	-4.5	6.75	40039.4	6.43	HUMAN	Q9Y376	Calcium-binding protein 39
26170	dirMS_041712_NAR_120mM_plus.8769.8769.2	2	3.31	0	1.70E+05		(K)HTGPNS	(K)H/T G/P N S|P D T A N D/G F V R(L)		99.13	842.8861	1684.767	-0.0025	-1.5	5.21	18511.8	5.62	HUMAN	D6R9T0	Heterogeneous nuclear ribonucleoprotein H (Fragment)
26171	dirMS_041712_NAR_20mM_plus.10564.10564.2	2	3.31	1	5.17E+04	M24m	(R)LVRLmQ	(R)L V|R\L m Q D K(E)	m:Oxidized methionine	145.8	509.8006	1002.577	16.0175	22.1	8.75	8592.6	4.7	HUMAN	H0YHP5	PRKC apoptosis WT1 regulator protein (Fragment)
26172	dirMS_041712_NAR_20mM_plus.13206.13206.2	2	3.31	0	2.66E+05		(K)LSELEAA	(K)L S\E|L/E A/A/L Q R(A)		162.38	565.3132	1129.621	-0.002	-1.8	4.53	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
26173	dirMS_041712_NAR_20mM_plus.13753.13753.2	2	3.31	0	1.30E+05	K559k	(K)EAVGLk	(K)E A V G L k S/T Q N/K(G)	k:Ubiquitin-K	166.72	644.8389	1174.643	114.0279	-11.7	8.69	68941.1	8.81	HUMAN	E9PGU5	Microcephalin
26174	dirMS_041712_NAR_20mM_plus.13790.13790.2	2	3.31	2	8.08E+04		(K)IERVGK	(K)I/E R/V G K/H G K(V)		167	512.3005	1023.606	-0.0121	-11.8	9.99	205145.1	5.89	HUMAN	Q16363	Laminin subunit alpha-4
26175	dirMS_041712_NAR_20mM_plus.16291.16291.3	3	3.31	1	1.47E+05	M1m T7t	(-)mATVTA	(-)m A T V T A t/T\K V P/E I R(D)	m:Oxidized methionine t:Pho	183.38	538.6101	1517.836	95.9802	11.7	8.5	51326.8	5.49	HUMAN	Q9Y230	RuvB-like 2
26176	dirMS_041712_NAR_20mM_plus.18563.18563.2	2	3.31	2	6.09E+04		(R)DSLSEKL	(R)D S/L/S E K L K S/K(Q)		199.4	567.8286	1134.637	0.0134	11.8	8.5	12088.6	9.74	HUMAN	Q86TU6	Putative uncharacterized protein encoded by LINC00523
26177	dirMS_041712_NAR_20mM_plus.7378.7378.2	2	3.31	0	2.44E+05		(R)TVGIVGI	(R)T V/G\I|V G N Q P K(V)		119.85	506.7922	1012.579	-0.0014	-1.4	8.41	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
26178	dirMS_041712_NAR_30mM_plus2.21339.21339.2	2	3.31	0	3.13E+05		(K)FDGILG	(K)F D\G\I|L/G M/A Y P R(I)		167.3	620.3199	1239.619	0.0135	10.9	5.83	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
26179	dirMS_041712_NAR_30mM_plus2.4713.4713.2	2	3.31	0	1.71E+05		(K)NCSETQ	(K)N C|S E T/Q/Y E S K(V)	C:Carbamidomethylation	75.8	623.256	1245.505	-0.0005	-0.4	4.53	28473.3	4.8	HUMAN	P61981	14-3-3 protein gamma
26180	dirMS_041712_NAR_40mM_plus2.12584.12584.3	3	3.31	1	1.28E+05		(K)LLQSIGC	(K)L L|Q S|I/G Q A P E S/I S E K E L K(L)		141.22	657.359	1970.08	-0.018	-9.1	4.79	60972	5.25	HUMAN	A6NCK0	NEDD8-activating enzyme E1 regulatory subunit
26181	dirMS_041712_NAR_40mM_plus2.16024.16024.3	3	3.31	1	8.11E+04		(K)VSLQEN	(K)V/S/L Q E N F P/D A S K P P K/K(R)		160.07	595.6489	1784.954	-0.022	-12.3	8.47	77561	8.85	HUMAN	Q6ZW33	MICAL C-terminal-like protein
26182	dirMS_041712_NAR_40mM_plus2.20011.20011.3	3	3.31	1	5.40E+05		(K)EGGLGP	(K)E G G L/G P L N I/P L L A D V T R R(L)		189.73	631.0288	1891.076	-0.0041	-2.2	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
26183	dirMS_041712_NAR_40mM_plus2.6394.6394.2	2	3.31	0	1.12E+04		(R)GGSEVE	(R)G G/S E V E/G G R(T)		96.92	424.1929	847.39	-0.0119	-14.1	4.53	164028.5	9.06	HUMAN	B7ZLX3	CLASP1 protein
26184	dirMS_041712_NAR_40mM_plus2.8135.8135.2	2	3.31	0	1.79E+04		(R)MGYMD	(R)M/G Y M/D/P/R(E)		108.18	435.1865	869.364	0.0013	1.5	5.59	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
26185	dirMS_041712_NAR_50mM_plus2.12137.12137.3	3	3.31	2	7.58E+05		(R)DARDW	(R)D/A/R D W L M K T E T/R(L)		131.25	507.9234	1521.748	0.0078	5.1	6.12	277072.9	6.23	HUMAN	B7WP88	TPR and ankyrin repeat-containing protein 1
26186	dirMS_041712_NAR_50mM_plus2.12722.12722.3	3	3.31	0	2.81E+05		(K)EMNPAL	(K)E M N/P/A L/G I D C L H K(G)	C:Carbamidomethylation	135.3	499.9106	1497.719	-0.0016	-1.1	5.32	49982	5.86	HUMAN	B4DYD8	T-complex protein 1 subunit epsilon
26187	dirMS_041712_NAR_50mM_plus2.12960.12960.3	3	3.31	0	5.78E+05		(R)ANTVQE	(R)A N/T/V Q E A T F Q M E L P K(K)		135.67	569.6265	1706.842	0.0231	13.6	4.53	104107.3	6.43	HUMAN	B7ZKJ8	35 kDa inter-alpha-trypsin inhibitor heavy chain H4
26188	dirMS_041712_NAR_50mM_plus2.13511.13511.3	3	3.31	0	6.34E+05	S5s	(-)XEHVsG	(-)X E H V s G G E/L F/D Y L V K(K)	s:N-acetylglucosamine (S)	139.28	636.9936	1705.88	203.0867	3.8	4.65	19561.2	6.73	HUMAN	H0YCS6	Serine/threonine-protein kinase BRSK2 (Fragment)
26189	dirMS_041712_NAR_50mM_plus2.8858.8858.3	3	3.31	1	8.79E+04	T44t	(R)tKSFLFV	(R)t/K S F L F V G C G/E T L R(D)	C:Carbamidomethylation t:Phosp	113.5	565.6079	1614.831	79.9783	7.1	8.41	20058.2	5.02	HUMAN	B4DY02	Protein FAM118A
26190	dirMS_041712_NAR_60mM_plus.13113.13113.3	3	3.31	0	7.59E+05	M1m	(-)mVNHFI	(-)m V N H F\I/A E/F K(R)	m:Oxidized methionine	125.68	417.8778	1235.624	15.9947	-0.2	6.5	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
26191	dirMS_041712_NAR_60mM_plus.16484.16484.3	3	3.31	0	7.03E+05		(K)SPYQEF	(K)S P/Y/Q E F T D/H L V K(T)		142.73	488.5776	1463.717	0.0017	1.2	5.3	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
26192	dirMS_041712_NAR_60mM_plus.17619.17619.3	3	3.31	0	2.39E+04	S226s	(R)LISQIVS	(R)L I S Q I V S S/I T A s L R(F)	s:Phosphorylated S	150.18	523.2911	1487.879	79.9796	8.4	9.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
26193	dirMS_041712_NAR_60mM_plus.17765.17765.3	3	3.31	0	2.98E+05	N140n	(K)LnFEQQ	(K)L n F E Q/Q P D/S R(E)	n:N-acetylglucosamine (N)	150.12	479.5642	1233.586	203.0922	8.9	4.37	52068.2	9.62	HUMAN	Q5QPV1	Recombining binding protein suppressor of hairless (Drosophila)-like
26194	dirMS_041712_NAR_60mM_plus.19424.19424.3	3	3.31	1	1.69E+04		(K)RSIQFV	(K)R S I Q F\V/D/W C P T/G F K(V)	C:Carbamidomethylation	159.92	580.9558	1740.853	0.0002	0.1	8.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
26195	dirMS_041712_NAR_60mM_plus.9208.9208.3	3	3.31	1	1.44E+05	N295n	(R)nTEVKS	(R)n/T E V K S A L R(H)	n:N-acetylglucosamine (N)	106.87	407.5532	1017.569	203.0763	-2.5	8.75	36002.9	7.2	HUMAN	Q8N628	Olfactory receptor 2C3
26196	dirMS_041712_NAR_120mM_minus.20565.20565.4	4	3.3	1	2.59E+04	T399t	(K)LKFMW	(K)L K F M W G/N L t L A S T/E/K(K)	t:N-acetylglucosamine (T)	169.28	486.2587	1738.92	203.0933	7.2	8.59	94031.2	4.9	HUMAN	B7Z5R6	Next to BRCA1 gene 1 protein
26197	dirMS_041712_NAR_120mM_minus.9594.9594.3	3	3.3	0	1.68E+04		(K)EDTGW	(K)E/D T G W/Y W C G I Q/R(D)	C:Carbamidomethylation	106.63	524.2361	1570.674	0.0194	12.4	4.37	13056.6	8.3	HUMAN	H0Y6K0	Adenosine receptor A3 (Fragment)
26198	dirMS_041712_NAR_20mM_minus.10524.10524.2	2	3.3	0	3.08E+04	M234m	(K)mVVESA	(K)m V/V/E/S A Y E V I K(L)	m:Oxidized methionine	153.82	642.3318	1267.66	15.9961	0.9	4.53	36923.1	5.71	HUMAN	P07195	L-lactate dehydrogenase B chain
26199	dirMS_041712_NAR_20mM_minus.11807.11807.2	2	3.3	1	9.14E+04		(R)LAELYVE	(R)L A E/L/Y/V E R A K(W)		167.07	596.3389	1191.673	-0.0027	-2.2	6.14	304955.6	7.24	HUMAN	Q13535	Serine/threonine-protein kinase ATR
26200	dirMS_041712_NAR_20mM_minus.11941.11941.3	3	3.3	1	2.69E+05	T83t	(K)DSKtEAS	(K)D S K t E A/S\G N I A I R(K)	t:N-acetylglucosamine (T)	167.37	522.2561	1361.702	203.0518	-17.6	6.07	174370.4	5.58	HUMAN	A4FU69	EF-hand calcium-binding domain-containing protein 5
26201	dirMS_041712_NAR_20mM_minus.7105.7105.2	2	3.3	0	1.67E+05		(R)AAQVA	(R)A A Q\V|A Q/D E E I A R(L)		118.8	650.8255	1300.649	-0.0054	-4.2	4.14	35935.5	6.2	HUMAN	Q8IVM0	Coiled-coil domain-containing protein 50
26202	dirMS_041712_NAR_20mM_minus.8661.8661.2	2	3.3	0	2.27E+04		(K)TIAPALV	(K)T I|A/P A L V S K(K)		136.12	450.2808	899.556	-0.0017	-1.9	8.41	21077	9.05	HUMAN	K7EM90	Alpha-enolase (Fragment)
26203	dirMS_041712_NAR_20mM_minus.8938.8938.2	2	3.3	0	2.78E+05		(R)ALGQN	(R)A L G Q|N|P T N\A E V|L K(V)		138.8	677.871	1354.733	0.0022	1.6	6.05	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
26204	dirMS_041712_NAR_30mM_minus2.17004.17004.2	2	3.3	0	4.44E+04		(K)LGINSLC	(K)L/G I/N S L\Q E/L\K(Q)		146.95	557.8242	1114.647	-0.0055	-5	6	25978.5	4.91	HUMAN	C9J502	Prostate leucine zipper variant 2
26205	dirMS_041712_NAR_30mM_minus2.18042.18042.2	2	3.3	0	2.92E+04		(K)LLEAQT	(K)L L/E A/Q T P S V R(K)		153.3	557.3216	1113.626	0.0097	8.7	6	28486.2	5.45	HUMAN	H3BRD6	Zinc finger protein 821 (Fragment)
26206	dirMS_041712_NAR_40mM_minus2.9476.9476.3	3	3.3	0	7.38E+04	M123m	(K)mMCES	(K)m M/C E S F I Y N Q T L\M/K(K)	C:Carbamidomethylation m:Oxid	138.18	604.6007	1795.789	15.999	2.2	5.75	60938	8.62	HUMAN	Q6UWM9	UDP-glucuronosyltransferase 2A3
26207	dirMS_041712_NAR_50mM_minus2.10787.10787.3	3	3.3	1	7.44E+03		(K)VAVVAG	(K)V A\V\V/A/G Y G D V G K G C A Q A L R(G)	C:Carbamidomethylation	129.78	630.9952	1890.985	-0.0144	-7.6	8.56	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
26208	dirMS_041712_NAR_50mM_minus2.11564.11564.3	3	3.3	1	1.67E+05		(K)SNQSYP	(K)S N Q S Y P T/P V T V E K D R(I)		134.2	574.2947	1720.85	0.0195	11.3	5.79	62286.2	5.54	HUMAN	B4DWG0	RCC1 and BTB domain-containing protein 2
26209	dirMS_041712_NAR_50mM_minus2.13039.13039.2	2	3.3	2	9.81E+04	N228n	(K)AQEYIR	(K)A Q/E Y/I/R Q K n K(G)	n:N-acetylglucosamine (N)	141.77	740.8864	1277.696	203.0695	-6.7	9.7	210066.3	9.23	HUMAN	Q14690	Protein RRP5 homolog
26210	dirMS_041712_NAR_50mM_minus2.13436.13436.3	3	3.3	1	2.32E+05		(K)LKSEFNE	(K)L K S E F N E P G T G I S H/R(Y)		144.85	557.9594	1671.845	0.0187	11.2	6.76	42179.1	4.56	HUMAN	E9PAZ2	H/ACA ribonucleoprotein complex non-core subunit NAF1
26211	dirMS_041712_NAR_50mM_minus2.16663.16663.3	3	3.3	0	1.06E+05	K356k	(K)NSSPPS	(K)N S/S/P P S S D k T I I A P K(V)	k:Ubiquitin-K	162.72	552.6273	1541.817	114.0504	4.5	8.59	136309.7	7.82	HUMAN	Q9NS40	Potassium voltage-gated channel subfamily H member 7
26212	dirMS_041712_NAR_50mM_minus2.18166.18166.3	3	3.3	1	2.19E+05		(K)LFKVSVF	(K)L F K\V S V P/H V L E M R(K)		171.98	518.9598	1554.882	-0.0176	-11.3	8.76	97088.9	6.62	HUMAN	H7C4E1	Uncharacterized protein C1orf222 (Fragment)
26213	dirMS_041712_NAR_60mM_minus.20096.20096.3	3	3.3	0	4.05E+05		(K)GHYTEG	(K)G H Y T E G A E\L|V/D S/V/L D V V R(K)		184.27	653.6647	1958.982	-0.0022	-1.1	4.31	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
26214	dirMS_041712_NAR_60mM_minus.5515.5515.3	3	3.3	1	3.85E+04		(K)SVQATT	(K)S V|Q/A T T E N K E/L K(T)		86.93	449.9037	1347.711	-0.0149	-11	5.86	36157.9	8.65	HUMAN	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial
26215	dirMS_041712_NAR_120mM_plus.12029.12029.4	4	3.3	0	3.20E+05		(K)TGTIVVE	(K)T G\T I V/V E/G H E L/H/D E D I R(L)		116.78	480.743	1919.946	0.0044	2.3	4.49	132902.3	5.82	HUMAN	J3KR24	Isoleucine--tRNA ligase, cytoplasmic
26216	dirMS_041712_NAR_120mM_plus.14923.14923.2	2	3.3	1	7.07E+05		(R)KFLDGIY	(R)K|F/L/D/G I Y V S\E K(G)		131.45	649.8522	1298.699	-0.002	-1.5	6.07	20931.1	10.28	HUMAN	D6RAN4	60S ribosomal protein L9 (Fragment)
26217	dirMS_041712_NAR_120mM_plus.7991.7991.2	2	3.3	0	2.65E+05		(K)FHSQLM	(K)F/H|S\Q/L M/R(L)		95.63	459.7341	918.461	-0.0005	-0.6	9.75	10225.7	7.97	HUMAN	P49458	Signal recognition particle 9 kDa protein
26218	dirMS_041712_NAR_20mM_plus.15978.15978.3	3	3.3	0	2.44E+04	K86k	(K)EYDAFIE	(K)E Y D A F/I E/T/I k/K(D)	k:Ubiquitin-K	180.73	490.9251	1356.705	114.0562	9	4.68	68275.5	6.09	HUMAN	Q8NHS4	Clathrin heavy chain linker domain-containing protein 1
26219	dirMS_041712_NAR_30mM_plus2.12357.12357.2	2	3.3	0	7.36E+05		(K)IVNYTVF	(K)I V N/Y T V/R(F)		117.3	432.7483	864.494	-0.0045	-5.2	8.75	135519.6	5.81	HUMAN	Q8TDY8	Immunoglobulin superfamily DCC subclass member 4
26220	dirMS_041712_NAR_30mM_plus2.22431.22431.2	2	3.3	0	1.74E+06		(R)VIFGLFG	(R)V I/F G L/F G K(T)		172.6	440.7682	880.529	0	0	8.72	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
26221	dirMS_041712_NAR_30mM_plus2.5487.5487.3	3	3.3	0	2.01E+05		(R)NQGGY	(R)N\Q\G G Y G G S\S S S|S/S Y/G/S G R(R)		83.03	565.5708	1694.7	-0.0022	-1.3	8.59	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
26222	dirMS_041712_NAR_40mM_plus2.8881.8881.2	2	3.3	0	1.06E+05		(K)TEWLDG	(K)T E|W/L D G K(H)		114.47	424.7133	848.415	0.0045	5.3	4.37	18393.6	9.55	HUMAN	A2BFH1	Peptidyl-prolyl cis-trans isomerase A-like 4G
26223	dirMS_041712_NAR_50mM_plus2.18249.18249.2	2	3.3	0	5.46E+05		(R)IHFPLAT	(R)I H/F|P L A T Y A\P V/I S A E K(A)		164.65	878.9842	1756.963	-0.0021	-1.2	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
26224	dirMS_041712_NAR_50mM_plus2.20800.20800.3	3	3.3	1	1.16E+05		(K)SVLTGGI	(K)S V|L/T G G L D A L E F I/G K K(T)		177.8	549.9834	1647.932	0.004	2.5	5.79	40220	4.95	HUMAN	Q6MZV4	Protein NOXP20
26225	dirMS_041712_NAR_60mM_plus.16172.16172.3	3	3.3	0	3.32E+05		(K)SLFEILILI	(K)S L F E I L I/L/M/G\K(Q)		141.55	421.9146	1263.738	-0.0089	-7	5.72	88843.5	5.58	HUMAN	O43422	52 kDa repressor of the inhibitor of the protein kinase
26226	dirMS_041712_NAR_60mM_plus.17813.17813.3	3	3.3	1	1.98E+05		(K)LALDIEI	(K)L/A|L/D/I E I A T Y\R K(L)		150.42	469.2709	1405.805	-0.0068	-4.8	6.07	49564	5.84	HUMAN	E9PAX3	Glial fibrillary acidic protein
26227	dirMS_041712_NAR_60mM_plus.19051.19051.3	3	3.3	1	1.08E+04		(-)MVAAG	(-)M V A A G/G G A R T E/G|A V R(R)		158.65	468.2401	1402.722	-0.0162	-11.6	9.35	19516.1	10.48	HUMAN	B4DJI5	HESB like domain containing 2, isoform CRA_b
26228	dirMS_041712_NAR_60mM_plus.19255.19255.3	3	3.3	1	1.85E+05		(R)AGEAGK	(R)A/G E A G K L E E/V|M/Q E L R(A)		159.03	553.9525	1659.837	0.0059	3.6	4.49	54918.3	5.61	HUMAN	Q9BR76	Coronin-1B
26229	dirMS_041712_NAR_60mM_plus.19542.19542.3	3	3.3	1	1.40E+05	M304m K3	(K)EmSLHE	(K)E m S L/H E/K A S/T P V L k(S)	m:Oxidized methionine k:Ub	160.6	567.2946	1569.831	130.0387	0.5	6.85	84112.2	6.8	HUMAN	Q04724	Transducin-like enhancer protein 1
26230	dirMS_041712_NAR_60mM_plus.19792.19792.3	3	3.3	1	1.05E+05		(K)ITLEAVL	(K)I T\L E A V L/N T/T C K K(C)	C:Carbamidomethylation	163.78	497.6187	1490.825	0.0169	11.3	8.59	27151.6	9.94	HUMAN	B4DY38	Nucleolar protein of 40 kDa
26231	dirMS_041712_NAR_60mM_plus.4583.4583.3	3	3.3	0	4.62E+05	S248s	(R)AQGsER	(R)A Q/G s E R P E/L G/R(S)	s:Phosphorylated S	76.23	427.2032	1199.613	79.9823	12.5	6.19	39904.6	11.42	HUMAN	C9JTQ0	Ankyrin repeat domain-containing protein 63
26232	dirMS_041712_NAR_60mM_plus.4811.4811.3	3	3.3	0	1.81E+05		(R)SSVSED	(R)S S|V S/E D D S H L\K(V)		79.18	401.8586	1203.549	0.0125	10.4	4.53	41977.7	6.73	HUMAN	E9PE01	Unconventional myosin-Vc
26233	dirMS_041712_NAR_60mM_plus.8854.8854.2	2	3.3	1	1.54E+04		(K)AFEAVD	(K)A F|E/A V D/K/A Y K(L)		105.83	571.2965	1141.589	-0.0031	-2.7	6.11	29841.1	9.04	HUMAN	O75937	DnaJ homolog subfamily C member 8
26234	dirMS_041712_NAR_120mM_minus.20084.20084.4	4	3.29	0	3.79E+05		(K)LAFPSPF	(K)L A F P/S/P F/G H L S E G F S H S R(W)		166	493.9968	1972.966	-0.0011	-0.5	6.92	16196.2	9.92	HUMAN	C9JRJ8	Sequestosome-1 (Fragment)
26235	dirMS_041712_NAR_120mM_minus.9330.9330.4	4	3.29	1	8.23E+04	N112n M1	(K)LKEIYEn	(K)L K E I Y/E n m A P G E N K(R)	n:N-acetylglucosamine (N) m	105.18	464.4735	1635.805	219.0675	-3.7	4.79	24799.7	5.16	HUMAN	C9JPC0	26S proteasome non-ATPase regulatory subunit 2 (Fragment)
26236	dirMS_041712_NAR_20mM_minus.10368.10480.2	2	3.29	1	2.17E+05	T362t	(R)SENSES	(R)S E N S/E S Q L t/S K S K(C)	t:Phosphorylated T	152.92	752.8365	1424.686	79.9794	8.7	5.86	47152.3	9.23	HUMAN	B4DZU0	Serine/threonine-protein kinase Nek2
26237	dirMS_041712_NAR_20mM_minus.13312.13312.2	2	3.29	0	4.98E+05		(K)DAGTIA	(K)D A G\T I/A G/L/N V L R(I)		184.62	600.3403	1199.674	-0.0009	-0.8	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
26238	dirMS_041712_NAR_30mM_minus2.13054.13054.2	2	3.29	0	3.55E+05		(R)EGIAFRF	(R)E G I/A F R/P A S K(T)		124.82	538.2931	1075.59	-0.0105	-9.8	8.85	108900.4	4.86	HUMAN	P32926	Desmoglein-3
26239	dirMS_041712_NAR_30mM_minus2.15488.15488.2	2	3.29	0	3.74E+05		(-)XGGITM	(-)X G G|I/T M A A R(M)		137	445.2523	889.492	0.0049	5.5	9.75	20283.9	9.18	HUMAN	H3BMS6	Sulfide:quinone oxidoreductase, mitochondrial (Fragment)
26240	dirMS_041712_NAR_40mM_minus2.15637.15637.3	3	3.29	1	3.98E+05	M145m	(R)GVmLA	(R)G V m/L/A\V D A/V I A E L K K(Q)	m:Oxidized methionine	181.67	524.9715	1556.908	15.9919	-1.9	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
26241	dirMS_041712_NAR_40mM_minus2.6311.6311.2	2	3.29	0	1.70E+05		(R)AQYDEL	(R)A Q|Y D/E L A R(K)		103.23	483.2366	965.469	-0.0028	-2.9	4.37	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
26242	dirMS_041712_NAR_50mM_minus2.11755.11755.3	3	3.29	0	1.75E+05		(K)LEDILESI	(K)L E\D I/L\E S I N/S I/K(S)		134.5	458.5927	1373.752	0.0113	8.2	4.14	26118.5	4.71	HUMAN	Q9Y3A6	Transmembrane emp24 domain-containing protein 5
26243	dirMS_041712_NAR_50mM_minus2.12573.12573.3	3	3.29	0	3.07E+04		(R)LATIANF	(R)L A\T I A N F/S A/L G L E P G R(D)		138.78	543.9658	1629.896	-0.013	-8	6	16079.9	5.3	HUMAN	F8WCC9	Solute carrier family 22 member 5
26244	dirMS_041712_NAR_50mM_minus2.15680.15680.3	3	3.29	1	1.17E+05	K51k	(R)ANLEISY	(R)A N L E I S Y A K/G L Q k\L A S K(L)	k:Ubiquitin-K	157.75	650.0294	1834.043	114.0304	-6.4	9.53	65188.3	9.39	HUMAN	I3L3C8	Uncharacterized protein
26245	dirMS_041712_NAR_50mM_minus2.16367.16367.3	3	3.29	1	5.41E+04		(K)SELVAM	(K)S E/L/V/A M L/E E E E L/R K(A)		161.32	559.2917	1675.857	0.0034	2	4.32	18679.2	5.61	HUMAN	B4DWW1	ADP-ribosylation factor-like protein 1
26246	dirMS_041712_NAR_50mM_minus2.5882.5882.3	3	3.29	0	5.83E+03	M224m	(K)TVQQH	(K)T V Q Q H A G E\T/D/P V T T m R(A)	m:Oxidized methionine	95.62	596.2904	1770.844	16.0127	10	5.29	26760.1	8.93	HUMAN	H3BPK3	Hydroxyacylglutathione hydrolase, mitochondrial (Fragment)
26247	dirMS_041712_NAR_50mM_minus2.9094.9094.3	3	3.29	0	1.28E+05		(K)LPATEKF	(K)L P/A T E/K/P/V L L/S K(D)		120.3	432.6022	1295.793	-0.0013	-1	8.59	105005	5.57	HUMAN	E9PL22	Hypoxia up-regulated protein 1
26248	dirMS_041712_NAR_50mM_minus2.9840.9840.3	3	3.29	1	8.48E+04		(R)ALRETLF	(R)A L R E T L/P A|E/Q D L T T K(N)		124.33	562.6354	1685.907	-0.0152	-9	4.68	26790	6.25	HUMAN	F5GX11	Proteasome subunit alpha type-1
26249	dirMS_041712_NAR_60mM_minus.11364.11364.3	3	3.29	1	1.35E+05		(R)MGIVGP	(R)M G\I V G P E F/K D/K(L)		123.85	407.5515	1220.634	0.0056	4.6	5.82	533778	5.74	HUMAN	Q15149	Plectin
26250	dirMS_041712_NAR_60mM_minus.15332.15332.3	3	3.29	0	1.17E+05		(R)QIFHPE	(R)Q I F H/P E\Q L I T G/K(E)		145.13	470.9285	1410.774	-0.003	-2.1	6.75	27836	8	HUMAN	Q9H853	Putative tubulin-like protein alpha-4B
26251	dirMS_041712_NAR_60mM_minus.5357.5357.3	3	3.29	0	1.69E+04	M110m	(K)LmELHG	(K)L/m/E L H\G/E G S S S G K(A)	m:Oxidized methionine	85.5	449.8802	1331.626	16.0001	3.8	5.4	16650	9.47	HUMAN	D6R9B6	40S ribosomal protein S3a
26252	dirMS_041712_NAR_60mM_minus.7549.7549.3	3	3.29	0	1.58E+05		(R)AAHSEG	(R)A A H S E G N T T/A/G\L D/M R(E)		101.22	510.9003	1530.697	-0.0102	-6.7	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
26253	dirMS_041712_NAR_120mM_plus.7356.7356.3	3	3.29	0	4.31E+05		(K)SWAGP	(K)S/W A G P G V/G C G G D G A R(G)	C:Carbamidomethylation	91.53	468.5449	1403.612	0.0081	5.8	5.55	18905.2	6.43	HUMAN	E9PAM5	Uncharacterized protein C11orf21
26254	dirMS_041712_NAR_20mM_plus.13038.13038.2	2	3.29	0	2.33E+04		(K)AVDSLV	(K)A V\D/S L\V|P I G R(G)		162.43	513.8007	1026.594	-0.0001	-0.1	5.88	48851.3	9.2	HUMAN	K7EK63	ATP synthase subunit alpha, mitochondrial
26255	dirMS_041712_NAR_20mM_plus.17280.17280.3	3	3.29	0	1.30E+05		(R)TTVPQLI	(R)T T V P Q\L\L\A/S V Q/R(W)		190.9	438.2581	1312.758	0.0014	1.1	9.41	266161	5.68	HUMAN	E9PPU0	Epiplakin
26256	dirMS_041712_NAR_20mM_plus.6682.6682.2	2	3.29	1	2.51E+04	M84m	(R)GVEEEEI	(R)G V E E|E|E E D/G E/m R E(-)	m:Oxidized methionine	110.62	777.2997	1537.596	15.9963	0.9	3.88	9782.1	4.7	HUMAN	P62306	Small nuclear ribonucleoprotein F
26257	dirMS_041712_NAR_50mM_plus2.11249.11249.3	3	3.29	1	3.14E+05		(R)DLDRIA	(R)D L D R I A|G\Q\V/A A A N K(K)		126.77	481.2661	1441.776	0.008	5.5	5.96	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
26258	dirMS_041712_NAR_50mM_plus2.15317.15317.3	3	3.29	0	7.60E+04		(R)QVLIASH	(R)Q V L\I/A S H\L/P S Y E L R(H)		148.3	542.6394	1625.901	0.0027	1.6	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
26259	dirMS_041712_NAR_50mM_plus2.15529.15529.3	3	3.29	1	5.41E+04		(R)GLNGGI	(R)G L/N/G/G I T/P L N S I S P L K K(N)		149.72	570.3327	1708.996	-0.012	-7.1	10	77923	6.41	HUMAN	B7ZLQ8	CPEB4 protein
26260	dirMS_041712_NAR_50mM_plus2.15612.15612.3	3	3.29	1	9.39E+05		(K)EAFSLFD	(K)E/A F S/L/F D K D G D G T I T/T K(E)		150.05	615.6348	1844.891	-0.0014	-0.8	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
26261	dirMS_041712_NAR_50mM_plus2.19553.19553.3	3	3.29	1	1.01E+05	M2101m K	(K)LQVHGA	(K)L Q V H/G A D H S/R T/S L m G k(S)	m:Oxidized methionine k:Ub	170.93	622.9846	1736.886	130.0532	8.2	8.76	319651.2	6.66	HUMAN	Q8TDX9	Polycystic kidney disease protein 1-like 1
26262	dirMS_041712_NAR_50mM_plus2.9611.9611.3	3	3.29	2	1.35E+05	N41n	(R)GRAnGL	(R)G R/A/n G L/D A P R A G A D R(G)	n:N-acetylglucosamine (N)	117.42	567.2893	1496.768	203.0857	3.7	9.51	125717	8.95	HUMAN	P36956-4	Isoform 4 of Sterol regulatory element-binding protein 1
26263	dirMS_041712_NAR_60mM_plus.18175.18175.3	3	3.29	0	1.66E+05		(R)QQVVA	(R)Q Q V/V/A A G T L/S P P G P E E A K(R)		152.23	593.6541	1778.928	0.0194	10.9	4.53	103230.2	9.17	HUMAN	P27987	Inositol-trisphosphate 3-kinase B
26264	dirMS_041712_NAR_60mM_plus.18796.18796.3	3	3.29	0	2.26E+04		(R)FLGVTQ	(R)F L/G V T\Q F S P T H A/R(K)		155.6	487.5963	1460.765	0.0099	6.8	9.75	22488.3	8.11	HUMAN	H0YHU0	Thyrotropin-releasing hormone-degrading ectoenzyme (Fragment)

26265	dirMS_041712_NAR_60mM_plus.19418.19418.3	3	3.29	0	6.28E+05		(K)VSHLLGI	(K)V S H L L\G\I\N\V|T/D F T R(G)		159.83	524.6233	1571.854	0.0013	0.8	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
26266	dirMS_041712_NAR_60mM_plus.19761.19761.3	3	3.29	0	1.53E+05	N556n	(R)nFPFYIT	(R)n F P F Y/I/T Y I R(A)	n:N-acetylglucosamine (N)	163.87	512.9411	1333.694	203.1148	23.1	8.59	115965.7	9.46	HUMAN	P10266	HERV-K_5q33.3 provirus ancestral Pol protein
26267	dirMS_041712_NAR_60mM_plus.8084.8084.3	3	3.29	0	1.32E+06		(R)LHQNVH	(R)L H Q N V H V G E K/P(-)		100.92	419.894	1257.67	-0.0024	-1.9	6.92	84960.2	9.74	HUMAN	Q9NZL3	Zinc finger protein 224
26268	dirMS_041712_NAR_60mM_plus.9103.9103.3	3	3.29	1	6.73E+05		(R)IVDLIKG	(R)I V D L I/K/G H H/H S K(E)		104.92	461.9268	1383.786	-0.0197	-14.2	8.61	28130.3	6.25	HUMAN	A8MPT4	Glutathione S-transferase theta-4
26269	dirMS_041712_NAR_120mM_minus.13111.13111.4	4	3.28	1	2.46E+05		(R)LASALA	(R)L A S A L\A/P S I Y E H E D I K K(G)		125.45	472.0044	1885.007	-0.0108	-5.7	5.45	31803.9	8.87	HUMAN	E5RG31	DNA replication licensing factor MCM4 (Fragment)
26270	dirMS_041712_NAR_120mM_minus.13156.13156.4	4	3.28	2	4.73E+05	K160k	(K)NAKEEIN	(K)N A K E E I N V L/H/G R L E k(L)	k:Ubiquitin-K	126.33	466.7525	1749.961	114.0276	-8.2	6.76	50855.3	7.14	HUMAN	Q14314	Fibroleukin
26271	dirMS_041712_NAR_120mM_minus.4975.4975.3	3	3.28	1	3.03E+05		(K)AGADEE	(K)A/G A D E/E R/A E T A R(L)		78.58	425.8687	1275.592	-0.0008	-0.7	4.41	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
26272	dirMS_041712_NAR_120mM_minus.8214.8214.2	2	3.28	1	3.09E+04		(K)FSEVLKR	(K)F/S/E V L K/R(L)		98.58	439.7574	878.509	-0.0019	-2.2	8.75	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
26273	dirMS_041712_NAR_20mM_minus.11181.11181.3	3	3.28	1	3.74E+05		(R)LGRDAE	(R)L G R D A E G/T E L\S/R(R)		159.7	435.2303	1303.66	0.0163	12.5	4.68	124488.2	9.65	HUMAN	Q5T0Z8	Uncharacterized protein C6orf132
26274	dirMS_041712_NAR_30mM_minus2.15556.15556.2	2	3.28	0	4.34E+05		(R)YPVNSV	(R)Y/P\V/N S/V N I L K(A)		137.33	573.8282	1146.652	-0.0026	-2.3	8.59	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
26275	dirMS_041712_NAR_30mM_minus2.16742.16742.2	2	3.28	0	3.00E+05	M2243m	(K)mSIYQA	(K)m S\I|Y Q A M W/K(G)	m:Oxidized methionine	144.75	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
26276	dirMS_041712_NAR_30mM_minus2.6993.6993.2	2	3.28	0	1.95E+05	M88m	(K)DVDEAY	(K)D V|D\E A/Y m N K(V)	m:Oxidized methionine	92.63	550.7326	1084.462	15.9964	1.3	4.03	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
26277	dirMS_041712_NAR_30mM_minus2.8043.8043.2	2	3.28	0	1.41E+05		(R)NYLSQP	(R)N Y/L/S Q P R(L)		98.65	439.2266	877.453	-0.0067	-7.7	8.75	6939	10.41	HUMAN	E5RGH6	V-type proton ATPase subunit B, brain isoform
26278	dirMS_041712_NAR_30mM_minus2.8440.8440.2	2	3.28	0	1.35E+05		(K)LTELSG	(K)L T/E/L/S G N P R(K)		100.15	493.7642	986.527	-0.0054	-5.5	6	28768.5	8.64	HUMAN	D6RID8	General transcription factor IIH subunit 2-like protein (Fragment)
26279	dirMS_041712_NAR_40mM_minus2.14547.14547.3	3	3.28	1	1.45E+05		(K)GTVPDD	(K)G T V/P D D A V E A L A D/S L G K K(E)		170.3	595.9791	1785.923	-0.0001	-0.1	4.23	81397.3	4.99	HUMAN	B7Z468	Calpastatin
26280	dirMS_041712_NAR_50mM_minus2.10780.10780.3	3	3.28	1	1.40E+05	S396s	(K)IsFLEGE	(K)I s/F L E G E G R\K G L K(G)	s:Phosphorylated S	129.58	505.2683	1433.811	79.9793	8.5	8.59	48376.2	6.73	HUMAN	P0CAP1-6	Isoform 6 of Myocardial zonula adherens protein
26281	dirMS_041712_NAR_60mM_minus.13486.13486.3	3	3.28	1	1.67E+05		(R)GAGGQ	(R)G A G G Q G K L D V T|I/L/S/P S R(K)		135.4	552.6388	1655.908	-0.0057	-3.4	8.75	258215.9	5.48	HUMAN	E7EN95	Filamin-B
26282	dirMS_041712_NAR_60mM_minus.13720.13720.3	3	3.28	0	1.27E+05		(R)ADHPPA	(R)A D H/P P A E\V T S H A A S G A K(A)		136.4	549.2742	1645.793	0.0152	9.2	6	43303.4	8.7	HUMAN	F8VRN8	LIM domain and actin-binding protein 1
26283	dirMS_041712_NAR_60mM_minus.17562.17562.2	2	3.28	1	1.90E+05		(K)AAGKIT	(K)A/A G K\I T D A F/S S L A K(R)		157.7	690.3818	1379.753	0.0034	2.5	8.64	60658.4	6.05	HUMAN	B3KQF6	Vacuolar protein sorting 33B (Yeast), isoform CRA_b
26284	dirMS_041712_NAR_120mM_plus.8585.8585.2	2	3.28	0	6.40E+04		(R)NGVMP	(R)N/G\V|M/P\S H F S R(G)		97.12	566.274	1131.536	0.0043	3.8	9.75	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
26285	dirMS_041712_NAR_20mM_plus.12228.12228.3	3	3.28	0	4.51E+04	M183m	(R)ALEmHL	(R)A L E m H/L N S/H S G V K(M)	m:Oxidized methionine	156.72	480.2359	1422.716	15.9773	-12.2	6.96	115356.9	7.84	HUMAN	E7ET52	Zinc finger protein ZFPM2
26286	dirMS_041712_NAR_20mM_plus.13458.13458.2	2	3.28	0	1.46E+05	M273m	(K)mISDAI	(K)m I/S D A/I|P E L K(A)	m:Oxidized methionine	165.18	566.7967	1116.597	15.9892	-5	4.37	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
26287	dirMS_041712_NAR_20mM_plus.17491.17491.2	2	3.28	0	3.09E+03		(K)EGSIEID	(K)E G S I/E/I D I/P V P K(Y)		192.22	648.852	1296.705	-0.0078	-6	4.14	66923.1	6.88	HUMAN	E9PG35	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (Fragment)
26288	dirMS_041712_NAR_30mM_plus2.21227.21227.2	2	3.28	0	3.48E+03		(R)GAFQNL	(R)G A F Q/N/L/F Q S V/R(E)		164.47	633.8315	1266.659	-0.0032	-2.5	9.75	68629.9	5.59	HUMAN	E7EVX6	Androgen receptor
26289	dirMS_041712_NAR_40mM_plus2.6778.6778.2	2	3.28	0	2.58E+04		(K)YQAECS	(K)Y Q/A E C/S Q F K(A)	C:Carbamidomethylation	100.03	580.7568	1160.504	0.0022	1.9	6	334221.3	6.44	HUMAN	P15924	Desmoplakin
26290	dirMS_041712_NAR_40mM_plus2.9978.9978.2	2	3.28	0	4.81E+03		(K)VWNLA	(K)V W/N/L A N/C K(L)	C:Carbamidomethylation	123.07	502.7511	1004.498	-0.0033	-3.3	8.72	33029.4	9.62	HUMAN	D6R9L0	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)
26291	dirMS_041712_NAR_50mM_plus2.17217.17217.3	3	3.28	1	3.37E+05		(R)VSFELFA	(R)V/S F E\L F A D K\V P K(T)		158.8	460.5906	1379.757	0.0003	0.2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
26292	dirMS_041712_NAR_50mM_plus2.19935.19935.3	3	3.28	0	2.50E+05		(K)LFLFHTS	(K)L F L F H T S\L|P I A E A/P G K(L)		172.83	580.9943	1740.968	0	0	6.75	108105.4	6.57	HUMAN	E7EP00	Protein transport protein Sec24C
26293	dirMS_041712_NAR_50mM_plus2.7290.7290.3	3	3.28	0	1.11E+05		(K)TNPPLIC	(K)T N|P/P L I Q E K/P A K(T)		104	445.9257	1335.763	-0.0005	-0.4	8.26	102841.5	6.73	HUMAN	D3DQV9	Eukaryotic translation initiation factor 4 gamma 2 (Fragment)
26294	dirMS_041712_NAR_50mM_plus2.9461.9461.3	3	3.28	1	2.24E+05	K1328k	(K)kLDSELS	(K)k L/D S E L S R A Q E K(A)	k:Ubiquitin-K	116.45	506.6003	1403.749	114.0375	-3.6	6.18	176978	9.15	HUMAN	O14514	Brain-specific angiogenesis inhibitor 1
26295	dirMS_041712_NAR_60mM_plus.15636.15636.3	3	3.28	1	5.51E+03	S2976s	(R)QNADsS	(R)Q N/A D/s/S R\I T F L K(G)	s:Phosphorylated S	137.47	487.2426	1379.728	79.9855	13.1	8.75	454925	5.33	HUMAN	E9PHH6	Extracellular matrix protein FRAS1
26296	dirMS_041712_NAR_60mM_plus.17021.17021.3	3	3.28	0	1.79E+05		(R)SGGLGG	(R)S/G/G L/G G S H\A L L L L R(S)		145.8	450.9323	1350.785	-0.0029	-2.1	9.49	56801.9	8.81	HUMAN	B8ZZ38	Leucine-rich PPR motif-containing protein, mitochondrial
26297	dirMS_041712_NAR_60mM_plus.19804.19804.3	3	3.28	0	2.83E+05		(R)NSVSNF	(R)N\S V/S/N F L H S L E R(G)		162.93	468.2401	1402.707	-0.0016	-1.1	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
26298	dirMS_041712_NAR_60mM_plus.7571.7571.3	3	3.28	0	2.93E+05		(K)NCPHV	(K)N C/P H/V V V/G T P G R(I)	C:Carbamidomethylation	97.75	431.5519	1292.653	-0.0117	-9	9.75	30944.2	6.52	HUMAN	B1Q2N1	ATP-dependent RNA helicase DDX39A
26299	dirMS_041712_NAR_20mM_minus.10808.10808.2	2	3.27	0	5.14E+04		(R)GSVLEP	(R)G S V/L/E/P E G T V E I K(F)		155.8	679.3706	1357.721	0.013	9.6	4.25	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
26300	dirMS_041712_NAR_20mM_minus.11846.11846.3	3	3.27	1	3.40E+05		(R)ISAEDG	(R)I S\A E D G L/K H E Y F R(E)		167.13	522.2561	1564.775	-0.0217	-13.9	5.45	85584.8	5.13	HUMAN	J3KTL7	Cyclin-dependent kinase 11B
26301	dirMS_041712_NAR_30mM_minus2.15307.15307.2	2	3.27	1	2.45E+05	K490k	(K)NLNQSK	(K)N L|N|Q/S K k(G)	k:Ubiquitin-K	135.53	473.2631	831.468	114.0506	8.1	10	151040	5.86	HUMAN	E9PEZ5	Uncharacterized protein KIAA1107
26302	dirMS_041712_NAR_30mM_minus2.15681.15681.2	2	3.27	0	3.46E+05		(K)LLYNNV	(K)L L/Y/N N V S N F G R(L)		137.97	648.8355	1296.67	-0.0058	-4.5	8.75	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
26303	dirMS_041712_NAR_30mM_minus2.16420.16420.2	2	3.27	1	1.58E+05	K90k M93	(K)EFKLTkT	(K)E F K|L/T k T A\m R(A)	k:Ubiquitin-K m:Oxidized me	142.38	677.8679	1224.677	130.0516	10.2	10	25482.5	10.06	HUMAN	G3V2E1	Spermatogenesis-associated protein 7 (Fragment)
26304	dirMS_041712_NAR_30mM_minus2.8582.8601.2	2	3.27	0	1.13E+06		(R)LLEVNS	(R)L L|E V N/S S/R(E)		101.32	459.2546	917.505	-0.0031	-3.4	6	16214.9	4.91	HUMAN	G3V5Q5	Thiamine triphosphatase
26305	dirMS_041712_NAR_40mM_minus2.7669.7669.3	3	3.27	1	7.75E+04	S349s	(K)ESDGLG	(K)E S D G L G I Q V s G G/R\G/S\K(R)	s:N-acetylglucosamine (S)	123.6	583.9659	1546.782	203.1012	12.5	6.17	304146	7.19	HUMAN	O15018	PDZ domain-containing protein 2
26306	dirMS_041712_NAR_50mM_minus2.11479.11479.3	3	3.27	1	9.59E+04		(R)LLIVSTT	(R)L L|I/V/S T T/P Y S E K D T K(Q)		133.12	565.6428	1694.921	-0.0072	-4.3	6.07	46476.4	5.33	HUMAN	B3KQ59	RuvB-like 2
26307	dirMS_041712_NAR_50mM_minus2.13833.13833.3	3	3.27	2	2.80E+05	Y114y	(K)LKVVITS	(K)L/K/V V I T S/K S G E I L y R(I)	y:Phosphorylated Y	146.68	595.9939	1706.021	79.9461	-11.3	9.7	76414.8	6.1	HUMAN	E9PGM4	1,4-alpha-glucan-branching enzyme
26308	dirMS_041712_NAR_50mM_minus2.6152.6152.3	3	3.27	1	1.83E+04		(K)AGSNT	(K)A G S N T/Q K/K W N L M L C Q S(-)	C:Carbamidomethylation	97.82	622.6372	1865.9	-0.0026	-1.4	10	7484.7	10.46	HUMAN	E5RGB8	Zinc fingers and homeoboxes protein 1
26309	dirMS_041712_NAR_50mM_minus2.8181.8181.3	3	3.27	0	2.05E+05	K101k	(K)AVIWP	(K)A V/I W P Q Y V/k D R(I)	k:Ubiquitin-K	114.37	496.9372	1374.753	114.0442	0.9	8.63	35395.5	10.24	HUMAN	Q5VT94	Growth hormone inducible transmembrane protein
26310	dirMS_041712_NAR_60mM_minus.17816.17816.3	3	3.27	1	3.60E+05		(K)NLRDID	(K)N L R D I D\E\V/S/S L/L R(T)		160.9	510.6099	1529.828	-0.013	-8.5	4.56	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
26311	dirMS_041712_NAR_60mM_minus.6085.6085.3	3	3.27	1	6.51E+03		(-)MDVDKE	(-)M D/V D/K E/L G M E S V K(A)		93.05	494.235	1480.702	-0.0117	-7.9	4.32	3913.2	4.23	HUMAN	E7EWV4	Thioredoxin domain-containing protein 2
26312	dirMS_041712_NAR_60mM_minus.8527.8527.3	3	3.27	0	2.71E+04		(K)ELQVNI	(K)E L/Q V/N I S\Q Q G E K(A)		107.28	458.2407	1372.707	0.0009	0.6	4.53	279771.8	9.54	HUMAN	Q8NDH2	Coiled-coil domain-containing protein 168
26313	dirMS_041712_NAR_120mM_plus.15188.15188.4	4	3.27	0	6.58E+05	K84k	(R)kGSVPL	(R)k G/S V/P L G L A T V L Q D/L L R(K)	k:Ubiquitin-K	132.47	474.2836	1780.069	114.0435	0.3	8.75	19024.4	11.62	HUMAN	B4DKJ6	Charged multivesicular body protein 7
26314	dirMS_041712_NAR_120mM_plus.15607.15607.3	3	3.27	0	4.94E+05	T160t	(R)tSPSSPA	(R)t S P S S P A P L|P H Q E A T P R(A)	t:Phosphorylated T	135.05	618.2835	1772.893	79.9434	-12.4	6.41	136757.5	5.83	HUMAN	F8W682	Anion exchange protein 2
26315	dirMS_041712_NAR_120mM_plus.20743.20743.4	4	3.27	1	2.18E+06		(R)LEEAGG	(R)L E E/A G G A/T S/V Q I E M\N K K/R(E)		160.77	491.0027	1961.012	-0.0231	-11.8	6.23	223892.1	5.63	HUMAN	P12883	Myosin-7
26316	dirMS_041712_NAR_120mM_plus.22891.22891.4	4	3.27	1	3.88E+06		(K)GLAPDLI	(K)G L A\P D L/P E/D L Y H/L I K K(A)		174.07	456.259	1822.011	0.0033	1.8	5.38	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
26317	dirMS_041712_NAR_120mM_plus.7653.7653.2	2	3.27	0	8.10E+05		(K)HFEALAI	(K)H/F|E/A L A N/R(A)		94.47	479.2487	957.49	0	0	6.75	63613.4	7.9	HUMAN	B3KXI2	Protein transport protein Sec23A
26318	dirMS_041712_NAR_20mM_plus.13667.13667.2	2	3.27	0	2.20E+05	M148m	(R)DLTDYL	(R)D L/T/D Y L/m K(I)	m:Oxidized methionine	165.43	507.7439	998.486	15.9942	-0.7	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
26319	dirMS_041712_NAR_20mM_plus.14536.14536.3	3	3.27	0	9.78E+04	M326m M	(K)FTVLLm	(K)F T V L L m/P N/G P m/R(I)	m:Oxidized methionine	171.72	469.9019	1375.723	31.9687	-15	9.75	42088	5.39	HUMAN	F8VTY8	Proliferation-associated protein 2G4
26320	dirMS_041712_NAR_20mM_plus.15070.15070.3	3	3.27	1	2.24E+04		(R)LDHTRA	(R)L D H T R A V N/Y/F S K(V)		175.22	484.2492	1450.744	-0.0107	-7.4	8.6	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
26321	dirMS_041712_NAR_20mM_plus.15257.15257.3	3	3.27	1	7.73E+04	T435t	(R)LRDWILI	(R)L R D W/I\L|E A t T K(A)	t:Phosphorylated T	176.58	475.9154	1345.747	79.9842	12.5	6.07	116186.9	9.34	HUMAN	Q7Z410	Transmembrane protease serine 9
26322	dirMS_041712_NAR_20mM_plus.16789.16789.2	2	3.27	0	9.63E+04		(R)SSIAGLL	(R)S S/I/A G L L L K(A)		187	451.2885	901.572	-0.002	-2.2	8.47	533778	5.74	HUMAN	Q15149	Plectin
26323	dirMS_041712_NAR_20mM_plus.16960.16960.3	3	3.27	0	2.88E+05		(K)VQIAVA	(K)V Q\I A/V A\N A Q/E/L/L Q R(M)		187.93	518.2975	1552.881	-0.0026	-1.7	5.97	10728.1	9.15	HUMAN	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13
26324	dirMS_041712_NAR_20mM_plus.18055.18055.2	2	3.27	0	8.33E+04		(K)SLESLDT	(K)S L|E/S/L\D T/S L F A K(N)		195.43	655.8428	1310.684	-0.0055	-4.2	4.37	52796.2	5.19	HUMAN	E7EUT8	Splicing factor 3A subunit 3
26325	dirMS_041712_NAR_20mM_plus.18977.18977.2	2	3.27	0	4.70E+04		(R)GLAVFIS	(R)G L/A|V/F/I S D I R(N)		201.8	545.8154	1090.626	-0.002	-1.8	5.84	75530.1	6.04	HUMAN	E9PJJ7	AP-2 complex subunit alpha-2
26326	dirMS_041712_NAR_20mM_plus.7794.7794.2	2	3.27	0	6.38E+04		(K)LITEDV	(K)L I/T E/D V Q G K(N)		123.35	501.7728	1002.547	-0.0083	-8.3	4.37	14616.7	10.16	HUMAN	D6RAS7	40S ribosomal protein S3a (Fragment)
26327	dirMS_041712_NAR_20mM_plus.7910.7910.2	2	3.27	0	8.55E+04	T207t	(K)FVQGLD	(K)F V Q G/L D I/G/P t K(T)	t:N-acetylglucosamine (T)	123.6	689.3745	1174.647	203.0951	11.4	5.84	89473.4	5.06	HUMAN	E7EMF1	Integrin alpha-2
26328	dirMS_041712_NAR_20mM_plus.8052.8052.3	3	3.27	0	4.57E+05	M239m	(K)EVDEQ	(K)E V D E/Q\m/L N V Q/N K(N)	m:Oxidized methionine	125.12	488.2328	1446.689	15.9945	-0.3	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
26329	dirMS_041712_NAR_20mM_plus.8275.8275.2	2	3.27	0	9.35E+04		(R)LATNTS	(R)L A|T|N/T/S A P D L K(N)		127.33	565.806	1130.605	-0.0005	-0.4	5.84	26233.5	10.95	HUMAN	B4DSQ1	Microtubule-associated protein
26330	dirMS_041712_NAR_30mM_plus2.17141.17141.2	2	3.27	1	4.04E+05		(R)GGETIRS	(R)G G E/T/I R S I C K(A)	C:Carbamidomethylation	142.68	560.7925	1120.578	-0.0002	-0.2	8.75	61918.7	4.86	HUMAN	Q5SZR4	Tudor and KH domain containing
26331	dirMS_041712_NAR_40mM_plus2.10573.10573.2	2	3.27	1	6.20E+03	M222m	(K)LGYSmT	(K)L G Y S/m/T R G K(I)	m:Oxidized methionine	127.35	514.7663	1012.524	16.0009	5.8	9.99	25811	5.23	HUMAN	B4DPH8	Tumor protein p63-regulated gene 1-like protein
26332	dirMS_041712_NAR_40mM_plus2.15339.15339.3	3	3.27	2	2.11E+04		(K)DVAKGS	(K)D V/A K G S E G E N P L T V P G R E K(E)		155.8	661.6783	1983.014	0.0062	3.1	4.87	54946.2	9.12	HUMAN	E7EX40	Rab11 family-interacting protein 1
26333	dirMS_041712_NAR_40mM_plus2.9118.9118.2	2	3.27	0	8.93E+04		(K)GSDFDC	(K)G S\D/F/D C E L/R(L)	C:Carbamidomethylation	115.47	549.7296	1098.452	-0.0001	-0.1	4.03	51260.6	5.39	HUMAN	P61978	Heterogeneous nuclear ribonucleoprotein K
26334	dirMS_041712_NAR_50mM_plus2.17477.17477.3	3	3.27	0	5.30E+05		(R)GGYVLH	(R)G G Y/V L/H I/G T I/Y/G D/L K(V)		160.33	535.9588	1605.863	-0.0017	-1	6.74	30427.2	7.21	HUMAN	H3BPK7	Alanine--tRNA ligase, cytoplasmic (Fragment)
26335	dirMS_041712_NAR_50mM_plus2.20710.20710.3	3	3.27	1	5.81E+05	M1m	(-)mTSLFA	(-)m T S L F A Q\E|I/R L S K(R)	m:Oxidized methionine	177.05	513.9492	1523.825	16.008	8.5	8.5	7355.4	6.72	HUMAN	C9JY17	Uncharacterized protein C3orf14 (Fragment)
26336	dirMS_041712_NAR_50mM_plus2.21183.21183.3	3	3.27	1	4.45E+05	M145m	(R)GVmLA	(R)G V/m\L A|V D/A V I A E L K K(Q)	m:Oxidized methionine	181.6	524.9717	1556.908	15.9925	-1.5	6.07	25225.7	9.52	HUMAN	E7ESH4	60 kDa heat shock protein, mitochondrial (Fragment)
26337	dirMS_041712_NAR_50mM_plus2.5265.5265.3	3	3.27	0	3.41E+05	M116m	(R)ATAPQT	(R)A T/A/P Q T Q H V/S/P m R(Q)	m:Oxidized methionine	87.48	480.5727	1423.711	15.9925	-1.7	9.8	29184.1	4.91	HUMAN	E9PBQ9	Elongation factor 1-delta
26338	dirMS_041712_NAR_60mM_plus.10218.10218.3	3	3.27	1	4.95E+05		(R)RQQEQ	(R)R Q Q\E/Q Q/V/P I L E K(F)		111.33	499.2786	1495.823	-0.0015	-1	6.14	276046.1	6.01	HUMAN	P49327	Fatty acid synthase
26339	dirMS_041712_NAR_60mM_plus.5062.5062.3	3	3.27	1	2.67E+05	T255t	(K)LYEtRSS	(K)L Y/E t R S S Q L R(K)	t:Phosphorylated T	83.22	444.8825	1252.664	79.9685	1.6	8.75	36669.5	10.42	HUMAN	Q6ZQR2	Uncharacterized protein C9orf171
26340	dirMS_041712_NAR_60mM_plus.8365.8365.3	3	3.27	0	3.74E+05		(R)SIRPDN	(R)S I R P D N\M|S/E/Y S K(Q)		101.98	476.2284	1426.663	0.0075	5.3	5.79	52511.1	5.48	HUMAN	B3KRS5	Histone deacetylase
26341	dirMS_041712_NAR_60mM_plus.8532.8532.3	3	3.27	0	6.38E+05		(K)EHDPVG	(K)E H D P V G Q/M/V/N N P K(I)		102.25	488.9052	1464.69	0.0111	7.6	5.32	86098.8	5.31	HUMAN	B4DUC5	Exportin-2
26342	dirMS_041712_NAR_30mM_minus2.11504.11504.2	2	3.26	0	1.42E+05		(R)GILIDTS	(R)G I/L/I/D/T S R(H)		115.87	437.7522	874.499	-0.0021	-2.4	5.84	63566.6	6.3	HUMAN	P07686	Beta-hexosaminidase subunit beta
26343	dirMS_041712_NAR_30mM_minus2.15644.15644.2	2	3.26	0	9.77E+04		(R)GSTDNL	(R)G S T/D/N/L/M/D D I E R(A)		138.77	683.3009	1365.595	-0.0006	-0.4	3.84	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
26344	dirMS_041712_NAR_30mM_minus2.16849.16849.2	2	3.26	0	3.94E+05	N2417n	(K)TFIEDVn	(K)T/F|I E D V n/K(F)	n:N-acetylglucosamine (N)	145	584.7961	965.494	203.0911	10	4.37	516964.4	6.59	HUMAN	P04114	Apolipoprotein B-100
26345	dirMS_041712_NAR_30mM_minus2.19732.19732.2	2	3.26	0	1.25E+05	M258m	(K)SmSLAT	(K)S m S L A T A G S A\F|Q|P(-)	m:Oxidized methionine	163.88	642.3005	1267.599	15.995	0.1	5.24	29605.1	9.37	HUMAN	P09067	Homeobox protein Hox-B5
26346	dirMS_041712_NAR_30mM_minus2.8144.8144.2	2	3.26	0	2.42E+05		(K)SFQQSS	(K)S/F/Q/Q S S/L S R(D)		99.28	520.2591	1039.517	-0.0058	-5.6	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
26347	dirMS_041712_NAR_50mM_minus2.12435.12435.3	3	3.26	0	2.81E+05		(K)QLTEED	(K)Q L|T/E/E D G V H S V I E E/N\I K(C)		138.65	647.3249	1939.961	-0.0006	-0.3	4.25	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
26348	dirMS_041712_NAR_50mM_minus2.13457.13457.3	3	3.26	1	1.37E+05		(K)IDSRLEQ	(K)I D/S R L E Q|Y/T\S A I/E G T K(S)		144.62	604.3145	1810.918	0.0108	6	4.68	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
26349	dirMS_041712_NAR_50mM_minus2.15604.15604.3	3	3.26	0	2.04E+05		(K)EGPFVH	(K)E G P F/V H I A S I C A A V L S/K(F)	C:Carbamidomethylation	157.83	600.3221	1798.952	-0.0003	-0.1	6.85	10691.6	9.52	HUMAN	H7C1F4	Chloride channel protein 1 (Fragment)
26350	dirMS_041712_NAR_60mM_minus.14367.14367.3	3	3.26	2	6.40E+03		(R)GKDISTI	(R)G K D I S T I T G/H/R G K(D)		139.95	457.2595	1369.755	0.0093	6.8	9.99	32522.5	5.29	HUMAN	H0YDG9	Remodeling and spacing factor 1 (Fragment)
26351	dirMS_041712_NAR_60mM_minus.17495.17495.3	3	3.26	0	1.10E+04	M251m M	(R)AHmGm	(R)A H\m G/m F T/E L|A\I L Y S K(F)	m:Oxidized methionine	157.03	581.9563	1711.855	31.9997	5.7	6.79	71165.3	5.57	HUMAN	J3KS13	Clathrin heavy chain 1
26352	dirMS_041712_NAR_60mM_minus.20277.20277.3	3	3.26	0	2.61E+05		(R)HDADG	(R)H D A D G Q A\T L/L/N L/L L R(N)		186.83	550.6362	1649.897	-0.0029	-1.8	5.21	41296.9	9.52	HUMAN	B4DT72	26S proteasome non-ATPase regulatory subunit 3
26353	dirMS_041712_NAR_60mM_minus.9973.9973.3	3	3.26	1	2.37E+04		(K)SLRENLL	(K)S L|R E N L L|Q H E K(S)		114.22	456.2517	1366.744	-0.0032	-2.3	6.48	24599.4	9.84	HUMAN	Q08499-12	Isoform 12 of cAMP-specific 3',5'-cyclic phosphodiesterase 4D
26354	dirMS_041712_NAR_120mM_plus.5396.5396.3	3	3.26	1	4.80E+05	T192t	(R)APEHLR	(R)A P\E H L R/A/t V R(W)	t:Phosphorylated T	81.45	410.5424	1149.649	79.9639	-2	9.65	39528.2	5.51	HUMAN	O15541	RING finger protein 113A
26355	dirMS_041712_NAR_120mM_plus.7036.7036.3	3	3.26	0	5.15E+05		(K)QSLSEE	(K)Q S/L S/E E N Y I K(L)		90.52	404.2038	1210.595	0.0018	1.5	4.53	11940.7	9.52	HUMAN	J3QQU0	Protein IMPACT (Fragment)
26356	dirMS_041712_NAR_20mM_plus.14637.14637.2	2	3.26	1	9.32E+04	K203k	(R)YVGVRH	(R)Y V/G V R\H S L|k(Y)	k:Ubiquitin-K	173.18	586.8315	1058.611	114.0452	1.9	9.99	61431.6	10.21	HUMAN	P25100	Alpha-1D adrenergic receptor
26357	dirMS_041712_NAR_20mM_plus.18176.18176.2	2	3.26	0	1.31E+05	M153m	(K)VVTYG	(K)V V T/Y\G/m/A N L L T G P K(R)	m:Oxidized methionine	196.32	740.3997	1463.793	15.9995	3.1	8.56	28454.5	6.24	HUMAN	B0AZP7	Synaptic vesicle membrane protein VAT-1 homolog
26358	dirMS_041712_NAR_20mM_plus.18866.18866.2	2	3.26	0	1.71E+05		(K)TAVETA	(K)T A|V/E|T A V L|L L R(I)		200.43	593.3625	1185.72	-0.0024	-2	5.66	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
26359	dirMS_041712_NAR_30mM_plus2.12820.12820.2	2	3.26	0	6.70E+04		(R)IYVSAN	(R)I Y|V S A N S G A R(I)		120.43	519.2668	1037.537	-0.0111	-10.7	8.75	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
26360	dirMS_041712_NAR_30mM_plus2.21698.21698.3	3	3.26	0	1.87E+05		(R)TTNFAG	(R)T T N F|A G\I L/S Q/G L R(I)		169.27	459.9204	1377.748	-0.0018	-1.3	9.41	113880.5	9.18	HUMAN	P09874	Poly [ADP-ribose] polymerase 1
26361	dirMS_041712_NAR_30mM_plus2.9270.9270.2	2	3.26	0	2.25E+05		(R)ALELEQ	(R)A L/E L E Q/E/R(K)		101.35	494.2566	987.511	-0.0046	-4.7	4.25	67933	6.08	HUMAN	P26038	Moesin
26362	dirMS_041712_NAR_40mM_plus2.8002.8002.2	2	3.26	0	1.57E+04		(K)IGNCPF	(K)I/G N/C/P F S Q R(L)	C:Carbamidomethylation	107.5	539.7602	1078.51	0.0033	3	9.75	27264.5	5.09	HUMAN	O00299	Chloride intracellular channel protein 1
26363	dirMS_041712_NAR_50mM_plus2.10933.10933.3	3	3.26	1	4.68E+05		(R)ALRETL	(R)A L R E T L|P\A E/Q D L T T K(N)		125.08	562.6377	1685.907	-0.0083	-4.9	4.68	26790	6.25	HUMAN	F5GX11	Proteasome subunit alpha type-1
26364	dirMS_041712_NAR_50mM_plus2.11236.11236.3	3	3.26	1	1.06E+04		(R)LVERDP	(R)L V E R/D P Q G S S L P E G G R(R)		126.42	566.2937	1696.861	0.0053	3.1	4.68	55259.1	4.76	HUMAN	Q8TBC5	Zinc finger and SCAN domain-containing protein 18
26365	dirMS_041712_NAR_50mM_plus2.13994.13994.3	3	3.26	1	9.56E+03	T170t	(K)TFLQTAt	(K)T F/L Q T\A t L I E D I L G V K K(E)	t:Phosphorylated T	141.2	657.3638	1890.095	79.9822	8.1	5.73	87380.4	8.96	HUMAN	B4E0Q1	Short transient receptor potential channel 4-associated protein
26366	dirMS_041712_NAR_50mM_plus2.16196.16196.3	3	3.26	1	4.90E+04		(K)VMLRLL	(K)V M L R/L L G D G S L/E S/W Q\R(Q)		152.25	620.658	1859.98	-0.0202	-10.9	6.04	15470.6	5.13	HUMAN	J3QSF8	Putative unconventional myosin-XVB (Fragment)
26367	dirMS_041712_NAR_50mM_plus2.8304.8304.3	3	3.26	0	6.93E+04		(R)EVEEEP	(R)E V E E\E/P G I/H S/L K(H)		110.4	456.2395	1366.685	0.0191	13.9	4.48	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
26368	dirMS_041712_NAR_60mM_plus.18706.18706.3	3	3.26	0	1.30E+05		(K)SPVTTLL	(K)S/P V/T T L/L E C M\H K(L)	C:Carbamidomethylation	155.05	472.5788	1415.702	0.0197	13.9	6.47	142137.5	9.17	HUMAN	E7ENU4	Double-stranded RNA-specific adenosine deaminase
26369	dirMS_041712_NAR_60mM_plus.19251.19251.3	3	3.26	0	2.50E+04	S266s	(R)LPPGLs	(R)L P P G L/s A S P/Q P S S V A P R(R)	s:Phosphorylated S	159.1	580.9558	1660.902	79.9512	-8.7	9.75	30941.6	7.12	HUMAN	P52945	Pancreas/duodenum homeobox protein 1
26370	dirMS_041712_NAR_60mM_plus.21139.21139.2	2	3.26	0	1.27E+05	N1472n	(R)QnTQG	(R)Q/n T Q G/A Q/A E F L F R(T)	n:N-acetylglucosamine (N)	174.23	856.912	1509.745	203.0723	-4.2	6	177994.4	5.37	HUMAN	Q12774	Rho guanine nucleotide exchange factor 5
26371	dirMS_041712_NAR_60mM_plus.8555.8555.3	3	3.26	0	6.31E+05		(K)EHDPVG	(K)E H D P V|G Q/M/V/N N P K(I)		102.27	488.9052	1464.69	0.0111	7.6	5.32	86098.8	5.31	HUMAN	B4DUC5	Exportin-2
26372	dirMS_041712_NAR_60mM_plus.8560.8560.3	3	3.26	1	4.93E+05	M2747m	(K)TLQEVT	(K)T L/Q E V T E m D/S V K R(Y)	m:Oxidized methionine	102.37	517.9269	1535.773	15.9928	-1.4	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
26373	dirMS_041712_NAR_120mM_minus.12062.12062.4	4	3.25	1	1.34E+06	S475s M47	(K)ICsPDK	(K)I C s P D K/m I G F S E T A K(C)	C:Carbamidomethylation s:N-ace	120.08	476.4733	1683.808	219.0633	-5.8	6.07	71924.9	6.25	HUMAN	B4DFA2	Vesicle-fusing ATPase

26374	dirMS_041712_NAR_120mM_minus.5376.5376.3	3	3.25	2	3.26E+03	T266t	(K)TKENLE	(K)T\K/E N L E/K\t R(H)	t:Phosphorylated T	84	400.1991	1118.616	79.9663	0	8.26	43475.4	5.51	HUMAN	Q6NZI2	Polymerase I and transcript release factor
26375	dirMS_041712_NAR_120mM_minus.9627.9627.2	2	3.25	0	3.20E+04		(K)HVVFIA	(K)H/V|V/F I/A Q R(R)		107.08	485.2837	969.563	-0.0027	-2.8	9.75	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
26376	dirMS_041712_NAR_20mM_minus.10449.10449.2	2	3.25	0	5.15E+04		(K)VLIANN	(K)V/L|I|A/N/N G I A A V K(C)		152.82	591.863	1182.72	-0.0018	-1.5	8.72	269989.9	5.92	HUMAN	F8W8T8	Acetyl-CoA carboxylase 2
26377	dirMS_041712_NAR_30mM_minus2.11361.11361.2	2	3.25	0	2.37E+05		(R)QPSQG	(R)Q P S Q/G P T F/G I/K(G)		115.4	580.3084	1159.611	-0.0011	-0.9	8.75	111409.8	9.02	HUMAN	F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic
26378	dirMS_041712_NAR_40mM_minus2.6679.6679.3	3	3.25	2	1.72E+03	S394s	(R)sTRIPGT	(R)s/T R\I P G/T D A Q A Q K K(F)	s:Phosphorylated S	106.42	527.6048	1500.813	79.987	13.1	9.99	49055.6	10.02	HUMAN	H7C1L3	ELM2 and SANT domain-containing protein 1 (Fragment)
26379	dirMS_041712_NAR_50mM_minus2.11326.11326.3	3	3.25	1	1.29E+05		(K)NQVAL	(K)N\Q|V|A L N/P Q N T V F D A K R(L)		132.68	605.6545	1814.951	-0.0018	-1	8.75	70336.2	5.48	HUMAN	P08107	Heat shock 70 kDa protein 1A/1B
26380	dirMS_041712_NAR_50mM_minus2.16213.16213.3	3	3.25	1	8.21E+04		(R)LGLSTL	(R)L G/L|S|T L G E L K Q/N L S R(S)		158.97	543.6477	1628.933	-0.0044	-2.7	8.75	22294.4	5.26	HUMAN	O43399	Tumor protein D54
26381	dirMS_041712_NAR_50mM_minus2.17500.17500.3	3	3.25	1	1.23E+04	T312t	(R)DFItLRL	(R)D/F|I\t L R L P P G F P V K(I)	t:N-acetylglucosamine (T)	167.78	601.6676	1599.926	203.0625	-9.3	8.75	58760.2	5.26	HUMAN	Q6ZTN6	Ankyrin repeat domain-containing protein 13D
26382	dirMS_041712_NAR_50mM_minus2.5929.5929.3	3	3.25	0	8.40E+04		(K)ANESSP	(K)A N/E/S S P K/P V G P P P E R(D)		95.83	521.2695	1561.797	-0.0029	-1.9	6.19	10501.2	5.81	HUMAN	A6PVM9	Allograft inflammatory factor 1-like
26383	dirMS_041712_NAR_50mM_minus2.9873.9873.3	3	3.25	1	1.13E+05		(K)IEKIGEG	(K)I E K/I G E G\T Y/G V V Y K(G)		124.48	519.2824	1555.837	-0.004	-2.6	6.14	21780.9	8.65	HUMAN	E5RIU6	Cyclin-dependent kinase 1 (Fragment)
26384	dirMS_041712_NAR_60mM_minus.15004.15004.3	3	3.25	0	2.26E+05	S61s	(K)LGTPTLL	(K)L G/T P/T L L A K P C/Y/I V I s K(R)	C:Carbamidomethylation s:Phos	143	652.0241	1874.082	79.9758	4.8	9.7	94356.4	8.95	HUMAN	Q9H5V8	CUB domain-containing protein 1
26385	dirMS_041712_NAR_60mM_minus.17988.17988.3	3	3.25	1	3.74E+05	K341k	(K)GTPEKV	(K)G T P E/K V F T/V/S/N I k(T)	k:Ubiquitin-K	160.42	511.9529	1419.784	114.0599	11.1	8.59	78298.8	5.26	HUMAN	Q7L1I2	Synaptic vesicle glycoprotein 2B
26386	dirMS_041712_NAR_60mM_minus.5548.5548.3	3	3.25	0	7.33E+04	M230m	(K)QVQmA	(K)Q V/Q m/A A T/H I/A R(K)	m:Oxidized methionine	86.88	414.5567	1225.647	16.0085	11	9.75	35345.8	9.26	HUMAN	Q00403	Transcription initiation factor IIB
26387	dirMS_041712_NAR_60mM_minus.5723.5723.3	3	3.25	1	5.90E+04		(K)EAEGAP	(K)E A/E/G A P Q V E A G K R(L)		88.77	447.8959	1341.676	-0.0026	-1.9	4.79	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
26388	dirMS_041712_NAR_60mM_minus.8358.8358.3	3	3.25	2	1.07E+05	S287s	(R)RGDSP	(R)R G D S P/W\Q V|V L L D s K K(K)	s:Phosphorylated S	106.7	603.3097	1727.944	79.9707	2.4	8.59	59095	6.24	HUMAN	B4DPQ7	Vitamin K-dependent protein C heavy chain
26389	dirMS_041712_NAR_60mM_minus.8919.8919.3	3	3.25	0	1.21E+05		(K)NCPHIV	(K)N C/P H/I V V G\T/P G R(I)	C:Carbamidomethylation	109.37	436.2271	1306.669	-0.0017	-1.3	9.75	28185.1	10.76	HUMAN	B4DIJ6	Spliceosome RNA helicase DDX39B
26390	dirMS_041712_NAR_120mM_plus.10674.10674.3	3	3.25	1	1.21E+06		(R)EKLEME	(R)E K L E M E/M E A/A/R(H)		109.52	446.2171	1336.623	0.0132	9.9	4.49	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)
26391	dirMS_041712_NAR_120mM_plus.14967.14967.3	3	3.25	1	6.73E+05	K13k	(-)XFQVSY	(-)X F/Q V S/Y F/A F K F/A k/K(D)	k:Ubiquitin-K	131.27	613.3369	1723.957	114.0391	-2.1	10	95759.3	5.87	HUMAN	H0Y9P1	BMP-2-inducible protein kinase (Fragment)
26392	dirMS_041712_NAR_120mM_plus.16109.16109.4	4	3.25	2	1.70E+06		(K)SIYGERF	(K)S I Y/G E R F P D E N F K/L K(H)		138.32	461.4898	1842.939	-0.0011	-0.6	5.9	23799.1	9.48	HUMAN	P23284	Peptidyl-prolyl cis-trans isomerase B
26393	dirMS_041712_NAR_120mM_plus.21614.21614.4	4	3.25	0	3.04E+05		(R)CPALHL	(R)C/P A L H L P/S L S V F/S/L R(W)	C:Carbamidomethylation	166.87	424.9891	1696.92	0.0142	8.4	9.75	31540.5	8.73	HUMAN	P59025	Receptor-transporting protein 1
26394	dirMS_041712_NAR_120mM_plus.6135.6135.3	3	3.25	1	2.28E+05	M357m	(K)AELDDT	(K)A E/L D D/T P m R G R(Q)	m:Oxidized methionine	85.37	426.2066	1260.6	16.0051	8	4.56	76262.2	9.53	HUMAN	P23246	Splicing factor, proline- and glutamine-rich
26395	dirMS_041712_NAR_120mM_plus.8557.8557.3	3	3.25	1	3.33E+05		(R)RLAEDE	(R)R L\A E\D\E\A/F Q R(R)		97.8	412.2128	1234.618	0.0064	5.2	4.68	533778	5.74	HUMAN	Q15149	Plectin
26396	dirMS_041712_NAR_20mM_plus.11954.11954.3	3	3.25	0	7.15E+04	M4040m	(R)SQVmD	(R)S Q\V\m D\E A T/A L Q L/R(E)	m:Oxidized methionine	155.68	493.2543	1461.737	16.0117	11.4	4.37	533778	5.74	HUMAN	Q15149	Plectin
26397	dirMS_041712_NAR_20mM_plus.12454.12454.2	2	3.25	0	6.91E+05		(R)NMTVA	(R)N M T V/A D S G T/N H D S R(L)		158.63	752.8363	1504.645	0.0208	13.8	5.21	205056.4	5.48	HUMAN	K7EKI8	Periplakin
26398	dirMS_041712_NAR_20mM_plus.15206.15206.2	2	3.25	1	4.01E+04	M244m Y2	(R)HmIRHT	(R)H m/I R H T/G D G P y K(C)	m:Oxidized methionine y:Ph	175.85	754.3261	1411.69	95.955	-4.1	8.61	65845.2	9.69	HUMAN	Q8TBZ8	Zinc finger protein 564
26399	dirMS_041712_NAR_20mM_plus.15342.15342.3	3	3.25	0	3.85E+04	M73m	(R)AILVDLE	(R)A I L V D L E/P G T\m D S V R(S)	m:Oxidized methionine	177.93	544.6139	1615.836	15.9912	-2.3	4.03	27549.9	4.39	HUMAN	E9PBJ4	Tubulin beta chain
26400	dirMS_041712_NAR_20mM_plus.17026.17026.2	2	3.25	0	1.40E+05		(K)FATEAA	(K)F A T\E/A/A/I/T I/L R(I)		188.77	603.3442	1205.689	-0.0077	-6.4	6	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
26401	dirMS_041712_NAR_30mM_plus2.11959.11959.2	2	3.25	1	5.36E+05		(R)LQKLPT	(R)L Q/K|L|P T S\M(-)		116.08	459.2593	917.513	-0.0011	-1.2	8.75	9148.5	9.4	HUMAN	C9JES7	COX assembly mitochondrial protein homolog
26402	dirMS_041712_NAR_30mM_plus2.16435.16435.3	3	3.25	0	4.29E+05		(K)LLDLVQ	(K)L L D\L|V\Q Q/S/C N Y K(Q)	C:Carbamidomethylation	139.03	494.2566	1480.746	0.0088	5.9	5.83	14855.1	9.26	HUMAN	B1AHD1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
26403	dirMS_041712_NAR_40mM_plus2.12140.12140.3	3	3.25	1	6.81E+04		(K)TSLVAT	(K)T S/L|V A/T/P G I D K L T E K(S)		137.78	524.9653	1572.884	-0.003	-1.9	5.73	89370.5	5.69	HUMAN	Q8IV36	Protein HID1
26404	dirMS_041712_NAR_40mM_plus2.20024.20024.3	3	3.25	1	5.68E+05		(K)EGGLGP	(K)E G G L/G/P L N/I P L L A D V T R R(L)		189.77	631.0288	1891.076	-0.0041	-2.2	6.17	15252.2	5.82	HUMAN	A6NIW5	Peroxiredoxin 2, isoform CRA_a
26405	dirMS_041712_NAR_50mM_plus2.10489.10489.2	2	3.25	1	1.53E+06		(R)DGKLVS	(R)D G K L|V S E S S/D V|L P K(-)		122.85	737.3925	1473.78	-0.0018	-1.2	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
26406	dirMS_041712_NAR_50mM_plus2.11986.11986.3	3	3.25	1	3.33E+06		(R)VVDLM	(R)V V|D/L M A H M A S K E(-)		130.52	444.2215	1330.649	0.0006	0.4	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
26407	dirMS_041712_NAR_50mM_plus2.13944.13944.3	3	3.25	1	7.16E+05	S81s	(R)DVLKGE	(R)D/V/L K G E S A A\s E I R(V)	s:N-acetylglucosamine (S)	140.85	526.5923	1374.722	203.04	-24.9	4.68	35549.6	10.18	HUMAN	Q96NR8	Retinol dehydrogenase 12
26408	dirMS_041712_NAR_50mM_plus2.14022.14022.3	3	3.25	0	6.73E+05		(K)QMVID	(K)Q M V/I/D|V L H P/G K(A)		142.2	412.894	1236.677	-0.0095	-7.6	6.74	32886.5	10.63	HUMAN	E7EPK6	40S ribosomal protein S24
26409	dirMS_041712_NAR_50mM_plus2.14226.14226.3	3	3.25	1	8.09E+04		(R)TQVELL	(R)T Q|V E L L E A P/T P A L K R(T)		143.53	555.9884	1665.953	-0.0027	-1.7	5.81	18460.6	5.48	HUMAN	C9IYM4	Glycogen [starch] synthase, muscle (Fragment)
26410	dirMS_041712_NAR_50mM_plus2.20165.20165.3	3	3.25	1	1.83E+04		(K)QNDQV	(K)Q N D/Q V/S F A S L/V E/E L K K(V)		173.72	612.3205	1834.955	-0.0076	-4.1	4.68	69285	5.2	HUMAN	G3V4Y7	Kinectin
26411	dirMS_041712_NAR_50mM_plus2.8318.8318.3	3	3.25	0	9.05E+04		(K)QQSIAG	(K)Q Q S I/A/G S A D S K/P I D V S R(L)		110.42	586.971	1758.898	0.0004	0.2	5.96	34637.3	8.91	HUMAN	Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1
26412	dirMS_041712_NAR_50mM_plus2.8446.8446.3	3	3.25	0	6.44E+04		(R)EPFHSIL	(R)E P F H S I L S/V L K(G)		111.17	423.9063	1269.72	-0.0158	-12.4	6.85	27027.7	6.85	HUMAN	Q5T3I4	Apolipoprotein A-I binding protein
26413	dirMS_041712_NAR_60mM_plus.11538.11538.3	3	3.25	1	4.83E+05		(R)GMDLQ	(R)G M/D L Q/P G N A L K R(F)		118	433.8981	1299.684	-0.004	-3.1	8.75	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
26414	dirMS_041712_NAR_60mM_plus.12915.12915.3	3	3.25	0	2.04E+05		(R)FLEDTF	(R)F L|E/D T/F G N D G R P R(V)		124.57	508.5817	1523.724	0.0068	4.5	4.56	114298.5	6.85	HUMAN	G5E928	Lysosomal alpha-mannosidase B peptide
26415	dirMS_041712_NAR_60mM_plus.19227.19227.3	3	3.25	0	5.02E+04		(K)VSHLLG	(K)V/S H L L G\I N\V/T D/F T R(G)		159.5	524.6233	1571.854	0.0013	0.8	6.71	227783.5	5.5	HUMAN	P35579	Myosin-9
26416	dirMS_041712_NAR_60mM_plus.19286.19286.3	3	3.25	1	8.48E+03	T20t	(K)EIGKIIP	(K)E/I G K I I P\F/t I A F K(R)	t:Phosphorylated T	159.73	519.6254	1476.882	79.9792	8.3	8.69	15415.3	6.64	HUMAN	Q8N812	Uncharacterized protein C12orf76
26417	dirMS_041712_NAR_60mM_plus.20867.20867.3	3	3.25	1	1.40E+05		(K)TFVNITP	(K)T F\V/N/I/T P A E V G V L V G K\D R(S)		170.55	639.0248	1915.065	-0.0049	-2.6	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
26418	dirMS_041712_NAR_60mM_plus.5789.5789.3	3	3.25	0	1.08E+05		(K)FASVQA	(K)F A S V/Q\A S\A P/Q G N S H K(E)		88.67	510.2582	1528.75	0.0098	6.4	8.76	46957	7.83	HUMAN	A2RRB2	ZNF608 protein
26419	dirMS_041712_NAR_120mM_minus.11178.11178.3	3	3.24	0	1.39E+05		(K)NFYQEH	(K)N/F/Y Q E H/P D L A R(R)		114.42	463.8944	1389.655	0.0141	10.1	5.32	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
26420	dirMS_041712_NAR_120mM_minus.18083.18083.4	4	3.24	1	2.27E+05		(R)ILEFFGL	(R)I L E F/F G L K K/E E C/P A V R(L)	C:Carbamidomethylation	154.08	484.763	1936.036	-0.0059	-3.1	6.23	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
26421	dirMS_041712_NAR_120mM_minus.5711.5711.3	3	3.24	1	7.04E+04		(R)REGGD	(R)R E G G D\G E\E|Q D\V/G/D A G R(L)		84.48	549.5713	1646.7	-0.0007	-0.5	4.02	64042.3	9.02	HUMAN	Q8N1G4	Leucine-rich repeat-containing protein 47
26422	dirMS_041712_NAR_120mM_minus.6472.6472.3	3	3.24	1	1.83E+04		(K)KMENCL	(K)K M/E N C\L/G E S R(H)	C:Carbamidomethylation	90.15	408.5232	1223.551	0.0043	3.5	6.14	43303.4	8.7	HUMAN	F8VRN8	LIM domain and actin-binding protein 1
26423	dirMS_041712_NAR_20mM_minus.11567.11567.2	2	3.24	0	2.97E+05		(R)GALQNI	(R)G A L\Q/N I/I\P A S T G A A K(A)		164.42	706.3976	1411.79	-0.0024	-1.7	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
26424	dirMS_041712_NAR_20mM_minus.12090.12090.3	3	3.24	1	3.81E+05		(-)XSTDTS	(-)X S T D T S/M N R S P/K(L)		170.48	446.227	1336.652	0.0139	10.4	8.75	4969.6	8.59	HUMAN	K7ELN8	Matrix metalloproteinase-28 (Fragment)
26425	dirMS_041712_NAR_20mM_minus.9299.9299.2	2	3.24	0	9.72E+04	M267m	(R)LITLEEE	(R)L I/T/L\E\E E m T K(Y)	m:Oxidized methionine	142.02	611.8143	1206.629	15.9927	-1.8	4.25	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
26426	dirMS_041712_NAR_30mM_minus2.18438.18438.2	2	3.24	0	1.34E+04		(R)LTAEDL	(R)L T|A E D\L F E/A R(I)		154.35	582.7922	1164.59	-0.0124	-10.7	4.14	533778	5.74	HUMAN	Q15149	Plectin
26427	dirMS_041712_NAR_50mM_minus2.15012.15012.3	3	3.24	0	1.44E+05		(K)IHYLDTT	(K)I H Y L D T\T T L/I E/P V/S R(S)		153.32	586.6522	1757.943	-0.0012	-0.7	5.32	25731.5	7.15	HUMAN	I3L297	Adapter molecule crk
26428	dirMS_041712_NAR_50mM_minus2.17020.17020.3	3	3.24	0	8.54E+04	K111k	(K)LLVMGT	(K)L L V M G T P P A V G A A S D/G k P K(S)	k:Ubiquitin-K	165.25	641.6908	1808.994	114.064	10.9	8.59	12816.5	10.23	HUMAN	G3V3I5	Uncharacterized protein
26429	dirMS_041712_NAR_50mM_minus2.8958.8958.3	3	3.24	1	1.16E+05	M88m	(K)DVDEAY	(K)D V/D/E A/Y m N K V E L E S R(L)	m:Oxidized methionine	118.62	605.2817	1797.832	15.9982	1.8	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
26430	dirMS_041712_NAR_50mM_minus2.9327.9327.3	3	3.24	0	2.64E+05	M167m	(R)ImLFTN	(R)I/m|L F/T N E D/N P H G N D\S A K(A)	m:Oxidized methionine	121.37	640.2914	1902.865	15.9946	-0.2	4.54	64302.5	6.4	HUMAN	B1AHC7	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)
26431	dirMS_041712_NAR_50mM_minus2.9349.9349.3	3	3.24	0	1.89E+05		(R)TYVTPP	(R)T Y/V T P P G T G F L P G D T A R(H)		121.02	583.963	1749.881	-0.0062	-3.5	5.5	19480	9.69	HUMAN	G3V282	Probable tRNA threonylcarbamoyladenosine biosynthesis protein OSGEP (Fragment)
26432	dirMS_041712_NAR_50mM_minus2.9357.9357.2	2	3.24	1	2.07E+04	K1596k	(R)GEAGVK	(R)G E A G V|K G E/k G G V G S K(G)	k:Ubiquitin-K	121.4	737.3927	1359.723	114.0555	8.5	8.5	248823.5	6.45	HUMAN	A6NMZ7	Collagen alpha-6(VI) chain
26433	dirMS_041712_NAR_60mM_minus.12870.12870.3	3	3.24	0	4.97E+05		(K)GIHPTIIS	(K)G I H|P T I\I|S E S F Q K(A)		131.52	486.2642	1456.78	-0.0014	-1	6.75	52843.5	6.17	HUMAN	B7Z9L0	T-complex protein 1 subunit delta
26434	dirMS_041712_NAR_60mM_minus.17097.17097.3	3	3.24	1	3.51E+04	M833m M	(K)mmALD	(K)m m/A/L/D R E V Q Y\L\L N/K(A)	m:Oxidized methionine	155.48	585.9628	1723.887	31.9869	-1.7	5.82	105005	5.57	HUMAN	E9PL22	Hypoxia up-regulated protein 1
26435	dirMS_041712_NAR_60mM_minus.18334.18334.3	3	3.24	0	1.21E+05		(R)LGIEGLS	(R)L G I E/G L S L/H/N V L K(L)		163.43	464.9423	1392.821	-0.0086	-6.2	6.75	177928	5.42	HUMAN	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1
26436	dirMS_041712_NAR_60mM_minus.8275.8275.3	3	3.24	0	4.59E+04	T519t	(R)SLAGFQ	(R)S L/A G/F Q E/S I L t D K(K)	t:N-acetylglucosamine (T)	105.9	537.9417	1408.732	203.0787	-0.4	4.37	87027	5.27	HUMAN	P83436	Conserved oligomeric Golgi complex subunit 7
26437	dirMS_041712_NAR_60mM_minus.8618.8618.3	3	3.24	0	2.43E+05	N128n	(K)IAVSLnY	(K)I A/V S L/n Y F K(I)	n:N-acetylglucosamine (N)	108.53	419.8951	1054.593	203.0776	-1.4	8.59	16194.4	9.92	HUMAN	E7EVQ5	Collagen triple helix repeat-containing protein 1
26438	dirMS_041712_NAR_60mM_minus.9717.9717.3	3	3.24	0	3.05E+05		(R)KPLLESG	(R)K P L L E|S G T/L/G T/K(G)		114.13	415.25	1243.726	0.0098	7.9	8.59	118930.9	5.49	HUMAN	P22314	Ubiquitin-like modifier-activating enzyme 1
26439	dirMS_041712_NAR_120mM_plus.16139.16139.3	3	3.24	1	1.91E+05		(R)GGRLEL	(R)G G R\L E L S G S A S G A A G/R(C)		138.35	482.5826	1445.746	-0.0123	-8.5	9.6	40477.6	5.18	HUMAN	A6NED2	RCC1 domain-containing protein 1
26440	dirMS_041712_NAR_20mM_plus.18320.18320.3	3	3.24	0	1.89E+04		(K)SSGPTSL	(K)S S G P T S L F A V\T/V A/P/P G A R(Q)		197.72	572.3108	1714.912	0.0056	3.3	9.47	91324.5	5.75	HUMAN	Q00839	Heterogeneous nuclear ribonucleoprotein U
26441	dirMS_041712_NAR_20mM_plus.6929.6929.2	2	3.24	0	9.56E+04		(K)AAAAA	(K)A A/A\A/A A\A\L\Q A K(S)		114.28	478.7792	956.552	-0.0012	-1.3	8.8	37884.5	11.27	HUMAN	H3BM89	60S ribosomal protein L4
26442	dirMS_041712_NAR_20mM_plus.7217.7217.2	2	3.24	0	1.02E+05		(R)SGAQAS	(R)S G A\Q/A\S S/T\P L S P T R(I)		117.42	680.3459	1359.686	-0.0018	-1.3	9.47	74423.5	6.57	HUMAN	P02545	Prelamin-A/C
26443	dirMS_041712_NAR_30mM_plus2.11329.11329.2	2	3.24	0	4.73E+04		(K)AFNWS	(K)A F|N W S S D/L N K(H)		112.23	591.286	1181.559	0.0062	5.2	5.88	59255.7	9.85	HUMAN	O75346	Zinc finger protein 253
26444	dirMS_041712_NAR_30mM_plus2.16974.16975.2	2	3.24	0	3.18E+04	K19k	(K)IYHPNV	(K)I Y H P/N\V D k(L)	k:Ubiquitin-K	141.93	550.2739	985.51	114.0304	-11.4	6.74	10145.6	9.15	HUMAN	F8VQQ8	Ubiquitin-conjugating enzyme E2 N
26445	dirMS_041712_NAR_30mM_plus2.5829.5829.2	2	3.24	0	8.42E+03		(R)ISSSSFS	(R)I/S\S S S/F S/R(V)		85.03	435.7193	870.432	-0.0002	-0.3	9.75	19288.4	10.19	HUMAN	F8VQY3	Keratin, type II cytoskeletal 8 (Fragment)
26446	dirMS_041712_NAR_30mM_plus2.6408.6408.2	2	3.24	0	1.46E+05		(R)FLEVDE	(R)F/L\E/V D E/R(N)		88.22	454.2274	907.452	-0.0044	-4.9	4.14	49798.6	5.52	HUMAN	H0YLH3	Geranylgeranyl transferase type-2 subunit alpha
26447	dirMS_041712_NAR_40mM_plus2.13712.13712.3	3	3.24	0	4.98E+03		(K)DQMQP	(K)D Q M Q P G G T A I S V T V|P Y R(V)		147.53	607.295	1819.901	-0.0303	-16.6	5.83	60689.6	9.68	HUMAN	Q6P1J9	Parafibromin
26448	dirMS_041712_NAR_40mM_plus2.19680.19680.3	3	3.24	1	3.21E+04		(R)LGSAIQ	(R)L G/S A I Q K I I T I\P A A L Q Q V K(N)		184.12	664.7445	1992.222	-0.0026	-1.3	10	265720.8	6.08	HUMAN	E7ETS8	DNA polymerase
26449	dirMS_041712_NAR_50mM_plus2.17945.17945.3	3	3.24	1	6.96E+05		(K)SLLGKD	(K)S L|L G K D V/L F L K(D)		161.7	411.5915	1232.761	-0.0013	-1.1	8.31	41827.5	7	HUMAN	B7Z7A9	Phosphoglycerate kinase
26450	dirMS_041712_NAR_50mM_plus2.19415.19415.3	3	3.24	0	3.50E+05		(R)GVPALV	(R)G V/P/A L V A L V A S S Q S V/R(E)		169.55	518.6453	1553.901	0.0204	13.1	9.75	97453.9	6.63	HUMAN	C9JJX6	Armadillo repeat protein deleted in velo-cardio-facial syndrome
26451	dirMS_041712_NAR_50mM_plus2.6512.6512.3	3	3.24	2	2.12E+04		(R)TERVEQ	(R)T E/R V E Q A/F R/A I D R(G)		98.88	530.9567	1590.835	0.0209	13.1	5.85	11901.1	4.72	HUMAN	E5RGG7	Protein-L-isoaspartate O-methyltransferase domain-containing protein 1
26452	dirMS_041712_NAR_50mM_plus2.8242.8242.3	3	3.24	1	3.49E+05		(R)VAVEAK	(R)V A/V E/A K N P A/D L/P K(L)		110.53	451.2563	1351.758	-0.0036	-2.7	6.04	96306.4	6.41	HUMAN	P13639	Elongation factor 2
26453	dirMS_041712_NAR_60mM_plus.10216.10216.3	3	3.24	1	8.18E+05		(K)TAVCDI	(K)T A/V/C D I/P P R G L/K(M)	C:Carbamidomethylation	111.95	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
26454	dirMS_041712_NAR_60mM_plus.16193.16193.3	3	3.24	1	5.46E+05	S891s	(K)IHRALN	(K)I H R A\L|N T\E/P P E G s K(E)	s:Phosphorylated S	142.18	543.6023	1548.813	79.9795	8.1	6.76	113960.2	9.93	HUMAN	O60391	Glutamate receptor ionotropic, NMDA 3B
26455	dirMS_041712_NAR_60mM_plus.20440.20440.3	3	3.24	1	2.66E+05		(R)FDITGV	(R)F D I T G V P A\N R T/L A K(V)		167.78	501.6108	1502.833	-0.0147	-9.8	8.75	295570.4	8.25	HUMAN	Q86UK0	ATP-binding cassette sub-family A member 12
26456	dirMS_041712_NAR_60mM_plus.21268.21268.3	3	3.24	0	2.23E+05		(R)QARPTY	(R)Q/A R P T Y\A T/A|M\L Q S L L/K(-)		175.57	597.9953	1791.979	-0.0072	-4	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
26457	dirMS_041712_NAR_60mM_plus.5248.5248.3	3	3.24	1	1.86E+05	M163m	(K)IYEDGD	(K)I/Y/E/D G D D D m K R(T)	m:Oxidized methionine	85.13	458.1946	1356.574	15.9956	0.5	4.03	21341.9	7.77	HUMAN	Q5R370	Calcyclin binding protein
26458	dirMS_041712_NAR_120mM_minus.20239.20239.4	4	3.23	0	4.90E+05		(K)LAFPSP	(K)L A\F P S|P F G H/L S E G F S H S R(W)		166.3	493.9968	1972.966	-0.0011	-0.5	6.92	16196.2	9.92	HUMAN	C9JRJ8	Sequestosome-1 (Fragment)
26459	dirMS_041712_NAR_20mM_minus.9237.9237.2	2	3.23	0	1.58E+04	S286s	(R)ILTAsQS	(R)I L|T/A s Q S R(S)	s:N-acetylglucosamine (S)	142.02	539.7915	875.495	203.0812	1.7	9.75	74404.7	6	HUMAN	B7Z7P5	E3 ubiquitin-protein ligase MARCH7
26460	dirMS_041712_NAR_30mM_minus2.12578.12578.2	2	3.23	0	2.09E+05		(K)YALSVG	(K)Y|A|L/S V G/Y R(H)		122.27	464.7493	928.489	0.0026	2.8	8.59	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
26461	dirMS_041712_NAR_30mM_minus2.13973.13973.2	2	3.23	0	3.15E+05		(R)LAGLFN	(R)L/A/G L/F N E Q R(K)		129.43	524.2789	1047.558	-0.0076	-7.3	6	63098.1	7.83	HUMAN	B7Z909	Hypoxia up-regulated protein 1
26462	dirMS_041712_NAR_30mM_minus2.16355.16355.2	2	3.23	1	1.09E+05	T234t	(R)HPDAFY	(R)H P|D/A F Y/L A R\t\A K(A)	t:Phosphorylated T	142.27	735.3466	1389.727	79.9586	-5.3	8.6	35854.2	9.41	HUMAN	F8W126	Microspherule protein 1 (Fragment)
26463	dirMS_041712_NAR_30mM_minus2.17760.17760.2	2	3.23	0	3.94E+05		(K)GNFNYI	(K)G N|F/N/Y/I E/F T/R(I)		151.3	630.8052	1260.601	0.0024	1.9	6	20513.6	4.62	HUMAN	J3QRS3	Myosin regulatory light chain 12A
26464	dirMS_041712_NAR_40mM_minus2.10991.10991.3	3	3.23	1	1.14E+05	M362m	(R)EGSVmL	(R)E G/S V/m/L Q/V D V/D\T V K G G L K(L)	m:Oxidized methionine	147.85	630.9989	1874.989	15.993	-1	4.56	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
26465	dirMS_041712_NAR_40mM_minus2.5265.5265.2	2	3.23	0	1.56E+04	M300m	(K)NMmAA	(K)N M/m A A C D/P R(H)	C:Carbamidomethylation m:Oxid	87.8	541.2153	1065.427	15.9959	0.9	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
26466	dirMS_041712_NAR_40mM_minus2.8489.8489.3	3	3.23	2	1.11E+05		(K)EDLRDT	(K)E D L R D/T F A A/M G\R L N V K(N)		130.85	612.6484	1835.943	-0.0126	-6.9	6.22	13151.8	5.56	HUMAN	H3BML9	Myosin regulatory light chain 2, skeletal muscle isoform (Fragment)
26467	dirMS_041712_NAR_50mM_minus2.10116.10116.3	3	3.23	1	5.70E+05		(K)LFQIYSK	(K)L F Q/I Y S/K S/P/F Y R(A)		124.85	516.9426	1548.821	-0.0077	-5	9.7	295096.7	9.32	HUMAN	B2RTY4	Unconventional myosin-IXa
26468	dirMS_041712_NAR_50mM_minus2.17512.17512.3	3	3.23	1	1.23E+05		(K)NAAGAL	(K)N A/A G A/L D L L K E/L K(N)		168.65	452.601	1355.789	-0.0008	-0.6	6.07	13786.8	9.33	HUMAN	B7Z4S1	Transcription elongation factor A protein 1
26469	dirMS_041712_NAR_50mM_minus2.18737.18737.3	3	3.23	1	7.67E+05		(K)EIINLKK	(K)E I/I/N/L K K D/L I R(S)		181.67	452.2862	1354.842	0.0024	1.8	8.69	15377.5	10.35	HUMAN	F5H2N8	Coiled-coil domain-containing protein 60
26470	dirMS_041712_NAR_50mM_minus2.8330.8330.3	3	3.23	0	5.48E+03		(K)VEGEAS	(K)V E G/E A S A L P T F W/G P R(G)		115.23	539.6119	1616.807	0.0144	8.9	4.53	28488	5.09	HUMAN	B0ZBF1	Atrial natriuretic peptide receptor 1
26471	dirMS_041712_NAR_60mM_minus.10693.10693.3	3	3.23	1	1.05E+06		(K)TAVCDI	(K)T|A|V/C D I/P P R G L K(M)	C:Carbamidomethylation	118.67	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
26472	dirMS_041712_NAR_60mM_minus.10820.10820.3	3	3.23	1	1.36E+05		(R)MASPV	(R)M/A S P V\N V K E E\V K(E)		120.32	444.2455	1330.704	0.0184	13.9	5.9	7852.8	5.3	HUMAN	H7BZ15	UPF0733 protein C2orf88 (Fragment)
26473	dirMS_041712_NAR_60mM_minus.7250.7250.3	3	3.23	0	1.49E+05		(K)TIEAEA	(K)T\I/E A E A A H G T/V T R(H)		99.87	452.5678	1355.691	-0.0025	-1.9	5.37	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
26474	dirMS_041712_NAR_60mM_minus.7511.7511.3	3	3.23	0	8.37E+04		(K)ALLQTH	(K)A L|L Q T H/P/E A\Q/R(A)		101.33	421.8989	1263.68	0.0017	1.4	6.79	15660.9	10.38	HUMAN	I3L1Y9	FLYWCH family member 2
26475	dirMS_041712_NAR_60mM_minus.9549.9549.3	3	3.23	1	4.47E+05		(K)TAVCDI	(K)T/A\V/C/D I/P P R G L/K(M)	C:Carbamidomethylation	112.42	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
26476	dirMS_041712_NAR_120mM_plus.10809.10809.4	4	3.23	2	8.30E+04	N90n	(K)QRHWL	(K)Q R H W L E P n K S I/F/K(Q)	n:N-acetylglucosamine (N)	109.63	472.2597	1682.912	203.1044	13.3	9.99	69683.6	5.97	HUMAN	A2A2Y4	FERM domain-containing protein 3
26477	dirMS_041712_NAR_120mM_plus.18854.18854.4	4	3.23	1	4.17E+05		(K)SPAAM	(K)S P A A M F L V G E/G S P D K K/A L K(K)		152.77	487.2719	1946.042	0.0242	12.4	8.22	60836.6	9.59	HUMAN	O00294	Tubby-related protein 1
26478	dirMS_041712_NAR_120mM_plus.7429.7429.3	3	3.23	0	3.61E+05	T174t	(K)VFFtLL	(K)V F\F t L L/W P G/K(V)	t:Phosphorylated T	91.22	429.8865	1207.687	79.9576	-6.8	8.72	64426	9.43	HUMAN	Q969Y0	NXPE family member 3
26479	dirMS_041712_NAR_20mM_plus.13772.13772.2	2	3.23	0	5.87E+04		(R)EVSADG	(R)E V S A D/G/P/I Q V T S T V K(N)		166.93	765.8991	1530.801	-0.0101	-6.6	4.37	34560.8	4.79	HUMAN	H0Y7R4	Kinesin-like protein KIF24 (Fragment)
26480	dirMS_041712_NAR_20mM_plus.18533.18533.2	2	3.23	0	1.36E+04		(R)APVPAS	(R)A P V/P A/S E L L|A\S G V L S R(A)		199.55	783.9444	1566.885	-0.0035	-2.2	6.05	533778	5.74	HUMAN	Q15149	Plectin
26481	dirMS_041712_NAR_20mM_plus.19123.19123.3	3	3.23	0	1.99E+05		(K)TLETQS	(K)T L E T Q S A L G|P A L/Q/A A F K(L)		202.6	582.6516	1745.943	-0.003	-1.7	5.66	120546	7.82	HUMAN	O95486	Protein transport protein Sec24A
26482	dirMS_041712_NAR_20mM_plus.19257.19257.2	2	3.23	1	2.52E+04	S832s	(K)DsGPET	(K)D s G P E/T/L E/K D L P R(K)	s:N-acetylglucosamine (S)	205.25	830.4161	1456.728	203.0971	10.7	4.32	112127.7	5.88	HUMAN	Q8N9B5	Junction-mediating and -regulatory protein

26483	dirMS_041712_NAR_20mM_plus.7267.7267.2	2	3.23	0	2.85E+04		(R)VLEEGS	(R)V L|E|E/G S V E A R(T)		118.03	544.7829	1088.558	0.0003	0.3	4.25	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
26484	dirMS_041712_NAR_30mM_plus2.4610.4610.2	2	3.23	0	1.92E+05		(K)EDAANN	(K)E D A A/N/N Y A/R(G)		73.87	512.2281	1023.449	-0.0001	-0.1	4.37	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
26485	dirMS_041712_NAR_40mM_plus2.10805.10805.3	3	3.23	1	4.32E+05		(R)DGKLVS	(R)D G K L V\S/E/S/S D/V L/P K(-)		128.65	491.9315	1473.78	0.0004	0.3	4.56	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
26486	dirMS_041712_NAR_40mM_plus2.12184.12184.2	2	3.23	0	2.65E+04		(R)IAAYLFK	(R)I/A/A Y L/F K(G)		137.85	413.2503	825.487	0.0064	7.8	8.59	15830.9	5.16	HUMAN	J3KRF5	Clathrin heavy chain 1 (Fragment)
26487	dirMS_041712_NAR_40mM_plus2.15704.15704.3	3	3.23	0	1.01E+04		(R)LQVIVCS	(R)L Q\V/I/V C S/A T L/H S F D V K(K)	C:Carbamidomethylation	158.6	606.3237	1816.963	-0.006	-3.3	6.74	83400.6	6.82	HUMAN	Q92499	ATP-dependent RNA helicase DDX1
26488	dirMS_041712_NAR_40mM_plus2.6198.6198.2	2	3.23	0	3.93E+04	S914s	(K)LSPsTAV	(K)L/S/P s/T A V K(Q)	s:Phosphorylated S	95.32	441.7142	802.467	79.9542	-13.7	8.75	114346.8	9.44	HUMAN	Q8IYT8	Serine/threonine-protein kinase ULK2
26489	dirMS_041712_NAR_40mM_plus2.6942.6942.2	2	3.23	0	7.45E+03		(K)SAAMTL	(K)S A/A/M T L/N E R(F)		101.07	496.7407	992.483	-0.0088	-8.9	5.72	83344.9	10.18	HUMAN	E9PK09	Bcl-2-associated transcription factor 1 (Fragment)
26490	dirMS_041712_NAR_40mM_plus2.7862.7862.2	2	3.23	1	1.45E+05		(K)EINISRK	(K)E I/N I/S\R K(M)		106.8	430.2474	859.5	-0.0121	-14	8.85	5116.9	9.77	HUMAN	D6RBG5	Serine/threonine-protein kinase Nek1
26491	dirMS_041712_NAR_50mM_plus2.17504.17504.3	3	3.23	0	1.02E+05		(K)GEMMD	(K)G E/M|M/D/L Q H G S L F L R(T)		159.92	545.2677	1633.783	0.006	3.7	5.32	12539.4	5.78	HUMAN	F5GXH2	L-lactate dehydrogenase A chain (Fragment)
26492	dirMS_041712_NAR_50mM_plus2.19599.19599.3	3	3.23	1	1.01E+05	T858t	(K)LSDALAI	(K)L S D A/L A M/V E E/t Q K T/K(A)	t:N-acetylglucosamine (T)	170.93	622.9846	1663.857	203.0821	1.5	4.68	162756.9	6.53	HUMAN	B1AJZ9	Forkhead-associated domain-containing protein 1
26493	dirMS_041712_NAR_50mM_plus2.8552.8552.3	3	3.23	0	4.72E+04		(K)ISNPTEF	(K)I S/N P\T E/F Q N H E K(Q)		112.13	481.9059	1443.686	0.0169	11.7	5.4	42522	9.96	HUMAN	E7ERR5	Nucleolar and spindle-associated protein 1
26494	dirMS_041712_NAR_50mM_plus2.9452.9452.3	3	3.23	0	5.99E+05		(K)GAVDGC	(K)G A\V|D G G L/S I/P H S/T K(R)		117.25	446.9057	1338.701	0.0013	1	6.74	34590.2	9.84	HUMAN	P46777	60S ribosomal protein L5
26495	dirMS_041712_NAR_60mM_plus.13217.13217.3	3	3.23	1	5.86E+05		(R)ICCDLD	(R)I/C/C D L D\V L A S K K(V)	C:Carbamidomethylation	125.33	474.5772	1421.713	0.0043	3.1	5.96	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
26496	dirMS_041712_NAR_60mM_plus.19021.19021.3	3	3.23	1	5.07E+03		(K)DAAVSK	(K)D A A V S K K A S/P E/A A S T P R(D)		158.1	562.6339	1685.882	0.0055	3.2	8.59	49966.5	5.76	HUMAN	E9PBR7	Protein PML
26497	dirMS_041712_NAR_60mM_plus.20814.20814.3	3	3.23	1	1.40E+05		(K)TFVNITP	(K)T F/V N I|T/P A E V G V L V/G K D R(S)		170.55	639.0248	1915.065	-0.0049	-2.6	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
26498	dirMS_041712_NAR_60mM_plus.6678.6678.3	3	3.23	0	1.20E+05	K267k	(K)MkTIWI	(K)M k T|I|W I A N K(H)	k:Ubiquitin-K	93.45	406.8878	1104.623	114.0254	-14.4	10	133110.4	5.68	HUMAN	E7EVD2	Epidermal growth factor
26499	dirMS_041712_NAR_120mM_minus.5604.5604.3	3	3.22	1	1.10E+05	T110t	(R)SSLSTVS	(R)S\S L S T V S/R t/L E K(L)	t:Phosphorylated T	84.03	463.2365	1307.717	79.9784	8.7	8.46	12945.8	9.98	HUMAN	A6PVL3	Kinocilin
26500	dirMS_041712_NAR_20mM_minus.7938.7938.2	2	3.22	1	4.72E+03		(K)TIKALDC	(K)T I K A L D G/D F S/E D N/R(N)		129	790.8823	1580.755	0.0022	1.4	4.22	156151	5.14	HUMAN	H0YMT1	Talin-2 (Fragment)
26501	dirMS_041712_NAR_30mM_minus2.10900.10900.2	2	3.22	0	7.88E+05		(R)GYSFTTT	(R)G Y|S F/T/T T A E R(E)		112.08	566.7699	1132.527	0.0056	4.9	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
26502	dirMS_041712_NAR_30mM_minus2.8496.8496.2	2	3.22	0	3.20E+06		(R)GTLDPV	(R)G T/L/D/P V E K(A)		100.33	429.7348	858.457	0.0056	6.5	4.37	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
26503	dirMS_041712_NAR_30mM_minus2.9511.9511.2	2	3.22	0	2.19E+05	M1m	(-)mFAWEI	(-)m F/A W E I/R(D)	m:Oxidized methionine	105.65	484.7299	952.471	15.9816	-13.8	5.75	30377	5.85	HUMAN	E7ERK2	Paired box protein Pax-5
26504	dirMS_041712_NAR_50mM_minus2.8539.8539.3	3	3.22	0	1.10E+04	M167m M	(R)LINANm	(R)L/I N A/N m m V L/G H E/P R(Q)	m:Oxidized methionine	116.57	542.9445	1594.819	31.9997	6.1	6.75	34747.6	6.06	HUMAN	O00487	26S proteasome non-ATPase regulatory subunit 14
26505	dirMS_041712_NAR_60mM_minus.10463.10463.3	3	3.22	0	2.04E+05		(R)LSNLAL	(R)L S N L/A L/V/K/P E K(T)		118.58	404.5829	1211.736	-0.0017	-1.4	8.59	15111	6.44	HUMAN	B4DE64	Programmed cell death protein 5
26506	dirMS_041712_NAR_60mM_minus.12898.12898.3	3	3.22	0	2.12E+05	T885t	(R)tNGVLLF	(R)t/N G V L L F/I P R(F)	t:N-acetylglucosamine (T)	131.28	444.9204	1129.673	203.0738	-4.1	9.41	122268.7	6.09	HUMAN	Q8TF46	DIS3-like exonuclease 1
26507	dirMS_041712_NAR_60mM_minus.14452.14452.3	3	3.22	0	1.62E+05		(R)AAAGGC	(R)A/A A G G Q/G S A V/A A E A E P G K(E)		139.95	514.591	1541.755	0.003	2	4.53	46876	9.38	HUMAN	Q9GZT9	Egl nine homolog 1
26508	dirMS_041712_NAR_60mM_minus.18728.18728.3	3	3.22	1	1.24E+04	T150t	(R)TTLRISE	(R)T T L R I S/E t P L/P I R(T)	t:Phosphorylated T	165.4	526.2842	1496.88	79.9585	-4.9	9.26	18657.1	9.97	HUMAN	H3BRW0	Ral guanine nucleotide dissociation stimulator-like 3 (Fragment)
26509	dirMS_041712_NAR_120mM_plus.14178.14178.4	4	3.22	1	1.80E+06	M294m	(R)ALQGAL	(R)A L|Q\G A/L m I Y F Y R/E E P R(F)	m:Oxidized methionine	127.23	494.0077	1957	16.0089	7.1	6.19	48041.8	6.46	HUMAN	P48775	Tryptophan 2,3-dioxygenase
26510	dirMS_041712_NAR_120mM_plus.5816.5816.2	2	3.22	1	1.28E+06		(K)IREEYPD	(K)I R/E E|Y P D|R(I)		84.52	539.2694	1077.532	-0.0008	-0.8	4.68	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
26511	dirMS_041712_NAR_20mM_plus.10664.10664.2	2	3.22	0	7.79E+03		(R)LLSTVAC	(R)L L|S T V A Q A/V K(G)		146.02	515.3183	1029.63	-0.0009	-0.9	8.75	60335	8.47	HUMAN	Q14554	Protein disulfide-isomerase A5
26512	dirMS_041712_NAR_20mM_plus.12656.12656.2	2	3.22	0	5.51E+04		(K)YGQISE	(K)Y G Q|I/S E\V V V V K(D)		160.02	610.8456	1220.689	-0.0046	-3.8	6	28815.3	9.52	HUMAN	B4E2X2	Cold-inducible RNA-binding protein
26513	dirMS_041712_NAR_30mM_plus2.20873.20873.2	2	3.22	0	3.45E+05		(R)QINWT	(R)Q I N W/T V/L Y/R(R)		163.25	596.8315	1192.647	0.0084	7	8.75	17656.4	11.01	HUMAN	C9JNW5	60S ribosomal protein L24
26514	dirMS_041712_NAR_40mM_plus2.4948.4948.2	2	3.22	0	1.87E+05	N467n	(K)CEDISnK	(K)C E D I/S n/K(L)	C:Carbamidomethylation n:N-ac	82.82	534.7263	865.372	203.0733	-5.7	4.37	118199	5.39	HUMAN	Q9H4L7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1
26515	dirMS_041712_NAR_50mM_plus2.11763.11763.3	3	3.22	1	1.81E+05	M698m	(K)AVISQGI	(K)A V I S Q/G M L/K C V G/S S m F L K(S)	C:Carbamidomethylation m:Oxid	130.45	658.0091	1956.012	16.0012	3.2	10	188058.8	6.52	HUMAN	E7ETD3	ATP-binding cassette sub-family A member 5
26516	dirMS_041712_NAR_50mM_plus2.12401.12401.3	3	3.22	0	4.98E+04		(R)ILAAANI	(R)I L/A A A N M P V Q G P L E K(S)		132.78	517.9575	1551.856	0.0016	1	6	86452.6	6.2	HUMAN	Q14765	Signal transducer and activator of transcription 4
26517	dirMS_041712_NAR_50mM_plus2.18385.18385.3	3	3.22	0	1.90E+04	N1567n	(K)LPKPDYr	(K)L/P K P D Y n|D L L A\A I K(D)	n:N-acetylglucosamine (N)	165.35	591.987	1570.884	203.0625	-9.5	5.96	464687.9	5.7	HUMAN	Q8WXX0	Dynein heavy chain 7, axonemal
26518	dirMS_041712_NAR_50mM_plus2.19662.19662.3	3	3.22	0	1.23E+04		(R)NVDPFH	(R)N V\D/P F H I/Y F C N L K(I)	C:Carbamidomethylation	171.83	556.277	1666.805	0.0118	7.1	6.74	36999.1	9.33	HUMAN	C9JVB6	Mitochondrial ribonuclease P protein 1 (Fragment)
26519	dirMS_041712_NAR_50mM_plus2.19759.19759.3	3	3.22	0	6.11E+04		(K)IFTPIVEI	(K)I F T/P/I V E H L G/L Q I R(F)		173.2	545.9893	1635.958	-0.0047	-2.9	6.75	15289.3	10.14	HUMAN	F8WBJ6	RNA-binding protein PNO1
26520	dirMS_041712_NAR_50mM_plus2.8899.8899.3	3	3.22	1	1.62E+04	Y71y	(R)ELyHILEI	(R)E L/y/H I L E/N H K F\T K(E)	y:Phosphorylated Y	113.83	584.6157	1671.885	79.9472	-10.9	7.01	27915.1	9.78	HUMAN	O95475	Homeobox protein SIX6
26521	dirMS_041712_NAR_60mM_plus.19842.19842.3	3	3.22	0	3.29E+04		(K)SFLIWVI	(K)S F/L/I W V N E E D/H/T R(V)		163.53	549.2699	1645.797	-0.0017	-1.1	4.65	29478.9	6.26	HUMAN	E9PCP8	Creatine kinase U-type, mitochondrial
26522	dirMS_041712_NAR_60mM_plus.6996.6996.3	3	3.22	0	2.75E+05		(R)QVQSQ	(R)Q V/Q/S\Q A H/G L Q M R(L)		94.97	461.5687	1382.696	-0.0042	-3	9.75	59390.2	9.41	HUMAN	G8JLG1	Structural maintenance of chromosomes protein 1A
26523	dirMS_041712_NAR_120mM_minus.12698.12698.3	3	3.21	1	2.33E+05	M5109m Y	(K)EmVQKI	(K)E/m V Q K I V N S/V y G/K(V)	m:Oxidized methionine y:Ph	123.33	530.9318	1494.799	95.9824	13.3	8.59	795633.2	6.26	HUMAN	J3QTJ6	Fibrous sheath-interacting protein 2
26524	dirMS_041712_NAR_120mM_minus.18203.18203.4	4	3.21	1	1.17E+05		(K)DGNLAS	(K)D G N L A/S/T/L G/Q H K G P I F A L/K(W)		154.2	492.5217	1967.071	-0.0059	-3	8.6	56221.5	5.28	HUMAN	Q9BZK7	F-box-like/WD repeat-containing protein TBL1XR1
26525	dirMS_041712_NAR_120mM_minus.6954.6954.4	4	3.21	1	1.75E+05		(K)ALASEKS	(K)A L/A S E K S P T A/D A K P A/P K(R)		92.37	421.2327	1681.912	-0.003	-1.8	8.54	58791	9.93	HUMAN	E9PDI4	Ladinin-1
26526	dirMS_041712_NAR_120mM_minus.7073.7073.3	3	3.21	0	1.14E+05		(K)HECQAN	(K)H E C Q A\N G|P/E/D L\N R(A)	C:Carbamidomethylation	92.9	513.8916	1539.661	-0.0002	-0.2	4.65	18961.8	8.63	HUMAN	P60981	Destrin
26527	dirMS_041712_NAR_20mM_minus.10176.10176.2	2	3.21	0	7.52E+03		(R)TIAQDY	(R)T I/A/Q D/Y G V/L K(A)		151.23	554.3035	1107.604	-0.0047	-4.3	5.5	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
26528	dirMS_041712_NAR_20mM_minus.13444.13444.2	2	3.21	2	5.07E+03		(K)SPEKSKF	(K)S P/E K S K P/D E K D P E K(S)		185.22	807.4137	1613.802	0.0184	11.4	4.94	474806.9	5.78	HUMAN	F8VWT9	Probable E3 ubiquitin-protein ligase HECTD4
26529	dirMS_041712_NAR_20mM_minus.8368.8368.2	2	3.21	0	2.07E+05	S594s	(R)DGEILAT	(R)D G\E I/L/A T G\s K(D)	s:N-acetylglucosamine (S)	132.67	597.3051	990.51	203.0927	11.2	4.37	112640.2	4.75	HUMAN	Q96MT7	WD repeat-containing protein 52
26530	dirMS_041712_NAR_20mM_minus.8606.8606.2	2	3.21	0	1.03E+05	K24k	(R)LYVNSEI	(R)L/Y|V N S|E k(Q)	k:Ubiquitin-K	135.8	483.7514	852.446	114.0494	6.7	6	57031.6	6.5	HUMAN	B0QZ65	GTPase activating protein and VPS9 domains 1
26531	dirMS_041712_NAR_20mM_minus.9853.9853.2	2	3.21	0	4.71E+04		(K)DVNAAI	(K)D V|N/A A I/A T I/K(T)		149.13	508.2919	1015.578	-0.0017	-1.7	5.84	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
26532	dirMS_041712_NAR_30mM_minus2.14487.14487.2	2	3.21	0	3.77E+05		(K)DLSIAAV	(K)D L|S I A A V G K(Y)		132.98	437.2551	873.504	-0.0011	-1.2	5.84	134148.1	6.48	HUMAN	O75182	Paired amphipathic helix protein Sin3b
26533	dirMS_041712_NAR_30mM_minus2.17936.17936.2	2	3.21	0	5.56E+04		(K)NLDENG	(K)N/L|D/E N G L/D/L L S K(M)		152.6	665.846	1330.685	-0.0002	-0.1	4.03	34151.9	8.46	HUMAN	P06493	Cyclin-dependent kinase 1
26534	dirMS_041712_NAR_30mM_minus2.20043.20043.2	2	3.21	0	1.29E+04	K101k	(R)kQVEIAC	(R)k|Q V E I A\Q R(E)	k:Ubiquitin-K	168.95	543.3132	971.563	114.0559	11.9	8.75	46814.8	8.33	HUMAN	P00966	Argininosuccinate synthase
26535	dirMS_041712_NAR_30mM_minus2.6276.6276.2	2	3.21	0	1.97E+05	M796m	(R)mNEAFC	(R)m N E|A/F G D|T/K(F)	m:Oxidized methionine	88.02	514.726	1012.44	16.0043	9.1	4.37	90316.8	5.52	HUMAN	Q13263	Transcription intermediary factor 1-beta
26536	dirMS_041712_NAR_50mM_minus2.11461.11461.3	3	3.21	0	2.35E+04		(R)LIAEQPF	(R)L I/A E Q/P/P H L T/P/G I R(E)		133.68	514.6309	1541.88	-0.0017	-1.1	6.75	20915.7	6.45	HUMAN	C9JBI3	Phosphoserine phosphatase (Fragment)
26537	dirMS_041712_NAR_50mM_minus2.12568.12568.3	3	3.21	0	3.06E+05		(K)AASDIAI	(K)A A\S D/I|A M/T\E L P P T H P I R(L)		139.55	607.3158	1819.937	-0.0042	-2.3	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
26538	dirMS_041712_NAR_50mM_minus2.17076.17076.3	3	3.21	1	8.59E+04		(R)QVNTAS	(R)Q V N T A S I K N L M G Q/E L R(R)		165.23	601.3217	1801.959	-0.0083	-4.6	8.75	55416.5	8.46	HUMAN	I3L077	HCG1987119, isoform CRA_a
26539	dirMS_041712_NAR_50mM_minus2.5265.5265.3	3	3.21	0	8.24E+05		(K)TATPQQ	(K)T A/T/P Q Q A Q E V/H E K(L)		88.02	489.5768	1466.723	-0.0075	-5.1	5.37	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
26540	dirMS_041712_NAR_50mM_minus2.7586.7586.3	3	3.21	1	1.66E+04	M22m	(K)LAEQAE	(K)L A/E/Q A E R Y D D m/A A C M K(S)	C:Carbamidomethylation m:Oxid	111.05	639.9402	1901.819	15.987	-4.1	4.32	5919.6	4.73	HUMAN	E5RGE1	14-3-3 protein zeta/delta (Fragment)
26541	dirMS_041712_NAR_60mM_minus.12858.12858.3	3	3.21	0	2.49E+05		(K)AQIHDL	(K)A Q I H D L\V\L|V G G/S T R(I)		131.42	489.2745	1465.812	-0.0032	-2.2	6.79	60126	5.44	HUMAN	E7EP94	Heat shock 70 kDa protein 1A/1B
26542	dirMS_041712_NAR_60mM_minus.13367.13367.3	3	3.21	1	2.90E+05		(K)FSIEDLK	(K)F/S/I E D L/K A Q P K(Q)		135.05	425.9025	1275.694	-0.0014	-1.1	6.07	13579.2	9.99	HUMAN	E9PPQ6	Thymocyte nuclear protein 1 (Fragment)
26543	dirMS_041712_NAR_60mM_minus.16028.16028.3	3	3.21	1	7.44E+04	T54t	(R)tLLEDGT	(R)t L L E D/G T/F K V R(V)	t:N-acetylglucosamine (T)	149.32	494.5973	1278.705	203.0721	-4.9	5.74	20958.6	8.78	HUMAN	I3L0Y6	NmrA-like family domain-containing protein 1 (Fragment)
26544	dirMS_041712_NAR_120mM_plus.11787.11787.4	4	3.21	2	5.53E+04	T28t	(R)KALStH	(R)K A/L S t H/A A G K Q A/E S S S K(A)	t:Phosphorylated T	116.2	445.9748	1700.893	79.9848	10.4	9.7	6901.6	9.99	HUMAN	F8WCU5	Biotinidase
26545	dirMS_041712_NAR_120mM_plus.8262.8262.3	3	3.21	1	9.06E+04	M208m	(R)EKLEME	(R)E K L E M E|m E/A A R(H)	m:Oxidized methionine	96.77	451.5439	1336.623	15.9936	-1	4.49	29678.2	9.57	HUMAN	C9JYS8	Non-POU domain-containing octamer-binding protein (Fragment)
26546	dirMS_041712_NAR_20mM_plus.13938.13938.3	3	3.21	0	4.54E+05	S12s	(-)MAPSTV	(-)M A P S T V A/V E/L L s P K(E)	s:Phosphorylated S	168.78	508.2519	1442.792	79.9488	-11.5	5.75	18339.9	9.7	HUMAN	Q5TA89	Transcription factor HES-5
26547	dirMS_041712_NAR_20mM_plus.7703.7703.2	2	3.21	0	4.02E+03		(R)VLADPSI	(R)V L A D/P S D\D T K(G)		122.45	530.7656	1060.516	0.0082	7.8	3.93	266161	5.68	HUMAN	E9PPU0	Epiplakin
26548	dirMS_041712_NAR_20mM_plus.8421.8421.2	2	3.21	0	3.29E+04	M87m	(R)NDLSPT	(R)N D\L|S\P T T/V/m S E G A R(N)	m:Oxidized methionine	128.28	747.3491	1477.695	15.9958	0.6	4.37	22233.1	7.14	HUMAN	P30043	Flavin reductase (NADPH)
26549	dirMS_041712_NAR_30mM_plus2.11164.11164.2	2	3.21	0	2.82E+05		(R)GTGIVS	(R)G T\G\I|V/S A/P V/P\K(K)		111.33	513.3006	1025.599	-0.005	-4.9	8.75	21898	11.33	HUMAN	E9PM36	40S ribosomal protein S2
26550	dirMS_041712_NAR_30mM_plus2.15446.15446.2	2	3.21	0	3.31E+05		(R)GLPWSC	(R)G L/P W/S/C S A D E V Q\R(F)	C:Carbamidomethylation	133.27	752.8375	1504.685	-0.0172	-11.4	4.37	4406.9	4.36	HUMAN	D6R9D3	Heterogeneous nuclear ribonucleoprotein H
26551	dirMS_041712_NAR_30mM_plus2.19205.19205.2	2	3.21	0	1.38E+05	S43s	(R)WLAAsP	(R)W/L/A A s P/T K(E)	s:N-acetylglucosamine (S)	153.68	538.7881	873.483	203.086	6.2	8.75	11725	11.11	HUMAN	C9IZW7	Protein FAM3D (Fragment)
26552	dirMS_041712_NAR_40mM_plus2.15852.15852.3	3	3.21	1	8.96E+04	M340m	(R)ALGTEVI	(R)A L|G T E/V I Q L/F P E K G N m G K(I)	m:Oxidized methionine	160.1	650.0097	1932.026	15.9886	-3.2	6.18	67184.7	9.24	HUMAN	O95831	Apoptosis-inducing factor 1, mitochondrial
26553	dirMS_041712_NAR_40mM_plus2.8048.8048.2	2	3.21	1	6.45E+04		(K)SMFAGI	(K)S M/F/A/G D K K(G)		108.08	442.2237	883.434	0.0059	6.7	8.31	20136.9	9.44	HUMAN	Q5TAE8	ERO1-like beta (S. cerevisiae) (Fragment)
26554	dirMS_041712_NAR_50mM_plus2.11553.11553.3	3	3.21	0	2.85E+05		(K)ITKPGSII	(K)I T K P G S I D S N N Q/L/F/A/P G G R(L)		128.32	658.0091	1972.025	-0.0119	-6	8.75	176357.7	5.25	HUMAN	D3DNT2	Eukaryotic translation initiation factor 4 gamma 1
26555	dirMS_041712_NAR_50mM_plus2.13953.13953.3	3	3.21	1	4.41E+04		(R)ALDPYKI	(R)A L D P Y K P R R/A G|F G E S/R(S)		142.8	607.3177	1819.956	-0.0176	-9.7	9.98	105966.5	9.75	HUMAN	Q8TE58	A disintegrin and metalloproteinase with thrombospondin motifs 15
26556	dirMS_041712_NAR_50mM_plus2.17204.17204.3	3	3.21	1	2.86E+05		(R)LESLDIPI	(R)L E S L/D I\P F T K A K(R)		158.6	454.6	1361.767	0.018	13.2	6.07	115807.5	5.38	HUMAN	Q9P2E2	Kinesin-like protein KIF17
26557	dirMS_041712_NAR_50mM_plus2.17310.17310.3	3	3.21	1	3.22E+05	T103t M10	(K)IIKtPmD	(K)I I|K/t P m D/M G T I K(K)	t:N-acetylglucosamine (T) m:	158.58	522.9433	1347.738	219.0779	2.3	8.59	152672.5	9.35	HUMAN	O60885	Bromodomain-containing protein 4
26558	dirMS_041712_NAR_50mM_plus2.20585.20585.3	3	3.21	1	3.17E+05		(R)VISGVLC	(R)V I|S G/V L Q/L G N I V\F K K(E)		176.33	539.0011	1614.994	-0.0054	-3.3	10	227783.5	5.5	HUMAN	P35579	Myosin-9
26559	dirMS_041712_NAR_50mM_plus2.20831.20831.3	3	3.21	0	1.28E+05		(R)ELSELSLI	(R)E L/S/E|L S L/L S L Y G I H K(Q)		178.87	567.984	1701.942	-0.0047	-2.8	5.4	44907.6	5.84	HUMAN	P15309	Prostatic acid phosphatase
26560	dirMS_041712_NAR_50mM_plus2.21557.21557.3	3	3.21	1	1.59E+05		(R)NPPLAE	(R)N P/P L/A E A L/L S/G D L E/K F S R(V)		183.07	653.0218	1957.039	0.0119	6.1	4.68	11963.3	4.8	HUMAN	H0YI90	Protein DDI1 homolog 2 (Fragment)
26561	dirMS_041712_NAR_50mM_plus2.5517.5517.3	3	3.21	1	9.44E+04	S761s	(K)LGLsKHT	(K)L G|L s/K/H T T N D R(T)	s:N-acetylglucosamine (S)	90.18	482.2464	1241.66	203.065	-10	8.76	93412.8	6.3	HUMAN	B3KP41	PHD finger protein 3 (Fragment)
26562	dirMS_041712_NAR_50mM_plus2.6668.6668.3	3	3.21	0	4.55E+05		(R)IEICVSD	(R)I E/I C V S D W W G A R(H)	C:Carbamidomethylation	99.23	497.9026	1491.705	-0.0117	-7.8	4.37	32307.5	10.46	HUMAN	Q8NI29	F-box only protein 27
26563	dirMS_041712_NAR_50mM_plus2.9281.9281.3	3	3.21	0	5.74E+05	M115m	(R)VmLGET	(R)V m/L/G/E/T N P A D S K P G T I R(G)	m:Oxidized methionine	115.57	601.3075	1785.916	15.9916	-1.8	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
26564	dirMS_041712_NAR_60mM_plus.10342.10342.3	3	3.21	1	1.30E+06		(K)AIQLEYS	(K)A I/Q/L/E\Y S E A R R(T)		112.13	445.9046	1335.701	-0.0023	-1.7	6.19	41296.9	9.52	HUMAN	B4DT72	26S proteasome non-ATPase regulatory subunit 3
26565	dirMS_041712_NAR_60mM_plus.21108.21108.3	3	3.21	2	1.05E+05	S179s	(K)EQGKSP	(K)E Q G K/S P\K A V I s I K(D)	s:N-acetylglucosamine (S)	173.75	529.9643	1384.816	203.0625	-10.6	9.7	39372.4	9.77	HUMAN	J3QRD3	Arf-GAP with dual PH domain-containing protein 2 (Fragment)
26566	dirMS_041712_NAR_60mM_plus.6066.6066.3	3	3.21	0	1.89E+05	M480m	(R)AAHSEG	(R)A A H\S E G N T T A/G L/D/m R(E)	m:Oxidized methionine	90.88	516.2346	1530.697	15.9927	-1.4	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
26567	dirMS_041712_NAR_60mM_plus.7991.7991.3	3	3.21	0	3.12E+05		(R)SQLLGS	(R)S Q/L/L/G S A H/E V Q R(F)		99.45	442.2342	1324.697	-0.0087	-6.6	6.47	285798.6	5.23	HUMAN	A6NG51	Spectrin alpha chain, non-erythrocytic 1
26568	dirMS_041712_NAR_120mM_minus.11538.11538.3	3	3.2	0	5.06E+06		(R)LFFVCG	(R)L F F V C G Q E G/L/R(A)	C:Carbamidomethylation	116.67	442.565	1325.667	0.0134	10.1	6	14481.7	6.05	HUMAN	A3KFI1	Neuroblastoma suppressor of tumorigenicity 1 (Fragment)
26569	dirMS_041712_NAR_120mM_minus.12846.12846.3	3	3.2	0	2.32E+05		(K)TFTAWC	(K)T F/T\A W/C N\S H L R(K)	C:Carbamidomethylation	123.62	464.8871	1392.648	-0.001	-0.7	9.44	104488.6	5.36	HUMAN	B2RCS5	Actinin, alpha 2, isoform CRA_b
26570	dirMS_041712_NAR_120mM_minus.13822.13822.3	3	3.2	0	2.31E+05	K467k	(K)LVDQFF	(K)L V/D Q F\F/V M k(S)	k:Ubiquitin-K	129.68	414.2125	1126.597	114.0264	-13.3	5.84	96842.2	9	HUMAN	F5GXW1	Dedicator of cytokinesis protein 4
26571	dirMS_041712_NAR_120mM_minus.17913.17913.3	3	3.2	1	1.37E+05		(R)AGKLDP	(R)A G K\L D/P H\L/V L D Q L R(C)		151.82	525.6385	1574.901	-0.0004	-0.2	6.79	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
26572	dirMS_041712_NAR_120mM_minus.18219.18219.4	4	3.2	2	1.95E+05	S14s	(-)MAVPAA	(-)M A V/P A A L/I/L R E S P s M K K(A)	s:Phosphorylated S	154.23	481.2594	1842.034	79.9818	8	9.99	15911.1	6.92	HUMAN	D6RC04	COMM domain-containing protein 10
26573	dirMS_041712_NAR_20mM_minus.10738.10738.3	3	3.2	0	8.54E+03	M78m K85	(K)GLCQLm	(K)G L C Q\L m G|D P A S G/k R(K)	C:Carbamidomethylation m:Oxid	155.15	540.5959	1489.725	130.0482	6.4	8.75	141364.5	9	HUMAN	A6NGG8	Uncharacterized protein C2orf71
26574	dirMS_041712_NAR_20mM_minus.7317.7317.2	2	3.2	0	3.99E+04		(K)AVTEQG	(K)A V/T E Q/G A E\L S N E/E R(N)		120.98	766.8612	1532.719	-0.0036	-2.3	4.09	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
26575	dirMS_041712_NAR_20mM_minus.9032.9032.2	2	3.2	0	6.54E+04	M68m M7	(R)NLAmG	(R)N/L A/m/G V N L T/S m S K(I)	m:Oxidized methionine	139.73	699.34	1365.687	31.9862	-2.6	8.75	29110.6	4.57	HUMAN	P12004	Proliferating cell nuclear antigen
26576	dirMS_041712_NAR_30mM_minus2.14614.14614.2	2	3.2	0	7.27E+04		(K)LSFGYVI	(K)L S|F/G Y V\R(S)		133.22	421.2267	841.457	-0.0105	-12.5	8.75	409090.1	5.82	HUMAN	Q15911	Zinc finger homeobox protein 3
26577	dirMS_041712_NAR_30mM_minus2.15340.15340.2	2	3.2	0	2.38E+05		(K)TNLPIFK	(K)T N|L|P I F K(L)		136.2	416.7494	832.493	-0.0012	-1.4	8.41	18819.1	8.89	HUMAN	O60493	Sorting nexin-3
26578	dirMS_041712_NAR_30mM_minus2.16366.16366.3	3	3.2	0	4.45E+05		(R)ASLEAAI	(R)A S L E\A A\I/A/D A/E/Q R(G)		143.23	448.8965	1344.675	-0.0004	-0.3	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
26579	dirMS_041712_NAR_30mM_minus2.9138.9138.2	2	3.2	0	6.12E+05		(R)ISPESGL	(R)I S P E/S G L A K(A)		103.48	451.2537	901.499	0.0012	1.3	6	84342.7	4.26	HUMAN	Q86TY3	Uncharacterized protein C14orf37
26580	dirMS_041712_NAR_50mM_minus2.15637.15637.3	3	3.2	0	2.54E+05	M460m	(R)ISIEmNC	(R)I S|I E/m N G/T L E D Q L S H L K(Q)	m:Oxidized methionine	157.28	648.6635	1927.979	15.9966	0.9	4.65	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
26581	dirMS_041712_NAR_50mM_minus2.15953.15953.3	3	3.2	2	2.17E+05	S476s	(R)KsLSELV	(R)K s/L S E/L V D D/K F G T G T K(K)	s:N-acetylglucosamine (S)	158.43	643.3412	1724.907	203.1025	12	6.12	85343.5	5.05	HUMAN	Q9BQI7	PH and SEC7 domain-containing protein 2
26582	dirMS_041712_NAR_50mM_minus2.6617.6617.3	3	3.2	0	3.68E+04		(K)IGEEEIQ	(K)I G E E E I Q/K P E E/K(V)		104	476.9108	1428.722	-0.0038	-2.7	4.32	81733.5	5.24	HUMAN	E9PAW1	Splicing factor 3A subunit 1
26583	dirMS_041712_NAR_50mM_minus2.7020.7020.3	3	3.2	2	1.43E+05	M291m	(K)KARmG	(K)K A/R m/G V V/E C A/K(H)	C:Carbamidomethylation m:Oxid	106.93	422.2224	1248.655	15.9975	2.1	9.99	42088	5.39	HUMAN	F8VTY8	Proliferation-associated protein 2G4
26584	dirMS_041712_NAR_60mM_minus.15460.15460.3	3	3.2	0	9.90E+04		(R)EHALLA	(R)E H A L L A|Y\T L/G V K(Q)		146.22	438.9202	1314.742	0.0044	3.4	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
26585	dirMS_041712_NAR_60mM_minus.15658.15658.3	3	3.2	1	1.09E+05	M332m	(R)AKFEELI	(R)A K F E\E\L N|m D L/F/R(S)	m:Oxidized methionine	147.6	510.255	1512.752	15.9989	2.6	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
26586	dirMS_041712_NAR_60mM_minus.6298.6298.3	3	3.2	1	6.81E+04		(R)ATEGM	(R)A T/E/G M/V V A D K N C S K(I)	C:Carbamidomethylation	94	503.9042	1509.704	-0.0055	-3.7	6.11	15607.8	9.99	HUMAN	B4E0P1	Proteasome (Prosome, macropain) subunit, beta type, 7, isoform CRA_b
26587	dirMS_041712_NAR_60mM_minus.8166.8166.3	3	3.2	1	8.67E+04		(K)GEFKDEI	(K)G E/F/K/D E E E T/V T T K(H)		105.5	504.913	1512.706	0.018	11.9	4.25	68315.4	6.01	HUMAN	Q14677	Clathrin interactor 1
26588	dirMS_041712_NAR_120mM_plus.7334.7334.3	3	3.2	1	4.50E+05		(R)ESNCYD	(R)E S/N C Y/D/P E R V K(N)	C:Carbamidomethylation	91.83	466.2133	1396.616	0.0092	6.6	4.68	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1
26589	dirMS_041712_NAR_120mM_plus.8565.8565.3	3	3.2	0	8.62E+05		(K)QHTFVE	(K)Q H T F V E/T/E/S V R(Y)		97.78	444.8857	1332.654	-0.0117	-8.8	5.4	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
26590	dirMS_041712_NAR_20mM_plus.12472.12472.3	3	3.2	0	5.11E+04		(K)VNQIGS	(K)V N Q I\G S/V\T E/S I Q A C K(L)	C:Carbamidomethylation	159.02	545.2781	1633.821	-0.0016	-1	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
26591	dirMS_041712_NAR_20mM_plus.13229.13229.2	2	3.2	0	3.22E+05	M148m	(R)DLTDYLr	(R)D L/T/D Y L m/K(I)	m:Oxidized methionine	164.32	507.7439	998.486	15.9942	-0.7	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle

26592	dirMS_041712_NAR_20mM_plus.17216.17216.3	3	3.2	0	1.85E+05		(R)AIVAIEN	(R)A I\V A I E N P A D/V S V/I S S R(N)		189.12	580.9864	1740.949	-0.0044	-2.5	4.37	33022.6	4.78	HUMAN	A6NE09	Protein RPSAP58
26593	dirMS_041712_NAR_20mM_plus.17343.17343.3	3	3.2	0	3.74E+05	M191m	(K)STGEAL	(K)S T G E A L V Q G L m/G A A V T L/K(N)	m:Oxidized methionine	191.22	587.9829	1745.947	15.9875	-4.2	5.72	23040.3	5.54	HUMAN	H3BRC0	Ubiquinone biosynthesis protein COQ9, mitochondrial
26594	dirMS_041712_NAR_20mM_plus.18214.18214.3	3	3.2	0	1.60E+05		(R)LSVLGAI	(R)L S V L G A I T/S/V/Q Q R(L)		196.2	457.9354	1371.795	-0.0038	-2.8	9.75	47760.5	5.39	HUMAN	B7Z7P8	Eukaryotic peptide chain release factor subunit 1
26595	dirMS_041712_NAR_20mM_plus.18463.18463.3	3	3.2	0	1.88E+04		(R)APVPAS	(R)A P\V P A S E L\L/A S/G V L S R(A)		199.92	522.9655	1566.885	-0.003	-1.9	6.05	533778	5.74	HUMAN	Q15149	Plectin
26596	dirMS_041712_NAR_20mM_plus.18495.18495.3	3	3.2	0	1.88E+04		(R)APVPAS	(R)A P\V P A S E L|L\A S/G\V L S R(A)		199.92	522.9655	1566.885	-0.003	-1.9	6.05	533778	5.74	HUMAN	Q15149	Plectin
26597	dirMS_041712_NAR_20mM_plus.8170.8170.2	2	3.2	0	7.99E+04	T282t M28	(K)YVVDtG	(K)Y/V/V D t G m V K(A)	t:N-acetylglucosamine (T) m:	126.28	615.8042	1011.518	219.0832	7.2	5.83	70280.6	8.97	HUMAN	I3L1L6	Putative ATP-dependent RNA helicase DHX33 (Fragment)
26598	dirMS_041712_NAR_20mM_plus.9844.9844.2	2	3.2	0	1.26E+05		(R)SSTDSLP	(R)S S T D S L/P/G P I S R(Q)		139.47	608.8139	1216.617	0.0037	3.1	5.55	65763.5	9.81	HUMAN	Q9HCD5	Nuclear receptor coactivator 5
26599	dirMS_041712_NAR_30mM_plus2.18365.18365.2	2	3.2	1	2.39E+05		(K)SDKSAV	(K)S D|K S A V S V/D S K(V)		149.22	561.7934	1122.564	0.0158	14.1	5.68	249766.9	6.66	HUMAN	B2RTR6	PCNX protein
26600	dirMS_041712_NAR_30mM_plus2.19364.19364.2	2	3.2	0	5.03E+04		(K)YPQLLP	(K)Y/P Q/L|L/P G I/R(G)		153.65	528.814	1056.62	0.0007	0.6	8.75	45228.3	6.03	HUMAN	F5H737	Adenosylhomocysteinase
26601	dirMS_041712_NAR_30mM_plus2.20589.20589.2	2	3.2	0	2.04E+05		(R)TTLLPGL	(R)T T|L/L/P G L L K(T)		161.22	478.3126	955.619	-0.0007	-0.8	8.41	55373.1	7.25	HUMAN	F5H6Y1	Phenylalanine--tRNA ligase beta subunit
26602	dirMS_041712_NAR_30mM_plus2.22528.22528.2	2	3.2	0	6.10E+04		(R)LEGLTD	(R)L E/G L/T/D E/I/N F\L R(Q)		174.63	710.3766	1419.748	-0.0019	-1.3	4.14	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
26603	dirMS_041712_NAR_30mM_plus2.6448.6448.2	2	3.2	0	1.26E+05		(K)SGYLSSE	(K)S G|Y|L/S S E R(L)		87.8	449.7152	898.427	-0.0034	-3.7	5.72	65692.2	5.7	HUMAN	E7EQR4	Ezrin
26604	dirMS_041712_NAR_30mM_plus2.8559.8559.2	2	3.2	0	4.00E+05		(R)FAQIVQ	(R)F/A|Q|I V Q K(G)		98.07	417.2466	833.488	-0.002	-2.4	8.75	11439.8	9.3	HUMAN	G3XAN8	Mitochondrial import inner membrane translocase subunit Tim8 B
26605	dirMS_041712_NAR_40mM_plus2.12655.12655.3	3	3.2	0	5.25E+04		(K)SLEDLIF	(K)S L/E/D L I F E S L P E N\A S H K(L)		141.12	643.6587	1928.96	0.0015	0.8	4.4	46401.7	6.35	HUMAN	B4DK25	Arginyl-tRNA--protein transferase 1
26606	dirMS_041712_NAR_40mM_plus2.9244.9244.3	3	3.2	0	7.25E+03	M115m	(R)VmLGET	(R)V m/L/G E/T N P A D/S K P G T I R(G)	m:Oxidized methionine	117.13	601.3077	1785.916	15.9922	-1.5	6.04	15431.7	9	HUMAN	E7ERL0	Nucleoside diphosphate kinase A
26607	dirMS_041712_NAR_50mM_plus2.10565.10565.3	3	3.2	1	2.09E+04		(R)VVKQEA	(R)V V K Q|E A/G G/L/G I S I K(G)		122.6	466.9434	1398.832	-0.0158	-11.3	8.56	58405	9.49	HUMAN	Q13425	Beta-2-syntrophin
26608	dirMS_041712_NAR_50mM_plus2.14224.14224.3	3	3.2	0	9.93E+05		(R)IVATKPL	(R)I/V/A T K/P L Y V A L/A Q R(K)		143.58	514.9831	1542.937	-0.0019	-1.2	9.99	65918.2	9.74	HUMAN	E7EQV3	Polyadenylate-binding protein 1
26609	dirMS_041712_NAR_60mM_plus.10169.10169.3	3	3.2	1	3.71E+05		(K)TAVCDI	(K)T A/V/C D I/P P R G L K(M)	C:Carbamidomethylation	110.05	442.9125	1326.72	0.0031	2.3	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
26610	dirMS_041712_NAR_60mM_plus.13173.13173.3	3	3.2	1	1.08E+05	S211s	(K)SLVsDKT	(K)S L\V s/D K T S/I S\E K(V)	s:N-acetylglucosamine (S)	125.67	499.594	1293.69	203.0778	-1	5.79	58791	9.93	HUMAN	E9PDI4	Ladinin-1
26611	dirMS_041712_NAR_60mM_plus.20861.20861.3	3	3.2	1	8.00E+03	K292k	(R)VALPDG	(R)V A L P/D G T T\V T V R V k(K)	k:Ubiquitin-K	170.57	523.9774	1455.853	114.0647	13.9	8.72	61891.7	6.06	HUMAN	Q96L92	Sorting nexin-27
26612	dirMS_041712_NAR_60mM_plus.8828.8828.3	3	3.2	0	5.51E+05		(K)VDNDEN	(K)V/D/N D E N E H Q L/S L R(T)		103.32	523.5814	1568.73	-0.0003	-0.2	4.31	6862.5	4.32	HUMAN	E5RGW4	Nucleophosmin (Fragment)
26613	dirMS_041712_NAR_60mM_plus.9792.9792.3	3	3.2	0	7.66E+05		(R)QQEGFK	(R)Q Q/E/G F/K/P\N Y M/E N R(E)		109.3	547.5879	1640.749	0.0006	0.4	6.14	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
26614	dirMS_041712_NAR_120mM_minus.12701.12701.4	4	3.19	2	9.80E+04		(K)QYESES	(K)Q Y E/S E S\V K L S V/S T T S/K R(E)		122.3	483.0061	1928.992	0.0102	5.3	8.5	260507.5	5.91	HUMAN	Q9Y3R5	Protein dopey-2
26615	dirMS_041712_NAR_120mM_minus.13926.13926.3	3	3.19	1	1.12E+05	S154s	(K)ESGGSG	(K)E S\G G S G s/S L F/S\R K K(F)	s:N-acetylglucosamine (S)	129.37	543.9536	1426.728	203.1178	23.6	10	22845.9	10.04	HUMAN	H0Y3W8	Monocarboxylate transporter 10 (Fragment)
26616	dirMS_041712_NAR_120mM_minus.18680.18680.3	3	3.19	0	7.86E+03		(R)HFNALG	(R)H F N A\L G\G W/G E/L Q N S V/K(T)		156.82	586.2907	1756.877	-0.019	-10.8	6.75	67307	6.24	HUMAN	F8VV40	Leukotriene A-4 hydrolase
26617	dirMS_041712_NAR_20mM_minus.8315.8315.2	2	3.19	0	7.00E+04	T270t	(K)ILAtAGW	(K)I L/A t A G W D H R(I)	t:N-acetylglucosamine (T)	132.53	671.8364	1139.596	203.0699	-7.1	6.74	36302	9.29	HUMAN	Q9BYB4	Guanine nucleotide-binding protein subunit beta-like protein 1
26618	dirMS_041712_NAR_30mM_minus2.11566.11566.2	2	3.19	0	4.29E+04		(R)LVDIICD	(R)L V|D I I C D K(M)	C:Carbamidomethylation	116.52	488.2587	975.518	-0.0078	-8	4.21	26180	5.09	HUMAN	Q96E17	Ras-related protein Rab-3C
26619	dirMS_041712_NAR_30mM_minus2.18832.18832.2	2	3.19	0	6.82E+04		(K)APDFVF	(K)A/P/D\F/V F/Y/A/P R(L)		157.32	591.8008	1182.594	0.0001	0.1	5.88	71218.8	6.3	HUMAN	A7YIJ8	Radixin
26620	dirMS_041712_NAR_40mM_minus2.10562.10562.3	3	3.19	2	4.13E+03	S4977s	(K)KSIsDIP	(K)K S/I s D I P V S\K I A\S F/I I K(E)	s:Phosphorylated S	145.02	642.6926	1846.105	79.9584	-4.1	9.7	795633.2	6.26	HUMAN	J3QTJ6	Fibrous sheath-interacting protein 2
26621	dirMS_041712_NAR_40mM_minus2.8152.8152.3	3	3.19	2	1.68E+05	S38s	(R)LLAEEIE	(R)L/L/A E/E I E K F Q G s D G K K(E)	s:N-acetylglucosamine (S)	128.68	665.6822	1791.949	203.0833	2	4.87	38926.6	5.94	HUMAN	Q5VWX1	KH domain-containing, RNA-binding, signal transduction-associated protein 2
26622	dirMS_041712_NAR_50mM_minus2.16356.16356.3	3	3.19	0	5.32E+04		(K)TTIENIQ	(K)T T/I/E/N I Q L/P H T L L S/R(F)		161.2	579.326	1735.97	-0.0067	-3.8	6.41	95792.4	6.36	HUMAN	J3KPV4	DNA replication licensing factor MCM4
26623	dirMS_041712_NAR_50mM_minus2.18673.18673.3	3	3.19	0	3.40E+05		(R)AGKPVI	(R)A G K\P V I C A T/Q M\L E/S M I/K(K)	C:Carbamidomethylation	180.9	626.3309	1876.969	0.0088	4.7	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
26624	dirMS_041712_NAR_50mM_minus2.9623.9623.3	3	3.19	0	1.28E+05		(R)MLQDVI	(R)M L/Q D V F/E T H F S K(I)		122.48	494.5757	1481.709	0.0032	2.2	5.3	53098.9	9.33	HUMAN	C9JJU3	Bromodomain testis-specific protein (Fragment)
26625	dirMS_041712_NAR_60mM_minus.11867.11867.3	3	3.19	0	1.92E+05		(R)ILHLLG	(R)I L H\L/L/G Q/E G P K(T)		126.37	402.2384	1204.705	-0.0042	-3.5	6.75	99028.8	5.32	HUMAN	Q9Y678	Coatomer subunit gamma-1
26626	dirMS_041712_NAR_60mM_minus.14570.14570.3	3	3.19	1	1.54E+05		(R)AVLYAD	(R)A V/L/Y A D Y R A P G P A/R(F)		141.03	507.2655	1519.802	-0.0196	-12.9	8.63	73233.7	5.52	HUMAN	B4DN67	Kin of IRRE-like protein 1
26627	dirMS_041712_NAR_60mM_minus.14837.14837.3	3	3.19	1	2.10E+05		(K)IDSRLE	(K)I/D S R L E\Q\Y/T S A\I E G T K(S)		142.88	604.3095	1810.918	-0.0042	-2.3	4.68	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
26628	dirMS_041712_NAR_60mM_minus.16859.16859.3	3	3.19	1	6.64E+04	S83s	(K)IsQRVIH	(K)I s/Q R V I H L F D E K(G)	s:Phosphorylated S	154.67	522.2733	1484.822	79.9834	10.9	6.75	31896	9.85	HUMAN	Q9H2K0	Translation initiation factor IF-3, mitochondrial
26629	dirMS_041712_NAR_60mM_minus.19464.19464.3	3	3.19	1	5.47E+05	M45m K47	(R)TTLGPR	(R)T T/L/G P R G m/D k L I V/D G R(G)	m:Oxidized methionine k:Ub	174.4	620.3279	1728.943	130.0266	-6	8.41	55284.8	7.77	HUMAN	B8ZZC9	T-complex protein 1 subunit eta
26630	dirMS_041712_NAR_60mM_minus.5671.5671.2	2	3.19	0	4.22E+02	N37n	(R)VYnTDP	(R)V Y/n T/D P L K(E)	n:N-acetylglucosamine (N)	86.55	576.7856	949.499	203.065	-12.5	5.8	19714.4	6.7	HUMAN	I3L1D0	WD repeat domain phosphoinositide-interacting protein 3
26631	dirMS_041712_NAR_60mM_minus.6974.6974.3	3	3.19	0	1.21E+05		(K)TQAYQ	(K)T Q|A Y Q/D\Q K/P G T S G L R(K)		97.4	550.6109	1649.824	-0.006	-3.7	8.25	61733.3	6.3	HUMAN	P36871	Phosphoglucomutase-1
26632	dirMS_041712_NAR_60mM_minus.9749.9749.3	3	3.19	1	2.21E+05		(R)LKAEAE	(R)L K A E\A\E\L/L/Q Q Q K(E)		114.58	466.9338	1398.795	-0.0083	-5.9	6.14	533778	5.74	HUMAN	Q15149	Plectin
26633	dirMS_041712_NAR_120mM_plus.14332.14332.4	4	3.19	1	1.42E+06		(-)IAELQEL	(-)I A/E L Q E L Q P S/A K D F/E V R(S)		127.37	494.0077	1973.034	-0.0249	-12.6	4.41	12631.3	7.04	HUMAN	H0YGG8	Citron Rho-interacting kinase (Fragment)
26634	dirMS_041712_NAR_120mM_plus.17729.17729.4	4	3.19	1	1.40E+05		(K)KTTIENI	(K)K T T I E/N\I/Q L/P/H T L L S R(F)		145.95	466.7655	1864.065	-0.0249	-13.4	8.76	95792.4	6.36	HUMAN	J3KPV4	DNA replication licensing factor MCM4
26635	dirMS_041712_NAR_120mM_plus.23181.23181.3	3	3.19	1	2.88E+05		(K)GLAPDLI	(K)G L\A/P D L P E D L Y H L I/K K(A)		174.42	608.0076	1822.011	-0.0027	-1.5	5.38	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
26636	dirMS_041712_NAR_120mM_plus.6751.6751.3	3	3.19	1	1.39E+05		(R)RQQEVE	(R)R Q\Q\E|V|E T E/L K(M)		88.68	420.5562	1259.659	-0.005	-3.9	4.79	51612.9	9.98	HUMAN	P08621	U1 small nuclear ribonucleoprotein 70 kDa
26637	dirMS_041712_NAR_20mM_plus.11674.11674.2	2	3.19	0	1.21E+05		(R)AQAALA	(R)A Q/A A/L/A/V/N I S A A R(G)		153.48	628.3565	1255.712	-0.006	-4.8	9.79	58479.6	6.23	HUMAN	P40227	T-complex protein 1 subunit zeta
26638	dirMS_041712_NAR_30mM_plus2.17663.17663.3	3	3.19	0	5.86E+05		(K)ISMPDV	(K)I S M P D/V/N L N L K(G)		146.12	415.225	1243.671	-0.011	-8.9	5.84	629603.7	5.8	HUMAN	Q09666	Neuroblast differentiation-associated protein AHNAK
26639	dirMS_041712_NAR_30mM_plus2.17666.17666.2	2	3.19	0	6.36E+05		(R)LMGLEA	(R)L/M|G\L E A L K(G)		146.48	437.7532	874.507	-0.0075	-8.6	6	4886.6	6.03	HUMAN	D6RIZ7	T-complex protein 1 subunit epsilon
26640	dirMS_041712_NAR_30mM_plus2.22522.22522.2	2	3.19	0	2.16E+04		(R)WLLDFA	(R)W L|L/D F A S K(R)		173.45	490.2728	979.525	0.0136	13.9	5.84	59384	7.79	HUMAN	B7Z3Z9	Long-chain-fatty-acid--CoA ligase 1
26641	dirMS_041712_NAR_30mM_plus2.5498.5498.2	2	3.19	1	2.82E+05		(K)ASPESR	(K)A S/P/E S R R(L)		82.23	401.709	802.417	-0.0059	-7.3	9.64	19435.1	10.87	HUMAN	J3KP49	Adenosine monophosphate-protein transferase FICD
26642	dirMS_041712_NAR_30mM_plus2.5642.5642.2	2	3.19	0	9.56E+03		(K)QSVVYG	(K)Q S V/V Y/G G K(S)		83.12	419.2286	837.447	0.0034	4.1	8.59	54993.5	5.63	HUMAN	E7EVX8	U4/U6 small nuclear ribonucleoprotein Prp31
26643	dirMS_041712_NAR_30mM_plus2.5742.5742.2	2	3.19	1	1.13E+05		(R)ISKECAR	(R)I S/K/E C A R(K)	C:Carbamidomethylation	84.83	432.2218	863.44	-0.004	-4.7	8.75	40449.4	7.82	HUMAN	C9J4D3	Neuroligin-1 (Fragment)
26644	dirMS_041712_NAR_50mM_plus2.21336.21336.3	3	3.19	0	7.33E+05		(R)AGKPVI	(R)A G K\P V I C A T/Q/M/L E S M I K(K)	C:Carbamidomethylation	181.38	626.3278	1876.969	-0.0005	-0.3	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
26645	dirMS_041712_NAR_50mM_plus2.21406.21406.3	3	3.19	1	1.97E+05		(R)TEGLSV	(R)T E|G L/S V L S Q A M/A\V I K E K(I)		182.8	602.0007	1803.988	-0.0009	-0.5	5.81	31604.9	6.88	HUMAN	G3V4T5	Eukaryotic translation initiation factor 2 subunit 1 (Fragment)
26646	dirMS_041712_NAR_50mM_plus2.6792.6792.3	3	3.19	1	1.30E+05		(K)EETQPP	(K)E E T Q|P/P V/A L K K(E)		100.88	413.9019	1239.694	-0.0032	-2.6	6.24	45021.6	8.74	HUMAN	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein
26647	dirMS_041712_NAR_50mM_plus2.9365.9365.3	3	3.19	1	3.84E+05	M633m M6	(R)MSQNV	(R)M S Q N V|D m|P K L H D A m G T/R(S)	m:Oxidized methionine	116.45	654.9726	1930.893	32.01	10.3	6.5	93984.9	9.34	HUMAN	Q5TB30	DEP domain-containing protein 1A
26648	dirMS_041712_NAR_60mM_plus.14030.14030.3	3	3.19	1	9.80E+05		(K)TTVKDL	(K)T T/V K D L S E\L/G S V R(T)		129.9	468.9268	1404.769	-0.0034	-2.4	5.74	533778	5.74	HUMAN	Q15149	Plectin
26649	dirMS_041712_NAR_60mM_plus.18385.18385.3	3	3.19	1	9.62E+04		(K)VTPNTV	(K)V T P/N T V L E N F/F K H\S T/R(Q)		153.17	630.661	1889.987	-0.0184	-9.7	8.73	13340.5	9.57	HUMAN	H0YK51	Ceramide synthase 3 (Fragment)
26650	dirMS_041712_NAR_60mM_plus.7306.7328.3	3	3.19	0	9.36E+05		(R)AAHSEG	(R)A A H S E G N T T/A/G L/D/M R(E)		96.68	510.9035	1530.697	-0.0006	-0.4	5.32	57829.5	6.01	HUMAN	P78371	T-complex protein 1 subunit beta
26651	dirMS_041712_NAR_60mM_plus.8305.8305.3	3	3.19	0	5.20E+05		(K)LHGAPK	(K)L/H G A P\K P H A/C P T/C A K(C)	C:Carbamidomethylation	101.58	548.9468	1644.81	0.0161	9.8	10	27457.2	10.18	HUMAN	K7EM76	Zinc finger and BTB domain-containing protein 48 (Fragment)
26652	dirMS_041712_NAR_60mM_plus.8653.8653.3	3	3.19	1	3.99E+04		(R)LLEEEDS	(R)L/L E E E D S K/L K(G)		103.8	401.8861	1203.647	-0.003	-2.5	4.41	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
26653	dirMS_041712_NAR_60mM_plus.9831.9831.3	3	3.19	1	7.09E+05		(R)TPGKEA	(R)T/P\G K E A\V/A|M/E S Y A K(A)		109.58	494.5808	1481.73	-0.0026	-1.8	5.81	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
26654	dirMS_041712_NAR_120mM_minus.15634.15634.3	3	3.18	2	4.34E+05		(R)ALKDEE	(R)A L/K/D E E K M E/L\Q E I Q L K(E)		138.58	649.0139	1945.031	-0.0039	-2	4.58	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
26655	dirMS_041712_NAR_120mM_minus.9441.9441.2	2	3.18	0	1.53E+05		(K)EFHLNE	(K)E/F/H L N E S\G D|P S S K(S)		106.17	723.8269	1446.65	-0.003	-2.1	4.65	30992.3	4.14	HUMAN	B2REB8	Protein SET
26656	dirMS_041712_NAR_120mM_minus.9585.9585.4	4	3.18	2	1.56E+05		(K)QMPQY	(K)Q M/P Q Y R G R T\E F/V K(D)		107.6	410.7166	1639.837	0.0072	4.4	9.99	52820.1	5.84	HUMAN	Q6UXE8	Butyrophilin-like protein 3
26657	dirMS_041712_NAR_20mM_minus.14428.14428.2	2	3.18	0	9.57E+04		(R)LTGQLF	(R)L/T/G Q L/F/L G G S I V K(G)		198.62	666.8967	1332.789	-0.0024	-1.8	8.75	45924.5	5.29	HUMAN	B4E1F3	Selenium-binding protein 1
26658	dirMS_041712_NAR_30mM_minus2.13709.13709.2	2	3.18	0	5.41E+05		(K)NLVTED	(K)N L\V|T E D/V M R(M)		127.1	538.7747	1076.541	0.0017	1.5	4.37	12797.5	10.58	HUMAN	K7EIL4	Glucose-6-phosphate isomerase (Fragment)
26659	dirMS_041712_NAR_30mM_minus2.14693.14693.2	2	3.18	1	2.93E+05	K64k	(K)kSGEVA	(K)k S/G E/V/A V L K/R(D)	k:Ubiquitin-K	132.9	600.8476	1086.663	114.025	-15	9.99	9837.1	7.97	HUMAN	C9J5P1	Chromosome 6 open reading frame 130, isoform CRA_a
26660	dirMS_041712_NAR_30mM_minus2.15235.15235.2	2	3.18	0	2.14E+05		(R)AGSLLM	(R)A/G\S\L/L\M L K(K)		136.02	416.7494	832.496	-0.0046	-5.5	8.8	111104.3	8.79	HUMAN	Q8NAT2	Tudor domain-containing protein 5
26661	dirMS_041712_NAR_30mM_minus2.16232.16232.2	2	3.18	0	2.68E+04		(K)FFVGGN	(K)F F|V/G G N W K(M)		141.38	477.745	954.483	-0.0005	-0.5	8.75	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
26662	dirMS_041712_NAR_40mM_minus2.9375.9375.3	3	3.18	2	2.76E+05	K1108k	(R)NSGPFA	(R)N S G P F A K N V S/L S/G K/E k(D)	k:Ubiquitin-K	138.13	592.9867	1662.881	114.0646	12.2	9.7	292466.7	7.12	HUMAN	O75417	DNA polymerase theta
26663	dirMS_041712_NAR_50mM_minus2.15239.15239.3	3	3.18	1	1.33E+05		(K)VSEQGL	(K)V/S E Q G/L/I E|I L/K K(V)		154.37	452.9385	1356.81	-0.0087	-6.4	6.11	12899.6	6.59	HUMAN	K7EL31	Programmed cell death protein 5
26664	dirMS_041712_NAR_50mM_minus2.16023.16023.3	3	3.18	1	5.41E+04		(K)FLSPQD	(K)F L/S/P Q D T/F E A L K R(N)		158.83	517.9421	1551.817	-0.0048	-3.1	6.07	97622	8.94	HUMAN	Q9NTZ6	RNA-binding protein 12
26665	dirMS_041712_NAR_50mM_minus2.8409.8409.3	3	3.18	2	5.66E+05	N207n	(K)ESnKCD	(K)E S/n K/C D R I|Q E N S S(-)	C:Carbamidomethylation n:N-ac	116.52	590.5989	1566.681	203.1009	12.1	4.68	24536.4	6.12	HUMAN	Q8WTR2	Dual specificity protein phosphatase 19
26666	dirMS_041712_NAR_60mM_minus.13277.13277.3	3	3.18	1	2.08E+03	M1616m	(K)ITESPRA	(K)I T E S P R A S/m G V L S G K(R)	m:Oxidized methionine	132.85	516.9421	1532.81	16.0016	4.3	8.75	211012.5	4.57	HUMAN	A6NNK5	Tumor suppressor p53-binding protein 1
26667	dirMS_041712_NAR_60mM_minus.17682.17682.3	3	3.18	1	2.30E+05		(R)LGLSTL	(R)L/G L/S/T/L G E L K Q N L/S R(S)		159.12	543.6476	1628.933	-0.0047	-2.9	8.75	22294.4	5.26	HUMAN	O43399	Tumor protein D54
26668	dirMS_041712_NAR_120mM_plus.16910.16910.3	3	3.18	1	1.33E+06		(K)LKVPEW	(K)L K V P E\W|V/D T V K(L)		141.93	438.5868	1313.746	-0.0005	-0.4	6.07	16060.2	10.31	HUMAN	P39019	40S ribosomal protein S19
26669	dirMS_041712_NAR_120mM_plus.19217.19217.3	3	3.18	1	6.13E+05		(R)HGVQEL	(R)H/G\V/Q E L\E\I E|L Q S Q L S K K(A)		153.85	656.0237	1966.06	-0.0038	-2	5.5	39641.8	4.93	HUMAN	K7EQQ3	Keratin, type I cytoskeletal 9
26670	dirMS_041712_NAR_120mM_plus.20189.20189.3	3	3.18	1	3.26E+05		(R)AKFEEL	(R)A K F E E\L/N M/D/L F R(S)		159.17	504.9201	1512.752	-0.0058	-3.8	4.68	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
26671	dirMS_041712_NAR_120mM_plus.20991.20991.3	3	3.18	1	1.61E+05		(R)DFIEKRY	(R)D/F I E K/R Y V E L K(K)		163.57	480.6058	1439.789	0.0136	9.4	6.18	8604.8	10.62	HUMAN	D6RJD6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2
26672	dirMS_041712_NAR_120mM_plus.24460.24460.3	3	3.18	1	2.33E+04		(R)GHYTIG	(R)G H\Y/T|I G K E I\I/D L V L D R(I)		183.73	614.6745	1842.012	-0.003	-1.6	5.38	58642	4.95	HUMAN	F5H5D3	Tubulin alpha-1C chain
26673	dirMS_041712_NAR_20mM_plus.11093.11093.2	2	3.18	0	1.26E+05		(K)YGVSGY	(K)Y G\V/S G Y P T L K(I)		149.6	542.7869	1084.567	-0.0008	-0.8	8.5	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
26674	dirMS_041712_NAR_20mM_plus.11781.11781.3	3	3.18	0	2.53E+05	S5s	(-)MTQTsP	(-)M/T Q T/s P F Y N G R(G)	s:N-acetylglucosamine (S)	154.73	502.2264	1301.594	203.0704	-6	8.5	22103.9	9.92	HUMAN	C9JSU7	STE20-related kinase adapter protein beta (Fragment)
26675	dirMS_041712_NAR_20mM_plus.12197.12197.2	2	3.18	0	5.30E+05	M494m	(R)GAHImN	(R)G A H/I m N S T C A A M P K(L)	C:Carbamidomethylation m:Oxid	157.35	752.8363	1488.676	15.9897	-3.5	8.76	114220.9	9.14	HUMAN	O43303	Centriolar coiled-coil protein of 110 kDa
26676	dirMS_041712_NAR_20mM_plus.6830.6830.2	2	3.18	0	4.54E+05	M132m	(R)DmVGIA	(R)D/m|V/G\I/A Q T G S G K(T)	m:Oxidized methionine	112.75	590.2864	1163.573	15.993	-1.6	5.84	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
26677	dirMS_041712_NAR_30mM_plus2.15655.15655.2	2	3.18	0	3.95E+05		(R)QPTPPF	(R)Q\P/T/P/P F F\G R(D)		134.25	523.7794	1046.542	0.0097	9.3	9.75	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
26678	dirMS_041712_NAR_30mM_plus2.18197.18197.2	2	3.18	0	2.22E+05		(K)MFGMV	(K)M/F|G M V L E K(I)		149.02	477.7447	954.479	0.0034	3.6	5.75	86098.8	5.31	HUMAN	B4DUC5	Exportin-2
26679	dirMS_041712_NAR_30mM_plus2.4702.4702.2	2	3.18	0	2.84E+05		(R)MDDYC	(R)M/D D/Y C R(R)	C:Carbamidomethylation	75.47	430.1579	859.307	0.0012	1.4	4.21	13246.4	9.21	HUMAN	Q5JY17	Nuclear receptor coactivator 5 (Fragment)
26680	dirMS_041712_NAR_40mM_plus2.10106.10106.3	3	3.18	0	5.15E+04		(K)EVVKPV	(K)E V V K P V\P I/T S P A V S K(V)		123.87	517.6421	1550.915	-0.0035	-2.2	8.69	65142.1	9.24	HUMAN	Q96HC4	PDZ and LIM domain protein 5
26681	dirMS_041712_NAR_40mM_plus2.17546.17546.3	3	3.18	0	1.65E+05		(R)VYAILTH	(R)V Y|A I L T H G I\F/S G P\A I S R(I)		169.45	601.3376	1801.996	0.0023	1.3	8.73	24482.9	7.96	HUMAN	B1ALA9	Phosphoribosyl pyrophosphate synthetase 1
26682	dirMS_041712_NAR_50mM_plus2.11706.11706.3	3	3.18	0	8.13E+05		(R)GATQQI	(R)G A T/Q Q I L D\E A E R(S)		129	444.2215	1330.66	-0.0098	-7.4	4.14	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
26683	dirMS_041712_NAR_50mM_plus2.15331.15331.3	3	3.18	1	9.75E+05	S965s	(K)LLTKsVA	(K)L L T/K s V A E T P V H K(Q)	s:N-acetylglucosamine (S)	149.48	542.6394	1422.832	203.0722	-4.4	8.6	212850	9.41	HUMAN	Q7Z2Z1	Treslin
26684	dirMS_041712_NAR_50mM_plus2.15611.15611.3	3	3.18	1	9.39E+05		(K)EAFSLF	(K)E A\F/S\L/F/D K/D G D G T I T T K(E)		150.05	615.6348	1844.891	-0.0014	-0.8	4.23	21860.1	4.45	HUMAN	E7EMB3	Calmodulin
26685	dirMS_041712_NAR_50mM_plus2.21527.21527.3	3	3.18	0	1.80E+05		(K)LHTVST	(K)L H T V S T T V W E A/L/P D V S R(A)		184.7	637.6781	1910.997	0.0227	11.9	5.32	72310.8	6.87	HUMAN	Q5SV97	Uncharacterized protein C1orf170
26686	dirMS_041712_NAR_50mM_plus2.6694.6694.3	3	3.18	1	4.76E+04		(K)DSKRVE	(K)D S K R\V\E/Q L/A R(E)		100.12	401.2301	1201.665	0.011	9.1	8.75	41644.3	5.64	HUMAN	F8VYN8	Coiled-coil domain-containing protein 41
26687	dirMS_041712_NAR_60mM_plus.10700.10700.3	3	3.18	0	1.17E+04		(R)CGAALA	(R)C/G A/A/L A/G H Q L I R(G)	C:Carbamidomethylation	113.38	422.8929	1266.674	-0.0094	-7.4	9.75	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
26688	dirMS_041712_NAR_60mM_plus.14037.14037.3	3	3.18	0	8.62E+05	N68n	(R)ELnAEIV	(R)E L/n/A E I V/V/N S/A K(V)	n:N-acetylglucosamine (N)	130.42	497.2559	1286.695	203.0581	-14.3	4.53	103586.6	8.51	HUMAN	Q5T655	Coiled-coil domain-containing protein 147
26689	dirMS_041712_NAR_60mM_plus.15874.15874.4	4	3.18	0	7.11E+05	M95m	(R)LPHAAG	(R)L P H\A A G H G C H E G P/H G m R(A)	C:Carbamidomethylation m:Oxid	139.45	459.9647	1820.818	16.019	13.1	7.1	12775.3	8.27	HUMAN	J3KSN5	Usher syndrome type-1G protein
26690	dirMS_041712_NAR_60mM_plus.16426.16426.3	3	3.18	0	4.22E+05		(R)FVFDRP	(R)F/V/F D/R/P L P V S R(L)		142.53	444.917	1332.742	-0.0058	-4.4	9.6	18685.5	9.45	HUMAN	B4DEV8	Proteasome subunit alpha type
26691	dirMS_041712_NAR_60mM_plus.18806.18806.3	3	3.18	1	2.15E+05		(K)GPREEI	(K)G P R E E I V|Y\L/P C I Y R(N)	C:Carbamidomethylation	156.02	588.9744	1764.91	-0.0015	-0.9	6.14	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
26692	dirMS_041712_NAR_60mM_plus.8254.8254.3	3	3.18	1	4.58E+05		(K)AALSEE	(K)A A|L/S E E E L E K K(S)		101.08	416.221	1246.652	-0.0041	-3.3	4.49	176357.7	5.25	HUMAN	D3DNT2	Eukaryotic translation initiation factor 4 gamma 1
26693	dirMS_041712_NAR_120mM_minus.13234.13234.3	3	3.17	1	5.47E+05		(R)TGPAG	(R)T G P A G G Q R Q S A S E|R(E)		125.92	467.9028	1401.683	0.0109	7.8	9.26	42501.3	7.13	HUMAN	Q0VG99	Mesoderm posterior protein 2
26694	dirMS_041712_NAR_120mM_minus.6046.6046.3	3	3.17	1	2.07E+04		(K)NVICDK	(K)N V/I/C D K C/E/G R(G)	C:Carbamidomethylation	86.4	417.525	1250.562	-0.0012	-0.9	6.07	45609.1	6.66	HUMAN	P31689	DnaJ homolog subfamily A member 1
26695	dirMS_041712_NAR_20mM_minus.13642.13642.3	3	3.17	0	2.12E+05		(K)LNGQQ	(K)L N/G Q Q/A A/L A S Q Y R(A)		187.05	473.9203	1419.734	0.0124	8.8	8.75	309341.6	9.2	HUMAN	E7EPN9	Protein PRRC2C
26696	dirMS_041712_NAR_20mM_minus.7307.7307.3	3	3.17	0	1.72E+04		(K)AVTEQG	(K)A V T E Q/G A\E L/S N E E/R(N)		121.03	511.5774	1532.719	-0.0011	-0.7	4.09	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
26697	dirMS_041712_NAR_30mM_minus2.12848.12848.2	2	3.17	0	4.06E+04		(R)GGEPQ	(R)G G\E/P Q G/P P F I/K(Y)		122.6	563.7964	1126.589	-0.0036	-3.2	6	266161	5.68	HUMAN	E9PPU0	Epiplakin
26698	dirMS_041712_NAR_30mM_minus2.14521.14521.2	2	3.17	0	4.86E+05		(K)YSEQTE	(K)Y S E Q/T E/F G I T\S D K(L)		132.68	752.8364	1504.68	-0.0147	-9.8	4.14	61388.9	5.43	HUMAN	B3KRB7	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta, isoform CRA_a
26699	dirMS_041712_NAR_30mM_minus2.15258.15258.2	2	3.17	0	4.79E+04		(K)LCDFGF	(K)L/C/D F/G F/A/R(A)	C:Carbamidomethylation	135.8	493.2343	985.456	0.0053	5.4	5.84	143554.7	5.57	HUMAN	A8MU99	Serine/threonine-protein kinase 36
26700	dirMS_041712_NAR_30mM_minus2.15947.15947.2	2	3.17	0	3.18E+04		(K)NLILVVR	(K)N L/I/L/V V R(G)		139.73	413.7746	826.551	-0.009	-10.9	9.75	193379.8	5.48	HUMAN	Q00610	Clathrin heavy chain 1

26701	dirMS_041712_NAR_30mM_minus2.5970.5970.2	2	3.17	0	7.36E+03	M43m M4	(R)LYAmQT	(R)L/Y|A\m/Q T G m/K(I)	m:Oxidized methionine	85.85	537.7506	1042.506	31.9879	-1.8	8.59	34163.9	5.87	HUMAN	Q9NP79	Vacuolar protein sorting-associated protein VTA1 homolog
26702	dirMS_041712_NAR_30mM_minus2.9638.9638.2	2	3.17	0	1.20E+05		(K)LAFGCQ	(K)L/A/F/G C Q/R(S)	C:Carbamidomethylation	107.05	426.2191	851.419	0.0117	13.7	9.75	18347.7	6.44	HUMAN	F8VUG8	Prickle-like protein 1 (Fragment)
26703	dirMS_041712_NAR_40mM_minus2.10859.10859.3	3	3.17	1	1.53E+04		(K)AVEGEG	(K)A V\E G E G G V R/S A T V P V S I W R(T)		147.35	657.3545	1970.045	0.0035	1.8	6.19	113511.3	6.35	HUMAN	Q5HYA8	Meckelin
26704	dirMS_041712_NAR_40mM_minus2.13003.13003.3	3	3.17	0	1.07E+04		(R)DGLAFN	(R)D G L A/F/N A L I/H R(H)		160.02	409.5572	1226.664	-0.007	-5.7	6.74	146974	5.55	HUMAN	C9JRP8	Spectrin beta chain, non-erythrocytic 4
26705	dirMS_041712_NAR_40mM_minus2.9981.9981.3	3	3.17	1	6.91E+05	M101m	(K)LENLQL	(K)L E/N L/Q L/W m G/R L N E T V R(G)	m:Oxidized methionine	141.53	663.3508	1972.043	15.9946	-0.2	6.14	13730.5	8.93	HUMAN	H7C436	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 1 (Fragment)
26706	dirMS_041712_NAR_50mM_minus2.8192.8192.3	3	3.17	1	2.09E+05		(K)GILAADE	(K)G I L/A/A/D E S T G S I A K R(L)		114.5	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
26707	dirMS_041712_NAR_60mM_minus.13913.13913.3	3	3.17	1	1.10E+05		(R)LLTFASC	(R)L L T F A S Q/L/K/A G K(G)		137.78	426.2545	1276.762	-0.0134	-10.5	10	107742.5	8.84	HUMAN	B3KXX3	Solute carrier family 12 member 6
26708	dirMS_041712_NAR_60mM_minus.7698.7698.3	3	3.17	1	6.40E+05		(K)IQDKEGI	(K)I Q|D K E G I/P/P D Q Q R(L)		102.18	508.5978	1523.781	-0.0024	-1.6	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
26709	dirMS_041712_NAR_60mM_minus.9519.9519.3	3	3.17	1	3.25E+04		(K)VLLQSKI	(K)V L L/Q/S K D Q\I|T/A G N A A R(K)		112.92	562.3149	1684.934	-0.0039	-2.3	8.72	46335.4	6.29	HUMAN	E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment)
26710	dirMS_041712_NAR_120mM_plus.10221.10221.3	3	3.17	0	2.55E+05	K9k	(K)LAkTGE(	(K)L A k T G E G/S Y G V/V/F K(C)	k:Ubiquitin-K	107.03	523.949	1455.784	114.0482	3.4	8.5	6666.7	9.69	HUMAN	F8WC88	Cyclin-dependent kinase-like 4
26711	dirMS_041712_NAR_120mM_plus.6209.6209.2	2	3.17	1	4.58E+04	S137s	(R)GSEsKS(	(R)G S/E s/K|S\G R(E)	s:N-acetylglucosamine (S)	85.22	505.7372	807.395	203.0716	-7.7	8.75	63508.9	9.55	HUMAN	Q8NEP4	Uncharacterized protein C17orf47
26712	dirMS_041712_NAR_20mM_plus.11935.11935.2	2	3.17	0	4.06E+04		(R)LVSHTVI	(R)L V|S H T V P/R(A)		155.68	454.7679	908.531	-0.0027	-3	9.75	47658	11.46	HUMAN	B7Z3M0	Podocan-like protein 1
26713	dirMS_041712_NAR_20mM_plus.13262.13262.3	3	3.17	1	3.57E+04		(R)CGFQDD	(R)C G F Q D D V A Y G K T K(I)	C:Carbamidomethylation	163.58	496.8956	1488.679	-0.0065	-4.4	5.96	111972.3	9.59	HUMAN	J3QRN6	Unconventional myosin-Id
26714	dirMS_041712_NAR_20mM_plus.7730.7730.3	3	3.17	0	1.18E+04	M886m	(R)YmEENN	(R)Y m E/E N\N\L E H I P/K(F)	m:Oxidized methionine	122.92	511.5761	1516.71	16.0037	5.7	4.75	107445.2	6.49	HUMAN	Q9BZF3	Oxysterol-binding protein-related protein 6
26715	dirMS_041712_NAR_20mM_plus.8513.8513.2	2	3.17	0	2.29E+04		(K)MAQYLE	(K)M A Q Y L E E E R(H)		128.52	584.7756	1168.53	0.0136	11.7	4.25	53461.2	6.87	HUMAN	Q16204	Coiled-coil domain-containing protein 6
26716	dirMS_041712_NAR_30mM_plus2.10177.10177.2	2	3.17	0	3.98E+04		(R)NAMGSI	(R)N/A|M/G S L A S Q\A T K(D)		106.68	589.7934	1178.583	-0.0039	-3.3	8.75	21119.9	4.34	HUMAN	H0Y3Y9	26S proteasome non-ATPase regulatory subunit 4 (Fragment)
26717	dirMS_041712_NAR_30mM_plus2.17086.17086.3	3	3.17	1	4.46E+05	M53m	(K)FLDTmA	(K)F L D T m A/G R/V Y R(L)	m:Oxidized methionine	143.4	448.8963	1328.678	15.9964	1.1	8.75	111607	8.89	HUMAN	Q6ZTR5	Uncharacterized protein CXorf22
26718	dirMS_041712_NAR_30mM_plus2.6839.6839.2	2	3.17	0	6.17E+04		(R)VYSTSVT	(R)V Y/S/T/S\V T G S R(E)		90.47	528.7673	1056.532	-0.0047	-4.4	8.72	9437.4	9.69	HUMAN	Q5T123	SH3 domain binding glutamic acid-rich protein like 3
26719	dirMS_041712_NAR_30mM_plus2.8410.8410.2	2	3.17	1	5.70E+05	K304k	(R)LSLREk(	(R)L/S/L/R/E k(A)	k:Ubiquitin-K	98.27	430.2487	745.457	114.0335	-11	8.75	71407.4	9.29	HUMAN	H0YBI6	Thioredoxin reductase 3 (Fragment)
26720	dirMS_041712_NAR_40mM_plus2.10292.10292.2	2	3.17	0	2.87E+04		(K)YNNCWI	(K)Y/N N/C W/L/A R(T)	C:Carbamidomethylation	125.6	548.7522	1096.499	-0.0022	-2	8.75	55416	8.63	HUMAN	H0YM31	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
26721	dirMS_041712_NAR_40mM_plus2.11362.11362.3	3	3.17	1	2.12E+03	N81n	(R)DIDNnLI	(R)D I D/N n L/I/T S T P R A G E\K(-)	n:N-acetylglucosamine (N)	132.7	649.6672	1743.887	203.0999	10.5	4.56	10443.5	10.42	HUMAN	H0YNU2	CTD small phosphatase-like protein 2 (Fragment)
26722	dirMS_041712_NAR_40mM_plus2.7975.7975.2	2	3.17	0	2.27E+04		(K)ASLENSI	(K)A/S L/E/N S L R(E)		107.33	445.2395	889.474	-0.002	-2.3	6.05	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
26723	dirMS_041712_NAR_40mM_plus2.8830.8830.2	2	3.17	0	3.85E+05		(K)VCADLIF	(K)V/C|A/D L I R(G)	C:Carbamidomethylation	113.28	423.7286	846.45	-0.0003	-0.3	5.81	6885.1	10.56	HUMAN	E5RJX2	40S ribosomal protein S20
26724	dirMS_041712_NAR_50mM_plus2.17502.17502.3	3	3.17	2	2.48E+05	M152m K1	(R)AMmEK	(R)A M/m E K L V K S/I/S Q L k(D)	m:Oxidized methionine k:Ub	159.62	579.3128	1605.907	130.0172	-11.9	9.7	53397.3	7.21	HUMAN	B4DLC8	Signal transducer and activator of transcription 2
26725	dirMS_041712_NAR_50mM_plus2.18949.18949.3	3	3.17	1	4.14E+05	S2452s	(K)KLLGSLS	(K)K L/L G S L S\G/S/L/T T V F H s(-)	s:N-acetylglucosamine (S)	167.17	617.3412	1646.911	203.0978	10	8.76	279771.8	9.54	HUMAN	Q8NDH2	Coiled-coil domain-containing protein 168
26726	dirMS_041712_NAR_50mM_plus2.21764.21764.3	3	3.17	0	1.12E+05		(R)GLAPVQ	(R)G L|A P V Q/A Y L H I P D I I K(V)		184.93	583.336	1748.011	-0.0171	-9.8	6.74	58266.4	9.46	HUMAN	B4DN00	Pyruvate carboxylase, mitochondrial
26727	dirMS_041712_NAR_60mM_plus.13074.13074.2	2	3.17	0	2.13E+05		(R)HGDLPD	(R)H G D L/P D|I/Q/I\K(H)		124.9	568.3082	1135.611	-0.0015	-1.3	5.21	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
26728	dirMS_041712_NAR_60mM_plus.15152.15152.3	3	3.17	1	2.70E+05		(K)KAEAAA	(K)K\A E A A A\S A\L\A\D\A D/A/D/L E E R(L)		135.37	639.6435	1916.92	-0.0036	-1.9	4.02	25103.6	5.88	HUMAN	O43633	Charged multivesicular body protein 2a
26729	dirMS_041712_NAR_60mM_plus.16464.16464.2	2	3.17	0	6.65E+05		(R)EHALLA	(R)E H|A/L/L\A/Y T L/G V K(Q)		143.6	657.8735	1314.742	-0.0019	-1.4	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
26730	dirMS_041712_NAR_60mM_plus.18295.18295.3	3	3.17	0	1.88E+05		(K)DHGLEV	(K)D H\G L E V|L/G L V R(V)		153.42	403.2318	1207.679	0.0015	1.2	5.32	17732.8	5.85	HUMAN	F5GYJ1	U8 snoRNA-decapping enzyme
26731	dirMS_041712_NAR_60mM_plus.5402.5402.3	3	3.17	1	1.83E+04		(R)YYGGGS	(R)Y/Y G G G S E G G R A P K(R)		85.83	433.5425	1298.612	0.0006	0.4	8.5	64759.2	8.88	HUMAN	P14866	Heterogeneous nuclear ribonucleoprotein L
26732	dirMS_041712_NAR_60mM_plus.5429.5429.3	3	3.17	0	4.17E+05	M21m	(R)SGSmDF	(R)S/G|S/m D P/S G A H/P S V R(Q)	m:Oxidized methionine	86.32	467.5464	1384.627	15.9973	1.7	6.46	48340.6	8.84	HUMAN	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
26733	dirMS_041712_NAR_60mM_plus.5973.5973.3	3	3.17	1	2.27E+05		(R)ALCDYK(	(R)A L/C/D/Y K Q D Q K(I)	C:Carbamidomethylation	90.4	423.5361	1268.594	-0.0002	-0.2	6.01	334221.3	6.44	HUMAN	P15924	Desmoplakin
26734	dirMS_041712_NAR_120mM_minus.20340.20340.4	4	3.16	1	3.14E+05	M189m M	(R)mVDmC	(R)m V D m Q K L/t H G/V/L H T K(F)	m:Oxidized methionine t:N-a	166.68	493.9968	1737.914	235.0515	-9	8.39	55160.8	6.02	HUMAN	Q8IV08	Phospholipase D3
26735	dirMS_041712_NAR_20mM_minus.10652.10652.2	2	3.16	1	7.07E+04		(K)YGSIPKL	(K)Y G S I P/K/L I(-)		154.42	445.7725	890.535	0.0031	3.5	8.59	9053.2	6.06	HUMAN	D6RBC5	OCIA domain-containing protein 1 (Fragment)
26736	dirMS_041712_NAR_20mM_minus.10768.10768.2	2	3.16	0	3.55E+05	T245t	(K)LGCDW	(K)L G C D/W\V A t I F S/R(D)	C:Carbamidomethylation t:Phosp	155.48	752.8365	1424.699	79.9666	0.2	5.84	73835.7	6.49	HUMAN	Q8TF42	Ubiquitin-associated and SH3 domain-containing protein B
26737	dirMS_041712_NAR_20mM_minus.13700.13700.2	2	3.16	0	3.23E+05		(K)LGGSAV	(K)L G G S A/V/I S L E/G K\P L(-)		188.47	670.8912	1340.778	-0.0033	-2.4	6	22956	8.8	HUMAN	E9PK25	Cofilin-1
26738	dirMS_041712_NAR_20mM_minus.13877.13877.2	2	3.16	0	5.25E+05	K58k	(K)IVEFNPN	(K)I|V/E F N P M V L k(G)	k:Ubiquitin-K	191.03	652.3653	1189.665	114.0584	11.9	6	7583.8	10.11	HUMAN	F8VZP2	Glycosyltransferase 8 domain-containing protein 2 (Fragment)
26739	dirMS_041712_NAR_30mM_minus2.12387.12387.2	2	3.16	1	8.53E+04		(R)IGLEVDF	(R)I G/L E V D R R(A)		121.53	479.2746	957.548	-0.0057	-5.9	6.07	85871.1	5.87	HUMAN	J3QR07	YTH domain-containing protein 1
26740	dirMS_041712_NAR_30mM_minus2.16540.16540.2	2	3.16	0	1.27E+05		(R)YLELLER	(R)Y L|E/L/L E R(T)		143.42	468.2614	935.52	-0.0041	-4.4	4.53	86321.7	5.29	HUMAN	I3L2B0	Protein CLUH
26741	dirMS_041712_NAR_30mM_minus2.17725.17725.2	2	3.16	0	6.65E+04		(K)IFFAGDT	(K)I/F|F A G D T I/P/K(S)		151.17	554.8038	1108.604	-0.0034	-3.1	5.84	258215.9	5.48	HUMAN	E7EN95	Filamin-B
26742	dirMS_041712_NAR_30mM_minus2.8447.8447.2	2	3.16	1	5.73E+05		(R)SKRGGE	(R)S/K R G G E E/R(V)		101.38	459.7452	918.475	0.008	8.7	8.46	46436.8	5.69	HUMAN	E9PIW9	Atherin
26743	dirMS_041712_NAR_40mM_minus2.14043.14043.3	3	3.16	0	4.86E+05		(R)IHFPLAT	(R)I H F P L A T Y A|P V I S A E K(A)		167.57	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
26744	dirMS_041712_NAR_40mM_minus2.9337.9337.2	2	3.16	0	1.02E+05		(K)MGSALF	(K)M G/S A L F V K(K)		137.82	426.7348	852.465	-0.0025	-2.9	8.5	46727.1	9.69	HUMAN	Q86WD7	Serpin A9
26745	dirMS_041712_NAR_50mM_minus2.10465.10465.3	3	3.16	1	5.73E+04		(R)MLFKDD	(R)M/L\F K D\D Y/P/S/S P P K(C)		127.57	508.9195	1524.74	0.0037	2.4	5.71	20685.4	9.18	HUMAN	B0QYN7	SUMO-conjugating enzyme UBC9
26746	dirMS_041712_NAR_50mM_minus2.13519.13519.3	3	3.16	0	3.51E+04	S643s	(R)TVLSIAs	(R)T\V/L S I A s A Q G/N V E/V V R(T)	s:Phosphorylated S	145.15	574.9724	1642.912	79.9904	14	5.66	137809.7	5.94	HUMAN	E9PDW0	Ankyrin repeat domain-containing protein 50
26747	dirMS_041712_NAR_50mM_minus2.15831.15831.3	3	3.16	1	8.21E+04		(K)DANAKL	(K)D A\N A K L S E\L|E/A/A/L Q R(A)		158.97	543.6248	1628.86	-0.0004	-0.2	4.68	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
26748	dirMS_041712_NAR_50mM_minus2.15897.15897.3	3	3.16	1	1.03E+05	T489t	(K)EMQSYS	(K)E M/Q S Y S/t/L K A V T T R(A)	t:N-acetylglucosamine (T)	157.65	606.6366	1614.816	203.0797	0.2	8.69	112769.3	9.14	HUMAN	P29322	Ephrin type-A receptor 8
26749	dirMS_041712_NAR_50mM_minus2.5853.5853.3	3	3.16	1	1.42E+05		(K)IQDKEGI	(K)I Q D K E\G I/P/P D Q Q R(L)		95.4	508.597	1523.781	-0.0048	-3.1	4.56	17271.6	6.75	HUMAN	B4DV12	Ubiquitin
26750	dirMS_041712_NAR_60mM_minus.10737.10737.3	3	3.16	1	1.21E+05		(K)GVAINM	(K)G V A\I N|M V\T E/E D K/R(T)		119.37	487.9154	1461.737	-0.005	-3.4	4.68	46381.4	5.32	HUMAN	P60842	Eukaryotic initiation factor 4A-I
26751	dirMS_041712_NAR_60mM_minus.10919.10919.3	3	3.16	0	2.57E+05		(R)ALPESLG	(R)A L|P/E/S L G Q/H A L R(S)		121.15	431.2376	1291.712	-0.0135	-10.4	6.79	31463.6	5.53	HUMAN	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1
26752	dirMS_041712_NAR_60mM_minus.16763.16763.3	3	3.16	1	2.04E+05		(K)YAVLYQ	(K)Y/A/V\L/Y/Q/P L F D K R(F)		154.33	504.9409	1512.821	-0.0128	-8.4	8.49	42989.1	4.45	HUMAN	B3KNT8	Nucleosome assembly protein 1-like 1
26753	dirMS_041712_NAR_60mM_minus.7450.7450.3	3	3.16	0	1.90E+05	K386k	(K)VIDEQAI	(K)V I/D/E Q\A F L/S P G S k(G)	k:Ubiquitin-K	101.43	502.2642	1390.721	114.0568	9.2	4.37	261285.6	8.17	HUMAN	Q5T1R4	Transcription factor HIVEP3
26754	dirMS_041712_NAR_60mM_minus.7541.7541.3	3	3.16	0	4.90E+04		(R)QSLGHP	(R)Q S L G H\P/P P E/P G P D R(V)		101.33	495.2483	1483.729	0.0015	1	5.32	12758.7	4.21	HUMAN	C9J830	cAMP-dependent protein kinase type II-alpha regulatory subunit (Fragment)
26755	dirMS_041712_NAR_60mM_minus.9626.9626.2	2	3.16	1	4.41E+05		(R)LQAEIEG	(R)L Q/A E/I/E/G L K G Q R(A)		114.13	671.3768	1341.748	-0.0022	-1.6	6.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
26756	dirMS_041712_NAR_120mM_plus.10471.10471.3	3	3.16	1	7.78E+05		(R)AQAGEL	(R)A Q A G/E L W V/K N E K(V)		107.1	458.2486	1372.722	0.0093	6.8	6.18	139774.5	6.28	HUMAN	C9JIN9	DEP domain-containing protein 5
26757	dirMS_041712_NAR_120mM_plus.3605.3605.3	3	3.16	1	3.84E+06	M139m	(R)QREmEE	(R)Q/R E m E E/Q/M/R(R)	m:Oxidized methionine	60.22	418.1852	1236.546	15.9951	0.1	4.79	26419.2	5.1	HUMAN	H0Y9K7	Splicing factor, proline- and glutamine-rich (Fragment)
26758	dirMS_041712_NAR_120mM_plus.4130.4130.2	2	3.16	1	1.31E+06	M310m	(R)TKTEISE	(R)T K/T E/I S/E/m N R(N)	m:Oxidized methionine	69.72	612.7976	1208.594	15.994	-0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
26759	dirMS_041712_NAR_120mM_plus.6790.6790.2	2	3.16	0	1.99E+05		(K)SFLKPGE	(K)S/F|L K P G E K(T)		89.1	453.2599	905.509	0.0034	3.8	8.31	58856.7	6.26	HUMAN	Q8WXF1	Paraspeckle component 1
26760	dirMS_041712_NAR_120mM_plus.8003.8003.2	2	3.16	0	4.64E+05		(K)STTTGHI	(K)S/T|T\T/G H L\I/Y K(C)		95.25	560.8014	1120.6	-0.0042	-3.7	8.34	12137.8	9.3	HUMAN	A6PW80	Elongation factor 1-alpha 1 (Fragment)
26761	dirMS_041712_NAR_20mM_plus.10386.10386.2	2	3.16	0	1.02E+05	T1009t	(K)EPEIItVT	(K)E P/E I I t/V T L K(K)	t:Phosphorylated T	145.08	611.8175	1142.667	79.961	-4.4	4.53	207812.6	6.06	HUMAN	A8MQ02	Afadin
26762	dirMS_041712_NAR_20mM_plus.10769.10769.2	2	3.16	0	2.19E+05	M33m	(K)VAGmD	(K)V A|G/m\D V E/L T V E E R(N)	m:Oxidized methionine	147.28	732.3555	1447.71	15.994	-0.6	4	10949.3	5.28	HUMAN	B4DJF2	14-3-3 protein epsilon
26763	dirMS_041712_NAR_20mM_plus.11469.11469.2	2	3.16	0	2.27E+05		(K)LITPAVV	(K)L I|T|P A/V V S E R(L)		151.1	542.8186	1084.636	-0.0062	-5.7	6	13798.9	10.17	HUMAN	P62851	40S ribosomal protein S25
26764	dirMS_041712_NAR_20mM_plus.15234.15234.2	2	3.16	2	6.89E+04	M122m	(K)KNLFERr	(K)K N/L F E R m E A R(A)	m:Oxidized methionine	175.98	655.3293	1293.673	15.9781	-12.8	8.75	174370.4	5.58	HUMAN	A4FU69	EF-hand calcium-binding domain-containing protein 5
26765	dirMS_041712_NAR_20mM_plus.6690.6690.2	2	3.16	0	7.62E+04	M1m M2m	(-)mmEVA	(-)m m E/V|A A/A D/V K(Q)	m:Oxidized methionine	110.9	548.754	1064.512	31.9892	-0.5	4.37	9475.6	4.64	HUMAN	J3KRD5	Cytosolic non-specific dipeptidase (Fragment)
26766	dirMS_041712_NAR_20mM_plus.7432.7432.2	2	3.16	0	7.51E+04	M33m	(R)IDEmPE	(R)I D E/m/P E A A\V/K(S)	m:Oxidized methionine	120.15	559.7742	1102.545	15.9962	1.2	4.14	26901.9	4.7	HUMAN	P51858	Hepatoma-derived growth factor
26767	dirMS_041712_NAR_20mM_plus.8194.8194.2	2	3.16	0	4.72E+03	M239m	(K)EVDEQn	(K)E V|D E Q m L N V/Q/N K(N)	m:Oxidized methionine	126.32	731.8435	1446.689	15.9904	-3.1	4.14	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
26768	dirMS_041712_NAR_30mM_plus2.10638.10638.2	2	3.16	0	5.36E+04		(K)TAVCDIF	(K)T A\V|C/D I/P|P R(G)	C:Carbamidomethylation	108.98	514.7643	1028.519	0.002	1.9	5.5	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
26769	dirMS_041712_NAR_40mM_plus2.10314.10314.2	2	3.16	0	2.87E+04		(K)YNNCWI	(K)Y/N|N C W/L/A R(T)	C:Carbamidomethylation	125.6	548.7522	1096.499	-0.0022	-2	8.75	55416	8.63	HUMAN	H0YM31	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial
26770	dirMS_041712_NAR_40mM_plus2.6830.6830.2	2	3.16	0	1.67E+04		(K)MMSFD	(K)M/M/S F D/T/R(A)		100.2	444.1966	887.375	0.0109	12.3	5.59	33457.6	6.02	HUMAN	F5H1G8	Guanine nucleotide-binding protein subunit alpha-13
26771	dirMS_041712_NAR_40mM_plus2.7490.7490.2	2	3.16	0	2.68E+04		(R)STFSTNY	(R)S T/F/S T N Y R(S)		103.65	488.2297	975.453	-0.0009	-0.9	8.46	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
26772	dirMS_041712_NAR_50mM_plus2.15569.15569.3	3	3.16	1	2.60E+05		(R)NAIENLI	(R)N A|I|E N L\L/G Y Q S G K T G F R(C)		149.67	623.3237	1867.966	-0.0095	-5.1	8.59	36304.5	8.62	HUMAN	P0C604	Putative olfactory receptor 4A8
26773	dirMS_041712_NAR_50mM_plus2.21339.21339.3	3	3.16	2	1.64E+05		(K)HIPRIGP	(K)H I P R I G P R/L G D A E W/A L R(R)		182.95	653.0385	1957.088	0.0131	6.7	9.52	29457.2	9.52	HUMAN	Q96NP5	HCG2008157
26774	dirMS_041712_NAR_50mM_plus2.21482.21482.3	3	3.16	0	4.01E+04		(K)NHEIVP(	(K)N H E\I V\P G S L|I A/S I A S/L\K(H)		184.62	583.67	1748.991	0.0049	2.8	6.75	54906.6	5.26	HUMAN	D6RDI3	Serine/threonine-protein kinase RIO2
26775	dirMS_041712_NAR_50mM_plus2.7986.7986.3	3	3.16	0	9.70E+03		(K)STAGDT	(K)S T/A G D T H/L/G G E/D F D N R(M)		108.98	564.5793	1691.726	-0.0022	-1.3	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
26776	dirMS_041712_NAR_60mM_plus.10886.10886.4	4	3.16	1	1.26E+06	M164m	(R)TEKGSD	(R)T\E K G S D P m F Y V N T S T/G G R(D)	m:Oxidized methionine	114.93	491.4815	1946.891	16.0129	9.2	5.73	59173.2	9.33	HUMAN	P60608	HERV-F(c)2_7q36.2 provirus ancestral Env polyprotein
26777	dirMS_041712_NAR_60mM_plus.14963.14963.2	2	3.16	1	2.62E+05		(K)GSLRAEI	(K)G S L\R A/E P G/A T P S R(D)		134.7	649.8514	1298.681	0.0144	11.1	9.6	280020.1	9.5	HUMAN	F8WBW8	BAH and coiled-coil domain-containing protein 1
26778	dirMS_041712_NAR_60mM_plus.15108.15108.3	3	3.16	1	2.51E+05		(R)LVDYLE(	(R)L/V D/Y/L E G/I R K(N)		135.35	402.5673	1205.689	-0.0015	-1.2	6.07	26450.3	5.66	HUMAN	Q96BR5	Sel1 repeat-containing protein 1
26779	dirMS_041712_NAR_60mM_plus.18791.18791.3	3	3.16	0	4.81E+04	S4s	(-)MEAsFV(	(-)M E A/s F/V Q T T M/A L G L S S K(K)	s:Phosphorylated S	155.72	627.6148	1800.887	79.9428	-12.5	5.75	50202.6	5.19	HUMAN	Q59EK9	RUN domain-containing protein 3A
26780	dirMS_041712_NAR_60mM_plus.20317.20317.3	3	3.16	1	2.58E+05	M100m M	(R)QAGAm	(R)Q A/G A m L L K V P L m L/T(-)	m:Oxidized methionine	167.3	506.6178	1485.853	31.9857	-2.7	8.75	11832.7	9.22	HUMAN	D6RCE5	Sodium-dependent phosphate transport protein 2A (Fragment)
26781	dirMS_041712_NAR_60mM_plus.20681.20681.3	3	3.16	2	1.68E+04	K1377k	(R)RFAKAS	(R)R F A\K A S S I/T E/I W S L/N/k(E)	k:Ubiquitin-K	168.58	655.6825	1851.012	114.0206	-11.3	9.99	525198.5	6.03	HUMAN	Q96DT5	Dynein heavy chain 11, axonemal
26782	dirMS_041712_NAR_60mM_plus.6963.6963.3	3	3.16	0	3.29E+05		(R)GPFRPEI	(R)G P|F R P E|P/G D G G E K(M)		94.62	448.2174	1342.639	-0.001	-0.7	4.68	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
26783	dirMS_041712_NAR_60mM_plus.7255.7255.3	3	3.16	1	1.38E+05		(R)GDASKE	(R)G D|A/S K/E D\I D T A M/K(L)		96.27	460.8814	1380.631	-0.0015	-1.1	4.23	35407.1	6.73	HUMAN	E9PF18	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial
26784	dirMS_041712_NAR_120mM_minus.10612.10612.3	3	3.15	0	4.91E+05		(R)GFCLPPI	(R)G F/C L P/P|H C S R(G)	C:Carbamidomethylation	113.22	410.858	1230.551	0.0088	7.1	9.75	14391.8	4.99	HUMAN	G3V461	Creatine kinase B-type (Fragment)
26785	dirMS_041712_NAR_120mM_minus.18155.18155.3	3	3.15	0	1.20E+05	S212s	(R)LLGPPPI	(R)L L G P P P H V A A/G/W s P D P/K(Y)	s:N-acetylglucosamine (S)	153.18	648.0089	1738.928	203.0846	2.7	6.74	32679.8	9.81	HUMAN	Q9H1R2	Dual specificity protein phosphatase 15
26786	dirMS_041712_NAR_120mM_minus.20214.20214.3	3	3.15	0	3.92E+05		(K)VHLVGII	(K)V H L\V G\I/D/I/F/T G K(K)		166.45	433.5866	1298.747	-0.0015	-1.1	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
26787	dirMS_041712_NAR_20mM_minus.7821.7821.3	3	3.15	1	9.09E+04		(K)TSPNEG	(K)T S P N E G\L S G|N P A D L E R R(E)		127.92	604.9578	1812.883	-0.0246	-13.6	4.68	139722.6	5.73	HUMAN	P20020	Plasma membrane calcium-transporting ATPase 1
26788	dirMS_041712_NAR_30mM_minus2.16391.16391.2	2	3.15	0	1.35E+05		(K)STFVNIL	(K)S T|F/V/N I L K(Q)		142.78	461.2712	921.54	-0.0053	-5.7	8.47	23232.7	5.07	HUMAN	D6RCP9	Deoxycytidine kinase
26789	dirMS_041712_NAR_30mM_minus2.5775.5775.2	2	3.15	0	5.20E+04		(K)AAQEEY	(K)A A Q/E E Y V|K(R)		85.57	469.2383	937.462	0.0068	7.2	4.53	39795.8	9.08	HUMAN	H3BQN4	Fructose-bisphosphate aldolase
26790	dirMS_041712_NAR_30mM_minus2.6152.6152.2	2	3.15	0	1.25E+05		(K)MAGAM	(K)M A/G\A M S/T T A K(T)		87.65	484.7299	968.454	-0.0014	-1.5	8.5	23963.2	8.9	HUMAN	Q9UQN3	Charged multivesicular body protein 2b
26791	dirMS_041712_NAR_50mM_minus2.14462.14462.3	3	3.15	0	4.40E+05		(R)QVLIASH	(R)Q V/L/I/A S H L/P S Y E L/R(H)		150.95	542.6354	1625.901	-0.0093	-5.7	6.75	267260.7	5.95	HUMAN	Q13085	Acetyl-CoA carboxylase 1
26792	dirMS_041712_NAR_50mM_minus2.16048.16048.3	3	3.15	0	2.60E+05		(R)GFGHIG	(R)G F G H I G I A\V/P D V Y S A C K(R)	C:Carbamidomethylation	159	597.6337	1790.889	-0.0029	-1.6	6.74	21005.6	5.12	HUMAN	Q04760	Lactoylglutathione lyase
26793	dirMS_041712_NAR_50mM_minus2.16725.16725.3	3	3.15	1	9.23E+04		(R)DSEQVA	(R)D/S/E Q V/A E\L K/Q E L A T L K(S)		163.05	601.3217	1801.954	-0.0036	-2	4.41	109459.8	4.94	HUMAN	F5GYR8	General vesicular transport factor p115
26794	dirMS_041712_NAR_60mM_minus.18355.18355.3	3	3.15	1	1.13E+04	T162t	(R)AtVIGSF	(R)A t V I G S|F K|L W/P T K(I)	t:N-acetylglucosamine (T)	163.17	550.9705	1447.831	203.0662	-8	10	71027.8	5.65	HUMAN	Q9C093-4	Isoform 4 of Sperm flagellar protein 2
26795	dirMS_041712_NAR_60mM_minus.8037.8037.3	3	3.15	1	3.52E+05	M230m M	(R)mSmKE\	(R)m S\m K E V\D E/Q\m\L N\V\Q N K(N)	m:Oxidized methionine	103.9	657.9647	1923.897	47.9823	-1.3	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
26796	dirMS_041712_NAR_60mM_minus.9907.9908.3	3	3.15	0	7.93E+05	M380m	(K)NGDmV	(K)N G D m V/I P S/D Y F K(I)	m:Oxidized methionine	114.85	467.8879	1385.641	16.0086	9.7	4.21	159566.1	6.15	HUMAN	B7ZKN0	NEO1 protein
26797	dirMS_041712_NAR_120mM_plus.23222.23222.4	4	3.15	1	6.17E+04		(K)GLAPDLI	(K)G L A P D L/P E D L Y/H L/I K K(A)		175.57	456.259	1822.011	0.0033	1.8	5.38	16789.5	10.63	HUMAN	J3KMX5	40S ribosomal protein S13
26798	dirMS_041712_NAR_120mM_plus.23904.23904.3	3	3.15	1	1.60E+05	K61k	(K)kLPGVG	(K)k/L/P G V G\T K I A E K(I)	k:Ubiquitin-K	179.85	452.2725	1240.762	114.0406	-1.7	9.7	21872.7	9.5	HUMAN	E5RIJ0	DNA polymerase beta
26799	dirMS_041712_NAR_120mM_plus.7826.7826.4	4	3.15	2	2.47E+05		(K)GKEIPLA	(K)G K E/I P L A/S L/R G E Q G P R(G)		94.97	427.7382	1707.95	-0.0191	-11.2	8.75	73476.9	9.67	HUMAN	P27658	Collagen alpha-1(VIII) chain
26800	dirMS_041712_NAR_20mM_plus.10360.10360.2	2	3.15	0	1.23E+05	M189m M	(K)SLAmEn	(K)S L/A m/E m V L/T G D R(I)	m:Oxidized methionine	144.17	677.8247	1322.644	31.9978	5.9	4.37	31843.3	8.87	HUMAN	P30084	Enoyl-CoA hydratase, mitochondrial
26801	dirMS_041712_NAR_20mM_plus.11713.11713.2	2	3.15	0	1.27E+05		(R)ANTFVA	(R)A N/T/F V A E/L K(G)		153.08	496.7735	992.541	-0.0014	-1.4	6.05	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
26802	dirMS_041712_NAR_20mM_plus.13406.13406.2	2	3.15	1	6.23E+03	S435s	(K)LsVEEEN	(K)L/s V/E/E/E M\K K(C)	s:N-acetylglucosamine (S)	166.1	648.3203	1092.561	203.0728	-5.1	4.79	52895.3	8.98	HUMAN	Q6ZWB6	BTB/POZ domain-containing protein KCTD8
26803	dirMS_041712_NAR_20mM_plus.13953.13953.3	3	3.15	2	1.90E+05	S321s	(R)FsDRSDI	(R)F s D\R S D L T/K H R(R)	s:N-acetylglucosamine (S)	167.92	522.2569	1361.692	203.0641	-9.8	8.75	52277.3	11.76	HUMAN	Q499Z4	Zinc finger protein 672
26804	dirMS_041712_NAR_20mM_plus.14783.14783.3	3	3.15	2	7.26E+04		(-)XPQEPYI	(-)X P Q E P Y D R G R/L G R(N)		172.73	519.6131	1556.829	-0.0045	-2.9	8.74	20025.2	5.3	HUMAN	K7EQ30	Tripartite motif-containing protein 47 (Fragment)
26805	dirMS_041712_NAR_20mM_plus.17746.17746.2	2	3.15	0	7.48E+04		(R)AVLDALI	(R)A V L|D A/L/L E G K(A)		193.93	514.8011	1028.599	-0.0037	-3.6	4.37	332906.7	4.86	HUMAN	E9PGC8	MAP1 light chain LC2
26806	dirMS_041712_NAR_20mM_plus.7713.7713.2	2	3.15	0	6.38E+04		(K)TIAEQLA	(K)T I A E/Q L A/E/K(I)		123.35	501.7728	1002.547	-0.0083	-8.3	4.53	117873.5	9.45	HUMAN	Q7L014	Probable ATP-dependent RNA helicase DDX46
26807	dirMS_041712_NAR_30mM_plus2.16051.16051.2	2	3.15	0	3.62E+05		(R)GLDIPSII	(R)G/L|D\I/P S I K(T)		137.32	421.7559	842.498	0.0063	7.5	5.84	103258.6	6.54	HUMAN	Q86XP3	ATP-dependent RNA helicase DDX42
26808	dirMS_041712_NAR_30mM_plus2.17102.17102.3	3	3.15	0	4.78E+05		(R)EFVSISSI	(R)E F V S I S S P A H V A/T(-)		143.45	448.8963	1344.679	-0.0051	-3.8	5.24	100943.3	6.1	HUMAN	P22681	E3 ubiquitin-protein ligase CBL
26809	dirMS_041712_NAR_30mM_plus2.5627.5627.3	3	3.15	1	1.09E+05	T68t	(K)EVPtKRS	(K)E V/P t/K R S F E C K(E)	C:Carbamidomethylation t:Phosp	82.75	487.5528	1380.694	79.9498	-11.3	8.69	59802	6.95	HUMAN	Q5T7W7	Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 2

26810	dirMS_041712_NAR_30mM_plus2.7397.7397.2	2	3.15	0	9.18E+05		(R)GSAQSS	(R)G S A Q/S|S E|R(R)		93.92	411.1964	821.375	0.0107	13.1	6	33928.5	6.4	HUMAN	A8MT20	Metabotropic glutamate receptor 5
26811	dirMS_041712_NAR_40mM_plus2.12305.12305.3	3	3.15	1	9.50E+04		(K)ILQEYIT	(K)I/L/Q/E Y/I/T Q Q S N K L/E T G K(S)		138.03	665.0257	1993.06	0.0025	1.3	6.14	28001.7	5.46	HUMAN	K7EJJ1	AP-1 complex subunit mu-2 (Fragment)
26812	dirMS_041712_NAR_40mM_plus2.12603.12603.3	3	3.15	0	1.25E+05	M114m M	(R)AGKPVI	(R)A G K P V\I C A T Q/m L E/S m I K(K)	C:Carbamidomethylation m:Oxid	139.8	637.0002	1876.969	32.0167	14.1	8.64	18466.1	5.78	HUMAN	H3BSU3	Pyruvate kinase (Fragment)
26813	dirMS_041712_NAR_40mM_plus2.5937.5937.2	2	3.15	0	2.31E+05		(R)MGANN	(R)M/G|A/N N L E/R(M)		93.93	452.7221	904.431	0.0064	7.1	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
26814	dirMS_041712_NAR_40mM_plus2.6826.6826.2	2	3.15	0	1.97E+04		(K)TPGPGA	(K)T/P/G|P G A/Q S A L R(A)		100.07	527.7842	1054.564	-0.0029	-2.7	9.41	14466.4	9.92	HUMAN	E5RH77	40S ribosomal protein S14
26815	dirMS_041712_NAR_40mM_plus2.8927.8927.2	2	3.15	0	1.05E+05		(K)FYEQFS	(K)F Y/E Q/F S/K(N)		115.03	474.7301	948.446	0.0068	7.1	6	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
26816	dirMS_041712_NAR_50mM_plus2.10249.10249.3	3	3.15	1	3.09E+05		(R)LGLPGD	(R)L G L/P G D E V D/N K V K(G)		120.28	461.9229	1383.748	0.0063	4.6	4.56	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
26817	dirMS_041712_NAR_50mM_plus2.11235.11235.3	3	3.15	1	1.06E+04	S580s	(K)AMEAA	(K)A M/E/A A S s L/K S Q A A\T\K(N)	s:N-acetylglucosamine (S)	126.42	566.2937	1493.763	203.1037	14.4	8.64	156306.5	9.65	HUMAN	O96028	Histone-lysine N-methyltransferase NSD2
26818	dirMS_041712_NAR_50mM_plus2.17957.17957.3	3	3.15	0	7.62E+04		(K)LNLSCIH	(K)L N|L/S C I/H S P V V N E L M R(G)	C:Carbamidomethylation	162.23	627.9943	1881.967	0.001	0.5	6.75	60090.6	9.25	HUMAN	Q9Y2X3	Nucleolar protein 58
26819	dirMS_041712_NAR_50mM_plus2.19641.19641.3	3	3.15	0	3.31E+04		(K)IFTPIVE	(K)I F/T/P/I V E/H L G L Q I R(F)		173.02	545.9893	1635.958	-0.0047	-2.9	6.75	15289.3	10.14	HUMAN	F8WBJ6	RNA-binding protein PNO1
26820	dirMS_041712_NAR_50mM_plus2.20969.20969.3	3	3.15	0	1.78E+05		(R)ELSELSL	(R)E L/S E\L S L L/S/L/Y G I H/K(Q)		179.43	567.984	1701.942	-0.0047	-2.8	5.4	44907.6	5.84	HUMAN	P15309	Prostatic acid phosphatase
26821	dirMS_041712_NAR_60mM_plus.11070.11070.2	2	3.15	0	6.40E+05	N5262n	(R)EMVET	(R)E M V E T Q/I n S|V K(C)	n:N-acetylglucosamine (N)	115.62	740.8612	1277.641	203.0745	-3.3	4.53	1011861	5.37	HUMAN	E9PEL9	Nesprin-1
26822	dirMS_041712_NAR_60mM_plus.13510.13510.3	3	3.15	1	3.50E+05	T1073t	(K)VKTDEV	(K)V/K T D E V\V t/L T P\R(I)	t:N-acetylglucosamine (T)	126.22	520.952	1357.769	203.0729	-4.2	6.04	178595.5	4.71	HUMAN	E9PF17	Versican core protein
26823	dirMS_041712_NAR_60mM_plus.14249.14249.3	3	3.15	1	8.71E+05		(K)TTVKDL	(K)T\T V K/D L/S E|L G S V R(T)		131.35	468.9268	1404.769	-0.0034	-2.4	5.74	533778	5.74	HUMAN	Q15149	Plectin
26824	dirMS_041712_NAR_60mM_plus.15888.15888.3	3	3.15	1	2.94E+04		(R)VEVERD	(R)V E|V E R D N L A/E D\I M R(L)		139.05	563.613	1688.827	-0.0028	-1.6	4.18	49709.6	5.19	HUMAN	B0YJC4	Vimentin
26825	dirMS_041712_NAR_60mM_plus.19124.19124.3	3	3.15	1	2.04E+05		(K)LEALKD	(K)L E A L/K D\L/A S L S R(D)		158.65	439.262	1315.758	0.0135	10.2	6.07	18679.9	4.7	HUMAN	C9IZR8	Engulfment and cell motility protein 1 (Fragment)
26826	dirMS_041712_NAR_60mM_plus.20010.20010.3	3	3.15	0	8.95E+05		(R)IHFPLAT	(R)I H F P L A T\Y A|P/V/I S A E K(A)		165.7	586.3246	1756.963	-0.004	-2.3	6.75	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
26827	dirMS_041712_NAR_60mM_plus.20020.20020.3	3	3.15	1	3.34E+05		(K)GPVREG	(K)G P V R E G D V\L/T/L/L/E S E R(E)		165.02	590.6485	1769.939	-0.0083	-4.7	4.41	7898	11.1	HUMAN	P62857	40S ribosomal protein S28
26828	dirMS_041712_NAR_60mM_plus.21218.21218.3	3	3.15	2	5.39E+05	T456t	(R)LREEtER	(R)L R E E t E R\I/V T/T Y I R(E)	t:Phosphorylated T	175.57	620.326	1778.976	79.9875	11.4	6.23	98249.7	7.05	HUMAN	E9PEQ4	Dynamin-2
26829	dirMS_041712_NAR_60mM_plus.7172.7172.2	2	3.15	1	5.01E+05		(K)GKGGEI	(K)G/K|G G E I\Q\P V S V/K(V)		95.43	599.8427	1198.679	-0.0009	-0.7	8.59	10803.5	9.82	HUMAN	B8ZZL8	10 kDa heat shock protein, mitochondrial
26830	dirMS_041712_NAR_60mM_plus.9832.9832.3	3	3.15	1	2.15E+05		(R)GPGLVK	(R)G P/G L V K/Q E D F R(D)		109.68	415.8936	1245.659	0.0076	6.1	6.07	180453.7	6.04	HUMAN	H0YIQ2	YLP motif-containing protein 1 (Fragment)
26831	dirMS_041712_NAR_120mM_minus.12991.12991.3	3	3.14	1	1.41E+05	S204s	(R)VTAKSQ	(R)V/T A/K S Q Q/s G E K(A)	s:N-acetylglucosamine (S)	124.98	455.898	1162.606	203.0732	-4.5	8.56	66740.7	5.73	HUMAN	E7EN86	Zinc finger protein 143
26832	dirMS_041712_NAR_120mM_minus.16381.16381.4	4	3.14	0	4.94E+04	T69t	(K)DHLVTA	(K)D H L V T\A Y N H L F E t K(R)	t:N-acetylglucosamine (T)	143.45	473.4926	1687.844	203.1047	13.4	5.99	25233.4	9.34	HUMAN	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3
26833	dirMS_041712_NAR_120mM_minus.5538.5538.3	3	3.14	0	2.91E+05	M46m M4	(R)HQGVm	(R)H\Q\G V\m\V/G m G Q K(D)	m:Oxidized methionine	83.3	401.8604	1171.571	31.9956	4.8	8.76	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
26834	dirMS_041712_NAR_20mM_minus.12583.12583.3	3	3.14	0	4.32E+05	M73m	(R)AVLVDL	(R)A V L V D L E/P G T m/D S V R(S)	m:Oxidized methionine	173.2	539.9423	1601.82	15.992	-1.8	4.03	13112.4	5.23	HUMAN	F8W813	Tubulin beta-8 chain
26835	dirMS_041712_NAR_20mM_minus.7623.7623.3	3	3.14	0	9.70E+05		(R)AEGLHQ	(R)A E\G/L\H Q L\E/A D H/S R(M)		124.87	488.2327	1462.703	-0.0198	-13.5	5.27	84818.2	5.38	HUMAN	B8QQJ3	CARD14 isoform 3
26836	dirMS_041712_NAR_20mM_minus.7651.7651.2	2	3.14	0	2.20E+05		(K)TVPVEA	(K)T V/P V E/A V T S K(T)		125.42	515.7883	1030.578	-0.0086	-8.3	5.66	35720	5.34	HUMAN	B4E358	Src substrate cortactin
26837	dirMS_041712_NAR_30mM_minus2.13541.13541.2	2	3.14	0	2.09E+05		(R)EGMLFI	(R)E G M/L/F/I S K(L)		126.77	462.7452	924.486	-0.0028	-3	6.1	302295.2	9.03	HUMAN	Q96L73	Histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific
26838	dirMS_041712_NAR_30mM_minus2.15242.15242.2	2	3.14	0	3.72E+04		(R)IAAYLFK	(R)I/A|A Y L F K(G)		136.48	413.2472	825.487	0.0002	0.3	8.59	15830.9	5.16	HUMAN	J3KRF5	Clathrin heavy chain 1 (Fragment)
26839	dirMS_041712_NAR_30mM_minus2.6115.6115.2	2	3.14	1	4.60E+04	M1840m	(R)NAESVK	(R)N A/E S V K G m/R(K)	m:Oxidized methionine	87.78	504.2543	991.499	16.0024	7.4	8.75	223892.1	5.63	HUMAN	P12883	Myosin-7
26840	dirMS_041712_NAR_50mM_minus2.12040.12040.3	3	3.14	0	2.82E+05	M22m	(K)QGPLH	(K)Q/G/P L H G m L\I/N T/P Y V/T K(D)	m:Oxidized methionine	136.68	595.6534	1768.941	16.0042	5.2	8.6	26744.2	7.15	HUMAN	K7EK64	Acetyl-CoA carboxylase 1 (Fragment)
26841	dirMS_041712_NAR_50mM_minus2.6488.6488.3	3	3.14	1	6.93E+05		(R)VVSSIE	(R)V V|S S I E Q K T E/G A E K(K)		103.08	502.2662	1504.785	-0.0013	-0.9	4.79	8491.4	6.28	HUMAN	E5RIR4	14-3-3 protein zeta/delta (Fragment)
26842	dirMS_041712_NAR_50mM_minus2.7487.7487.3	3	3.14	0	4.49E+04	M289m	(K)ATVmD	(K)A T\V/m/D V K P V D/Y R(E)	m:Oxidized methionine	108.95	470.5755	1393.714	15.9975	1.9	6	35399.1	5.17	HUMAN	I3L4R8	Replication protein A 70 kDa DNA-binding subunit (Fragment)
26843	dirMS_041712_NAR_60mM_minus.17578.17578.3	3	3.14	1	2.32E+05		(K)GPREEI	(K)G P R E E I\V Y/L|P/C I Y R(N)	C:Carbamidomethylation	157.98	588.9733	1764.91	-0.0048	-2.7	6.14	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
26844	dirMS_041712_NAR_60mM_minus.8722.8722.3	3	3.14	1	1.40E+04	S299s	(K)LLGFsES	(K)L L/G F s E/S E K K(S)	s:Phosphorylated S	110.1	406.5363	1137.615	79.9793	10.7	6.14	115820.5	6.08	HUMAN	Q7RTR0	NACHT, LRR and PYD domains-containing protein 9
26845	dirMS_041712_NAR_60mM_minus.9467.9467.3	3	3.14	0	2.46E+05	S179s	(R)STPTPEL	(R)S T|P T P E/L I/s K(K)	s:N-acetylglucosamine (S)	112.25	425.8906	1072.589	203.0688	-8.3	5.72	28550.5	6.88	HUMAN	F6R8P8	SH3-containing GRB2-like protein 3-interacting protein 1 (Fragment)
26846	dirMS_041712_NAR_120mM_plus.10717.10717.3	3	3.14	1	5.61E+05		(K)IKGEHP	(K)I/K/G E H P G L\S I G D V A K(K)		108.78	507.6167	1520.843	-0.0076	-5	6.75	24408.7	5.92	HUMAN	B2RPK0	Putative high mobility group protein B1-like 1
26847	dirMS_041712_NAR_120mM_plus.11409.11409.3	3	3.14	1	8.84E+05		(R)ARSEQF	(R)A R S E\Q\F/I/N L R(E)		112.93	411.8988	1233.67	0.012	9.7	9.64	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
26848	dirMS_041712_NAR_120mM_plus.11808.11808.3	3	3.14	1	4.16E+06		(K)LLKITGC	(K)L L K I T G C A S P G K(T)	C:Carbamidomethylation	114.02	415.5688	1244.703	-0.0113	-9.1	10	42755	7.81	HUMAN	B7Z2F4	T-complex protein 1 subunit delta
26849	dirMS_041712_NAR_20mM_plus.11576.11576.2	2	3.14	0	1.27E+05		(R)ANTFVA	(R)A N|T/F V/A/E/L K(G)		152.88	496.7735	992.541	-0.0014	-1.4	6.05	24936.4	8.67	HUMAN	G3XAL0	Malate dehydrogenase
26850	dirMS_041712_NAR_20mM_plus.13039.13039.2	2	3.14	0	3.89E+04		(K)ILSDTYT	(K)I/L S/D T Y T V E K(V)		162.18	584.808	1168.61	-0.0009	-0.7	4.37	16797.2	7.93	HUMAN	G3V2T6	Uncharacterized protein
26851	dirMS_041712_NAR_20mM_plus.18221.18221.3	3	3.14	0	1.04E+05		(K)LAAELS	(K)L A A E L S/A T L E Q A/A A/T A R(V)		197.35	562.9694	1686.902	-0.0084	-5	4.53	558007.1	5.44	HUMAN	P58107	Epiplakin
26852	dirMS_041712_NAR_20mM_plus.7698.7698.2	2	3.14	0	1.53E+04		(K)TNEAQA	(K)T N/E|A Q A\I E T A R(A)		122.68	602.3004	1203.596	-0.0029	-2.4	4.53	10145.6	9.15	HUMAN	F8VQQ8	Ubiquitin-conjugating enzyme E2 N
26853	dirMS_041712_NAR_30mM_plus2.16001.16001.2	2	3.14	0	4.81E+05		(R)MGPNIY	(R)M G/P/N|I|Y E L R(T)		136.78	546.7844	1092.551	0.0109	10	5.75	8641.9	9.77	HUMAN	C9JDV8	Protein NipSnap homolog 1 (Fragment)
26854	dirMS_041712_NAR_40mM_plus2.6868.6868.2	2	3.14	0	4.44E+04		(K)SFQQSS	(K)S F|Q\Q/S S L S R(D)		100.17	520.2619	1039.517	-0.0002	-0.2	9.47	100478.9	5.71	HUMAN	A8MXP9	Matrin-3
26855	dirMS_041712_NAR_50mM_plus2.10694.10694.3	3	3.14	1	1.16E+05		(K)AVPREE	(K)A V|P R E E L/F V T S K(L)		123.92	459.2547	1375.758	-0.0084	-6.1	6.19	36914.7	6.33	HUMAN	P14550	Alcohol dehydrogenase [NADP(+)]
26856	dirMS_041712_NAR_50mM_plus2.11317.11317.3	3	3.14	0	5.84E+04	T219t	(K)CMLFSS	(K)C M L F S S G T V Q/L t/T T S/R(A)	C:Carbamidomethylation t:N-ace	127.85	664.6463	1788.862	203.0625	-8.5	9.75	38768.8	9.65	HUMAN	B4E0G4	PHD finger protein 6
26857	dirMS_041712_NAR_50mM_plus2.19966.19966.2	2	3.14	1	5.13E+05	S272s	(K)EsQRKF	(K)E s Q\R K F|E E E T\V K(S)	s:N-acetylglucosamine (S)	173.3	856.9122	1509.754	203.0628	-9.7	4.95	139280.8	5.39	HUMAN	O60841	Eukaryotic translation initiation factor 5B
26858	dirMS_041712_NAR_50mM_plus2.6239.6239.3	3	3.14	0	9.45E+04		(K)AGYSTD	(K)A G Y|S/T/D\E S S S S S L H A T R(T)		97.43	585.9333	1755.778	0.0073	4.2	5.32	74564.3	5.95	HUMAN	P51116	Fragile X mental retardation syndrome-related protein 2
26859	dirMS_041712_NAR_50mM_plus2.8455.8455.3	3	3.14	0	5.53E+05		(R)ASGNYA	(R)A S/G/N/Y A T V I S H N/P E T K(K)		111.85	563.6145	1688.824	0.0051	3	6.79	24115.6	11.59	HUMAN	E9PIZ3	60S ribosomal protein L8
26860	dirMS_041712_NAR_50mM_plus2.8724.8724.3	3	3.14	1	9.82E+04		(R)GDPAV	(R)G D\P A/V G K/T A L A Q I F R(S)		112.42	515.284	1543.859	-0.0217	-14	8.75	20124.7	5.5	HUMAN	F5GZ09	Intraflagellar transport protein 27 homolog (Fragment)
26861	dirMS_041712_NAR_60mM_plus.15277.15277.3	3	3.14	1	2.00E+05	N221n	(K)DGnVVT	(K)D G n V/V\T/S F K K R(M)	n:N-acetylglucosamine (N)	136.2	485.2663	1250.685	203.0992	13.6	9.99	62965	9.18	HUMAN	C9JS87	Histone deacetylase 9
26862	dirMS_041712_NAR_60mM_plus.5055.5055.3	3	3.14	0	2.71E+05		(R)YINTEH	(R)Y/I/N T E/H G G S Q A R(F)		83.2	444.8825	1332.629	0.0038	2.9	6.75	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
26863	dirMS_041712_NAR_60mM_plus.5126.5126.3	3	3.14	0	8.43E+04		(R)AEAEAG	(R)A E|A\E A/G S P R P D/P R(E)		85.22	451.5555	1352.655	-0.0034	-2.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
26864	dirMS_041712_NAR_60mM_plus.5498.5498.3	3	3.14	1	1.34E+05		(K)CDSSPD	(K)C\D S S P D/S A E/D V R K(V)	C:Carbamidomethylation	86.15	489.2128	1465.622	0.0015	1	4.23	40122.7	5.43	HUMAN	P02765	Alpha-2-HS-glycoprotein
26865	dirMS_041712_NAR_60mM_plus.6624.6624.3	3	3.14	1	3.47E+05		(-)RSTSGAE	(-)R|S T S G A/E P E S A/R(A)		93.58	416.5412	1247.598	0.0116	9.3	6.14	78626.3	9.32	HUMAN	H3BSH7	Cirhin (Fragment)
26866	dirMS_041712_NAR_120mM_minus.10516.10516.2	2	3.13	0	2.67E+05	M103m M	(R)LmmDF	(R)L m m D/F/D G K(N)	m:Oxidized methionine	112.05	494.7161	956.422	32.0033	13.7	4.21	64554.4	7.74	HUMAN	A0AV96	RNA-binding protein 47
26867	dirMS_041712_NAR_120mM_minus.20228.20228.4	4	3.13	1	2.98E+05		(R)GIEKPPF	(R)G I E K P P/F E\L/P D/F I K R(T)		166.82	447.2523	1785.99	-0.0024	-1.4	6.18	98282.7	5.49	HUMAN	E9PPJ0	Splicing factor 3B subunit 2
26868	dirMS_041712_NAR_20mM_minus.10776.10776.2	2	3.13	0	3.77E+05	K397k	(R)ALVTVD	(R)A L V|T/V D E|V L k(D)	k:Ubiquitin-K	155.6	600.8502	1086.641	114.0526	8.1	4.37	54996.4	5.61	HUMAN	C9J6G4	WAP, kazal, immunoglobulin, kunitz and NTR domain-containing protein 2
26869	dirMS_041712_NAR_20mM_minus.12581.12581.2	2	3.13	0	2.76E+05	M185m	(K)LAVNm	(K)L A/V N m V/P F/P R(L)	m:Oxidized methionine	173.25	580.3173	1143.634	15.993	-1.6	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
26870	dirMS_041712_NAR_20mM_minus.14492.14492.3	3	3.13	0	1.37E+05		(R)LSVEEA	(R)L S V\E E A V A A G V|V|G G E I Q E K(L)		199.57	629.0005	1884.991	-0.0044	-2.3	4.09	266161	5.68	HUMAN	E9PPU0	Epiplakin
26871	dirMS_041712_NAR_20mM_minus.8308.8308.2	2	3.13	0	7.57E+04		(K)DPNIVIA	(K)D P/N I V I A K(M)		133.1	435.2582	869.509	0	0	5.84	55361.8	6.42	HUMAN	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b
26872	dirMS_041712_NAR_30mM_minus2.10504.10504.2	2	3.13	0	1.03E+06	M234m	(K)TIVmGA	(K)T\I/V/m/G A S F R(N)	m:Oxidized methionine	111.57	499.2567	981.519	15.9875	-7.4	9.41	35556.4	9.3	HUMAN	F2Z393	Transaldolase
26873	dirMS_041712_NAR_30mM_minus2.16021.16021.2	2	3.13	0	2.17E+04		(R)NVYSLEI	(R)N/V|Y S L E I R(N)		140.85	497.265	993.536	-0.0136	-13.7	6	4024332	6.06	HUMAN	K7ENY1	Titin
26874	dirMS_041712_NAR_30mM_minus2.17368.17368.2	2	3.13	0	1.11E+04		(R)EQLAIAE	(R)E Q\L/A/I/A/E F A R(S)		148.28	574.3084	1147.611	-0.0011	-0.9	4.53	44227.3	7.81	HUMAN	E7EQR6	T-complex protein 1 subunit alpha
26875	dirMS_041712_NAR_30mM_minus2.18307.18307.2	2	3.13	0	1.03E+05		(K)SCDFLSS	(K)S C|D\F/L|S/S F R(D)	C:Carbamidomethylation	153.83	559.7501	1118.494	-0.0006	-0.5	5.55	42963.5	5.19	HUMAN	P35237	Serpin B6
26876	dirMS_041712_NAR_30mM_minus2.6655.6655.2	2	3.13	0	2.55E+04		(R)ASTALS	(R)A S/T|A L S/N E/Q/Q A R(R)		90.43	638.3134	1275.629	-0.0092	-7.2	6.05	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
26877	dirMS_041712_NAR_50mM_minus2.11072.11072.3	3	3.13	1	4.04E+05		(R)DNADLR	(R)D N/A D L R C E L P K(L)	C:Carbamidomethylation	131.43	444.2213	1330.642	0.0074	5.5	4.56	99395.5	5.82	HUMAN	E9PET8	Kinesin heavy chain isoform 5C
26878	dirMS_041712_NAR_50mM_minus2.18782.18782.3	3	3.13	1	5.91E+05		(K)EIINLKK	(K)E I/I/N L K K D L I R(S)		181.93	452.2862	1354.842	0.0024	1.8	8.69	15377.5	10.35	HUMAN	F5H2N8	Coiled-coil domain-containing protein 60
26879	dirMS_041712_NAR_60mM_minus.12079.12079.3	3	3.13	0	1.88E+05	M908m	(R)mTIIGVI	(R)m T\I I\G V I L\S F R(A)	m:Oxidized methionine	126.9	422.5787	1249.734	15.9879	-5.6	9.5	129634.5	6.4	HUMAN	P55160	Nck-associated protein 1-like
26880	dirMS_041712_NAR_60mM_minus.13692.13692.3	3	3.13	1	6.76E+05		(R)TLEGFR	(R)T L E G F/R/L L V E/K(E)		136.15	435.5926	1304.757	0.006	4.6	5.81	210550.5	6.46	HUMAN	G5E933	Myotubularin-related protein 5
26881	dirMS_041712_NAR_60mM_minus.17684.17684.3	3	3.13	1	1.91E+05	S154s	(R)AGKPPG	(R)A G K/P P G A E|P P s A A A K G/R(K)	s:N-acetylglucosamine (S)	158.18	588.9733	1561.844	203.0608	-10.5	9.99	210777.5	6.03	HUMAN	Q9Y4B5	Protein SOGA2
26882	dirMS_041712_NAR_60mM_minus.17690.17690.3	3	3.13	1	2.31E+05		(R)LGLSTLG	(R)L G L/S T L/G E L K/Q N L S R(S)		159.18	543.6476	1628.933	-0.0047	-2.9	8.75	22294.4	5.26	HUMAN	O43399	Tumor protein D54
26883	dirMS_041712_NAR_60mM_minus.7466.7466.3	3	3.13	1	2.56E+04	M2211m	(R)STTQEL	(R)S T/T/Q E L m E D D R V K(R)	m:Oxidized methionine	101.02	523.2497	1551.732	16.0026	4.9	4.32	266161	5.68	HUMAN	E9PPU0	Epiplakin
26884	dirMS_041712_NAR_60mM_minus.7651.7651.3	3	3.13	0	1.62E+05	S828s	(R)AGLEVL	(R)A G L/E V L G S S D/P T T s A S R(V)	s:Phosphorylated S	102.03	576.5915	1647.818	79.9415	-14.4	4.37	94860.9	9.41	HUMAN	Q15398-3	Isoform 3 of Disks large-associated protein 5
26885	dirMS_041712_NAR_120mM_plus.4161.4161.2	2	3.13	1	1.45E+06	M310m	(R)TKTEISE	(R)T K|T/E\I S E m N R(N)	m:Oxidized methionine	69.8	612.7976	1208.594	15.994	-0.8	5.81	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
26886	dirMS_041712_NAR_120mM_plus.4438.4438.3	3	3.13	1	2.90E+05		(R)AAEEED	(R)A A|E E/E/D E A D P/K R(Q)		72.35	453.8721	1359.602	-0.0005	-0.4	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
26887	dirMS_041712_NAR_120mM_plus.6462.6462.3	3	3.13	1	1.10E+05		(R)RTAQEV	(R)R T A Q E\V/E/T/Y/R(R)		87.97	418.2137	1252.628	-0.0015	-1.2	6.14	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
26888	dirMS_041712_NAR_20mM_plus.11256.11256.2	2	3.13	0	1.18E+05		(K)VGLQVV	(K)V/G L/Q\V V A/V K(A)		150.45	456.7977	912.588	0.0004	0.5	8.72	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
26889	dirMS_041712_NAR_20mM_plus.19180.19180.3	3	3.13	0	8.23E+04		(R)GQVPPL	(R)G Q V P P L|V/T/T/N F L V K(D)		203.7	504.9651	1512.878	0.0023	1.5	8.75	108105.4	6.57	HUMAN	E7EP00	Protein transport protein Sec24C
26890	dirMS_041712_NAR_20mM_plus.8282.8282.2	2	3.13	0	1.39E+05		(K)LYACSSL	(K)L Y|A C S S L/D C T V R(I)	C:Carbamidomethylation	127.48	722.8163	1444.656	-0.0306	-21.2	5.83	182528.5	7.97	HUMAN	A6NE52	WD repeat-containing protein KIAA1875
26891	dirMS_041712_NAR_20mM_plus.8800.8800.2	2	3.13	0	2.28E+04	M863m	(K)LmSDAL	(K)L m/S D A L Q H A Q C T L/K(S)	C:Carbamidomethylation m:Oxid	130.13	816.3904	1615.793	15.9805	-8.9	6.74	127697.7	6.18	HUMAN	Q86W24	NACHT, LRR and PYD domains-containing protein 14
26892	dirMS_041712_NAR_30mM_plus2.16615.16615.2	2	3.13	0	3.72E+05		(K)QLQEM	(K)Q L Q/E/M/L G L/S/K(V)		140.13	573.8112	1146.619	-0.0036	-3.1	6	83880.6	7.33	HUMAN	F5H365	Protein transport protein Sec23A
26893	dirMS_041712_NAR_30mM_plus2.17380.17380.2	2	3.13	0	8.32E+04		(R)VPFTDIF	(R)V P F T/D\I F K(K)		143.97	483.7736	966.529	0.0104	10.8	5.81	20492.5	4.36	HUMAN	H3BNQ4	Dynein assembly factor 1, axonemal (Fragment)
26894	dirMS_041712_NAR_30mM_plus2.20162.20162.2	2	3.13	0	1.03E+05		(R)ALTDFF	(R)A L/T\D/F F R(K)		159	435.2316	869.452	0.0043	5	5.88	22336.7	5.02	HUMAN	H7BXD5	Grancalcin
26895	dirMS_041712_NAR_30mM_plus2.21953.21953.2	2	3.13	0	2.28E+05		(K)ALELNM	(K)A L/E/L/N M L S L/K(G)		170.38	566.3204	1131.644	-0.0107	-9.4	6.05	40821.3	7.79	HUMAN	Q9Y617	Phosphoserine aminotransferase
26896	dirMS_041712_NAR_30mM_plus2.22142.22142.3	3	3.13	0	3.20E+05		(K)TQDVLP	(K)T/Q D V L P T S Q G V D H K(Q)		172.5	508.9306	1524.765	0.012	7.9	5.18	170856.3	5.85	HUMAN	E9PD49	Roundabout homolog 1
26897	dirMS_041712_NAR_30mM_plus2.8492.8492.2	2	3.13	0	6.78E+05		(R)LANQQS	(R)L A\N/Q/Q S\L K(N)		97.98	451.2545	901.51	-0.0084	-9.4	8.75	93493.8	9.47	HUMAN	B4DZN9	Rho GTPase-activating protein 11A
26898	dirMS_041712_NAR_40mM_plus2.10781.10781.2	2	3.13	0	5.88E+04		(R)YYGYTG	(R)Y/Y/G|Y T G A F R(C)		128.98	549.2569	1097.505	0.0015	1.3	8.5	78507.3	9.14	HUMAN	E7EQB2	Kaliocin-1 (Fragment)
26899	dirMS_041712_NAR_40mM_plus2.13601.13601.3	3	3.13	0	1.89E+05		(R)LSAMLV	(R)L S/A/M L V P V/T P/E V K P K(R)		145.9	536.9848	1608.939	0.0005	0.3	8.59	31524.1	4.5	HUMAN	P82970	High mobility group nucleosome-binding domain-containing protein 5
26900	dirMS_041712_NAR_40mM_plus2.9390.9390.2	2	3.13	0	6.70E+04		(K)SLLSSPT	(K)S L/L S/S/P T K(D)		118.4	416.7466	832.477	0.0085	10.2	8.47	39475.1	5.72	HUMAN	I3NI36	A-kinase anchor protein 1, mitochondrial (Fragment)
26901	dirMS_041712_NAR_50mM_plus2.10569.10569.3	3	3.13	1	1.07E+05		(K)LAEQAE	(K)L/A/E/Q A E R Y D D M/A T C M K(A)	C:Carbamidomethylation	123.33	644.6132	1931.83	-0.0045	-2.4	4.32	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
26902	dirMS_041712_NAR_50mM_plus2.13774.13774.3	3	3.13	1	1.88E+06		(R)QATKDA	(R)Q A T K D A G T I/A/G/L N\V L R(I)		140	543.3085	1627.913	-0.0016	-1	8.75	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
26903	dirMS_041712_NAR_60mM_plus.18962.18962.3	3	3.13	0	9.80E+03		(K)LYFKPIG	(K)L Y F K P I G D/P V F A/R(D)		156.52	508.2852	1522.842	-0.0006	-0.4	8.59	228081	6.98	HUMAN	A6NHR9	Structural maintenance of chromosomes flexible hinge domain-containing protein 1
26904	dirMS_041712_NAR_60mM_plus.20103.20103.3	3	3.13	0	5.22E+04		(K)VHLVGI	(K)V H L\V\G I|D\I F\T G K(K)		165.22	433.5839	1298.747	-0.0096	-7.4	6.71	13048.7	6.42	HUMAN	C9J4W5	Eukaryotic translation initiation factor 5A-2 (Fragment)
26905	dirMS_041712_NAR_120mM_minus.10631.10631.3	3	3.12	1	8.70E+04		(R)RGVVG	(R)R G V V G\P E/L Y G/R(L)		111.63	401.559	1202.664	-0.0016	-1.3	8.75	266161	5.68	HUMAN	E9PPU0	Epiplakin
26906	dirMS_041712_NAR_120mM_minus.11009.11009.3	3	3.12	1	1.83E+05		(R)NREILDE	(R)N R E I|L/D E/S/L/R(L)		114.83	415.5534	1244.659	-0.0137	-11	4.68	96649	6.13	HUMAN	Q8WUM4	Programmed cell death 6-interacting protein
26907	dirMS_041712_NAR_120mM_minus.11254.11254.3	3	3.12	1	1.61E+05		(K)SKHGSIE	(K)S K H G S/I E A N F/R(A)		114.68	415.8884	1245.633	0.0172	13.8	8.49	77915	5.87	HUMAN	Q6NUM6	tRNA wybutosine-synthesizing protein 1 homolog B
26908	dirMS_041712_NAR_120mM_minus.16046.16046.3	3	3.12	1	2.26E+05		(K)STFVLDE	(K)S T|F\V L/D E F K/R(K)		141.13	414.5544	1241.652	-0.0038	-3.1	5.79	56491.1	7.78	HUMAN	B4DTG2	Elongation factor 1-gamma
26909	dirMS_041712_NAR_120mM_minus.4547.4547.2	2	3.12	0	1.65E+05	S198s	(K)DITEEIM	(K)D/I T/E E I/M s G A R(T)	s:Phosphorylated S	74.27	651.2674	1221.578	79.9495	-12.9	4.14	89423.4	4.85	HUMAN	C9J2Z7	Eukaryotic translation initiation factor 4 gamma 1 (Fragment)
26910	dirMS_041712_NAR_120mM_minus.5971.5971.3	3	3.12	1	5.59E+05		(K)TCEESSF	(K)T C|E/E S S F C K/R(Q)	C:Carbamidomethylation	86.78	435.1849	1303.541	-0.0004	-0.3	5.81	10576.1	11.44	HUMAN	E9PRF8	Neutral alpha-glucosidase AB
26911	dirMS_041712_NAR_120mM_minus.9668.9668.3	3	3.12	0	3.83E+05		(K)NCPHIV	(K)N C/P H I\V/V\G T/P\G R(I)	C:Carbamidomethylation	107.45	436.2293	1306.669	0.0049	3.7	9.75	28185.1	10.76	HUMAN	B4DIJ6	Spliceosome RNA helicase DDX39B
26912	dirMS_041712_NAR_20mM_minus.11571.11571.3	3	3.12	1	8.58E+04	S51s	(K)GSLKNG	(K)G/S L K N G s M G S P/V N Q Q P K(K)	s:Phosphorylated S	164.17	603.6175	1728.87	79.9682	1	10	18425	4.34	HUMAN	Q5T586	Chromosome 9 open reading frame 25
26913	dirMS_041712_NAR_20mM_minus.13207.13207.2	2	3.12	0	1.40E+05		(K)VGINYQ	(K)V G I N Y Q|P P T V V/P G G D L A K(V)		183.15	912.9938	1824.985	-0.0051	-2.8	5.8	49012.3	4.9	HUMAN	A8MUB1	Tubulin alpha-4A chain
26914	dirMS_041712_NAR_30mM_minus2.16440.16440.2	2	3.12	0	1.28E+05		(K)QCFLVL	(K)Q C|F/L/V/L R(Q)	C:Carbamidomethylation	143.23	468.2614	935.513	0.0024	2.6	9.75	20139.7	9.34	HUMAN	C9J7S3	Aspartate--tRNA ligase, cytoplasmic (Fragment)
26915	dirMS_041712_NAR_40mM_minus2.8330.8330.3	3	3.12	1	4.74E+03		(R)IAEFTTN	(R)I/A|E F/T T N L T/E E E E K S K(S)		129.48	623.6417	1868.912	-0.0018	-1	4.32	227783.5	5.5	HUMAN	P35579	Myosin-9
26916	dirMS_041712_NAR_50mM_minus2.17834.17834.3	3	3.12	1	4.47E+04		(R)QGIEKLI	(R)Q G I E K L/I D V/I/E H R(A)		170.37	517.2991	1549.87	0.0131	8.4	5.45	58292.8	10.25	HUMAN	Q6UWH4	Protein FAM198B
26917	dirMS_041712_NAR_50mM_minus2.18071.18071.3	3	3.12	0	2.72E+05		(K)ISSIQSIV	(K)I/S S I Q/S/I V/P A L E I A N A/H/R(K)		171.43	640.361	1919.071	-0.0024	-1.3	6.75	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
26918	dirMS_041712_NAR_50mM_minus2.8308.8308.3	3	3.12	1	6.81E+04		(K)NVSEEL	(K)N V/S/E E L D R T P/P E V/S K(K)		115.55	567.289	1699.85	0.0027	1.6	4.41	136658.9	5.13	HUMAN	Q15393	Splicing factor 3B subunit 3

26919	dirMS_041712_NAR_50mM_minus2.8400.8400.3	3	3.12	1	1.94E+05		(K)GILAADE	(K)G I/L A/A D E S/T G S I/A K R(L)		115.23	496.9372	1488.802	-0.0046	-3.1	6.07	30711.4	7.15	HUMAN	H3BPS8	Fructose-bisphosphate aldolase A (Fragment)
26920	dirMS_041712_NAR_50mM_minus2.9264.9264.3	3	3.12	1	1.57E+05		(R)VHNATL	(R)V H/N A T L I L/S E G L/K R(A)		121.18	517.639	1550.901	0.0011	0.7	8.73	114325.3	6.69	HUMAN	P23378	Glycine dehydrogenase [decarboxylating], mitochondrial
26921	dirMS_041712_NAR_50mM_minus2.9983.9983.3	3	3.12	1	1.17E+05		(R)VGEPVA	(R)V G/E|P V A L/S E E E R L K(L)		124.95	519.2824	1555.833	0	0	4.49	8516.9	5.1	HUMAN	E9PIL8	Splicing factor 3B subunit 2 (Fragment)
26922	dirMS_041712_NAR_60mM_minus.11567.11567.3	3	3.12	1	2.94E+05		(R)VFDKEG	(R)V/F D K E G\N G T/V/M/G A E I R(H)		124.35	574.9539	1722.848	-0.0008	-0.5	4.68	26991.7	5.01	HUMAN	B7Z6Z4	Myosin light polypeptide 6
26923	dirMS_041712_NAR_60mM_minus.12383.12383.3	3	3.12	0	1.80E+05		(K)LTSSSIDI	(K)L T S S S I/D P G L S I K(Q)		128.38	439.9167	1317.726	0.0095	7.2	5.84	84866.9	5.86	HUMAN	Q5QJE6	Deoxynucleotidyltransferase terminal-interacting protein 2
26924	dirMS_041712_NAR_60mM_minus.12672.12672.3	3	3.12	0	1.18E+04	T54t	(R)TQNPM	(R)T Q/N/P M V T G t S V L G V K(F)	t:N-acetylglucosamine (T)	130.48	578.961	1531.815	203.0536	-14.9	8.41	29260.8	5.72	HUMAN	P28070	Proteasome subunit beta type-4
26925	dirMS_041712_NAR_60mM_minus.14311.14311.3	3	3.12	1	1.25E+05		(R)DLEEKLE	(R)D L/E E K/L/E/T L R(L)		139.63	415.8949	1245.669	0.0016	1.3	4.41	141626	5.5	HUMAN	A8MY36	Dynactin subunit 1
26926	dirMS_041712_NAR_60mM_minus.16204.16204.3	3	3.12	0	1.20E+05		(R)LIDDMV	(R)L/I D D M/V A Q V L/K(S)		150.3	415.5713	1244.692	0.0075	6	4.21	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
26927	dirMS_041712_NAR_60mM_minus.17108.17108.3	3	3.12	0	2.08E+05		(R)DTYNQS	(R)D T Y N Q S I/P Q P/P\P R(K)		154.82	504.913	1512.744	-0.0197	-13	5.83	56541.9	9.36	HUMAN	G5EA07	HCG1647660, isoform CRA_a
26928	dirMS_041712_NAR_60mM_minus.19658.19658.3	3	3.12	1	3.16E+05		(R)ARDDLIT	(R)A R D D L I T|D\L/L/N E A K(Q)		176.93	529.6145	1586.838	-0.0095	-6	4.23	23653.1	9.28	HUMAN	C9J8H1	V-type proton ATPase subunit E 1 (Fragment)
26929	dirMS_041712_NAR_60mM_minus.5766.5766.3	3	3.12	0	6.91E+05	K1105k	(K)SFFSSCG	(K)S\F/F/S S/C G S L H k(L)	C:Carbamidomethylation k:Ubiqu	88.05	457.5434	1256.573	114.0428	-0.1	8.49	150311.9	6.33	HUMAN	B7ZKT6	SOS2 protein
26930	dirMS_041712_NAR_60mM_minus.9656.9656.3	3	3.12	1	2.83E+05		(K)TAVCDIF	(K)T A V/C D I/P P R G L K(M)	C:Carbamidomethylation	112.42	442.9098	1326.72	-0.005	-3.8	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
26931	dirMS_041712_NAR_120mM_plus.6736.6736.2	2	3.12	0	3.07E+05		(R)SHEGET	(R)S H|E|G\E/T A Y I\R(V)		88.3	581.7777	1162.549	-0.0006	-0.5	5.38	16510	11.51	HUMAN	J3KSR8	Serine/arginine-rich-splicing factor 1 (Fragment)
26932	dirMS_041712_NAR_120mM_plus.7353.7353.3	3	3.12	1	7.86E+05		(R)KTGQAP	(R)K T G\Q A|P G Y|S Y T A A N K(N)		91.62	519.5943	1556.77	-0.002	-1.3	9.53	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
26933	dirMS_041712_NAR_20mM_plus.12186.12186.2	2	3.12	1	3.28E+04	S274s	(K)QLNQGE	(K)Q L/N Q/G E G T I/R s R(S)	s:Phosphorylated S	156.7	719.8475	1358.714	79.9742	5.5	9.6	32478.2	7.88	HUMAN	Q9UN19	Dual adapter for phosphotyrosine and 3-phosphotyrosine and 3-phosphoinositide
26934	dirMS_041712_NAR_20mM_plus.14639.14639.2	2	3.12	1	9.83E+04		(R)KAVESIC	(R)K A/V E S I Q A E D E S A K(L)		173.2	752.8674	1504.749	-0.0214	-14.2	4.41	40466	9.39	HUMAN	B4DQT1	Macrophage erythroblast attacher
26935	dirMS_041712_NAR_20mM_plus.17001.17001.2	2	3.12	0	1.73E+05		(K)LFLVQLC	(K)L F|L|V|Q L Q E K(A)		189.28	559.3342	1117.662	-0.0004	-0.4	6	17283.8	5.95	HUMAN	H3BND3	Cleavage and polyadenylation-specificity factor subunit 5 (Fragment)
26936	dirMS_041712_NAR_30mM_plus2.11183.11183.2	2	3.12	0	2.63E+05		(R)GTGIVS/	(R)G T G I/V/S A P V/P K(K)		111.4	513.3006	1025.599	-0.005	-4.9	8.75	21898	11.33	HUMAN	E9PM36	40S ribosomal protein S2
26937	dirMS_041712_NAR_30mM_plus2.22661.22661.3	3	3.12	1	1.17E+04		(R)LMNSQL	(R)L M N/S Q L V T T E K/R(F)		176.07	473.9205	1419.762	-0.0155	-10.9	8.75	47117.2	9.42	HUMAN	P15907	Beta-galactoside alpha-2,6-sialyltransferase 1
26938	dirMS_041712_NAR_30mM_plus2.6394.6394.2	2	3.12	0	6.15E+04	T604t M60	(K)GTVQtG	(K)G T/V Q/t\G m D t T K(T)	t:Phosphorylated T m:Oxidiz	87.8	657.7467	1138.541	175.9453	13.5	5.84	135284.8	9.24	HUMAN	Q96Q06	Perilipin-4
26939	dirMS_041712_NAR_30mM_plus2.6710.6710.2	2	3.12	0	1.24E+05		(K)SCATFSS	(K)S\C A/T/F S S S H S(-)	C:Carbamidomethylation	89.43	535.7086	1070.421	-0.0108	-10.1	6.46	7480.2	4.69	HUMAN	D6RAB3	Protein transport protein Sec31A
26940	dirMS_041712_NAR_40mM_plus2.17476.17476.3	3	3.12	0	7.92E+04		(R)LLLDGAI	(R)L L\L D/G A/P L/I A I H K(A)		169.23	458.6226	1373.852	0.0017	1.3	6.74	16469.8	8	HUMAN	K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)
26941	dirMS_041712_NAR_50mM_plus2.15547.15547.3	3	3.12	1	3.24E+04		(R)ALLKDQ	(R)A L/L K D Q Q/P G/T/F L/L R(F)		149.62	533.9764	1599.922	-0.0071	-4.4	8.79	83929.4	6.02	HUMAN	J3KPM9	Signal transducer and activator of transcription 1-alpha/beta
26942	dirMS_041712_NAR_50mM_plus2.21637.21637.3	3	3.12	1	1.01E+05		(R)SVMEAF	(R)S V M E A P F/P|A L G K T I L V K(N)		183.97	601.0191	1801.029	0.0135	7.5	8.31	98165.4	9.97	HUMAN	F8WAT8	DENN domain-containing protein 2A
26943	dirMS_041712_NAR_50mM_plus2.6034.6034.3	3	3.12	1	4.14E+04	M625m M6	(K)AQALRD	(K)A Q|A L R D N S T m/G Y m A A K(K)	m:Oxidized methionine	95.82	587.2736	1727.82	31.9859	-2.2	8.63	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
26944	dirMS_041712_NAR_60mM_plus.12858.12858.3	3	3.12	1	8.89E+05	M232m	(R)MSmKE	(R)M S m K E V D E\Q|M/L/N V Q N K(N)	m:Oxidized methionine	123.58	647.3021	1923.897	15.9945	-0.2	4.68	40069.4	4.83	HUMAN	E7EWR1	Tubulin beta chain
26945	dirMS_041712_NAR_120mM_minus.11621.11621.4	4	3.11	1	2.74E+05	S311s	(R)LsQYFEK	(R)L s Q Y F E K F D/V K(E)	s:N-acetylglucosamine (S)	117.63	402.461	1403.72	203.1016	13.9	6.07	155915	5.75	HUMAN	H7C1J4	Chromosome 6 open reading frame 107, isoform CRA_b
26946	dirMS_041712_NAR_120mM_minus.16806.16806.3	3	3.11	0	4.41E+05		(R)EHALLA	(R)E H A\L L/A\Y/T L/G V K(Q)		145.82	438.9186	1314.742	-0.0004	-0.3	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
26947	dirMS_041712_NAR_120mM_minus.7019.7019.3	3	3.11	1	9.49E+03	S50s	(R)EDsYHVI	(R)E\D|s Y H V R S R(S)	s:N-acetylglucosamine (S)	92.82	451.2073	1148.544	203.063	-12.1	6.85	60330.3	9.9	HUMAN	B1AVT0	CDC-like kinase 2
26948	dirMS_041712_NAR_120mM_minus.7482.7482.3	3	3.11	1	2.75E+05	M1m S3s	(-)mGsGEP	(-)m G s G E/P N/P A G K K K(K)	m:Oxidized methionine s:Pho	95.12	466.2202	1300.668	95.9783	12.2	9.7	43672.2	9.75	HUMAN	Q96DU9	Polyadenylate-binding protein 5
26949	dirMS_041712_NAR_120mM_minus.8654.8654.3	3	3.11	0	2.42E+05		(R)HGGGG	(R)H G G G G G G/F/G G/G/G/F G/S R(S)		101.48	440.8694	1320.583	0.0108	8.2	9.75	65717	8.32	HUMAN	P35908	Keratin, type II cytoskeletal 2 epidermal
26950	dirMS_041712_NAR_120mM_minus.9570.9570.3	3	3.11	0	3.45E+05		(K)NCPHIV	(K)N C/P/H I/V V G T/P G R(I)	C:Carbamidomethylation	107.37	436.2293	1306.669	0.0049	3.7	9.75	28185.1	10.76	HUMAN	B4DIJ6	Spliceosome RNA helicase DDX39B
26951	dirMS_041712_NAR_20mM_minus.6411.6411.2	2	3.11	0	1.57E+05		(R)VLADPSI	(R)V L|A|D/P S D D T K(G)		107.4	530.7615	1060.516	0	0	3.93	266161	5.68	HUMAN	E9PPU0	Epiplakin
26952	dirMS_041712_NAR_30mM_minus2.14397.14397.2	2	3.11	0	2.48E+05		(R)GIFTSEI	(R)G I|F/T/S E I G T K(Q)		132.1	526.7803	1052.562	-0.0089	-8.5	6	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
26953	dirMS_041712_NAR_30mM_minus2.17745.17745.2	2	3.11	0	2.77E+05		(K)SDVETIF	(K)S D V E\T I F/S/K(Y)		151.57	513.2571	1025.515	-0.008	-7.8	4.37	24721.8	10.58	HUMAN	Q5QPL9	RNA binding protein, autoantigenic (HnRNP-associated with lethal yellow homolog (Mouse)) (Fragment)
26954	dirMS_041712_NAR_30mM_minus2.18210.18210.2	2	3.11	0	1.25E+04		(R)ACLLCSL	(R)A C|L|L C/S L/V K(V)	C:Carbamidomethylation	153.23	532.2854	1063.564	-0.0003	-0.3	8.8	4709.5	6.52	HUMAN	J3KSQ6	Transcription elongation factor SPT4
26955	dirMS_041712_NAR_30mM_minus2.19229.19229.2	2	3.11	1	1.27E+05	M792m	(K)FGTIRAD	(K)F G/T I R A D/L I E Q m R(F)	m:Oxidized methionine	160.15	783.4108	1549.815	15.9988	2.5	6.07	144424.4	5.18	HUMAN	Q6ZT07	TBC1 domain family member 9
26956	dirMS_041712_NAR_30mM_minus2.5800.5800.2	2	3.11	0	7.96E+04		(R)SLLSWD	(R)S L L/S|W D S R(S)		85.35	482.244	963.489	-0.0087	-9	5.55	93096.1	6.18	HUMAN	B4DYV8	Roundabout homolog 4
26957	dirMS_041712_NAR_30mM_minus2.9159.9181.2	2	3.11	1	2.85E+04		(R)ATWAN	(R)A T W\A N/S K/E R(S)		105.82	531.7651	1062.533	-0.0098	-9.2	8.79	110910.1	9.73	HUMAN	Q6ZN55-2	Isoform 2 of Zinc finger protein 574
26958	dirMS_041712_NAR_40mM_minus2.11028.11028.3	3	3.11	0	8.43E+04		(K)MLDAED	(K)M/L/D/A E D/I V N T A R P D E K(A)		148.55	606.297	1816.875	0.0019	1	4.1	105308.6	5.27	HUMAN	O43707	Alpha-actinin-4
26959	dirMS_041712_NAR_40mM_minus2.13103.13103.3	3	3.11	1	7.25E+04		(R)VTTVTEI	(R)V/T/T V T E/I G K D V I/G L R(I)		160.8	534.3113	1600.927	-0.0075	-4.7	6.04	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
26960	dirMS_041712_NAR_40mM_minus2.9066.9066.3	3	3.11	0	7.48E+04		(R)LAQDHS	(R)L A Q D H S/I L N P Q/K(W)		135.53	455.2461	1363.733	-0.0091	-6.7	6.74	4528.1	8.38	HUMAN	A6PVU2	Ubiquitin carboxyl-terminal hydrolase 49 (Fragment)
26961	dirMS_041712_NAR_40mM_minus2.9723.9723.2	2	3.11	0	1.91E+06		(R)VAPEEH	(R)V A/P E E H/P V L/L T E A\P L N P K(A)		140.2	977.5343	1954.064	-0.0031	-1.6	4.75	18032.2	5.25	HUMAN	E7EVS6	Actin, cytoplasmic 1 (Fragment)
26962	dirMS_041712_NAR_40mM_minus2.9808.9808.3	3	3.11	1	3.95E+04	K558k	(K)TFAIKPE	(K)T\F/A I K P E/V A P E L S E G R k(N)	k:Ubiquitin-K	140.9	662.684	1872.023	114.0149	-14.1	5.9	81321	6.7	HUMAN	Q9UH90	F-box only protein 40
26963	dirMS_041712_NAR_50mM_minus2.17060.17060.3	3	3.11	1	4.79E+04		(K)LVGQSI	(K)L V G Q/S/I/I A Y L Q K K(G)		165.03	487.6328	1460.883	0.0003	0.2	9.7	139883.7	8.06	HUMAN	P53621	Coatomer subunit alpha
26964	dirMS_041712_NAR_50mM_minus2.5902.5902.3	3	3.11	1	5.83E+03		(K)DGDPRK	(K)D G D P R K A/S T P Q/E E Q T K(E)		95.62	596.2904	1786.857	0.0001	0	4.79	151738.6	5.95	HUMAN	B5MEG5	Ubiquitin carboxyl-terminal hydrolase
26965	dirMS_041712_NAR_60mM_minus.13557.13557.3	3	3.11	1	2.12E+05		(R)NDEELN	(R)N/D\E/E/L N K/L/L G K(V)		135.2	424.8995	1272.679	0.0045	3.6	4.68	9975.4	9.7	HUMAN	H0YFX9	Histone H2A (Fragment)
26966	dirMS_041712_NAR_60mM_minus.8590.8590.3	3	3.11	1	1.25E+05		(R)QLQLAC	(R)Q L/Q L A Q/E A A Q K/R(L)		107.87	461.9241	1383.77	-0.0125	-9.1	8.75	533778	5.74	HUMAN	Q15149	Plectin
26967	dirMS_041712_NAR_120mM_plus.14798.14798.3	3	3.11	1	9.20E+05		(K)LDKSQIH	(K)L D K S Q I H D/I/V|L/V\G G S T R(I)		130.88	613.3369	1838.013	-0.0169	-9.2	6.75	45508.6	5.5	HUMAN	A8K7Q2	Heat shock cognate 71 kDa protein
26968	dirMS_041712_NAR_120mM_plus.4316.4316.3	3	3.11	0	6.78E+05	M76m M7	(R)LTNSmM	(R)L/T/N S m M m H G R(N)	m:Oxidized methionine	71.2	403.8446	1177.527	31.9918	1.6	9.75	23047.2	9.95	HUMAN	P46782	40S ribosomal protein S5
26969	dirMS_041712_NAR_120mM_plus.4510.4510.3	3	3.11	0	2.28E+04		(R)THSQGC	(R)T H S Q G G\Y/G/S Q/G\Y K(Y)		73.05	457.2092	1369.613	-0.0001	-0.1	8.2	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
26970	dirMS_041712_NAR_120mM_plus.9927.9927.3	3	3.11	1	2.45E+05		(-)MEMVGI	(-)M E M V/G F L P K T/R(R)		104.88	436.8969	1308.68	-0.0041	-3.2	8.5	151307	9.67	HUMAN	H3BMM1	Unconventional myosin-IXa
26971	dirMS_041712_NAR_20mM_plus.12658.12658.3	3	3.11	0	1.47E+04	S20s	(K)IFINNEW	(K)I F I N N/E W Q N s/E S G R(V)	s:N-acetylglucosamine (S)	160.13	632.9689	1693.793	203.0993	10.5	4.53	54217.9	6.52	HUMAN	H0YMG7	Retinal dehydrogenase 2
26972	dirMS_041712_NAR_20mM_plus.13177.13177.2	2	3.11	0	2.38E+05	M148m	(R)DLTDYLr	(R)D L|T/D Y L m K(I)	m:Oxidized methionine	164.13	507.7439	998.486	15.9942	-0.7	4.21	37482.1	5.36	HUMAN	E9PG30	Actin, gamma-enteric smooth muscle
26973	dirMS_041712_NAR_20mM_plus.17589.17589.2	2	3.11	0	3.20E+04		(K)LFVTND	(K)L F|V/T N D A/A\T I L R(E)		192.63	667.3752	1333.747	-0.0043	-3.2	5.84	58214.7	5.25	HUMAN	B4DEM7	T-complex protein 1 subunit theta
26974	dirMS_041712_NAR_20mM_plus.9903.9903.2	2	3.11	1	6.81E+04	S2195s	(R)VDENRs	(R)V D/E N\R s E F L/L H E G R(L)	s:Phosphorylated S	139.12	890.9015	1700.835	79.9607	-3.2	4.83	237639.1	6.17	HUMAN	G3XAA0	AT rich interactive domain 1B (SWI1-like), isoform CRA_a
26975	dirMS_041712_NAR_30mM_plus2.20421.20421.2	2	3.11	0	2.87E+05	M233m	(K)LVLPmIK	(K)L V|L P m/I K(E)	m:Oxidized methionine	161.53	415.2703	813.527	16.0067	14.2	8.75	110726	4.76	HUMAN	B4E0R6	Importin-5
26976	dirMS_041712_NAR_30mM_plus2.20509.20509.2	2	3.11	0	8.83E+04		(K)TENLLGS	(K)T E/N L|L/G/S Y/F P K(K)		161.33	634.8311	1268.652	0.0028	2.2	5.66	28772.3	6.28	HUMAN	A6NJG9	Proteasome activator complex subunit 1
26977	dirMS_041712_NAR_30mM_plus2.20568.20568.2	2	3.11	0	9.48E+04		(K)SVVTSIF	(K)S V|V|T S I/F G V K(N)		162.62	518.799	1036.604	-0.013	-12.5	8.47	132902.3	5.82	HUMAN	J3KR24	Isoleucine--tRNA ligase, cytoplasmic
26978	dirMS_041712_NAR_30mM_plus2.21171.21171.2	2	3.11	1	8.69E+04		(K)VFLKETE	(K)V F|L/K E T E/R(Q)		164.35	511.2941	1021.568	0.0133	13	6.11	244993.9	9.17	HUMAN	Q13459	Unconventional myosin-IXb
26979	dirMS_041712_NAR_30mM_plus2.21833.21833.2	2	3.11	0	3.14E+05		(R)DLLFQAI	(R)D L|L/F Q/A L/G R(T)		170.52	516.7959	1032.584	0.0009	0.8	5.84	66742	6.4	HUMAN	Q9NSD9	Phenylalanine--tRNA ligase beta subunit
26980	dirMS_041712_NAR_30mM_plus2.8257.8257.2	2	3.11	1	9.18E+05	Y488y	(R)YDDKySI	(R)Y D|D/K y S K(Y)	y:Phosphorylated Y	96.48	499.6972	918.42	79.9668	0.5	5.96	63184.5	9.73	HUMAN	J3KNK5	PiggyBac transposable element derived 5
26981	dirMS_041712_NAR_40mM_plus2.10139.10139.2	2	3.11	0	6.24E+04		(K)LGITQLR	(K)L/G I/T/Q L R(F)		124.1	400.7509	800.499	-0.0043	-5.4	9.75	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
26982	dirMS_041712_NAR_40mM_plus2.6492.6492.2	2	3.11	0	1.80E+03	M609m	(K)SLSAmD	(K)S L S/A m D/V E K(C)	m:Oxidized methionine	97.78	498.2392	979.476	15.9947	-0.3	4.37	136926.3	6.08	HUMAN	F8VY01	FYVE, RhoGEF and PH domain-containing protein 6
26983	dirMS_041712_NAR_50mM_plus2.5534.5534.3	3	3.11	2	7.63E+04	M90m	(K)mKTTSQ	(K)m K T\T\S Q R E G N S\G G K(I)	m:Oxidized methionine	90.35	499.5721	1480.717	15.9845	-7	9.99	15089.9	5.22	HUMAN	K7EIT6	Zinc finger protein 221 (Fragment)
26984	dirMS_041712_NAR_50mM_plus2.9738.9738.3	3	3.11	0	5.62E+05		(R)DNIQGIT	(R)D N\I Q/G I T K/P A I R(R)		117.37	442.5902	1325.754	0.0025	1.9	8.75	11367.1	11.36	HUMAN	P62805	Histone H4
26985	dirMS_041712_NAR_60mM_plus.13281.13281.3	3	3.11	1	2.21E+05		(K)LLCFDDE	(K)L L C F D D/E|G T P R T K(E)	C:Carbamidomethylation	126.12	517.9269	1551.747	0.019	12.2	4.56	17457.4	5.14	HUMAN	C9JNW7	Zinc finger protein 425 (Fragment)
26986	dirMS_041712_NAR_60mM_plus.19208.19208.3	3	3.11	0	3.60E+05		(R)ILSDEQL	(R)I\L/S D E Q\L\L S T E R(L)		159.17	468.5804	1403.738	-0.011	-7.8	4.14	56390.6	9.81	HUMAN	Q6ZSJ9	Protein shisa-6 homolog
26987	dirMS_041712_NAR_60mM_plus.5898.5898.3	3	3.11	1	6.14E+03		(K)KEAGEG	(K)K E A G/E\G G/E A E A\P A A E G G/K(D)		89.55	553.2578	1657.766	-0.0075	-4.5	4.32	31725.3	4.48	HUMAN	P29966	Myristoylated alanine-rich C-kinase substrate
26988	dirMS_041712_NAR_60mM_plus.8340.8340.3	3	3.11	0	4.53E+05	K42k	(R)LGAAVA	(R)L G A A V A P/E G N Q k/K(K)	k:Ubiquitin-K	101.7	466.2562	1282.711	114.0427	-0.2	8.59	21455.2	6.6	HUMAN	B4DFT4	ATP synthase subunit s-like protein
26989	dirMS_041712_NAR_120mM_minus.8536.8536.3	3	3.1	1	4.61E+05		(R)LKVTEG	(R)L K V T E G G E|P Y/R(L)		100.53	416.885	1248.658	-0.0178	-14.3	6.14	96827.3	5.58	HUMAN	E9PKU7	Neutral alpha-glucosidase AB
26990	dirMS_041712_NAR_20mM_minus.8501.8501.3	3	3.1	0	5.95E+04	M1m	(-)mGPLAG	(-)m G P L\A G L/G P G S T P R(T)	m:Oxidized methionine	134.22	442.895	1310.689	15.9819	-9.8	9.5	128366.8	4.92	HUMAN	F5H5C2	Nuclear pore complex protein Nup133
26991	dirMS_041712_NAR_30mM_minus2.15575.15575.2	2	3.1	0	3.35E+04	M1342m	(R)ASLSLW	(R)A S/L\S/L/W Q|A m E K(G)	m:Oxidized methionine	138.07	640.3185	1263.64	15.9895	-4.2	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
26992	dirMS_041712_NAR_30mM_minus2.15992.15992.2	2	3.1	1	2.18E+05		(R)DLSERAI	(R)D\L\S/E R A/L\P R(R)		140.42	528.7959	1056.58	0.0049	4.6	6.07	87190.9	6.22	HUMAN	Q86TB9	Protein PAT1 homolog 1
26993	dirMS_041712_NAR_50mM_minus2.11525.11525.3	3	3.1	2	2.25E+04	T825t	(K)AEQKGt	(K)A E/Q K G/t L K H G/G L R(E)	t:N-acetylglucosamine (T)	133.7	533.2928	1394.786	203.0776	-1.1	10	125496.3	8.82	HUMAN	E9PE87	Partitioning defective 3 homolog B
26994	dirMS_041712_NAR_50mM_minus2.13869.13869.3	3	3.1	2	3.05E+04		(R)KQCDV	(R)K Q C D/V V D T A F K N/G L K(D)	C:Carbamidomethylation	147.05	574.9724	1722.884	0.0183	10.6	8.5	31322.1	5.95	HUMAN	F5GZX2	Tektin-1
26995	dirMS_041712_NAR_50mM_minus2.14002.14002.3	3	3.1	0	1.88E+04		(R)LTEDLEY	(R)L/T/E D/L E Y/H E L L/D R(A)		147.45	549.2731	1645.807	-0.002	-1.2	4.17	19946.4	5.79	HUMAN	H0YCV6	Oxysterol-binding protein 1 (Fragment)
26996	dirMS_041712_NAR_50mM_minus2.14343.14343.3	3	3.1	1	8.33E+04		(R)LSQELEY	(R)L S/Q E L E Y/L/T E D/V K R(L)		149.87	574.9724	1722.891	0.0118	6.8	4.41	267687.4	4.97	HUMAN	P12270	Nucleoprotein TPR
26997	dirMS_041712_NAR_50mM_minus2.15610.15610.3	3	3.1	1	4.72E+05		(K)QGGLGF	(K)Q G/G L G P M N\I/P L V S D/P K R(T)		157.45	593.6566	1778.958	-0.0029	-1.6	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
26998	dirMS_041712_NAR_50mM_minus2.7156.7156.3	3	3.1	1	1.42E+04		(K)SELLMG	(K)S E/L L M G G C/S/W/I R G/K(I)	C:Carbamidomethylation	107.42	531.9316	1593.788	-0.0073	-4.6	8.46	19911.5	5.39	HUMAN	Q53HV7-2	Isoform 2 of Single-strand selective monofunctional uracil DNA glycosylase
26999	dirMS_041712_NAR_60mM_minus.15067.15067.2	2	3.1	0	3.90E+05		(R)EHALLA	(R)E/H\A/L/L A Y T\L G V K(Q)		144.58	657.873	1314.742	-0.0029	-2.2	6.85	50482.3	9.31	HUMAN	P68104	Elongation factor 1-alpha 1
27000	dirMS_041712_NAR_60mM_minus.18027.18027.3	3	3.1	0	1.11E+04	K560k M5	(K)VkAGDS	(K)V k|A/G D S L m V m I A M K(M)	k:Ubiquitin-K m:Oxidized me	160.05	547.2829	1493.789	146.0453	7.7	8.56	68787.2	6.34	HUMAN	E9PHF7	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial
27001	dirMS_041712_NAR_60mM_minus.18135.18135.3	3	3.1	0	1.82E+03		(K)THVADF	(K)T H V A D F\A/P E\V A W V/T R(S)		163.82	566.9562	1698.86	-0.0058	-3.4	5.29	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
27002	dirMS_041712_NAR_60mM_minus.8801.8801.3	3	3.1	1	1.72E+04		(K)AFTKCS	(K)A F T K/C S Y/L/T K(H)	C:Carbamidomethylation	109.98	406.8804	1218.619	0.0079	6.5	9.7	93743.8	9.6	HUMAN	Q96MR9	Zinc finger protein 560
27003	dirMS_041712_NAR_120mM_plus.24707.24707.3	3	3.1	1	1.57E+05	N26n	(R)SVPELK	(R)S V P E L K V G I/V G n L A S\G/K(S)	n:N-acetylglucosamine (N)	185.98	624.3546	1667.969	203.0802	0.4	8.31	13262.6	4.87	HUMAN	C9J8Z2	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 1 (Fragment)
27004	dirMS_041712_NAR_20mM_plus.10596.10596.2	2	3.1	0	4.49E+03		(K)AVGQG	(K)A V G Q G\C/V E/I G/S Q/R(Y)	C:Carbamidomethylation	145.67	680.8384	1360.664	0.0057	4.2	6.05	107013.3	8.48	HUMAN	P06400	Retinoblastoma-associated protein
27005	dirMS_041712_NAR_20mM_plus.13738.13738.2	2	3.1	1	3.01E+04		(K)DCNLSV	(K)D/C/N L S V K\N\A F\K(L)	C:Carbamidomethylation	166.77	648.3203	1295.641	-0.0079	-6.1	8.59	59774.9	6.46	HUMAN	E9PFR9	Spermatogenesis-associated protein 13
27006	dirMS_041712_NAR_20mM_plus.5976.5976.3	3	3.1	0	1.02E+06	M295m M	(R)mGQmA	(R)m G Q m A m G\G A/m/G I/N N R(G)	m:Oxidized methionine	100.27	534.8861	1538.67	63.9743	-3.4	9.5	43979.5	8.92	HUMAN	F5GYZ3	Non-POU domain-containing octamer-binding protein
27007	dirMS_041712_NAR_20mM_plus.8644.8644.2	2	3.1	0	1.02E+05		(K)EQVANS	(K)E Q|V/A N S/A F V E R(C)		130.5	625.3102	1249.617	-0.004	-3.2	4.53	17664	8.77	HUMAN	H0Y6E4	Heat shock protein HSP 90-beta (Fragment)
27008	dirMS_041712_NAR_30mM_plus2.8073.8073.2	2	3.1	0	1.28E+06		(K)QGGGG	(K)Q G G G/G G/G G S V/P G I E R(M)		97.12	642.8178	1284.629	-0.0008	-0.6	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
27009	dirMS_041712_NAR_40mM_plus2.11615.11615.2	2	3.1	0	1.47E+05		(R)FPGQLN	(R)F/P G Q/L N/A/D L R(K)		134.6	565.7995	1130.595	-0.0036	-3.1	5.84	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
27010	dirMS_041712_NAR_40mM_plus2.12625.12625.3	3	3.1	0	3.31E+05		(K)AASDIAI	(K)A A\S D I/A M T E L/P P T H P I R(L)		140.45	607.3167	1819.937	-0.0015	-0.9	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
27011	dirMS_041712_NAR_50mM_plus2.10165.10165.3	3	3.1	2	3.85E+04		(K)ESLRNCI	(K)E S/L R N C P G I K G/P K(E)	C:Carbamidomethylation	122.18	485.9273	1455.774	-0.0063	-4.3	10	52932	9.14	HUMAN	C9JJD1	Dimethylaniline monooxygenase [N-oxide-forming] 5
27012	dirMS_041712_NAR_50mM_plus2.13035.13035.3	3	3.1	0	1.96E+06		(R)LLIQALY	(R)L L I Q\A L Y D P/I N P D/R(E)		136.6	547.6436	1640.901	0.0156	9.5	4.21	47773.7	9.98	HUMAN	B4DMT0	Transmembrane protein 143
27013	dirMS_041712_NAR_50mM_plus2.13107.13107.3	3	3.1	0	5.16E+05		(K)QVLNQI	(K)Q V/L N|Q D\L/T F Q/H I K(I)		137.17	528.6227	1583.854	-0.0005	-0.3	6.74	26601.2	7.98	HUMAN	Q5VWZ2	Lysophospholipase-like protein 1
27014	dirMS_041712_NAR_50mM_plus2.18024.18024.3	3	3.1	1	4.74E+05		(R)EFTRLEI	(R)E F T R L E\I|C/N\L T P D A L K(S)	C:Carbamidomethylation	161.88	640.6666	1919.989	-0.0043	-2.2	4.68	82516.1	5.49	HUMAN	P07384	Calpain-1 catalytic subunit
27015	dirMS_041712_NAR_50mM_plus2.6064.6064.3	3	3.1	1	7.03E+04		(R)IQEAGTI	(R)I/Q\E\A\G T E V V K A K(A)		96.12	424.9102	1272.716	0.0003	0.2	6.14	31330.8	9.26	HUMAN	E9PDB2	Malate dehydrogenase, mitochondrial
27016	dirMS_041712_NAR_60mM_plus.20108.20108.3	3	3.1	1	1.24E+05		(K)LDPRYT	(K)L D P R Y T A D L/L E V L(-)		165.08	506.6178	1517.821	0.0179	11.8	4.03	7008	5.34	HUMAN	C9J2I5	Organic solute transporter subunit alpha (Fragment)
27017	dirMS_041712_NAR_60mM_plus.6411.6411.3	3	3.1	0	2.57E+05		(R)QAGEVT	(R)Q A G E V T/Y/A/D/A H K(G)		92.2	430.5486	1289.612	0.0192	14.9	5.32	56791.5	11.56	HUMAN	Q08170	Serine/arginine-rich splicing factor 4
27018	dirMS_041712_NAR_120mM_minus.12440.12440.3	3	3.09	1	2.95E+05	Y925y	(K)LFNKAL	(K)L F/N K A/L A T y S K(D)	y:Phosphorylated Y	121.87	445.9006	1255.705	79.9827	12.3	9.7	135048.7	6.35	HUMAN	Q05GC8	Breast cancer anti-estrogen resistance 2
27019	dirMS_041712_NAR_120mM_minus.16069.16069.4	4	3.09	1	7.65E+03	S55s	(K)DTKIsIP	(K)D T K I s I P A|F\S V T L I K(K)	s:Phosphorylated S	141.92	428.9878	1632.957	79.9723	3.5	8.59	36382.8	7.18	HUMAN	B7Z4W8	GRAM domain-containing protein 3
27020	dirMS_041712_NAR_120mM_minus.18031.18031.4	4	3.09	2	3.15E+05		(R)RYEIAVN	(R)R Y E I A V/N L/D L/T E\R Q V K(V)		154.12	487.5223	1947.066	0.0016	0.8	6.18	33878.6	8.14	HUMAN	P50222	Homeobox protein MOX-2
27021	dirMS_041712_NAR_120mM_minus.7036.7036.3	3	3.09	1	5.77E+05		(K)DSYVGD	(K)D S/Y/V/G D E A Q S K/R(G)		92.07	452.2134	1354.623	0.0023	1.7	4.56	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
27022	dirMS_041712_NAR_20mM_minus.11245.11245.2	2	3.09	1	4.09E+05		(K)IMVCEK	(K)I M/V/C/E K/D P A L K(N)	C:Carbamidomethylation	159.8	652.3395	1303.675	-0.0031	-2.4	6.07	41145.9	6.26	HUMAN	P26992	Ciliary neurotrophic factor receptor subunit alpha
27023	dirMS_041712_NAR_20mM_minus.8426.8426.2	2	3.09	0	1.07E+05		(R)GYSFTT	(R)G Y/S\F/T T T A E R(E)		133.37	566.771	1132.527	0.0078	6.9	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
27024	dirMS_041712_NAR_40mM_minus2.6411.6411.3	3	3.09	2	7.03E+04	M409m K4	(K)KENSET	(K)K E N S E T T/L T R S A S/m k(L)	m:Oxidized methionine k:Ub	104.45	604.9568	1682.838	130.0181	-10.9	8.59	58791	9.93	HUMAN	E9PDI4	Ladinin-1
27025	dirMS_041712_NAR_50mM_minus2.11135.11135.3	3	3.09	1	5.51E+05		(K)QQEAAL	(K)Q Q E/A A L/E/L E/E L K K(K)		131.12	510.2775	1528.822	-0.0038	-2.5	4.49	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
27026	dirMS_041712_NAR_50mM_minus2.12023.12023.3	3	3.09	1	1.78E+05		(K)APSSLSD	(K)A P S/S L/S D/A V P Q R A D H R(V)		137.22	569.6251	1706.857	0.0039	2.3	6.79	96409.7	8.92	HUMAN	E7ETX7	SURP and G-patch domain-containing protein 2
27027	dirMS_041712_NAR_50mM_minus2.12806.12806.3	3	3.09	1	1.12E+04		(K)NAAQFL	(K)N A|A Q F/L/L S T N D K T I/K(L)		140.88	555.3037	1663.901	-0.0048	-2.9	8.59	52204.6	5.82	HUMAN	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform

27028	dirMS_041712_NAR_50mM_minus2.16359.16359.3	3	3.09	1	1.25E+05	S713s	(K)VLPPCIIS	(K)V/L\P/P C I I S G G N T/A K s K(E)	C:Carbamidomethylation s:N-ace	160.55	615.6611	1641.899	203.0695	-5.4	10	141996.1	8.78	HUMAN	F8W6J4	AF4/FMR2 family member 2
27029	dirMS_041712_NAR_50mM_minus2.7449.7449.3	3	3.09	2	1.77E+04	S278s	(K)ILWKERI	(K)I/L\W K E\R D L/s F K(S)	s:Phosphorylated S	107.72	505.6001	1434.81	79.9754	6	8.59	49641.1	5.95	HUMAN	C9JV39	Coiled-coil domain-containing protein 102B
27030	dirMS_041712_NAR_50mM_minus2.8106.8106.3	3	3.09	1	9.52E+04		(K)TAVCDIF	(K)T/A V/C D I/P P R G L K(M)	C:Carbamidomethylation	112.42	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
27031	dirMS_041712_NAR_60mM_minus.11390.11390.3	3	3.09	2	1.19E+05		(K)YAPAEQ	(K)Y A/P A/E Q F R G S K R(F)		123.3	470.5828	1409.728	0.0054	3.8	9.99	65440.2	9.24	HUMAN	F5GX30	Polyhomeotic-like protein 1
27032	dirMS_041712_NAR_60mM_minus.16537.16537.3	3	3.09	1	9.23E+04		(R)KQSLGE	(R)K Q\S L G E\L\I/G T L N A A K(V)		152.13	514.9657	1542.885	-0.0024	-1.6	8.59	31075.7	5.65	HUMAN	P60174	Triosephosphate isomerase
27033	dirMS_041712_NAR_60mM_minus.16873.16873.3	3	3.09	0	1.02E+05		(K)ICDQWD	(K)I C\D Q W D A\L/G/S L/T H S R(R)	C:Carbamidomethylation	153.88	586.9446	1758.823	-0.0035	-2	5.21	80254.2	5.05	HUMAN	D6PXK4	Alpha actinin 4 short isoform
27034	dirMS_041712_NAR_60mM_minus.17668.17668.3	3	3.09	0	3.84E+05	M3139m	(K)DELVmE	(K)D E/L V m/E\I L/S D L L K(R)	m:Oxidized methionine	159.22	511.9372	1517.813	15.9839	-7.2	3.91	404166.4	6.52	HUMAN	Q0VDD8	Dynein heavy chain 14, axonemal
27035	dirMS_041712_NAR_60mM_minus.18397.18397.3	3	3.09	0	1.06E+05		(R)ILVTLLH	(R)I L|V/T L L/H T L E R(M)		163.88	436.6046	1307.805	-0.0053	-4.1	6.75	45212.4	9.41	HUMAN	B7Z233	Acetyl-CoA acetyltransferase, cytosolic
27036	dirMS_041712_NAR_60mM_minus.8402.8402.3	3	3.09	1	2.30E+04		(R)VASSTLL	(R)V A/S/S T L L D D R R(N)		106.95	411.5582	1232.659	0.0007	0.6	5.93	108806.2	4.84	HUMAN	O60763	General vesicular transport factor p115
27037	dirMS_041712_NAR_60mM_minus.9131.9131.3	3	3.09	0	3.16E+05		(K)GPQGPF	(K)G P\Q G P/P G P G G E A G/N Q G\R(L)		110.53	511.5711	1532.72	-0.0213	-13.9	6	248823.5	6.45	HUMAN	A6NMZ7	Collagen alpha-6(VI) chain
27038	dirMS_041712_NAR_120mM_plus.11899.11899.3	3	3.09	1	1.23E+05	K128k	(R)ISEVTDV	(R)I S\E V T D/V/K/N k(L)	k:Ubiquitin-K	116.33	416.2263	1132.621	114.0435	0.5	6.07	22074.7	6.12	HUMAN	I3L1F7	Tektin-5 (Fragment)
27039	dirMS_041712_NAR_120mM_plus.5602.5602.3	3	3.09	1	1.25E+05		(R)SGGGYG	(R)S G/G G Y/G G D R S S G G G Y S G D R(S)		82.28	583.5787	1748.722	-0.0003	-0.2	5.68	21563.9	10.01	HUMAN	K7EKB2	TATA-binding protein-associated factor 2N (Fragment)
27040	dirMS_041712_NAR_120mM_plus.5976.5976.2	2	3.09	1	1.33E+05	S229s S231	(K)SSsAsKK	(K)S S/s A s K K/D\R(K)	s:Phosphorylated S	84.98	563.2166	965.501	159.9249	-6.9	9.99	197316.7	9.58	HUMAN	Q5T200	Zinc finger CCCH domain-containing protein 13
27041	dirMS_041712_NAR_120mM_plus.7658.7658.3	3	3.09	1	2.76E+05		(R)EVQQGE	(R)E V/Q/Q/G E E F E R R(I)		92.77	469.5586	1406.666	-0.0046	-3.3	4.49	15567.5	8.13	HUMAN	H0Y4J6	Adenylate kinase isoenzyme 1 (Fragment)
27042	dirMS_041712_NAR_120mM_plus.7818.7818.3	3	3.09	0	3.52E+05		(K)LQEQEG	(K)L/Q E\Q E G S L A A E\G R(H)		94.83	463.2276	1387.681	-0.013	-9.3	4.25	55284	7.24	HUMAN	G3V2W1	Protein Z-dependent protease inhibitor
27043	dirMS_041712_NAR_120mM_plus.9317.9317.3	3	3.09	0	4.33E+04	N109n	(R)AFALnCS	(R)A F A L n/C S W R(G)	C:Carbamidomethylation n:N-ace	102.23	443.2145	1124.531	203.0984	14.3	9.79	24958.9	11.08	HUMAN	F2Z333	Fibronectin type-III domain-containing transmembrane protein C1orf233
27044	dirMS_041712_NAR_20mM_plus.10913.10996.2	2	3.09	0	1.28E+05		(K)LAEYVIT	(K)L A E\Y V\I T K(S)		148.33	468.7674	936.54	-0.0125	-13.4	6	236508.3	9.06	HUMAN	E7EUA9	Neuron navigator 3
27045	dirMS_041712_NAR_20mM_plus.11630.11630.2	2	3.09	0	9.66E+04	T660t S666	(R)APLPtSP	(R)A P L/P t S/P Q P P/s P R(Q)	t:Phosphorylated T s:Phosph	153.47	752.8363	1344.727	159.9383	3.7	9.79	73666	6.97	HUMAN	E7EWG4	Ubiquitin-associated protein 2
27046	dirMS_041712_NAR_20mM_plus.13241.13241.3	3	3.09	1	6.83E+04	M224m	(K)IVLFmKV	(K)I V L|F\m K W S D N K(D)	m:Oxidized methionine	163.75	466.244	1380.734	15.983	-8.5	8.59	83030.7	5.78	HUMAN	B7ZMI3	ITPR1 protein
27047	dirMS_041712_NAR_20mM_plus.14595.14595.3	3	3.09	0	1.43E+05		(R)LQEAGIL	(R)L Q E A G\I/L S/A/E E\L Q R(L)		172.05	519.6131	1556.828	-0.0031	-2	4.25	533778	5.74	HUMAN	Q15149	Plectin
27048	dirMS_041712_NAR_20mM_plus.17663.17663.2	2	3.09	1	9.22E+04	K192k	(K)GELERAI	(K)G E L E R A L|S A V I A T E|k(K)	k:Ubiquitin-K	193.5	850.9546	1586.875	114.0271	-9.3	4.79	72215.4	5.98	HUMAN	H3BV12	Uncharacterized protein
27049	dirMS_041712_NAR_40mM_plus2.15892.15892.3	3	3.09	1	7.42E+04		(K)VLDSGA	(K)V L|D S G A/P I K/I/P V G P E T L G R(I)		160.05	640.3668	1919.096	-0.0102	-5.3	6.04	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
27050	dirMS_041712_NAR_40mM_plus2.6517.6517.2	2	3.09	0	1.54E+05		(K)AGFAGD	(K)A G F/A/G D/D\A/P R(A)		98.67	488.728	976.448	0.0004	0.4	4.21	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
27051	dirMS_041712_NAR_50mM_plus2.10290.10290.3	3	3.09	1	9.15E+03	S1388s	(R)sKEEVGI	(R)s K E E V G I N T\E T/S S A E R(K)	s:N-acetylglucosamine (S)	120.92	647.303	1736.83	203.0647	-7.5	4.49	164512	5.96	HUMAN	Q14191	Werner syndrome ATP-dependent helicase
27052	dirMS_041712_NAR_50mM_plus2.19933.19933.3	3	3.09	1	9.89E+05		(K)LKEAELL	(K)L K E A E L L|E|P L/M/P A I R(A)		172.6	574.9989	1722.982	-0.0001	-0.1	4.79	56164.6	6.01	HUMAN	E9PP73	Coatomer subunit beta (Fragment)
27053	dirMS_041712_NAR_50mM_plus2.21483.21483.3	3	3.09	1	1.48E+05		(K)AKNEILD	(K)A K N E I L\D\E\V I/S/L S Q V T/P K(H)		183.82	662.036	1984.096	-0.0027	-1.3	4.68	118312	7.77	HUMAN	E5KLJ5	Dynamin-like 120 kDa protein, mitochondrial
27054	dirMS_041712_NAR_50mM_plus2.7693.7693.3	3	3.09	1	9.32E+04	S348s	(K)VAAIsES	(K)V A A I s E S P V A\E K S A/S/T(-)	s:N-acetylglucosamine (S)	106.45	583.9631	1546.796	203.0789	-0.3	4.53	40852.6	9.93	HUMAN	P43088	Prostaglandin F2-alpha receptor
27055	dirMS_041712_NAR_60mM_plus.10171.10171.3	3	3.09	1	8.55E+05	S155s	(K)LAREsSL	(K)L/A R E s S L M A/R(E)	s:N-acetylglucosamine (S)	112.08	446.2368	1133.61	203.0863	5.2	9.6	168293.9	6.29	HUMAN	A2A2E9	OTTHUMP00000030968
27056	dirMS_041712_NAR_60mM_plus.15271.15271.3	3	3.09	1	8.29E+04		(R)KEFSPFG	(R)K E F S\P\F/G T I/T S A K(V)		137.1	471.585	1412.742	-0.0016	-1.1	8.59	65918.2	9.74	HUMAN	E7EQV3	Polyadenylate-binding protein 1
27057	dirMS_041712_NAR_60mM_plus.16085.16085.3	3	3.09	0	3.62E+05		(K)MTHLPE	(K)M T H L P E\L\D\T/L/S S E R(A)		141.95	543.6023	1628.795	-0.0025	-1.5	4.65	141616.6	6.1	HUMAN	B7ZKM8	Protein transport protein Sec24B
27058	dirMS_041712_NAR_60mM_plus.16683.16683.3	3	3.09	1	2.29E+04		(R)YRSDGA	(R)Y R S D G A L\L|L/G A S S L S/G R(C)		143.73	574.9718	1722.913	-0.0125	-7.2	8.75	30278.5	5.29	HUMAN	B4DP38	Methylosome protein 50
27059	dirMS_041712_NAR_60mM_plus.5824.5824.3	3	3.09	1	1.32E+05	S249s	(R)AYDIAGs	(R)A Y/D I/A G s T K D V K(V)	s:Phosphorylated S	88.53	449.8794	1267.653	79.9708	3.3	6.01	175123.7	8.97	HUMAN	P11388	DNA topoisomerase 2-alpha
27060	dirMS_041712_NAR_60mM_plus.6990.6990.3	3	3.09	2	3.83E+05		(-)MKEAGV	(-)M K E/A/G V D H R Q W/R(G)		94.97	504.9258	1512.749	0.014	9.3	8.52	37293.3	4.52	HUMAN	B4DI46	Testican-3
27061	dirMS_041712_NAR_120mM_minus.10033.10033.3	3	3.08	0	1.02E+06	N527n	(K)ATHEGL	(K)A T H\E G L\n A H/L/K(Q)	n:N-acetylglucosamine (N)	109.28	465.2334	1190.628	203.058	-15.3	6.96	191330.6	8.28	HUMAN	Q4KWH8	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-1
27062	dirMS_041712_NAR_120mM_minus.11326.11326.3	3	3.08	0	1.40E+05		(K)LEHEYIQ	(K)L E H\E Y\I/Q N F K(I)		116.33	440.8914	1320.658	0.0014	1	5.4	30169.7	5.02	HUMAN	Q15691	Microtubule-associated protein RP/EB family member 1
27063	dirMS_041712_NAR_120mM_minus.6801.6801.2	2	3.08	0	2.42E+05		(K)VSDSPSH	(K)V S D S P/S H/I A T K(T)		91.35	571.2929	1141.585	-0.0063	-5.5	6.71	226980	6.78	HUMAN	Q9P2D3	HEAT repeat-containing protein 5B
27064	dirMS_041712_NAR_20mM_minus.11078.11078.2	2	3.08	0	1.45E+05		(K)IDIIPNP(	(K)I D I\I/P N|P Q E R(T)		157.8	597.8271	1194.648	-0.0008	-0.7	4.37	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
27065	dirMS_041712_NAR_20mM_minus.11718.11718.3	3	3.08	0	2.51E+05		(R)GALQNI	(R)G A L Q N\I\I/P A S T G A A K(A)		165.27	471.2674	1411.79	-0.0027	-1.9	8.75	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
27066	dirMS_041712_NAR_30mM_minus2.10167.10188.2	2	3.08	0	4.19E+05		(R)YAVHTN	(R)Y A|V H|T/N Q C/R(R)	C:Carbamidomethylation	109.7	574.7655	1148.527	-0.0028	-2.5	8.75	14730.3	10.27	HUMAN	E7EP86	Uncharacterized protein
27067	dirMS_041712_NAR_30mM_minus2.10363.10363.2	2	3.08	0	4.22E+05		(R)VGQAVA	(R)V/G Q A/V A L/R(A)		110.38	407.2465	813.494	-0.0084	-10.3	9.72	20631.5	6.98	HUMAN	D6RAX2	C-terminal-binding protein 1 (Fragment)
27068	dirMS_041712_NAR_30mM_minus2.12469.12469.2	2	3.08	0	1.20E+05	M158m	(R)DmALLL	(R)D m A L L/L N A/E|N K(T)	m:Oxidized methionine	121.58	624.3176	1231.635	15.9928	-1.7	4.37	42336	9.92	HUMAN	Q9NTX9	Protein FAM217B
27069	dirMS_041712_NAR_30mM_minus2.19677.19677.2	2	3.08	0	3.74E+05		(R)ASLSLW	(R)A S L/S L|W Q/A M E\K(G)		163.02	632.3234	1263.64	-0.0007	-0.5	6.05	266161	5.68	HUMAN	E9PPU0	Epiplakin
27070	dirMS_041712_NAR_30mM_minus2.9111.9111.2	2	3.08	0	6.32E+05		(K)LAQLEEA	(K)L A|Q\L/E E A K(Q)		103.47	451.2537	901.499	0.0012	1.3	4.53	28965.2	9.43	HUMAN	P24539	ATP synthase subunit b, mitochondrial
27071	dirMS_041712_NAR_40mM_minus2.7212.7212.2	2	3.08	0	2.47E+05		(R)VAGIIDV	(R)V/A|G I I\D V R(H)		116.75	421.7585	842.509	0.0003	0.4	5.81	20841.7	10.49	HUMAN	E7EQU4	Uncharacterized protein
27072	dirMS_041712_NAR_50mM_minus2.16111.16111.3	3	3.08	0	1.46E+05		(K)VVDELN	(K)V V|D E L N L L/H T E/L A K(Q)		160.4	531.9638	1593.885	-0.0078	-4.9	4.65	16381.6	5.83	HUMAN	F8VWV2	DCC-interacting protein 13-beta (Fragment)
27073	dirMS_041712_NAR_50mM_minus2.18400.18400.3	3	3.08	1	1.31E+04		(R)VISGVLC	(R)V I|S\G V L Q L/G N I V F K K(E)		176.05	539.0018	1614.994	-0.0033	-2	10	227783.5	5.5	HUMAN	P35579	Myosin-9
27074	dirMS_041712_NAR_60mM_minus.17823.17823.3	3	3.08	1	5.94E+05		(R)KVESLQI	(R)K V E\S L Q/E/E/I/A F L K(K)		159.97	511.9529	1533.852	-0.0081	-5.3	4.79	49709.6	5.19	HUMAN	B0YJC4	Vimentin
27075	dirMS_041712_NAR_60mM_minus.18711.18711.3	3	3.08	0	9.08E+04	K249k	(R)VYIPCIY	(R)V/Y/I P C I Y/V L N k(I)	C:Carbamidomethylation k:Ubiqu	165.42	499.2763	1381.755	114.0595	11.1	8.47	40826.7	9.22	HUMAN	Q9Y295	Developmentally-regulated GTP-binding protein 1
27076	dirMS_041712_NAR_60mM_minus.19199.19199.3	3	3.08	0	1.83E+03		(K)LSGLHG	(K)L/S/G L H G Q D L F/G I W S K(V)		170.5	553.301	1657.87	0.0188	11.3	6.74	44907.6	5.84	HUMAN	P15309	Prostatic acid phosphatase
27077	dirMS_041712_NAR_120mM_plus.11705.11705.4	4	3.08	0	8.01E+05	M388m	(R)AEISEFA	(R)A E I S E F A\P P N T P V/V m V K(A)	m:Oxidized methionine	113.8	461.9971	1828.951	16.0152	11	4.53	54090.7	6.89	HUMAN	D6RCE4	Protocadherin Fat 1 (Fragment)
27078	dirMS_041712_NAR_120mM_plus.23732.23732.3	3	3.08	1	2.72E+05	K364k	(R)kLLLSAT	(R)k L/L L S A/T S G/E K G V R(I)	k:Ubiquitin-K	179.2	524.9713	1458.864	114.0355	-4.7	9.99	70206.9	8.81	HUMAN	E9PDD9	RNA-binding protein 28
27079	dirMS_041712_NAR_20mM_plus.15965.15965.2	2	3.08	0	1.31E+05		(K)SILFVPT	(K)S I L/F V|P T S A P R(G)		181.23	594.3403	1187.678	-0.005	-4.2	9.47	92752.5	4.76	HUMAN	P14625	Endoplasmin
27080	dirMS_041712_NAR_20mM_plus.16910.16910.3	3	3.08	0	1.00E+05		(R)AAFTAFI	(R)A A F T A F E E/A/Q\L P R(L)		187.72	484.2492	1450.733	0.0005	0.4	4.53	25834.8	9.54	HUMAN	Q96CT7	Coiled-coil domain-containing protein 124
27081	dirMS_041712_NAR_20mM_plus.8750.8750.2	2	3.08	0	2.94E+04		(R)LNQDQL	(R)L/N/Q D Q/L\D/A V S K(Y)		130.13	615.823	1230.632	0.0063	5.1	4.21	20235.4	6.77	HUMAN	E9PLA9	Caprin-1 (Fragment)
27082	dirMS_041712_NAR_30mM_plus2.23649.23649.2	2	3.08	0	2.77E+04		(R)IAIYELLF	(R)I A|I/Y E L L F/K(E)		192.48	555.3331	1109.661	-0.0016	-1.4	6	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
27083	dirMS_041712_NAR_30mM_plus2.7109.7109.2	2	3.08	0	2.18E+05		(K)AAFQSQ	(K)A/A|F Q/S Q Y/K(S)		91.63	471.7412	942.468	0.0072	7.6	8.63	103258.6	6.54	HUMAN	Q86XP3	ATP-dependent RNA helicase DDX42
27084	dirMS_041712_NAR_30mM_plus2.9103.9103.2	2	3.08	0	1.79E+05		(K)DVPITHI	(K)D V|P I T H R(R)		100.8	419.2286	837.458	-0.0078	-9.3	6.74	35887.1	6.64	HUMAN	B4DMG2	Transmembrane protein 131
27085	dirMS_041712_NAR_40mM_plus2.18629.18629.3	3	3.08	0	6.98E+04		(R)QGTPLIA	(R)Q G\T P L I/A F S L L/P/H E Q K(R)		175.37	593.6623	1778.98	-0.0076	-4.3	6.75	6068.8	5.09	HUMAN	I3L4E8	Pre-rRNA-processing protein TSR1 homolog (Fragment)
27086	dirMS_041712_NAR_40mM_plus2.7086.7086.2	2	3.08	0	3.89E+04		(K)VTLTSEE	(K)V T|L/T\S E\E/E A R(L)		101.7	567.78	1134.564	-0.011	-9.7	4.25	33940.9	9.27	HUMAN	F5H308	L-lactate dehydrogenase
27087	dirMS_041712_NAR_50mM_plus2.11492.11492.3	3	3.08	0	3.46E+05		(R)MLTGPV	(R)M L/T/G/P/V Y/S Q S T A L T H K(Q)		127.68	578.6334	1733.889	-0.0034	-2	8.37	138084.9	5.52	HUMAN	Q86VP6	Cullin-associated NEDD8-dissociated protein 1
27088	dirMS_041712_NAR_50mM_plus2.13505.13505.3	3	3.08	1	1.88E+06		(R)MAALEE	(R)M A A L E/E K L/A/A T R P/A R(V)		140	543.3085	1627.895	0.0161	9.9	8.5	9699.8	9.29	HUMAN	F8VWG6	Liprin-alpha-2
27089	dirMS_041712_NAR_50mM_plus2.19117.19117.3	3	3.08	0	9.44E+04		(R)EAIDSPV	(R)E A\I/D S P/V S F/L A L H N Q I R(N)		169.3	637.3362	1910.013	-0.019	-9.9	5.32	125655.3	6.18	HUMAN	Q92900	Regulator of nonsense transcripts 1
27090	dirMS_041712_NAR_50mM_plus2.19998.19998.2	2	3.08	1	3.80E+05		(R)KAIIIFVP	(R)K A I I I/F/V/P V\P Q L K(S)		173.13	733.4779	1465.95	-0.002	-1.3	10	21311.5	10.28	HUMAN	B5MCP9	40S ribosomal protein S7
27091	dirMS_041712_NAR_50mM_plus2.21055.21055.3	3	3.08	2	3.71E+04	S551s	(R)KEAEsSF	(R)K E A E s S P/F/V/E R L L K(K)	s:N-acetylglucosamine (S)	178.88	612.6632	1632.896	203.0795	0.1	6.23	92752.5	4.76	HUMAN	P14625	Endoplasmin
27092	dirMS_041712_NAR_50mM_plus2.8070.8070.3	3	3.08	0	9.70E+03		(K)STAGDT	(K)S T|A/G D T/H L G G E D F D N R(M)		108.98	564.5793	1691.726	-0.0022	-1.3	4.22	69032.8	5.37	HUMAN	E9PKE3	Heat shock cognate 71 kDa protein
27093	dirMS_041712_NAR_60mM_plus.17482.17482.3	3	3.08	1	2.78E+04	N44n	(K)AIQKGnI	(K)A I Q K G n M E/V A/R(I)	n:N-acetylglucosamine (N)	148.57	473.9176	1216.647	203.0916	8.6	8.79	22166.1	7.91	HUMAN	Q7LBR1	Charged multivesicular body protein 1b
27094	dirMS_041712_NAR_60mM_plus.18524.18524.3	3	3.08	1	2.05E+05		(K)KGVLFG	(K)K G V L F G V P G\A\F T/P/G C S\K(V)	C:Carbamidomethylation	154.43	574.6347	1721.904	-0.0148	-8.6	10	17625	9.57	HUMAN	A6NG06	Peroxiredoxin-5, mitochondrial
27095	dirMS_041712_NAR_60mM_plus.18827.18827.2	2	3.08	1	1.53E+05		(R)VSFELFA	(R)V S F E L/F A D/K V\P K(T)		155.82	690.3813	1379.757	-0.0016	-1.2	6.04	13378.8	6.27	HUMAN	C9J5S7	Peptidyl-prolyl cis-trans isomerase
27096	dirMS_041712_NAR_60mM_plus.7193.7193.3	3	3.08	0	1.96E+05		(R)LENQEG	(R)L/E/N Q E G I D/F I K(A)		95.67	435.8976	1305.669	0.0097	7.5	4.14	46872	4.99	HUMAN	Q8IX90	Spindle and kinetochore-associated protein 3
27097	dirMS_041712_NAR_120mM_minus.12480.12480.2	2	3.07	1	4.55E+05		(K)SDCKEFS	(K)S D C K/E F S/S/E A/R(V)	C:Carbamidomethylation	121.6	658.2849	1315.558	0.0042	3.2	4.68	74494.3	7.79	HUMAN	F5H897	Heat shock protein 75 kDa, mitochondrial
27098	dirMS_041712_NAR_120mM_minus.7918.7918.3	3	3.07	0	3.83E+05		(K)QTPAPA	(K)Q T P A P A A S V T G/S R(R)		97.43	414.8854	1242.644	-0.002	-1.6	9.75	360912.4	9.65	HUMAN	P46013	Antigen KI-67
27099	dirMS_041712_NAR_120mM_minus.9716.9716.2	2	3.07	0	3.66E+05	K1282k	(R)SASLETk	(R)S\A S/L/E T k/K(D)	k:Ubiquitin-K	107.83	489.2735	863.483	114.0565	13.8	8.31	197797.8	6.21	HUMAN	G3V1L9	Tight junction protein 1 (Zona occludens 1), isoform CRA_a
27100	dirMS_041712_NAR_20mM_minus.11488.11488.2	2	3.07	0	1.40E+05	M98m	(R)TLTIVDT	(R)T L|T\I/V/D T G I G m T/K(A)	m:Oxidized methionine	163.17	683.3669	1349.735	15.992	-2.1	5.5	20151.2	4.58	HUMAN	G3V2J8	Heat shock protein HSP 90-alpha (Fragment)
27101	dirMS_041712_NAR_20mM_minus.8005.8005.2	2	3.07	0	8.63E+04		(R)DQVTYC	(R)D Q/V/T Y/Q Q L R(E)		129.78	575.7953	1150.585	-0.0018	-1.6	5.83	266161	5.68	HUMAN	E9PPU0	Epiplakin
27102	dirMS_041712_NAR_30mM_minus2.16436.16436.2	2	3.07	0	1.34E+05		(K)STFVNIL	(K)S T|F V/N I L K(Q)		142.92	461.2712	921.54	-0.0053	-5.7	8.47	23232.7	5.07	HUMAN	D6RCP9	Deoxycytidine kinase
27103	dirMS_041712_NAR_30mM_minus2.16598.16598.2	2	3.07	1	2.57E+05	M1m T3t	(-)mStLPSK	(-)m S\t/L P S K/W/K(R)	m:Oxidized methionine t:Pho	144.07	587.2756	1077.576	95.9678	5.6	10	35205.8	5.36	HUMAN	B4DLQ9	Transcription factor Dp-1
27104	dirMS_041712_NAR_30mM_minus2.18617.18617.2	2	3.07	0	1.80E+04		(K)FIIPNVV	(K)F I|I/P N/V V K(Y)		155.68	465.2877	929.582	-0.0137	-14.8	8.75	17529.3	9.3	HUMAN	F5GXY2	L-lactate dehydrogenase A chain (Fragment)
27105	dirMS_041712_NAR_30mM_minus2.8552.8552.2	2	3.07	1	1.01E+05		(K)AGVKQF	(K)A G V\K Q\P E R(S)		100.98	442.7519	884.495	0.0017	1.9	8.79	93412.8	6.3	HUMAN	B3KP41	PHD finger protein 3 (Fragment)
27106	dirMS_041712_NAR_30mM_minus2.9675.9675.2	2	3.07	0	1.20E+05		(K)LAFGCQ	(K)L A|F G/C Q/R(S)	C:Carbamidomethylation	107.05	426.2191	851.419	0.0117	13.7	9.75	18347.7	6.44	HUMAN	F8VUG8	Prickle-like protein 1 (Fragment)
27107	dirMS_041712_NAR_40mM_minus2.11582.11582.3	3	3.07	1	1.28E+05	S44s	(K)GsFVGN	(K)G/s/F V G N\I S K D L G L E/P R(E)	s:N-acetylglucosamine (S)	151.02	631.3335	1688.897	203.0893	5.3	6.07	101940.5	4.81	HUMAN	Q9Y5H2	Protocadherin gamma-A11
27108	dirMS_041712_NAR_50mM_minus2.16442.16442.3	3	3.07	0	2.19E+05		(K)FLNDTTI	(K)F/L/N D T T K P V G L L\L S E\R(F)		162.18	601.6676	1803.001	-0.0128	-7.1	6.07	30082.2	4.7	HUMAN	B4E318	BRCA2 and CDKN1A-interacting protein
27109	dirMS_041712_NAR_50mM_minus2.6166.6166.3	3	3.07	1	1.83E+04	T152t	(R)TAEQTE	(R)T A/E Q/T E R R L P t/Q A E R(R)	t:Phosphorylated T	97.82	622.6372	1785.92	79.9768	5.6	5.9	60147.2	5.51	HUMAN	E9PFE5	Uncharacterized protein C3orf30
27110	dirMS_041712_NAR_50mM_minus2.7694.7694.3	3	3.07	1	3.75E+04		(K)NSDEAD	(K)N\S|D/E A D L/V P A K E A N V K(C)		110.73	567.289	1699.85	0.0027	1.6	4.32	19439.5	4.97	HUMAN	B5MD17	Chromobox protein homolog 1 (Fragment)
27111	dirMS_041712_NAR_50mM_minus2.8009.8009.3	3	3.07	2	5.62E+04	K454k	(R)SREEELT	(R)S R/E E/E L T R A/A L Q/Q\k(S)	k:Ubiquitin-K	112.35	591.6389	1658.882	114.0201	-12.9	5.95	115095.7	9.44	HUMAN	Q5TCX8	Mitogen-activated protein kinase kinase kinase MLK4
27112	dirMS_041712_NAR_60mM_minus.14181.14181.3	3	3.07	1	1.02E+05		(K)GPNVFC	(K)G P N V/F Q\G Y L K D/P A/K(T)		138.67	511.9372	1533.806	-0.009	-5.8	8.5	59384	7.79	HUMAN	B7Z3Z9	Long-chain-fatty-acid--CoA ligase 1
27113	dirMS_041712_NAR_60mM_minus.16086.16086.3	3	3.07	0	1.60E+05	M241m	(R)HNVmIS	(R)H N V m I S\T E|W/A/A/P N V L R(D)	m:Oxidized methionine	149.25	618.6483	1837.938	15.9926	-1.3	6.75	39066	6.61	HUMAN	A6PVW9	Selenium binding protein 1 (Fragment)
27114	dirMS_041712_NAR_60mM_minus.16187.16187.3	3	3.07	1	1.10E+05		(R)LIELVDR	(R)L I E L V D R/G L/V E K(V)		150.33	461.9435	1383.821	-0.0046	-3.4	4.68	31542.1	6.41	HUMAN	Q68D91	Metallo-beta-lactamase domain-containing protein 2
27115	dirMS_041712_NAR_60mM_minus.18608.18608.3	3	3.07	0	5.42E+04	T1236t	(R)FIPVtSV	(R)F I/P V t S/V V L L Y H/R(V)	t:Phosphorylated T	164.75	541.9639	1543.9	79.9776	7	8.75	156931.9	6.52	HUMAN	E9PE50	NACHT, LRR and PYD domains-containing protein 1
27116	dirMS_041712_NAR_60mM_minus.5858.5858.2	2	3.07	0	6.14E+03	T312t	(R)TtFGELI(	(R)T t/F G E L I Q P/F F E K(E)	t:Phosphorylated T	89.15	818.8981	1556.8	79.9894	14.1	4.53	55266.8	5.77	HUMAN	Q96MA6	Adenylate kinase 8
27117	dirMS_041712_NAR_120mM_plus.5071.5071.3	3	3.07	0	1.59E+04		(R)AGCDTS	(R)A G C D T S S T P S N T/A P R(I)	C:Carbamidomethylation	78.92	507.8874	1521.66	-0.0122	-8	5.88	21409.6	10.21	HUMAN	Q8IYB0	Putative uncharacterized protein MGC39545
27118	dirMS_041712_NAR_120mM_plus.9164.9164.3	3	3.07	1	1.54E+05		(R)VTEVRA	(R)V/T|E V R A D T G G/L\G R(S)		101.28	444.2411	1330.707	0.0014	1	6.04	74208.3	6.51	HUMAN	F5H837	Retinoblastoma-like protein 2 (Fragment)
27119	dirMS_041712_NAR_20mM_plus.11075.11075.3	3	3.07	0	3.68E+04	K662k	(K)SSMkTN	(K)S S M k T N/N/P L K(L)	k:Ubiquitin-K	148.77	411.8807	1119.583	114.0449	1.6	10	96731.7	8.74	HUMAN	Q14721	Potassium voltage-gated channel subfamily B member 1
27120	dirMS_041712_NAR_20mM_plus.16358.16358.2	2	3.07	0	1.18E+05	M578m	(K)ASMHP\	(K)A S M H P V T A m L/V/G/K(D)	m:Oxidized methionine	184.35	679.3577	1341.702	16.0064	8.4	8.8	67307	6.24	HUMAN	F8VV40	Leukotriene A-4 hydrolase
27121	dirMS_041712_NAR_20mM_plus.18600.18600.3	3	3.07	2	4.28E+04	K601k	(K)IVSKLQE	(K)I V\S K|L\Q E/M K E k(K)	k:Ubiquitin-K	199.9	482.9449	1332.756	114.0646	15	8.5	113203.9	8.73	HUMAN	Q8IYE0	Coiled-coil domain-containing protein 146
27122	dirMS_041712_NAR_20mM_plus.9707.9707.2	2	3.07	0	7.32E+04	M113m	(R)TIAmDG	(R)T I|A m D G T E G L V R(G)	m:Oxidized methionine	138.22	639.825	1262.641	16.0018	5.4	4.37	55307.5	5.25	HUMAN	F8VPV9	ATP synthase subunit beta
27123	dirMS_041712_NAR_30mM_plus2.17423.17423.2	2	3.07	0	3.75E+04		(K)DAGTIA(	(K)D A/G T/I/A/G L/N V M R(I)		143.38	609.3176	1217.631	-0.0028	-2.3	5.84	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
27124	dirMS_041712_NAR_30mM_plus2.6513.6513.2	2	3.07	0	3.24E+04		(K)SGYLSSE	(K)S G|Y\L/S S E/R(L)		89.43	449.7152	898.427	-0.0034	-3.7	5.72	65692.2	5.7	HUMAN	E7EQR4	Ezrin
27125	dirMS_041712_NAR_40mM_plus2.10812.10812.3	3	3.07	1	4.32E+05		(K)ASLENSI	(K)A S/L E N S L R/E|V E A R(Y)		128.65	491.9315	1473.766	0.0144	9.7	4.79	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
27126	dirMS_041712_NAR_40mM_plus2.7692.7692.2	2	3.07	0	1.48E+05		(R)SGYFDEI	(R)S G|Y|F D E R(Y)		104.58	437.1906	873.374	0.0002	0.2	4.37	22761.5	9.91	HUMAN	C9J6W7	Creatine kinase U-type, mitochondrial (Fragment)
27127	dirMS_041712_NAR_50mM_plus2.13989.13989.3	3	3.07	1	1.28E+06	M320m	(K)YmACCL	(K)Y m/A/C C/L L Y R G D V V P K(E)	C:Carbamidomethylation m:Oxid	140.83	620.9622	1844.886	15.9865	-4.5	8.49	50706.6	5.68	HUMAN	A6NHL2	Tubulin alpha chain-like 3
27128	dirMS_041712_NAR_50mM_plus2.17105.17105.3	3	3.07	1	3.44E+05		(K)FIQPNIG	(K)F I Q/P N I/G E L/P T A L K G R(L)		157.68	585.3302	1753.996	-0.0199	-11.3	8.75	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
27129	dirMS_041712_NAR_50mM_plus2.17806.17806.3	3	3.07	1	2.23E+05		(K)MGVGKI	(K)M/G V/G K L E M/Y V L N/P V K(S)		161.72	559.9739	1677.907	0.0005	0.3	8.26	75482.2	6.34	HUMAN	D6RA32	Microtubule-associated protein 1B (Fragment)
27130	dirMS_041712_NAR_50mM_plus2.20351.20351.3	3	3.07	1	1.04E+04		(K)SSVLESL	(K)S S V|L/E S L V\G R D L L P R(G)		175.6	547.6436	1640.933	-0.0167	-10.2	5.79	19884.2	4.87	HUMAN	B4DDQ3	Dynamin-1-like protein
27131	dirMS_041712_NAR_50mM_plus2.7163.7163.3	3	3.07	0	5.30E+04		(K)VNMPAI	(K)V N|M/P\A K P A/P\P T K(A)		103.3	417.5684	1250.693	-0.0019	-1.5	10	227202.2	8.26	HUMAN	Q14008	Cytoskeleton-associated protein 5
27132	dirMS_041712_NAR_50mM_plus2.7325.7325.3	3	3.07	1	2.03E+03	M617m M	(K)AQALRD	(K)A Q/A L R D N\S T m|G/Y m M A K(K)	m:Oxidized methionine	104.23	607.2766	1787.824	31.9915	0.9	8.63	83605	4.97	HUMAN	P08238	Heat shock protein HSP 90-beta
27133	dirMS_041712_NAR_50mM_plus2.8936.8936.3	3	3.07	1	3.10E+05		(K)TAVCDIF	(K)T A|V/C D I/P P R G L K(M)	C:Carbamidomethylation	114.82	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
27134	dirMS_041712_NAR_60mM_plus.14669.14669.3	3	3.07	2	6.99E+05	S195s	(K)MDLRsR	(K)M D L/R s R Y/L D/S\L K(A)	s:Phosphorylated S	133	526.2613	1496.789	79.9804	8.9	8.34	39725	9.34	HUMAN	Q96H22	Centromere protein N
27135	dirMS_041712_NAR_60mM_plus.19870.19870.3	3	3.07	1	1.53E+05		(R)GEIYVKG	(R)G E I/Y V K/G I S E Q/E G K(I)		163.87	512.9411	1536.79	0.0183	11.9	4.79	126185.9	6.52	HUMAN	E7EVL1	Adenylate cyclase type 8
27136	dirMS_041712_NAR_60mM_plus.5583.5583.3	3	3.07	0	6.64E+03	S459s	(R)GTsFDLI	(R)G T s\F D L/I G E S T I/R(C)	s:N-acetylglucosamine (S)	87.32	533.5989	1395.711	203.0707	-5.4	4.37	281477	6.63	HUMAN	E9PDY4	Complement receptor type 1

27137	dirMS_041712_NAR_60mM_plus.5913.5913.3	3	3.07	0	1.08E+05	Y204y	(K)VAVyIIV	(K)V A V y I/I V D E/S N V K(Y)	y:Phosphorylated Y	88.67	510.2582	1448.8	79.9605	-3.8	4.37	91118.6	5.96	HUMAN	A6ND36	Protein FAM83G
27138	dirMS_041712_NAR_60mM_plus.7919.7919.3	3	3.07	0	5.90E+05	M1201m K	(K)EVQTAIF	(K)E V/Q T A\I P m G I k(A)	m:Oxidized methionine k:Ub	99.57	439.5631	1186.65	130.0247	-10	6.1	464687.9	5.7	HUMAN	Q8WXX0	Dynein heavy chain 7, axonemal
27139	dirMS_041712_NAR_60mM_plus.8011.8011.3	3	3.07	0	3.01E+05		(R)SQLLGS	(R)S Q\L/L/G/S A H E/V Q R(F)		99.55	442.2342	1324.697	-0.0087	-6.6	6.47	285798.6	5.23	HUMAN	A6NG51	Spectrin alpha chain, non-erythrocytic 1
27140	dirMS_041712_NAR_60mM_plus.8595.8595.2	2	3.07	0	4.27E+05		(R)FACHSA	(R)F/A/C/H S/A S L T V R(N)	C:Carbamidomethylation	102.73	624.8118	1248.615	0.001	0.8	9.75	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
27141	dirMS_041712_NAR_120mM_minus.11911.11911.4	4	3.06	2	6.76E+05		(K)GTVIKVF	(K)G T V I K V/P L K V E Q/A\N/N A R(D)		119.27	460.021	1837.065	-0.0032	-1.8	9.99	150202.8	9.1	HUMAN	E7EW20	Unconventional myosin-VI
27142	dirMS_041712_NAR_120mM_minus.12985.12985.3	3	3.06	1	1.97E+05		(K)KTSCEFT	(K)K T S C E F|T G D/I L/R(T)	C:Carbamidomethylation	124.97	476.2347	1426.699	-0.0099	-7	6.07	21230	6.36	HUMAN	H0YC04	V-type proton ATPase subunit B, brain isoform (Fragment)
27143	dirMS_041712_NAR_120mM_minus.13100.13100.3	3	3.06	1	1.42E+04	M72m	(R)TEmENE	(R)T\E|m\E N E F/V L I K K(D)	m:Oxidized methionine	125.45	499.5949	1480.772	15.9986	2.4	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
27144	dirMS_041712_NAR_120mM_minus.17880.17880.3	3	3.06	1	1.54E+05		(R)AGKLDP	(R)A G K L\D|P H/L/V L D Q L R(C)		151.7	525.6385	1574.901	-0.0004	-0.2	6.79	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
27145	dirMS_041712_NAR_20mM_minus.10737.10737.2	2	3.06	0	6.61E+04		(K)VNQIGS	(K)V N/Q I/G/S/V T/E S I Q A C K(L)	C:Carbamidomethylation	155.45	817.4099	1633.821	-0.0089	-5.4	5.97	47328.4	7.76	HUMAN	P13929	Beta-enolase
27146	dirMS_041712_NAR_20mM_minus.13627.13627.2	2	3.06	1	1.05E+05		(R)SNAYTIT	(R)S N A Y/T I\T T S S/R M A K(K)		187.62	765.8936	1530.758	0.0219	14.3	9.99	48142.3	9.88	HUMAN	Q15760	Probable G-protein coupled receptor 19
27147	dirMS_041712_NAR_20mM_minus.7312.7312.3	3	3.06	0	1.72E+04		(K)AVTEQG	(K)A V T E Q G\A|E L/S N E E R(N)		121.03	511.5774	1532.719	-0.0011	-0.7	4.09	17219.2	5.69	HUMAN	E9PG15	14-3-3 protein theta (Fragment)
27148	dirMS_041712_NAR_20mM_minus.8326.8326.2	2	3.06	0	4.27E+03		(R)VLTVINC	(R)V L|T V/I/N Q T Q K(E)		132.92	572.338	1143.673	-0.0045	-3.9	8.72	10815.7	10.72	HUMAN	F2Z388	60S ribosomal protein L35
27149	dirMS_041712_NAR_20mM_minus.9841.9841.2	2	3.06	0	1.50E+05		(K)LSELEPG	(K)L S E L|E|P G T G D/L R(F)		147.83	643.8318	1286.659	-0.0023	-1.8	4.14	266161	5.68	HUMAN	E9PPU0	Epiplakin
27150	dirMS_041712_NAR_30mM_minus2.14293.14293.2	2	3.06	0	5.10E+04	M20m	(R)LGLAEPI	(R)L G|L A E P D/m/L R(K)	m:Oxidized methionine	129.92	565.7971	1114.593	15.9944	-0.4	4.37	18928.5	8.86	HUMAN	H3BTQ7	Origin recognition complex subunit 6
27151	dirMS_041712_NAR_30mM_minus2.5449.5449.2	2	3.06	0	9.84E+04		(K)DSYVGD	(K)D/S Y|V/G D E A Q S K(R)		83.85	599.7632	1198.522	-0.0031	-2.6	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
27152	dirMS_041712_NAR_30mM_minus2.5487.5487.2	2	3.06	0	2.91E+05		(K)GEGSTA	(K)G E/G/S T A/E V/R(E)		84.13	453.2209	905.432	0.0022	2.5	4.53	84108.3	6.39	HUMAN	Q33E94	Transcription factor RFX4
27153	dirMS_041712_NAR_40mM_minus2.8293.8293.3	3	3.06	0	2.03E+05	M35m	(K)AASDIAr	(K)A A S/D I/A m T E L/P P T H/P I R(L)	m:Oxidized methionine	128.85	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
27154	dirMS_041712_NAR_40mM_minus2.9360.9360.3	3	3.06	1	6.96E+05	M356m	(K)VGEVIVT	(K)V/G E|V/I V T K D D A m L L K(G)	m:Oxidized methionine	136.93	549.6354	1630.908	15.9832	-7.1	4.56	61224.7	5.7	HUMAN	P10809	60 kDa heat shock protein, mitochondrial
27155	dirMS_041712_NAR_50mM_minus2.7872.7872.3	3	3.06	0	5.88E+04	M24m	(K)mIISSLQ	(K)m I I S S L Q V I A/A/D C K(R)	C:Carbamidomethylation m:Oxid	111.92	522.2727	1548.812	15.9911	-2.4	5.59	38091.8	5.35	HUMAN	Q86US8-2	Isoform 2 of Telomerase-binding protein EST1A
27156	dirMS_041712_NAR_60mM_minus.10300.10300.3	3	3.06	1	2.36E+04	M88m	(K)DVDEAY	(K)D V/D/E A/Y m N\K/V E L E S R(L)	m:Oxidized methionine	116.03	605.2791	1797.832	15.9904	-2.5	4.18	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
27157	dirMS_041712_NAR_60mM_minus.12023.12023.3	3	3.06	1	4.11E+04		(R)LYIDSYE	(R)L/Y|I D/S Y/E K D V A K(I)		126.87	481.9183	1443.737	0.0038	2.6	4.56	61733.3	6.3	HUMAN	P36871	Phosphoglucomutase-1
27158	dirMS_041712_NAR_60mM_minus.13776.13776.3	3	3.06	0	1.42E+05		(K)ADFCIIH	(K)A D/F C/I/I H/Y A/G K(V)	C:Carbamidomethylation	137.43	432.2132	1294.625	0.0002	0.1	6.79	233493.8	5.45	HUMAN	F8VTL3	Myosin-10
27159	dirMS_041712_NAR_60mM_minus.18375.18375.3	3	3.06	0	1.09E+05		(R)ILVTLLH	(R)I L/V/T/L L H T L E R(M)		163.85	436.6046	1307.805	-0.0053	-4.1	6.75	45212.4	9.41	HUMAN	B7Z233	Acetyl-CoA acetyltransferase, cytosolic
27160	dirMS_041712_NAR_60mM_minus.19336.19336.3	3	3.06	1	1.56E+04		(K)AKINEA	(K)A K I N E A V E/C L/L S L\K(A)	C:Carbamidomethylation	172.08	529.9633	1587.878	-0.0021	-1.3	6.18	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
27161	dirMS_041712_NAR_60mM_minus.5347.5347.3	3	3.06	1	1.52E+04	T623t	(R)WSVMIF	(R)W S V M/I R E/t/P R(Q)	t:Phosphorylated T	85.35	452.2129	1274.667	79.9567	-7.1	9.6	143766.3	5.36	HUMAN	Q5KSL6	Diacylglycerol kinase kappa
27162	dirMS_041712_NAR_120mM_plus.11480.11546.3	3	3.06	1	2.83E+06		(K)LGLRPGI	(K)L G L R P G|I|H H S\L F G D V K K(L)		113.63	625.3557	1874.076	-0.0234	-12.5	9.99	63309.2	9.46	HUMAN	H7BXW3	Melanoma-associated antigen D2
27163	dirMS_041712_NAR_120mM_plus.13960.13960.3	3	3.06	1	4.03E+05		(K)WKDSDE	(K)W/K D S D E\A/D L V/L/A/K(E)		126.42	497.2584	1489.753	0.0073	4.9	4.23	20982.2	5.23	HUMAN	Q13185	Chromobox protein homolog 3
27164	dirMS_041712_NAR_120mM_plus.5932.5932.3	3	3.06	2	1.80E+05		(R)KTGQAP	(R)K\T G Q A/P\G Y\S\Y/T A A\N K N K(G)		83.88	600.3013	1798.908	-0.0189	-10.5	9.83	11447.2	9.81	HUMAN	C9JFR7	Cytochrome c (Fragment)
27165	dirMS_041712_NAR_120mM_plus.9834.9834.3	3	3.06	0	1.73E+06	S7s	(-)XYLSEVsI	(-)X Y L S/E V/s L Q/K(Y)	s:Phosphorylated S	104.62	420.5413	1179.662	79.9474	-15	6	13791.7	9.36	HUMAN	H0YFK3	C-type lectin-like domain family 1 (Fragment)
27166	dirMS_041712_NAR_20mM_plus.13595.13595.2	2	3.06	0	5.50E+04		(K)IFVGGLS	(K)I F|V/G G\L|S P D T P E E K(I)		165.28	744.8731	1488.758	-0.0191	-12.8	4.14	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
27167	dirMS_041712_NAR_20mM_plus.14817.14817.2	2	3.06	0	1.48E+05		(K)VSTLPAI	(K)V/S/T L/P A I T L K(L)		172.9	521.8283	1042.651	-0.0013	-1.3	8.72	20599.3	9.19	HUMAN	H7C1V0	Cathepsin D light chain (Fragment)
27168	dirMS_041712_NAR_20mM_plus.15053.15053.2	2	3.06	0	7.93E+04		(K)VVNIVP	(K)V V|N|I V P V I A\K(A)		174.72	526.3453	1051.687	-0.0041	-3.9	8.72	22387.6	9.64	HUMAN	K7EK18	Septin-9 (Fragment)
27169	dirMS_041712_NAR_30mM_plus2.10067.10067.2	2	3.06	0	3.02E+05	M1385m	(R)IWmLEN	(R)I/W|m L/E M K(Q)	m:Oxidized methionine	105.75	483.7442	950.484	15.9973	2.5	6	335976	5.62	HUMAN	O43149	Zinc finger ZZ-type and EF-hand domain-containing protein 1
27170	dirMS_041712_NAR_40mM_plus2.15319.15319.3	3	3.06	1	8.47E+03		(K)QGGLGF	(K)Q G/G L/G P M N I/P L\V S D P K R(T)		156.17	593.6623	1778.958	0.0142	8	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
27171	dirMS_041712_NAR_40mM_plus2.6288.6288.2	2	3.06	1	2.84E+05		(R)YSGGNY	(R)Y/S/G G N Y R D N\Y/D\N(-)		95.58	719.2857	1437.567	-0.0024	-1.7	4.21	17170.1	8.86	HUMAN	P98179	Putative RNA-binding protein 3
27172	dirMS_041712_NAR_40mM_plus2.8007.8007.2	2	3.06	0	3.33E+04		(R)SGQGAF	(R)S G\Q/G A|F|G N M C R(G)	C:Carbamidomethylation	107.53	592.7523	1184.494	0.0038	3.2	9.47	18988.7	11.2	HUMAN	H3BTP7	60S ribosomal protein L4 (Fragment)
27173	dirMS_041712_NAR_50mM_plus2.10585.10585.3	3	3.06	1	1.85E+05		(K)KSWFGN	(K)K S W F/G N F/I S L E K(E)		122.8	485.9273	1455.763	0.0043	2.9	8.59	40694.4	9.71	HUMAN	B4DM60	Serine/threonine-protein kinase BRSK2
27174	dirMS_041712_NAR_50mM_plus2.10610.10610.3	3	3.06	0	5.66E+05		(K)SFPAAA	(K)S F/P A A A V L P T G A A|R(G)		123.8	443.5761	1328.732	-0.0184	-13.8	9.47	18035.5	11.4	HUMAN	C9JYT9	Vacuolar protein sorting-associated protein 37D
27175	dirMS_041712_NAR_50mM_plus2.11991.11991.3	3	3.06	1	8.60E+05	M654m	(K)mSAVSC	(K)m S A V S/Q/D A I E D S R Q A R(T)	m:Oxidized methionine	131.22	593.9395	1763.834	15.9699	-14.1	4.56	79718	10.14	HUMAN	E9PEW0	Ubiquitin carboxyl-terminal hydrolase 36
27176	dirMS_041712_NAR_50mM_plus2.12526.12526.3	3	3.06	1	5.93E+05		(K)AVLFCLS	(K)A V/L/F/C L S E D K/K(N)	C:Carbamidomethylation	134.23	437.2325	1309.682	0.0009	0.7	6.11	22956	8.8	HUMAN	E9PK25	Cofilin-1
27177	dirMS_041712_NAR_50mM_plus2.14132.14132.3	3	3.06	0	1.36E+05		(K)QIGNVA	(K)Q I/G N V A A L/P/G I V H R(S)		142.23	482.2828	1444.838	-0.0045	-3.1	9.75	19338.9	5.33	HUMAN	E7EQS9	tRNA-splicing ligase RtcB homolog
27178	dirMS_041712_NAR_50mM_plus2.8385.8385.3	3	3.06	1	2.28E+05	M172m T1	(K)LmLRRtE	(K)L m L R R/t E/S V/V\E K(L)	m:Oxidized methionine t:Phc	110.8	519.6023	1460.825	95.967	3.7	8.75	71553.1	6.2	HUMAN	B4DHQ7	Plexin-C1
27179	dirMS_041712_NAR_50mM_plus2.8594.8594.3	3	3.06	1	8.10E+04		(K)NSDEAD	(K)N/S|D/E A D L V/P A K E A N V\K(C)		112.2	567.2893	1699.85	0.0036	2.1	4.32	19439.5	4.97	HUMAN	B5MD17	Chromobox protein homolog 1 (Fragment)
27180	dirMS_041712_NAR_50mM_plus2.8914.8914.3	3	3.06	1	2.72E+05		(K)TAVCDIF	(K)T A V C D I/P P R G L K(M)	C:Carbamidomethylation	114.72	442.9121	1326.72	0.0019	1.4	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
27181	dirMS_041712_NAR_60mM_plus.13764.13764.3	3	3.06	1	4.08E+05		(K)SGYLAGI	(K)S G Y L A/G D K/L|L/P Q/R(V)		128.58	473.2654	1417.78	0.0019	1.3	8.31	67933	6.08	HUMAN	P26038	Moesin
27182	dirMS_041712_NAR_60mM_plus.16075.16075.3	3	3.06	1	1.57E+05		(R)ILNPLLD	(R)I L/N/P L L\D R V R(T)		141.2	403.5863	1208.747	-0.003	-2.5	9.6	87537	9.67	HUMAN	Q9Y446	Plakophilin-3
27183	dirMS_041712_NAR_60mM_plus.16485.16485.3	3	3.06	0	7.03E+05		(K)SPYQEFT	(K)S/P/Y Q/E F T D H L V K(T)		142.73	488.5776	1463.717	0.0017	1.2	5.3	25381.9	10.49	HUMAN	E9PQD7	40S ribosomal protein S2
27184	dirMS_041712_NAR_60mM_plus.18444.18444.3	3	3.06	0	1.35E+04		(K)SPVTTLL	(K)S P/V/T T L L/E C\M\H K(L)	C:Carbamidomethylation	153.65	472.5788	1415.702	0.0197	13.9	6.47	142137.5	9.17	HUMAN	E7ENU4	Double-stranded RNA-specific adenosine deaminase
27185	dirMS_041712_NAR_60mM_plus.7884.7884.3	3	3.06	1	1.16E+04		(R)LQRELQ	(R)L Q/R E L/Q S L/S Q R(L)		100.17	453.2595	1357.755	0.0093	6.9	9.6	110876.7	5.76	HUMAN	Q8N283	Ankyrin repeat domain-containing protein 35
27186	dirMS_041712_NAR_120mM_minus.7420.7420.2	2	3.05	0	4.94E+03		(R)HMEMY	(R)H/M/E/M Y A D/R(E)		94.33	526.7192	1052.429	0.0023	2.2	5.32	54427.4	5.96	HUMAN	K4DID9	Acetyl-CoA carboxylase 1
27187	dirMS_041712_NAR_120mM_minus.9694.9694.3	3	3.05	1	3.90E+05		(K)YAGKDG	(K)Y/A/G K D G Y N/Y T L S K(T)		107.47	493.9089	1479.711	0.0007	0.5	8.38	11854.4	6.57	HUMAN	P31949	Protein S100-A11
27188	dirMS_041712_NAR_20mM_minus.10407.10407.3	3	3.05	1	2.05E+05	S373s	(R)LDsAFR	(R)L D s A F/R|C M\S S K(G)	C:Carbamidomethylation s:N-ace	152.88	502.2275	1301.598	203.0703	-6	8.75	55504.9	9.2	HUMAN	F8W840	YTH domain family protein 1
27189	dirMS_041712_NAR_20mM_minus.10739.10739.2	2	3.05	0	8.75E+04		(K)FLIPNAS	(K)F/L/I/P N A S Q A E S K(V)		154.72	652.8447	1304.685	-0.0024	-1.8	6	19186.1	4.48	HUMAN	B0AZS6	14-3-3 protein zeta/delta
27190	dirMS_041712_NAR_30mM_minus2.13332.13332.2	2	3.05	0	4.40E+04	T141t	(R)SQtVLN	(R)S Q|t\V L N Q L R(Y)	t:Phosphorylated T	125.92	569.7841	1058.595	79.9656	-0.6	9.47	82948.6	6.59	HUMAN	B7ZKL3	EPS8L2 protein
27191	dirMS_041712_NAR_30mM_minus2.13706.13706.2	2	3.05	0	2.30E+05		(K)FAFQAE	(K)F A|F/Q/A\E V N/R(M)		127.28	541.2823	1081.543	0.0148	13.7	6	92752.5	4.76	HUMAN	P14625	Endoplasmin
27192	dirMS_041712_NAR_30mM_minus2.18082.18082.2	2	3.05	0	2.13E+04		(R)LSLGPEG	(R)L S L/G P/E G I\T/K(G)		152.73	507.7939	1014.583	-0.0025	-2.4	6	17859.6	10.27	HUMAN	Q5VZT2	Putative uncharacterized protein C10orf113
27193	dirMS_041712_NAR_30mM_minus2.19047.19047.3	3	3.05	0	1.68E+05		(K)SYELPDG	(K)S Y\E\L/P D G Q\V|I T I/G N E R(F)		158.8	597.6343	1790.892	-0.0036	-2	4.14	123097.1	5.83	HUMAN	A5A3E0	POTE ankyrin domain family member F
27194	dirMS_041712_NAR_30mM_minus2.5923.5923.2	2	3.05	0	1.13E+05		(R)APSFGTI	(R)A P S F G/T D/Q K(I)		85.87	475.7392	950.458	0.0133	14	5.88	55958.5	9.67	HUMAN	F2Z2J7	Tubulin polyglutamylase TTLL7
27195	dirMS_041712_NAR_30mM_minus2.6798.6798.2	2	3.05	0	3.88E+05		(K)SPEDLEF	(K)S/P/E/D L E/R(L)		90.92	423.2044	845.4	0.0016	1.9	4.14	63374.2	8.64	HUMAN	P06744	Glucose-6-phosphate isomerase
27196	dirMS_041712_NAR_30mM_minus2.9109.9109.2	2	3.05	0	3.92E+04		(K)ITTADVN	(K)I T|T/A D V N E/K(N)		103.85	495.7528	990.51	-0.0119	-12	4.37	107784.8	10.06	HUMAN	Q6ZNB6	NF-X1-type zinc finger protein NFXL1
27197	dirMS_041712_NAR_30mM_minus2.9382.9382.2	2	3.05	0	4.36E+05		(K)NDPSLPI	(K)N D|P S L P E/P K(C)		105.4	498.7592	996.5	0.0115	11.5	4.37	20203.8	9.79	HUMAN	B4DG16	Asparagine--tRNA ligase, cytoplasmic
27198	dirMS_041712_NAR_40mM_minus2.10948.10948.3	3	3.05	0	1.02E+05	M56m	(K)VAIVKPG	(K)V/A I\V K P G V/P m E I V/L N K(E)	m:Oxidized methionine	147.13	575.0112	1707.024	15.9953	0.2	8.56	73146.9	5.45	HUMAN	E9PJ21	Hypoxia up-regulated protein 1 (Fragment)
27199	dirMS_041712_NAR_40mM_minus2.13193.13193.3	3	3.05	1	2.07E+05	M2447m	(R)AKFFEVF	(R)A K F F E V\F|D N S\m K(R)	m:Oxidized methionine	161.92	493.5654	1462.704	15.9781	-11.3	6.11	440352.7	8.98	HUMAN	F2Z2U4	Transformation/transcription domain-associated protein
27200	dirMS_041712_NAR_50mM_minus2.10439.10439.3	3	3.05	0	2.62E+05		(R)TFIAIKPI	(R)T F|I A I K P D G V Q R(G)		126.87	448.923	1344.763	-0.009	-6.7	8.41	6640.6	8.25	HUMAN	C9K028	Nucleoside diphosphate kinase A (Fragment)
27201	dirMS_041712_NAR_50mM_minus2.6601.6601.3	3	3.05	0	6.22E+04		(K)EGVTNP	(K)E G|V|T N P S N S S Q Q A/L L K(A)		104.1	558.2834	1672.85	-0.0144	-8.6	6.1	95012.8	9.6	HUMAN	A6NNM8	Tubulin polyglutamylase TTLL13
27202	dirMS_041712_NAR_50mM_minus2.7115.7115.3	3	3.05	1	2.74E+04		(R)LAEEKA	(R)L A|E E K A Q\A S/S\I/P V G S R(C)		107.42	548.29	1642.876	-0.0204	-12.4	6.14	23811.2	6.78	HUMAN	A8MVD5	Tubulin-folding cofactor B
27203	dirMS_041712_NAR_120mM_plus.7704.7704.3	3	3.05	2	2.01E+05	K134k	(R)RYSRYLN	(R)R Y S R Y/L N/E k(A)	k:Ubiquitin-K	93.68	448.2316	1228.643	114.037	-4.5	9.7	17023.1	9.82	HUMAN	E5RFC6	Clathrin coat assembly protein AP180 (Fragment)
27204	dirMS_041712_NAR_20mM_plus.10167.10167.2	2	3.05	0	1.51E+05		(K)GEATVSI	(K)G E A T/V/S F D D P P S A K(A)		142.13	710.8324	1420.659	-0.0015	-1.1	4.03	53724.2	9.54	HUMAN	H3BPE7	RNA-binding protein FUS
27205	dirMS_041712_NAR_20mM_plus.11291.11291.3	3	3.05	0	7.77E+04	Y224y	(R)ADLTEYI	(R)A D\L T E Y L S/T/H y/K(A)	y:Phosphorylated Y	149.38	507.5583	1440.7	79.9598	-4.3	5.32	53329.5	5.94	HUMAN	P31930	Cytochrome b-c1 complex subunit 1, mitochondrial
27206	dirMS_041712_NAR_20mM_plus.18666.18666.2	2	3.05	0	5.56E+04		(K)SVLIGEF	(K)S V/L|I/G E F L E K(V)		199.67	567.8286	1134.641	0.0094	8.3	4.53	35352	7.68	HUMAN	K7EP06	mRNA cap guanine-N7 methyltransferase
27207	dirMS_041712_NAR_20mM_plus.9109.9109.2	2	3.05	0	3.60E+05	M161m	(K)LLIEmEC	(K)L L/I E/m E Q R(L)	m:Oxidized methionine	133.05	524.278	1031.555	15.9933	-1.5	4.53	20203.9	6.24	HUMAN	H0YJG0	Creatine kinase B-type (Fragment)
27208	dirMS_041712_NAR_20mM_plus.9463.9463.2	2	3.05	0	1.86E+05		(K)SVTNED	(K)S V|T N E D/V T Q/E E/L G G A K(T)		136	838.9014	1676.797	-0.0018	-1.1	4	61363	8.73	HUMAN	C9JQS9	Propionyl-CoA carboxylase beta chain, mitochondrial
27209	dirMS_041712_NAR_30mM_plus2.10031.10031.2	2	3.05	0	3.21E+05	T555t	(K)TDVtVVI	(K)T D V/t V V/R(F)	t:N-acetylglucosamine (T)	105.62	496.774	789.447	203.0942	15	5.5	155846.3	5.52	HUMAN	Q99683	Mitogen-activated protein kinase kinase kinase 5
27210	dirMS_041712_NAR_30mM_plus2.6580.6580.2	2	3.05	0	1.26E+05		(R)TGVVTD	(R)T/G/V\V/T D G V K(H)		88.7	438.2432	875.483	-0.0041	-4.7	5.5	28071.3	8.6	HUMAN	P38117	Electron transfer flavoprotein subunit beta
27211	dirMS_041712_NAR_30mM_plus2.6700.6700.2	2	3.05	0	2.62E+05	M529m	(R)MGLSmI	(R)M/G|L|S m E R(M)	m:Oxidized methionine	89.73	420.1949	823.38	16.0025	9	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
27212	dirMS_041712_NAR_30mM_plus2.7753.7753.2	2	3.05	0	6.90E+05		(R)QGANIN	(R)Q G\A N\I/N E/I/R(Q)		94.57	507.769	1014.533	-0.002	-1.9	6	38010.7	6.67	HUMAN	Q15365	Poly(rC)-binding protein 1
27213	dirMS_041712_NAR_40mM_plus2.15388.15388.3	3	3.05	1	8.47E+03		(K)QGGLGF	(K)Q G/G L G|P M N I/P L V S D P K R(T)		156.17	593.6623	1778.958	0.0142	8	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
27214	dirMS_041712_NAR_40mM_plus2.19798.19798.3	3	3.05	0	4.02E+03	S71s	(R)LPHNLsL	(R)L P H N L/s L E L V V A A P\P A/R(D)	s:Phosphorylated S	185.6	626.3485	1797.038	79.9928	14.1	6.75	113960.2	9.93	HUMAN	O60391	Glutamate receptor ionotropic, NMDA 3B
27215	dirMS_041712_NAR_40mM_plus2.8889.8889.2	2	3.05	0	1.19E+05		(R)GYSFTTT	(R)G Y|S|F/T T T\A E R(E)		114.9	566.7672	1132.527	0.0002	0.2	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
27216	dirMS_041712_NAR_50mM_plus2.10578.10578.3	3	3.05	1	2.19E+05		(K)SVEAAA	(K)S V|E/A A A E L/S A K D L K(E)		122.85	477.9286	1431.769	0.0023	1.6	4.68	12131.5	11.14	HUMAN	F5GXR3	Parathymosin
27217	dirMS_041712_NAR_50mM_plus2.11836.11836.3	3	3.05	1	3.33E+06		(R)VVDLM	(R)V V/D L/M A/H M A S K E(-)		130.52	444.2215	1330.649	0.0006	0.4	5.51	31718.5	7.17	HUMAN	E7EUT4	Glyceraldehyde-3-phosphate dehydrogenase
27218	dirMS_041712_NAR_50mM_plus2.12232.12232.3	3	3.05	0	3.10E+05		(-)MLLSLVL	(-)M L L S L\V/L H\T Y S M R(Y)		132.17	521.9495	1563.839	-0.0046	-3	8.52	10260	9.6	HUMAN	E5RH21	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon
27219	dirMS_041712_NAR_50mM_plus2.12793.12793.3	3	3.05	1	3.20E+04		(K)IGNVCKI	(K)I/G/N V C K K L/S S P S N Y/K(L)	C:Carbamidomethylation	135.27	565.6269	1694.889	-0.0233	-13.7	10	50975.3	7.79	HUMAN	B4DDV1	Interferon-induced protein with tetratricopeptide repeats 5
27220	dirMS_041712_NAR_50mM_plus2.18064.18064.3	3	3.05	0	4.40E+05	M311m S3	(K)LGmLSV	(K)L G m L S V L s T L S G T I A I/K(H)	m:Oxidized methionine s:N-a	162.85	641.6959	1703.998	219.0756	0.7	8.75	108087.2	8.84	HUMAN	Q9NVH2	Integrator complex subunit 7
27221	dirMS_041712_NAR_50mM_plus2.18070.18070.3	3	3.05	0	4.02E+05		(R)YPSLSLH	(R)Y/P/S L S L/H G I E G A/F S G S G A/K(T)		162.92	626.6508	1877.939	-0.0014	-0.7	6.75	53219.8	5.66	HUMAN	Q96KP4	Cytosolic non-specific dipeptidase
27222	dirMS_041712_NAR_60mM_plus.16208.16208.3	3	3.05	0	1.12E+06	N649n	(K)LLnNLTS	(K)L L n N/L/T S I K(I)	n:N-acetylglucosamine (N)	141.08	406.908	1015.615	203.0948	12.7	8.75	183305.2	5.01	HUMAN	P11047	Laminin subunit gamma-1
27223	dirMS_041712_NAR_60mM_plus.19617.19617.3	3	3.05	0	1.25E+03	K18k	(R)NLFSQTI	(R)N L F S Q T L S/L/G\S Q k(E)	k:Ubiquitin-K	162.42	512.9411	1422.759	114.05	4.6	8.75	19809.3	6.3	HUMAN	B5MCS1	NAD-dependent protein deacetylase sirtuin-2 (Fragment)
27224	dirMS_041712_NAR_60mM_plus.21228.21228.3	3	3.05	1	5.45E+05		(R)SKALGSI	(R)S K A L\G\S D H C P I T L\Y L|A/L(-)	C:Carbamidomethylation	175.57	620.326	1858.973	-0.0097	-5.2	6.46	5634.5	9.82	HUMAN	G3V574	DNA-(apurinic or apyrimidinic site) lyase
27225	dirMS_041712_NAR_120mM_minus.13120.13120.4	4	3.04	1	2.66E+05	S94s	(R)SPASLRG	(R)S P A S L R G G H A G T T/Y I F s K(G)	s:Phosphorylated S	125.07	483.2345	1849.956	79.9606	-2.9	9.99	47087.9	7.88	HUMAN	P58400	Neurexin-1-beta
27226	dirMS_041712_NAR_120mM_minus.14898.14898.4	4	3.04	1	4.81E+05		(K)KKELEEI	(K)K K E L\E E\I V Q P I/I S K(L)		135.12	414.2486	1653.978	-0.006	-3.6	6.23	72445.7	5.07	HUMAN	P11021	78 kDa glucose-regulated protein
27227	dirMS_041712_NAR_120mM_minus.17137.17137.4	4	3.04	1	5.35E+05		(R)NEELNV	(R)N E E/L N V E/T L V V/V D K/K(M)		148.72	432.9911	1728.938	0.0048	2.8	4.41	64675.9	9.36	HUMAN	Q2XQZ0	A disintegrin and metalloproteinase with thrombospondin motifs 16
27228	dirMS_041712_NAR_120mM_minus.4894.4894.3	3	3.04	1	3.49E+05		(R)AAEEED	(R)A A|E/E E D\E\A D P K R(Q)		78.73	453.8716	1359.602	-0.002	-1.5	4.08	11529.7	4.14	HUMAN	P20962	Parathymosin
27229	dirMS_041712_NAR_120mM_minus.6310.6310.3	3	3.04	0	1.54E+05		(K)LHQSLH	(K)L/H Q/S L H\Q S Q K(Q)		87.88	402.5466	1205.639	-0.0133	-11	8.76	121492.5	9.43	HUMAN	O95625	Zinc finger and BTB domain-containing protein 11
27230	dirMS_041712_NAR_120mM_minus.9102.9102.3	3	3.04	0	4.24E+05	T35t S48s	(R)TtTVNIG	(R)T t T V N I G S/I S T\A D G s A L/V K(L)	t:Phosphorylated T s:Phosph	103.82	665.6353	1834.976	159.9157	-8.5	5.5	30609.6	5.17	HUMAN	Q96B26	Exosome complex component RRP43
27231	dirMS_041712_NAR_120mM_minus.9830.9830.2	2	3.04	1	1.22E+06	Y66y M67n	(K)TQGVIK	(K)T/Q G V/I K y m G P A/G A K(N)	y:Phosphorylated Y m:Oxidiz	108.05	758.8539	1420.762	95.9388	-14.8	9.7	104041.1	5.8	HUMAN	E9PHA6	DNA mismatch repair protein Msh2
27232	dirMS_041712_NAR_30mM_minus2.11949.11949.2	2	3.04	0	6.12E+05		(K)VQTAVT	(K)V Q|T\A V T M K(G)		117.73	439.2467	877.481	0.005	5.7	8.72	14312.9	4.69	HUMAN	F5H875	Charged multivesicular body protein 1a
27233	dirMS_041712_NAR_30mM_minus2.12242.12242.2	2	3.04	1	1.78E+05		(-)MEQVNE	(-)M/E|Q V/N E L K E K(G)		120.12	624.3176	1247.63	-0.0021	-1.7	4.78	15808.4	8.71	HUMAN	F5GXD8	Stress-induced-phosphoprotein 1
27234	dirMS_041712_NAR_30mM_minus2.16888.16888.2	2	3.04	0	2.62E+05	M2243m	(K)mSIYQA	(K)m S I|Y Q A M/W/K(G)	m:Oxidized methionine	145.35	587.2756	1157.548	15.9957	0.7	8.34	266161	5.68	HUMAN	E9PPU0	Epiplakin
27235	dirMS_041712_NAR_30mM_minus2.19167.19179.2	2	3.04	0	1.56E+05		(K)FTSPPGI	(K)F T/S/P P G D K(F)		159.8	424.7117	848.415	0.0013	1.5	5.84	183793.9	7.08	HUMAN	F5GWN5	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit beta
27236	dirMS_041712_NAR_30mM_minus2.7835.7835.2	2	3.04	0	1.35E+05		(K)SLTAEPC	(K)S/L T A E/P\Q K(A)		98.22	437.2408	873.468	0.0067	7.7	5.72	555035.4	6.1	HUMAN	Q9Y6V0	Protein piccolo
27237	dirMS_041712_NAR_40mM_minus2.12655.12655.3	3	3.04	0	1.07E+04	S314s	(R)HSPIAPS	(R)H S P I A P S S/P s/P Q V L A Q K(Y)	s:N-acetylglucosamine (S)	158.23	649.6858	1743.939	203.104	12.7	8.76	105826.3	9.6	HUMAN	Q9NQS7	Inner centromere protein
27238	dirMS_041712_NAR_40mM_minus2.14939.14939.3	3	3.04	1	1.01E+06		(K)TFVNITP	(K)T F/V|N I\T P A E V G V L V G\K D R(S)		172.05	639.0252	1915.065	-0.0037	-1.9	5.74	17630.6	11.62	HUMAN	I3L3D5	Profilin-1 (Fragment)
27239	dirMS_041712_NAR_40mM_minus2.5384.5384.2	2	3.04	0	1.03E+05		(K)DSYVGD	(K)D S\Y|V G/D E A Q S K(R)		89.65	599.7638	1198.522	-0.0019	-1.6	4.03	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
27240	dirMS_041712_NAR_60mM_minus.11234.11234.3	3	3.04	0	7.43E+04		(R)LGSTVVI	(R)L/G S/T V V D L S V P G K(F)		122.25	424.5804	1271.72	0.0061	4.8	5.84	29726.7	9.68	HUMAN	Q86U90	YrdC domain-containing protein, mitochondrial
27241	dirMS_041712_NAR_60mM_minus.13303.13303.3	3	3.04	1	5.11E+05		(R)KLVIIEGI	(R)K L V I\I\E/G D L/E/R(T)		135.05	428.9221	1284.752	-0.0004	-0.3	4.68	33450.2	4.73	HUMAN	J3KN67	Tropomyosin alpha-3 chain
27242	dirMS_041712_NAR_60mM_minus.18128.18128.3	3	3.04	0	8.73E+03		(K)EFSHIAF	(K)E F S H I A/F/L/T I K(G)		162.55	435.9153	1305.72	0.0112	8.6	6.85	54978.6	6.16	HUMAN	P10619	Lysosomal protective protein
27243	dirMS_041712_NAR_120mM_plus.11289.11289.2	2	3.04	0	5.12E+05		(-)XALAFYR	(-)X/A L/A F Y R(A)		112.25	427.2494	853.493	-0.0015	-1.8	8.75	5785.5	9.31	HUMAN	I3L4E7	Cytochrome c oxidase assembly protein COX11, mitochondrial (Fragment)
27244	dirMS_041712_NAR_120mM_plus.13576.13576.3	3	3.04	1	1.17E+06	T188t	(K)NYLAtRC	(K)N Y|L A t R/G L T\W K(N)	t:Phosphorylated T	123.58	468.2345	1322.722	79.9674	0.8	9.99	33386	5.9	HUMAN	F5H7R8	E3 ubiquitin-protein ligase CHFR
27245	dirMS_041712_NAR_120mM_plus.4875.4875.3	3	3.04	1	2.67E+04		(R)KENSMI	(R)K E/N S\M D T/A S/Q A I K(-)		77.15	474.896	1422.689	-0.0159	-11.2	6.07	23891.7	5.1	HUMAN	Q9BRV8	Suppressor of IKBKE 1

27246	dirMS_041712_NAR_120mM_plus.8578.8578.2	2	3.04	1	1.66E+05		(R)LHIRNEF	(R)L/H I R N E F\M\R(C)		98.05	608.3168	1215.642	-0.0152	-12.5	9.61	138192.7	6.56	HUMAN	C9JDG0	Protein diaphanous homolog 3
27247	dirMS_041712_NAR_20mM_plus.10542.10542.2	2	3.04	0	1.05E+05		(R)AVLLGPI	(R)A/V|L L|G/P P G/A G K(G)		144.92	490.2992	979.593	-0.0024	-2.4	8.8	4460.2	8.14	HUMAN	F8VPP1	Adenylate kinase 2, mitochondrial
27248	dirMS_041712_NAR_20mM_plus.13506.13506.2	2	3.04	1	9.85E+04	K463k M46	(R)kLREVm	(R)k|L/R E/V m H K(K)	k:Ubiquitin-K m:Oxidized me	164.85	585.8253	1040.603	130.04	1.8	9.99	54996.4	5.61	HUMAN	C9J6G4	WAP, kazal, immunoglobulin, kunitz and NTR domain-containing protein 2
27249	dirMS_041712_NAR_20mM_plus.8600.8600.2	2	3.04	0	6.29E+04		(R)LDAEPRI	(R)L D A E/P R\P P P T Q E\A\A(-)		129.63	746.3743	1491.744	-0.0025	-1.7	4.14	54213.9	7.33	HUMAN	B4E363	Phenylalanine--tRNA ligase alpha subunit
27250	dirMS_041712_NAR_30mM_plus2.16894.16894.2	2	3.04	1	1.24E+04		(-)MVGCA	(-)M/V G C A/K|K G E/R(E)	C:Carbamidomethylation	140.73	568.2831	1135.571	-0.0121	-10.7	9.99	20318.6	5.45	HUMAN	B4DIP9	BTB/POZ domain-containing protein KCTD20
27251	dirMS_041712_NAR_30mM_plus2.20827.20827.2	2	3.04	0	1.02E+05		(R)DWVLNI	(R)D W|V/L/N E F K(H)		163.85	525.767	1050.526	0.0013	1.2	4.37	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
27252	dirMS_041712_NAR_30mM_plus2.4551.4551.2	2	3.04	0	3.69E+05		(R)SYTSGP	(R)S Y|T/S/G P G S\R(I)		73.57	456.2155	911.422	0.002	2.2	8.46	19288.4	10.19	HUMAN	F8VQY3	Keratin, type II cytoskeletal 8 (Fragment)
27253	dirMS_041712_NAR_40mM_plus2.13926.13926.3	3	3.04	1	3.86E+05		(R)QVFGEA	(R)Q V/F G E A T K Q/P G I\T F I A A K(F)		147.62	636.0176	1906.043	-0.005	-2.6	8.59	32905.8	5.88	HUMAN	C9JH19	Cathepsin D light chain (Fragment)
27254	dirMS_041712_NAR_40mM_plus2.5927.5927.2	2	3.04	0	1.88E+03		(K)MMYDC	(K)M/M/Y D/Q R(Q)		93.45	422.1766	843.349	-0.0028	-3.4	5.59	38299.3	5.27	HUMAN	Q9Y266	Nuclear migration protein nudC
27255	dirMS_041712_NAR_40mM_plus2.6079.6079.3	3	3.04	1	2.42E+04	S854s	(R)sRSVSP	(R)s R S V S P/C/S N V E S R(L)	C:Carbamidomethylation s:Phosp	94.68	515.558	1464.686	79.9735	4.6	9.32	99885.2	12.36	HUMAN	I3L182	Serine/arginine repetitive matrix protein 2 (Fragment)
27256	dirMS_041712_NAR_40mM_plus2.8900.8900.2	2	3.04	0	1.19E+05		(R)GYSFTT	(R)G Y S/F/T/T/T A E R(E)		114.9	566.7672	1132.527	0.0002	0.2	6	23901.9	5.28	HUMAN	I3L1U9	Actin, cytoplasmic 2, N-terminally processed (Fragment)
27257	dirMS_041712_NAR_50mM_plus2.13606.13606.3	3	3.04	1	9.86E+05		(R)LLLSTSL	(R)L/L/L S T/S L D A/K D E L E E/R(L)		138.95	611.3256	1831.965	-0.0025	-1.4	4.18	119608.2	5.53	HUMAN	Q68E01	Integrator complex subunit 3
27258	dirMS_041712_NAR_50mM_plus2.7640.7640.3	3	3.04	1	4.96E+04	S289s	(K)SRHDSIT	(K)S R H D S I T/G s/L K(K)	s:N-acetylglucosamine (S)	105.97	468.5732	1200.633	203.0719	-5.3	8.49	49011.6	7.89	HUMAN	A6NI17	E3 ubiquitin-protein ligase TRIM31
27259	dirMS_041712_NAR_50mM_plus2.8275.8275.3	3	3.04	0	1.26E+05		(K)QLAVAE	(K)Q L A V/A E G K/P P E A/P K(G)		109.72	478.9337	1434.795	-0.0086	-6	6.14	24364.9	9.64	HUMAN	H0YIP0	Methionine--tRNA ligase, cytoplasmic (Fragment)
27260	dirMS_041712_NAR_50mM_plus2.8509.8509.3	3	3.04	1	1.69E+05	T70t	(K)KDPPAt	(K)K D P/P A t E H G N L\E K(K)	t:N-acetylglucosamine (T)	111.82	546.9401	1435.718	203.0882	5.4	5.44	16128.1	9.43	HUMAN	H7C375	WD repeat-containing and planar cell polarity effector protein fritz homolog (Fragment)
27261	dirMS_041712_NAR_50mM_plus2.9142.9142.3	3	3.04	1	2.23E+05	M28m	(K)LAEQAE	(K)L/A/E/Q A E R Y D D M A A A/m K(A)	m:Oxidized methionine	114.55	610.2777	1812.825	15.9931	-1	4.32	28196	4.76	HUMAN	P31946	14-3-3 protein beta/alpha
27262	dirMS_041712_NAR_120mM_minus.10593.10593.2	2	3.03	1	1.56E+05		(K)IKIIAPPE	(K)I K I|I/A\P/P E R(K)		111.57	518.8303	1036.651	0.002	1.9	8.75	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
27263	dirMS_041712_NAR_120mM_minus.17019.17019.4	4	3.03	0	6.85E+05		(K)HLEINP	(K)H\L\E\I N/P D H S\I I E T L/R(Q)		146.87	447.4904	1786.945	-0.0049	-2.7	5.27	85057.6	4.94	HUMAN	P07900	Heat shock protein HSP 90-alpha
27264	dirMS_041712_NAR_120mM_minus.4360.4360.2	2	3.03	0	3.95E+05		(K)HYAMQ	(K)H Y|A|M Q E\A\K(Q)		72.92	489.2307	977.451	0.0032	3.3	6.75	39309.6	4.32	HUMAN	F8WCY5	Reticulocalbin-2
27265	dirMS_041712_NAR_120mM_minus.7964.7964.3	3	3.03	1	4.85E+05	M215m	(R)MRGLH	(R)M R G L H D\m G V T V R(D)	m:Oxidized methionine	97.23	463.2365	1371.698	15.9966	1.2	9.37	26720.1	7.18	HUMAN	Q92994-4	Isoform 4 of Transcription factor IIIB 90 kDa subunit
27266	dirMS_041712_NAR_120mM_minus.9865.9865.3	3	3.03	1	9.45E+04		(R)SRAEAE	(R)S R A E\A E\S\M/Y Q/I K(Y)		108.07	471.5662	1412.684	0.0002	0.1	5.86	37296.3	5.3	HUMAN	F8VU64	Keratin, type II cytoskeletal 8
27267	dirMS_041712_NAR_20mM_minus.11833.11833.3	3	3.03	0	3.26E+05	M297m T2	(K)TLEVNP	(K)T L\E V N P m t|G E V R(L)	m:Oxidized methionine t:N-a	167.08	522.2561	1345.678	219.0757	0.9	4.53	85381.1	5	HUMAN	Q9NRJ7	Protocadherin beta-16
27268	dirMS_041712_NAR_20mM_minus.8906.8906.2	2	3.03	0	8.70E+03		(K)MDYNS	(K)M D/Y N S F Q A/V/T I\R(T)		137.63	722.8406	1444.689	-0.015	-10.4	5.59	135472.3	6.98	HUMAN	Q8IZF2-3	Isoform 3 of Probable G-protein coupled receptor 116
27269	dirMS_041712_NAR_30mM_minus2.14107.14107.2	2	3.03	0	1.75E+05		(R)VPELFA	(R)V/P|E L F A N R(G)		129.9	473.2631	945.515	0.0037	3.9	5.97	29854.8	9.49	HUMAN	C9J3R0	Regulator of chromosome condensation (Fragment)
27270	dirMS_041712_NAR_30mM_minus2.15181.15181.2	2	3.03	0	4.61E+04	M316m	(R)ISEQFTA	(R)I S|E Q/F/T A m F R(R)	m:Oxidized methionine	136.38	623.3014	1229.598	15.9972	1.8	6	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
27271	dirMS_041712_NAR_30mM_minus2.16873.16873.2	2	3.03	0	1.69E+05		(R)ASLEAAI	(R)A S L E A/A/I A/D A\E Q R(G)		144.92	672.8404	1344.675	-0.0019	-1.4	4.14	56607.4	5.37	HUMAN	F8VXB4	Keratin, type II cytoskeletal 8
27272	dirMS_041712_NAR_30mM_minus2.18105.18105.2	2	3.03	1	5.00E+05		(R)RSSLLTE	(R)R/S S L L T E/K(L)		153.77	467.2718	933.536	0	-0.1	8.75	376926.5	4.99	HUMAN	H0Y5W0	E3 ubiquitin-protein ligase HUWE1 (Fragment)
27273	dirMS_041712_NAR_30mM_minus2.18770.18770.2	2	3.03	0	1.61E+05		(K)ADGLLG	(K)A D G/L L G M F L K(R)		157.23	532.7918	1064.581	-0.0046	-4.3	5.88	70204.6	9.22	HUMAN	H7BYA9	ER membrane protein complex subunit 1 (Fragment)
27274	dirMS_041712_NAR_40mM_minus2.14400.14400.3	3	3.03	0	2.04E+05		(R)DIKPQN	(R)D I K P Q/N\L\L/L/D\P D/T A V L K(L)		169.47	631.6945	1893.069	-0.0002	-0.1	4.43	47257	9.38	HUMAN	P49841	Glycogen synthase kinase-3 beta
27275	dirMS_041712_NAR_40mM_minus2.7493.7493.2	2	3.03	1	1.82E+05	M73m	(K)mEVRAE	(K)m|E V R/A E E P K(E)	m:Oxidized methionine	120.23	552.7711	1088.541	15.9945	-0.4	4.78	38024.2	11.27	HUMAN	A6NL46	Putative UPF0607 protein ENSP00000332738
27276	dirMS_041712_NAR_50mM_minus2.8003.8003.3	3	3.03	1	1.21E+05		(K)TAVCDI	(K)T A|V/C D I/P P R G L K(M)	C:Carbamidomethylation	112.2	442.9126	1326.72	0.0034	2.6	8.41	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
27277	dirMS_041712_NAR_60mM_minus.17497.17497.3	3	3.03	1	1.17E+04		(R)KNVLCG	(R)K N\V L\C G N I/P/P/D L F A R(M)	C:Carbamidomethylation	156.23	571.9695	1713.911	-0.0165	-9.7	8.75	34425.5	9.08	HUMAN	P23193	Transcription elongation factor A protein 1
27278	dirMS_041712_NAR_60mM_minus.19236.19236.3	3	3.03	0	1.04E+06		(R)SLHDAL	(R)S L H\D A/L C V\L/A Q T/V/K(D)	C:Carbamidomethylation	171.22	518.9484	1554.831	-0.0002	-0.1	6.46	57204.9	6.01	HUMAN	F5GWF6	T-complex protein 1 subunit beta
27279	dirMS_041712_NAR_60mM_minus.5599.5599.3	3	3.03	1	1.63E+04	T9t	(-)MRPLTE	(-)M R P L T/E E/E t R/V M/F E K(I)	t:Phosphorylated T	87.02	659.3066	1895.935	79.9699	1.8	4.95	12624.3	8.83	HUMAN	J3QLW7	60S ribosome subunit biogenesis protein NIP7 homolog
27280	dirMS_041712_NAR_60mM_minus.6048.6048.3	3	3.03	0	1.54E+05		(K)SAWDQ	(K)S A W D Q P S/L P E G N|K(N)		92.13	476.895	1428.675	-0.0049	-3.5	4.37	214673.3	8.33	HUMAN	E7ENT4	Exophilin-5
27281	dirMS_041712_NAR_60mM_minus.7964.7964.3	3	3.03	1	1.80E+05		(K)EASKQA	(K)E A\S K Q A D\V N L/V/N A\K(L)		104.17	496.2639	1486.786	-0.0089	-6	6.17	57391.2	6.29	HUMAN	O43175	D-3-phosphoglycerate dehydrogenase
27282	dirMS_041712_NAR_60mM_minus.9263.9263.3	3	3.03	0	8.83E+04	T7t M9m	(R)EtQmTP	(R)E t Q m/T P L S L K(V)	t:N-acetylglucosamine (T) m:	111.42	456.229	1147.603	219.0697	-3.3	6.1	39660.8	9.13	HUMAN	H7C3K9	Melanophilin (Fragment)
27283	dirMS_041712_NAR_120mM_plus.16879.16879.4	4	3.03	1	1.67E+04		(R)IYLDLPQ	(R)I Y L D L P Q/N/F K I F V S E K(L)		140.92	489.2725	1954.068	-0.0003	-0.1	6.07	20345.4	4.53	HUMAN	B7Z3J5	E3 ubiquitin-protein ligase RNF14
27284	dirMS_041712_NAR_120mM_plus.23582.23582.4	4	3.03	2	1.65E+05	M21m	(R)IAIYELLF	(R)I A I/Y E L L F K E G V m/V A K K(D)	m:Oxidized methionine	178.22	492.7854	1952.129	15.9909	-2.1	8.43	19924.8	9.99	HUMAN	F6U211	40S ribosomal protein S10
27285	dirMS_041712_NAR_120mM_plus.3569.3569.3	3	3.03	2	3.85E+06	T274t	(R)EEKEREt	(R)E E K E/R/E t E(-)	t:N-acetylglucosamine (T)	59.63	418.1852	1049.475	203.0665	-10.3	4.5	31216.1	4.95	HUMAN	F8WBJ0	CDK5 regulatory subunit-associated protein 2
27286	dirMS_041712_NAR_120mM_plus.9533.9533.3	3	3.03	1	5.95E+05		(R)NYRDNY	(R)N Y R D N|Y\Q/A F C/K(W)	C:Carbamidomethylation	103.37	493.5549	1478.648	0.002	1.4	8.49	334221.3	6.44	HUMAN	P15924	Desmoplakin
27287	dirMS_041712_NAR_20mM_plus.16728.16728.3	3	3.03	0	1.52E+05	T678t	(R)LVVPtH	(R)L V\V/P t H G/N S S A/A V S T P/K(N)	t:Phosphorylated T	185.9	582.2872	1664.897	79.9504	-9.1	8.76	115054.2	9.41	HUMAN	F8VVB8	Meiosis arrest female protein 1
27288	dirMS_041712_NAR_20mM_plus.8463.8463.3	3	3.03	1	3.29E+05	S110s M11	(R)QDGsG	(R)Q D G s/G\V R A D V/V m K(F)	s:N-acetylglucosamine (S) m:	128.08	527.5924	1361.684	219.0785	2.6	5.96	46776.1	9.32	HUMAN	O60235	Transmembrane protease serine 11D
27289	dirMS_041712_NAR_30mM_plus2.10784.10784.2	2	3.03	0	1.01E+06		(R)GCAVVE	(R)G C|A|V V E F K(M)	C:Carbamidomethylation	109.38	455.2298	909.45	0.0025	2.7	6	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
27290	dirMS_041712_NAR_30mM_plus2.13111.13111.2	2	3.03	0	4.13E+05		(R)LGATILD	(R)L G/A/T\I L D/R(I)		121.83	429.7522	858.504	-0.0072	-8.4	5.84	43706.2	5.85	HUMAN	Q5VZM2	Ras-related GTP-binding protein B
27291	dirMS_041712_NAR_30mM_plus2.20878.20878.2	2	3.03	0	2.93E+05		(K)FIIPQIV	(K)F I|I P Q I V\K(Y)		164.35	479.3092	957.613	-0.002	-2.1	8.75	25445.8	5.52	HUMAN	A8MW50	L-lactate dehydrogenase (Fragment)
27292	dirMS_041712_NAR_30mM_plus2.4518.4518.2	2	3.03	0	2.50E+05	S124s	(K)SAPsMV	(K)S A|P/s M V D/R(L)	s:Phosphorylated S	73	471.6876	862.409	79.9592	-7.6	5.55	66838.5	6.6	HUMAN	Q8N584	Tetratricopeptide repeat protein 39C
27293	dirMS_041712_NAR_30mM_plus2.6822.6822.2	2	3.03	0	2.71E+05		(K)GDAGE	(K)G/D A\G E N G P/K(G)		90.4	422.6944	844.38	0.002	2.4	4.37	63751.6	8.36	HUMAN	A8MWQ5	Collagen-like Alzheimer amyloid plaque component
27294	dirMS_041712_NAR_30mM_plus2.9336.9336.2	2	3.03	0	1.37E+05		(R)SLAQAT	(R)S L A\Q A/T/S A/P R(A)		103.53	501.2717	1001.537	-0.0013	-1.3	9.47	10049.4	10.42	HUMAN	G3V4N9	Vasohibin-1
27295	dirMS_041712_NAR_30mM_plus2.9716.9716.2	2	3.03	0	6.65E+05		(K)QTTCW	(K)Q T/T|C/W/D|G V R(N)	C:Carbamidomethylation	104.97	561.7585	1122.5	0.0101	9	5.84	25868	9.48	HUMAN	Q9P016	Thymocyte nuclear protein 1
27296	dirMS_041712_NAR_40mM_plus2.10680.10680.3	3	3.03	1	6.95E+04	S71s	(R)AAAAAL	(R)A A|A\A/A L S\Q Q Q s L Q E R L R(L)	s:Phosphorylated S	127.65	640.9931	1840.999	79.966	-0.2	9.64	99930.3	8.46	HUMAN	J3KMW8	Cactin
27297	dirMS_041712_NAR_40mM_plus2.11703.11703.3	3	3.03	1	6.34E+04	T333t	(K)GtMPKE	(K)G t M P K E/V N L G L L A K(K)	t:N-acetylglucosamine (T)	135.05	558.6431	1470.835	203.0799	0.3	8.59	194702.2	5.43	HUMAN	Q9UKK3	Poly [ADP-ribose] polymerase 4
27298	dirMS_041712_NAR_40mM_plus2.17716.17716.3	3	3.03	0	2.50E+05		(R)DIKPQN	(R)D I K P Q N L\L|L D/P D T A V L K(L)		170.77	631.6874	1893.069	-0.0215	-11.4	4.43	47257	9.38	HUMAN	P49841	Glycogen synthase kinase-3 beta
27299	dirMS_041712_NAR_40mM_plus2.5417.5417.2	2	3.03	0	2.45E+05	M300m	(K)NMmAA	(K)N M m A A/C D|P R(H)	C:Carbamidomethylation m:Oxid	89.2	541.2145	1065.427	15.9943	-0.6	5.84	50199.4	4.75	HUMAN	A6NNZ2	Tubulin beta-8 chain-like protein LOC260334
27300	dirMS_041712_NAR_50mM_plus2.12924.12924.3	3	3.03	0	8.87E+04	K2955k	(K)FTSVTD	(K)F T/S V T D S L E Q V L A k(N)	k:Ubiquitin-K	135.15	551.2824	1537.811	114.0218	-12.8	4.37	990583.7	9.16	HUMAN	F8WCL5	Nebulin
27301	dirMS_041712_NAR_50mM_plus2.13007.13007.3	3	3.03	1	5.75E+05	K106k	(R)HHLLQG	(R)H H L L Q/G G/G A R D I S G T S k(E)	k:Ubiquitin-K	135.85	616.6476	1733.904	114.0241	-10.2	8.76	11643.8	10.79	HUMAN	J3KTB2	ATP synthase mitochondrial F1 complex assembly factor 2
27302	dirMS_041712_NAR_50mM_plus2.18322.18322.3	3	3.03	1	2.28E+05		(R)NNYRLA	(R)N N|Y R L A Q/A Y L D/K(Y)		164.42	490.2558	1468.754	-0.0015	-1	8.49	54557	9.04	HUMAN	O60882	Matrix metalloproteinase-20
27303	dirMS_041712_NAR_50mM_plus2.19099.19099.3	3	3.03	1	4.04E+05		(R)LKVPPAI	(R)L K/V/P P A I N Q F|T Q A L D R(Q)		169.77	604.3351	1811.017	-0.0266	-14.7	8.75	30166.2	10.79	HUMAN	P62424	60S ribosomal protein L7a
27304	dirMS_041712_NAR_60mM_plus.10128.10128.3	3	3.03	0	2.28E+05		(R)ENNTVS	(R)E N N/T V S N I H/P\K(L)		111.4	418.2158	1252.628	0.0048	3.8	6.85	121492.5	9.43	HUMAN	O95625	Zinc finger and BTB domain-containing protein 11
27305	dirMS_041712_NAR_60mM_plus.18005.18005.3	3	3.03	0	1.57E+05		(K)ILLQPTS	(K)I L L Q P T S S|I/S/T T K(T)		151.27	463.6084	1388.8	0.0111	8	8.75	192522.7	5.74	HUMAN	Q9P1Z9	Uncharacterized protein C9orf174
27306	dirMS_041712_NAR_60mM_plus.19162.19162.3	3	3.03	0	8.59E+04		(K)LYFKPIG	(K)L Y/F K P I G D|P V F A R(D)		157.82	508.2852	1522.842	-0.0006	-0.4	8.59	228081	6.98	HUMAN	A6NHR9	Structural maintenance of chromosomes flexible hinge domain-containing protein 1
27307	dirMS_041712_NAR_60mM_plus.7444.7444.3	3	3.03	1	1.00E+06		(K)GGETIK	(K)G G|E T/I K/Q L\Q E/R(A)		97.45	420.23	1258.675	0.0005	0.4	6.14	70034.8	6.89	HUMAN	B4DT31	Far upstream element-binding protein 1
27308	dirMS_041712_NAR_120mM_minus.10916.10916.4	4	3.02	1	2.32E+05	M976m	(K)QPGLV	(K)Q P G L V m E\R A/L/L S D E/R(V)	m:Oxidized methionine	113.65	433.2296	1713.895	16.0013	3.7	4.68	114344.7	7.28	HUMAN	J3QRV5	Lethal(2) giant larvae protein homolog 2
27309	dirMS_041712_NAR_120mM_minus.13683.13683.2	2	3.02	0	2.18E+05	M644m	(K)mFVTSS	(K)m F V T/S S H/L Q\L/K(S)	m:Oxidized methionine	129.08	653.8514	1290.688	16.0081	10.1	8.52	256666.6	6.03	HUMAN	O60287	Nucleolar pre-ribosomal-associated protein 1
27310	dirMS_041712_NAR_120mM_minus.20143.20143.4	4	3.02	1	2.40E+05		(R)GIEKPPF	(R)G I E K/P P\F E L P D/F I K R(T)		166.33	447.2523	1785.99	-0.0024	-1.4	6.18	98282.7	5.49	HUMAN	E9PPJ0	Splicing factor 3B subunit 2
27311	dirMS_041712_NAR_120mM_minus.4582.4582.2	2	3.02	0	7.49E+05		(R)HSDGNL	(R)H/S\D G N L\C\V K(V)	C:Carbamidomethylation	73.97	515.2423	1029.478	-0.0009	-0.9	6.74	7781.8	6.82	HUMAN	E9PE20	Signal recognition particle 9 kDa protein
27312	dirMS_041712_NAR_120mM_minus.5705.5705.2	2	3.02	0	9.25E+04		(R)AEAEAG	(R)A E/A|E A G S P R P D|P R(E)		84.4	676.8296	1352.655	-0.0034	-2.5	4.68	558007.1	5.44	HUMAN	P58107	Epiplakin
27313	dirMS_041712_NAR_120mM_minus.8170.8170.3	3	3.02	0	2.50E+05		(R)VTEALS	(R)V T/E/A L S A\N F N H K(K)		99.05	444.2318	1330.675	0.0059	4.4	6.72	82753.4	5.9	HUMAN	E7EV89	Lysine-specific demethylase 5A (Fragment)
27314	dirMS_041712_NAR_120mM_minus.8238.8238.3	3	3.02	1	4.70E+05		(K)TDEPGK	(K)T D/E/P G K Y\T A N R(G)		99.97	417.8682	1251.596	-0.0064	-5.1	5.73	18089.3	4.93	HUMAN	Q5VSP4	Putative lipocalin 1-like protein 1
27315	dirMS_041712_NAR_20mM_minus.8594.8594.2	2	3.02	0	8.25E+04		(R)YEIEETE	(R)Y/E|I E E/T/E T V T K(S)		134.9	671.3246	1341.642	-0.0001	-0.1	4.09	54214.9	5.66	HUMAN	C9J813	Caldesmon (Fragment)
27316	dirMS_041712_NAR_30mM_minus2.12258.12258.2	2	3.02	0	2.22E+05		(R)IFYDMK	(R)I F/Y/D/M K(V)		119.33	408.702	816.396	0.0007	0.8	5.83	15739.2	9.3	HUMAN	F6RFD5	Destrin
27317	dirMS_041712_NAR_30mM_minus2.14208.14208.2	2	3.02	0	8.29E+04		(K)DSNFAG	(K)D S N/F/A/G D L/V R(N)		130.45	547.265	1093.527	-0.0045	-4.2	4.21	103258.6	6.54	HUMAN	Q86XP3	ATP-dependent RNA helicase DDX42
27318	dirMS_041712_NAR_30mM_minus2.17635.17635.2	2	3.02	0	1.17E+05	K131k	(K)LFSKPD	(K)L/F S K P D/G k(L)	k:Ubiquitin-K	150.63	503.2741	891.493	114.0475	4.5	8.59	58388.1	6.04	HUMAN	Q86WT6	E3 ubiquitin-protein ligase TRIM69
27319	dirMS_041712_NAR_30mM_minus2.5671.5671.2	2	3.02	0	1.60E+05	T854t	(K)tDQQG	(K)t/D Q Q/G D T/P R(Q)	t:Phosphorylated T	85.28	549.2137	1017.46	79.9605	-5.3	4.21	102170	8.79	HUMAN	A8MVN1	Diacylglycerol kinase zeta
27320	dirMS_041712_NAR_30mM_minus2.9152.9152.2	2	3.02	0	3.92E+04		(K)VDTKPS	(K)V D/T K/P S S E/K(K)		103.85	495.7528	990.51	-0.0119	-12	6.04	181960.4	6.43	HUMAN	A2VDJ0	Transmembrane protein 131-like
27321	dirMS_041712_NAR_30mM_minus2.9798.9798.2	2	3.02	0	4.12E+05		(R)LLSSEDS	(R)L/L S S E D S/A K(V)		107.73	475.2457	949.484	0.0005	0.5	4.37	15363	4.76	HUMAN	C9JFK0	Zinc finger CW-type PWWP domain protein 2 (Fragment)
27322	dirMS_041712_NAR_40mM_minus2.11365.11365.3	3	3.02	0	8.13E+03	T583t	(K)YQAIFD	(K)Y Q A I F D N/T T/S/L t D/K(H)	t:N-acetylglucosamine (T)	149.95	607.293	1616.78	203.0842	2.7	4.21	76500.1	5.92	HUMAN	Q13546	Receptor-interacting serine/threonine-protein kinase 1
27323	dirMS_041712_NAR_50mM_minus2.13544.13544.3	3	3.02	2	6.86E+04		(K)EAGKGG	(K)E A/G/K G G V A D S R E L K P/M I/K(-)		144.72	629.345	1886.016	0.004	2.1	8.59	74551.1	9.65	HUMAN	Q8WWI5-3	Isoform 3 of Choline transporter-like protein 1
27324	dirMS_041712_NAR_50mM_minus2.8647.8647.3	3	3.02	0	5.96E+04	M272m	(K)MISGm	(K)M/I S/G m Y M G E L V R(L)	m:Oxidized methionine	117.43	468.2185	1386.658	15.9831	-8.4	5.75	100397.6	5.71	HUMAN	E9PB90	Hexokinase-2
27325	dirMS_041712_NAR_60mM_minus.13520.13520.3	3	3.02	0	3.61E+05	M330m	(K)LKPmYG	(K)L K P m Y G P G/Y T\G/L K(N)	m:Oxidized methionine	135.32	480.9239	1424.761	15.9965	1.1	9.53	98067.1	5.34	HUMAN	Q92995	Ubiquitin carboxyl-terminal hydrolase 13
27326	dirMS_041712_NAR_60mM_minus.18202.18202.3	3	3.02	1	1.21E+05	S6s	(-)XAEQQs	(-)X/A/E\Q Q s/K A V F G R(S)	s:N-acetylglucosamine (S)	162.82	512.9419	1333.722	203.0889	6.2	8.75	21418.7	5.32	HUMAN	K7EIU2	Serine/threonine-protein kinase ULK2 (Fragment)
27327	dirMS_041712_NAR_60mM_minus.6387.6387.2	2	3.02	1	1.72E+05		(K)IIAPPER	(K)I I|A/P P E R K(Y)		94	462.287	923.567	-0.0006	-0.6	8.75	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
27328	dirMS_041712_NAR_120mM_plus.7217.7217.3	3	3.02	0	3.53E+05	K136k	(K)MGPFLT	(K)M G/P F L T S/Q E k(E)	k:Ubiquitin-K	91.08	417.8755	1137.561	114.0511	6.5	5.75	162425.9	6.1	HUMAN	H0YME5	Eukaryotic translation initiation factor 2-alpha kinase 4 (Fragment)
27329	dirMS_041712_NAR_20mM_plus.10594.10594.3	3	3.02	0	2.90E+04		(R)AQPSVS	(R)A Q\P S V S/L/G A A Y R(A)		145.98	407.2191	1219.643	-0.0002	-0.2	8.79	69661.6	9.75	HUMAN	Q96PK6	RNA-binding protein 14
27330	dirMS_041712_NAR_20mM_plus.12087.12087.2	2	3.02	0	5.00E+05	S200s T20	(K)sLALSPG	(K)s L A L S P G W/S/t V A R(S)	s:Phosphorylated S t:Phosph	156.6	752.8363	1344.727	159.9383	3.7	9.47	24142.6	9.52	HUMAN	G3V3R6	Galectin-3
27331	dirMS_041712_NAR_20mM_plus.12624.12624.2	2	3.02	0	1.23E+05		(R)GVEICIA	(R)G V\E I|C/I/A T/P G R(L)	C:Carbamidomethylation	159.2	586.8084	1172.609	0.0003	0.3	6	61018.6	9.44	HUMAN	B4DLW8	Probable ATP-dependent RNA helicase DDX5
27332	dirMS_041712_NAR_20mM_plus.14049.14049.2	2	3.02	0	1.13E+05	M185m	(K)LAVNm	(K)L A V/N m|V/P F P/R(L)	m:Oxidized methionine	169.77	580.3169	1143.634	15.9922	-2.3	9.75	42230.8	4.77	HUMAN	A6NKZ8	Putative tubulin beta chain-like protein ENSP00000290377
27333	dirMS_041712_NAR_20mM_plus.14400.14400.2	2	3.02	0	6.82E+04		(R)ELAQQV	(R)E L A/Q Q V Q Q\V\A D/D Y|G K(C)		170.75	846.4161	1691.824	0.0014	0.8	4.03	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
27334	dirMS_041712_NAR_20mM_plus.14859.14859.2	2	3.02	0	6.83E+04		(R)IMNTFS	(R)I M N T/F/S V V/P S|P K(V)		173.27	660.3527	1319.703	-0.0047	-3.5	8.75	42831.5	4.86	HUMAN	A8K854	HCG1983504, isoform CRA_f
27335	dirMS_041712_NAR_20mM_plus.16227.16227.3	3	3.02	0	1.70E+05		(K)DAGTIA	(K)D A\G T I|A G\L/N V/L/R(I)		183.65	400.5627	1199.674	-0.0007	-0.6	5.84	17973	5.16	HUMAN	E9PI65	Heat shock cognate 71 kDa protein (Fragment)
27336	dirMS_041712_NAR_20mM_plus.6742.6742.2	2	3.02	0	3.36E+04		(R)SLASPH	(R)S L A|S P H T/S G T M|R(T)		111.17	622.8147	1244.605	0.0169	13.6	9.49	19678.9	11.3	HUMAN	F5GYW2	Acetoacetyl-CoA synthetase
27337	dirMS_041712_NAR_20mM_plus.6780.6780.2	2	3.02	0	2.68E+05		(R)IANFQE	(R)I A|N/F Q/E K(L)		111.43	425.2226	849.447	-0.0086	-10.1	6	25730.9	6.52	HUMAN	A0PK11	Clarin-2
27338	dirMS_041712_NAR_30mM_plus2.17169.17169.2	2	3.02	0	1.48E+05		(K)WPLYM	(K)W/P L/Y M/S T/K(N)		143.55	513.2647	1025.513	0.0097	9.4	8.59	45578.2	7.83	HUMAN	B4DFL2	Isocitrate dehydrogenase [NADP]
27339	dirMS_041712_NAR_30mM_plus2.18640.18640.3	3	3.02	0	1.66E+05		(-)SDVLELT	(-)S D V\L E L T D D/N/F E S R(I)		150.85	547.2595	1639.745	0.0194	11.8	3.77	13747.3	6.8	HUMAN	H7BZJ3	Thioredoxin (Fragment)
27340	dirMS_041712_NAR_30mM_plus2.7693.7693.2	2	3.02	0	1.97E+05		(K)ITLTCGR	(K)I/T|L/T C G R(D)	C:Carbamidomethylation	93.9	410.7181	820.434	-0.0056	-6.9	9.75	62195.8	5.63	HUMAN	B0YIW6	Archain 1, isoform CRA_a
27341	dirMS_041712_NAR_40mM_plus2.15300.15300.3	3	3.02	1	8.47E+03		(K)QGGLGF	(K)Q G G L/G P M N I/P L V S D P K R(T)		156.17	593.6623	1778.958	0.0142	8	8.75	22338.2	8.65	HUMAN	Q06830	Peroxiredoxin-1
27342	dirMS_041712_NAR_40mM_plus2.17320.17320.3	3	3.02	0	2.47E+04		(R)GTEDITS	(R)G T E D\I/T S/P/H G I/P L D\L/L D R(V)		169.42	650.3372	1948.997	-0.0004	-0.2	4.22	35067	5.55	HUMAN	E7ETR0	RuvB-like 1
27343	dirMS_041712_NAR_40mM_plus2.6015.6015.2	2	3.02	0	2.48E+05		(R)MGANN	(R)M G A|N N L/E R(M)		94.25	452.7221	904.431	0.0064	7.1	5.75	77799.7	9.09	HUMAN	P52272	Heterogeneous nuclear ribonucleoprotein M
27344	dirMS_041712_NAR_40mM_plus2.8143.8143.2	2	3.02	0	4.70E+04	T65t	(R)LAtAMK	(R)L/A|t/A M K(L)	t:N-acetylglucosamine (T)	108.52	419.2273	634.359	203.0881	10.4	8.75	15599.4	8.24	HUMAN	J3QRX8	Angiotensin-converting enzyme (Fragment)
27345	dirMS_041712_NAR_40mM_plus2.9950.9950.3	3	3.02	0	1.48E+04		(R)AQIFAN	(R)A Q\I F A N T V/D N/A R(I)		122.43	440.561	1319.67	-0.0018	-1.4	5.88	43773.3	5.26	HUMAN	F8VZY9	Keratin, type I cytoskeletal 18
27346	dirMS_041712_NAR_50mM_plus2.19707.19707.3	3	3.02	2	7.67E+04		(K)DLYGAK	(K)D L|Y/G A K L I A Q K C Q V R(N)	C:Carbamidomethylation	172.23	588.3256	1762.963	-0.001	-0.6	9.7	18141.8	10.11	HUMAN	E5RGP0	rRNA-processing protein UTP23 homolog (Fragment)
27347	dirMS_041712_NAR_60mM_plus.10635.10635.3	3	3.02	1	3.21E+04		(R)LRQLAE	(R)L R Q L A E|E|D\L/A Q Q R(A)		112.7	523.9486	1569.834	-0.0031	-2	4.68	533778	5.74	HUMAN	Q15149	Plectin
27348	dirMS_041712_NAR_60mM_plus.13129.13129.3	3	3.02	0	1.08E+05		(K)DAHNAL	(K)D A H N A\L L/D\I/Q/S/S G R(A)		125.67	499.594	1496.745	0.0223	14.9	5.21	106155.7	5.45	HUMAN	B5ME19	Eukaryotic translation initiation factor 3 subunit C
27349	dirMS_041712_NAR_60mM_plus.13682.13682.3	3	3.02	1	4.71E+05		(R)KYEMFA	(R)K\Y E M F\A\Q/T|L/Q Q S R(G)		128.72	543.9389	1629.805	-0.0032	-2	8.59	90004.9	5.14	HUMAN	P55072	Transitional endoplasmic reticulum ATPase
27350	dirMS_041712_NAR_60mM_plus.17017.17017.3	3	3.02	0	3.49E+05	K619k	(R)LAAAIG	(R)L A A A\I G k H/S E S V/K(T)	k:Ubiquitin-K	146.07	475.5976	1310.743	114.0356	-5.2	8.6	94819.8	8.87	HUMAN	Q5CZ79	Ankyrin repeat domain-containing protein 20B
27351	dirMS_041712_NAR_60mM_plus.17247.17247.3	3	3.02	1	3.41E+05		(K)YQLDKD	(K)Y Q|L D/K/D G\V V L F K(K)		146.82	475.5976	1424.778	-0.0001	-0.1	5.96	51524.1	4.82	HUMAN	F5H8J2	Protein disulfide-isomerase
27352	dirMS_041712_NAR_60mM_plus.19973.19973.3	3	3.02	1	5.38E+03	K689k	(K)DMEQH	(K)D M E Q H/R A L I E k/S K(R)	k:Ubiquitin-K	164.25	566.9611	1584.816	114.0525	5.6	6.76	112821.3	9.27	HUMAN	Q63HK3	Zinc finger protein with KRAB and SCAN domains 2
27353	dirMS_041712_NAR_60mM_plus.5063.5063.3	3	3.02	0	2.67E+05		(R)YINTEH	(R)Y/I|N T E/H/G G S Q A R(F)		83.22	444.8825	1332.629	0.0038	2.9	6.75	87447.6	6.44	HUMAN	Q15437	Protein transport protein Sec23B
27354	dirMS_041712_NAR_120mM_minus.5958.5958.3	3	3.01	1	2.07E+04		(K)NVICDK	(K)N V|I/C D/K C E G/R(G)	C:Carbamidomethylation	86.4	417.525	1250.562	-0.0012	-0.9	6.07	45609.1	6.66	HUMAN	P31689	DnaJ homolog subfamily A member 1

27355	dirMS_041712_NAR_20mM_minus.12452.12452.3	3	3.01	1	8.32E+04	S587s	(K)VVSTPG	(K)V V S T P G K\T/V/P V P s G K(V)	s:Phosphorylated S	172.67	511.6052	1452.842	79.959	-4.8	10	103196.3	8.73	HUMAN	Q7Z2K8	G protein-regulated inducer of neurite outgrowth 1
27356	dirMS_041712_NAR_30mM_minus2.18952.18952.2	2	3.01	0	1.91E+05		(K)CFSVLG	(K)C/F/S V/L|G F C/K(S)	C:Carbamidomethylation	157.42	559.2673	1117.517	0.0104	9.3	8.75	83273.6	5.55	HUMAN	P13010	X-ray repair cross-complementing protein 5
27357	dirMS_041712_NAR_30mM_minus2.6586.6586.2	2	3.01	0	1.67E+05	N6900n	(R)ESEnIR	(R)E S E/n I R(I)	n:N-acetylglucosamine (N)	90.17	475.7203	747.363	203.0702	-9.7	4.53	4024332	6.06	HUMAN	K7ENY1	Titin
27358	dirMS_041712_NAR_30mM_minus2.8825.8825.2	2	3.01	0	5.08E+05	S365s	(R)YGVSITL	(R)Y G|V S I T L s G R(T)	s:Phosphorylated S	101.4	566.7699	1052.574	79.959	-6.4	8.75	52585.6	5.66	HUMAN	E9PRT6	Pancreatic lipase-related protein 1
27359	dirMS_041712_NAR_40mM_minus2.12765.12765.3	3	3.01	0	8.16E+03		(K)EAPCVLI	(K)E A\P C V L I\Y/I/P D G H T K(E)	C:Carbamidomethylation	158.37	571.6284	1712.868	0.003	1.8	5.32	172185.3	7.06	HUMAN	P07814	Bifunctional glutamate/proline--tRNA ligase
27360	dirMS_041712_NAR_40mM_minus2.8232.8232.3	3	3.01	0	2.47E+05	M35m	(K)AASDIA	(K)A A S/D I A m T/E L/P P T H P I R(L)	m:Oxidized methionine	128.65	612.6484	1819.937	15.9936	-0.7	5.32	12926.1	4.4	HUMAN	K7EM20	14-3-3 protein epsilon (Fragment)
27361	dirMS_041712_NAR_50mM_minus2.13156.13156.3	3	3.01	1	1.01E+05		(R)TEMENE	(R)T/E/M E N E/F/V/L I K K(D)		142.92	494.2621	1480.772	0.0002	0.1	4.78	13588.1	4.66	HUMAN	F8VP67	Keratin, type II cytoskeletal 8 (Fragment)
27362	dirMS_041712_NAR_50mM_minus2.15702.15702.3	3	3.01	0	1.01E+05		(-)MAPSTA	(-)M A P S T A V S V V/S D S/I/K(V)		157.95	497.9267	1491.772	-0.0068	-4.5	5.59	36888.4	9.6	HUMAN	B1AHC5	PHD finger protein 21B
27363	dirMS_041712_NAR_50mM_minus2.8518.8518.3	3	3.01	1	4.13E+04	M88m	(K)ALDDmI	(K)A L/D D m/I S T L K K(I)	m:Oxidized methionine	116.17	417.5602	1234.671	15.9949	0	6	56186.7	5.47	HUMAN	B4DUR8	T-complex protein 1 subunit gamma
27364	dirMS_041712_NAR_60mM_minus.18068.18068.3	3	3.01	0	7.10E+03		(R)CRPQED	(R)C R P Q E D\T G W\V/L/F/P V N K(A)	C:Carbamidomethylation	161.5	649.3238	1945.959	-0.002	-1.1	6.07	558007.1	5.44	HUMAN	P58107	Epiplakin
27365	dirMS_041712_NAR_60mM_minus.7121.7121.3	3	3.01	1	2.74E+05		(R)IVDGKV	(R)I V D G K V/V/S E T N D\T K(V)		97.95	502.2642	1504.785	-0.0073	-4.8	4.56	48057	5.34	HUMAN	P05783	Keratin, type I cytoskeletal 18
27366	dirMS_041712_NAR_60mM_minus.8841.8841.3	3	3.01	1	1.02E+05		(K)SAVGFD	(K)S A/V/G F D Y Q G K\T E K(H)		108.85	477.2381	1429.696	0.004	2.8	5.79	25153.2	6.6	HUMAN	H7C314	Src substrate cortactin (Fragment)
27367	dirMS_041712_NAR_60mM_minus.9030.9030.3	3	3.01	0	6.62E+05		(R)ADGKPY	(R)A D G K P Y S G/P V/E A R(V)		111.03	449.5563	1346.67	-0.0156	-11.6	6.11	129136.9	9.58	HUMAN	K7EPJ4	Cartilage intermediate layer protein 2 C1
27368	dirMS_041712_NAR_120mM_plus.20657.20657.4	4	3.01	2	3.87E+05		(R)TLAEIAK	(R)T L A E/I A K V E/L D N M/P L R G K(Q)		161.73	500.2814	1998.105	-0.0015	-0.7	5.85	23729.5	9.89	HUMAN	C9IZL7	Non-POU domain-containing octamer-binding protein (Fragment)
27369	dirMS_041712_NAR_120mM_plus.8389.8389.2	2	3.01	0	3.77E+04		(R)HSVGVV	(R)H/S/V/G V V I G R(S)		97.47	462.2744	923.542	-0.0006	-0.7	9.75	73399.3	6.86	HUMAN	Q92945	Far upstream element-binding protein 2
27370	dirMS_041712_NAR_120mM_plus.9431.9431.2	2	3.01	1	5.81E+05		(K)ERLEGF	(K)E R L\E G F|V\K(T)		102.77	489.2725	977.542	-0.0037	-3.8	6.24	132819.4	9.48	HUMAN	Q8N1G1	RNA exonuclease 1 homolog
27371	dirMS_041712_NAR_20mM_plus.13611.13611.2	2	3.01	0	5.50E+04		(K)IFVGGLS	(K)I F|V/G G L/S P D T|P E E K(I)		165.28	744.8731	1488.758	-0.0191	-12.8	4.14	33782.7	8.78	HUMAN	B4DTC3	Heterogeneous nuclear ribonucleoprotein D0
27372	dirMS_041712_NAR_20mM_plus.17205.17205.2	2	3.01	0	1.45E+04		(R)LLALNSL	(R)L L|A L/N S L Y|S P K(I)		189.98	609.8583	1218.709	0.0001	0.1	8.59	470342.8	6.83	HUMAN	E7EUY0	DNA-dependent protein kinase catalytic subunit
27373	dirMS_041712_NAR_20mM_plus.6761.6761.2	2	3.01	0	2.15E+05	M132m	(R)DmVGIA	(R)D m\V|G\I\A/Q T G S G K(T)	m:Oxidized methionine	112.18	590.2864	1163.573	15.993	-1.6	5.84	73202	9.19	HUMAN	C9JMU5	Probable ATP-dependent RNA helicase DDX17
27374	dirMS_041712_NAR_20mM_plus.8861.8861.2	2	3.01	0	8.98E+05	M239m	(K)EITALAP	(K)E I/T A/L/A P S T m\K(I)	m:Oxidized methionine	132.37	589.309	1161.618	15.9923	-2.2	6.1	32616.5	5.18	HUMAN	A6NL76	Actin, alpha skeletal muscle
27375	dirMS_041712_NAR_30mM_plus2.19678.19678.2	2	3.01	0	2.42E+05	S78s	(K)ALGQLIs	(K)A L|G\Q L\I s K(Y)	s:N-acetylglucosamine (S)	156.55	516.7959	829.514	203.0703	-8.7	8.8	66268.9	9.06	HUMAN	Q969N2	GPI transamidase component PIG-T
27376	dirMS_041712_NAR_30mM_plus2.21291.21291.2	2	3.01	0	7.29E+03		(K)GQVWI	(K)G Q/V/W/I\N G F N L G R(Y)		166.3	680.8538	1360.712	-0.0117	-8.6	9.75	60881	6.36	HUMAN	E7EQ29	Beta-galactosidase
27377	dirMS_041712_NAR_40mM_plus2.19687.19687.3	3	3.01	0	1.06E+06		(R)GLAPVQ	(R)G L|A P V Q A Y L H I P D I I/K(V)		183.65	583.3378	1748.011	-0.0117	-6.7	6.74	58266.4	9.46	HUMAN	B4DN00	Pyruvate carboxylase, mitochondrial
27378	dirMS_041712_NAR_40mM_plus2.6103.6103.2	2	3.01	0	5.46E+04	S132s	(R)LSPTAsR	(R)L/S|P T/A s/R(S)	s:Phosphorylated S	94.97	406.1921	731.405	79.9723	7.4	9.75	34653.1	11.06	HUMAN	Q99988	Growth/differentiation factor 15
27379	dirMS_041712_NAR_50mM_plus2.11550.11550.3	3	3.01	0	2.85E+05		(R)FCGLPQ	(R)F/C/G L P/Q P E T V G Q L G T V L R(N)	C:Carbamidomethylation	128.32	658.0091	1972.032	-0.0193	-9.8	6	84837	9.79	HUMAN	P05164	Myeloperoxidase
27380	dirMS_041712_NAR_50mM_plus2.13089.13089.3	3	3.01	1	2.93E+05	S1001s	(K)IIRRYVS	(K)I I R\R Y\V S/s E G T E K(E)	s:N-acetylglucosamine (S)	136.75	580.9801	1537.833	203.0925	7.5	8.59	118870	4.85	HUMAN	E9PCH6	Ankyrin-2
27381	dirMS_041712_NAR_50mM_plus2.7390.7390.3	3	3.01	1	4.24E+04		(K)DFGNAL	(K)D F G N A L N W/A K Q A/K(I)		105.02	488.2509	1462.744	-0.0056	-3.8	8.59	149959.2	6.73	HUMAN	C9JKF1	Sterile alpha motif domain-containing protein 9 (Fragment)
27382	dirMS_041712_NAR_60mM_plus.10530.10530.3	3	3.01	0	9.43E+04		(R)SSGPYG	(R)S S G P/Y/G G G G Q Y F/A K P R(N)		112.77	543.6023	1628.782	0.0108	6.6	9.7	33268.7	9.31	HUMAN	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1
27383	dirMS_041712_NAR_60mM_plus.16706.16706.3	3	3.01	1	3.09E+05		(-)MKLNISF	(-)M K L N I S F/P/A T/G C Q K(L)	C:Carbamidomethylation	142.9	532.2733	1594.808	-0.0026	-1.7	10	10471.9	5.4	HUMAN	A2A3R7	40S ribosomal protein S6
27384	dirMS_041712_NAR_60mM_plus.17226.17226.3	3	3.01	0	5.80E+05	K731k	(K)VAETVTI	(K)V A E/T V T k/I L R(K)	k:Ubiquitin-K	147.62	415.2483	1129.694	114.0364	-5.2	8.72	263152.8	8.75	HUMAN	A6NE01	Protein FAM186A
27385	dirMS_041712_NAR_60mM_plus.17471.17471.3	3	3.01	1	5.45E+05		(R)LKDLEAL	(R)L K D L E A|L/L/N S K(E)		147.8	415.2483	1243.726	0.0047	3.8	6.07	63136.9	5.83	HUMAN	D6RAQ3	Prelamin-A/C
27386	dirMS_041712_NAR_60mM_plus.17746.17746.3	3	3.01	0	9.06E+04		(K)TFKPIDL	(K)T F\K/P/I D L S D/L K(R)		149.98	426.2424	1276.715	-0.0021	-1.6	5.63	10920	9.39	HUMAN	C9JLW8	Protein FAM195B
27387	dirMS_041712_NAR_60mM_plus.19017.19017.3	3	3.01	1	1.44E+04	K817k	(R)RLPDQF	(R)R\L P D Q F/S k\L A D/R(I)	k:Ubiquitin-K	157.23	520.622	1445.786	114.0655	14.5	8.75	137811.6	6.21	HUMAN	B7Z7Y1	Rap guanine nucleotide exchange factor 6
27388	dirMS_041712_NAR_60mM_plus.7468.7468.3	3	3.01	1	7.00E+05	M176m	(K)GmVQA	(K)G m/V Q A V R L I A E\G K(A)	m:Oxidized methionine	97.73	463.2618	1371.778	15.9932	-1.3	8.75	99683.2	5.63	HUMAN	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase
27389	dirMS_041712_NAR_60mM_plus.7780.7780.3	3	3.01	1	2.95E+05	T136t	(K)ISKVECG	(K)I S K V/E/C G\F A t I/K(D)	C:Carbamidomethylation t:N-ace	99.02	519.2682	1352.724	203.0658	-8.7	8.59	35163.4	5.67	HUMAN	B4E1F4	ER degradation-enhancing alpha-mannosidase-like 2
27390	dirMS_041712_NAR_60mM_plus.8866.8866.3	3	3.01	0	2.16E+05		(R)SVITFGS	(R)S V I T F G S/Y/S/P R(I)		103.85	405.2162	1213.621	0.0129	10.6	8.46	65982.3	8.42	HUMAN	Q9NSB2	Keratin, type II cuticular Hb4
27391	dirMS_041712_NAR_60mM_minus.9558.9558.3	3	3	0	2.04E+05	N516n	(R)ISGALFT	(R)I/S|G\A L F T n D K(F)	n:N-acetylglucosamine (N)	112.4	423.5497	1065.557	203.077	-1.8	5.84	228081	6.98	HUMAN	A6NHR9	Structural maintenance of chromosomes flexible hinge domain-containing protein 1