Type of file:	table
Label:	Table 1
Filename:	PubMed_17911086_Hojlund_Table1.pdf

Supplemental Table I. Proteins identified in human muscle biopsy tissue

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
1	IPI00000690; IPI00157908	AIFM1	609	613	611	6.6E+04	6.7E+04	6.7E+04	28.4	12	1	1	1	1	ISOFORM 1 OF APOPTOSIS-INDUCING FACTOR 1, MITOCHONDRIAL PRECURSOR.; ISOFORM 3 OF APOPTOSIS-INDUCING FACTOR 1, MITOCHONDRIAL PRECURSOR.	O95831; Q1L6K4; Q1L6K6; Q5JUZ7; Q5RZ99; Q5RZA0; Q6I9X6; Q9Y3I3; Q9Y3I4	AIFM1_HUMAN; Q1L6K4_HUMAN; Q1L6K6_HUMAN; Q5RZ99_HUMAN; Q5RZA0_HUMAN
2	IPI00000792; IPI00641565; IPI00642016; IPI00647366	CRYZ	206	329	268	2.2E+04	3.5E+04	2.9E+04	18.4	3	1	1	1	0	QUINONE OXIDOREDUCTASE.; 26 KDA PROTEIN.; 22 KDA PROTEIN.; 32 KDA PROTEIN.	Q08257; Q53FT0; Q59EU7; Q6NSK9	; QOR_HUMAN
3	IPI00000811; IPI00789119; IPI00796198	PSMB6	114	239	181	1.2E+04	2.5E+04	1.9E+04	13.4	3	0	0	1	1	PROTEASOME SUBUNIT BETA TYPE 6 PRECURSOR.; 20 KDA PROTEIN.; 12 KDA PROTEIN.	P28072; Q6IAT9; Q96J55	; PSB6_HUMAN; Q6IAT9_HUMAN
4	IPI00000816	YWHAE	255	255	255	2.9E+04	2.9E+04	2.9E+04	37.6	9	1	1	1	1	14-3-3 PROTEIN EPSILON.	P29360; P42655; P62258; Q4VJB6; Q53XZ5; Q63631	1433E_HUMAN; Q4VJB6_HUMAN; Q53XZ5_HUMAN
5	IPI00000874; IPI00640741	PRDX1	171	199	185	1.9E+04	2.2E+04	2.1E+04	54.4	12	1	1	1	1	PEROXIREDOXIN-1.; 19 KDA PROTEIN.	P35703; Q06830; Q2V576; Q5T154; Q5T155	; PRDX1_HUMAN
6	IPI00000875; IPI00747497	EEF1G	436	437	437	5.0E+04	5.0E+04	5.0E+04	14.0	5	1	1	1	1	ELONGATION FACTOR 1-GAMMA.; 50 KDA PROTEIN.	P26641; Q2F838; Q2F840; Q53YD7; Q6PJ62; Q6PK31; Q96CU2; Q9P196	; EF1G_HUMAN; Q2F838_HUMAN; Q2F840_HUMAN; Q53YD7_HUMAN
7	IPI00001091	AFG3L2	797	797	797	8.9E+04	8.9E+04	8.9E+04	10.5	7	1	1	1	1	AFG3-LIKE PROTEIN 2.	Q6P1L0; Q8TA92; Q9Y4W6	AFG32_HUMAN; Q8TA92_HUMAN
8	IPI00001539	ACAA2	397	397	397	4.2E+04	4.2E+04	4.2E+04	39.0	11	1	1	1	1	3-KETOACYL-COA THIOLASE, MITOCHONDRIAL.	P42765; Q9BUT6	THIM_HUMAN
9	IPI00001589	TIMM13	95	95	95	1.1E+04	1.1E+04	1.1E+04	26.3	2	0	0	1	0	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM13.	P62206; Q9UHL8; Q9WTL1; Q9Y5L4	TIM13_HUMAN
10	IPI00001639	KPNB1	876	876	876	9.7E+04	9.7E+04	9.7E+04	8.7	5	1	1	1	1	IMPORTIN BETA-1 SUBUNIT.	Q14637; Q14974; Q53XN2; Q96J27	IMB1_HUMAN; Q53XN2_HUMAN
11	IPI00001730	FHOD1	1164	1164	1164	1.3E+05	1.3E+05	1.3E+05	7.4	7	1	1	1	1	FH1/FH2 DOMAIN-CONTAINING PROTEIN.	Q59F76; Q6Y1F2; Q76MS8; Q8N521; Q9Y613	FHOD1_HUMAN
12	IPI00002149	SAR1B	198	198	198	2.2E+04	2.2E+04	2.2E+04	19.7	2	0	0	1	1	GTP-BINDING PROTEIN SAR1B.	Q53F37; Q567T4; Q9H029; Q9Y6B6	Q53F37_HUMAN; Q9H029_HUMAN; SAR1B_HUMAN
13	IPI00002352	MYLPF	170	170	170	1.9E+04	1.9E+04	1.9E+04	61.8	18	1	1	1	1	MYOSIN LIGHT CHAIN 2.	Q14843; Q6IB41; Q96A32	MLRS_HUMAN
14	IPI00002459; IPI00221226	ANXA6	667	673	670	7.5E+04	7.6E+04	7.6E+04	52.8	32	1	1	1	1	ANNEXIN VI ISOFORM 2.; ANNEXIN A6.	P08133; Q6ZT79	; ANXA6_HUMAN
15	IPI00002460; IPI00021771; IPI00514510	ANXA7	466	488	481	5.0E+04	5.3E+04	5.2E+04	10.9	4	1	1	1	1	ISOFORM 1 OF ANNEXIN A7.; ISOFORM 2 OF ANNEXIN A7.; ANNEXIN VII ISOFORM 2.	P20073; Q53HM8; Q5T0M6; Q5T0M7	ANXA7_HUMAN; Q53HM8_HUMAN; Q5T0M6_HUMAN; Q5T0M7_HUMAN
16	IPI00002521; IPI00456008	ATP5J	108	116	112	1.3E+04	1.3E+04	1.3E+04	45.4	5	0	0	1	1	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR.; ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F0 COMPLEX, SUBUNIT F6ISOFORM B PRECURSOR.	P18859; Q6IB54; Q6NZ59	; ATP5J_HUMAN; Q6IB54_HUMAN; Q6NZ59_HUMAN
17	IPI00002536; IPI00216155; IPI00216156	SESN1	426	551	490	5.0E+04	6.4E+04	5.7E+04	5.9	2	0	0	1	0	ISOFORM T2 OF SESTRIN-1.; ISOFORM T1 OF SESTRIN-1.; ISOFORM T3 OF SESTRIN-1.	Q2M2B7; Q5T316; Q5T318; Q9NV00; Q9UPD5; Q9Y6P5; Q9Y6P6	Q2M2B7_HUMAN; Q5T316_HUMAN; Q5T318_HUMAN; SESN1_HUMAN
18	IPI00002966	HSPA4	840	840	840	9.4E+04	9.4E+04	9.4E+04	10.8	6	1	1	1	1	HEAT SHOCK 70 KDA PROTEIN 4.	O14992; O95756; P34932; Q2TAL4; Q59GF8; Q7KYN0	HSP74_HUMAN; O14992_HUMAN; Q2TAL4_HUMAN; Q59GF8_HUMAN; Q7KYN0_HUMAN
19	IPI00003021; IPI00640401	ATP1A2	1009	1020	1015	1.1E+05	1.1E+05	1.1E+05	13.3	10	1	1	1	1	SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-2 CHAIN PRECURSOR.; CATION-TRANSPORTING ATPASE.	P50993; Q07059; Q58I22; Q5JW73; Q5JW74; Q86UZ5; Q9UQ25	AT1A2_HUMAN; Q58I22_HUMAN; Q5JW73_HUMAN; Q5JW74_HUMAN
20	IPI00003362	HSPA5	655	655	655	7.2E+04	7.2E+04	7.2E+04	35.1	19	1	1	1	1	HSPA5 PROTEIN.	Q2KHP4	Q2KHP4_HUMAN
21	IPI00003482	DECR1	335	335	335	3.6E+04	3.6E+04	3.6E+04	20.6	5	1	1	1	1	2,4-DIENOYL-COA REDUCTASE, MITOCHONDRIAL PRECURSOR.	Q16698; Q2M304; Q7LDK6; Q93085	DECR_HUMAN; Q7LDK6_HUMAN
22	IPI00003814	MAP2K6	334	334	334	3.7E+04	3.7E+04	3.7E+04	12.6	3	1	1	1	0	ISOFORM 1 OF DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE6.	P52564	MP2K6_HUMAN
23	IPI00003815; IPI00794402; IPI00796541	ARHGDIA	204	249	229	2.3E+04	2.8E+04	2.6E+04	15.2	4	0	0	1	1	RHO GDP-DISSOCIATION INHIBITOR 1.; 28 KDA PROTEIN.; 26 KDA PROTEIN.	P52565; Q6IBM5	; GDIR_HUMAN; Q6IBM5_HUMAN
24	IPI00003833	MTCH2	303	303	303	3.3E+04	3.3E+04	3.3E+04	15.2	3	0	0	1	1	MITOCHONDRIAL CARRIER HOMOLOG 2.	Q53G34; Q9Y6C9	MTCH2_HUMAN; Q53G34_HUMAN
25	IPI00003865	HSPA8	646	646	646	7.1E+04	7.1E+04	7.1E+04	43.6	23	1	1	1	1	ISOFORM 1 OF HEAT SHOCK COGNATE 71 KDA PROTEIN.	P11142; Q53GZ6; Q96BE0; Q96H53; Q96IS6; Q9H3R6; Q9NWW3; Q9NZ87	HSP7C_HUMAN; Q53GZ6_HUMAN; Q96BE0_HUMAN; Q96H53_HUMAN; Q96IS6_HUMAN; Q9NWW3_HUMAN; Q9NZ87_HUMAN
26	IPI00003933; IPI00745553	HAGH	260	308	284	2.9E+04	3.4E+04	3.1E+04	17.2	5	0	0	1	1	HYDROXYACYL GLUTATHIONE HYDROLASE ISOFORM 1.; HYDROXYACYLGLUTATHIONE HYDROLASE.	Q16775	; GLO2_HUMAN
27	IPI00003949	UBE2N	152	152	152	1.7E+04	1.7E+04	1.7E+04	27.0	3	0	0	1	1	UBIQUITIN-CONJUGATING ENZYME E2 N.	P61088; Q16781; Q53Y81	UBE2N_HUMAN
28	IPI00003968	NDUFA9	377	377	377	4.3E+04	4.3E+04	4.3E+04	26.3	7	1	1	1	1	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 9,MITOCHONDRIAL PRECURSOR.	Q14076; Q16795; Q2NKX0; Q9BTT5	NDUA9_HUMAN; Q9BTT5_HUMAN
29	IPI00004247; IPI00216725; IPI00446678	PHKA1	1181	1240	1215	1.3E+05	1.4E+05	1.4E+05	15.5	17	1	1	1	1	ISOFORM 1 OF PHOSPHORYLASE B KINASE REGULATORY SUBUNIT ALPHA, SKELETALMUSCLE ISOFORM.; ISOFORM 2 OF PHOSPHORYLASE B KINASE REGULATORY SUBUNIT ALPHA, SKELETALMUSCLE ISOFORM.; 133 KDA PROTEIN.	P46020; Q2M3D7	; KPB1_HUMAN
30	IPI00004471	PDLIM3	364	364	364	3.9E+04	3.9E+04	3.9E+04	30.8	10	1	1	1	1	ISOFORM 1 OF PDZ AND LIM DOMAIN PROTEIN 3.	O43590; O60439; O60440; Q53GG5; Q8N6Y6; Q9BVP4	PDLI3_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]				Detection							
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
31	IPI00004860; IPI00759723	RARS	588	660	624	6.7E+04	7.5E+04	7.1E+04	3.9	2	0	0	1	0	ISOFORM COMPLEXED OF ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC.; ISOFORM MONOMERIC OF ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC.	P54136; Q53GY4; Q9BWA1	Q53GY4_HUMAN; SYRC_HUMAN
32	IPI00004902; IPI00556451	ETFB	255	346	301	2.8E+04	3.7E+04	3.3E+04	32.9	9	0	0	1	1	ISOFORM 1 OF ELECTRON TRANSFER FLAVOPROTEIN SUBUNIT BETA.; ISOFORM 2 OF ELECTRON TRANSFER FLAVOPROTEIN SUBUNIT BETA.	P38117; Q6IBH7; Q71RF6; Q9Y3S7	ETFB_HUMAN
33	IPI00005040; IPI00513827	ACADM	421	454	438	4.7E+04	5.0E+04	4.8E+04	35.1	11	1	1	1	1	MEDIUM-CHAIN SPECIFIC ACYL-COA DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.; HYPOTHETICAL PROTEIN DKFZP686M24262.	P11310; Q5HYG7; Q5T4U4; Q5T4U5; Q9NYF1	ACADM_HUMAN; Q5HYG7_HUMAN; Q5T4U4_HUMAN; Q5T4U5_HUMAN
34	IPI00005158; IPI00334291	LONP1	896	959	928	1.0E+05	1.1E+05	1.0E+05	12.2	9	1	1	1	1	LON PROTEASE HOMOLOG, MITOCHONDRIAL PRECURSOR.; CDNA FLJ39307 FIS, CLONE OCBBF2013208, HIGHLY SIMILAR TO MITOCHONDRIALLON PROTEASE.	P36776; P36777; Q2VPA0; Q8N8K8; Q9UQ95	LONM_HUMAN; Q2VPA0_HUMAN; Q8N8K8_HUMAN
35	IPI00005668; IPI00029733; IPI00289524; IPI00291483; IPI00394704; IPI00455167; IPI00514814; IPI00736657	AKR1C1; AKR1C2;	223	323	287	2.5E+04	3.7E+04	3.3E+04	13.0	3	1	1	1	1	ALDO-KETO REDUCTASE FAMILY 1 MEMBER C2.; ALDO-KETO REDUCTASE FAMILY 1 MEMBER C1.; ALDO-KETO REDUCTASE FAMILY 1 MEMBER C4.; ALDO-KETO REDUCTASE FAMILY 1 MEMBER C3.; DIHYDRODIOL DEHYDROGENASE DD1 (FRAGMENT).; DIHYDRODIOL DEHYDROGENASE DD2.; ALDO-KETO REDUCTASE FAMILY 1, MEMBER C1.; SIMILAR TO ALDO-KETO REDUCTASE FAMILY 1 MEMBER C1 (20-ALPHA-HYDROXYSTEROID DEHYDROGENASE) (20-ALPHA-HSD) (TRANS-1,2-DIHYDROBENZENE-1,2-DIOL DEHYDROGENASE) (HIGH-AFFINITY HEPATIC BILEACID-BINDING PROTEIN) (HBAB) (CHLORDECONE REDUCTASE HOMOLOG HAKRC...ISOFORM 1.	P17516; P42330; P52895; P52896; Q04828; Q14133; Q2XPP3; Q59GU2; Q5SR14; Q5SR15; Q5SR16; Q5T2L1; Q5T6A3; Q7M4N1; Q7M4N2; Q8WW84; Q96A71; Q96DJ1; Q96KI8; Q96SD9; Q99530; Q9NS54; Q9UCX1; Q9UCX2; Q9UII3; Q9UKL9	; AK1C1_HUMAN; AK1C2_HUMAN; AK1C3_HUMAN; AK1C4_HUMAN; Q2XPP3_HUMAN; Q59GU2_HUMAN; Q5SR14_HUMAN; Q5SR16_HUMAN; Q7M4N1_HUMAN; Q7M4N2_HUMAN; Q96SD9_HUMAN
36	IPI00005957	SMPX	88	88	88	9.6E+03	9.6E+03	9.6E+03	43.2	2	0	0	1	0	SMALL MUSCLE PROTEIN, X-LINKED.	Q5VSM2	Q5VSM2_HUMAN
37	IPI00006091; IPI00304639; IPI00375141; IPI00472316	DMD	3562	3685	3651	4.1E+05	4.3E+05	4.2E+05	5.4	15	0	0	1	0	ISOFORM 4 OF DYSTROPHIN.; ISOFORM 3 OF DYSTROPHIN.; DYSTROPHIN DP427L ISOFORM.; DYSTROPHIN DP427P1 ISOFORM.	P11532; Q02295; Q14169; Q14170; Q548X2; Q5JXQ4; Q5JXW4; Q5JYU0; Q6PK12; Q7KZ40; Q7KZ48; Q8WYD8; Q8WYD9; Q8WYE0; Q8WYE1; Q8WYE2; Q8WYE3; Q8WYE4; Q8WYE5; Q8WYE6; Q8WYE7; Q8WYE8; Q8WYE9; Q8WYF0; Q8WYF1; Q8WYF2;	DMD_HUMAN; Q548X2_HUMAN; Q5JXQ4_HUMAN; Q5JXW4_HUMAN; Q6PK12_HUMAN; Q7KZ40_HUMAN; Q8WYD8_HUMAN; Q8WYD9_HUMAN; Q8WYE0_HUMAN; Q8WYE1_HUMAN; Q8WYE2_HUMAN; Q8WYE3_HUMAN; Q8WYE4_HUMAN; Q8WYE5_HUMAN; Q8WYE6_HUMAN; Q8WYE7_HUMAN; Q8WYE8_HUMAN; Q8WYE9_HUMAN; Q8WYF0_HUMAN; Q8WYF1_HUMAN; Q8WYF2_HUMAN; Q8WYF5_HUMAN; Q9UEH4_HUMAN; Q9UMG1_HUMAN; Q9UPB4_HUMAN; Q9UPB5_HUMAN
38	IPI00006211	VAPB	243	243	243	2.7E+04	2.7E+04	2.7E+04	17.3	3	0	0	1	1	ISOFORM 1 OF VESICLE-ASSOCIATED MEMBRANE PROTEIN-ASSOCIATED PROTEINB/C.	O95292; O95293; Q53XM7; Q9P0H0	Q53XM7_HUMAN; VAPB_HUMAN
39	IPI00006579	COX4I1	169	169	169	2.0E+04	2.0E+04	2.0E+04	46.1	8	1	1	1	1	CYTOCHROME C OXIDASE SUBUNIT 4 ISOFORM 1, MITOCHONDRIAL PRECURSOR.	P13073; Q6P666	COX41_HUMAN; Q6P666_HUMAN
40	IPI00006663; IPI00792207	ALDH2	517	517	517	5.6E+04	5.6E+04	5.6E+04	21.7	8	1	1	1	1	ALDEHYDE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.; MITOCHONDRIAL ALDEHYDE DEHYDROGENASE 2 VARIANT (FRAGMENT).	P05091; Q03639; Q53FB6; Q6IB13; Q6IV71; Q9UN17	ALDH2_HUMAN; Q53FB6_HUMAN; Q9UN17_HUMAN
41	IPI00007052	FIS1	152	152	152	1.7E+04	1.7E+04	1.7E+04	15.8	2	1	0	1	1	MITOCHONDRIAL FISSION 1 PROTEIN.	Q9BTP3; Q9Y3D6	FIS1_HUMAN
42	IPI00007402; IPI00784008	IPO7	1038	1040	1039	1.2E+05	1.2E+05	1.2E+05	5.3	4	1	1	1	0	120 KDA PROTEIN.; IMPORTIN-7.	O95373; Q1RMF7; Q9H177; Q9NTE3	; IPO7_HUMAN
43	IPI00007611	ATP5O	213	213	213	2.3E+04	2.3E+04	2.3E+04	35.2	6	1	1	1	1	ATP SYNTHASE O SUBUNIT, MITOCHONDRIAL PRECURSOR.	P48047; Q53HH2; Q5U042; Q6IBI2	ATPO_HUMAN; Q53HH2_HUMAN
44	IPI00007673; IPI00401259	CHCHD2; CHCHD9	151	151	151	1.5E+04	1.6E+04	1.6E+04	18.5	2	0	0	1	0	COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN-CONTAINING PROTEIN 2.; COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN-CONTAINING PROTEIN 9.	Q498C3; Q5T1J5; Q6NZ50; Q9Y6H1	CHCH2_HUMAN; Q5T1J5_HUMAN
45	IPI00007702	HSPA2	639	639	639	7.0E+04	7.0E+04	7.0E+04	32.9	19	1	1	1	1	HEAT SHOCK-RELATED 70 KDA PROTEIN 2.	P54652; Q15508; Q53XM3; Q9UE78	HSP72_HUMAN; Q53XM3_HUMAN
46	IPI00007750; IPI00794663	TUBA4A	433	448	441	4.8E+04	5.0E+04	4.9E+04	37.7	12	1	1	1	1	TUBULIN ALPHA-1 CHAIN.; 48 KDA PROTEIN.	P05215; P68366	; TBA1_HUMAN
47	IPI00007752	TUBB2C	445	445	445	5.0E+04	5.0E+04	5.0E+04	51.2	20	1	1	1	1	TUBULIN BETA-2C CHAIN.	A2BFA2; P05217; P68371; Q8IWP6; Q8IZ29; Q8N6N5;	A2BFA2_HUMAN; Q8IWP6_HUMAN; Q8IZ29_HUMAN; Q8N6N5_HUMAN; Q96HX0_HUMAN; TBB2C_HUMAN
48	IPI00007765	HSPA9	679	679	679	7.4E+04	7.4E+04	7.4E+04	37.6	19	1	1	1	1	STRESS-70 PROTEIN, MITOCHONDRIAL PRECURSOR.	A1XP52; P30036; P31932; P38646; Q1HB43; Q2F839; Q6GU03; Q8N1C8; Q9BWB7	A1XP52_HUMAN; GRP75_HUMAN; Q1HB43_HUMAN; Q2F839_HUMAN; Q8N1C8_HUMAN
49	IPI00007856	MYH2	1941	1941	1941	2.2E+05	2.2E+05	2.2E+05	65.3	253	1	1	1	1	MYOSIN-2.	A0AVL4; Q14322; Q16229; Q86T56; Q9UKX2	MYH2_HUMAN; Q86T56_HUMAN
50	IPI00007926	C6orf108	174	174	174	1.9E+04	1.9E+04	1.9E+04	20.1	2	0	0	1	0	C-MYC-RESPONSIVE PROTEIN RCL.	O43598	RCL_HUMAN
51	IPI00008215	ME1	572	572	572	6.4E+04	6.4E+04	6.4E+04	7.5	3	1	1	1	0	NADP-DEPENDENT MALIC ENZYME.	P48163; Q16797; Q16855; Q53F72; Q5VWA2; Q8WVX2; Q9BWX8; Q9H1W3; Q9UIY4	MAOX_HUMAN; Q8WVX2_HUMAN
52	IPI00008418; IPI00219865; IPI00789460; IPI00794003	DIABLO	157	239	187	1.8E+04	2.7E+04	2.1E+04	14.6	3	0	0	1	1	ISOFORM 1 OF DIABLO HOMOLOG, MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF DIABLO HOMOLOG, MITOCHONDRIAL PRECURSOR.; 19 KDA PROTEIN.; 18 KDA PROTEIN.	Q502X2; Q53HB7; Q96LV0; Q9BT11; Q9HAV6; Q9NR28	; DBLOH_HUMAN; Q502X2_HUMAN; Q53HB7_HUMAN
53	IPI00008485	ACO1	889	889	889	9.8E+04	9.8E+04	9.8E+04	10.0	5	1	1	1	1	IRON-RESPONSIVE ELEMENT-BINDING PROTEIN 1.	P21399; Q14652; Q5VZA7; Q9HBB2	IREB1_HUMAN; Q5VZA7_HUMAN; Q9HBB2_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
54	IPI00008530; IPI00556485; IPI00791188; IPI00792267; IPI00793002; IPI00793584; IPI00794884	RPLP0	147	317	212	1.6E+04	3.4E+04	2.3E+04	16.4	4	1	1	1	1	60S ACIDIC RIBOSOMAL PROTEIN P0.; RPLP0 PROTEIN.; 18 KDA PROTEIN.; 16 KDA PROTEIN.; 19 KDA PROTEIN.; 23 KDA PROTEIN.; 24 KDA PROTEIN.	P05388; Q3B7A4; Q53HK9; Q53HW2; Q6NSF2; Q8NHW5;	; Q3B7A4_HUMAN; Q53HK9_HUMAN; Q53HW2_HUMAN; Q6NSF2_HUMAN; Q8NHW5_HUMAN; RLA0_HUMAN
55	IPI00008994; IPI00218108; IPI00218109; IPI00382995	NDRG2	356	371	361	3.9E+04	4.1E+04	4.0E+04	31.0	6	1	1	1	1	ISOFORM 1 OF PROTEIN NDRG2.; ISOFORM 2 OF PROTEIN NDRG2.; ISOFORM 3 OF PROTEIN NDRG2.; CYTOPLASMIC PROTEIN NDR1.	Q567T1; Q68DW2; Q86U08; Q86U46; Q8TDR6; Q96FD3; Q96FT0; Q96JU0; Q96PN0; Q9BQH5; Q9ULH2; Q9UN36	NDRG2_HUMAN; Q8TDR6_HUMAN
56	IPI00009236	CAV1	178	178	178	2.0E+04	2.0E+04	2.0E+04	13.5	2	0	0	1	0	ISOFORM ALPHA OF CAVEOLIN-1.	Q03135; Q2TNI1; Q59E85; Q7Z4F3; Q9UGP1; Q9UNG1; Q9UQH6	CAV1_HUMAN; Q2TNI1_HUMAN; Q59E85_HUMAN; Q7Z4F3_HUMAN
57	IPI00009253	NAPA	295	295	295	3.3E+04	3.3E+04	3.3E+04	11.2	2	0	0	1	1	ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN.	P54920; Q96IK3; Q9BVJ3	SNAA_HUMAN
58	IPI00009550	APOBEC2	224	224	224	2.6E+04	2.6E+04	2.6E+04	32.1	5	1	1	1	1	PROBABLE C-]U-EDITING ENZYME APOBEC-2.	Q53F28; Q5TGU5; Q5TGU6; Q9Y235	ABEC2_HUMAN; Q53F28_HUMAN
59	IPI00009551	MYOT	498	498	498	5.5E+04	5.5E+04	5.5E+04	33.9	10	1	1	1	1	MYOTILIN.	A0A4R6; Q9UBF9	MYOTI_HUMAN
60	IPI00009896	EPHX1	455	455	455	5.3E+04	5.3E+04	5.3E+04	16.5	6	1	1	1	1	EPOXIDE HYDROLASE 1.	P07099; Q5VTJ6; Q6FGZ3; Q9NP75; Q9NPE7; Q9NQU6; Q9NQU7; Q9NQU8; Q9NQU9; Q9NQV0; Q9NQV1; Q9NQV2	HYEP_HUMAN; Q6FGZ3_HUMAN
61	IPI00009943; IPI00550900	TPT1	172	188	180	2.0E+04	2.2E+04	2.1E+04	10.6	2	0	0	1	1	TUMOR PROTEIN, TRANSLATIONALLY-CONTROLLED 1.; TRANSLATIONALLY-CONTROLLED TUMOR PROTEIN.	P13693; Q5W0H4; Q6YLS2; Q7Z4J4; Q96EE2; Q9UC70	Q5W0H4_HUMAN; TCTP_HUMAN
62	IPI00010080	OXSR1	527	527	527	5.8E+04	5.8E+04	5.8E+04	14.2	6	1	1	1	1	SERINE/THREONINE-PROTEIN KINASE OSR1.	O95747; Q3LR53; Q7Z501; Q9UPQ1	OXSR1_HUMAN
63	IPI00010182; IPI00218836; IPI00815745	DBI	87	104	93	1.0E+04	1.2E+04	1.1E+04	61.4	5	0	0	1	1	ISOFORM A 1 OF ACYL-COA-BINDING PROTEIN.; ISOFORM 2 OF ACYL-COA-BINDING PROTEIN.; DIAZEPAM BINDING INHIBITOR ISOFORM 2.	P07108; P08869; Q4VWZ6; Q53SQ7; Q6IB48; Q9UCI8	ACBP_HUMAN; Q4VWZ6_HUMAN; Q9UCI8_HUMAN
64	IPI00010271; IPI00219675; IPI00394837	RAC1	148	211	184	1.7E+04	2.3E+04	2.1E+04	7.1	2	0	0	1	0	ISOFORM A OF RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 PRECURSOR.; ISOFORM B OF RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 PRECURSOR.; RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 ISOFORM RAC1C.	O95501; P15154; P63000; Q3Y4D3; Q5JAA8; Q9BTB4	; RAC1_HUMAN
65	IPI00010331; IPI00016807	SIRT5	299	310	305	3.3E+04	3.4E+04	3.3E+04	10.0	2	0	0	1	1	ISOFORM 2 OF NAD-DEPENDENT DEACETYLASE SIRTUIN-5.; ISOFORM 1 OF NAD-DEPENDENT DEACETYLASE SIRTUIN-5.	Q5T294; Q5T295; Q7Z3A0; Q9NXA8; Q9Y6E6	Q5T295_HUMAN; Q7Z3A0_HUMAN; SIRT5_HUMAN
66	IPI00010414; IPI00798196	PDLIM1	268	329	299	2.9E+04	3.6E+04	3.2E+04	13.1	2	1	1	1	0	PDZ AND LIM DOMAIN PROTEIN 1.; 29 KDA PROTEIN.	O00151; Q5VZH5; Q9BPZ9	; PDLI1_HUMAN
67	IPI00010418; IPI00743335; IPI00829992	MYO1C	1028	1063	1045	1.2E+05	1.2E+05	1.2E+05	9.0	7	1	1	1	1	MYOSIN-IC.; MYOSIN IC ISOFORM A.; MYOSIN IC ISOFORM B.	A1L180; O00159; Q4LE56; Q6NVJ7; Q86Y95	; A1L180_HUMAN; MYO1C_HUMAN; Q4LE56_HUMAN; Q86Y95_HUMAN
68	IPI00010796	P4HB	508	508	508	5.7E+04	5.7E+04	5.7E+04	44.5	18	1	1	1	1	PROTEIN DISULFIDE-ISOMERASE PRECURSOR.	P07237; P30037; P32079; Q15205; Q6LDE5; Q96C96	PDIA1_HUMAN; Q96C96_HUMAN
69	IPI00010810	ETFA	333	333	333	3.5E+04	3.5E+04	3.5E+04	26.7	6	1	1	1	1	ELECTRON TRANSFER FLAVOPROTEIN SUBUNIT ALPHA, MITOCHONDRIAL PRECURSOR.	P13804; Q53XN3	ETFA_HUMAN; Q53XN3_HUMAN
70	IPI00011107	IDH2	452	452	452	5.1E+04	5.1E+04	5.1E+04	39.8	28	1	1	1	1	ISOCITRATE DEHYDROGENASE [NADP], MITOCHONDRIAL PRECURSOR.	P48735; Q53GL5; Q96GT3	IDHP_HUMAN; Q53GL5_HUMAN
71	IPI00011126	PSMC1	440	440	440	4.9E+04	4.9E+04	4.9E+04	19.1	5	1	1	1	0	26S PROTEASE REGULATORY SUBUNIT 4.	P49014; P62191; Q03527; Q53HB3; Q53XL8; Q6IAW0; Q6NW36; Q96AZ3	PRS4_HUMAN; Q53HB3_HUMAN; Q53XL8_HUMAN; Q6NW36_HUMAN
72	IPI00011201	ME2	584	584	584	6.5E+04	6.5E+04	6.5E+04	3.8	2	0	1	1	0	NAD-DEPENDENT MALIC ENZYME, MITOCHONDRIAL PRECURSOR.	P23368; Q9BYG1; Q9H4B2	MAOM_HUMAN
73	IPI00011229	CTSD	412	412	412	4.5E+04	4.5E+04	4.5E+04	9.5	3	0	0	1	0	CATHEPSIN D PRECURSOR.	P07339; Q6IB57	CATD_HUMAN
74	IPI00011250; IPI00647149	UCHL3	147	230	189	1.7E+04	2.6E+04	2.1E+04	18.7	3	0	0	1	1	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L3.; 17 KDA PROTEIN.	P15374; Q5TBK8; Q6IBE9	; UCHL3_HUMAN
75	IPI00011285	CAPN1	714	714	714	8.2E+04	8.2E+04	8.2E+04	22.0	12	1	1	1	1	CALPAIN-1 CATALYTIC SUBUNIT.	P07384; Q2TTR0; Q6DHV4	CAN1_HUMAN; Q2TTR0_HUMAN; Q6DHV4_HUMAN
76	IPI00011416	ECH1	328	328	328	3.6E+04	3.6E+04	3.6E+04	33.2	10	1	1	1	1	DELTA(3,5)-DELTA(2,4)-DIENOYL-COA ISOMERASE, MITOCHONDRIAL PRECURSOR.	Q13011; Q8WVX0; Q96EZ9	ECH1_HUMAN
77	IPI00011525	CASQ1	396	396	396	4.5E+04	4.5E+04	4.5E+04	28.3	15	1	1	1	1	CALSEQUESTRIN 1.	Q5JW76	Q5JW76_HUMAN
78	IPI00011635	BCL2L13	485	485	485	5.3E+04	5.3E+04	5.3E+04	13.4	5	1	1	1	1	ISOFORM 2 OF BCL-2-LIKE 13 PROTEIN.	Q96B37; Q96IB7; Q9BXK5; Q9BY01; Q9HC05; Q9UFE0; Q9UKN3	B2L13_HUMAN
79	IPI00011770	NDUFA4	81	81	81	9.4E+03	9.4E+03	9.4E+03	22.2	2	0	0	1	1	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 4.	O00483; Q6FHN5	NDUA4_HUMAN
80	IPI00012007; IPI00827743	AHCY	285	432	359	3.1E+04	4.8E+04	3.9E+04	15.5	6	1	1	1	1	ADENOSYLHOMOCYSTEINASE.; 31 KDA PROTEIN.	P23526; Q1RMG2; Q96A36	; Q1RMG2_HUMAN; SAHH_HUMAN
81	IPI00012048; IPI00375531	NME1	152	177	165	1.7E+04	2.0E+04	1.8E+04	32.9	5	0	0	1	0	NUCLEOSIDE DIPHOSPHATE KINASE A.; NON-METASTATIC CELLS 1, PROTEIN (NM23A) EXPRESSED IN ISOFORM A.	P15531; Q6FGK3; Q86XQ2	NDKA_HUMAN; Q6FGK3_HUMAN; Q86XQ2_HUMAN
82	IPI00012268	PSMD2	908	908	908	1.0E+05	1.0E+05	1.0E+05	12.3	8	1	1	1	1	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 2.	Q12932; Q13200; Q15321; Q53XQ4; Q59EG8; Q96I12; Q9NSM5	PSMD2_HUMAN; Q53XQ4_HUMAN; Q59EG8_HUMAN; Q9NSM5_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
83	IPI00012726; IPI00555747; IPI00642904; IPI00642944	PABPC4	615	660	638	6.8E+04	7.2E+04	7.0E+04	12.2	5	1	1	1	1	ISOFORM 1 OF POLYADENYLATE-BINDING PROTEIN 4.; ISOFORM 2 OF POLYADENYLATE-BINDING PROTEIN 4.; POLY(A) BINDING PROTEIN, CYTOPLASMIC 4.; POLY(A) BINDING PROTEIN, CYTOPLASMIC 4.	Q13310; Q147Y3; Q15164; Q3B867; Q53GL4; Q59GZ7; Q5SPS4; Q5SPS5; Q5SPS6; Q5T3B4; Q6IQ30; Q6P0N3	PABP4_HUMAN; Q147Y3_HUMAN; Q15164_HUMAN; Q3B867_HUMAN; Q53GL4_HUMAN; Q59GZ7_HUMAN; Q5SPS4_HUMAN; Q5SPS5_HUMAN; Q5SPS6_HUMAN; Q5T3B4_HUMAN; Q6IQ30_HUMAN
84	IPI00012728	ACSL1	698	698	698	7.8E+04	7.8E+04	7.8E+04	29.9	19	1	1	1	1	ISOFORM 1 OF LONG-CHAIN-FATTY-ACID--COA LIGASE 1.	P33121; P41215; Q108N1; Q8N8V7; Q8TA99	ACSL1_HUMAN; Q108N1_HUMAN
85	IPI00012750; IPI00401105; IPI00478694; IPI00740757	RPS25; hCG_1640	124	125	124	1.4E+04	1.4E+04	1.4E+04	24.0	3	0	0	1	1	40S RIBOSOMAL PROTEIN S25.; SIMILAR TO 40S RIBOSOMAL PROTEIN S25.; 14 KDA PROTEIN.; SIMILAR TO 40S RIBOSOMAL PROTEIN S25.	P25111; P62851	; RS25_HUMAN
86	IPI00012912	CPT2	658	658	658	7.4E+04	7.4E+04	7.4E+04	17.5	8	1	1	1	0	CARNITINE O-PALMITOYLTRANSFERASE 2, MITOCHONDRIAL PRECURSOR.	P23786; Q53G79; Q5SW68; Q9BQ26	CPT2_HUMAN; Q53G79_HUMAN
87	IPI00013459; IPI00556190; IPI00791036	NDUFB5	137	189	171	1.6E+04	2.2E+04	2.0E+04	12.2	3	0	0	1	1	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 5,MITOCHONDRIAL PRECURSOR.; NDUFB5 PROTEIN.; 22 KDA PROTEIN.	O43674; Q05D62; Q561V6	; NDUB5_HUMAN; Q05D62_HUMAN; Q561V6_HUMAN
88	IPI00013723	PIN1	163	163	163	1.8E+04	1.8E+04	1.8E+04	25.8	3	0	0	1	0	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA-INTERACTING 1.	Q13526; Q53X75; Q8NFL2	PIN1_HUMAN; Q53X75_HUMAN; Q8NFL2_HUMAN
89	IPI00013745	PLCD4	763	763	763	8.8E+04	8.8E+04	8.8E+04	13.4	6	1	1	1	1	PHOSPHOLIPASE C DELTA 4.	Q53FS8; Q9BRC7	Q53FS8_HUMAN; Q9BRC7_HUMAN
90	IPI00013847	UQCRC1	480	480	480	5.3E+04	5.3E+04	5.3E+04	27.7	11	1	1	1	1	UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN 1, MITOCHONDRIALPRECURSOR.	P31930; Q96DD2	UQCR1_HUMAN
91	IPI00013860; IPI00479966	HIBADH	336	360	348	3.5E+04	3.8E+04	3.7E+04	21.7	5	1	1	1	1	3-HYDROXYISOBUTYRATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.; HYPOTHETICAL PROTEIN (FRAGMENT).	P31937; Q546Z2; Q9UDN3	; 3HIDH_HUMAN; Q546Z2_HUMAN
92	IPI00013894	STIP1	543	543	543	6.3E+04	6.3E+04	6.3E+04	17.3	10	1	1	1	1	STRESS-INDUCED-PHOSPHOPROTEIN 1.	P31948; Q5TZU9	Q5TZU9_HUMAN; STIP1_HUMAN
93	IPI00013933	DSP	2871	2871	2871	3.3E+05	3.3E+05	3.3E+05	1.7	4	0	0	1	1	ISOFORM DPI OF DESMOPLAKIN.	O75993; P15924; Q14189; Q9UHN4	DESP_HUMAN
94	IPI00013991	TPM2	284	284	284	3.3E+04	3.3E+04	3.3E+04	65.5	31	1	1	1	1	ISOFORM 1 OF TROPOMYOSIN BETA CHAIN.	P06468; P07951; Q13894; Q53FM4; Q5TCU4; Q5TCU7; Q9UH67	TPM2_HUMAN
95	IPI00014398	FHL1	296	296	296	3.4E+04	3.4E+04	3.4E+04	17.6	6	1	1	1	1	FOUR AND A HALF LIM DOMAINS 1 VARIANT.	Q53FI7	Q53FI7_HUMAN
96	IPI00014399	FHL3	280	280	280	3.1E+04	3.1E+04	3.1E+04	6.1	2	0	0	1	1	FOUR AND A HALF LIM DOMAINS PROTEIN 3.	Q13643; Q6I9T0; Q96C98; Q9BVA2; Q9P100	FHL3_HUMAN; Q6I9T0_HUMAN; Q96C98_HUMAN; Q9BVA2_HUMAN; Q9P100_HUMAN
97	IPI00014424	EEF1A2	463	463	463	5.0E+04	5.0E+04	5.0E+04	32.0	15	1	1	1	1	ELONGATION FACTOR 1-ALPHA 2.	P54266; Q05639; Q0VGC7	EF1A2_HUMAN
98	IPI00014439	QDPR	244	244	244	2.6E+04	2.6E+04	2.6E+04	21.3	3	0	0	1	1	DIHYDROPTERIDINE REDUCTASE.	P09417; Q53F52; Q9H3M5	DHPR_HUMAN
99	IPI00014581; IPI00296039	TPM1	284	284	284	3.3E+04	3.3E+04	3.3E+04	78.9	37	1	1	1	1	ISOFORM 1 OF TROPOMYOSIN-1 ALPHA CHAIN.; ISOFORM 4 OF TROPOMYOSIN-1 ALPHA CHAIN.	P09493; P09494; P10469; Q6DV89; Q86W64; Q8TCG4; Q96IK2; Q9UCY9	Q6DV89_HUMAN; Q8TCG4_HUMAN; TPM1_HUMAN
100	IPI00014852	PGM5	506	506	506	5.6E+04	5.6E+04	5.6E+04	13.4	5	1	1	1	1	PHOSPHOGLUCOMUTASE-LIKE PROTEIN 5.	Q15124; Q5VYV3; Q8N527	PGM5_HUMAN; Q5VYV3_HUMAN; Q8N527_HUMAN
101	IPI00015141	CKMT2	419	419	419	4.8E+04	4.8E+04	4.8E+04	41.8	22	1	1	1	1	CREATINE KINASE, SARCOMERIC MITOCHONDRIAL PRECURSOR.	P17540; Q6ICS8; Q8N1E1	KCRS_HUMAN
102	IPI00015421	KLHL31	634	634	634	7.0E+04	7.0E+04	7.0E+04	3.8	2	1	0	1	0	KELCH-LIKE PROTEIN 31.	Q9H511	KLH31_HUMAN
103	IPI00015833	CHCHD3	227	227	227	2.6E+04	2.6E+04	2.6E+04	16.3	6	0	0	1	1	COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN-CONTAINING PROTEIN 3.	Q9NX63	CHCH3_HUMAN
104	IPI00015865	ADPRHL2	363	363	363	3.9E+04	3.9E+04	3.9E+04	11.6	3	1	1	1	1	POLY(ADP-RIBOSE) GLYCOHYDROLASE ARH3.	Q53G94; Q6IAB8; Q9BY47; Q9NX46	ARHL2_HUMAN
105	IPI00015911	DLD	509	509	509	5.4E+04	5.4E+04	5.4E+04	24.2	9	1	1	1	1	DIHYDROLIPOYL DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.	P09622; Q14131; Q14167; Q59EV8; Q8WTS4	DLDH_HUMAN; Q59EV8_HUMAN; Q8WTS4_HUMAN
106	IPI00015972	COX6C	75	75	75	8.8E+03	8.8E+03	8.8E+03	37.3	5	0	0	1	1	CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR.	P09669	COX6C_HUMAN
107	IPI00016006; IPI00184477; IPI00797784	GPHN	380	769	628	4.1E+04	8.3E+04	6.8E+04	4.2	2	0	0	1	0	ISOFORM 1 OF GEPHYRIN.; ISOFORM 2 OF GEPHYRIN.; 41 KDA PROTEIN.	Q96KU4; Q9H4E9; Q9NQX3; Q9P2G2	; GEPH_HUMAN; Q96KU4_HUMAN
108	IPI00016077	GBAS	286	286	286	3.4E+04	3.4E+04	3.4E+04	23.4	4	1	1	1	1	PROTEIN NIPSNAP2.	O43801; O75323; Q53X96	NIPS2_HUMAN; Q53X96_HUMAN
109	IPI00016342; IPI00791850; IPI00792578; IPI00795370	RAB7A	78	207	116	8.7E+03	2.3E+04	1.3E+04	17.9	3	0	0	1	1	RAS-RELATED PROTEIN RAB-7.; 9 KDA PROTEIN.; 11 KDA PROTEIN.; 9 KDA PROTEIN.		
110	IPI00016346	PROSC	275	275	275	3.0E+04	3.0E+04	3.0E+04	9.5	2	0	0	1	0	PROLINE SYNTHETASE CO-TRANSCRIBED BACTERIAL HOMOLOG PROTEIN.	O94903; Q6FI94	PROSC_HUMAN
111	IPI00016457; IPI00029140; IPI00514595	CRAT	548	626	593	6.2E+04	7.1E+04	6.7E+04	23.6	11	1	1	1	1	ISOFORM 1 OF CARNITINE O-ACETYLTRANSFERASE.; ISOFORM 3 OF CARNITINE O-ACETYLTRANSFERASE.; ISOFORM 2 OF CARNITINE O-ACETYLTRANSFERASE.	P43155; Q5T952; Q9BW16	; CACP_HUMAN; Q5T952_HUMAN
112	IPI00016513	RAB10	200	200	200	2.3E+04	2.3E+04	2.3E+04	28.5	4	0	0	1	1	RAS-RELATED PROTEIN RAB-10.	O88386; P61026; Q53SX4; Q53T70; Q6IA52; Q9D7X6; Q9H0T3; Q9UL28	Q53SX4_HUMAN; Q53T70_HUMAN; Q9UL28_HUMAN; RAB10_HUMAN
113	IPI00016862; IPI00759575	GSR	479	522	501	5.2E+04	5.6E+04	5.4E+04	10.5	3	1	1	1	1	ISOFORM MITOCHONDRIAL OF GLUTATHIONE REDUCTASE, MITOCHONDRIALPRECURSOR.; ISOFORM CYTOPLASMIC OF GLUTATHIONE REDUCTASE, MITOCHONDRIAL PRECURSOR.	P00390; Q03504; Q7Z5C9; Q9NP63	GSHR_HUMAN; Q03504_HUMAN
114	IPI00016910; IPI00646839	EIF3S8; LOC7286	913	914	914	1.1E+05	1.1E+05	1.1E+05	6.5	5	1	1	1	1	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 8.; SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 8,110KDA ISOFORM 1.	A1KYQ7; O00215; Q3B7B9; Q99613	; A1KYQ7_HUMAN; IF38_HUMAN; Q3B7B9_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
115	IPI00017283	IARS2	1012	1012	1012	1.1E+05	1.1E+05	1.1E+05	8.3	6	1	1	1	1	ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR.	Q1M2P9; Q6PI85; Q7L439; Q86WU9; Q96D91; Q9H9Q8; Q9NSE4	Q1M2P9_HUMAN; Q9H9Q8_HUMAN; SYIM_HUMAN
116	IPI00017334; IPI00791634	PHB	272	272	272	3.0E+04	3.0E+04	3.0E+04	29.4	7	1	0	1	1	PROHIBITIN.; PROHIBITIN VARIANT (FRAGMENT).	P35232; Q4VBQ0; Q53FV0; Q6FHP5; Q6PUJ7	PHB_HUMAN; Q53FV0_HUMAN; Q6FHP5_HUMAN; Q6PUJ7_HUMAN
117	IPI00017367	RDX	583	583	583	6.9E+04	6.9E+04	6.9E+04	19.6	9	1	1	1	1	RADIXIN.	P35241; Q05CU6; Q6PKD3; Q86Y61; Q9NST9	Q05CU6_HUMAN; Q6PKD3_HUMAN; Q9NST9_HUMAN; RADI_HUMAN
118	IPI00017510	COX2	227	227	227	2.6E+04	2.6E+04	2.6E+04	39.2	6	1	1	1	1	CYTOCHROME C OXIDASE SUBUNIT 2.	A0S3D8; A0SA07; A1Z455; A1Z4V2; P00403; Q06TE6; Q09U41; Q0Z7D8; Q0Z7F1; Q0Z7J0; Q0Z7K3; Q0Z7S0; Q14XI3; Q14XT3; Q15HH9; Q19MP7; Q2QDD3; Q305H0; Q37526; Q4EYL1; Q4EZD4; Q4F4V6; Q4F6A2; Q4GCC3; Q4GCG2; Q4GCZ4; Q4GHE1; Q4GQP0; Q4GVP5; Q4GW12; Q4R1L3; Q4R1L5; Q5S971; Q5SA98; Q5SAP1; Q5SB08; Q5XRW8; Q6R0V6; Q6RKW8; Q6RNN7; Q6RQ80; Q6VIG7; Q6VJD8; Q6VJJ3; Q7GXZ8; Q7Y626; Q7Y6M3; Q7Y6N0; Q7YCE6; Q7YEH2; Q85KR6; Q85KS0; Q85KS5; Q85KS8; Q85KT6; Q85KV5; Q85KW8; Q85KX8; Q85L00; Q86WE9; Q8HNR1; Q8HNR6; Q8HQB7; Q8WCW3;	A0S3D8_HUMAN; A0SA07_HUMAN; A1Z455_HUMAN; A1Z4V2_HUMAN; COX2_HUMAN; Q06TE6_HUMAN; Q09U41_HUMAN; Q0Z7D8_HUMAN; Q0Z7F1_HUMAN; Q0Z7J0_HUMAN; Q0Z7K3_HUMAN; Q0Z7S0_HUMAN; Q14XI3_HUMAN; Q14XT3_HUMAN; Q15HH9_HUMAN; Q19MP7_HUMAN; Q305H0_HUMAN; Q4EYL1_HUMAN; Q4EZD4_HUMAN; Q4F4V6_HUMAN; Q4F6A2_HUMAN; Q4GCC3_HUMAN; Q4GCG2_HUMAN; Q4GCZ4_HUMAN; Q4GHE1_HUMAN; Q4GQP0_HUMAN; Q4GVP5_HUMAN; Q4GW12_HUMAN; Q4R1L3_HUMAN; Q4R1L5_HUMAN; Q5S971_HUMAN; Q5SA98_HUMAN; Q5SAP1_HUMAN; Q5SB08_HUMAN; Q5XRW8_HUMAN; Q6R0V6_HUMAN; Q6RKW8_HUMAN; Q6RNN7_HUMAN; Q6RQ80_HUMAN; Q6VIG7_HUMAN; Q6VJD8_HUMAN; Q6VJJ3_HUMAN; Q7GXZ8_HUMAN; Q7Y626_HUMAN; Q7Y6M3_HUMAN; Q7Y6N0_HUMAN; Q7YCE6_HUMAN; Q7YEH2_HUMAN; Q85KR6_HUMAN; Q85KS0_HUMAN; Q85KS5_HUMAN; Q85KS8_HUMAN; Q85KT6_HUMAN; Q85KV5_HUMAN; Q85KW8_HUMAN; Q85KX8_HUMAN; Q85L00_HUMAN; Q86WE9_HUMAN; Q8HNR1_HUMAN; Q8HNR6_HUMAN; Q8HQB7_HUMAN; Q8WCW3_HUMAN; Q9B138_HUMAN; Q9B1F9_HUMAN;
119	IPI00017726; IPI00336094	HSD17B10	252	261	257	2.6E+04	2.7E+04	2.6E+04	24.1	4	0	0	1	1	ISOFORM 1 OF 3-HYDROXYACYL-COA DEHYDROGENASE TYPE-2.; ISOFORM 2 OF 3-HYDROXYACYL-COA DEHYDROGENASE TYPE-2.	Q5H927; Q6IBS9; Q8TCV9; Q96HD5; Q99714	HCD2_HUMAN; Q5H927_HUMAN; Q6IBS9_HUMAN
120	IPI00017855; IPI00790739	ACO2	780	805	793	8.5E+04	8.8E+04	8.7E+04	47.3	37	1	1	1	1	ACONITATE HYDRATASE, MITOCHONDRIAL PRECURSOR.; ACONITASE 2, MITOCHONDRIAL.	A2A274; O75809; Q5JZ41; Q6FHX0; Q71UF1; Q8TAQ6; Q99798	A2A274_HUMAN; ACON_HUMAN; Q5JZ41_HUMAN; Q6FHX0_HUMAN; Q71UF1_HUMAN; Q8TAQ6_HUMAN
121	IPI00018206	GOT2	430	430	430	4.7E+04	4.7E+04	4.7E+04	44.2	23	1	1	1	1	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR.	P00505; Q53FL3; Q9BWA3	AATM_HUMAN; Q53FL3_HUMAN
122	IPI00018246; IPI00220663; IPI00220665; IPI00220667	HK1	905	921	915	1.0E+05	1.0E+05	1.0E+05	20.2	18	1	1	1	1	ISOFORM 1 OF HEXOKINASE-1.; ISOFORM 2 OF HEXOKINASE-1.; ISOFORM 3 OF HEXOKINASE-1.; ISOFORM 4 OF HEXOKINASE-1.	O43443; O43444; O75574; P19367; P78542; Q59FD4; Q5VTC3; Q5VTC4; Q5VTC5; Q5VTC6; Q71V75; Q96HC8; Q9NNZ4; Q9NNZ5	HXK1_HUMAN; P78542_HUMAN; Q59FD4_HUMAN; Q5VTC4_HUMAN; Q5VTC5_HUMAN; Q5VTC6_HUMAN; Q71V75_HUMAN
123	IPI00018342; IPI00640817	AK1	194	210	202	2.2E+04	2.3E+04	2.3E+04	63.4	13	1	1	1	1	ADENYLATE KINASE ISOENZYME 1.; ADENYLATE KINASE 1.	P00568; Q53EY8; Q5T9B7; Q6FGX9; Q9BVK9; Q9UQC7	KAD1_HUMAN; Q53EY8_HUMAN; Q5T9B7_HUMAN; Q6FGX9_HUMAN
124	IPI00018398	PSMC3	439	439	439	4.9E+04	4.9E+04	4.9E+04	44.0	13	1	1	1	0	26S PROTEASE REGULATORY SUBUNIT 6A.	P17980; Q3B757; Q3B865; Q53HU5; Q6GPG8; Q6IBS1; Q96HD3	PRS6A_HUMAN; Q3B757_HUMAN; Q53HU5_HUMAN; Q6GPG8_HUMAN; Q6IBS1_HUMAN
125	IPI00018465	CCT7	543	543	543	5.9E+04	5.9E+04	5.9E+04	19.7	7	1	1	1	0	T-COMPLEX PROTEIN 1 SUBUNIT ETA.	O14871; Q53HV2; Q6FI26; Q6IBT3; Q99832	Q53HV2_HUMAN; Q6IBT3_HUMAN; TCPH_HUMAN
126	IPI00018671; IPI00790757	DUSP3	185	210	198	2.0E+04	2.3E+04	2.2E+04	40.0	6	0	0	1	1	DUAL SPECIFICITY PROTEIN PHOSPHATASE 3.; 23 KDA PROTEIN.	P51452; Q5U0J1	; DUS3_HUMAN; Q5U0J1_HUMAN
127	IPI00018740	IDI2	227	227	227	2.7E+04	2.7E+04	2.7E+04	10.1	2	0	0	1	1	ISOPENTENYL-DIPHOSPHATE DELTA-ISOMERASE 2.	Q9BXS1	IDI2_HUMAN
128	IPI00018755; IPI00335132; IPI00419258; IPI00644653; IPI00645948; IPI00742929; IPI00815806	HMG1L10; HMGB1	158	215	184	1.8E+04	2.5E+04	2.1E+04	17.2	2	0	0	1	0	HIGH MOBILITY GROUP PROTEIN 1-LIKE 10.; 22 KDA PROTEIN.; HIGH MOBILITY GROUP PROTEIN B1.; HIGH-MOBILITY GROUP BOX 1.; HIGH-MOBILITY GROUP BOX 1.; SIMILAR TO HIGH MOBILITY GROUP PROTEIN 1.; HIGH-MOBILITY GROUP BOX 1 VARIANT (FRAGMENT).	P09429; Q14321; Q59GW1; Q5T7C3; Q5T7C4; Q5T7C6; Q6IBE1; Q9UGV6	; HMG1X_HUMAN; HMGB1_HUMAN; Q14321_HUMAN; Q59GW1_HUMAN; Q5T7C3_HUMAN; Q5T7C4_HUMAN; Q5T7C6_HUMAN
129	IPI00018804; IPI00168849	TRIP10	545	601	573	6.3E+04	6.8E+04	6.5E+04	13.1	4	1	1	1	0	ISOFORM 2 OF CDC42-INTERACTING PROTEIN 4.; ISOFORM 1 OF CDC42-INTERACTING PROTEIN 4.	O15184; Q15642; Q53G22; Q5TZN1; Q6FI24; Q8NFL1; Q8TCY1; Q8TDX3; Q96RJ1	CIP4_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
130	IPI00018942; IPI00645172	FLJ10769	347	390	369	3.7E+04	4.1E+04	3.9E+04	7.8	2	0	0	1	1	FLJ10769 PROTEIN.; HYPOTHETICAL PROTEIN LOC55739.	Q5T9X3; Q8IW45; Q9H7W1; Q9NVF5	Q5T9X3_HUMAN; Q8IW45_HUMAN; Q9H7W1_HUMAN; Q9NVF5_HUMAN
131	IPI00019600	UBE2V2	145	145	145	1.6E+04	1.6E+04	1.6E+04	31.0	4	0	0	1	1	UBIQUITIN-CONJUGATING ENZYME E2 VARIANT 2.	A0M8W4; Q15819	A0M8W4_HUMAN; UB2V2_HUMAN
132	IPI00019755; IPI00642936; IPI00797661	GSTO1	146	241	196	1.7E+04	2.8E+04	2.3E+04	12.9	4	1	0	1	1	GLUTATHIONE TRANSFERASE OMEGA-1.; GLUTATHIONE S-TRANSFERASE OMEGA 1.; 17 KDA PROTEIN.	P78417; Q5TA02; Q5TA03; Q7Z3T2	; GSTO1_HUMAN; Q5TA02_HUMAN
133	IPI00019884	ACTN2	894	894	894	1.0E+05	1.0E+05	1.0E+05	38.3	29	1	1	1	1	ALPHA-ACTININ-2.	P35609; Q59FD9; Q5VXF1; Q86TF4; Q86TI8	ACTN2_HUMAN; Q59FD9_HUMAN; Q5VXF1_HUMAN
134	IPI00019888; IPI00336008	ALDH5A1	535	548	542	5.7E+04	5.9E+04	5.8E+04	10.7	4	1	1	1	1	SUCCINATE SEMIALDEHYDE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.; ALDEHYDE DEHYDROGENASE 5A1 PRECURSOR, ISOFORM 1.	P51649; Q546H9; Q8N3W6; Q8N3W7	Q546H9_HUMAN; Q8N3W6_HUMAN; Q8N3W7_HUMAN; SSDH_HUMAN
135	IPI00019987	SUOX	545	545	545	6.0E+04	6.0E+04	6.0E+04	7.3	3	0	0	1	0	SULFITE OXIDASE.		
136	IPI00020035	NIPSNAP3B	247	247	247	2.8E+04	2.8E+04	2.8E+04	22.3	4	0	0	1	1	PROTEIN NIPSNAP3B.	Q5VX30; Q9BS92; Q9NUM2	NPS3B_HUMAN; Q5VX30_HUMAN
137	IPI00020210	DYSF	2081	2081	2081	2.4E+05	2.4E+05	2.4E+05	5.6	7	1	1	1	1	DYSFERLIN_V1.	Q0H395; Q53QY3; Q53TD2; Q7Z6P1; Q8TEL8	Q0H395_HUMAN; Q53QY3_HUMAN; Q53TD2_HUMAN; Q7Z6P1_HUMAN; Q8TEL8_HUMAN
138	IPI00020436; IPI00429190; IPI00790785; IPI00795676	RAB11A; RAB11B	198	218	211	2.2E+04	2.4E+04	2.4E+04	10.6	2	0	0	1	0	RAS-RELATED PROTEIN RAB-11B.; RAS-RELATED PROTEIN RAB-11A.; 24 KDA PROTEIN.; 22 KDA PROTEIN.	P24410; P62491; Q15907; Q2YDT2; Q5TZN9; Q5U0I1; Q6FHR0; Q6FI42; Q8NI07; Q9JLX1	; Q5U0I1_HUMAN; Q6FHR0_HUMAN; Q6FI42_HUMAN; RB11A_HUMAN; RB11B_HUMAN
139	IPI00020495	MRPS36	103	103	103	1.1E+04	1.1E+04	1.1E+04	33.0	2	0	0	1	0	MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S36.	P82909; Q9H2H4	RT36_HUMAN
140	IPI00020510	ZCD1	108	108	108	1.2E+04	1.2E+04	1.2E+04	34.3	3	0	0	1	1	ZINC FINGER CDGSH DOMAIN-CONTAINING PROTEIN 1.	Q1X902; Q9NZ45	Q1X902_HUMAN; ZCD1_HUMAN
141	IPI00020530	THEM2	140	140	140	1.5E+04	1.5E+04	1.5E+04	17.9	2	0	0	1	1	THIOESTERASE SUPERFAMILY MEMBER 2.	O95549; Q9NPJ3	THEM2_HUMAN
142	IPI00020906	IMPA1	277	277	277	3.0E+04	3.0E+04	3.0E+04	15.9	4	0	0	1	1	INOSITOL MONOPHOSPHATASE.	P29218	IMPA1_HUMAN
143	IPI00020984	CANX	592	592	592	6.8E+04	6.8E+04	6.8E+04	11.3	5	1	1	1	1	CALNEXIN PRECURSOR.	P27824	CALX_HUMAN
144	IPI00020986; IPI00794403; IPI00796888	LUM	202	338	257	2.3E+04	3.8E+04	2.9E+04	27.5	7	1	1	1	1	LUMICAN PRECURSOR.; 23 KDA PROTEIN.; 26 KDA PROTEIN.	P51884; Q53FV4; Q96QM7	; LUM_HUMAN; Q53FV4_HUMAN
145	IPI00021263; IPI00790768	YWHAZ	229	245	237	2.6E+04	2.8E+04	2.7E+04	27.1	5	0	0	1	1	14-3-3 PROTEIN ZETA/DELTA.; 26 KDA PROTEIN.	P29213; P29312; P63104; Q32P43; Q5XJ08; Q6GPI2; Q6IN74; Q6NUR9; Q6P3U9; Q86V33	; 1433Z_HUMAN
146	IPI00021338	DLAT	614	614	614	6.6E+04	6.6E+04	6.6E+04	13.4	7	0	0	1	0	DIHYDROLIPOYLLYSINE-RESIDUE ACETYLTRANSFERASE COMPONENT OF PYRUVATEDEHYDROGENASE COMPLEX, MITOCHONDRIAL PRECURSOR.	P10515; Q16783	ODP2_HUMAN
147	IPI00021347	UBE2L3	154	154	154	1.8E+04	1.8E+04	1.8E+04	24.0	2	1	1	1	1	UBIQUITIN-CONJUGATING ENZYME E2 L3.	P51966; P68036; P70653; Q9HAV1	UB2L3_HUMAN
148	IPI00021369	CRYAB	175	175	175	2.0E+04	2.0E+04	2.0E+04	44.0	10	1	1	1	1	ALPHA CRYSTALLIN B CHAIN.	O43416; P02511	CRYAB_HUMAN
149	IPI00021405; IPI00216952; IPI00216953; IPI00514204; IPI00644087; IPI00655812	LMNA	465	664	573	5.3E+04	7.4E+04	6.5E+04	18.2	10	1	1	1	1	ISOFORM A OF LAMIN-A/C.; ISOFORM C OF LAMIN-A/C.; ISOFORM ADELTA10 OF LAMIN-A/C.; LAMIN A/C.; PROGERIN.; RHABDOMYOSARCOMA ANTIGEN MU-RMS-40.12.	P02545; P02546; Q3BDU5; Q5I6Y4; Q5I6Y5; Q5I6Y6; Q5TCJ2; Q5TCJ3; Q5TCJ4; Q6UYC3; Q8N519; Q969I8; Q96JA2	LMNA_HUMAN; Q3BDU5_HUMAN; Q5I6Y4_HUMAN; Q5I6Y5_HUMAN; Q5I6Y6_HUMAN; Q5TCJ2_HUMAN; Q5TCJ3_HUMAN; Q5TCJ4_HUMAN; Q6UYC3_HUMAN; Q8N519_HUMAN
150	IPI00021428	ACTA1	377	377	377	4.2E+04	4.2E+04	4.2E+04	71.9	43	1	1	1	1	ACTIN, ALPHA SKELETAL MUSCLE.	P02568; P68133; P99020; Q5T8M9	ACTS_HUMAN; Q5T8M9_HUMAN
151	IPI00021435	PSMC2	433	433	433	4.9E+04	4.9E+04	4.9E+04	8.8	3	1	1	1	1	26S PROTEASE REGULATORY SUBUNIT 7.	P35998; Q3LIA5; Q75L23	PRS7_HUMAN; Q3LIA5_HUMAN; Q75L23_HUMAN
152	IPI00021785	COX5B	129	129	129	1.4E+04	1.4E+04	1.4E+04	9.3	2	0	0	1	1	CYTOCHROME C OXIDASE SUBUNIT 5B, MITOCHONDRIAL PRECURSOR.	P10606; Q53YB7; Q6FHJ9; Q6FHM4; Q96J18; Q99610	COX5B_HUMAN; Q53YB7_HUMAN; Q6FHJ9_HUMAN; Q6FHM4_HUMAN
153	IPI00021812; IPI00555610	AHNAK	2960	2961	2961	3.1E+05	3.1E+05	3.1E+05	1.4	3	0	0	1	0	NEUROBLAST DIFFERENTIATION-ASSOCIATED PROTEIN AHNAK (FRAGMENT).; 313 KDA PROTEIN.	Q09666; Q13727; Q6ZQN2; Q8N274	; AHNK_HUMAN; Q13727_HUMAN; Q6ZQN2_HUMAN; Q8N274_HUMAN
154	IPI00021831	PRKAR1A	381	381	381	4.3E+04	4.3E+04	4.3E+04	32.3	11	1	1	1	1	CAMP-DEPENDENT PROTEIN KINASE TYPE I-ALPHA REGULATORY SUBUNIT.	P10644; Q567S7; Q68DQ4	KAP0_HUMAN; Q68DQ4_HUMAN
155	IPI00021841	APOA1	267	267	267	3.1E+04	3.1E+04	3.1E+04	42.3	12	1	1	1	1	APOLIPOPROTEIN A-I PRECURSOR.	P02647; Q6LDN9; Q6LEJ8; Q6Q785; Q8TDB0; Q9UCT8; Q9Y355	APOA1_HUMAN; Q6LEJ8_HUMAN; Q8TDB0_HUMAN; Q9UCT8_HUMAN; Q9Y355_HUMAN
156	IPI00021890; IPI00747151	HSD17B8	231	261	246	2.4E+04	2.7E+04	2.5E+04	16.1	3	0	0	1	1	ESTRADIOL 17-BETA-DEHYDROGENASE 8.; 24 KDA PROTEIN.	Q5STP7; Q92506; Q9UIQ1	; DHB8_HUMAN; Q5STP7_HUMAN
157	IPI00021925	CPT1B	843	843	843	9.5E+04	9.5E+04	9.5E+04	5.8	4	1	0	1	1	CARNITINE O-PALMITOYLTRANSFERASE I, MUSCLE ISOFORM.	A2RRE8; Q53FV7	A2RRE8_HUMAN; Q53FV7_HUMAN
158	IPI00022143; IPI00746655	FAM62A	1104	1114	1109	1.2E+05	1.2E+05	1.2E+05	8.6	6	1	1	1	0	ISOFORM 1 OF PROTEIN FAM62A.; ISOFORM 2 OF PROTEIN FAM62A.	A0FGR7; O94848; Q6PJN4; Q9BSJ8; Q9H6J1; Q9H6W2; Q9Y416	A0FGR7_HUMAN; FA62A_HUMAN
159	IPI00022200; IPI00072917; IPI00072918; IPI00220701; IPI00376964	COL6A3	2971	3177	3022	3.2E+05	3.4E+05	3.3E+05	1.4	3	0	1	1	1	ALPHA 3 TYPE VI COLLAGEN ISOFORM 1 PRECURSOR.; ALPHA 3 TYPE VI COLLAGEN ISOFORM 3 PRECURSOR.; ALPHA 3 TYPE VI COLLAGEN ISOFORM 4 PRECURSOR.; ISOFORM 2 OF COLLAGEN ALPHA-3(VI) CHAIN PRECURSOR.; ALPHA 3 TYPE VI COLLAGEN ISOFORM 2 PRECURSOR.	P12111; Q16501; Q53QF4; Q53QF6; Q59F25; Q63HQ4; Q6MZG6; Q8N4Z1	; CO6A3_HUMAN; Q53QF4_HUMAN; Q53QF6_HUMAN; Q59F25_HUMAN; Q63HQ4_HUMAN; Q6MZG6_HUMAN; Q8N4Z1_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
160	IPI00022202; IPI00215777; IPI00788624; IPI00789657; IPI00790115; IPI00793177	SLC25A3	215	362	316	2.4E+04	4.0E+04	3.5E+04	12.2	4	1	1	1	1	ISOFORM A OF PHOSPHATE CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR.; ISOFORM B OF PHOSPHATE CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR.; 31 KDA PROTEIN.; 36 KDA PROTEIN.; CDNA FLJ90278 FIS, CLONE NT2RP1000325, HIGHLY SIMILAR TO PHOSPHATECARRIER PROTEIN, MITOCHONDRIALPRECURSOR.; 24 KDA PROTEIN.	Q00325; Q53HC3; Q7Z7N7; Q8NCF7; Q96A03	; MPCP_HUMAN; Q53HC3_HUMAN; Q7Z7N7_HUMAN; Q8NCF7_HUMAN
161	IPI00022305	BZW2	419	419	419	4.8E+04	4.8E+04	4.8E+04	9.3	3	1	1	1	0	BASIC LEUCINE ZIPPER AND W2 DOMAIN-CONTAINING PROTEIN 2.	Q3B779; Q75MG1; Q9H3F7; Q9Y6E2	BZW2_HUMAN; Q75MG1_HUMAN
162	IPI00022314	SOD2	222	222	222	2.5E+04	2.5E+04	2.5E+04	33.3	8	1	1	1	1	SUPEROXIDE DISMUTASE [MN], MITOCHONDRIAL PRECURSOR.	P04179; P78434; Q16792; Q4ZJI1; Q5TCM1; Q7Z7M4; Q7Z7M5; Q7Z7M6; Q7Z7M7; Q96EE6; Q9P2Z3	Q4ZJI1_HUMAN; Q7Z7M4_HUMAN; Q7Z7M5_HUMAN; Q7Z7M6_HUMAN; Q7Z7M7_HUMAN; SODM_HUMAN
163	IPI00022361; IPI00791534	SLC4A1	911	929	920	1.0E+05	1.0E+05	1.0E+05	20.2	13	1	1	1	1	BAND 3 ANION TRANSPORT PROTEIN.; SOLUTE CARRIER FAMILY 4 ANION EXCHANGER MEMBER 1 VARIANT.	P02730; P78487; Q1ZZ45; Q4KKW9; Q4VB84	B3AT_HUMAN; Q1ZZ45_HUMAN; Q4KKW9_HUMAN
164	IPI00022433	HSPB6	175	175	175	1.9E+04	1.9E+04	1.9E+04	41.7	6	1	1	1	1	ALPHA CRYSTALLIN FAMILY PROTEIN.		
165	IPI00022442	NDUFAB1	156	156	156	1.7E+04	1.7E+04	1.7E+04	15.4	3	0	0	1	1	ACYL CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR.	O14561; Q9UNV1	ACPM_HUMAN
166	IPI00022463; IPI00798430	TF	698	698	698	7.7E+04	7.7E+04	7.7E+04	29.1	17	1	1	1	1	SEROTRANSFERRIN PRECURSOR.; TRANSFERRIN VARIANT (FRAGMENT).	A0PJA6; O43890; P02787; Q06AH7; Q1HBA5; Q53H26; Q9NQB8; Q9UHV0	A0PJA6_HUMAN; Q06AH7_HUMAN; Q1HBA5_HUMAN; Q53H26_HUMAN; TRFE_HUMAN
167	IPI00022744; IPI00219994	CSE1L	945	971	958	1.1E+05	1.1E+05	1.1E+05	8.7	7	1	1	1	1	ISOFORM 1 OF EXPORTIN-2.; ISOFORM 3 OF EXPORTIN-2.	O75432; P55060; Q32M40; Q9H5B7; Q9NTS0; Q9UP98; Q9UP99; Q9UPA0	XPO2_HUMAN
168	IPI00022774	VCP	806	806	806	8.9E+04	8.9E+04	8.9E+04	29.7	19	1	1	1	1	TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE.	P55072; Q0IIN5; Q0V924; Q5VYM0; Q969G7; Q96IF9; Q9HAP0; Q9HAP1; Q9NTC4	Q0IIN5_HUMAN; Q0V924_HUMAN; Q5VYM0_HUMAN; Q96IF9_HUMAN; Q9HAP0_HUMAN; Q9HAP1_HUMAN; Q9NTC4_HUMAN; TERA_HUMAN
169	IPI00022793	HADHB	475	475	475	5.1E+04	5.1E+04	5.1E+04	40.6	19	1	1	1	1	TRIFUNCTIONAL ENZYME BETA SUBUNIT, MITOCHONDRIAL PRECURSOR.	Q9T2V8	Q9T2V8_HUMAN
170	IPI00022891	SLC25A4	298	298	298	3.3E+04	3.3E+04	3.3E+04	34.9	10	1	1	1	1	ADP/ATP TRANSLOCASE 1.	P12235	ADT1_HUMAN
171	IPI00023191	TOM1	493	493	493	5.4E+04	5.4E+04	5.4E+04	10.1	4	1	1	1	0	TARGET OF MYB1.	Q86X74	Q86X74_HUMAN
172	IPI00023635; IPI00555726	IMPA2	261	288	275	2.9E+04	3.1E+04	3.0E+04	7.6	2	0	0	1	0	ISOFORM 1 OF INOSITOL MONOPHOSPHATASE 2.; ISOFORM 2 OF INOSITOL MONOPHOSPHATASE 2.	O14732; Q9UJT3; Q9UNV4; Q9UNV5; Q9UNV6; Q9UPE5; Q9UPE6; Q9UPE7; Q9UPE8	IMPA2_HUMAN; Q9UNV4_HUMAN; Q9UNV5_HUMAN; Q9UNV6_HUMAN; Q9UPE5_HUMAN; Q9UPE6_HUMAN; Q9UPE7_HUMAN; Q9UPE8_HUMAN
173	IPI00023640	PDCD5	125	125	125	1.4E+04	1.4E+04	1.4E+04	28.8	3	0	0	1	1	PROGRAMMED CELL DEATH PROTEIN 5.	O14737; Q53YC9; Q6IB70	PDCD5_HUMAN
174	IPI00024046	CDH13	713	713	713	7.8E+04	7.8E+04	7.8E+04	7.6	4	1	1	1	1	CADHERIN-13 PRECURSOR.	P55290; Q6GTW4; Q8TBX3	CAD13_HUMAN
175	IPI00024157	FKBP3	224	224	224	2.5E+04	2.5E+04	2.5E+04	25.0	6	0	0	1	1	FK506-BINDING PROTEIN 3.	Q00688; Q14317; Q53GD8	FKBP3_HUMAN; Q53GD8_HUMAN
176	IPI00024175	PSMA7	248	248	248	2.8E+04	2.8E+04	2.8E+04	26.2	5	0	0	1	1	ISOFORM 1 OF PROTEASOME SUBUNIT ALPHA TYPE 7.	O14818; Q05DH1; Q9BR53; Q9H4K5; Q9UEU8	PSA7_HUMAN; Q05DH1_HUMAN
177	IPI00024664; IPI00375145	USP5	835	858	847	9.3E+04	9.6E+04	9.5E+04	15.2	7	1	1	1	1	ISOFORM LONG OF UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 5.; ISOFORM SHORT OF UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 5.	P45974; Q96J22	UBP5_HUMAN
178	IPI00024670; IPI00744902	REEP5	185	189	187	2.1E+04	2.1E+04	2.1E+04	6.4	2	0	0	1	0	RECEPTOR EXPRESSION-ENHANCING PROTEIN 5.; 21 KDA PROTEIN.	Q00765; Q04198; Q5QGT0; Q9BWH9	; REEP5_HUMAN
179	IPI00024804; IPI00396118; IPI00794585	ATP2A1	807	1001	934	8.8E+04	1.1E+05	1.0E+05	35.9	42	1	1	1	1	ISOFORM SERCA1B OF SARCOPLASMIC/ENDOPLASMIC RETICULUM CALCIUM ATPASE1.; ISOFORM SERCA1A OF SARCOPLASMIC/ENDOPLASMIC RETICULUM CALCIUM ATPASE1.; SIMILAR TO ATPASE, CA++ TRANSPORTING, CARDIAC MUSCLE, FAST TWITCH 1.	O14983; O14984; Q7Z675; Q7Z6E5; Q8N3X5	AT2A1_HUMAN; Q7Z675_HUMAN; Q7Z6E5_HUMAN; Q8N3X5_HUMAN
180	IPI00024915; IPI00759663	PRDX5	162	214	188	1.7E+04	2.2E+04	2.0E+04	27.2	4	1	0	1	1	ISOFORM MITOCHONDRIAL OF PEROXIREDOXIN-5, MITOCHONDRIAL PRECURSOR.; ISOFORM CYTOPLASMIC+PEROXISOMAL OF PEROXIREDOXIN-5, MITOCHONDRIALPRECURSOR.	P30044; Q14CK0; Q6IAF2; Q9UBU5; Q9UJU4; Q9UKX4	PRDX5_HUMAN
181	IPI00024919; IPI00374151	PRDX3	238	256	247	2.6E+04	2.8E+04	2.7E+04	18.4	4	0	1	1	1	THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE, MITOCHONDRIAL PRECURSOR.; PEROXIREDOXIN 3 ISOFORM B.	P30048; P35690; Q0D2H1; Q13776; Q14579; Q53HC2; Q5T5V2; Q96HK4	PRDX3_HUMAN; Q14579_HUMAN; Q53HC2_HUMAN
182	IPI00024920	ATP5D	168	168	168	1.7E+04	1.7E+04	1.7E+04	22.6	3	1	0	1	1	ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR.	P30049; Q6FG90	ATPD_HUMAN; Q6FG90_HUMAN
183	IPI00024983; IPI00410134	RTN2	205	545	375	2.2E+04	5.9E+04	4.1E+04	14.2	5	1	1	1	1	ISOFORM RTN2-A OF RETICULON-2.; ISOFORM RTN2-C OF RETICULON-2.	O60509; O75298; Q6GMT0; Q7RTM6; Q7RTN0; Q7RTN1; Q7RTN2	Q6GMT0_HUMAN; Q7RTN0_HUMAN; RTN2_HUMAN
184	IPI00024993	ECHS1	290	290	290	3.1E+04	3.1E+04	3.1E+04	18.6	5	0	0	1	1	ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR.	O00739; P30084; Q5VWY1; Q96H54	ECHM_HUMAN
185	IPI00025019	PSMB1	241	241	241	2.6E+04	2.6E+04	2.6E+04	8.3	2	0	0	1	0	PROTEASOME SUBUNIT BETA TYPE 1 PRECURSOR.	P20618; Q53FT8; Q9BWA8	PSB1_HUMAN; Q53FT8_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
186	IPI00025084; IPI00794720	CAPNS1	268	322	295	2.8E+04	3.4E+04	3.1E+04	18.3	4	0	0	1	1	CALPAIN SMALL SUBUNIT 1.; 34 KDA PROTEIN.	P04632; Q8WTX3; Q96EW0	; CPNS1_HUMAN
187	IPI00025086	COX5A	150	150	150	1.7E+04	1.7E+04	1.7E+04	24.7	3	1	0	1	1	CYTOCHROME C OXIDASE SUBUNIT 5A, MITOCHONDRIAL PRECURSOR.	P20674; P30045; Q71UP1; Q8TB65	COX5A_HUMAN; Q71UP1_HUMAN; Q8TB65_HUMAN
188	IPI00025092; IPI00791650; IPI00797657	MYBPC1	1123	1141	1130	1.3E+05	1.3E+05	1.3E+05	54.4	72	1	1	1	1	MYOSIN-BINDING PROTEIN C, SLOW-TYPE.; 127 KDA PROTEIN.; MYOSIN BINDING PROTEIN C, SLOW TYPE ISOFORM 4.	Q00872; Q15497; Q569K7; Q63HJ3	; MYPC1_HUMAN; Q569K7_HUMAN; Q63HJ3_HUMAN
189	IPI00025239	NDUFS2	463	463	463	5.3E+04	5.3E+04	5.3E+04	45.1	15	1	1	1	1	NADH DEHYDROGENASE [UBIQUINONE] IRON-SULFUR PROTEIN 2, MITOCHONDRIALPRECURSOR.	O75306; Q53HG2; Q5VTW0; Q969P3; Q9HC11; Q9HC12; Q9UEV3	NDUS2_HUMAN; Q53HG2_HUMAN; Q5VTW0_HUMAN; Q9HC11_HUMAN; Q9HC12_HUMAN
190	IPI00025252; IPI00657680	PDIA3	485	505	495	5.5E+04	5.7E+04	5.6E+04	22.0	8	1	1	1	0	PROTEIN DISULFIDE-ISOMERASE A3 PRECURSOR.; 55 KDA PROTEIN.	P30101; Q13453; Q14255; Q8IYF8; Q9UMU7	; PDIA3_HUMAN
191	IPI00025366	CS	466	466	466	5.2E+04	5.2E+04	5.2E+04	31.8	14	1	1	1	1	CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR.	O75390; Q71UT9; Q7KZH0; Q96FZ8; Q9BWN8	CISY_HUMAN
192	IPI00025512	HSPB1	205	205	205	2.3E+04	2.3E+04	2.3E+04	74.6	14	1	1	1	1	HEAT-SHOCK PROTEIN BETA-1.	P04792; Q6FI47; Q96C20; Q96EI7; Q9UC31; Q9UC35	HSPB1_HUMAN; Q96C20_HUMAN; Q96EI7_HUMAN; Q9UC35_HUMAN
193	IPI00025753	DSG1	1049	1049	1049	1.1E+05	1.1E+05	1.1E+05	7.7	6	0	0	1	1	DESMOGLEIN-1 PRECURSOR.	Q02413; Q712V6	DSG1_HUMAN; Q712V6_HUMAN
194	IPI00025796	NDUFS3	264	264	264	3.0E+04	3.0E+04	3.0E+04	20.4	5	1	1	1	1	NADH DEHYDROGENASE [UBIQUINONE] IRON-SULFUR PROTEIN 3, MITOCHONDRIALPRECURSOR.	O75489; Q53FM7; Q9UF24; Q9UNQ8	NDUS3_HUMAN; Q53FM7_HUMAN; Q9UF24_HUMAN
195	IPI00025819	CAPN3	821	821	821	9.4E+04	9.4E+04	9.4E+04	12.6	7	1	1	1	1	ISOFORM I OF CALPAIN-3.	P20807; Q9BTU4; Q9Y5S6; Q9Y5S7	CAN3_HUMAN
196	IPI00025874	RPN1	646	646	646	7.3E+04	7.3E+04	7.3E+04	15.8	7	1	1	1	1	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 67 KDASUBUNIT PRECURSOR.	Q53EP4; Q68DT1; Q6IBR0; Q96HX3	Q53EP4_HUMAN; Q68DT1_HUMAN; Q6IBR0_HUMAN; Q96HX3_HUMAN
197	IPI00025879	MYH1	1939	1939	1939	2.2E+05	2.2E+05	2.2E+05	62.0	224	1	1	1	1	MYOSIN-1.	P12882; Q14CA4; Q9Y622	MYH1_HUMAN
198	IPI00025880	MYH7	1935	1935	1935	2.2E+05	2.2E+05	2.2E+05	67.4	238	1	1	1	1	MYOSIN-7.	A2TDB6; P12883; Q14836; Q14837; Q14904; Q14905; Q16579; Q2M1Y6; Q2XUS2; Q59EV3; Q5GJ54; Q92679; Q9H1D5; Q9UDA2; Q9UMM8	A2TDB6_HUMAN; MYH7_HUMAN; Q14905_HUMAN; Q2XUS2_HUMAN; Q59EV3_HUMAN; Q5GJ54_HUMAN; Q9UDA2_HUMAN
199	IPI00025974	CHMP4B	224	224	224	2.5E+04	2.5E+04	2.5E+04	17.9	3	0	1	1	1	CHARGED MULTIVESICULAR BODY PROTEIN 4B.	Q53ZD6; Q9H444	CHM4B_HUMAN
200	IPI00026154; IPI00792916; IPI00829824	PRKCSH	181	528	412	2.0E+04	5.9E+04	4.6E+04	6.3	3	1	1	1	0	GLUCOSIDASE 2 SUBUNIT BETA PRECURSOR.; GLUCOSIDASE II BETA SUBUNIT PRECURSOR.; HAPLN4 PROTEIN (FRAGMENT).	A2VCQ4; P14314; Q96BU9; Q96D06; Q9P0W9	; A2VCQ4_HUMAN; GLU2B_HUMAN
201	IPI00026185	CAPZB	277	277	277	3.1E+04	3.1E+04	3.1E+04	8.7	2	0	0	1	0	ISOFORM 1 OF F-ACTIN CAPPING PROTEIN SUBUNIT BETA.	P47756; Q5U0L4; Q8TB49; Q9NUC4	CAPZB_HUMAN
202	IPI00026216	NPEPPS	919	919	919	1.0E+05	1.0E+05	1.0E+05	34.9	25	1	1	1	1	PUROMYCIN-SENSITIVE AMINOPEPTIDASE.	P55786; Q6P145; Q9NP16; Q9UEM2	PSA_HUMAN
203	IPI00026271	RPS14	151	151	151	1.6E+04	1.6E+04	1.6E+04	15.2	2	0	0	1	0	40S RIBOSOMAL PROTEIN S14.	P06366; P62263; Q5BJI0	RS14_HUMAN
204	IPI00026272; IPI00031562; IPI00081836; IPI00102165; IPI00216456; IPI00216457; IPI00220855; IPI00255316; IPI00291764; IPI00339274; IPI00552873	H2AFJ; HIST1H2AB; HIST1H2AC; HIST1H2AD; HIST1H2AE; HIST1H2AG; HIST1H2AH; HIST1H2AI; HIST1H2AJ; HIST1H2AK; HIST1H2AL; HIST1H2AM; HIST2H2AA3; HIST2H2AA4;	128	155	132	1.4E+04	1.7E+04	1.4E+04	35.7	4	1	0	1	1	HISTONE H2A TYPE 1-B.; HISTONE H2A TYPE 3.; HISTONE H2A TYPE 1-H.; H2A HISTONE FAMILY, MEMBER J ISOFORM 1.; HISTONE H2A TYPE 1-C.; HISTONE H2A TYPE 2-A.; H2A HISTONE FAMILY, MEMBER J ISOFORM 2.; HISTONE H2A TYPE 1-D.; HISTONE H2A TYPE 1.; HISTONE H2A TYPE 2-C.; HISTONE H2A TYPE 1-J.	A0PK91; A2RUU6; O00775; O00776; O00777; O00778; P02261; P04908; P0C0S8; P20670; P20671; P57754; Q08AJ9; Q16777; Q2M1R2; Q540R1; Q5JXQ5; Q6DRA7; Q6FGY6; Q6FI13; Q76PA6; Q7L7L0; Q8IUE5; Q93077; Q96KK5; Q99878; Q9BTM1; Q9NV63	A2RUU6_HUMAN; H2A1B_HUMAN; H2A1C_HUMAN; H2A1D_HUMAN; H2A1H_HUMAN; H2A1J_HUMAN; H2A1_HUMAN; H2A2A_HUMAN; H2A2C_HUMAN; H2A3_HUMAN; Q08AJ9_HUMAN; Q9BTM1_HUMAN; Q9NV63_HUMAN
205	IPI00026314; IPI00646773	GSN	731	782	757	8.1E+04	8.6E+04	8.3E+04	25.4	12	1	1	1	1	ISOFORM 1 OF GELSOLIN PRECURSOR.; ISOFORM 2 OF GELSOLIN PRECURSOR.	A2A418; P06396; Q5T0I2; Q8WVV7	A2A418_HUMAN; GELS_HUMAN; Q5T0I2_HUMAN
206	IPI00026538	SH3BGR	239	239	239	2.6E+04	2.6E+04	2.6E+04	23.9	4	0	0	1	1	SH3 DOMAIN-BINDING GLUTAMIC ACID-RICH PROTEIN.	P55822; Q53Y47; Q9BRB8	Q53Y47_HUMAN; SH3BG_HUMAN
207	IPI00026665	QARS	793	793	793	9.0E+04	9.0E+04	9.0E+04	9.5	6	1	1	1	1	GLUTAMINYL-TRNA SYNTHETASE.	Q53HS0; Q96AW5	Q53HS0_HUMAN; Q96AW5_HUMAN
208	IPI00026904	ADSL	484	484	484	5.5E+04	5.5E+04	5.5E+04	32.2	10	1	1	1	1	ISOFORM 1 OF ADENYLOSUCCINATE LYASE.	O75495; P30566; Q5TI34; Q71UA4	PUR8_HUMAN; Q71UA4_HUMAN
209	IPI00026964	UQCRFS1	274	274	274	3.0E+04	3.0E+04	3.0E+04	21.5	5	1	1	1	1	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIALPRECURSOR.	P47985; Q6NVX5; Q9UPH2	UCRI_HUMAN
210	IPI00027107	TUFM	455	455	455	5.0E+04	5.0E+04	5.0E+04	44.2	15	1	1	1	1	TU TRANSLATION ELONGATION FACTOR, MITOCHONDRIAL.		
211	IPI00027146	GLUD2	558	558	558	6.1E+04	6.1E+04	6.1E+04	3.4	2	0	0	1	0	GLUTAMATE DEHYDROGENASE 2, MITOCHONDRIAL PRECURSOR.	P49448; Q9BSD0; Q9UDQ4	DHE4_HUMAN; Q9BSD0_HUMAN
212	IPI00027230	HSP90B1	803	803	803	9.2E+04	9.2E+04	9.2E+04	10.1	7	1	1	1	1	ENDOPLASMIN PRECURSOR.	P14625; Q59FC6; Q5CAQ5; Q96A97; Q96GW1	ENPL_HUMAN; Q59FC6_HUMAN; Q5CAQ5_HUMAN; Q96GW1_HUMAN
213	IPI00027252	PHB2	299	299	299	3.3E+04	3.3E+04	3.3E+04	37.1	10	1	1	1	1	PROHIBITIN-2.	Q2YDA4; Q7KYU3; Q92978; Q99623; Q9BXV3	PHB2_HUMAN; Q9BXV3_HUMAN
214	IPI00027255	MYL6; MYL6B	208	208	208	2.3E+04	2.3E+04	2.3E+04	45.7	9	1	1	1	1	MYOSIN LIGHT POLYPEPTIDE 6B.	P14649	MYL6B_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
215	IPI00027350; IPI00375400	PRDX2	148	198	173	1.6E+04	2.2E+04	1.9E+04	58.8	11	1	1	1	1	PEROXIREDOXIN-2.; 16 KDA PROTEIN.	P31945; P32118; P32119; P35701; Q6FHG4; Q92763	; PRDX2_HUMAN
216	IPI00027448	ATP5L	103	103	103	1.1E+04	1.1E+04	1.1E+04	54.4	7	1	0	1	1	ATP SYNTHASE SUBUNIT G, MITOCHONDRIAL.	O75964; Q96BV6; Q9UBZ7	ATP5L_HUMAN
217	IPI00027487	CKM	381	381	381	4.3E+04	4.3E+04	4.3E+04	59.8	46	1	1	1	1	CREATINE KINASE M-TYPE.	P06732; Q96QL9	KCRM_HUMAN
218	IPI00027497	GPI	558	558	558	6.3E+04	6.3E+04	6.3E+04	47.0	24	1	1	1	1	GLUCOSE-6-PHOSPHATE ISOMERASE.	P06744; Q9BRD3; Q9BSK5; Q9UHE6	G6PI_HUMAN; Q9BRD3_HUMAN
219	IPI00027547	DCD	110	110	110	1.1E+04	1.1E+04	1.1E+04	22.7	3	0	0	1	0	DERMCIDIN PRECURSOR.	P58461; P81605; Q53YJ2	DCD_HUMAN; Q53YJ2_HUMAN
220	IPI00027809; IPI00181738; IPI00218862; IPI00748557	PPP3CB	496	525	512	5.6E+04	5.9E+04	5.8E+04	10.3	4	1	1	1	1	PROTEIN PHOSPHATASE 3 (FORMERLY 2B), CATALYTIC SUBUNIT, BETA ISOFORM.; ISOFORM 3 OF SERINE/THREONINE-PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNITBETA ISOFORM.; ISOFORM 2 OF SERINE/THREONINE-PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNITBETA ISOFORM.; SERINE/THREONINE PROTEIN PHOSPHATASE.	P16298; P16299; Q5F2F8; Q5F2F9; Q8N1F0; Q8N3W4; Q9UMB2	PP2BB_HUMAN; Q5F2F8_HUMAN; Q5F2F9_HUMAN; Q8N1F0_HUMAN; Q9UMB2_HUMAN
221	IPI00028004; IPI00788896; IPI00789577	PSMB3	107	205	141	1.2E+04	2.3E+04	1.6E+04	19.0	3	0	0	1	0	PROTEASOME SUBUNIT BETA TYPE 3.; 13 KDA PROTEIN.; 12 KDA PROTEIN.	P31147; P49720; Q0P6J7; Q96E27	; PSB3_HUMAN
222	IPI00028520; IPI00221298	NDUFV1	455	464	460	5.0E+04	5.1E+04	5.0E+04	24.1	12	1	1	1	1	ISOFORM 1 OF NADH DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN 1,MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF NADH DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN 1,MITOCHONDRIAL PRECURSOR.	O60924; O60940; P49821; Q16104; Q53G70; Q6IBR3; Q96BF8; Q96HS7; Q96ID4	NDUV1_HUMAN; Q53G70_HUMAN; Q6IBR3_HUMAN; Q96ID4_HUMAN
223	IPI00029111	DPYSL3	684	684	684	7.4E+04	7.4E+04	7.4E+04	15.8	7	1	1	1	1	DPYSL3 PROTEIN.	Q6DEN2; Q8IXW6	Q6DEN2_HUMAN; Q8IXW6_HUMAN
224	IPI00029133; IPI00456747	ATP5F1	195	256	226	2.2E+04	2.9E+04	2.6E+04	35.6	9	1	1	1	1	ATP SYNTHASE B CHAIN, MITOCHONDRIAL PRECURSOR.; ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F0 COMPLEX, SUBUNIT B1.	P24539; Q08ET0; Q53GB3; Q5QNZ2; Q9BQ68; Q9BRU8	AT5F1_HUMAN; Q08ET0_HUMAN; Q53GB3_HUMAN; Q5QNZ2_HUMAN
225	IPI00029264	CYC1	325	325	325	3.5E+04	3.5E+04	3.5E+04	16.3	5	0	0	1	1	CYTOCHROME C1 HEME PROTEIN, MITOCHONDRIAL PRECURSOR.	P08574; Q5U062; Q6FHS7; Q8TBT6	CY1_HUMAN; Q8TBT6_HUMAN
226	IPI00029558	NDUFC2	119	119	119	1.4E+04	1.4E+04	1.4E+04	16.8	2	0	0	1	1	NADH DEHYDROGENASE [UBIQUINONE] 1 SUBUNIT C2.	O95298; Q549M5; Q6FIH8; Q9UBJ9	NDUC2_HUMAN; Q549M5_HUMAN; Q6FIH8_HUMAN
227	IPI00029561	NDUFA10	355	355	355	4.1E+04	4.1E+04	4.1E+04	15.8	6	1	1	1	0	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 10,MITOCHONDRIAL PRECURSOR.	O95299; Q53QE8; Q53SW4; Q7Z518	NDUAA_HUMAN; Q53QE8_HUMAN; Q53SW4_HUMAN; Q7Z518_HUMAN
228	IPI00029623	PSMA6	246	246	246	2.7E+04	2.7E+04	2.7E+04	14.2	3	0	0	1	1	PROTEASOME SUBUNIT ALPHA TYPE 6.	P34062; P60900; Q6IB60; Q9BZ93	PSA6_HUMAN; Q9BZ93_HUMAN
229	IPI00029722	KIF5A	1032	1032	1032	1.2E+05	1.2E+05	1.2E+05	2.4	2	0	0	1	0	KINESIN HEAVY CHAIN ISOFORM 5A.	Q12840; Q4LE26	KIF5A_HUMAN
230	IPI00030104	MYBPC2	1142	1142	1142	1.3E+05	1.3E+05	1.3E+05	43.4	47	1	1	1	1	MYOSIN-BINDING PROTEIN C, FAST-TYPE.	A1L4G9; Q14324	A1L4G9_HUMAN; MYPC2_HUMAN
231	IPI00030182	GAMT	236	236	236	2.6E+04	2.6E+04	2.6E+04	18.6	3	0	0	1	0	GUANIDINOACETATE N-METHYLTRANSFERASE.	Q14353; Q53Y34; Q8WVJ1	GAMT_HUMAN
232	IPI00030275	TRAP1	704	704	704	8.0E+04	8.0E+04	8.0E+04	16.8	8	1	1	1	1	HEAT SHOCK PROTEIN 75 KDA, MITOCHONDRIAL PRECURSOR.	O43642; O75235; Q12931; Q53FS6; Q53G55; Q59EK6; Q5CAQ4; Q8N9Z3; Q9BV61; Q9UHL5	Q53FS6_HUMAN; Q53G55_HUMAN; Q59EK6_HUMAN; Q5CAQ4_HUMAN; Q8N9Z3_HUMAN; Q9BV61_HUMAN; TRAP1_HUMAN
233	IPI00030363	ACAT1	427	427	427	4.5E+04	4.5E+04	4.5E+04	53.6	24	1	1	1	1	ACETYL-COA ACETYLTRANSFERASE, MITOCHONDRIAL PRECURSOR.	P24752	THIL_HUMAN
234	IPI00030405	HSPB3	150	150	150	1.7E+04	1.7E+04	1.7E+04	16.0	2	0	0	1	0	HEAT-SHOCK PROTEIN BETA-3.	Q12988; Q6ICS9	HSPB3_HUMAN; Q6ICS9_HUMAN
235	IPI00030702; IPI00607898; IPI00792971; IPI00795359; IPI00795821	IDH3A	217	366	304	2.3E+04	4.0E+04	3.3E+04	21.0	6	1	1	1	0	ISOFORM 1 OF ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT ALPHA,MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT ALPHA,MITOCHONDRIAL PRECURSOR.; ISOCITRATE DEHYDROGENASE 3 (NAD+) ALPHA VARIANT (FRAGMENT).; 28 KDA PROTEIN.; 23 KDA PROTEIN.	P50213; Q53GF8; Q9H3X0	; IDH3A_HUMAN; Q53GF8_HUMAN
236	IPI00030828; IPI00607861	H6PD	791	802	797	8.9E+04	9.0E+04	9.0E+04	3.4	2	0	1	1	0	90 KDA PROTEIN.; GDH/6PGL ENDOPLASMIC BIFUNCTIONAL PROTEIN PRECURSOR.	O95479; Q4TT33; Q66I35; Q68DT3	; G6PE_HUMAN
237	IPI00030986; IPI00220297	KBTBD10	596	606	601	6.7E+04	6.8E+04	6.7E+04	15.7	8	1	1	1	1	ISOFORM LONG OF KELCH REPEAT AND BTB DOMAIN-CONTAINING PROTEIN 10.; ISOFORM SHORT OF KELCH REPEAT AND BTB DOMAIN-CONTAINING PROTEIN 10.	O60662; Q3ZTS6; Q53R42	KBTBA_HUMAN; Q3ZTS6_HUMAN; Q53R42_HUMAN
238	IPI00031107; IPI00414384	HSDL2	345	418	382	3.7E+04	4.5E+04	4.1E+04	23.9	8	1	1	1	1	HSDL2 PROTEIN.; HYDROXYSTEROID DEHYDROGENASE-LIKE PROTEIN.	Q658M8; Q6YN16; Q9BT58	Q658M8_HUMAN; Q6YN16_HUMAN; Q9BT58_HUMAN
239	IPI00031169	RAB2A	212	212	212	2.4E+04	2.4E+04	2.4E+04	19.3	3	0	0	1	1	RAS-RELATED PROTEIN RAB-2A.	O75546; P08886; P61019	O75546_HUMAN; RAB2A_HUMAN
240	IPI00031397	ACSL3	720	720	720	8.0E+04	8.0E+04	8.0E+04	8.6	4	1	1	1	0	LONG-CHAIN-FATTY-ACID--COA LIGASE 3.	O95573; Q60I92; Q6PIM8; Q8IUM9	ACSL3_HUMAN; Q6PIM8_HUMAN
241	IPI00031461	GDI2	445	445	445	5.1E+04	5.1E+04	5.1E+04	31.2	11	1	1	1	1	RAB GDP DISSOCIATION INHIBITOR BETA.	O43928; P50395; Q6IAT1; Q9UQM6	GDIB_HUMAN; Q6IAT1_HUMAN
242	IPI00031522	HADHA	763	763	763	8.3E+04	8.3E+04	8.3E+04	48.4	34	1	1	1	1	TRIFUNCTIONAL ENZYME SUBUNIT ALPHA, MITOCHONDRIAL PRECURSOR.	P40939; Q16679; Q53T69; Q53TA2; Q96GT7; Q9UQC5	ECHA_HUMAN; Q53T69_HUMAN; Q53TA2_HUMAN; Q9UQC5_HUMAN
243	IPI00031697	TMEM109	243	243	243	2.6E+04	2.6E+04	2.6E+04	5.4	2	0	0	1	0	TRANSMEMBRANE PROTEIN 109 PRECURSOR.	Q9BVC6	TM109_HUMAN
244	IPI00031804; IPI00294779	VDAC3	283	284	284	3.1E+04	3.1E+04	3.1E+04	28.3	7	1	0	1	1	ISOFORM 1 OF VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 3.; ISOFORM 2 OF VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 3.	Q9UIS0; Q9Y277	VDAC3_HUMAN
245	IPI00032137	ACTN3	901	901	901	1.0E+05	1.0E+05	1.0E+05	17.9	13	0	0	1	1	ALPHA-ACTININ-3.	Q08043; Q4JCP9; Q4KKV2; Q4VAM3	ACTN3_HUMAN; Q4JCP9_HUMAN; Q4VAM3_HUMAN
246	IPI00032195	HSPB2	307	307	307	3.3E+04	3.3E+04	3.3E+04	20.2	4	0	0	1	1	HEAT-SHOCK PROTEIN BETA-2.		

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]				Detection							
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
247	IPI00032450; IPI00783617	ASPH	210	225	218	2.4E+04	2.6E+04	2.5E+04	12.9	2	0	0	1	0	ASPARTATE BETA-HYDROXYLASE ISOFORM D.; ASPARTATE BETA-HYDROXYLASE ISOFORM E.	Q9NRI0; Q9NRI1	Q9NRI0_HUMAN; Q9NRI1_HUMAN
248	IPI00032561	CAB39	341	341	341	4.0E+04	4.0E+04	4.0E+04	17.9	6	1	1	1	0	CALCIUM-BINDING PROTEIN 39.	Q53RN7; Q7Z4X0; Q9Y376	CAB39_HUMAN; Q53RN7_HUMAN; Q7Z4X0_HUMAN
249	IPI00032826; IPI00168839	FAM10A5; ST13	369	369	369	4.1E+04	4.1E+04	4.1E+04	16.5	5	1	1	1	1	HSC70-INTERACTING PROTEIN.; PROTEIN FAM10A5.	A0AUJ6; O14999; P50502; Q0IJ56; Q1XBU6; Q1XBU7; Q2TU77; Q3KNR6; Q8NFI4	A0AUJ6_HUMAN; F10A1_HUMAN; F10A5_HUMAN; Q0IJ56_HUMAN; Q1XBU6_HUMAN; Q1XBU7_HUMAN; Q2TU77_HUMAN; Q3KNR6_HUMAN
250	IPI00032875; IPI00455179	ETFDH	584	617	601	6.5E+04	6.9E+04	6.7E+04	19.6	9	1	1	1	1	ISOFORM 1 OF ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE,MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE,MITOCHONDRIAL PRECURSOR.	Q16134; Q547S8; Q7Z347	ETFD_HUMAN; Q547S8_HUMAN
251	IPI00032959	GPD1L	351	351	351	3.8E+04	3.8E+04	3.8E+04	16.8	6	0	0	1	1	GLYCEROL-3-PHOSPHATE DEHYDROGENASE 1-LIKE.	Q14702; Q8N335; Q9BRM5	Q14702_HUMAN; Q8N335_HUMAN; Q9BRM5_HUMAN
252	IPI00033022; IPI00181352; IPI00218889; IPI00477431; IPI00514550; IPI00743573; IPI00794575	DNM2	866	872	869	9.8E+04	9.8E+04	9.8E+04	4.2	3	0	1	1	0	ISOFORM 1 OF DYNAMIN-2.; DYNAMIN 2 ISOFORM 4.; ISOFORM 2 OF DYNAMIN-2.; 98 KDA PROTEIN.; DYNAMIN 2 ISOFORM 2.; 98 KDA PROTEIN.; 98 KDA PROTEIN.	P50570; Q5I0Y0; Q7Z5S3; Q8N1K8; Q9UPH4; Q9UPH5	; DYN2_HUMAN; Q8N1K8_HUMAN; Q9UPH5_HUMAN
253	IPI00033036	METAP2	478	478	478	5.3E+04	5.3E+04	5.3E+04	7.3	3	0	0	1	0	METHIONINE AMINOPEPTIDASE 2.	P50579	AMPM2_HUMAN
254	IPI00033494; IPI00220573; IPI00604523; IPI00719669	MRCL3; MRLC2	171	177	173	2.0E+04	2.0E+04	2.0E+04	11.6	2	0	0	1	0	MYOSIN REGULATORY LIGHT CHAIN.; MYOSIN REGULATORY LIGHT CHAIN 2, NONSARCOMERIC.; MYOSIN REGULATORY LIGHT CHAIN MRCL3 VARIANT.; SIMILAR TO MYOSIN REGULATORY LIGHT CHAIN MRCL2.	O14950; P19105; Q13182; Q2F834; Q53HL1; Q53X45; Q7Z5Z4	MLRM_HUMAN; O14950_HUMAN; Q13182_HUMAN; Q2F834_HUMAN; Q53HL1_HUMAN; Q53X45_HUMAN; Q7Z5Z4_HUMAN
255	IPI00037283; IPI00146935; IPI00235412; IPI00473085; IPI00555883	DNM1L	699	736	716	7.8E+04	8.2E+04	8.0E+04	28.3	13	1	1	1	0	ISOFORM 5 OF DYNAMIN-1-LIKE PROTEIN.; ISOFORM 1 OF DYNAMIN-1-LIKE PROTEIN.; ISOFORM 3 OF DYNAMIN-1-LIKE PROTEIN.; ISOFORM 4 OF DYNAMIN-1-LIKE PROTEIN.; ISOFORM 2 OF DYNAMIN-1-LIKE PROTEIN.	O00429; O14541; O60709; Q32Q67; Q59GN9; Q7L6B3; Q8TBT7; Q9BWM1; Q9Y5J2	DNM1L_HUMAN; Q32Q67_HUMAN; Q59GN9_HUMAN
256	IPI00044608	KIAA1881	1357	1357	1357	1.3E+05	1.3E+05	1.3E+05	16.2	15	1	0	1	0	PLASMA MEMBRANE ASSOCIATED PROTEIN, S3-12.		
257	IPI00062037	DYNLL2	89	89	89	1.0E+04	1.0E+04	1.0E+04	20.2	2	0	0	1	0	DYNEIN LIGHT CHAIN 2, CYTOPLASMIC.	Q96FJ2	DYL2_HUMAN
258	IPI00063234; IPI00219774	PRKAR2A	382	404	393	4.3E+04	4.6E+04	4.4E+04	47.6	13	1	1	1	1	PRKAR2A PROTEIN.; CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY SUBUNIT.	P13861; Q16823; Q9BUB1	KAP2_HUMAN; Q9BUB1_HUMAN
259	IPI00063827	ABHD14B	210	210	210	2.2E+04	2.2E+04	2.2E+04	17.6	3	0	0	1	1	ISOFORM 1 OF ABHYDROLASE DOMAIN-CONTAINING PROTEIN 14B.	Q86VK8; Q8N8W5; Q96IU4	ABHEB_HUMAN
260	IPI00063903; IPI00640630	USMG5	58	58	58	6.5E+03	6.6E+03	6.5E+03	44.8	4	0	0	1	1	UP-REGULATED DURING SKELETAL MUSCLE GROWTH PROTEIN 5.; 7 KDA PROTEIN.	Q96IX5	; USMG5_HUMAN
261	IPI00065501	JSRP1	331	331	331	3.6E+04	3.6E+04	3.6E+04	21.8	4	1	1	1	1	JUNCTIONAL SARCOPLASMIC RETICULUM PROTEIN 1.	Q96MG2	Q96MG2_HUMAN
262	IPI00069693		215	215	215	2.3E+04	2.3E+04	2.3E+04	11.6	2	0	0	1	0	SIMILAR TO RIBOSOMAL PROTEIN L14.		
263	IPI00075248; IPI00386621; IPI00794543	CALM1; CALM2; CALM3	147	152	149	1.7E+04	1.7E+04	1.7E+04	41.6	4	0	0	1	1	CALMODULIN.; CALM3 PROTEIN.; 17 KDA PROTEIN.	P02593; P62158; P70667; P99014; Q13942; Q53S29; Q61379; Q61380; Q96HK3; Q96HY3; Q9BRL5	; CALM_HUMAN; Q96HY3_HUMAN; Q9BRL5_HUMAN
264	IPI00098902	OGDH	1023	1023	1023	1.2E+05	1.2E+05	1.2E+05	34.6	28	1	1	1	1	OXOGLUTARATE (ALPHA-KETOGLUTARATE) DEHYDROGENASE (LIPOAMIDE) ISOFORM 1PRECURSOR.	A2VCT3; Q9UDX0	A2VCT3_HUMAN; Q9UDX0_HUMAN
265	IPI00100160; IPI00746694	CAND1	1230	1230	1230	1.4E+05	1.4E+05	1.4E+05	7.9	7	1	1	1	0	ISOFORM 1 OF CULLIN-ASSOCIATED NEDD8-DISSOCIATED PROTEIN 1.; SIMILAR TO TIP120.	O94918; Q6PIY4; Q86VP6; Q8NDJ4; Q96JZ9; Q96T19; Q9BTC4; Q9H0G2; Q9P0H7; Q9UF85	; CAND1_HUMAN
266	IPI00100192; IPI00619911; IPI00647805; IPI00807412	NT5C3	285	336	301	3.3E+04	3.8E+04	3.4E+04	20.6	6	0	0	1	1	ISOFORM 3 OF CYTOSOLIC 5'-NUCLEOTIDASE III.; ISOFORM 1 OF CYTOSOLIC 5'-NUCLEOTIDASE III.; ISOFORM 4 OF CYTOSOLIC 5'-NUCLEOTIDASE III.; ISOFORM 2 OF CYTOSOLIC 5'-NUCLEOTIDASE III.	Q6IPZ1; Q6NXS6; Q7L3G6; Q9H0P0; Q9P0P5; Q9UC42; Q9UC43; Q9UC44; Q9UC45	5NT3_HUMAN
267	IPI00100775	C11orf67	122	122	122	1.3E+04	1.3E+04	1.3E+04	45.1	5	1	0	1	1	ISOFORM 1 OF UPF0366 PROTEIN C11ORF67.	Q96AQ4; Q9H7C9; Q9Y6B1	CK067_HUMAN
268	IPI00100980	EHD2	543	543	543	6.1E+04	6.1E+04	6.1E+04	32.2	13	1	1	1	1	EH DOMAIN-CONTAINING PROTEIN 2.	Q8NCJ3; Q96CB6; Q9NZN4	EHD2_HUMAN; Q8NCJ3_HUMAN
269	IPI00007935; IPI00103146; IPI00552367; IPI00553102	PDLIM5	214	596	383	2.4E+04	6.4E+04	4.2E+04	55.6	11	1	1	1	1	PDZ AND LIM DOMAIN PROTEIN 5.; PDZ AND LIM DOMAIN 5 ISOFORM E.; PDZ AND LIM DOMAIN 5 ISOFORM D.; PDZ AND LIM DOMAIN 5 ISOFORM B.	O60705; Q4W5K9; Q5UW38; Q8WVK0; Q96HC4; Q9P1D1	; PDLI5_HUMAN; Q4W5K9_HUMAN; Q5UW38_HUMAN; Q8WVK0_HUMAN; Q9P1D1_HUMAN
270	IPI00103467	ALDH1B1	517	517	517	5.7E+04	5.7E+04	5.7E+04	30.2	11	1	1	1	1	ALDEHYDE DEHYDROGENASE X, MITOCHONDRIAL PRECURSOR.	P30837; Q8WX76; Q9BV45	AL1B1_HUMAN
271	IPI00103994	LARS	1176	1176	1176	1.3E+05	1.3E+05	1.3E+05	4.2	4	0	1	1	0	LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC.	A2RRR4; Q2TU79; Q6NVI4; Q9H8E3; Q9HAM7; Q9NPU8; Q9NSE1; Q9NVC0; Q9NVP8; Q9P2J5	A2RRR4_HUMAN; Q2TU79_HUMAN; Q6NVI4_HUMAN; Q9H8E3_HUMAN; Q9HAM7_HUMAN; Q9NPU8_HUMAN; Q9NVC0_HUMAN; Q9NVP8_HUMAN; SYLC_HUMAN
272	IPI00152330; IPI00647802	LRRC20	175	184	180	2.0E+04	2.1E+04	2.0E+04	41.3	7	0	0	1	1	ISOFORM 1 OF LEUCINE-RICH REPEAT-CONTAINING PROTEIN 20.; 20 KDA PROTEIN.	Q5T6D4; Q5T6D6; Q8TCA0; Q9NVA6; Q9NVG3	; LRC20_HUMAN
273	IPI00155601	LRP16	325	325	325	3.6E+04	3.6E+04	3.6E+04	10.2	2	0	0	1	1	PROTEIN LRP16.	Q9BQ69; Q9UH96	LRP16_HUMAN
274	IPI00156282; IPI00414289	GPS1	491	527	509	5.6E+04	5.9E+04	5.7E+04	6.3	3	1	1	1	1	G PROTEIN PATHWAY SUPPRESSOR 1 ISOFORM 2.; G PROTEIN PATHWAY SUPPRESSOR 1 ISOFORM 1.		

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
275	IPI00157144; IPI00303868	GYS1	673	737	705	7.6E+04	8.4E+04	8.0E+04	29.0	17	1	1	1	1	GYS1 PROTEIN.; GLYCOGEN [STARCH] SYNTHASE, MUSCLE.	P13807; Q53ER0; Q9BTT9	GYS1_HUMAN; Q53ER0_HUMAN; Q9BTT9_HUMAN
276	IPI00164623; IPI00783987	C3	1663	1665	1664	1.9E+05	1.9E+05	1.9E+05	23.8	24	1	1	1	1	187 KDA PROTEIN.; COMPLEMENT C3 PRECURSOR (FRAGMENT).	P01024; Q6LDJ0	; CO3_HUMAN; Q6LDJ0_HUMAN
277	IPI00168081; IPI00784073	SMYD1	490	493	492	5.7E+04	5.7E+04	5.7E+04	29.6	11	1	1	1	1	57 KDA PROTEIN.; SET AND MYND DOMAIN-CONTAINING PROTEIN 1.	A0AV30; Q5GJ32; Q5GJ33; Q5HYE8; Q8NB12	; Q5GJ32_HUMAN; Q5GJ33_HUMAN; Q5HYE8_HUMAN; SMYD1_HUMAN
278	IPI00169383	PGK1	417	417	417	4.5E+04	4.5E+04	4.5E+04	63.6	29	1	1	1	1	PHOSPHOGLYCERATE KINASE 1.	P00558; Q5J7W1; Q6IBT6; Q8NI87	PGK1_HUMAN
279	IPI00170914	ADSSL1	457	457	457	5.0E+04	5.0E+04	5.0E+04	48.8	16	1	1	1	1	ISOFORM 1 OF ADENYLOSUCCINATE SYNTHETASE ISOZYME 1.	Q86TT6; Q8N142; Q8N714	PURA1_HUMAN
280	IPI00170935	LRRC47	583	583	583	6.3E+04	6.3E+04	6.3E+04	13.9	6	1	1	1	1	LEUCINE-RICH REPEAT-CONTAINING PROTEIN 47.	Q8N1G4; Q9ULN5	LRC47_HUMAN
281	IPI00171199; IPI00419249	PSMA3	248	255	252	2.8E+04	2.8E+04	2.8E+04	12.9	3	0	0	1	0	ISOFORM 2 OF PROTEASOME SUBUNIT ALPHA TYPE 3.; ISOFORM 1 OF PROTEASOME SUBUNIT ALPHA TYPE 3.	P25788; Q6IB71; Q86U83; Q8N1D8; Q9BS70	PSA3_HUMAN; Q6IB71_HUMAN
282	IPI00171573; IPI00185975	CCDC109A	330	351	341	3.7E+04	4.0E+04	3.8E+04	14.3	4	0	0	1	1	COILED-COIL DOMAIN CONTAINING 109A.; CCDC109A PROTEIN.	Q8NE86; Q96FL3	; C109A_HUMAN
283	IPI00171761; IPI00171769; IPI00552881	FUNDC2	189	218	199	2.1E+04	2.3E+04	2.2E+04	12.7	4	0	0	1	1	21 KDA PROTEIN.; FUN14 DOMAIN CONTAINING 2.; FUN14 DOMAIN CONTAINING 2.	Q5HYP8; Q8NHX8; Q9BWH2	; Q5HYP8_HUMAN; Q9BWH2_HUMAN
284	IPI00173461	JPH1	661	661	661	7.2E+04	7.2E+04	7.2E+04	6.4	3	1	1	1	1	JUNCTOPHILIN-1.	Q4KMX3; Q6AHW6; Q7Z682; Q86VR1; Q9HDC5	JPH1_HUMAN; Q4KMX3_HUMAN; Q6AHW6_HUMAN; Q7Z682_HUMAN; Q86VR1_HUMAN
285	IPI00173549; IPI00735855; IPI00737694; IPI00742098	SYNPO2	1093	1261	1195	1.2E+05	1.4E+05	1.3E+05	4.4	3	1	1	1	1	SYNAPTOPODIN 2.; SYNAPTOPODIN-2.; SIMILAR TO SYNAPTOPODIN 2 ISOFORM 3.; SIMILAR TO SYNAPTOPODIN 2 ISOFORM 2.	Q9UK89; Q9UMS6	; SYNP2_HUMAN
286	IPI00176469; IPI00641178; IPI00644715; IPI00645029	CABC1	492	647	577	5.6E+04	7.2E+04	6.5E+04	24.9	13	1	1	1	1	ISOFORM 1 OF CHAPERONE-ACTIVITY OF BC1 COMPLEX-LIKE, MITOCHONDRIALPRECURSOR.; ISOFORM 3 OF CHAPERONE-ACTIVITY OF BC1 COMPLEX-LIKE, MITOCHONDRIALPRECURSOR.; CHAPERONE, ABC1 ACTIVITY OF BC1 COMPLEX HOMOLOG.; CHAPERONE, ABC1 ACTIVITY OF BC1 COMPLEX HOMOLOG.	A1L377; Q5T7A2; Q5T7A4; Q5T7A5; Q63HK0; Q8NCJ6; Q8NI60; Q9HBQ1; Q9NQ67	A1L377_HUMAN; ADCK3_HUMAN; Q5T7A2_HUMAN; Q5T7A4_HUMAN
287	IPI00176532	JPH2	696	696	696	7.4E+04	7.4E+04	7.4E+04	8.2	3	1	1	1	1	ISOFORM 1 OF JUNCTOPHILIN-2.	O95913; Q5JY74; Q86VZ3; Q9BR39; Q9UJN4	JPH2_HUMAN; Q86VZ3_HUMAN
288	IPI00176903	PTRF	390	390	390	4.3E+04	4.3E+04	4.3E+04	28.2	10	1	1	1	1	ISOFORM 1 OF POLYMERASE I AND TRANSCRIPT RELEASE FACTOR.	O00535; Q6GMY1; Q6NZI2; Q96H74; Q9BT85; Q9HAP4	PTRF_HUMAN
289	IPI00177817	ATP2A2	997	997	997	1.1E+05	1.1E+05	1.1E+05	33.2	41	1	1	1	1	ISOFORM SERCA2A OF SARCOPLASMIC/ENDOPLASMIC RETICULUM CALCIUM ATPASE2.	P16614; P16615	AT2A2_HUMAN
290	IPI00028031; IPI00178744	ACADVL	679	701	690	7.3E+04	7.5E+04	7.4E+04	42.2	30	1	1	1	1	ISOFORM 1 OF VERY-LONG-CHAIN SPECIFIC ACYL-COA DEHYDROGENASE,MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF VERY-LONG-CHAIN SPECIFIC ACYL-COA DEHYDROGENASE,MITOCHONDRIAL PRECURSOR.	Q53HR2	; Q53HR2_HUMAN
291	IPI00179330; IPI00418813; IPI00456429; IPI00719280; IPI00743241; IPI00743650; IPI00744274; IPI00783060; IPI00784990; IPI00789107; IPI00789823; IPI00790633; IPI00792712	RPS27A; UBA52; UBB; UBC	76	388	239	8.6E+03	4.4E+04	2.7E+04	34.0	6	1	1	1	1	UBIQUITIN AND RIBOSOMAL PROTEIN S27A PRECURSOR.; CDNA FLJ46113 FIS, CLONE TESTI2036285, HIGHLY SIMILAR TO RATTUSNORVEGICUS UBIQUITIN C.; UBIQUITIN AND RIBOSOMAL PROTEIN L40 PRECURSOR.; UBIQUITIN B PRECURSOR.; 44 KDA PROTEIN.; 44 KDA PROTEIN.; 44 KDA PROTEIN.; UBIQUITIN.; UBIQUITIN C SPLICE VARIANT.; 30 KDA PROTEIN.; 16 KDA PROTEIN.; 25 KDA PROTEIN.; 39 KDA PROTEIN.	P02248; P02249; P02250; P62988; Q29120; Q3MIH3; Q5RKT7; Q5U5U6; Q5UGI3; Q6LBL4; Q6LDU5; Q6ZRT8; Q91887; Q91888; Q9BWD6; Q9BX98; Q9UEF2; Q9UEG1; Q9UEK8; Q9UPK7	; Q3MIH3_HUMAN; Q5RKT7_HUMAN; Q5U5U6_HUMAN; Q5UGI3_HUMAN; Q6ZRT8_HUMAN; UBIQ_HUMAN
292	IPI00183968	TPM3	285	285	285	3.3E+04	3.3E+04	3.3E+04	78.6	33	1	1	1	1	TROPOMYOSIN 3 ISOFORM 1.	Q5VU71	Q5VU71_HUMAN
293	IPI00185631; IPI00448879; IPI00794112	AMPD1	747	780	768	8.6E+04	9.0E+04	8.9E+04	33.9	25	1	1	1	1	ADENOSINE MONOPHOSPHATE DEAMINASE 1.; AMP DEAMINASE 1.; 90 KDA PROTEIN.	P23109; Q5TF00; Q5TF02; Q5W9V2; Q6F4B5; Q6F4B6; Q6F4B7; Q6F4B8; Q6F4B9; Q6I6Y1; Q6I6Y2; Q6I6Y3; Q6PH79; Q6PJ57	; AMPD1_HUMAN; Q5TF02_HUMAN; Q5W9V2_HUMAN; Q6F4B5_HUMAN; Q6F4B6_HUMAN; Q6F4B7_HUMAN; Q6F4B8_HUMAN; Q6F4B9_HUMAN; Q6I6Y1_HUMAN; Q6I6Y2_HUMAN; Q6I6Y3_HUMAN; Q6PH79_HUMAN; Q6PJ57_HUMAN
294	IPI00186290	EEF2	858	858	858	9.5E+04	9.5E+04	9.5E+04	25.8	18	1	1	1	1	ELONGATION FACTOR 2.	P13639; Q58J86; Q6PK56; Q8TA90	EF2_HUMAN; Q6PK56_HUMAN; Q8TA90_HUMAN
295	IPI00186966; IPI00220586; IPI00220587; IPI00220996; IPI00220997; IPI00220998; IPI00220999; IPI00221000; IPI00221001; IPI00329733; IPI00395680	BIN1	409	593	486	4.6E+04	6.5E+04	5.3E+04	38.8	15	1	1	1	1	ISOFORM IIA OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM BIN1-13 OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM BIN1+12A OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM IIB OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM IIC1 OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM II2 OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM II3 OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM BIN1 OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM BIN1-10-13 OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM IIC2 OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM IID OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.	O00297; O00499; O00545; O43867; O60552; O60553; O60554; O60555; O75514; O75515; O75516; O75517; O75518; Q659B7; Q8WWH9; Q92944; Q99688; Q9BTH3	; BIN1_HUMAN; Q659B7_HUMAN; Q8WWH9_HUMAN; Q9BTH3_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
296	IPI00215715; IPI00745082	CAMK2A	478	478	478	5.4E+04	5.4E+04	5.4E+04	13.0	4	0	0	1	1	ISOFORM A OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II ALPHACHAIN.; CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE IIA ISOFORM 2.	Q7LDD5; Q9UL21; Q9UQM7; Q9Y2H4; Q9Y352	KCC2A_HUMAN; Q7LDD5_HUMAN; Q9Y2H4_HUMAN
297	IPI00215746	FABP4	132	132	132	1.5E+04	1.5E+04	1.5E+04	25.0	2	0	0	1	1	FATTY ACID-BINDING PROTEIN, ADIPOCYTE.	P15090; Q6IBA1	FABPA_HUMAN; Q6IBA1_HUMAN
298	IPI00215780	RPS19	145	145	145	1.6E+04	1.6E+04	1.6E+04	13.8	2	0	0	1	0	40S RIBOSOMAL PROTEIN S19.	P39019; Q8WVX7	Q8WVX7_HUMAN; RS19_HUMAN
299	IPI00215790	RPL38	70	70	70	8.2E+03	8.2E+03	8.2E+03	50.0	4	0	0	1	1	60S RIBOSOMAL PROTEIN L38.	P23411; P63173	RL38_HUMAN
300	IPI00215901; IPI00218988	AK2	232	239	236	2.6E+04	2.6E+04	2.6E+04	10.0	2	0	0	1	0	ISOFORM 1 OF ADENYLATE KINASE ISOENZYME 2, MITOCHONDRIAL.; ISOFORM 2 OF ADENYLATE KINASE ISOENZYME 2, MITOCHONDRIAL.	P54819; Q16856; Q5TIF7; Q5TIF8; Q8TCY2; Q8TCY3	KAD2_HUMAN; Q5TIF8_HUMAN
301	IPI00215914; IPI00215917; IPI00797941	ARF1; ARF3	129	181	164	1.4E+04	2.1E+04	1.9E+04	24.3	4	0	0	1	1	ADP-RIBOSYLATION FACTOR 1.; ADP-RIBOSYLATION FACTOR 3.; 14 KDA PROTEIN.	P10947; P16587; P32889; P61204; P84077	; ARF1_HUMAN; ARF3_HUMAN
302	IPI00215920	ARF6	175	175	175	2.0E+04	2.0E+04	2.0E+04	12.6	2	0	0	1	1	ADP-RIBOSYLATION FACTOR 6.	P26438; P62330; Q5U025; Q6FGZ2; Q6FH17	ARF6_HUMAN; Q5U025_HUMAN; Q6FGZ2_HUMAN; Q6FH17_HUMAN
303	IPI00215983	CA1	261	261	261	2.9E+04	2.9E+04	2.9E+04	48.3	10	1	1	1	1	CARBONIC ANHYDRASE 1.	P00915	CAH1_HUMAN
304	IPI00024145; IPI00216024; IPI00216026; IPI00216027; IPI00411815; IPI00455531; IPI00718908; IPI00737171	LOC647153; LOC729317; VDAC2	283	347	309	3.0E+04	3.8E+04	3.3E+04	27.4	8	1	1	1	1	ISOFORM 1 OF VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2.; ISOFORM 2 OF VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2.; ISOFORM 3 OF VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2.; ISOFORM 4 OF VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2.; ISOFORM 5 OF VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2.; SIMILAR TO VOLTAGE-DEPENDENT ANION CHANNEL 2.; ISOFORM 6 OF VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2.; SIMILAR TO VOLTAGE-DEPENDENT ANION CHANNEL 2.	A2A3S1; P45880; Q5VWK1; Q5VWK3; Q6IB40; Q7L3J5; Q9BWK8; Q9Y5I6	; A2A3S1_HUMAN; VDAC2_HUMAN
305	IPI00216049; IPI00216746; IPI00514561; IPI00647717; IPI00807545	HNRPK	379	464	435	4.2E+04	5.1E+04	4.8E+04	25.2	7	1	1	1	1	ISOFORM 1 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K.; ISOFORM 2 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K.; HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K.; HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K.; ISOFORM 3 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K.	P61978; Q07244; Q15671; Q59F98; Q5EC54; Q5T6W2; Q5T6W4; Q5T6W5; Q60577; Q6IBN1; Q922Y7; Q96J62	HNRPK_HUMAN; Q5EC54_HUMAN; Q5T6W2_HUMAN; Q5T6W4_HUMAN; Q5T6W5_HUMAN; Q6IBN1_HUMAN
306	IPI00216070	MYL1	194	194	194	2.1E+04	2.1E+04	2.1E+04	76.8	23	1	1	1	1	MYOSIN LIGHT CHAIN 1, SKELETAL MUSCLE ISOFORM.	P05976; Q53SD2; Q6IBD5	MLE1_HUMAN; Q53SD2_HUMAN
307	IPI00216138	TAGLN	201	201	201	2.3E+04	2.3E+04	2.3E+04	12.4	2	0	0	1	1	TRANSGELIN.	O15542; Q01995; Q53GC9; Q5U0D2; Q6FI52	Q53GC9_HUMAN; Q5U0D2_HUMAN; Q6FI52_HUMAN; TAGL_HUMAN
308	IPI00216236; IPI00657955	TNNI2	182	182	182	2.1E+04	2.1E+04	2.1E+04	24.2	6	0	1	1	1	TROPONIN I, FAST SKELETAL MUSCLE.; 21 KDA PROTEIN.	P48788	; TNNI2_HUMAN
309	IPI00216298; IPI00382841; IPI00552768	TXN	84	105	91	9.3E+03	1.2E+04	1.0E+04	22.9	2	0	0	1	1	THIOREDOXIN.; THIOREDOXIN DELTA 3 (FRAGMENT).; THIOREDOXIN.	O60744; P10599; Q5T936; Q5T937; Q96KI3; Q9UDG5	O60744_HUMAN; Q5T936_HUMAN; Q5T937_HUMAN; Q9UDG5_HUMAN; THIO_HUMAN
310	IPI00216308	VDAC1	283	283	283	3.1E+04	3.1E+04	3.1E+04	60.8	15	1	1	1	1	VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1.	P21796; Q5FVE7; Q9UIQ5; Q9UPL0	VDAC1_HUMAN
311	IPI00216348; IPI00302712; IPI00744015; IPI00827813; IPI00827859	DYNC1I2	611	641	628	6.8E+04	7.2E+04	7.0E+04	5.7	2	0	0	1	0	ISOFORM 2C OF CYTOPLASMIC DYNEIN 1 INTERMEDIATE CHAIN 2.; ISOFORM 2B OF CYTOPLASMIC DYNEIN 1 INTERMEDIATE CHAIN 2.; ISOFORM 2A OF CYTOPLASMIC DYNEIN 1 INTERMEDIATE CHAIN 2.; ISOFORM 2F OF CYTOPLASMIC DYNEIN 1 INTERMEDIATE CHAIN 2.; ISOFORM 2E OF CYTOPLASMIC DYNEIN 1 INTERMEDIATE CHAIN 2.	Q13409; Q32LY9; Q53S84; Q59GU5; Q5BJF8; Q7Z4X1; Q96NG7; Q96S87; Q9BXZ5; Q9NT58	DC1I2_HUMAN; Q32LY9_HUMAN; Q53S84_HUMAN; Q59GU5_HUMAN; Q5BJF8_HUMAN; Q7Z4X1_HUMAN
312	IPI00216461; IPI00784259	ACYP2	99	127	113	1.1E+04	1.4E+04	1.3E+04	45.5	6	0	0	1	1	ACYLPHOSPHATASE-2.; ACYLPHOSPHATASE, MUSCLE TYPE ISOZYME.	P14621; Q4ZFV7; Q53TK7	; ACYP2_HUMAN; Q4ZFV7_HUMAN; Q53TK7_HUMAN
313	IPI00216798	MYL2	166	166	166	1.9E+04	1.9E+04	1.9E+04	84.9	20	1	1	1	1	MYOSIN REGULATORY LIGHT CHAIN 2, VENTRICULAR/CARDIAC MUSCLE ISOFORM.	P10916; Q14908; Q16123; Q6IB42; Q7Z3Z1	MLRV_HUMAN; Q14908_HUMAN; Q6IB42_HUMAN; Q7Z3Z1_HUMAN
314	IPI00216983	CA3	260	260	260	3.0E+04	3.0E+04	3.0E+04	66.5	16	1	1	1	1	CARBONIC ANHYDRASE 3.	O60842; P07451	CAH3_HUMAN
315	IPI00217030	RPS4X	263	263	263	3.0E+04	3.0E+04	3.0E+04	8.4	2	0	0	1	0	40S RIBOSOMAL PROTEIN S4, X ISOFORM.	P12631; P12750; P27576; P55831; P62701; Q14727; Q53HV1; Q6IPY4; Q96IR1	Q53HV1_HUMAN; Q96IR1_HUMAN; RS4X_HUMAN
316	IPI00217232; IPI00464979	SUCLA2	441	463	452	4.8E+04	5.0E+04	4.9E+04	34.0	10	1	1	1	1	ISOFORM 2 OF SUCCINYL-COA LIGASE [ADP-FORMING] BETA-CHAIN,MITOCHONDRIAL PRECURSOR.; ISOFORM 1 OF SUCCINYL-COA LIGASE [ADP-FORMING] BETA-CHAIN,MITOCHONDRIAL PRECURSOR.	O95194; Q5T9Q4; Q5T9Q6; Q6N0B1; Q7Z503; Q9NV21; Q9NVP7; Q9P2R7	Q5T9Q4_HUMAN; Q5T9Q6_HUMAN; Q6N0B1_HUMAN; Q7Z503_HUMAN; SUCB1_HUMAN
317	IPI00217428; IPI00644184; IPI00651724	UNC45B	850	931	903	9.5E+04	1.0E+05	1.0E+05	13.5	12	1	1	1	1	ISOFORM 1 OF UNC45 HOMOLOG B.; ISOFORM 2 OF UNC45 HOMOLOG B.; ISOFORM 3 OF UNC45 HOMOLOG B.	Q495Q8; Q495Q9; Q8IWX7	UN45B_HUMAN
318	IPI00217458	GPT	496	496	496	5.5E+04	5.5E+04	5.5E+04	27.2	9	1	1	1	1	ALANINE AMINOTRANSFERASE 1.	P24298; P78398; Q93076	ALAT1_HUMAN
319	IPI00217466	HIST1H1D	221	221	221	2.2E+04	2.2E+04	2.2E+04	21.3	5	0	0	1	1	HISTONE H1.3.	P16402; Q2M2I2	H13_HUMAN
320	IPI00217493	MB	154	154	154	1.7E+04	1.7E+04	1.7E+04	74.0	24	1	1	1	1	MYOGLOBIN.	P02144; Q52H51; Q5THY7; Q8WVH6	MYG_HUMAN; Q8WVH6_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
321	IPI00217871	ALDH4A1	563	563	563	6.2E+04	6.2E+04	6.2E+04	28.6	11	1	1	1	1	DELTA-1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR.	P30038; Q16882; Q53HU4; Q5JNV6; Q8IZ38; Q96IF0	AL4A1_HUMAN; Q53HU4_HUMAN; Q5JNV6_HUMAN
322	IPI00217966	LDHA	332	332	332	3.7E+04	3.7E+04	3.7E+04	52.4	20	1	1	1	1	ISOFORM 1 OF L-LACTATE DEHYDROGENASE A CHAIN.	P00338; Q53G53; Q6IBM7; Q6ZNV1	LDHA_HUMAN
323	IPI00217976; IPI00747283	MAPT	758	776	767	7.9E+04	8.1E+04	8.0E+04	13.2	6	1	1	1	0	MICROTUBULE-ASSOCIATED PROTEIN TAU.; ISOFORM PNS-TAU OF MICROTUBULE-ASSOCIATED PROTEIN TAU.	P10636; P18518; Q14799; Q15549; Q15550; Q15551; Q5CZI7; Q9UDJ3; Q9UMH0; Q9UQ96	Q5CZI7_HUMAN; TAU_HUMAN
324	IPI00218130	PYGM	842	842	842	9.7E+04	9.7E+04	9.7E+04	62.5	73	1	1	1	1	GLYCOGEN PHOSPHORYLASE, MUSCLE FORM.	A0AVK1; P11217	PYGM_HUMAN
325	IPI00218192; IPI00294193; IPI00556036; IPI00760855; IPI00790993	ITIH4; TMEM110	699	940	879	7.7E+04	1.0E+05	9.7E+04	6.6	5	1	1	1	1	ISOFORM 2 OF INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR.; ISOFORM 1 OF INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR.; INTER-ALPHA (GLOBULIN) INHIBITOR H4 (PLASMA KALLIKREIN-SENSITIVEGLYCOPROTEIN) VARIANT (FRAGMENT).; 101 KDA PROTEIN.; 104 KDA PROTEIN.	Q14624; Q15135; Q59FS1; Q68DH2; Q9P190; Q9UQ54	; ITIH4_HUMAN; Q59FS1_HUMAN; Q68DH2_HUMAN
326	IPI00218236	PPP1CB	327	327	327	3.7E+04	3.7E+04	3.7E+04	16.8	4	1	1	1	1	SERINE/THREONINE-PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT.	P37140; P62140; Q5U087; Q6FG45	PP1B_HUMAN
327	IPI00218342; IPI00794900	MTHFD1	935	974	955	1.0E+05	1.1E+05	1.0E+05	17.7	15	1	1	1	1	C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC.; 105 KDA PROTEIN.	P11586; Q86VC9; Q9BVP5	; C1TC_HUMAN
328	IPI00218343; IPI00387144; IPI00792677	TUBA1B; TUBA1C	416	451	439	4.6E+04	5.0E+04	4.9E+04	23.8	8	0	0	1	1	TUBULIN ALPHA-6 CHAIN.; TUBULIN ALPHA-UBIQUITOUS CHAIN.; 46 KDA PROTEIN.	P04687; P05209; P68363; Q27I68; Q53GA7; Q9BQE3	; Q27I68_HUMAN; Q53GA7_HUMAN; TBA6_HUMAN; TBAK_HUMAN
329	IPI00218414	CA2	260	260	260	2.9E+04	2.9E+04	2.9E+04	36.5	9	1	1	1	1	CARBONIC ANHYDRASE 2.	P00918; Q6FI12; Q6LD99; Q96ET9	CAH2_HUMAN; Q6LD99_HUMAN
330	IPI00218474	ENO3	434	434	434	4.7E+04	4.7E+04	4.7E+04	60.8	39	1	1	1	1	BETA-ENOLASE.	P13929; Q96AE2; Q9NPL4	ENOB_HUMAN; Q9NPL4_HUMAN
331	IPI00218568	PCBD1	104	104	104	1.2E+04	1.2E+04	1.2E+04	17.3	2	0	0	1	0	PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE.	P61457; P70519; P80095; Q6FGB3; Q6LEE0; Q6LEE1; Q6LEE2; Q9D930	PHS_HUMAN; Q6FGB3_HUMAN; Q6LEE0_HUMAN; Q6LEE1_HUMAN; Q6LEE2_HUMAN
332	IPI00218570	PGAM2	253	253	253	2.9E+04	2.9E+04	2.9E+04	48.2	14	1	1	1	1	PHOSPHOGLYCERATE MUTASE 2.	P15259	PGAM2_HUMAN
333	IPI00218571; IPI00514085	PHKB	1086	1093	1090	1.2E+05	1.2E+05	1.2E+05	11.6	11	1	1	1	1	ISOFORM 1 OF PHOSPHORYLASE B KINASE REGULATORY SUBUNIT BETA.; ISOFORM 2 OF PHOSPHORYLASE B KINASE REGULATORY SUBUNIT BETA.	Q8N4T5; Q93100	KPBB_HUMAN
334	IPI00218733; IPI00783680	SOD1	154	156	155	1.6E+04	1.6E+04	1.6E+04	16.7	2	0	0	1	1	16 KDA PROTEIN.; SUPEROXIDE DISMUTASE.	P00441; Q16669; Q16711; Q16838; Q16839; Q16840; Q6NR85	; Q6NR85_HUMAN; SODC_HUMAN
335	IPI00218847; IPI00219861; IPI00410615	ACP1	124	158	147	1.4E+04	1.8E+04	1.7E+04	31.7	4	0	0	1	1	ISOFORM 2 OF LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE.; ISOFORM 1 OF LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE.; ISOFORM 3 OF LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE.	P24666; P24667; Q16035; Q16036; Q16725; Q3KQX8; Q53RU0; Q59EH3	PPAC_HUMAN; Q3KQX8_HUMAN; Q53RU0_HUMAN; Q59EH3_HUMAN
336	IPI00218848	ATP5I	72	72	72	8.3E+03	8.3E+03	8.3E+03	50.0	3	0	0	1	1	ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F0 COMPLEX, SUBUNIT E.		
337	IPI00218914	ALDH1A1	501	501	501	5.5E+04	5.5E+04	5.5E+04	39.9	14	1	1	1	1	RETINAL DEHYDROGENASE 1.	O00768; P00352; Q5SYR1	AL1A1_HUMAN; Q5SYR1_HUMAN
338	IPI00219018; IPI00789134; IPI00795257	GAPDH	260	335	296	2.8E+04	3.6E+04	3.2E+04	69.0	32	1	1	1	1	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE.; GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE.; 32 KDA PROTEIN.	P00354; P04406; Q16768; Q2TSD0; Q53X65; Q5ZEY3	; G3P_HUMAN; Q16768_HUMAN; Q2TSD0_HUMAN; Q53X65_HUMAN; Q5ZEY3_HUMAN
339	IPI00219025	GLRX	106	106	106	1.2E+04	1.2E+04	1.2E+04	11.3	2	0	0	1	0	GLUTAREDOXIN-1.	P35754; Q3KQS1; Q6ICT1	GLRX1_HUMAN
340	IPI00219029	GOT1	413	413	413	4.6E+04	4.6E+04	4.6E+04	62.5	24	1	1	1	1	ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC.	P17174; Q2TU84; Q5VW80	AATC_HUMAN; Q2TU84_HUMAN
341	IPI00219034	NDUFA8	172	172	172	2.0E+04	2.0E+04	2.0E+04	30.2	3	0	0	1	1	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 8.	P51970; Q5VZ50; Q9Y6N0	NDUA8_HUMAN; Q5VZ50_HUMAN
342	IPI00219067; IPI00639805; IPI00645360; IPI00645711	GSTM2	193	237	217	2.3E+04	2.8E+04	2.6E+04	32.6	7	1	0	1	1	GLUTATHIONE S-TRANSFERASE MU 2.; 26 KDA PROTEIN.; GLUTATHIONE TRANSFERASE.; 28 KDA PROTEIN.	P28161; Q0D2I8; Q2M318; Q5TZY5; Q8WWE1; Q9UE37	; GSTM2_HUMAN; Q0D2I8_HUMAN; Q9UE37_HUMAN
343	IPI00219077	LTA4H	611	611	611	6.9E+04	6.9E+04	6.9E+04	22.6	9	1	1	1	1	ISOFORM 1 OF LEUKOTRIENE A-4 HYDROLASE.	P09960; Q6IAT6	LKHA4_HUMAN; Q6IAT6_HUMAN
344	IPI00031801; IPI00219147; IPI00219148; IPI00555698	CSDA	134	372	288	1.5E+04	4.0E+04	3.1E+04	34.6	5	1	1	1	1	ISOFORM 1 OF DNA-BINDING PROTEIN A.; ISOFORM 2 OF DNA-BINDING PROTEIN A.; ISOFORM 3 OF DNA-BINDING PROTEIN A.; CSDA PROTEIN VARIANT (FRAGMENT).	P16989; Q14121; Q59EB5; Q969N6; Q96B76; Q96GD7	DBPA_HUMAN; Q59EB5_HUMAN; Q96B76_HUMAN; Q96GD7_HUMAN
345	IPI00219207	RTN4	199	199	199	2.2E+04	2.2E+04	2.2E+04	23.1	4	1	1	1	1	ISOFORM 3 OF RETICULON-4.	O94962; Q53SY1; Q7L7Q5; Q9BXG5; Q9H212; Q9H3I3; Q9NQC3; Q9UQ42; Q9Y293; Q9Y2Y7; Q9Y5U6	Q53SY1_HUMAN; Q7L7Q5_HUMAN; RTN4_HUMAN
346	IPI00219217	LDHB	334	334	334	3.7E+04	3.7E+04	3.7E+04	32.9	12	1	1	1	1	L-LACTATE DEHYDROGENASE B CHAIN.	P07195; Q5U077	LDHB_HUMAN; Q5U077_HUMAN
347	IPI00219219	LGALS1	135	135	135	1.5E+04	1.5E+04	1.5E+04	25.2	3	1	0	1	1	GALECTIN-1.	P09382; Q15954	LEG1_HUMAN; Q15954_HUMAN
348	IPI00219226; IPI00796706	HRC	699	706	703	8.0E+04	8.1E+04	8.1E+04	12.0	4	1	1	1	1	SARCOPLASMIC RETICULUM HISTIDINE-RICH CALCIUM-BINDING PROTEINPRECURSOR.; 81 KDA PROTEIN.	P23327; Q2M1I0; Q504Y6	; Q2M1I0_HUMAN; SRCH_HUMAN
349	IPI00219381	NDUFA2	99	99	99	1.1E+04	1.1E+04	1.1E+04	20.2	3	0	0	1	0	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 2.	O43678; Q6IAY8	NDUA2_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
350	IPI00219383	NDUFB3	98	98	98	1.1E+04	1.1E+04	1.1E+04	21.4	2	1	0	1	0	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 3.	O43676; Q6IB80	NDUB3_HUMAN; Q6IB80_HUMAN
351	IPI00219446; IPI00795288	PEBP1	187	196	192	2.1E+04	2.2E+04	2.1E+04	44.9	7	1	1	1	1	PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN 1.; 22 KDA PROTEIN.	P30086	; PEBP1_HUMAN
352	IPI00219525; IPI00747533	PGD	483	485	484	5.3E+04	5.3E+04	5.3E+04	19.5	6	1	1	1	0	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING.; 53 KDA PROTEIN.	P52209; Q4VXH6; Q9BWD8	; 6PGD_HUMAN; Q4VXH6_HUMAN
353	IPI00219526	PGM1	562	562	562	6.1E+04	6.1E+04	6.1E+04	65.1	37	1	1	1	1	ISOFORM 1 OF PHOSPHOGLUCOMUTASE-1.	P36871; Q16105; Q5BKZ9; Q6NW22; Q86U74; Q96J40; Q9H1D2; Q9NTY4	PGM1_HUMAN; Q5BKZ9_HUMAN; Q6NW22_HUMAN; Q86U74_HUMAN; Q9H1D2_HUMAN
354	IPI00218371; IPI00219616; IPI00643000; IPI00816572	PRPS1; PRPS1L1	168	318	281	1.8E+04	3.5E+04	3.1E+04	9.4	2	0	0	1	1	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE III.; RIBOSE-PHOSPHATE PYROPHOSPHOKINASE I.; PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1.; PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1 VARIANT (FRAGMENT).	P09329; P21108; P60891; Q15244; Q53FW2; Q5JPM8; Q5JV75; Q6P5P6	PRPS1_HUMAN; PRPS3_HUMAN; Q15244_HUMAN; Q53FW2_HUMAN; Q5JPM8_HUMAN; Q5JV75_HUMAN; Q6P5P6_HUMAN
355	IPI00219684	FABP3	133	133	133	1.5E+04	1.5E+04	1.5E+04	58.7	9	1	1	1	1	FATTY ACID-BINDING PROTEIN, HEART.	P05413; Q5VV93; Q6IBD7; Q99957	FABPH_HUMAN; Q6IBD7_HUMAN
356	IPI00219685	NDUFA13	227	227	227	2.6E+04	2.6E+04	2.6E+04	22.0	4	1	0	1	1	CELL DEATH-REGULATORY PROTEIN GRIM19.		
357	IPI00219729	SLC25A11	314	314	314	3.4E+04	3.4E+04	3.4E+04	25.5	7	1	1	1	1	MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN.	O75537; Q02978; Q6IBH0; Q969P7	M2OM_HUMAN; Q6IBH0_HUMAN
358	IPI00219757; IPI00796076; IPI00797321	GSTP1	191	210	203	2.1E+04	2.3E+04	2.3E+04	40.0	5	1	1	1	1	GLUTATHIONE S-TRANSFERASE P.; 23 KDA PROTEIN.; 21 KDA PROTEIN.	O00460; P09211; Q15690; Q5TZY3	; GSTP1_HUMAN
359	IPI00219796	TNNC2	160	160	160	1.8E+04	1.8E+04	1.8E+04	53.1	10	1	1	1	1	TROPONIN C, SKELETAL MUSCLE.	P02585; Q6FH92	Q6FH92_HUMAN; TNNC2_HUMAN
360	IPI00219910; IPI00783862	BLVRB	206	211	209	2.2E+04	2.3E+04	2.2E+04	31.8	6	1	1	1	1	23 KDA PROTEIN.; FLAVIN REDUCTASE.	P30043; P32078; P53005; Q32LZ2	; BLVRB_HUMAN
361	IPI00219913; IPI00640357	USP14	459	494	477	5.2E+04	5.6E+04	5.4E+04	25.3	9	1	1	1	1	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 14.; UBIQUITIN SPECIFIC PROTEASE 14 ISOFORM B.	P54578; Q53XY5	; Q53XY5_HUMAN; UBP14_HUMAN
362	IPI00219953; IPI00514049; IPI00514929	CMPK	168	228	188	1.9E+04	2.6E+04	2.1E+04	18.0	3	0	0	1	1	CYTIDYLATE KINASE.; CYTIDYLATE KINASE.; CYTIDYLATE KINASE.	Q5SVZ1; Q5SVZ2	; Q5SVZ1_HUMAN; Q5SVZ2_HUMAN
363	IPI00219983; IPI00796892	CACNB1	523	643	583	5.8E+04	7.1E+04	6.4E+04	23.3	9	1	1	1	1	ISOFORM 2 OF VOLTAGE-DEPENDENT L-TYPE CALCIUM CHANNEL SUBUNIT BETA-1.; 71 KDA PROTEIN.	O15331; Q02639; Q02640; Q02641; Q9C085	; CACB1_HUMAN
364	IPI00220063	NDUFS5	106	106	106	1.3E+04	1.3E+04	1.3E+04	24.5	3	1	0	1	1	NADH DEHYDROGENASE [UBIQUINONE] IRON-SULFUR PROTEIN 5.	O43920; Q6IBA0	NDUS5_HUMAN; Q6IBA0_HUMAN
365	IPI00220301	PRDX6	224	224	224	2.5E+04	2.5E+04	2.5E+04	54.5	12	1	1	1	1	PEROXIREDOXIN-6.	P30041; P32077; Q5TAH4; Q5ZEZ8	PRDX6_HUMAN
366	IPI00220342	DDAH1	285	285	285	3.1E+04	3.1E+04	3.1E+04	17.9	3	1	1	1	0	NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1.	O94760; Q5HYC8; Q5VWX2; Q86XK5	DDAH1_HUMAN; Q5HYC8_HUMAN; Q5VWX2_HUMAN
367	IPI00220362	HSPE1	102	102	102	1.1E+04	1.1E+04	1.1E+04	51.0	6	0	0	1	1	10 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL.	O95421; P61604; Q04984; Q53X54; Q9UNM1	CH10_HUMAN; Q53X54_HUMAN; Q9UNM1_HUMAN
368	IPI00220373	IDE	1019	1019	1019	1.2E+05	1.2E+05	1.2E+05	2.8	3	0	1	1	0	INSULIN-DEGRADING ENZYME.	P14735; Q59GA5; Q5T5N2	IDE_HUMAN; Q59GA5_HUMAN; Q5T5N2_HUMAN
369	IPI00220391; IPI00220558; IPI00783826	RYR1	5035	5040	5038	5.6E+05	5.7E+05	5.7E+05	2.5	8	0	0	1	1	565 KDA PROTEIN.; ISOFORM 2 OF RYANODINE RECEPTOR 1.; ISOFORM 1 OF RYANODINE RECEPTOR 1.	O75591; P21817; Q16314; Q16368; Q59FN5; Q8WYM7; Q8WYM8; Q9NPK1; Q9P1U4	; O75591_HUMAN; Q59FN5_HUMAN; Q8WYM7_HUMAN; Q8WYM8_HUMAN; RYR1_HUMAN
370	IPI00220416; IPI00643836; IPI00790644; IPI00798386	UQCRB	91	140	110	1.1E+04	1.6E+04	1.3E+04	31.5	3	1	0	1	1	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KDA PROTEIN.; UQCRB PROTEIN.; 16 KDA PROTEIN.; 12 KDA PROTEIN.	P14927; Q49AB7; Q6FGD1	; Q49AB7_HUMAN; Q6FGD1_HUMAN; UCR6_HUMAN
371	IPI00220467; IPI00395442; IPI00643758	TNNT1	251	278	264	3.0E+04	3.3E+04	3.1E+04	39.0	13	1	1	1	1	ISOFORM 2 OF TROPONIN T, SLOW SKELETAL MUSCLE.; ISOFORM 1 OF TROPONIN T, SLOW SKELETAL MUSCLE.; ISOFORM 3 OF TROPONIN T, SLOW SKELETAL MUSCLE.	O95472; P13805; Q16061; Q3B759; Q56R93; Q56R94; Q5U0E1	Q3B759_HUMAN; Q56R93_HUMAN; Q56R94_HUMAN; Q5U0E1_HUMAN; TNNT1_HUMAN
372	IPI00220487	ATP5H	161	161	161	1.8E+04	1.8E+04	1.8E+04	51.6	9	0	0	1	1	ISOFORM 1 OF ATP SYNTHASE D CHAIN, MITOCHONDRIAL.	O75947; Q9H3J4	ATP5H_HUMAN
373	IPI00220642	YWHAG	247	247	247	2.8E+04	2.8E+04	2.8E+04	31.6	8	0	0	1	1	14-3-3 PROTEIN GAMMA.	O70457; P35214; P61981; Q6FH52; Q9UDP2; Q9UN99	1433G_HUMAN
374	IPI00220644	PKM2	531	531	531	5.8E+04	5.8E+04	5.8E+04	63.7	53	1	1	1	1	ISOFORM M1 OF PYRUVATE KINASE ISOZYMES M1/M2.	P14618; P14786; Q96E76; Q9BWB5; Q9UPF2	KPYM_HUMAN
375	IPI00220706; IPI00554676; IPI00749035; IPI00816084; IPI00816618	HBE1; HBG1; HBG2	147	158	152	1.6E+04	1.7E+04	1.7E+04	36.7	5	0	0	1	1	HEMOGLOBIN SUBUNIT GAMMA-1.; HEMOGLOBIN SUBUNIT GAMMA-2.; 17 KDA PROTEIN.; GAMMA-G GLOBIN (FRAGMENT).; HEMOGLOBIN GAMMA-G (FRAGMENT).	P02096; P62027; P69891; P69892; Q14403; Q14474; Q14476; Q14491; Q549G1; Q68NH9; Q8TDA1; Q96FH6; Q96FH7; Q9UNL6	; HBG1_HUMAN; HBG2_HUMAN; Q14403_HUMAN; Q14474_HUMAN; Q14476_HUMAN; Q14491_HUMAN; Q549G1_HUMAN; Q8TDA1_HUMAN; Q96FH6_HUMAN; Q9UNL6_HUMAN
376	IPI00220741; IPI00641363	SPTA1	2416	2431	2424	2.8E+05	2.8E+05	2.8E+05	5.4	10	0	1	1	1	SPECTRIN ALPHA CHAIN, ERYTHROCYTE.; SPECTRIN, ALPHA, ERYTHROCYTIC 1.	O60686; Q5VYL1; Q5VYL2	O60686_HUMAN; Q5VYL1_HUMAN; Q5VYL2_HUMAN
377	IPI00220766	GLO1	184	184	184	2.1E+04	2.1E+04	2.1E+04	18.5	5	0	0	1	1	LACTOYLGLUTATHIONE LYASE.	P78375; Q04760; Q59EL0; Q5TZW3; Q96FC0; Q96J41	LGUL_HUMAN; Q59EL0_HUMAN
378	IPI00220916; IPI00375714	HSPB7	175	258	217	1.9E+04	2.8E+04	2.4E+04	32.0	4	0	0	1	1	ISOFORM 2 OF HEAT-SHOCK PROTEIN BETA-7.; HEAT SHOCK 27KDA PROTEIN FAMILY, MEMBER 7.	Q5T5Q2; Q7Z3C1; Q9NU17; Q9UBY9	HSPB7_HUMAN; Q5T5Q2_HUMAN; Q7Z3C1_HUMAN
379	IPI00221092	RPS16	146	146	146	1.6E+04	1.6E+04	1.6E+04	22.6	3	0	0	1	0	40S RIBOSOMAL PROTEIN S16.	P17008; P62249	RS16_HUMAN
380	IPI00221127	MYLK2	596	596	596	6.5E+04	6.5E+04	6.5E+04	21.5	9	1	1	1	1	MYOSIN LIGHT CHAIN KINASE 2, SKELETAL/CARDIAC MUSCLE.	Q569L1; Q96I84; Q9H1R3	MYLK2_HUMAN
381	IPI00221222	SUB1	127	127	127	1.4E+04	1.4E+04	1.4E+04	15.8	2	0	0	1	0	ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15.	P53999; Q59G24; Q6IBA2; Q96L29	Q59G24_HUMAN; Q6IBA2_HUMAN; TCP4_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
382	IPI00221305	CAMK2B	666	666	666	7.3E+04	7.3E+04	7.3E+04	12.6	7	1	1	1	1	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE IIB ISOFORM 1.		
383	IPI00239077	HINT1	126	126	126	1.4E+04	1.4E+04	1.4E+04	50.0	3	1	0	1	1	HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN 1.	P49773; Q9H5W8	HINT1_HUMAN
384	IPI00243742	MYL3	195	195	195	2.2E+04	2.2E+04	2.2E+04	68.2	21	1	1	1	1	MYOSIN LIGHT POLYPEPTIDE 3.	P08590; Q14909; Q9NRS8	MYL3_HUMAN; Q14909_HUMAN
385	IPI00246058	PDCD6IP	873	873	873	9.7E+04	9.7E+04	9.7E+04	8.7	6	1	1	1	1	PDCD6IP PROTEIN.	Q4W4Y1; Q6NUS1	Q4W4Y1_HUMAN; Q6NUS1_HUMAN
386	IPI00246975	GSTM3	225	225	225	2.7E+04	2.7E+04	2.7E+04	13.8	3	0	0	1	0	GLUTATHIONE S-TRANSFERASE MU 3.	O60550; P21266; Q59EJ5; Q6FGJ9; Q96HA3	GSTM3_HUMAN; Q59EJ5_HUMAN; Q6FGJ9_HUMAN
387	IPI00255554; IPI00410073	GPR123	1280	1280	1280	1.4E+05	1.4E+05	1.4E+05	1.4	2	0	0	1	0	ISOFORM 1 OF PROBABLE G-PROTEIN COUPLED RECEPTOR 123.; ISOFORM 2 OF PROBABLE G-PROTEIN COUPLED RECEPTOR 123.	Q5T234; Q86SN7; Q86SQ6; Q96JJ9	GP123_HUMAN
388	IPI00289499	ATIC	592	592	592	6.5E+04	6.5E+04	6.5E+04	19.3	7	1	1	1	0	BIFUNCTIONAL PURINE BIOSYNTHESIS PROTEIN PURH.	P31939; Q13856; Q53S28	PUR9_HUMAN; Q53S28_HUMAN
389	IPI00289758	CAPN2	700	700	700	8.0E+04	8.0E+04	8.0E+04	4.6	3	0	0	1	0	CALPAIN-2 CATALYTIC SUBUNIT PRECURSOR.	P17655; Q16738; Q59EF6; Q6PJT3; Q8WU26; Q9HBB1	CAN2_HUMAN; Q59EF6_HUMAN
390	IPI00290416	GTPBP9	396	396	396	4.5E+04	4.5E+04	4.5E+04	20.7	7	1	1	1	1	ISOFORM 1 OF PUTATIVE GTP-BINDING PROTEIN 9.	Q5BJD7; Q8NCI8; Q96CU1; Q96SV2; Q9NTK5; Q9P1D3; Q9UNY9; Q9Y6G4	GTPB9_HUMAN
391	IPI00290553; IPI00793673	ALDH1L1	902	912	907	9.9E+04	1.0E+05	9.9E+04	13.9	9	1	1	1	1	10-FORMYLTETRAHYDROFOLATE DEHYDROGENASE.; FORMYLTETRAHYDROFOLATE DEHYDROGENASE ISOFORM A VARIANT.	O75891; Q49A47; Q53H87; Q53HP5; Q59G10; Q68CS1	FTHFD_HUMAN; Q49A47_HUMAN; Q53H87_HUMAN; Q53HP5_HUMAN; Q59G10_HUMAN
392	IPI00290566	TCP1	556	556	556	6.0E+04	6.0E+04	6.0E+04	18.0	6	1	1	1	1	T-COMPLEX PROTEIN 1 SUBUNIT ALPHA.	P17987; Q15556; Q5TCM3	TCPA_HUMAN
393	IPI00290770; IPI00552715; IPI00553185; IPI00744315	CCT3	507	545	535	5.6E+04	6.1E+04	5.9E+04	17.8	7	1	1	1	1	CHAPERONIN CONTAINING TCP1, SUBUNIT 3 ISOFORM B.; CHAPERONIN CONTAINING TCP1, SUBUNIT 3 ISOFORM C.; T-COMPLEX PROTEIN 1 SUBUNIT GAMMA.; 60 KDA PROTEIN.	P49368; Q2TU64; Q59H77; Q5SZY0; Q5SZY1; Q9BR64	; Q2TU64_HUMAN; Q59H77_HUMAN; Q5SZY0_HUMAN; TCPG_HUMAN
394	IPI00291005	MDH1	334	334	334	3.6E+04	3.6E+04	3.6E+04	40.1	11	1	1	1	1	MALATE DEHYDROGENASE, CYTOPLASMIC.	P40925; Q6I9V0	MDHC_HUMAN
395	IPI00291006	MDH2	338	338	338	3.6E+04	3.6E+04	3.6E+04	48.8	16	1	1	1	1	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.	O43682; P40926; Q0QF37; Q6FHZ0; Q75MP7; Q75MT9	MDHM_HUMAN; Q0QF37_HUMAN; Q6FHZ0_HUMAN; Q75MP7_HUMAN; Q75MT9_HUMAN
396	IPI00291175; IPI00307162	VCL	1066	1134	1100	1.2E+05	1.2E+05	1.2E+05	37.6	31	1	1	1	1	ISOFORM 1 OF VINCULIN.; ISOFORM 2 OF VINCULIN.	P18206; Q16450; Q5JQ13; Q5SWX2; Q7Z3B8; Q8IXU7	Q5JQ13_HUMAN; VINC_HUMAN
397	IPI00291922	PSMA5	241	241	241	2.6E+04	2.6E+04	2.6E+04	13.3	2	0	0	1	1	PROTEASOME SUBUNIT ALPHA TYPE 5.	P28066; Q3T1C1; Q5U0A0; Q6IBF7	PSA5_HUMAN; Q5U0A0_HUMAN
398	IPI00291928; IPI00646415	RAB14	181	215	198	2.0E+04	2.4E+04	2.2E+04	19.3	3	0	0	1	0	RAS-RELATED PROTEIN RAB-14.; 20 KDA PROTEIN.	P35287; P61106; Q5JVD4; Q6Q7K5; Q969L0; Q9UI11	; RAB14_HUMAN
399	IPI00293464; IPI00784120; IPI00786914; IPI00787250	DDB1	1057	1140	1119	1.2E+05	1.3E+05	1.2E+05	5.5	5	0	1	1	1	DNA DAMAGE-BINDING PROTEIN 1.; 127 KDA PROTEIN.; DAMAGE-SPECIFIC DNA BINDING PROTEIN 1.; SIMILAR TO DNA DAMAGE-BINDING PROTEIN 1 (DAMAGE-SPECIFIC DNA-BINDINGPROTEIN 1) (UV-DAMAGED DNA-BINDING FACTOR) (DDB P127 SUBUNIT) (DDBA)(UV-DAMAGED DNA-BINDING PROTEIN 1) (UV-DDB 1) (XERODERMA PIGMENTOSUMGROUP E-COMPLEMENTING PROTEIN) (XPCE) (XP...	O15176; Q13289; Q16531; Q58F96	; DDB1_HUMAN
400	IPI00293867; IPI00472043	DDT	118	134	126	1.3E+04	1.4E+04	1.3E+04	21.2	2	0	0	1	0	D-DOPACHROME DECARBOXYLASE.; SIMILAR TO D-DOPACHROME TAUTOMERASE.	O00774; O60787; P30046; Q13534; Q53Y51	; DOPD_HUMAN; Q53Y51_HUMAN
401	IPI00293975	GPX1	203	203	203	2.2E+04	2.2E+04	2.2E+04	17.2	3	0	0	1	1	GLUTATHIONE PEROXIDASE 1 ISOFORM 1.	Q6NSD4	Q6NSD4_HUMAN
402	IPI00294073	COQ7	217	217	217	2.4E+04	2.4E+04	2.4E+04	13.4	2	0	0	1	1	UBIQUINONE BIOSYNTHESIS PROTEIN COQ7 HOMOLOG.	Q49A71; Q8NI45; Q99807; Q9BTT7; Q9H0T5; Q9UEW5; Q9UNR5	COQ7_HUMAN; Q49A71_HUMAN; Q8NI45_HUMAN; Q9BTT7_HUMAN; Q9H0T5_HUMAN
403	IPI00294186; IPI00749059	LACTB	547	547	547	6.1E+04	6.1E+04	6.1E+04	17.0	6	1	1	1	0	ISOFORM 1 OF SERINE BETA-LACTAMASE-LIKE PROTEIN LACTB, MITOCHONDRIALPRECURSOR.; LACTB PROTEIN.	P83096; P83111	; LACTB_HUMAN
404	IPI00294187	PADI2	665	665	665	7.6E+04	7.6E+04	7.6E+04	20.9	11	1	1	1	1	PROTEIN-ARGININE DEIMINASE TYPE-2.	Q9UPN2; Q9Y2J8	PADI2_HUMAN
405	IPI00294398; IPI00298406	HADH	314	390	352	3.4E+04	4.2E+04	3.8E+04	34.4	9	1	1	1	1	ISOFORM 1 OF HYDROXYACYL-COENZYME A DEHYDROGENASE, MITOCHONDRIALPRECURSOR.; ISOFORM 2 OF HYDROXYACYL-COENZYME A DEHYDROGENASE, MITOCHONDRIALPRECURSOR.	O00324; O00397; O00753; Q16836; Q4W5B4	HCDH_HUMAN; Q4W5B4_HUMAN
406	IPI00294911	SDHB	280	280	280	3.2E+04	3.2E+04	3.2E+04	23.6	6	1	1	1	1	SUCCINATE DEHYDROGENASE [UBIQUINONE] IRON-SULFUR SUBUNIT,MITOCHONDRIAL PRECURSOR.	P21912; Q0QEY7; Q70SX8; Q9NQ12	DHSB_HUMAN; Q0QEY7_HUMAN; Q70SX8_HUMAN
407	IPI00294959	LDB3	617	617	617	6.7E+04	6.7E+04	6.7E+04	40.4	22	1	1	1	1	ISOFORM 2 OF LIM DOMAIN-BINDING PROTEIN 3.	O75112; Q5K6N9; Q5K6P0; Q5K6P1; Q96FH2; Q9Y4Z3; Q9Y4Z4; Q9Y4Z5	LDB3_HUMAN
408	IPI00295386	CBR1	277	277	277	3.0E+04	3.0E+04	3.0E+04	18.4	4	0	0	1	1	CARBONYL REDUCTASE [NADPH] 1.		
409	IPI00295400; IPI00412737	WARS	430	471	451	4.9E+04	5.3E+04	5.1E+04	18.7	5	1	1	1	0	TRYPTOPHANYL-TRNA SYNTHETASE, CYTOPLASMIC.; TRYPTOPHANYL-TRNA SYNTHETASE ISOFORM B.	P23381; P78534; P78535; Q502Y0; Q53XB6; Q9UDL3	; P78534_HUMAN; Q502Y0_HUMAN; Q53XB6_HUMAN; SYWC_HUMAN
410	IPI00295777; IPI00797300	GPD1	326	349	338	3.5E+04	3.8E+04	3.6E+04	41.6	14	1	1	1	1	GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+], CYTOPLASMIC.; 35 KDA PROTEIN.	P21695; Q8N1B0	; GPDA_HUMAN
411	IPI00296053; IPI00759715	FH	467	510	489	5.0E+04	5.5E+04	5.2E+04	40.2	14	1	1	1	1	ISOFORM MITOCHONDRIAL OF FUMARATE HYDRATASE, MITOCHONDRIAL PRECURSOR.; ISOFORM CYTOPLASMIC OF FUMARATE HYDRATASE, MITOCHONDRIAL PRECURSOR.	P07954; Q5SY06	FUMH_HUMAN; Q5SY06_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
412	IPI00296190; IPI00646289; IPI00646889	C10orf58	218	229	224	2.4E+04	2.6E+04	2.5E+04	10.0	2	0	0	1	0	UNCHARACTERIZED PROTEIN C10ORF58 PRECURSOR.; 25 KDA PROTEIN.; 24 KDA PROTEIN.	Q6UW08; Q8N2K3; Q8NBK9; Q96JR0; Q9BRX8	; CJ058_HUMAN
413	IPI00296635	GBE1	702	702	702	8.0E+04	8.0E+04	8.0E+04	9.3	5	1	1	1	0	1,4-ALPHA-GLUCAN BRANCHING ENZYME.	Q04446; Q59ET0; Q96EN0	GLGB_HUMAN; Q59ET0_HUMAN
414	IPI00297779	CCT2	535	535	535	5.7E+04	5.7E+04	5.7E+04	28.4	10	1	1	1	1	T-COMPLEX PROTEIN 1 SUBUNIT BETA.	P78371; Q14D36; Q6IAT3; Q9H369	Q9H369_HUMAN; TCPB_HUMAN
415	IPI00298423	PDHX	501	501	501	5.4E+04	5.4E+04	5.4E+04	30.3	11	1	1	1	1	PYRUVATE DEHYDROGENASE PROTEIN X COMPONENT, MITOCHONDRIAL PRECURSOR.	O00330; O60221; Q96FV8; Q99783	ODPX_HUMAN
416	IPI00298547	PARK7	189	189	189	2.0E+04	2.0E+04	2.0E+04	31.8	4	1	1	1	1	PROTEIN DJ-1.	O14805; Q6DR95; Q7LFU2; Q99497	PARK7_HUMAN
417	IPI00298933	CASQ2	399	399	399	4.6E+04	4.6E+04	4.6E+04	28.8	10	1	1	1	1	CALSEQUESTRIN-2 PRECURSOR.	O14958; Q5T1D2; Q8TBW8	CASQ2_HUMAN; Q5T1D2_HUMAN
418	IPI00298961; IPI00784388	XPO1	1070	1071	1071	1.2E+05	1.2E+05	1.2E+05	6.6	5	1	1	1	0	EXPORTIN-1.; 123 KDA PROTEIN.	O14980; Q63HP8; Q68CP3; Q99433	; XPO1_HUMAN
419	IPI00299000; IPI00794875; IPI00807557	PA2G4	372	406	391	4.1E+04	4.5E+04	4.3E+04	13.6	5	1	1	1	1	PROLIFERATION-ASSOCIATED PROTEIN 2G4.; 41 KDA PROTEIN.; HYPOTHETICAL PROTEIN (FRAGMENT).	O43846; Q05D08; Q6PIN5; Q9UM59; Q9UQ80	; PA2G4_HUMAN; Q05D08_HUMAN; Q6PIN5_HUMAN
420	IPI00299033	KPNA3	521	521	521	5.8E+04	5.8E+04	5.8E+04	14.8	6	1	1	1	1	IMPORTIN ALPHA-3 SUBUNIT.	O00191; O00505; O43195; Q53F09; Q5W0Z8; Q8IYQ9; Q96AA7	IMA3_HUMAN; Q53F09_HUMAN; Q5W0Z8_HUMAN; Q8IYQ9_HUMAN
421	IPI00299155; IPI00789638; IPI00790038; IPI00790207; IPI00795606	PSMA4	225	261	238	2.5E+04	2.9E+04	2.7E+04	9.7	3	0	0	1	1	PROTEASOME SUBUNIT ALPHA TYPE 4.; PSMA4 PROTEIN.; 25 KDA PROTEIN.; 27 KDA PROTEIN.; 26 KDA PROTEIN.	P25789; Q53XP2; Q7Z474; Q8TBD1	; PSA4_HUMAN; Q53XP2_HUMAN; Q7Z474_HUMAN
422	IPI00299456	FBP2	339	339	339	3.7E+04	3.7E+04	3.7E+04	33.0	10	1	1	1	1	FRUCTOSE-1,6-BISPHOSPHATASE ISOZYME 2.	O00757; Q17R39; Q6FI53; Q9UJ73; Q9UMQ9; Q9UMR0	F16P2_HUMAN; Q9UJ73_HUMAN; Q9UMQ9_HUMAN; Q9UMR0_HUMAN
423	IPI00299608; IPI00456695	PSMD1	922	953	938	1.0E+05	1.1E+05	1.0E+05	8.8	5	1	1	1	1	ISOFORM 1 OF 26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 1.; ISOFORM 2 OF 26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 1.	Q05BX4; Q05CW6; Q24JU0; Q53TI2; Q6GMU5; Q6P2P4; Q6PJM7; Q6PKG9; Q86VU1; Q8IV79; Q99460	PSMD1_HUMAN; Q05BX4_HUMAN; Q05CW6_HUMAN
424	IPI00299977	PHPT1	125	125	125	1.4E+04	1.4E+04	1.4E+04	26.4	3	0	0	1	1	14 KDA PHOSPHOHISTIDINE PHOSPHATASE.	Q5T5S3; Q6FIE5; Q9H0Y3; Q9NRX4	PHP14_HUMAN; Q5T5S3_HUMAN; Q6FIE5_HUMAN
425	IPI00300074	FARSB	589	589	589	6.6E+04	6.6E+04	6.6E+04	9.5	5	1	1	1	1	PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN.	O95708; Q4ZFX1; Q57ZJ5; Q9BR63; Q9NSD9; Q9NZZ6	Q4ZFX1_HUMAN; Q57ZJ5_HUMAN; Q9BR63_HUMAN; SYFB_HUMAN
426	IPI00300285; IPI00783874	HDHD2	259	266	263	2.9E+04	2.9E+04	2.9E+04	8.1	2	0	0	1	1	29 KDA PROTEIN.; HALOACID DEHALOGENASE-LIKE HYDROLASE DOMAIN CONTAINING 2.	Q96NV4; Q9H0R4	; Q96NV4_HUMAN; Q9H0R4_HUMAN
427	IPI00300567; IPI00398758	DCI	285	302	294	3.1E+04	3.3E+04	3.2E+04	14.6	4	1	1	1	1	ISOFORM 1 OF 3,2-TRANS-ENOYL-COA ISOMERASE, MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF 3,2-TRANS-ENOYL-COA ISOMERASE, MITOCHONDRIAL PRECURSOR.	P42126; Q13290; Q7Z2L6; Q7Z2L7; Q96DC0; Q9BUB8; Q9BW05	D3D2_HUMAN; Q96DC0_HUMAN
428	IPI00301028	TRIM72	477	477	477	5.3E+04	5.3E+04	5.3E+04	37.3	14	1	1	1	1	ISOFORM 1 OF TRIPARTITE MOTIF-CONTAINING PROTEIN 72.	Q6ZMU5; Q8N4X6; Q8NBD9	TRI72_HUMAN
429	IPI00301419; IPI00798179	COPS7A	166	275	221	1.8E+04	3.0E+04	2.4E+04	7.6	2	0	0	1	1	COP9 SIGNALOSOME COMPLEX SUBUNIT 7A.; 18 KDA PROTEIN.	Q567U8; Q9NVX3; Q9UBW8; Q9UJW4	; CSN7A_HUMAN; Q567U8_HUMAN
430	IPI00301464; IPI00412663; IPI00783326	SGCA	263	387	346	2.9E+04	4.3E+04	3.8E+04	10.3	3	1	1	1	0	ISOFORM SGCA-1 OF ALPHA-SARCOGLYCAN PRECURSOR.; ISOFORM SGCA-2 OF ALPHA-SARCOGLYCAN PRECURSOR.; 43 KDA PROTEIN.	Q13710; Q13712; Q16586	; SGCA_HUMAN
431	IPI00302592; IPI00333541; IPI00644576	FLNA	2607	2647	2631	2.8E+05	2.8E+05	2.8E+05	6.0	11	1	0	1	1	FILAMIN A, ALPHA.; FILAMIN-A.; FILAMIN A, ALPHA.	P21333; Q5HY53; Q5HY54; Q5HY55; Q60FE5; Q60FE6; Q6NXF2; Q86TQ3; Q8NF52; Q8TES4; Q96C61	FLNA_HUMAN; Q5HY53_HUMAN; Q5HY54_HUMAN; Q5HY55_HUMAN; Q60FE5_HUMAN; Q60FE6_HUMAN; Q6NXF2_HUMAN; Q86TQ3_HUMAN; Q8NF52_HUMAN; Q8TES4_HUMAN; Q96C61_HUMAN
432	IPI00302925; IPI00784090	CCT8	548	550	549	6.0E+04	6.0E+04	6.0E+04	21.0	10	1	1	1	1	CHAPERONIN CONTAINING TCP1, SUBUNIT 8 (THETA) VARIANT.; T-COMPLEX PROTEIN 1 SUBUNIT THETA.	P50990; Q4VBP8; Q53HU0; Q7Z759	Q53HU0_HUMAN; Q7Z759_HUMAN; TCPQ_HUMAN
433	IPI00303258	LMCD1	365	365	365	4.1E+04	4.1E+04	4.1E+04	34.3	10	1	1	1	1	LIM AND CYSTEINE-RICH DOMAINS PROTEIN 1.	Q9NZU5	LMCD1_HUMAN
434	IPI00303476	ATP5B	529	529	529	5.7E+04	5.7E+04	5.7E+04	75.4	40	1	1	1	1	ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL PRECURSOR.	P06576; Q0QEN7; Q14283	ATPB_HUMAN; Q0QEN7_HUMAN
435	IPI00303568; IPI00395565; IPI00514138	PTGES2	186	377	276	2.1E+04	4.2E+04	3.1E+04	14.0	2	0	0	1	1	PROSTAGLANDIN E SYNTHASE 2.; PROSTAGLANDIN E SYNTHASE 2 ISOFORM 2.; 29 KDA PROTEIN.	Q53EW9; Q5SYV6; Q96GI0; Q96GL2; Q9H7Z7	; PGES2_HUMAN
436	IPI00303882	M6PRBP1	434	434	434	4.7E+04	4.7E+04	4.7E+04	28.3	8	1	1	1	1	ISOFORM B OF MANNOSE-6-PHOSPHATE RECEPTOR-BINDING PROTEIN 1.	O60664; Q53G77; Q9BS03; Q9UBD7; Q9UP92	M6PBP_HUMAN
437	IPI00304925; IPI00807640	HSPA1A; HSPA1B	641	641	641	7.0E+04	7.0E+04	7.0E+04	38.5	19	1	1	1	1	HEAT SHOCK 70 KDA PROTEIN 1.; HEAT SHOCK 70KDA PROTEIN 1B.	P08107; P19790; Q59EJ3; Q5JQI4; Q5SP17; Q9UQC1; Q9UQL9; Q9UQM0	HSP71_HUMAN; Q59EJ3_HUMAN; Q5JQI4_HUMAN; Q9UQC1_HUMAN
438	IPI00305166	SDHA	664	664	664	7.3E+04	7.3E+04	7.3E+04	21.8	12	1	1	1	1	SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT,MITOCHONDRIAL PRECURSOR.	P31040; Q0QF12; Q16395; Q59GW8; Q9UMY5	DHSA_HUMAN; Q0QF12_HUMAN; Q59GW8_HUMAN
439	IPI00305383	UQCRC2	453	453	453	4.8E+04	4.8E+04	4.8E+04	40.8	12	1	1	1	1	UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN 2, MITOCHONDRIALPRECURSOR.	P22695; Q9BQ05	UQCR2_HUMAN
440	IPI00305978	AKR7A2	359	359	359	4.0E+04	4.0E+04	4.0E+04	9.5	2	1	1	1	1	AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2.	O43488; O75749; Q5TG63	ARK72_HUMAN

			Amino Acids in Sequence^1			Protein Molecular Weight^1			Detection								
Protein Group^2	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
441	IPI00306301	PDHA1	390	390	390	4.3E+04	4.3E+04	4.3E+04	34.6	14	1	1	1	1	PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT, SOMATIC FORM,MITOCHONDRIAL PRECURSOR.	P08559; Q53GE3; Q53H41; Q5JPT8; Q9NP12; Q9UBJ8; Q9UBU0; Q9UNG4; Q9UNG5	ODPA_HUMAN; Q53GE3_HUMAN; Q53H41_HUMAN; Q5JPT8_HUMAN
442	IPI00306720; IPI00796142	COX7A1	79	109	94	9.1E+03	1.2E+04	1.1E+04	29.1	2	0	0	1	1	CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-HEART, MITOCHONDRIAL PRECURSOR.; PROTEIN.	P24310; Q6FGI7	; CX7A1_HUMAN; Q6FGI7_HUMAN
443	IPI00307749; IPI00419604	NDUFS7	213	298	256	2.3E+04	3.3E+04	2.8E+04	15.0	3	0	0	1	1	NADH DEHYDROGENASE [UBIQUINONE] IRON-SULFUR PROTEIN 7, MITOCHONDRIALPRECURSOR.; CDNA FLJ34850 FIS, CLONE NT2NE2011758, HIGHLY SIMILAR TO NADH-UBIQUINONE OXIDOREDUCTASE 20 KDA SUBUNIT.	Q7LD69; Q8NAS7	Q7LD69_HUMAN; Q8NAS7_HUMAN
444	IPI00307755	PRKAA2	552	552	552	6.2E+04	6.2E+04	6.2E+04	13.0	5	1	1	1	1	5'-AMP-ACTIVATED PROTEIN KINASE CATALYTIC SUBUNIT ALPHA-2.	A0MZF5; P54646; Q9H1E8; Q9UD43	A0MZF5_HUMAN; AAPK2_HUMAN
445	IPI00328156; IPI00639878	MAOB	520	520	520	5.9E+04	5.9E+04	5.9E+04	25.8	12	1	1	1	1	AMINE OXIDASE [FLAVIN-CONTAINING] B.; MONOAMINE OXIDASE B.	P27338; Q7Z6S2; Q8TBI1	AOFB_HUMAN; Q8TBI1_HUMAN
446	IPI00328318; IPI00514126	AGL	1532	1534	1533	1.7E+05	1.8E+05	1.7E+05	35.0	46	1	1	1	1	AMYLO-1,6-GLUCOSIDASE, 4-ALPHA-GLUCANOTRANSFERASE ISOFORM 1 VARIANT.; ISOFORM 1 OF GLYCOGEN DEBRANCHING ENZYME.	P35573; P78354; P78544; Q59H92; Q6AZ90; Q9UF08	GDE_HUMAN; Q59H92_HUMAN
447	IPI00328328; IPI00409717	EIF4A2	407	408	408	4.6E+04	4.6E+04	4.6E+04	29.2	9	1	1	1	1	ISOFORM 1 OF EUKARYOTIC INITIATION FACTOR 4A-II.; ISOFORM 2 OF EUKARYOTIC INITIATION FACTOR 4A-II.	Q14240; Q53XJ6; Q86WD0; Q96B90; Q96EA8	IF4A2_HUMAN; Q53XJ6_HUMAN; Q86WD0_HUMAN
448	IPI00328534; IPI00658052	SRL	857	932	895	9.3E+04	1.0E+05	9.7E+04	25.6	20	1	1	1	1	ISOFORM 2 OF SARCALUMENIN PRECURSOR.; ISOFORM 1 OF SARCALUMENIN PRECURSOR.	Q86TD4	; SRCA_HUMAN
449	IPI00329200; IPI00783829; IPI00793443	RANBP5	1097	1123	1112	1.2E+05	1.3E+05	1.3E+05	12.5	10	1	1	1	0	127 KDA PROTEIN.; IMPORTIN BETA-3.; RAN BINDING PROTEIN 5.	O00410; O15257; Q5T578; Q86XC7; Q9BVS9	; IMB3_HUMAN; Q5T578_HUMAN; Q86XC7_HUMAN; Q9BVS9_HUMAN
450	IPI00329331	UGP2	508	508	508	5.7E+04	5.7E+04	5.7E+04	51.4	21	1	1	1	1	ISOFORM 1 OF UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE 2.	Q0P6K2; Q16851; Q53QE9; Q86Y81; Q9BU15	Q53QE9_HUMAN; UGPA2_HUMAN
451	IPI00329572; IPI00783170	PACSIN3	424	425	425	4.8E+04	4.9E+04	4.9E+04	24.9	8	1	1	1	1	49 KDA PROTEIN.; PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE IN NEURONS PROTEIN 3.	Q9H331; Q9NWV9; Q9UKS6	; PACN3_HUMAN
452	IPI00329745; IPI00477140; IPI00783271	LRPPRC	1278	1402	1358	1.5E+05	1.6E+05	1.5E+05	20.9	22	1	1	1	1	CDNA FLJ43793 FIS, CLONE TESTI4000014, HIGHLY SIMILAR TO 130 KDALEUCINE-RICH PROTEIN.; HYPOTHETICAL PROTEIN LRPPRC.; LEUCINE-RICH PPR MOTIF-CONTAINING PROTEIN.	A0PJE3; Q53PC0; Q53QN7; Q6ZUD8; Q7Z7A6; Q96D84	A0PJE3_HUMAN; Q53PC0_HUMAN; Q53QN7_HUMAN; Q6ZUD8_HUMAN; Q7Z7A6_HUMAN; Q96D84_HUMAN
453	IPI00329801	ANXA5	320	320	320	3.6E+04	3.6E+04	3.6E+04	41.6	14	0	0	1	1	ANNEXIN A5.	P08758; Q6FHB3; Q6FI16; Q8WV69	ANXA5_HUMAN; Q6FHB3_HUMAN
454	IPI00332106; IPI00645060	PBXIP1	702	731	717	7.8E+04	8.1E+04	7.9E+04	14.6	8	1	1	1	1	PRE-B-CELL LEUKEMIA HOMEOBOX INTERACTING PROTEIN 1.; PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR INTERACTING PROTEIN 1.	Q5T176; Q96AQ6; Q9HA02; Q9HD85	Q5T176_HUMAN; Q96AQ6_HUMAN; Q9HA02_HUMAN; Q9HD85_HUMAN
455	IPI00220906; IPI00333838	ACOT1; ACOT2	421	483	452	4.6E+04	5.3E+04	5.0E+04	40.1	11	1	1	1	1	ISOFORM 1 OF ACYL-COENZYME A THIOESTERASE 2.; ACYL-COENZYME A THIOESTERASE 1.	A1L172; A1L173; P49753; Q3I5F8; Q3I5F9; Q53EK4; Q86TX2; Q9NUX4	A1L172_HUMAN; A1L173_HUMAN; ACOT1_HUMAN; ACOT2_HUMAN; Q3I5F8_HUMAN; Q53EK4_HUMAN
456	IPI00334775; IPI00414676	HSP90AB1	724	736	730	8.3E+04	8.5E+04	8.4E+04	42.4	27	1	1	1	1	85 KDA PROTEIN.; HEAT SHOCK PROTEIN HSP 90-BETA.	P08238; Q5T9W7; Q6PK50; Q9H6X9; Q9NQW0; Q9NTK6	; HS90B_HUMAN; Q6PK50_HUMAN; Q9H6X9_HUMAN
457	IPI00337541	NNT	1086	1086	1086	1.1E+05	1.1E+05	1.1E+05	13.5	11	1	1	1	1	NAD(P) TRANSHYDROGENASE, MITOCHONDRIAL PRECURSOR.	Q13423; Q16796; Q2TB59; Q2TB60; Q8N3V4; Q8N5H5	NNTM_HUMAN; Q2TB59_HUMAN; Q8N5H5_HUMAN
458	IPI00337741	APEH	732	732	732	8.1E+04	8.1E+04	8.1E+04	16.3	8	1	1	1	1	ACYLAMINO-ACID-RELEASING ENZYME.	P13798; Q9BQ33; Q9P0Y2	ACPH_HUMAN
459	IPI00374208	CAND2	1119	1119	1119	1.2E+05	1.2E+05	1.2E+05	13.3	10	1	1	1	1	CULLIN-ASSOCIATED NEDD8-DISSOCIATED PROTEIN 2.	O75155	CAND2_HUMAN
460	IPI00374657	VAPA	294	294	294	3.3E+04	3.3E+04	3.3E+04	15.3	5	0	0	1	1	VESICLE-ASSOCIATED MEMBRANE PROTEIN-ASSOCIATED PROTEIN A ISOFORM 1.		
461	IPI00376005; IPI00411704	EIF5A	154	184	169	1.7E+04	2.0E+04	1.9E+04	25.5	3	1	0	1	1	ISOFORM 2 OF EUKARYOTIC TRANSLATION INITIATION FACTOR 5A-1.; ISOFORM 1 OF EUKARYOTIC TRANSLATION INITIATION FACTOR 5A-1.	P10159; P63241; Q16182; Q7L7L3; Q7Z4L1; Q9D0G2	IF5A1_HUMAN
462	IPI00377167	SMTNL1	512	512	512	5.5E+04	5.5E+04	5.5E+04	18.0	5	1	1	1	1	SIMILAR TO SMOOTHELIN-LIKE 1.		
463	IPI00377214; IPI00465264	NLRX1	921	975	948	1.0E+05	1.1E+05	1.0E+05	3.9	3	0	1	1	1	NLR FAMILY MEMBER X1 ISOFORM 2.; NLR FAMILY MEMBER X1 ISOFORM 1.	Q7RTR3; Q86UT6; Q96D51; Q9H724	Q7RTR3_HUMAN; Q86UT6_HUMAN; Q96D51_HUMAN; Q9H724_HUMAN
464	IPI00382470; IPI00784295; IPI00789847	HSP90AA1	732	854	790	8.5E+04	9.8E+04	9.1E+04	33.0	26	1	1	1	1	HEAT SHOCK PROTEIN HSP 90-ALPHA 2.; HEAT SHOCK PROTEIN HSP 90-ALPHA.; PROTEIN.	P07900; Q2PP14; Q2VPJ6; Q5CAQ6; Q5CAQ7; Q86SX1; Q8TBA7; Q96HX7; Q9BVQ5	; HS90A_HUMAN; Q2VPJ6_HUMAN; Q5CAQ6_HUMAN; Q5CAQ7_HUMAN; Q86SX1_HUMAN; Q8TBA7_HUMAN; Q96HX7_HUMAN
465	IPI00382894	TPM3	248	248	248	2.9E+04	2.9E+04	2.9E+04	66.5	22	0	0	1	1	TROPOMYOSIN 3.	Q5VU58; Q8TCG3	Q5VU58_HUMAN; Q8TCG3_HUMAN
466	IPI00383046	CMBL	245	245	245	2.8E+04	2.8E+04	2.8E+04	22.4	7	0	0	1	1	CARBOXYMETHYLENEBUTENOLIDASE-LIKE.	Q8TED6; Q96DG6	Q8TED6_HUMAN; Q96DG6_HUMAN
467	IPI00011454; IPI00383581; IPI00441414; IPI00472068	GANAB	847	966	925	9.6E+04	1.1E+05	1.0E+05	9.4	5	1	1	1	1	ISOFORM 2 OF NEUTRAL ALPHA-GLUCOSIDASE AB PRECURSOR.; ISOFORM 1 OF NEUTRAL ALPHA-GLUCOSIDASE AB PRECURSOR.; ISOFORM 3 OF NEUTRAL ALPHA-GLUCOSIDASE AB PRECURSOR.; 107 KDA PROTEIN.	Q14697; Q8WTS9; Q9P0X0	; GANAB_HUMAN
468	IPI00384280	PCYOX1	505	505	505	5.7E+04	5.7E+04	5.7E+04	28.7	10	1	1	1	1	PRENYLCYSTEINE OXIDASE PRECURSOR.	O94982; Q53ST0; Q584P1; Q8N4N5; Q96QM8; Q9UHG3	PCYOX_HUMAN; Q53ST0_HUMAN; Q584P1_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
469	IPI00384938; IPI00423463; IPI00423464; IPI00423466; IPI00448925; IPI00448938; IPI00472610; IPI00645363; IPI00761159; IPI00784810; IPI00784817; IPI00784822; IPI00784828; IPI00784842; IPI00785084; IPI00807531; IPI00815926; IPI00816314; IPI00816681; IPI00829944	IGHG1; IGHM	348	544	472	3.8E+04	6.0E+04	5.2E+04	22.8	10	1	1	1	1	HYPOTHETICAL PROTEIN DKFZP686N02209.; HYPOTHETICAL PROTEIN DKFZP686O01196.; HYPOTHETICAL PROTEIN DKFZP686K03196.; HYPOTHETICAL PROTEIN DKFZP686H20196.; IGHG1 PROTEIN.; IGHG1 PROTEIN.; IGHM PROTEIN.; HYPOTHETICAL PROTEIN DKFZP686P15220.; IGHM PROTEIN.; IGHG1 PROTEIN.; ANTI-RHD MONOCLONAL T125 GAMMA1 HEAVY CHAIN PRECURSOR.; IGHV4-31 PROTEIN.; HYPOTHETICAL PROTEIN DKFZP686C11235.; HYPOTHETICAL PROTEIN DKFZP686G11190.; HYPOTHETICAL PROTEIN IGHG1.; IGHG1 PROTEIN.; IGHG1 PROTEIN.; HYPOTHETICAL PROTEIN DKFZP686I15196.; HEPATITIS B VIRUS RECEPTOR BINDING PROTEIN (FRAGMENT).; IGHG1 PROTEIN.	Q569F4; Q5EFE5; Q6GMW7; Q6GMX1; Q6GMX6; Q6IN78; Q6MZQ6; Q6MZV7; Q6N089; Q6N094; Q6N095; Q6N096; Q6N097; Q6P055; Q6PI81; Q6PJ95; Q6PJA4; Q6PJF1; Q6PYX1; Q7Z351; Q7Z5W1; Q7Z7P5	Q569F4_HUMAN; Q5EFE5_HUMAN; Q6GMW7_HUMAN; Q6GMX1_HUMAN; Q6GMX6_HUMAN; Q6IN78_HUMAN; Q6MZQ6_HUMAN; Q6MZV7_HUMAN; Q6N089_HUMAN; Q6N094_HUMAN; Q6N095_HUMAN; Q6N096_HUMAN; Q6N097_HUMAN; Q6P055_HUMAN; Q6PI81_HUMAN; Q6PJ95_HUMAN; Q6PJA4_HUMAN; Q6PJF1_HUMAN; Q6PYX1_HUMAN; Q7Z351_HUMAN; Q7Z5W1_HUMAN; Q7Z7P5_HUMAN
470	IPI00386271	SLC25A12	678	678	678	7.5E+04	7.5E+04	7.5E+04	52.2	28	1	1	1	1	CALCIUM-BINDING MITOCHONDRIAL CARRIER PROTEIN ARALAR1.	O75746; Q96AM8	CMC1_HUMAN; Q96AM8_HUMAN
471	IPI00394740	TNNT3	252	252	252	3.0E+04	3.0E+04	3.0E+04	31.0	9	0	0	1	0	ISOFORM 4 OF TROPONIN T, FAST SKELETAL MUSCLE.		
472	IPI00394847; IPI00784051	SMTNL2	317	461	389	3.5E+04	5.0E+04	4.3E+04	9.5	3	0	1	1	0	SMOOTHELIN-LIKE 2.; CDNA FLJ42461 FIS, CLONE BRACE2026836, MODERATELY SIMILAR TO MUSMUSCULUS SMOOTHELIN L1, LARGE ISOFORM.	Q2TAL5; Q6ZVK6	Q2TAL5_HUMAN; Q6ZVK6_HUMAN
473	IPI00395769; IPI00478410	ATP5C1	297	298	298	3.3E+04	3.3E+04	3.3E+04	18.2	5	1	1	1	1	ISOFORM HEART OF ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR.; ISOFORM LIVER OF ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR.	P36542; Q5VYP3; Q6I9V2; Q8TAS0; Q96AS8	ATPG_HUMAN; Q6I9V2_HUMAN; Q8TAS0_HUMAN
474	IPI00396171; IPI00745518	MAP4	1152	1163	1158	1.2E+05	1.2E+05	1.2E+05	11.3	9	0	0	1	0	ISOFORM 1 OF MICROTUBULE-ASSOCIATED PROTEIN 4.; MICROTUBULE-ASSOCIATED PROTEIN 4 ISOFORM 1 VARIANT (FRAGMENT).	P27816; Q05D06; Q13082; Q59FT2; Q6NX68; Q96A76	MAP4_HUMAN; Q05D06_HUMAN; Q59FT2_HUMAN; Q6NX68_HUMAN
475	IPI00396378; IPI00414696	HNRPA2B1	341	353	347	3.6E+04	3.7E+04	3.7E+04	7.3	2	1	0	1	1	ISOFORM B1 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1.; ISOFORM A2 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1.	P22626; P22627	ROA2_HUMAN
476	IPI00100197; IPI00397571	NSFL1C	370	372	371	4.1E+04	4.1E+04	4.1E+04	30.3	7	1	1	1	0	ISOFORM 1 OF NSFL1 COFACTOR P47.; ISOFORM 3 OF NSFL1 COFACTOR P47.	Q53FE8; Q53FF5; Q5JXA5; Q7Z533; Q9H102; Q9NVL9; Q9UI06; Q9UNZ2	NSF1C_HUMAN; Q53FE8_HUMAN; Q53FF5_HUMAN; Q5JXA5_HUMAN
477	IPI00398121; IPI00470891	CSDE1	798	813	806	8.9E+04	9.1E+04	9.0E+04	2.6	2	0	0	1	0	HYPOTHETICAL PROTEIN DKFZP779B0247.; ISOFORM LONG OF COLD SHOCK DOMAIN-CONTAINING PROTEIN E1.	O75534; O94961; Q5TF04; Q5TF05; Q68DF1; Q68DI9; Q8WU01; Q96L66; Q9GZV0; Q9UG12; Q9UG93; Q9Y2S4	CSDE1_HUMAN; Q68DF1_HUMAN; Q8WU01_HUMAN; Q96L66_HUMAN; Q9GZV0_HUMAN; Q9UG12_HUMAN; Q9UG93_HUMAN
478	IPI00398958	LOC387867	295	295	295	3.3E+04	3.3E+04	3.3E+04	7.1	2	0	0	1	0	SIMILAR TO 40S RIBOSOMAL PROTEIN SA.		
479	IPI00220402; IPI00410126	PPP1R2; PPP1R2P3	205	205	205	2.3E+04	2.3E+04	2.3E+04	21.9	3	0	0	1	1	PROTEIN PHOSPHATASE INHIBITOR 2.; PPP1R2P3 PROTEIN.	P41236; Q6NXS1	IPP2_HUMAN; Q6NXS1_HUMAN
480	IPI00410261	MYBPC1	1171	1171	1171	1.3E+05	1.3E+05	1.3E+05	57.1	75	1	1	1	1	MYOSIN BINDING PROTEIN C, SLOW TYPE ISOFORM 1.	Q17RR7; Q86T39; Q86T48; Q86TA8; Q86TC8; Q8N3R4	Q17RR7_HUMAN; Q86T39_HUMAN; Q86T48_HUMAN; Q86TA8_HUMAN; Q86TC8_HUMAN; Q8N3R4_HUMAN
481	IPI00410714	HBA1; HBA2	142	142	142	1.5E+04	1.5E+04	1.5E+04	76.8	15	1	1	1	1	HEMOGLOBIN SUBUNIT ALPHA.	P01922; P69905; P78461; Q1HDT5; Q3MIF5; Q4ZGM8; Q53F97; Q6J1Z9; Q7Z6G4; Q7Z7B4; Q86YL2; Q86YQ1; Q86YQ4; Q86YQ5; Q96KF1; Q96T46; Q9BX83; Q9NQT3; Q9NYR7	HBA_HUMAN; P78461_HUMAN; Q1HDT5_HUMAN; Q4ZGM8_HUMAN; Q53F97_HUMAN; Q6J1Z9_HUMAN; Q7Z6G4_HUMAN; Q7Z7B4_HUMAN; Q86YL2_HUMAN; Q86YQ1_HUMAN; Q86YQ4_HUMAN; Q86YQ5_HUMAN; Q96T46_HUMAN; Q9BX83_HUMAN; Q9NQT3_HUMAN
482	IPI00411375; IPI00743873	MAP4	716	887	802	7.6E+04	9.3E+04	8.4E+04	6.9	4	0	1	1	0	MICROTUBULE-ASSOCIATED PROTEIN 4 ISOFORM 2.; 76 KDA PROTEIN.	Q6ZUW9; Q86Y04	; Q6ZUW9_HUMAN; Q86Y04_HUMAN
483	IPI00024989; IPI00411680; IPI00828189	PCMT1	227	228	228	2.5E+04	2.5E+04	2.5E+04	32.2	7	1	0	1	1	PROTEIN-L-ISOASPARTATE (D-ASPARTATE) O-METHYLTRANSFERASE.; ISOFORM 1 OF PROTEIN-L-ISOASPARTATE(D-ASPARTATE) O-METHYLTRANSFERASE.; ISOFORM 2 OF PROTEIN-L-ISOASPARTATE(D-ASPARTATE) O-METHYLTRANSFERASE.	P22061; Q14661; Q16556; Q5VYC1; Q5VYC2; Q93061; Q96II9; Q99625; Q9BQV7; Q9BQV8; Q9NP03	PIMT_HUMAN; Q5VYC1_HUMAN; Q5VYC2_HUMAN; Q9BQV7_HUMAN; Q9BQV8_HUMAN; Q9NP03_HUMAN
484	IPI00412713	SAMM50	469	469	469	5.2E+04	5.2E+04	5.2E+04	22.2	8	1	1	1	1	SORTING AND ASSEMBLY MACHINERY COMPONENT 50 HOMOLOG.	Q53HC4; Q56VW7; Q969Y9; Q96I46; Q9NW85; Q9UQM9; Q9Y512	Q53HC4_HUMAN; Q56VW7_HUMAN; SAM50_HUMAN
485	IPI00413318; IPI00473047	PRKAG1	331	340	336	3.8E+04	3.9E+04	3.8E+04	17.1	4	0	1	1	0	5'-AMP-ACTIVATED PROTEIN KINASE SUBUNIT GAMMA-1.; CDNA FLJ40287 FIS, CLONE TESTI2027909, HIGHLY SIMILAR TO 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT.	P54619; Q8N7V9	AAKG1_HUMAN; Q8N7V9_HUMAN
486	IPI00413344; IPI00796024	CFL2	166	182	174	1.9E+04	2.0E+04	1.9E+04	41.6	7	1	1	1	1	COFILIN-2.; PROTEIN.	Q549N0; Q9Y281	; COF2_HUMAN; Q549N0_HUMAN
487	IPI00413641	AKR1B1	316	316	316	3.6E+04	3.6E+04	3.6E+04	41.1	11	1	1	1	1	ALDOSE REDUCTASE.	O15289; P15121; Q5U031; Q6FGA4; Q6ICP2; Q9BS21; Q9UCI9	ALDR_HUMAN; O15289_HUMAN; Q5U031_HUMAN; Q6FGA4_HUMAN; Q6ICP2_HUMAN
488	IPI00414320	ANXA11	505	505	505	5.4E+04	5.4E+04	5.4E+04	22.0	8	1	1	1	1	ANNEXIN A11.	P50995; Q59EP1; Q5T0G8; Q6ICS0	ANX11_HUMAN; Q59EP1_HUMAN; Q5T0G8_HUMAN; Q6ICS0_HUMAN

Protein Group[2]	IPI ID	IPI gene name	Amino Acids in Sequence[1]			Protein Molecular Weight[1]			Seq. Cov. (max)	Unique Peptides (max)	Detection				Protein name	Uniprot Id	Uniprot Entry Name
			Min.	Max.	Mean	Min.	Max.	Mean			Expt. I-1	Expt. I-2	Expt. II	Expt. iii			
489	IPI00418169; IPI00455315	ANXA2	339	357	348	3.9E+04	4.0E+04	4.0E+04	47.9	15	1	1	1	1	ANNEXIN A2 ISOFORM 1.; ANNEXIN A2.	P07355; Q567R4; Q6N0B3; Q8TBV2; Q96DD5	ANXA2_HUMAN; Q6N0B3_HUMAN; Q8TBV2_HUMAN
490	IPI00418217; IPI00797844	ANKRD2	333	360	347	3.7E+04	4.0E+04	3.8E+04	49.3	11	1	1	1	1	ISOFORM 1 OF ANKYRIN REPEAT DOMAIN-CONTAINING PROTEIN 2.; ANKYRIN REPEAT DOMAIN 2.	Q3B778; Q5T456; Q70EZ9; Q8WUD7; Q96MG0; Q9GZV1	ANKR2_HUMAN; Q3B778_HUMAN; Q70EZ9_HUMAN; Q96MG0_HUMAN
491	IPI00418471; IPI00827679	VIM	431	466	449	5.0E+04	5.4E+04	5.2E+04	42.3	18	1	1	1	1	VIMENTIN.; 50 KDA PROTEIN.	P08670; Q15867; Q15868; Q15869; Q53HU8; Q548L2; Q6LER9; Q8N850; Q8N9S6; Q96ML2; Q9NTM3	; Q53HU8_HUMAN; Q548L2_HUMAN; Q8N9S6_HUMAN; VIME_HUMAN
492	IPI00419273; IPI00549919	CUL4A	659	763	711	7.7E+04	8.8E+04	8.3E+04	3.5	2	0	0	1	0	ISOFORM 1 OF CULLIN-4A.; ISOFORM 2 OF CULLIN-4A.	A2A2W2; O75834; Q13619; Q589T6; Q5TC62; Q6UP08; Q9UP17	A2A2W2_HUMAN; CUL4A_HUMAN
493	IPI00419307; IPI00554737	PPP2R1A	589	589	589	6.5E+04	6.5E+04	6.5E+04	22.8	9	1	1	1	1	ALPHA ISOFORM OF REGULATORY SUBUNIT A, PROTEIN PHOSPHATASE 2.; SERINE/THREONINE-PROTEIN PHOSPHATASE 2A 65 KDA REGULATORY SUBUNIT AALPHA ISOFORM.	P30153; Q13773; Q6ICQ3; Q96DH3	; 2AAA_HUMAN
494	IPI00419424; IPI00430808; IPI00430820; IPI00430847; IPI00440577; IPI00472961; IPI00478600; IPI00550731; IPI00554675; IPI00746963; IPI00761125; IPI00784070; IPI00784661; IPI00784773; IPI00784865; IPI00784985; IPI00807459; IPI00816118; IPI00827488	IGKC; IGKV1-5	234	294	239	2.6E+04	3.2E+04	2.6E+04	27.1	4	0	1	1	1	IGKV1-5 PROTEIN.; IGKC PROTEIN.; IGKV1-5 PROTEIN.; IGKC PROTEIN.; IGKV2-24 PROTEIN.; IGKC PROTEIN.; IGKV1-5 PROTEIN.; HYPOTHETICAL PROTEIN.; ANTI-RHD MONOCLONAL T125 KAPPA LIGHT CHAIN PRECURSOR.; IGKC PROTEIN.; IGKC PROTEIN.; IGKC PROTEIN.; HYPOTHETICAL PROTEIN.; HYPOTHETICAL PROTEIN.; HYPOTHETICAL PROTEIN.; HYPOTHETICAL PROTEIN.; HYPOTHETICAL PROTEIN.; IGKC PROTEIN.; IGKC PROTEIN.	A0A5E5; Q0KKI6; Q502W4; Q5EFE6; Q6GMV9; Q6GMW0; Q6GMW1; Q6GMX0; Q6GMX8; Q6GMX9; Q6P491; Q6P5R5; Q6P5S8; Q6PIH4; Q6PIH6; Q6PIH7; Q6PIT5; Q6PJF2; Q7Z3Y4; Q7Z473; Q8NEK0; Q8TCD0	A0A5E5_HUMAN; Q0KKI6_HUMAN; Q502W4_HUMAN; Q5EFE6_HUMAN; Q6GMV9_HUMAN; Q6GMW0_HUMAN; Q6GMW1_HUMAN; Q6GMX0_HUMAN; Q6GMX8_HUMAN; Q6GMX9_HUMAN; Q6P491_HUMAN; Q6P5R5_HUMAN; Q6P5S8_HUMAN; Q6PIH4_HUMAN; Q6PIH6_HUMAN; Q6PIH7_HUMAN; Q6PIT5_HUMAN; Q6PJF2_HUMAN; Q7Z3Y4_HUMAN; Q7Z473_HUMAN; Q8NEK0_HUMAN; Q8TCD0_HUMAN
495	IPI00419585	LOC653214; LOC654188; PPIA	165	165	165	1.8E+04	1.8E+04	1.8E+04	27.3	5	1	0	1	1	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A.	P05092; P62937; Q3KQW3; Q6IBU5; Q71V99; Q96IX3; Q9BRU4; Q9BTY9; Q9UC61	PPIA_HUMAN; Q71V99_HUMAN
496	IPI00420049; IPI00739670	C1orf170	696	696	696	7.2E+04	7.2E+04	7.2E+04	13.7	5	1	1	1	1	SIMILAR TO ZK84.1.; SIMILAR TO ZK84.1.	Q5SV97; Q6ZVZ7; Q9BRF2	Q5SV97_HUMAN; Q6ZVZ7_HUMAN; Q9BRF2_HUMAN
497	IPI00420108	DLST	453	453	453	4.9E+04	4.9E+04	4.9E+04	24.7	11	1	1	1	1	DIHYDROLIPOYLLYSINE-RESIDUE SUCCINYLTRANSFERASE COMPONENT OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX, MITOCHONDRIAL PRECURSOR.	P36957; Q6IBS5; Q7LDY7; Q9BQ32	ODO2_HUMAN; Q6IBS5_HUMAN; Q7LDY7_HUMAN
498	IPI00427330	SBDS	250	250	250	2.9E+04	2.9E+04	2.9E+04	11.6	3	0	0	1	0	SHWACHMAN-BODIAN-DIAMOND SYNDROME PROTEIN.	Q96FX0; Q9NV53; Q9Y3A5	SBDS_HUMAN
499	IPI00434580; IPI00479390	MYOM1	1589	1685	1637	1.8E+05	1.9E+05	1.8E+05	34.2	45	1	1	1	1	MYOMESIN 1.; MYOM1 PROTEIN.	Q14BD6; Q6H969; Q6ZUU0; Q9NZL8	Q14BD6_HUMAN; Q6H969_HUMAN; Q6ZUU0_HUMAN; Q9NZL8_HUMAN
500	IPI00440493	ATP5A1	553	553	553	6.0E+04	6.0E+04	6.0E+04	62.0	39	1	1	1	1	ATP SYNTHASE SUBUNIT ALPHA, MITOCHONDRIAL PRECURSOR.	P25705; Q53XX6; Q8IXV2; Q96FB4; Q96HW2; Q96IR6; Q9BTV8	ATPA_HUMAN; Q53XX6_HUMAN
501	IPI00440828; IPI00552360; IPI00604759	FAHD1	224	248	233	2.5E+04	2.7E+04	2.6E+04	13.3	2	0	0	1	0	ISOFORM 2 OF FUMARYLACETOACETATE HYDROLASE DOMAIN-CONTAINING PROTEIN1.; ISOFORM 1 OF FUMARYLACETOACETATE HYDROLASE DOMAIN-CONTAINING PROTEIN1.; FUMARYLACETOACETATE HYDROLASE DOMAIN CONTAINING 1.	A2A2C2; A2A2C3; Q6FIC7; Q6P587; Q96RY1; Q9H0N6	A2A2C2_HUMAN; A2A2C3_HUMAN; FAHD1_HUMAN
502	IPI00448095; IPI00797249; IPI00797917	DCXR	242	244	243	2.6E+04	2.6E+04	2.6E+04	16.4	4	0	0	1	1	L-XYLULOSE REDUCTASE.; 26 KDA PROTEIN.; 26 KDA PROTEIN.	Q7Z4W1; Q9BTZ3; Q9UHY9	; DCXR_HUMAN
503	IPI00453474; IPI00473081	TNNI1	187	187	187	2.2E+04	2.2E+04	2.2E+04	21.4	7	0	0	1	1	TROPONIN I, SLOW SKELETAL MUSCLE.; 22 KDA PROTEIN.	P19237; Q659A5; Q6FGS7; Q6FGW1; Q6ICU2; Q86T57; Q96DT9	; Q659A5_HUMAN; Q6FGS7_HUMAN; Q6FGW1_HUMAN; Q6ICU2_HUMAN; Q86T57_HUMAN; Q96DT9_HUMAN; TNNI1_HUMAN
504	IPI00456626	TXLNB	684	684	684	7.7E+04	7.7E+04	7.7E+04	16.2	8	1	1	1	1	BETA-TAXILIN.	Q5HYH7; Q5HYK6; Q5VTF3; Q76L25; Q86T52; Q8N3L3; Q8N3S2	Q5HYH7_HUMAN; Q5HYK6_HUMAN; TXLNB_HUMAN
505	IPI00456965	COQ5	327	327	327	3.7E+04	3.7E+04	3.7E+04	17.7	5	0	0	1	1	ISOFORM 1 OF UBIQUINONE BIOSYNTHESIS METHYLTRANSFERASE COQ5,MITOCHONDRIAL PRECURSOR.	Q32Q28; Q53HH0; Q5HYK3; Q96LV1; Q9BSP8	COQ5_HUMAN
506	IPI00465028; IPI00797687	TPI1	249	286	268	2.7E+04	3.1E+04	2.9E+04	44.2	12	1	1	1	1	TRIOSEPHOSPHATE ISOMERASE 1 VARIANT.; ISOFORM 1 OF TRIOSEPHOSPHATE ISOMERASE.	P00938; P60174; Q53HE2; Q6FHP9; Q6IS07; Q8WWD0; Q96AG5	Q53HE2_HUMAN; Q6FHP9_HUMAN; TPIS_HUMAN
507	IPI00465084; IPI00658057; IPI00793833	DES	402	470	447	4.7E+04	5.4E+04	5.1E+04	50.6	20	1	1	1	1	DESMIN.; MUTANT DESMIN.; 47 KDA PROTEIN.	P17661; Q15787; Q45VM6; Q45VM7; Q45VM8; Q53SB5; Q549R7; Q549R8; Q549R9; Q8IZR1; Q8IZR6; Q8NES2; Q8NEU6; Q8TAC4; Q8TCX2; Q8TD99; Q9H319; Q9UHN5; Q9UJ80	; DESM_HUMAN; Q45VM6_HUMAN; Q45VM7_HUMAN; Q45VM8_HUMAN; Q53SB5_HUMAN; Q549R7_HUMAN; Q549R8_HUMAN; Q549R9_HUMAN; Q9H319_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
508	IPI00465179; IPI00743142	PFKM	780	851	816	8.5E+04	9.3E+04	8.9E+04	38.7	36	1	1	1	1	CDNA FLJ44241 FIS, CLONE THYMU3008436, HIGHLY SIMILAR TO 6-PHOSPHOFRUCTOKINASE, MUSCLE TYPE.; ISOFORM 1 OF 6-PHOSPHOFRUCTOKINASE, MUSCLE TYPE.	P08237; Q16814; Q16815; Q6ZTT1	K6PF_HUMAN; Q6ZTT1_HUMAN
509	IPI00465248	ENO1	434	434	434	4.7E+04	4.7E+04	4.7E+04	49.8	19	1	1	1	1	ISOFORM ALPHA-ENOLASE OF ALPHA-ENOLASE.	P06733; P22712; Q16704; Q4TUS4; Q53FT9; Q53HR3; Q658M5; Q6GMP2; Q71V37; Q7Z3V6; Q8WU71; Q96GV1; Q9BT62; Q9UCG5; Q9UCH6; Q9UM55	ENOA_HUMAN; Q53FT9_HUMAN; Q53HR3_HUMAN; Q96GV1_HUMAN; Q9BT62_HUMAN; Q9UCG5_HUMAN; Q9UCH6_HUMAN
510	IPI00465256	AK3	227	227	227	2.6E+04	2.6E+04	2.6E+04	41.9	9	0	0	1	1	GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL.	Q5VYW6; Q7Z4Y4; Q7Z531; Q9H576; Q9NPB4; Q9UIJ7	KAD3_HUMAN; Q7Z4Y4_HUMAN; Q7Z531_HUMAN
511	IPI00465315	CYCS	105	105	105	1.2E+04	1.2E+04	1.2E+04	49.5	6	1	0	1	1	CYTOCHROME C.	P00001; P99999; Q6LER6; Q6NUR2; Q6NX69; Q96BV4	CYC_HUMAN; Q6LER6_HUMAN
512	IPI00465436	CAT	527	527	527	6.0E+04	6.0E+04	6.0E+04	44.4	20	1	1	1	1	CATALASE.	P04040; Q2M1U4; Q4VXX5; Q8TAK2; Q9BWT9; Q9UC85	CATA_HUMAN; Q8TAK2_HUMAN; Q9UC85_HUMAN
513	IPI00465439	ALDOA	364	364	364	3.9E+04	3.9E+04	3.9E+04	70.9	38	1	1	1	1	FRUCTOSE-BISPHOSPHATE ALDOLASE A.	P04075; Q6FH76; Q6FI10; Q96B15; Q9BWD9; Q9UCN2	ALDOA_HUMAN; Q6FI10_HUMAN; Q9UCN2_HUMAN
514	IPI00470359	TNNC1	161	161	161	1.8E+04	1.8E+04	1.8E+04	46.0	7	1	1	1	1	TROPONIN C, SLOW SKELETAL AND CARDIAC MUSCLES.	O14800; P02590; P04463; P63316; Q6FH91	Q6FH91_HUMAN; TNNC1_HUMAN
515	IPI00470535	CACNA2D1	1110	1110	1110	1.3E+05	1.3E+05	1.3E+05	12.6	10	1	1	1	1	DIHYDROPYRIDINE RECEPTOR ALPHA 2 SUBUNIT.	O95026; Q9UD81; Q9UDL7; Q9UDU5; Q9UIU0	O95026_HUMAN; Q9UD81_HUMAN; Q9UDL7_HUMAN; Q9UDU5_HUMAN; Q9UIU0_HUMAN
516	IPI00470631; IPI00746245	COQ9	318	324	321	3.6E+04	3.6E+04	3.6E+04	23.6	4	1	1	1	1	ISOFORM 1 OF UBIQUINONE BIOSYNTHESIS PROTEIN COQ9, MITOCHONDRIALPRECURSOR.; 36 KDA PROTEIN.	O75208; Q7L5V7; Q7Z5T6; Q8NBL4; Q9NTJ2; Q9P056	; COQ9_HUMAN
517	IPI00470674	CYB5R1	305	305	305	3.4E+04	3.4E+04	3.4E+04	41.6	12	1	1	1	1	NAD(P)H:QUINONE OXIDOREDUCTASE TYPE 3, POLYPEPTIDE A2.	A0PK21; O95329; Q53F73; Q8NCL5; Q9UHJ1; Q9UHQ9	A0PK21_HUMAN; O95329_HUMAN; Q53F73_HUMAN; Q8NCL5_HUMAN; Q9UHJ1_HUMAN; Q9UHQ9_HUMAN
518	IPI00470829	IMMT	726	726	726	8.0E+04	8.0E+04	8.0E+04	33.5	21	1	0	1	0	ISOFORM 3 OF MITOCHONDRIAL INNER MEMBRANE PROTEIN.	Q14539; Q15092; Q16891; Q68D41; Q69HW5; Q6IBL0; Q7Z3X1; Q8TAJ5; Q9P0V2	IMMT_HUMAN
519	IPI00472102; IPI00784154	HSPD1	573	575	574	6.1E+04	6.1E+04	6.1E+04	57.4	25	1	1	1	1	61 KDA PROTEIN.; 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL PRECURSOR.	P10809; Q38L19; Q53QD5	; CH60_HUMAN; Q53QD5_HUMAN
520	IPI00472442	PSMA1	269	269	269	3.0E+04	3.0E+04	3.0E+04	21.6	5	0	0	1	0	ISOFORM LONG OF PROTEASOME SUBUNIT ALPHA TYPE 1.	P25786; Q53YE8; Q9BRV9	PSA1_HUMAN; Q53YE8_HUMAN
521	IPI00473011	HBB; HBD	147	147	147	1.6E+04	1.6E+04	1.6E+04	75.5	13	1	1	1	1	HEMOGLOBIN SUBUNIT DELTA.	A0N071; P02042; Q3Y5H3; Q8WXT7	A0N071_HUMAN; HBD_HUMAN
522	IPI00477090; IPI00479708; IPI00549291; IPI00828205; IPI00829729; IPI00829768; IPI00829843; IPI00829854; IPI00829911	IGHM	595	625	605	6.5E+04	6.9E+04	6.6E+04	15.4	7	1	1	1	1	IGHM PROTEIN.; IGHM PROTEIN.; IGHM PROTEIN.; IGHM PROTEIN.; IGHM PROTEIN.; IGHM PROTEIN.; IGHM PROTEIN.; IGHM PROTEIN.; IGHM PROTEIN.	A2J1N3; Q5FWG0; Q6GMX5; Q6GMY2; Q86TT1; Q8WUK1; Q8WUX4; Q96AA6; Q96BB9; Q96EY0; Q9BQB8; Q9BU10	A2J1N3_HUMAN; Q5FWG0_HUMAN; Q6GMX5_HUMAN; Q6GMY2_HUMAN; Q86TT1_HUMAN; Q8WUK1_HUMAN; Q8WUX4_HUMAN; Q96AA6_HUMAN; Q96BB9_HUMAN; Q96EY0_HUMAN; Q9BQB8_HUMAN; Q9BU10_HUMAN
523	IPI00477131	SYPL2	272	272	272	3.0E+04	3.0E+04	3.0E+04	21.7	3	0	0	1	0	ISOFORM 1 OF SYNAPTOPHYSIN-LIKE PROTEIN 2.	Q5VXT5; Q6ZMX1	SYPL2_HUMAN
524	IPI00375704; IPI00479306	PSMB5	263	266	265	2.8E+04	2.9E+04	2.9E+04	15.8	4	0	0	1	1	HYPOTHETICAL PROTEIN DKFZP686I0180 (FRAGMENT).; PROTEASOME BETA 5 SUBUNIT.	Q7Z3B5; Q9TNN9	Q7Z3B5_HUMAN; Q9TNN9_HUMAN
525	IPI00479877	ALDH9A1	518	518	518	5.6E+04	5.6E+04	5.6E+04	15.6	7	1	1	1	1	ALDEHYDE DEHYDROGENASE 9A1.	Q6NSM2	Q6NSM2_HUMAN
526	IPI00479905	NDUFB10	172	172	172	2.1E+04	2.1E+04	2.1E+04	30.8	4	0	0	1	1	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 10.	O96000	NDUBA_HUMAN
527	IPI00513979	SEPW1	89	89	89	9.6E+03	9.6E+03	9.6E+03	11.2	3	0	0	1	1	SELENOPROTEIN W.		
528	IPI00549467	NIT2	276	276	276	3.1E+04	3.1E+04	3.1E+04	13.8	3	0	0	1	0	NITRILASE FAMILY MEMBER 2.	Q8WUF0; Q9NQR4	Q8WUF0_HUMAN; Q9NQR4_HUMAN
529	IPI00003925; IPI00549885; IPI00798351	PDHB	317	359	339	3.5E+04	3.9E+04	3.7E+04	31.8	10	1	1	1	1	ISOFORM 1 OF PYRUVATE DEHYDROGENASE E1 COMPONENT SUBUNIT BETA,MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF PYRUVATE DEHYDROGENASE E1 COMPONENT SUBUNIT BETA,MITOCHONDRIAL PRECURSOR.; 35 KDA PROTEIN.	P11177; Q6FH45; Q9BQ27; Q9UFK3	; ODPB_HUMAN
530	IPI00550069; IPI00783491	RNH1	461	461	461	5.0E+04	5.0E+04	5.0E+04	9.8	4	1	1	1	1	RIBONUCLEASE INHIBITOR.; RIBONUCLEASE/ANGIOGENIN INHIBITOR.	P13489; Q59GB3; Q8IZK8; Q96FD7; Q9BQ80	Q59GB3_HUMAN; Q8IZK8_HUMAN; Q96FD7_HUMAN; Q9BQ80_HUMAN; RINI_HUMAN
531	IPI00550165	DHRS7B	325	325	325	3.5E+04	3.5E+04	3.5E+04	8.3	2	0	0	1	0	DEHYDROGENASE/REDUCTASE (SDR FAMILY) MEMBER 7B.	Q6IAN0; Q6UX59; Q9BTF9; Q9UFM6	Q6IAN0_HUMAN; Q6UX59_HUMAN; Q9BTF9_HUMAN; Q9UFM6_HUMAN
532	IPI00550239	H1F0	194	194	194	2.1E+04	2.1E+04	2.1E+04	10.8	2	0	0	1	0	HISTONE H1.0.	P07305; Q6FG88; Q8N6R3	H10_HUMAN
533	IPI00551024	DAK	575	575	575	5.9E+04	5.9E+04	5.9E+04	5.7	2	0	0	1	0	DIHYDROXYACETONE KINASE.	Q2L9C1; Q3LXA3; Q53EQ9; Q9BVA7; Q9H895; Q9UFX5	DAK_HUMAN; Q2L9C1_HUMAN; Q9UFX5_HUMAN
534	IPI00553177	SERPINA1	418	418	418	4.7E+04	4.7E+04	4.7E+04	51.7	18	1	1	1	1	ALPHA-1-ANTITRYPSIN PRECURSOR.	P01009; Q0PVP5; Q13672; Q53XB8; Q5U0M1; Q96BF9; Q96ES1; Q9P1P0	A1AT_HUMAN; Q0PVP5_HUMAN; Q53XB8_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
535	IPI00554521	FTH1	183	183	183	2.1E+04	2.1E+04	2.1E+04	33.3	5	0	0	1	1	FERRITIN HEAVY CHAIN.	P02794; Q3KRA8; Q3SWW1; Q6NS36; Q6NZ44	FRIH_HUMAN; Q6NS36_HUMAN; Q6NZ44_HUMAN
536	IPI00554701	UCRC	63	63	63	7.3E+03	7.3E+03	7.3E+03	38.1	2	0	0	1	1	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.2 KDA PROTEIN.	Q9T2V6; Q9UDW1	UCR10_HUMAN
537	IPI00444262; IPI00604620; IPI00827674	NCL	603	710	667	6.6E+04	7.7E+04	7.2E+04	9.8	4	1	1	1	0	CDNA FLJ45706 FIS, CLONE FEBRA2028457, HIGHLY SIMILAR TO NUCLEOLIN.; ISOFORM 1 OF NUCLEOLIN.; ISOFORM 2 OF NUCLEOLIN.	P19338; Q53SK1; Q6ZS99; Q8NB06	NUCL_HUMAN; Q6ZS99_HUMAN
538	IPI00604664	NDUFS1	727	727	727	7.9E+04	7.9E+04	7.9E+04	36.2	21	1	1	1	1	NADH-UBIQUINONE OXIDOREDUCTASE 75 KDA SUBUNIT, MITOCHONDRIALPRECURSOR.	P28331; Q53TR8; Q8N1C4; Q8TCC9	NDUS1_HUMAN
539	IPI00641582	BAG3	575	575	575	6.2E+04	6.2E+04	6.2E+04	4.7	2	1	1	1	0	BAG FAMILY MOLECULAR CHAPERONE REGULATOR 3.	O95817; Q3B763; Q53GY1; Q9NT20; Q9P120	BAG3_HUMAN; Q53GY1_HUMAN
540	IPI00023048; IPI00642971	EEF1D	281	647	464	3.1E+04	7.1E+04	5.1E+04	22.1	4	1	1	1	1	ELONGATION FACTOR 1-DELTA.; EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 DELTA ISOFORM 1.	P29692; Q71RH4; Q969J1; Q96I38; Q9BW34; Q9H7G6	EF1D_HUMAN; Q71RH4_HUMAN; Q96I38_HUMAN; Q9BW34_HUMAN; Q9H7G6_HUMAN
541	IPI00644697	HEBP2	214	214	214	2.4E+04	2.4E+04	2.4E+04	9.4	2	0	0	1	0	HEBP2 PROTEIN (FRAGMENT).	Q05DB4	Q05DB4_HUMAN
542	IPI00645016	S100A1	94	94	94	1.1E+04	1.1E+04	1.1E+04	38.3	2	0	0	1	1	PROTEIN S100-A1.	P23297; Q5T7Y3	S10A1_HUMAN
543	IPI00645078	UBE1	1058	1058	1058	1.2E+05	1.2E+05	1.2E+05	24.1	16	1	1	1	1	UBIQUITIN-ACTIVATING ENZYME E1.	P22314; Q5JRR8; Q96E13	Q5JRR8_HUMAN; UBE1_HUMAN
544	IPI00645194	ITGB1	798	798	798	8.8E+04	8.8E+04	8.8E+04	3.3	2	1	0	1	0	INTEGRIN BETA 1 ISOFORM 1A PRECURSOR.	Q8WUM6	Q8WUM6_HUMAN
545	IPI00645836	ESD	230	230	230	2.5E+04	2.5E+04	2.5E+04	18.7	3	0	0	1	0	PROTEIN.		
546	IPI00654755	HBB	147	147	147	1.6E+04	1.6E+04	1.6E+04	96.6	21	1	1	1	1	HEMOGLOBIN SUBUNIT BETA.	P02023; P68871; Q13852; Q14477; Q14481; Q14510; Q3LR79; Q3Y9I8; Q45KT0; Q4F786; Q4JLR8; Q4TWB7; Q4TZM4; Q52MT0; Q549N7; Q6FI08; Q6J1Z7; Q6J1Z8; Q6R7N2; Q6VFQ5; Q6VFQ6; Q8IUL9; Q8IZI0; Q8IZI1; Q9BX96; Q9GZL9; Q9UCP8; Q9UCP9; Q9UE58; Q9UK54	HBB_HUMAN; Q14477_HUMAN; Q3LR79_HUMAN; Q3Y9I8_HUMAN; Q4F786_HUMAN; Q4JLR8_HUMAN; Q4TWB7_HUMAN; Q4TZM4_HUMAN; Q52MT0_HUMAN; Q549N7_HUMAN; Q6J1Z7_HUMAN; Q6J1Z8_HUMAN; Q6R7N2_HUMAN; Q6VFQ5_HUMAN; Q6VFQ6_HUMAN; Q8IUL9_HUMAN; Q8IZI0_HUMAN; Q9GZL9_HUMAN; Q9UE58_HUMAN; Q9UK54_HUMAN
547	IPI00719622; IPI00787692	LOC645899;	69	69	69	7.8E+03	7.8E+03	7.8E+03	30.4	2	0	0	1	0	40S RIBOSOMAL PROTEIN S28.; 8 KDA PROTEIN.	P25112; P62857	; RS28_HUMAN
548	IPI00741097	GSTT1	240	240	240	2.7E+04	2.7E+04	2.7E+04	20.8	4	0	0	1	0	GLUTATHIONE S-TRANSFERASE THETA-1.	O00226; P30711; Q5TZY2; Q969K8; Q96IY3	GSTT1_HUMAN; Q5TZY2_HUMAN
549	IPI00031583; IPI00743314	VDP	962	973	968	1.1E+05	1.1E+05	1.1E+05	12.3	9	1	1	1	1	HYPOTHETICAL PROTEIN DKFZP451D234.; GENERAL VESICULAR TRANSPORT FACTOR P115.	O60763; Q6PK63; Q86TB8; Q8N592	Q86TB8_HUMAN; VDP_HUMAN
550	IPI00745335	GPX4	234	234	234	2.7E+04	2.7E+04	2.7E+04	15.8	3	0	0	1	0	GLUTATHIONE PEROXIDASE 4 ISOFORM C PRECURSOR.	Q6PJX4	Q6PJX4_HUMAN
551	IPI00745729	SELENBP1	478	478	478	5.3E+04	5.3E+04	5.3E+04	35.6	15	1	1	1	1	SELENIUM BINDING PROTEIN 1.	Q49AQ8; Q96GX7	Q49AQ8_HUMAN; Q96GX7_HUMAN
552	IPI00745872	ALB	609	609	609	6.9E+04	6.9E+04	6.9E+04	38.1	31	1	1	1	1	ISOFORM 1 OF SERUM ALBUMIN PRECURSOR.	O95574; P02768; P04277; Q13140; Q645G4; Q68DN5; Q6UXK4; Q86YG0; Q9P157; Q9P1I7; Q9UHS3; Q9UJZ0	ALBU_HUMAN; Q645G4_HUMAN
553	IPI00746165	WDR1	606	606	606	6.6E+04	6.6E+04	6.6E+04	21.6	7	1	1	1	1	ISOFORM 1 OF WD REPEAT PROTEIN 1.	O75083; O75313; Q53GN4; Q53H17; Q59ER5; Q8N6E5; Q9UG05; Q9UG78; Q9UQE0	Q53GN4_HUMAN; Q53H17_HUMAN; Q59ER5_HUMAN; WDR1_HUMAN
554	IPI00747355	PREP	710	710	710	8.1E+04	8.1E+04	8.1E+04	33.1	17	1	1	1	1	PROLYL ENDOPEPTIDASE.	Q8N6D4; Q9UM02	Q8N6D4_HUMAN; Q9UM02_HUMAN
555	IPI00759493	SUCLG1	346	346	346	3.6E+04	3.6E+04	3.6E+04	22.8	6	0	0	1	1	SUCCINATE-COA LIGASE, GDP-FORMING, ALPHA SUBUNIT.	Q6IAL5	Q6IAL5_HUMAN
556	IPI00759542; IPI00759754	TTN	34350	34474	34412	3.8E+06	3.8E+06	3.8E+06	0.1	3	0	0	1	1	ISOFORM 8 OF TITIN.; ISOFORM 1 OF TITIN.	Q10465; Q10466; Q15598; Q2XUS3; Q32Q60; Q4U1Z6; Q6NSG0; Q6PDB1; Q6PJP0; Q7KYM2; Q7KYN4; Q7KYN5; Q7LDM3; Q7Z2X3; Q8TCG8; Q8WZ42; Q8WZ51; Q8WZ52; Q8WZ53; Q8WZB3; Q92761; Q92762; Q9UD97; Q9UP84; Q9Y6L9	TITIN_HUMAN
557	IPI00783128	FLNC	2705	2705	2705	2.9E+05	2.9E+05	2.9E+05	33.8	71	1	1	1	1	GAMMA FILAMIN VARIANT.	Q59H94	Q59H94_HUMAN
558	IPI00024913; IPI00218482; IPI00784162; IPI00784277; IPI00793677; IPI00794316; IPI00795385	C21orf33	217	268	244	2.3E+04	2.8E+04	2.6E+04	19.8	3	1	0	1	1	ISOFORM LONG OF ES1 PROTEIN HOMOLOG, MITOCHONDRIAL PRECURSOR.; ISOFORM SHORT OF ES1 PROTEIN HOMOLOG, MITOCHONDRIAL PRECURSOR.; 25 KDA PROTEIN.; 28 KDA PROTEIN.; PROTEIN.; 24 KDA PROTEIN.; 23 KDA PROTEIN.	O00650; O00660; O15011; O15012; P30042; P55346; P78474; Q92505; Q92507	; ES1_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
559	IPI00216704; IPI00237806; IPI00783228; IPI00784382	SPTB	2106	2328	2225	2.4E+05	2.7E+05	2.6E+05	4.8	10	1	1	1	1	ISOFORM 2 OF SPECTRIN BETA CHAIN, ERYTHROCYTE.; ISOFORM 3 OF SPECTRIN BETA CHAIN, ERYTHROCYTE.; ISOFORM 1 OF SPECTRIN BETA CHAIN, ERYTHROCYTE.; SPECTRIN BETA ISOFORM A.	O14724; O14725; O14726; P11277; Q15510; Q15519; Q59FP5; Q71VG0; Q71VG1; Q71VG2	O14724_HUMAN; O14725_HUMAN; O14726_HUMAN; Q59FP5_HUMAN; Q71VG0_HUMAN; Q71VG1_HUMAN; Q71VG2_HUMAN; SPTB1_HUMAN
560	IPI00787298	KIAA1881	1423	1423	1423	1.4E+05	1.4E+05	1.4E+05	14.2	14	0	1	1	1	SIMILAR TO PLASMA MEMBRANE ASSOCIATED PROTEIN, S3-12.	Q96Q06	Q96Q06_HUMAN
561	IPI00787362	LOC730839	1885	1885	1885	1.9E+05	1.9E+05	1.9E+05	3.5	3	0	0	1	0	SIMILAR TO HORNERIN.		
562	IPI00789324	JUP	745	745	745	8.2E+04	8.2E+04	8.2E+04	8.2	5	0	0	1	0	JUP PROTEIN.	Q7L3S5	Q7L3S5_HUMAN
563	IPI00792715	ENO2	341	341	341	3.7E+04	3.7E+04	3.7E+04	7.3	4	0	0	1	0	37 KDA PROTEIN.		
564	IPI00793379		1463	1463	1463	1.6E+05	1.6E+05	1.6E+05	28.8	38	1	1	1	1	165 KDA PROTEIN.		
565	IPI00020599; IPI00793605	CALR	322	417	370	3.7E+04	4.8E+04	4.2E+04	9.3	2	1	1	1	0	CALRETICULIN PRECURSOR.; 37 KDA PROTEIN.	P27797; Q3B830; Q53G71; Q6IAT4	; CALR_HUMAN; Q3B830_HUMAN; Q53G71_HUMAN; Q6IAT4_HUMAN
566	IPI00794080		1968	1968	1968	2.3E+05	2.3E+05	2.3E+05	22.9	77	0	1	1	1	227 KDA PROTEIN.		
567	IPI00794464	CMYA1	1843	1843	1843	2.0E+05	2.0E+05	2.0E+05	7.3	9	1	1	1	1	CARDIOMYOPATHY-ASSOCIATED PROTEIN 1.	Q68DF2; Q702N8; Q702N9; Q8TCG7	Q68DF2_HUMAN; Q702N8_HUMAN; Q702N9_HUMAN; Q8TCG7_HUMAN
568	IPI00794849	SLMAP	409	409	409	4.7E+04	4.7E+04	4.7E+04	5.6	2	0	0	1	0	PROTEIN.		
569	IPI00797126	NACA	925	925	925	9.5E+04	9.5E+04	9.5E+04	9.1	6	0	0	1	1	SIMILAR TO NASCENT POLYPEPTIDE ASSOCIATED COMPLEX ALPHA SUBUNIT.		
570	IPI00798211	TBCB	214	214	214	2.4E+04	2.4E+04	2.4E+04	10.3	2	0	0	1	0	24 KDA PROTEIN.		
571	IPI00815770	SNX3	162	162	162	1.9E+04	1.9E+04	1.9E+04	10.5	2	0	0	1	0	ISOFORM 1 OF SORTING NEXIN-3.	O60493; O60718; Q4TT31; Q5JXJ7; Q5JXJ8; Q96AP9; Q9C0J5; Q9NU45	Q4TT31_HUMAN; SNX3_HUMAN
572	IPI00000335	HINT2	163	163	163	1.7E+04	1.7E+04	1.7E+04	31.3	3	1	0	0	1	HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN 2.	Q53HJ8; Q5TCW3; Q8WYJ5; Q9BX68	HINT2_HUMAN; Q53HJ8_HUMAN; Q5TCW3_HUMAN; Q8WYJ5_HUMAN
573	IPI00000935	PLN	52	52	52	6.1E+03	6.1E+03	6.1E+03	23.1	3	0	0	0	1	CARDIAC PHOSPHOLAMBAN.	P26678; Q5R352	PPLA_HUMAN; Q5R352_HUMAN
574	IPI00001580	FYCO1	1478	1478	1478	1.7E+05	1.7E+05	1.7E+05	1.8	2	0	0	0	1	ISOFORM 1 OF FYVE AND COILED-COIL DOMAIN-CONTAINING PROTEIN 1.	Q3MJE6; Q86T41; Q86TB1; Q8TEF9; Q96IV5; Q9BQS8; Q9H8P9	FYCO1_HUMAN
575	IPI00001952	ENDOD1	500	500	500	5.5E+04	5.5E+04	5.5E+04	9.0	3	1	1	0	1	ENDONUCLEASE DOMAIN-CONTAINING 1 PROTEIN PRECURSOR.	O94919; Q8TAQ8	ENDD1_HUMAN
576	IPI00003091	PPP1R3A	1122	1122	1122	1.3E+05	1.3E+05	1.3E+05	2.4	2	0	0	0	1	ISOFORM 1 OF PROTEIN PHOSPHATASE 1 REGULATORY SUBUNIT 3A.	A0AVQ2; O43476; Q16821; Q75LN8; Q7KYM8; Q86UI6	PPR3A_HUMAN
577	IPI00003348; IPI00012451; IPI00026268; IPI00639998; IPI00640462; IPI00640949	GNB1; GNB2; GNE	108	340	235	1.2E+04	3.8E+04	2.6E+04	6.2	2	0	0	0	1	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) SUBUNIT BETA 2.; GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA 4.; GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) SUBUNIT BETA 1.; GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), BETA POLYPEPTIDE 1.; GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), BETA POLYPEPTIDE 1.; GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), BETA POLYPEPTIDE 1.	P04697; P04901; P11016; P54312; P62873; P62879; Q1RMY8; Q4VXS9; Q4VXT0; Q4VXT1; Q5QPR5; Q6FHM2; Q71UM6; Q9HAV0	GBB1_HUMAN; GBB2_HUMAN; GBB4_HUMAN; Q1RMY8_HUMAN; Q4VXS9_HUMAN; Q4VXT0_HUMAN; Q4VXT1_HUMAN; Q5QPR5_HUMAN; Q6FHM2_HUMAN; Q71UM6_HUMAN
578	IPI00003420	MAPRE2	327	327	327	3.7E+04	3.7E+04	3.7E+04	11.3	2	0	0	0	1	ISOFORM 1 OF MICROTUBULE-ASSOCIATED PROTEIN RP/EB FAMILY MEMBER 2.	Q15555; Q9UQ33	MARE2_HUMAN
579	IPI00003921; IPI00218697; IPI00218698; IPI00218699; IPI00218700; IPI00218701; IPI00739613; IPI00791144	EPB41	566	864	695	6.3E+04	9.7E+04	7.8E+04	4.9	2	1	0	0	1	ISOFORM 1 OF PROTEIN 4.1.; ISOFORM 2 OF PROTEIN 4.1.; ISOFORM 3 OF PROTEIN 4.1.; ISOFORM 4 OF PROTEIN 4.1.; ISOFORM 5 OF PROTEIN 4.1.; ISOFORM 6 OF PROTEIN 4.1.; EPB41 PROTEIN (FRAGMENT).; HYPOTHETICAL PROTEIN (FRAGMENT).	P11171; P11176; Q14245; Q1WWM3; Q29RX4; Q4VB86; Q4VB87; Q59F12; Q5TB33; Q5TB35; Q5TB36; Q5VXN8; Q8IXV9; Q9Y578; Q9Y579	41_HUMAN; Q1WWM3_HUMAN; Q29RX4_HUMAN; Q4VB86_HUMAN; Q4VB87_HUMAN; Q59F12_HUMAN; Q5TB33_HUMAN; Q5TB36_HUMAN
580	IPI00004457	AOC3	763	763	763	8.5E+04	8.5E+04	8.5E+04	5.1	3	0	0	0	1	MEMBRANE COPPER AMINE OXIDASE.	Q16853; Q45F94; Q9UEU7	AOC3_HUMAN; Q9UEU7_HUMAN
581	IPI00005202	PGRMC2	247	247	247	2.6E+04	2.6E+04	2.6E+04	11.3	2	0	0	0	1	MEMBRANE-ASSOCIATED PROGESTERONE RECEPTOR COMPONENT 2.		
582	IPI00005537	MRPL12	198	198	198	2.1E+04	2.1E+04	2.1E+04	11.6	2	0	0	0	1	39S RIBOSOMAL PROTEIN L12, MITOCHONDRIAL PRECURSOR.	P52815; Q969U0; Q96Q74; Q9HCA2; Q9UQJ3	Q96Q74_HUMAN; RM12_HUMAN
583	IPI00005614	SPTBN1	2364	2364	2364	2.7E+05	2.7E+05	2.7E+05	1.4	2	0	0	0	1	ISOFORM LONG OF SPECTRIN BETA CHAIN, BRAIN 1.	O60837; Q01082; Q16057; Q53R99	Q53R99_HUMAN; SPTB2_HUMAN
584	IPI00005755	TCAP	167	167	167	1.9E+04	1.9E+04	1.9E+04	13.2	2	0	0	0	1	TELETHONIN.	A2TDC0; O15273; Q96L27	A2TDC0_HUMAN; TELT_HUMAN
585	IPI00005966	NDUFA12	146	146	146	1.7E+04	1.7E+04	1.7E+04	19.9	2	1	0	0	1	13KDA DIFFERENTIATION-ASSOCIATED PROTEIN VARIANT (FRAGMENT).	Q53HG1; Q53XX0	Q53HG1_HUMAN; Q53XX0_HUMAN
586	IPI00006252; IPI00793201	SCYE1	312	336	324	3.4E+04	3.7E+04	3.6E+04	12.2	2	0	0	0	1	MULTISYNTHETASE COMPLEX AUXILIARY COMPONENT P43.; 37 KDA PROTEIN.	Q12904; Q6FG28; Q96CQ9	; MCA1_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
587	IPI00006721; IPI00107749; IPI00107750; IPI00107751; IPI00107752; IPI00107753; IPI00375149; IPI00375150; IPI00789199; IPI00797488	OPA1	942	1015	979	1.1E+05	1.2E+05	1.1E+05	9.4	6	1	1	0	1	ISOFORM 1 OF DYNAMIN-LIKE 120 KDA PROTEIN, MITOCHONDRIAL PRECURSOR.; ISOFORM 5 OF DYNAMIN-LIKE 120 KDA PROTEIN, MITOCHONDRIAL PRECURSOR.; OPTIC ATROPHY 1 ISOFORM 5.; OPTIC ATROPHY 1 ISOFORM 6.; ISOFORM 2 OF DYNAMIN-LIKE 120 KDA PROTEIN, MITOCHONDRIAL PRECURSOR.; OPTIC ATROPHY 1 ISOFORM 8.; ISOFORM 8 OF DYNAMIN-LIKE 120 KDA PROTEIN, MITOCHONDRIAL PRECURSOR.; OPTIC ATROPHY 1 ISOFORM 3.; ISOFORM 7 OF DYNAMIN-LIKE 120 KDA PROTEIN, MITOCHONDRIAL PRECURSOR.; ISOFORM 3 OF DYNAMIN-LIKE 120 KDA PROTEIN, MITOCHONDRIAL PRECURSOR.	O60313; Q6PEK6	; OPA1_HUMAN; Q6PEK6_HUMAN
588	IPI00006865	SEC22B	215	215	215	2.5E+04	2.5E+04	2.5E+04	12.1	2	0	0	0	1	VESICLE-TRAFFICKING PROTEIN SEC22B.	O75396	SC22B_HUMAN
589	IPI00007755	RAB21	225	225	225	2.4E+04	2.4E+04	2.4E+04	10.2	2	0	0	0	1	RAS-RELATED PROTEIN RAB-21.	Q14466; Q569H3; Q96GX3; Q9UL25	Q96GX3_HUMAN; RAB21_HUMAN
590	IPI00008438; IPI00478810	RPS10	165	172	169	1.9E+04	2.0E+04	1.9E+04	14.6	2	0	0	0	1	40S RIBOSOMAL PROTEIN S10.; RIBOSOMAL PROTEIN S10.	P46783; Q5TZB9; Q5TZC0	Q5TZB9_HUMAN; Q5TZC0_HUMAN; RS10_HUMAN
591	IPI00009480; IPI00377080	COPS8	160	209	185	1.8E+04	2.3E+04	2.1E+04	19.1	2	0	0	0	1	COP9 SIGNALOSOME COMPLEX SUBUNIT 8.; COP9 SIGNALOSOME SUBUNIT 8 ISOFORM 2.	Q53QS9; Q99627	; CSN8_HUMAN; Q53QS9_HUMAN
592	IPI00009747; IPI00792647	LSS	262	732	497	3.0E+04	8.3E+04	5.6E+04	10.7	2	1	1	0	1	LANOSTEROL SYNTHASE.; 30 KDA PROTEIN.	P48449; Q8IYL6; Q9UEZ1	; ERG7_HUMAN
593	IPI00009960; IPI00554469	IMMT	747	758	753	8.3E+04	8.4E+04	8.3E+04	33.6	19	0	1	0	1	ISOFORM 1 OF MITOCHONDRIAL INNER MEMBRANE PROTEIN.; ISOFORM 2 OF MITOCHONDRIAL INNER MEMBRANE PROTEIN.	Q05DN3; Q14539; Q15092; Q16891; Q68D41; Q69HW5; Q6IBL0; Q7Z3X1; Q8TAJ5; Q9P0V2	IMMT_HUMAN; Q05DN3_HUMAN
594	IPI00010154	GDI1	447	447	447	5.1E+04	5.1E+04	5.1E+04	23.5	7	1	1	0	1	RAB GDP DISSOCIATION INHIBITOR ALPHA.	P31150; P50394; Q6FG50; Q7Z2G6; Q7Z2G9; Q7Z2H5; Q7Z2I6	GDIA_HUMAN; Q6FG50_HUMAN
595	IPI00010402	SH3BGRL3	226	226	226	2.4E+04	2.4E+04	2.4E+04	8.4	2	0	0	0	1	HYPOTHETICAL PROTEIN.	Q86Z22	Q86Z22_HUMAN
596	IPI00010740	SFPQ	707	707	707	7.6E+04	7.6E+04	7.6E+04	3.7	2	0	0	0	1	ISOFORM LONG OF SPLICING FACTOR, PROLINE- AND GLUTAMINE-RICH.	P23246; P30808; Q5SZ71; Q6PIX2; Q86VG2; Q9BSV4	Q5SZ71_HUMAN; Q6PIX2_HUMAN; Q86VG2_HUMAN; Q9BSV4_HUMAN; SFPQ_HUMAN
597	IPI00010845	NDUFS8	210	210	210	2.4E+04	2.4E+04	2.4E+04	15.2	3	0	0	0	1	NADH DEHYDROGENASE [UBIQUINONE] IRON-SULFUR PROTEIN 8, MITOCHONDRIALPRECURSOR.	O00217; Q08E91; Q0VDA8; Q53G17	NDUS8_HUMAN; Q08E91_HUMAN; Q53G17_HUMAN
598	IPI00011217	NDUFS4	175	175	175	2.0E+04	2.0E+04	2.0E+04	14.9	2	0	0	0	1	NADH DEHYDROGENASE [UBIQUINONE] IRON-SULFUR PROTEIN 4, MITOCHONDRIALPRECURSOR.	O43181; Q9BS69	NDUS4_HUMAN
599	IPI00011253	RPS3	243	243	243	2.7E+04	2.7E+04	2.7E+04	16.1	3	0	0	0	1	40S RIBOSOMAL PROTEIN S3.	P23396; Q498B5; Q53G83; Q6IPX9; Q8NI95; Q9NQS8	Q53G83_HUMAN; Q6IPX9_HUMAN; Q9NQS8_HUMAN; RS3_HUMAN
600	IPI00011603	PSMD3	534	534	534	6.1E+04	6.1E+04	6.1E+04	26.6	9	1	1	0	1	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 3.	O43242; Q6IBN0; Q8N9M2; Q96EI2; Q96N86; Q9BQA4	PSMD3_HUMAN; Q6IBN0_HUMAN; Q8N9M2_HUMAN; Q96N86_HUMAN
601	IPI00011654; IPI00645452	TUBB	426	444	435	4.8E+04	5.0E+04	4.9E+04	51.1	19	1	1	0	1	TUBULIN BETA CHAIN.; TUBULIN, BETA POLYPEPTIDE.	P05218; P07437; Q5JP53; Q5SU16; Q6LC01; Q8WUC1; Q9CY33	Q5JP53_HUMAN; Q5SU16_HUMAN; Q6LC01_HUMAN; TBB5_HUMAN
602	IPI00012119; IPI00794413; IPI00795042	DCN	179	359	252	2.0E+04	4.0E+04	2.8E+04	20.7	4	1	1	0	1	ISOFORM A OF DECORIN PRECURSOR.; 20 KDA PROTEIN.; 24 KDA PROTEIN.	P07585; Q6FH10; Q9P0Z0; Q9P0Z1; Q9Y5N8; Q9Y5N9	; PGS2_HUMAN; Q6FH10_HUMAN
603	IPI00012272	MYBPH	477	477	477	5.2E+04	5.2E+04	5.2E+04	21.6	7	1	1	0	1	MYOSIN-BINDING PROTEIN H.	Q13203; Q16886; Q86YC5	MYBPH_HUMAN
604	IPI00012493; IPI00794659	RPS20	119	142	131	1.3E+04	1.6E+04	1.5E+04	10.6	2	0	0	0	1	40S RIBOSOMAL PROTEIN S20.; 16 KDA PROTEIN.	P17075; P60866; Q5M8S9	; RS20_HUMAN
605	IPI00013297	PDAP1	181	181	181	2.1E+04	2.1E+04	2.1E+04	13.3	2	0	0	0	1	28 KDA HEAT- AND ACID-STABLE PHOSPHOPROTEIN.	Q13442; Q92906	HAP28_HUMAN
606	IPI00013452	EPRS	1512	1512	1512	1.7E+05	1.7E+05	1.7E+05	1.7	2	0	0	0	1	GLUTAMYL-PROLYL TRNA SYNTHETASE.	A0AVA9; Q05BP6; Q05DF8; Q3KQZ8; Q5DSM1; Q5H9S5; Q6PD57; Q86X73	A0AVA9_HUMAN; Q05BP6_HUMAN; Q05DF8_HUMAN; Q3KQZ8_HUMAN; Q5DSM1_HUMAN; Q5H9S5_HUMAN; Q6PD57_HUMAN; Q86X73_HUMAN
607	IPI00013455; IPI00027172; IPI00217113	CLIP1	1392	1438	1419	1.6E+05	1.6E+05	1.6E+05	3.5	4	0	0	0	1	CLIP1 PROTEIN.; ISOFORM LONG OF CAP-GLY DOMAIN-CONTAINING LINKER PROTEIN 1.; ISOFORM SHORT OF CAP-GLY DOMAIN-CONTAINING LINKER PROTEIN 1.	A0AVD3; O43667; P30622; Q17RS4; Q29RG0; Q6P5Z9; Q6Q318	A0AVD3_HUMAN; CLIP1_HUMAN; O43667_HUMAN; Q17RS4_HUMAN; Q29RG0_HUMAN; Q6P5Z9_HUMAN; Q6Q318_HUMAN
608	IPI00013808	ACTN4	911	911	911	1.0E+05	1.0E+05	1.0E+05	9.6	6	0	0	0	1	ALPHA-ACTININ-4.	O43707; O76048; Q96BG6	ACTN4_HUMAN; Q96BG6_HUMAN
609	IPI00013917; IPI00456898	LOC440055; RPS12	132	132	132	1.5E+04	1.5E+04	1.5E+04	13.6	2	0	0	0	1	40S RIBOSOMAL PROTEIN S12.; SIMILAR TO RIBOSOMAL PROTEIN S12.	P25398; Q76M58	; Q76M58_HUMAN; RS12_HUMAN
610	IPI00014230; IPI00794855	C1QBP	225	282	254	2.5E+04	3.1E+04	2.8E+04	9.6	2	0	1	0	1	COMPLEMENT COMPONENT 1 Q SUBCOMPONENT-BINDING PROTEIN, MITOCHONDRIALPRECURSOR.; 25 KDA PROTEIN.	Q07021; Q2HXR8; Q9NNY8	; C1QBP_HUMAN
611	IPI00014310	CUL1	776	776	776	9.0E+04	9.0E+04	9.0E+04	11.9	5	1	1	0	1	CULLIN-1.	O60719; Q08AL6; Q13616; Q75MQ1; Q8IYW1	CUL1_HUMAN; Q75MQ1_HUMAN
612	IPI00014312; IPI00382458; IPI00382459	CUL3	702	768	738	8.1E+04	8.9E+04	8.5E+04	7.8	4	1	1	0	1	ISOFORM 1 OF CULLIN-3.; ISOFORM 2 OF CULLIN-3.; ISOFORM 3 OF CULLIN-3.	O75415; Q13618; Q53RD1; Q53S54; Q569L3; Q9UBI8; Q9UET7	CUL3_HUMAN; Q53RD1_HUMAN; Q53S54_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
613	IPI00017030; IPI00402167; IPI00477329; IPI00760846; IPI00760925; IPI00828082	MYO18A; TIAF1	2002	2057	2033	2.3E+05	2.3E+05	2.3E+05	1.6	2	0	0	0	1	234 KDA PROTEIN.; 232 KDA PROTEIN.; 227 KDA PROTEIN.; ISOFORM 1 OF MYOSIN-XVIIIA.; ISOFORM 3 OF MYOSIN-XVIIIA.; ISOFORM 4 OF MYOSIN-XVIIIA.	Q5H9U3; Q5QD01; Q5W9F9; Q5W9G1; Q8IXP8; Q92614; Q9NYE8	; MY18A_HUMAN; Q5QD01_HUMAN; Q9NYE8_HUMAN
614	IPI00017344	RAB5B	215	215	215	2.4E+04	2.4E+04	2.4E+04	14.0	2	0	0	0	1	RAS-RELATED PROTEIN RAB-5B.	P35239; P35277; P61020; Q6FI54; Q6PIK9; Q86TH0; Q8IXL2	Q6FI54_HUMAN; RAB5B_HUMAN
615	IPI00017601	CP	1065	1065	1065	1.2E+05	1.2E+05	1.2E+05	11.9	9	0	1	0	1	CERULOPLASMIN PRECURSOR.	P00450; Q14063; Q1L857; Q2PP18; Q6NSB2; Q9UKS4	CERU_HUMAN; Q1L857_HUMAN; Q6NSB2_HUMAN
616	IPI00017672	NP	293	293	293	3.3E+04	3.3E+04	3.3E+04	14.7	3	0	0	0	1	CDNA FLJ25678 FIS, CLONE TST04067, HIGHLY SIMILAR TO PURINE NUCLEOSIDEPHOSPHORYLASE.	Q8N7G1; Q9P1G4	Q8N7G1_HUMAN; Q9P1G4_HUMAN
617	IPI00018931	VPS35	796	796	796	9.2E+04	9.2E+04	9.2E+04	12.2	7	1	1	0	1	VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN 35.	Q53FR4; Q561W2; Q5HYM2; Q96QK1; Q9H016; Q9H096; Q9H4P3; Q9H8J0; Q9NRS7; Q9NVG2; Q9NX80; Q9NZK2	Q53FR4_HUMAN; Q5HYM2_HUMAN; VPS35_HUMAN
618	IPI00019345; IPI00640287	RAP1A	184	184	184	2.1E+04	2.1E+04	2.1E+04	14.1	2	0	0	0	1	RAS-RELATED PROTEIN RAP-1A PRECURSOR.; RAP1A, MEMBER OF RAS ONCOGENE FAMILY.	P10113; P62834; Q5QPH6; Q5U0C3	Q5QPH6_HUMAN; Q5U0C3_HUMAN; RAP1A_HUMAN
619	IPI00019580	PLG	810	810	810	9.1E+04	9.1E+04	9.1E+04	3.8	3	0	0	0	1	PLASMINOGEN PRECURSOR.	P00747; Q15146; Q5TEH4; Q68DS2; Q6PA00; Q9UMI2	PLMN_HUMAN; Q68DS2_HUMAN; Q9UMI2_HUMAN
620	IPI00019591; IPI00639937	CFB	764	764	764	8.6E+04	8.6E+04	8.6E+04	3.3	2	0	0	0	1	ISOFORM 1 OF COMPLEMENT FACTOR B PRECURSOR (FRAGMENT).; B-FACTOR, PROPERDIN.	O15006; P00751; Q29944; Q53F89; Q5JP67; Q5ST50; Q96HX6; Q9BTF5; Q9BX92	CFAB_HUMAN; Q53F89_HUMAN; Q5JP67_HUMAN
621	IPI00019906; IPI00218019; IPI00795150	BSG	269	432	362	2.9E+04	4.6E+04	3.9E+04	11.9	2	0	1	0	1	ISOFORM 2 OF BASIGIN PRECURSOR.; ISOFORM 1 OF BASIGIN PRECURSOR.; 46 KDA PROTEIN.	P35613; Q54A51; Q7Z796; Q8IZL7	; BASI_HUMAN; Q54A51_HUMAN
622	IPI00020416; IPI00640197	TPP2	1249	1262	1256	1.4E+05	1.4E+05	1.4E+05	3.0	3	0	1	0	1	TRIPEPTIDYL-PEPTIDASE 2.; TRIPEPTIDYL PEPTIDASE II.	P29144; Q5VZU8; Q5VZU9	Q5VZU8_HUMAN; Q5VZU9_HUMAN; TPP2_HUMAN
623	IPI00020898	RPS6KA3	740	740	740	8.4E+04	8.4E+04	8.4E+04	7.4	4	1	1	0	1	RIBOSOMAL PROTEIN S6 KINASE ALPHA-3.	P51812; Q4VAP3; Q59H26; Q5JPK8; Q7Z2J3; Q7Z2J4; Q7Z3Z7	KS6A3_HUMAN; Q7Z2J3_HUMAN; Q7Z2J4_HUMAN
624	IPI00020987	PRELP	382	382	382	4.4E+04	4.4E+04	4.4E+04	15.7	5	0	0	0	1	PROLARGIN PRECURSOR.	P51888; Q6FG38; Q6FHG6; Q7Z4B2	PRELP_HUMAN; Q6FG38_HUMAN; Q6FHG6_HUMAN; Q7Z4B2_HUMAN
625	IPI00021439; IPI00021440	ACTB; ACTG1	375	375	375	4.2E+04	4.2E+04	4.2E+04	53.1	26	1	1	0	1	ACTIN, CYTOPLASMIC 1.; ACTIN, CYTOPLASMIC 2.	A1E282; P02570; P02571; P14104; P60709; P63261; P70514; P99021; P99022; Q11211; Q1KLZ0; Q53G76; Q53G99; Q53GK6; Q562L3; Q562L5; Q562L6; Q562L9; Q562M3; Q562M5; Q562N0; Q562N2; Q562N8; Q562P0; Q562R8; Q562S0; Q562U1; Q562U2; Q562V5; Q562X2; Q562X9; Q562Y6; Q562Y8; Q562Z4; Q562Z6; Q562Z7; Q5U032; Q64316; Q75MN2; Q8WVW5; Q96B34; Q96E67; Q96HG5; Q9UE89; Q9UMN3	A1E282_HUMAN; ACTB_HUMAN; ACTG_HUMAN; Q1KLZ0_HUMAN; Q53G76_HUMAN; Q53G99_HUMAN; Q53GK6_HUMAN; Q562L3_HUMAN; Q562L5_HUMAN; Q562L6_HUMAN; Q562L9_HUMAN; Q562M3_HUMAN; Q562M5_HUMAN; Q562N0_HUMAN; Q562N2_HUMAN; Q562N8_HUMAN; Q562P0_HUMAN; Q562R8_HUMAN; Q562S0_HUMAN; Q562U1_HUMAN; Q562U2_HUMAN; Q562V5_HUMAN; Q562X2_HUMAN; Q562X9_HUMAN; Q562Y6_HUMAN; Q562Y8_HUMAN; Q562Z4_HUMAN; Q562Z6_HUMAN; Q562Z7_HUMAN; Q5U032_HUMAN; Q8WVW5_HUMAN; Q96HG5_HUMAN; Q9UE89_HUMAN; Q9UMN3_HUMAN
626	IPI00021842	APOE	317	317	317	3.6E+04	3.6E+04	3.6E+04	28.4	7	0	0	0	1	APOLIPOPROTEIN E PRECURSOR.	P02649; Q13791; Q6LA97; Q6LBZ1; Q8TCZ8; Q9P2S4	APOE_HUMAN; Q13791_HUMAN; Q6LA97_HUMAN; Q6LBZ1_HUMAN; Q8TCZ8_HUMAN
627	IPI00021854	APOA2	100	100	100	1.1E+04	1.1E+04	1.1E+04	21.0	2	0	0	0	1	APOLIPOPROTEIN A-II PRECURSOR.	P02652	APOA2_HUMAN
628	IPI00022391	APCS	223	223	223	2.5E+04	2.5E+04	2.5E+04	9.0	2	0	0	0	1	SERUM AMYLOID P-COMPONENT PRECURSOR.	P02743	SAMP_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
629	IPI00022418; IPI00339223; IPI00339225; IPI00339226; IPI00339227; IPI00339228; IPI00414283; IPI00470919; IPI00479723; IPI00642991	FN1	2176	2446	2298	2.4E+05	2.7E+05	2.5E+05	2.3	3	0	0	0	1	ISOFORM 1 OF FIBRONECTIN PRECURSOR.; ISOFORM 3 OF FIBRONECTIN PRECURSOR.; ISOFORM 5 OF FIBRONECTIN PRECURSOR.; ISOFORM 6 OF FIBRONECTIN PRECURSOR.; ISOFORM 7 OF FIBRONECTIN PRECURSOR.; ISOFORM 8 OF FIBRONECTIN PRECURSOR.; FIBRONECTIN 1 ISOFORM 4 PREPROPROTEIN.; FIBRONECTIN 1 ISOFORM 2 PREPROPROTEIN.; ISOFORM 10 OF FIBRONECTIN PRECURSOR.; FIBRONECTIN 1 ISOFORM 6 PREPROPROTEIN.	O95609; O95610; O95617; P02751; Q14312; Q14325; Q14326; Q17RV7; Q585T2; Q59EH1; Q59G22; Q60FE4; Q68CX6; Q68DP8; Q68DT4; Q6LDP6; Q6MZF4; Q6MZM7; Q6MZS0; Q6MZU5; Q6N025; Q6N084; Q6N0A6; Q7Z391; Q86T27; Q8IVI8; Q96KP7; Q96KP8; Q96KP9; Q9H1B8; Q9HAP3; Q9UMK2	; FINC_HUMAN; O95617_HUMAN; Q17RV7_HUMAN; Q585T2_HUMAN; Q59EH1_HUMAN; Q59G22_HUMAN; Q60FE4_HUMAN; Q68CX6_HUMAN; Q68DP8_HUMAN; Q68DT4_HUMAN; Q6MZF4_HUMAN; Q6MZM7_HUMAN; Q6MZS0_HUMAN; Q6MZU5_HUMAN; Q6N025_HUMAN; Q6N084_HUMAN; Q6N0A6_HUMAN; Q7Z391_HUMAN
630	IPI00022429	ORM1	201	201	201	2.4E+04	2.4E+04	2.4E+04	17.9	3	1	1	0	1	ALPHA-1-ACID GLYCOPROTEIN 1 PRECURSOR.	P02763; Q5T539; Q5U067; Q8TC16	A1AG1_HUMAN; Q5T539_HUMAN; Q5U067_HUMAN
631	IPI00022431	AHSG	367	367	367	3.9E+04	3.9E+04	3.9E+04	8.2	2	0	1	0	1	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR.	O14961; O14962; P02765; Q9P152	FETUA_HUMAN
632	IPI00022432	TTR	147	147	147	1.6E+04	1.6E+04	1.6E+04	25.2	3	1	0	0	1	TRANSTHYRETIN PRECURSOR.	P02766; Q53WY6; Q549C7; Q6IB96; Q8TDB1; Q8TDB2; Q9UBZ6; Q9UCM9	Q53WY6_HUMAN; Q549C7_HUMAN; Q8TDB1_HUMAN; Q8TDB2_HUMAN; TTHY_HUMAN
633	IPI00022488	HPX	462	462	462	5.2E+04	5.2E+04	5.2E+04	5.8	2	1	1	0	1	HEMOPEXIN PRECURSOR.	P02790; Q9BS19	HEMO_HUMAN; Q9BS19_HUMAN
634	IPI00022977	CKB	381	381	381	4.3E+04	4.3E+04	4.3E+04	34.4	10	1	1	0	1	CREATINE KINASE B-TYPE.	P12277; Q2LE07; Q6FG40	KCRB_HUMAN; Q6FG40_HUMAN
635	IPI00024067; IPI00455383	CLTC	1639	1675	1657	1.9E+05	1.9E+05	1.9E+05	3.8	5	0	0	0	1	ISOFORM 1 OF CLATHRIN HEAVY CHAIN 1.; ISOFORM 2 OF CLATHRIN HEAVY CHAIN 1.	Q00610; Q49AL0; Q6N0A0; Q86TF2	CLH1_HUMAN; Q49AL0_HUMAN
636	IPI00024107; IPI00218467; IPI00788661	SNCA	112	140	122	1.1E+04	1.4E+04	1.3E+04	45.0	4	0	0	0	1	ISOFORM 1 OF ALPHA-SYNUCLEIN.; ISOFORM 2-4 OF ALPHA-SYNUCLEIN.; 12 KDA PROTEIN.	P37840; Q13701; Q4JHI3; Q4W5L2; Q6IAU6; Q6QBS3	; Q4W5L2_HUMAN; Q6QBS3_HUMAN; SYUA_HUMAN
637	IPI00024266; IPI00639812	MGST3	152	166	159	1.7E+04	1.8E+04	1.7E+04	18.4	3	0	0	0	1	MICROSOMAL GLUTATHIONE S-TRANSFERASE 3.; MICROSOMAL GLUTATHIONE S-TRANSFERASE 3.	O14880; Q53GB9; Q5VV89; Q6ICN4	MGST3_HUMAN; Q53GB9_HUMAN; Q5VV89_HUMAN
638	IPI00024401	USP13	863	863	863	9.7E+04	9.7E+04	9.7E+04	4.2	2	0	0	0	1	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 13.	Q92995; Q96B25	Q96B25_HUMAN; UBP13_HUMAN
639	IPI00024976	TOMM22	142	142	142	1.6E+04	1.6E+04	1.6E+04	16.2	2	0	0	0	1	MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM22 HOMOLOG.	Q53GB0; Q5JZD3; Q9NS69	Q53GB0_HUMAN; Q5JZD3_HUMAN; TOM22_HUMAN
640	IPI00025156	STUB1	303	303	303	3.5E+04	3.5E+04	3.5E+04	12.5	3	0	0	0	1	ISOFORM 1 OF STIP1 HOMOLOGY AND U BOX-CONTAINING PROTEIN 1.	A2IDB9; O60526; Q969U2; Q9HBT1; Q9UNE7	A2IDB9_HUMAN; STUB1_HUMAN
641	IPI00025341	BDH1	343	343	343	3.8E+04	3.8E+04	3.8E+04	5.0	2	0	0	0	1	D-BETA-HYDROXYBUTYRATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.	A1E284; Q02338; Q96ET1; Q9BRZ4	A1E284_HUMAN; BDH_HUMAN
642	IPI00025717; IPI00477773	MTX2	253	263	258	2.9E+04	3.0E+04	2.9E+04	9.1	2	0	0	0	1	METAXIN-2.; METAXIN 2 ISOFORM B.	O75431; Q53S50; Q53SQ2; Q5M7Z6; Q8IZ68	MTX2_HUMAN; Q53S50_HUMAN; Q53SQ2_HUMAN; Q8IZ68_HUMAN
643	IPI00026260; IPI00604590; IPI00795292	NME1; NME1-NME2; NME2	152	292	237	1.7E+04	3.3E+04	2.7E+04	31.6	4	0	0	0	1	NUCLEOSIDE DIPHOSPHATE KINASE B.; NME1-NME2 PROTEIN.; NME1-NME2 PROTEIN.	P22392; Q1WM23; Q32Q12; Q6FHN3	NDKB_HUMAN; Q1WM23_HUMAN; Q32Q12_HUMAN; Q6FHN3_HUMAN
644	IPI00027223	IDH1	414	414	414	4.7E+04	4.7E+04	4.7E+04	22.2	6	1	1	0	1	ISOCITRATE DEHYDROGENASE [NADP] CYTOPLASMIC.	O75874; Q0QER2; Q567U4; Q6FHQ6; Q6FI37; Q6FIA4; Q7Z3V0; Q93090; Q9NTJ9; Q9UKW8	IDHC_HUMAN; Q0QER2_HUMAN; Q567U4_HUMAN; Q6FHQ6_HUMAN; Q6FI37_HUMAN; Q6FIA4_HUMAN; Q7Z3V0_HUMAN
645	IPI00027342; IPI00552929; IPI00792495	CAP2	406	477	452	4.5E+04	5.3E+04	5.0E+04	7.6	2	1	0	0	1	ADENYLYL CYCLASE-ASSOCIATED PROTEIN 2.; HYPOTHETICAL PROTEIN DKFZP686D0714.; CAP, ADENYLATE CYCLASE-ASSOCIATED PROTEIN, 2.	P40123; Q5JPJ8; Q6IAY2; Q9BYW9	CAP2_HUMAN; Q5JPJ8_HUMAN; Q9BYW9_HUMAN
646	IPI00027463	S100A6	90	90	90	1.0E+04	1.0E+04	1.0E+04	16.7	2	0	0	0	1	PROTEIN S100-A6.	P06703; Q5RHS4	S10A6_HUMAN
647	IPI00027626	CCT6A	531	531	531	5.8E+04	5.8E+04	5.8E+04	21.5	7	1	1	0	1	T-COMPLEX PROTEIN 1 SUBUNIT ZETA.	A1JUI8; P40227; Q3KP28; Q59ET3; Q75LP4; Q96S46	A1JUI8_HUMAN; Q59ET3_HUMAN; TCPZ_HUMAN
648	IPI00027701	ACADS	412	412	412	4.4E+04	4.4E+04	4.4E+04	34.5	10	1	1	0	1	SHORT-CHAIN SPECIFIC ACYL-COA DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.	P16219; P78331	ACADS_HUMAN
649	IPI00028120; IPI00028614; IPI00619961; IPI00790118; IPI00827872	EPB42	240	721	592	2.7E+04	8.0E+04	6.6E+04	12.9	5	1	1	0	1	ISOFORM LONG OF ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2.; EPB42 PROTEIN.; EPB42 PROTEIN.; 27 KDA PROTEIN.; ISOFORM SHORT OF ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2.	P16452; Q4KKX0; Q4VB96; Q4VB97	; EPB42_HUMAN; Q4KKX0_HUMAN; Q4VB96_HUMAN; Q4VB97_HUMAN
650	IPI00028883; IPI00642807	NDUFB8	155	186	171	1.8E+04	2.2E+04	2.0E+04	21.9	2	0	0	0	1	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 8,MITOCHONDRIAL PRECURSOR.; NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUBCOMPLEX, 8, 19KDA.	O95169; Q5W144; Q5W145; Q9UG53; Q9UJR4; Q9UQF3	NDUB8_HUMAN; Q5W145_HUMAN
651	IPI00029468	ACTR1A	376	376	376	4.3E+04	4.3E+04	4.3E+04	18.6	4	1	1	0	1	ALPHA-CENTRACTIN.	P42024; P61163	ACTZ_HUMAN
652	IPI00029739	CFH	1231	1231	1231	1.4E+05	1.4E+05	1.4E+05	1.7	2	0	0	0	1	ISOFORM 1 OF COMPLEMENT FACTOR H PRECURSOR.	P08603; P78435; Q14006; Q14570; Q2TAZ5; Q38G77; Q5TFM3; Q8N708; Q9NU86	CFAH_HUMAN; Q14006_HUMAN; Q2TAZ5_HUMAN
653	IPI00030154; IPI00479722; IPI00748256	PSME1	249	253	251	2.9E+04	2.9E+04	2.9E+04	18.1	4	0	0	0	1	PROTEASOME ACTIVATOR COMPLEX SUBUNIT 1.; 29 KDA PROTEIN.; PROTEASOME ACTIVATOR SUBUNIT 1 ISOFORM 2.	Q06323; Q6FHU3; Q6IBM2; Q9UEF4	; PSME1_HUMAN; Q6FHU3_HUMAN; Q6IBM2_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
654	IPI00030531; IPI00791574; IPI00794566	SLMAP	790	828	810	9.1E+04	9.5E+04	9.3E+04	5.1	2	0	0	0	1	ISOFORM 3 OF SARCOLEMMAL MEMBRANE-ASSOCIATED PROTEIN.; ISOFORM 1 OF SARCOLEMMAL MEMBRANE-ASSOCIATED PROTEIN.; ISOFORM 2 OF SARCOLEMMAL MEMBRANE-ASSOCIATED PROTEIN.	Q14BN4; Q14C95; Q6AI54; Q6UXC9; Q6ZVQ8; Q8NCW9; Q9H297; Q9HCH1; Q9Y681	SLMAP_HUMAN
655	IPI00030929; IPI00220278	MYL9	118	172	145	1.4E+04	2.0E+04	1.7E+04	17.8	2	0	0	0	1	MYOSIN REGULATORY LIGHT CHAIN 9 ISOFORM B.; MYOSIN REGULATORY LIGHT CHAIN 2, SMOOTH MUSCLE ISOFORM.	P24844; Q6IBG1; Q71U02; Q9BQL9; Q9BUF9; Q9H136	MLRN_HUMAN; Q6IBG1_HUMAN; Q71U02_HUMAN; Q9BUF9_HUMAN
656	IPI00031564	C7orf24	188	188	188	2.1E+04	2.1E+04	2.1E+04	10.6	2	0	0	0	1	UNCHARACTERIZED PROTEIN C7ORF24.	O75223	CG024_HUMAN
657	IPI00032633	COQ6	468	468	468	5.1E+04	5.1E+04	5.1E+04	13.9	6	1	1	0	1	UBIQUINONE BIOSYNTHESIS MONOOXYGENASE COQ6.	Q53GG6; Q96CA1; Q96CK2; Q9Y2Z9	COQ6_HUMAN; Q53GG6_HUMAN
658	IPI00032957; IPI00450472	UBE2I	158	184	171	1.8E+04	2.0E+04	1.9E+04	16.5	2	0	0	0	1	SUMO-CONJUGATING ENZYME UBC9.; UBIQUITIN-CONJUGATING ENZYME E2I.	P50550; P63279; Q15698; Q59GX1; Q7KZS0; Q86VB3	Q7KZS0_HUMAN; UBC9_HUMAN
659	IPI00037448; IPI00550682	GRHPR	328	341	335	3.6E+04	3.7E+04	3.6E+04	32.6	8	1	1	0	1	GLYOXYLATE REDUCTASE/HYDROXYPYRUVATE REDUCTASE.; GRHPR PROTEIN (FRAGMENT).	Q5M7Z5; Q5T945; Q9H3E9; Q9UBQ7; Q9UKX1	GRHPR_HUMAN; Q5M7Z5_HUMAN; Q5T945_HUMAN
660	IPI00042580; IPI00647123; IPI00797546	APOO	114	198	164	1.3E+04	2.2E+04	1.9E+04	13.1	2	0	0	0	1	ISOFORM 1 OF APOLIPOPROTEIN O PRECURSOR.; 13 KDA PROTEIN.; ISOFORM 2 OF APOLIPOPROTEIN O PRECURSOR.	Q9BUR5; Q9H3J9	; APOO_HUMAN
661	IPI00045496	USP28	1077	1077	1077	1.2E+05	1.2E+05	1.2E+05	2.0	2	0	0	0	1	ISOFORM 1 OF UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 28.	Q96RU2; Q9P213	UBP28_HUMAN
662	IPI00065495; IPI00152070; IPI00736624	COQ10A	215	247	231	2.4E+04	2.8E+04	2.6E+04	7.7	2	0	0	0	1	ISOFORM 1 OF PROTEIN COQ10 A, MITOCHONDRIAL PRECURSOR.; COQ10A PROTEIN.; ISOFORM 2 OF PROTEIN COQ10 A, MITOCHONDRIAL PRECURSOR.	Q6GMR6; Q6UWB9; Q86X16; Q8TAL2; Q96MF1; Q96MF6; Q9BUP4	CQ10A_HUMAN; Q8TAL2_HUMAN
663	IPI00105916	NOL3	219	219	219	2.4E+04	2.4E+04	2.4E+04	12.3	2	0	0	0	1	ISOFORM 1 OF NUCLEOLAR PROTEIN 3.	O60936; O60937	NOL3_HUMAN
664	IPI00152692; IPI00829870	DTD1; HARS2	209	209	209	2.3E+04	2.3E+04	2.3E+04	14.8	2	0	0	0	1	PROBABLE D-TYROSYL-TRNA(TYR) DEACYLASE 1.; HISTIDYL-TRNA SYNTHETASE 2.	Q496C9; Q496D1; Q5W184; Q8TEA8; Q8WXU8; Q9BW67; Q9H464; Q9H474	; DTD1_HUMAN; Q496C9_HUMAN
665	IPI00157790	KIAA0368	2017	2017	2017	2.2E+05	2.2E+05	2.2E+05	1.9	3	0	0	0	1	KIAA0368 PROTEIN.		
666	IPI00168620	ADPRHL1	354	354	354	4.0E+04	4.0E+04	4.0E+04	16.4	6	1	1	0	1	ISOFORM 1 OF [PROTEIN ADP-RIBOSYLARGININE] HYDROLASE-LIKE PROTEIN 1.	Q5JUG2; Q8NDY3; Q96GD1	ARHL1_HUMAN
667	IPI00171844	COPS4	406	406	406	4.6E+04	4.6E+04	4.6E+04	31.0	8	1	1	0	1	COP9 SIGNALOSOME COMPLEX SUBUNIT 4.	Q53FV3; Q561W7; Q9BT78; Q9NW31; Q9Y677	CSN4_HUMAN; Q53FV3_HUMAN
668	IPI00180408	MYH15	1946	1946	1946	2.2E+05	2.2E+05	2.2E+05	1.5	5	0	0	0	1	MYOSIN-15.	Q9Y2K3	MYH15_HUMAN
669	IPI00215719	RPL18	188	188	188	2.2E+04	2.2E+04	2.2E+04	13.8	2	0	0	0	1	60S RIBOSOMAL PROTEIN L18.	Q07020; Q0QEW2; Q8WTZ6	Q0QEW2_HUMAN; RL18_HUMAN
670	IPI00215894; IPI00789376; IPI00797833	KNG1	291	427	382	3.3E+04	4.8E+04	4.3E+04	4.9	2	0	0	0	1	ISOFORM LMW OF KININOGEN-1 PRECURSOR.; KNG1 PROTEIN.; KININOGEN 1.	P01042; P01043; Q05CF8; Q53EQ0; Q6PAU9	KNG1_HUMAN; Q05CF8_HUMAN; Q53EQ0_HUMAN; Q6PAU9_HUMAN
671	IPI00215979	BPGM	259	259	259	3.0E+04	3.0E+04	3.0E+04	20.1	4	0	0	0	1	BISPHOSPHOGLYCERATE MUTASE.	P07738	PMGE_HUMAN
672	IPI00216691	PFN1	140	140	140	1.5E+04	1.5E+04	1.5E+04	40.0	4	1	0	0	1	PROFILIN-1.	P07737; Q53Y44	PROF1_HUMAN; Q53Y44_HUMAN
673	IPI00216697; IPI00297532; IPI00374973; IPI00646300; IPI00654646; IPI00744408; IPI00744846; IPI00744895; IPI00744986; IPI00745246; IPI00745348; IPI00747536; IPI00747552; IPI00748074; IPI00748330; IPI00748439; IPI00748895; IPI00749301	ANK1	1519	1983	1796	1.7E+05	2.2E+05	2.0E+05	5.5	7	0	1	0	1	ISOFORM ER1 OF ANKYRIN-1.; ISOFORM ER2 OF ANKYRIN-1.; ISOFORM ER3 OF ANKYRIN-1.; ISOFORM ER16 OF ANKYRIN-1.; ISOFORM ER5 OF ANKYRIN-1.; ISOFORM ER7 OF ANKYRIN-1.; ISOFORM ER10 OF ANKYRIN-1.; ISOFORM ER6 OF ANKYRIN-1.; ISOFORM ER9 OF ANKYRIN-1.; 207 KDA PROTEIN.; ISOFORM ER4 OF ANKYRIN-1.; ISOFORM ER11 OF ANKYRIN-1.; ISOFORM ER8 OF ANKYRIN-1.; ISOFORM ER15 OF ANKYRIN-1.; ISOFORM BR21 OF ANKYRIN-1.; ISOFORM ER14 OF ANKYRIN-1.; ISOFORM ER13 OF ANKYRIN-1.; ISOFORM ER12 OF ANKYRIN-1.	O43400; P16157; Q13768; Q59FP2; Q8N604; Q99407; Q9UMG4	; ANK1_HUMAN; Q9UMG4_HUMAN
674	IPI00217960; IPI00396630	LOC730418; PRKACA	343	351	347	4.0E+04	4.1E+04	4.0E+04	29.2	8	1	1	0	1	ISOFORM 2 OF CAMP-DEPENDENT PROTEIN KINASE, ALPHA-CATALYTIC SUBUNIT.; ISOFORM 1 OF CAMP-DEPENDENT PROTEIN KINASE, ALPHA-CATALYTIC SUBUNIT.	P17612; Q15136; Q32P54; Q9H2Y0; Q9NRB4; Q9NRH9	KAPCA_HUMAN; Q15136_HUMAN; Q32P54_HUMAN
675	IPI00218465; IPI00759657	PLAA	738	795	767	8.1E+04	8.7E+04	8.4E+04	4.0	2	0	0	0	1	PHOSPHOLIPASE A-2-ACTIVATING PROTEIN.; PHOSPHOLIPASE A2-ACTIVATING PROTEIN ISOFORM 2.	Q53EU5; Q5VY33; Q9NUL8; Q9NVE9; Q9UF53; Q9Y263; Q9Y5L1	; PLAP_HUMAN
676	IPI00218728	PAFAH1B1	410	410	410	4.7E+04	4.7E+04	4.7E+04	11.7	3	1	1	0	1	ISOFORM 1 OF PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB SUBUNITALPHA.	P43034; Q8WZ88; Q8WZ89	LIS1_HUMAN
677	IPI00218918	ANXA1	346	346	346	3.9E+04	3.9E+04	3.9E+04	28.3	7	1	1	0	1	ANNEXIN A1.	P04083; Q05BR2; Q5TZZ9	ANXA1_HUMAN; Q05BR2_HUMAN; Q5TZZ9_HUMAN
678	IPI00219291; IPI00220300; IPI00456013; IPI00719814	ATP5J2	49	94	72	5.7E+03	1.1E+04	8.3E+03	43.6	2	0	0	0	1	ISOFORM 2 OF ATP SYNTHASE F CHAIN, MITOCHONDRIAL.; ISOFORM 1 OF ATP SYNTHASE F CHAIN, MITOCHONDRIAL.; ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F0 COMPLEX, SUBUNIT F2ISOFORM 2C.; ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F0 COMPLEX, SUBUNIT F2ISOFORM 2D.	O76079; P56134; Q53FE1; Q6IBB3; Q96L83; Q9BTI8	; ATPK_HUMAN; Q53FE1_HUMAN; Q6IBB3_HUMAN
679	IPI00219365	MSN	577	577	577	6.8E+04	6.8E+04	6.8E+04	16.1	8	1	1	0	1	MOESIN.	P26038; Q6PJT4	MOES_HUMAN; Q6PJT4_HUMAN
680	IPI00219682; IPI00377081	STOM	123	288	206	1.3E+04	3.2E+04	2.3E+04	16.3	3	0	0	0	1	ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN.; STOMATIN ISOFORM B.	P27105; Q14087; Q15609; Q5VX95; Q5VX96; Q96FK4	Q5VX95_HUMAN; STOM_HUMAN
681	IPI00219772	NDUFB7	137	137	137	1.6E+04	1.6E+04	1.6E+04	12.4	2	0	0	0	1	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 7.	P17568; Q6ICN9; Q9UI16	NDUB7_HUMAN; Q6ICN9_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
682	IPI00220059	LOC727762; NDUFB4	129	129	129	1.5E+04	1.5E+04	1.5E+04	17.1	2	0	0	0	1	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 4.	O95168	NDUB4_HUMAN
683	IPI00220503; IPI00793544	DCTN2	377	406	392	4.2E+04	4.5E+04	4.3E+04	20.2	6	1	1	0	1	DYNACTIN 2.; 42 KDA PROTEIN.	Q53H88	; Q53H88_HUMAN
684	IPI00220834	XRCC5	732	732	732	8.3E+04	8.3E+04	8.3E+04	9.8	6	0	1	0	1	ATP-DEPENDENT DNA HELICASE 2 SUBUNIT 2.	P13010; Q0Z7V0; Q4VBQ5; Q53HH7; Q9UCQ0; Q9UCQ1	KU86_HUMAN; Q0Z7V0_HUMAN; Q53HH7_HUMAN
685	IPI00220991; IPI00333383; IPI00784156; IPI00784366; IPI00790702	AP2B1	880	953	932	9.8E+04	1.1E+05	1.0E+05	3.5	2	0	0	0	1	HYPOTHETICAL PROTEIN DKFZP781K0743.; 105 KDA PROTEIN.; ISOFORM 1 OF AP-2 COMPLEX SUBUNIT BETA-1.; ISOFORM 2 OF AP-2 COMPLEX SUBUNIT BETA-1.; BETA ADAPTIN SUBUNIT.	P21851; P63010; Q68DI0; Q7Z451; Q96EL6; Q96J19	; AP2B1_HUMAN; Q68DI0_HUMAN; Q7Z451_HUMAN; Q96EL6_HUMAN
686	IPI00255052; IPI00790752	NDUFB9	168	179	174	2.0E+04	2.2E+04	2.1E+04	26.8	3	0	0	0	1	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 9.; NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT.	Q5JVG7; Q9UQE8; Q9UQS5; Q9Y6M9	NDUB9_HUMAN; Q5JVG7_HUMAN; Q9UQS5_HUMAN
687	IPI00289334; IPI00382696; IPI00477536; IPI00480131	FLNB	2578	2602	2593	2.8E+05	2.8E+05	2.8E+05	2.9	7	0	0	0	1	ISOFORM 1 OF FILAMIN-B.; ISOFORM 2 OF FILAMIN-B.; FILAMIN B.; 278 KDA PROTEIN.	O75369; Q13706; Q59EC2; Q60FE7; Q68CT4; Q6MZJ1; Q8WXS9; Q8WXT0; Q8WXT1; Q8WXT2; Q9NRB5; Q9NT26; Q9UEV9	; FLNB_HUMAN; Q60FE7_HUMAN; Q68CT4_HUMAN
688	IPI00291136	COL6A1	1028	1028	1028	1.1E+05	1.1E+05	1.1E+05	5.1	4	0	1	0	1	COLLAGEN ALPHA-1(VI) CHAIN PRECURSOR.	O00117; O00118; P12109; Q05BT9; Q14040; Q14041; Q16258; Q7Z645; Q8TBN2; Q9BSA8	CO6A1_HUMAN; Q05BT9_HUMAN; Q8TBN2_HUMAN
689	IPI00291328; IPI00646556; IPI00793910	NDUFV2	212	252	238	2.4E+04	2.8E+04	2.6E+04	11.3	2	1	1	0	1	NADH DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN 2, MITOCHONDRIALPRECURSOR.; 28 KDA PROTEIN.; 24-KDA SUBUNIT OF COMPLEX I.	P19404; Q6IB76; Q6IPW4; Q6LEN9; Q9BV41; Q9UEH5	; NDUV2_HUMAN; Q6IB76_HUMAN; Q6IPW4_HUMAN; Q6LEN9_HUMAN; Q9UEH5_HUMAN
690	IPI00291866; IPI00556459	SERPING1	333	500	417	3.7E+04	5.5E+04	4.6E+04	10.2	4	0	1	0	1	PLASMA PROTEASE C1 INHIBITOR PRECURSOR.; SERINE/CYSTEINE PROTEINASE INHIBITOR CLADE G MEMBER 1 SPLICE VARIANT 2(FRAGMENT).	P05155; Q16304; Q547W3; Q59EI5; Q5UGI6; Q96FE0; Q9UC49; Q9UCF9	IC1_HUMAN; Q16304_HUMAN; Q5UGI6_HUMAN; Q9UC49_HUMAN; Q9UCF9_HUMAN
691	IPI00292530	ITIH1	911	911	911	1.0E+05	1.0E+05	1.0E+05	5.3	3	0	0	0	1	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H1 PRECURSOR.	P19827; P78455; Q01746; Q562G1	ITIH1_HUMAN
692	IPI00294216; IPI00373875; IPI00746318	SGCD	256	290	279	2.9E+04	3.2E+04	3.1E+04	7.2	2	0	0	0	1	DELTA-SARCOGLYCAN.; DELTA-SARCOGLYCAN ISOFORM 2.; DELTA-SARCOGLYCAN ISOFORM 1.	Q53XA5; Q92629; Q99644	; Q53XA5_HUMAN; SGCD_HUMAN
693	IPI00297084	DDOST	456	456	456	5.1E+04	5.1E+04	5.1E+04	24.6	8	1	1	0	1	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOSYLTRANSFERASEPRECURSOR.	Q5VWA5	Q5VWA5_HUMAN
694	IPI00297626	STXBP3	592	592	592	6.8E+04	6.8E+04	6.8E+04	3.6	2	0	0	0	1	SYNTAXIN-BINDING PROTEIN 3.	O00186; Q53FW1; Q5VTL6; Q86YJ3; Q9UPD7	Q53FW1_HUMAN; Q5VTL6_HUMAN; STXB3_HUMAN
695	IPI00298497	FGB	491	491	491	5.6E+04	5.6E+04	5.6E+04	10.6	3	1	1	0	1	FIBRINOGEN BETA CHAIN PRECURSOR.	P02675; Q32Q65; Q3KPF2	FIBB_HUMAN; Q32Q65_HUMAN
696	IPI00298994; IPI00784273	TLN1	2541	2553	2547	2.7E+05	2.7E+05	2.7E+05	1.9	4	1	0	0	1	271 KDA PROTEIN.; TALIN-1.	Q5TCU6; Q86YD0; Q9NZQ2; Q9UHH8; Q9UPX3; Q9Y490	; Q5TCU6_HUMAN; TLN1_HUMAN
697	IPI00300502	MYOZ1	299	299	299	3.2E+04	3.2E+04	3.2E+04	14.4	2	0	0	0	1	MYOZENIN-1.	Q9H1I7; Q9NP98	MYOZ1_HUMAN
698	IPI00302328	MYH6	1939	1939	1939	2.2E+05	2.2E+05	2.2E+05	42.0	147	1	1	0	1	MYOSIN-6.	A2RTX1; O60661; P13533; Q13943; Q14906; Q14907; Q9UQV1	A2RTX1_HUMAN; MYH6_HUMAN; O60661_HUMAN; Q9UQV1_HUMAN
699	IPI00302927	CCT4	539	539	539	5.8E+04	5.8E+04	5.8E+04	21.5	9	1	1	0	1	T-COMPLEX PROTEIN 1 SUBUNIT DELTA.	O14870; P50991; Q53QP9; Q96C51	TCPD_HUMAN
700	IPI00304273; IPI00784338	APOA4	396	396	396	4.5E+04	4.5E+04	4.5E+04	21.2	7	1	1	0	1	APOLIPOPROTEIN A-IV PRECURSOR.; SIMILAR TO APOA4 PROTEIN.	P06727; Q13784; Q14CW8; Q6Q787	APOA4_HUMAN; Q13784_HUMAN
701	IPI00304417; IPI00304419; IPI00643978	IDH3B	383	389	386	4.2E+04	4.3E+04	4.2E+04	18.6	5	1	1	0	1	ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT BETA, MITOCHONDRIAL PRECURSOR.; ISOFORM A OF ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT BETA,MITOCHONDRIAL PRECURSOR.; 42 KDA PROTEIN.	O43837; O95106; Q5JXS8; Q9NQ06; Q9NQ07; Q9UEX0; Q9UG99	; IDH3B_HUMAN
702	IPI00073454; IPI00220613; IPI00304840	COL6A2	828	1019	922	8.7E+04	1.1E+05	9.8E+04	4.4	4	0	1	0	1	ISOFORM 2C2A' OF COLLAGEN ALPHA-2(VI) CHAIN PRECURSOR.; ISOFORM 2C2A OF COLLAGEN ALPHA-2(VI) CHAIN PRECURSOR.; ISOFORM 2C2 OF COLLAGEN ALPHA-2(VI) CHAIN PRECURSOR.	P12110; Q13909; Q13910; Q13911; Q14048; Q14049; Q16259; Q16597; Q6P0Q1; Q9BUM6; Q9UML3; Q9Y4S8	CO6A2_HUMAN; Q9BUM6_HUMAN
703	IPI00305461; IPI00645038	ITIH2	935	946	941	1.1E+05	1.1E+05	1.1E+05	4.8	3	0	0	0	1	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR.; INTER-ALPHA (GLOBULIN) INHIBITOR H2.	A2RTY6; P19823; Q14659; Q15484; Q5T985; Q5T986	A2RTY6_HUMAN; ITIH2_HUMAN; Q5T985_HUMAN; Q5T986_HUMAN
704	IPI00305692; IPI00642032	TXNL1	289	325	307	3.2E+04	3.7E+04	3.4E+04	15.9	4	0	0	0	1	THIOREDOXIN-LIKE PROTEIN 1.; 37 KDA PROTEIN.	O43396; Q59G46	; Q59G46_HUMAN; TXNL1_HUMAN
705	IPI00306280	DENR	199	199	199	2.2E+04	2.2E+04	2.2E+04	10.1	2	0	0	0	1	DENSITY-REGULATED PROTEIN.		
706	IPI00328415; IPI00446235	CYB5R3	278	301	290	3.2E+04	3.4E+04	3.3E+04	16.3	4	1	1	0	1	ISOFORM 1 OF NADH-CYTOCHROME B5 REDUCTASE.; ISOFORM 2 OF NADH-CYTOCHROME B5 REDUCTASE.	O75675; P00387; Q6TGM4; Q6TGM5; Q6ZVI6; Q8TDL8; Q8WTS8; Q9UEN4; Q9UEN5; Q9UL55; Q9UL56	NCB5R_HUMAN; Q6TGM4_HUMAN; Q6TGM5_HUMAN; Q6ZVI6_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
707	IPI00328650; IPI00411520; IPI00784009	C14orf159	616	621	618	6.6E+04	6.7E+04	6.7E+04	23.9	9	1	1	0	1	ISOFORM 1 OF UPF0317 PROTEIN C14ORF159, MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF UPF0317 PROTEIN C14ORF159, MITOCHONDRIAL PRECURSOR.; 67 KDA PROTEIN.	Q4LE40; Q53HP9; Q6IA66; Q7Z3D6; Q86SW3; Q86SX8; Q86SX9; Q86T08; Q86TV5; Q8NB88; Q96GW5; Q9H7G0; Q9H8Y9; Q9H9W6	; CN159_HUMAN; Q4LE40_HUMAN; Q53HP9_HUMAN; Q6IA66_HUMAN; Q8NB88_HUMAN
708	IPI00329389; IPI00741742; IPI00790342	RPL6	288	289	288	3.3E+04	3.3E+04	3.3E+04	9.3	2	0	0	0	1	60S RIBOSOMAL PROTEIN L6.; RIBOSOMAL PROTEIN L6.; DNA-BINDING PROTEIN TAXREB107.	Q02878; Q2M3Q3; Q8N5Z7; Q8TBK5; Q8WW97; Q9HBB3	Q8N5Z7_HUMAN; Q8TBK5_HUMAN; Q9HBB3_HUMAN; RL6_HUMAN
709	IPI00329646	PCBD2	130	130	130	1.4E+04	1.4E+04	1.4E+04	13.9	2	0	0	0	1	PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE 2.		
710	IPI00335085; IPI00783374	RNF123	1314	1316	1315	1.5E+05	1.5E+05	1.5E+05	4.3	3	1	1	0	1	ISOFORM 1 OF E3 UBIQUITIN-PROTEIN LIGASE RNF123.; ISOFORM 2 OF E3 UBIQUITIN-PROTEIN LIGASE RNF123.	A1L4Q3; Q5I022; Q5XPI4; Q6PFW4; Q71RH0; Q8IW18; Q9H0M8; Q9H5L8; Q9H9T2	A1L4Q3_HUMAN; RN123_HUMAN
711	IPI00337454; IPI00337455; IPI00477427; IPI00641544; IPI00747742	TNNT3	256	269	261	3.0E+04	3.2E+04	3.1E+04	38.7	15	1	1	0	1	ISOFORM 1 OF TROPONIN T, FAST SKELETAL MUSCLE.; TROPONIN T3, SKELETAL, FAST ISOFORM 3.; ISOFORM 2 OF TROPONIN T, FAST SKELETAL MUSCLE.; ISOFORM 3 OF TROPONIN T, FAST SKELETAL MUSCLE.; HYPOTHETICAL PROTEIN DKFZP779M2348.	P45378; Q12975; Q12976; Q12977; Q12978; Q17RG9; Q6FH29; Q6N056; Q86TH6	Q17RG9_HUMAN; Q6FH29_HUMAN; Q6N056_HUMAN; TNNT3_HUMAN
712	IPI00375676	FTL	191	191	191	2.1E+04	2.1E+04	2.1E+04	12.0	2	0	0	0	1	FERRITIN LIGHT POLYPEPTIDE VARIANT.	Q6IBT7; Q6S4P3; Q86WI9; Q8WU07; Q96AU9; Q96CU0	Q6IBT7_HUMAN; Q6S4P3_HUMAN; Q86WI9_HUMAN; Q8WU07_HUMAN; Q96AU9_HUMAN; Q96CU0_HUMAN
713	IPI00394809	APOOL	268	268	268	2.9E+04	2.9E+04	2.9E+04	10.8	2	0	0	0	1	APOLIPOPROTEIN O-LIKE PRECURSOR.	Q3KNU7; Q5H9D1; Q68DW4; Q6UXV4	APOOL_HUMAN; Q68DW4_HUMAN
714	IPI00398162; IPI00478974; IPI00745227; IPI00786896	NRAP	1695	1738	1717	1.9E+05	2.0E+05	2.0E+05	5.1	6	0	0	0	1	ISOFORM 2 OF NEBULIN-RELATED-ANCHORING PROTEIN.; ISOFORM 3 OF NEBULIN-RELATED-ANCHORING PROTEIN.; ISOFORM 1 OF NEBULIN-RELATED-ANCHORING PROTEIN.; ISOFORM 4 OF NEBULIN-RELATED-ANCHORING PROTEIN.	A0AVL2; O15500; Q05D68; Q5VWI3; Q5VWI4; Q6MZK3; Q6N026; Q6N059; Q6NSH8; Q6PDB0; Q719H6; Q86TC5; Q86TD6; Q86TE6; Q86VF6; Q86VF7; Q8N3R6; Q8N8F9; Q8TCH0; Q96MG4	A0AVL2_HUMAN; NRAP_HUMAN; Q05D68_HUMAN
715	IPI00398837	CCDC88	1476	1476	1476	1.6E+05	1.6E+05	1.6E+05	1.6	2	0	0	0	1	COILED-COIL DOMAIN CONTAINING 88.	Q8NF44	Q8NF44_HUMAN
716	IPI00399007; IPI00426051; IPI00829767	IGHG2	393	464	425	4.4E+04	5.1E+04	4.7E+04	19.2	7	1	1	0	1	HYPOTHETICAL PROTEIN DKFZP686I04196 (FRAGMENT).; HYPOTHETICAL PROTEIN DKFZP686C15213.; PROTEIN.	A2J1N1; Q0ZCI1; Q6MZU6; Q6N093	; A2J1N1_HUMAN; Q0ZCI1_HUMAN; Q6MZU6_HUMAN; Q6N093_HUMAN
717	IPI00409750	OTUB1	315	315	315	3.5E+04	3.5E+04	3.5E+04	6.0	2	0	0	0	1	ISOFORM 2 OF UBIQUITIN THIOESTERASE PROTEIN OTUB1.	Q32Q78; Q96FW1; Q96II3; Q9NXQ4; Q9P0B8	OTUB1_HUMAN
718	IPI00411706; IPI00641040	ESD	253	282	268	2.8E+04	3.1E+04	3.0E+04	26.5	6	0	0	0	1	S-FORMYLGLUTATHIONE HYDROLASE.; 28 KDA PROTEIN.	P10768; Q5TBU8; Q5TBV0; Q5TBV2; Q9BVJ2	; ESTD_HUMAN
719	IPI00418163	C4B	1744	1744	1744	1.9E+05	1.9E+05	1.9E+05	13.1	15	0	1	0	1	COMPLEMENT COMPONENT 4B PREPROPROTEIN.	Q6U2E9; Q6U2F8; Q6U2G0; Q6U2G1; Q6U2H4; Q6U2L1; Q6U2L6; Q6U2L7; Q6U2M2; Q6U2M5; Q6VCV8; Q96SA7; Q96SA8; Q9UNU2	Q6U2E9_HUMAN; Q6U2F8_HUMAN; Q6U2G0_HUMAN; Q6U2G1_HUMAN; Q6U2H4_HUMAN; Q6U2L1_HUMAN; Q6U2L6_HUMAN; Q6U2L7_HUMAN; Q6U2M2_HUMAN; Q6U2M5_HUMAN; Q6VCV8_HUMAN; Q96SA7_HUMAN; Q96SA8_HUMAN; Q9UNU2_HUMAN
720	IPI00418495	CD36	472	472	472	5.3E+04	5.3E+04	5.3E+04	8.9	3	1	1	0	1	PLATELET GLYCOPROTEIN 4.	P16671; Q13966; Q16093; Q8TCV7; Q9BPZ8; Q9BQA7; Q9BQC2; Q9BZM7; Q9BZM8; Q9BZM9; Q9BZN0; Q9BZN1; Q9BZN2; Q9BZN3; Q9BZN4; Q9BZN5	CD36_HUMAN; Q9BQA7_HUMAN; Q9BZM7_HUMAN; Q9BZM9_HUMAN; Q9BZN0_HUMAN; Q9BZN1_HUMAN; Q9BZN2_HUMAN
721	IPI00419266	NDUFA6	154	154	154	1.8E+04	1.8E+04	1.8E+04	12.3	2	1	0	0	1	NADH DEHYDROGENASE (UBIQUINONE) 1 ALPHA SUBCOMPLEX, 6, 14KDA.	Q6FGW0; Q6IBT8	Q6FGW0_HUMAN; Q6IBT8_HUMAN
722	IPI00419802	HIBCH	386	386	386	4.3E+04	4.3E+04	4.3E+04	26.4	10	1	1	0	1	3-HYDROXYISOBUTYRYL-COENZYME A HYDROLASE ISOFORM 1.	Q53GA8; Q53GF2; Q53TC6; Q6NVY1; Q92931	Q53GA8_HUMAN; Q53GF2_HUMAN; Q53TC6_HUMAN; Q6NVY1_HUMAN; Q92931_HUMAN
723	IPI00423460	IGHA1	506	506	506	5.4E+04	5.4E+04	5.4E+04	10.1	4	1	0	0	1	HYPOTHETICAL PROTEIN DKFZP686G21220 (FRAGMENT).	Q6N090	Q6N090_HUMAN
724	IPI00452731	NDUFA7	113	113	113	1.3E+04	1.3E+04	1.3E+04	34.5	3	0	0	0	1	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 7.	O95182; Q32Q14; Q6FG42; Q6IB89	NDUA7_HUMAN; Q32Q14_HUMAN; Q6FG42_HUMAN; Q6IB89_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
725	IPI00453473	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4	103	103	103	1.1E+04	1.1E+04	1.1E+04	40.8	4	1	0	0	1	HISTONE H4.	A2VCL0; P02304; P02305; P62805; Q0VAS5; Q6B823; Q6DRA9; Q6FGB8; Q6NWP7	A2VCL0_HUMAN; H4_HUMAN; Q0VAS5_HUMAN; Q6B823_HUMAN; Q6DRA9_HUMAN; Q6FGB8_HUMAN; Q6NWP7_HUMAN
726	IPI00478003	A2M	1474	1474	1474	1.6E+05	1.6E+05	1.6E+05	22.4	26	1	1	0	1	ALPHA-2-MACROGLOBULIN PRECURSOR.	P01023; Q13677; Q59F47; Q5QTS0; Q68DN2; Q6PIY3; Q6PN97; Q9BQ22	A2MG_HUMAN; Q9BQ22_HUMAN
727	IPI00478292; IPI00744706; IPI00745092	SPTAN1	2460	2485	2475	2.8E+05	2.9E+05	2.8E+05	1.3	2	0	0	0	1	ISOFORM 1 OF SPECTRIN ALPHA CHAIN, BRAIN.; ISOFORM 3 OF SPECTRIN ALPHA CHAIN, BRAIN.; ISOFORM 2 OF SPECTRIN ALPHA CHAIN, BRAIN.	Q9UG16	; Q9UG16_HUMAN
728	IPI00478450	NDUFB11	163	163	163	1.8E+04	1.8E+04	1.8E+04	20.9	2	0	0	0	1	ISOFORM 2 OF NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT11, MITOCHONDRIAL PRECURSOR.	Q5JRR3; Q5JRR4; Q6IAB6; Q8WZ96; Q9BXX9; Q9NX14	NDUBB_HUMAN
729	IPI00478774	MYOM3	1441	1441	1441	1.6E+05	1.6E+05	1.6E+05	9.7	11	1	1	0	1	MYOMESIN-3.	Q5VTT5; Q6AWC0; Q6AWC1; Q6NXF9; Q6ZRG7; Q7Z3G9; Q96C54	Q5VTT5_HUMAN; Q6AWC0_HUMAN; Q6AWC1_HUMAN; Q6NXF9_HUMAN; Q6ZRG7_HUMAN; Q7Z3G9_HUMAN; Q96C54_HUMAN
730	IPI00550363; IPI00647915	CCDC19; TAGLN2	199	220	210	2.2E+04	2.4E+04	2.3E+04	13.1	2	0	0	0	1	TRANSGELIN-2.; 24 KDA PROTEIN.	P37802; Q5JRQ6; Q5JRQ7; Q6FGI1; Q9BUH5; Q9H4P0	; Q6FGI1_HUMAN; TAGL2_HUMAN
731	IPI00550991	SERPINA3	448	448	448	5.1E+04	5.1E+04	5.1E+04	13.6	4	1	1	0	1	ISOFORM 1 OF ALPHA-1-ANTICHYMOTRYPSIN PRECURSOR.	Q2TU87; Q2TU88	Q2TU87_HUMAN; Q2TU88_HUMAN
732	IPI00412545; IPI00554681	NDUFA5	116	116	116	1.3E+04	1.4E+04	1.4E+04	31.0	3	1	0	0	1	HYPOTHETICAL PROTEIN DKFZP781K1356.; NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 5.	Q16718; Q5H9R2; Q6IRX7	NDUA5_HUMAN; Q5H9R2_HUMAN
733	IPI00555692; IPI00793199	ANXA4	299	321	310	3.4E+04	3.6E+04	3.5E+04	8.4	2	0	0	0	1	ANXA4 PROTEIN.; ANNEXIN IV.	Q59FK3; Q6LES2; Q6MZI0; Q6P452	Q59FK3_HUMAN; Q6LES2_HUMAN; Q6MZI0_HUMAN; Q6P452_HUMAN
734	IPI00555956	PSMB4	264	264	264	2.9E+04	2.9E+04	2.9E+04	9.1	2	0	0	0	1	PROTEASOME SUBUNIT BETA TYPE 4 PRECURSOR.	P28070; P31148; Q5SZS5; Q6IBI4; Q969L6	PSB4_HUMAN; Q5SZS5_HUMAN; Q6IBI4_HUMAN
735	IPI00604707	DLAT	647	647	647	6.9E+04	6.9E+04	6.9E+04	18.9	12	1	1	0	1	DIHYDROLIPOAMIDE S-ACETYLTRANSFERASE (E2 COMPONENT OF PYRUVATEDEHYDROGENASE COMPLEX) VARIANT.	Q16791; Q53EP3; Q86YI5	Q16791_HUMAN; Q53EP3_HUMAN; Q86YI5_HUMAN
736	IPI00431645; IPI00478493; IPI00641737	HP	281	420	349	3.1E+04	4.7E+04	3.9E+04	17.1	5	1	1	0	1	HP PROTEIN.; HP PROTEIN.; HAPTOGLOBIN PRECURSOR.	Q0VAC5; Q6NSB4; Q6PEJ8	; Q0VAC5_HUMAN; Q6NSB4_HUMAN; Q6PEJ8_HUMAN
737	IPI00645720	COQ7	179	179	179	2.0E+04	2.0E+04	2.0E+04	15.1	2	0	0	0	1	20 KDA PROTEIN.		
738	IPI00742696	GC	474	474	474	5.3E+04	5.3E+04	5.3E+04	12.0	6	1	1	0	1	VITAMIN D-BINDING PROTEIN PRECURSOR.	Q53F31; Q6GTG1; Q6LDC6	Q53F31_HUMAN; Q6GTG1_HUMAN; Q6LDC6_HUMAN
739	IPI00745471	SYNE1	8410	8410	8410	9.7E+05	9.7E+05	9.7E+05	0.2	2	0	0	0	1	OTTHUMP00000017444.	Q7Z6R3	Q7Z6R3_HUMAN
740	IPI00785200		236	236	236	2.5E+04	2.5E+04	2.5E+04	23.3	2	0	0	0	1	HYPOTHETICAL PROTEIN.	Q8NEJ1	Q8NEJ1_HUMAN
741	IPI00792352	RAN	236	236	236	2.6E+04	2.6E+04	2.6E+04	18.6	3	0	0	0	1	26 KDA PROTEIN.		
742	IPI00000030; IPI00219543; IPI00219544	PPP2R5D	496	602	556	5.8E+04	7.0E+04	6.5E+04	4.5	2	0	1	0	0	ISOFORM DELTA-1 OF SERINE/THREONINE-PROTEIN PHOSPHATASE 2A 56 KDAREGULATORY SUBUNIT DELTA ISOFORM.; ISOFORM DELTA-2 OF SERINE/THREONINE-PROTEIN PHOSPHATASE 2A 56 KDAREGULATORY SUBUNIT DELTA ISOFORM.; ISOFORM DELTA-3 OF SERINE/THREONINE-PROTEIN PHOSPHATASE 2A 56 KDAREGULATORY SUBUNIT DELTA ISOFORM.	O00494; O00696; Q14738; Q15171; Q59EF0; Q5TC39	2A5D_HUMAN; Q59EF0_HUMAN; Q5TC39_HUMAN
743	IPI00000146	NT5C1A	368	368	368	4.1E+04	4.1E+04	4.1E+04	28.3	7	1	1	0	0	CYTOSOLIC 5'-NUCLEOTIDASE 1A.	Q3SYB9; Q5TG98; Q9BWT8; Q9BXI3	5NT1A_HUMAN
744	IPI00000663; IPI00759655	MLYCD	454	493	474	5.1E+04	5.5E+04	5.3E+04	7.5	2	1	1	0	0	ISOFORM MITOCHONDRIAL OF MALONYL-COA DECARBOXYLASE, MITOCHONDRIALPRECURSOR.; ISOFORM CYTOPLASMIC+PEROXISOMAL OF MALONYL-COA DECARBOXYLASE,MITOCHONDRIAL PRECURSOR.	O95822; Q9UNU5; Q9Y3F2	DCMC_HUMAN
745	IPI00000873; IPI00829641	VARS	1264	1264	1264	1.4E+05	1.4E+05	1.4E+05	2.1	2	0	1	0	0	VALYL-TRNA SYNTHETASE.; 140 KDA PROTEIN.	A2BEY0; P26640; Q5JQ90; Q96E77; Q9UQM2	; A2BEY0_HUMAN; SYV_HUMAN
746	IPI00002270	C6orf211	441	441	441	5.1E+04	5.1E+04	5.1E+04	11.6	4	1	1	0	0	UPF0364 PROTEIN C6ORF211.	Q96FC6; Q9H993; Q9UFY5	CF211_HUMAN
747	IPI00002311	SCRN3	426	426	426	4.9E+04	4.9E+04	4.9E+04	6.1	2	1	1	0	0	SECERNIN-3.	Q0VDG5	Q0VDG5_HUMAN
748	IPI00002375	TMOD1	359	359	359	4.1E+04	4.1E+04	4.1E+04	11.1	3	0	1	0	0	TROPOMODULIN-1.	P28289; Q9BUF1	TMOD1_HUMAN
749	IPI00002519; IPI00220668	SHMT1	444	483	464	4.9E+04	5.3E+04	5.1E+04	6.2	2	0	1	0	0	ISOFORM 1 OF SERINE HYDROXYMETHYLTRANSFERASE, CYTOSOLIC.; ISOFORM 2 OF SERINE HYDROXYMETHYLTRANSFERASE, CYTOSOLIC.	P34896; Q53ET7; Q96HY0; Q9UMD1; Q9UMD2	GLYC_HUMAN; Q53ET7_HUMAN; Q96HY0_HUMAN
750	IPI00003918	RPL4	427	427	427	4.8E+04	4.8E+04	4.8E+04	8.2	3	1	1	0	0	60S RIBOSOMAL PROTEIN L4.	P36578; P39029; Q4VBR0; Q53G74; Q59GY2; Q969Z9	Q53G74_HUMAN; Q59GY2_HUMAN; RL4_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
751	IPI00003944	DBT	482	482	482	5.3E+04	5.3E+04	5.3E+04	6.9	2	1	1	0	0	LIPOAMIDE ACYLTRANSFERASE COMPONENT OF BRANCHED-CHAIN ALPHA-KETO ACIDDEHYDROGENASE COMPLEX, MITOCHONDRIAL PRECURSOR.	P11182; Q5VVL8	ODB2_HUMAN; Q5VVL8_HUMAN
752	IPI00004839	CRKL	303	303	303	3.4E+04	3.4E+04	3.4E+04	19.8	4	1	1	0	0	CRK-LIKE PROTEIN.	P46109	CRKL_HUMAN
753	IPI00005198; IPI00641665	ILF2	115	390	253	1.2E+04	4.3E+04	2.8E+04	8.0	2	1	1	0	0	INTERLEUKIN ENHANCER-BINDING FACTOR 2.; 12 KDA PROTEIN.	Q12905; Q53FG3; Q5SR10; Q5SR11; Q7L7R3; Q9BWD4; Q9P1N0	; ILF2_HUMAN; Q53FG3_HUMAN
754	IPI00005809	SDPR	425	425	425	4.7E+04	4.7E+04	4.7E+04	11.8	3	1	1	0	0	SERUM DEPRIVATION-RESPONSE PROTEIN.	O95810	SDPR_HUMAN
755	IPI00006114	SERPINF1	418	418	418	4.6E+04	4.6E+04	4.6E+04	12.9	4	1	1	0	0	PIGMENT EPITHELIUM-DERIVED FACTOR PRECURSOR.	P36955; Q13236; Q2TU83; Q96CT1; Q96R01; Q9BWA4	PEDF_HUMAN; Q2TU83_HUMAN
756	IPI00006451	NSF	744	744	744	8.3E+04	8.3E+04	8.3E+04	5.8	3	1	1	0	0	VESICLE-FUSING ATPASE.	P46459; Q8N6D7; Q96D47; Q9H3V6; Q9UKZ2	NSF_HUMAN; Q96D47_HUMAN; Q9H3V6_HUMAN
757	IPI00006558; IPI00022824	SH3GLB1	365	386	376	4.1E+04	4.3E+04	4.2E+04	7.4	2	1	1	0	0	ISOFORM 1 OF SH3 DOMAIN GRB2-LIKE PROTEIN B1.; ISOFORM 2 OF SH3 DOMAIN GRB2-LIKE PROTEIN B1.	Q5H8U5; Q9H3Z0; Q9NR47; Q9NYA9; Q9Y371	Q5H8U5_HUMAN; SHLB1_HUMAN
758	IPI00006957; IPI00339238	DHRS7	289	339	314	3.2E+04	3.8E+04	3.5E+04	13.6	3	1	1	0	0	ISOFORM 1 OF DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER 7 PRECURSOR.; ISOFORM 2 OF DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER 7 PRECURSOR.	Q9UKU2; Q9Y394	DHRS7_HUMAN
759	IPI00007183; IPI00169267	ARL6IP2	579	583	581	6.6E+04	6.6E+04	6.6E+04	5.9	2	1	1	0	0	HYPOTHETICAL PROTEIN ARL6IP2.; ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 6-INTERACTING PROTEIN 2.	Q4ZG30; Q7Z630; Q8NHH8; Q8NHH9; Q9H5M7	Q4ZG30_HUMAN; Q7Z630_HUMAN; Q8NHH8_HUMAN; Q8NHH9_HUMAN; Q9H5M7_HUMAN
760	IPI00007675	DYNC1LI1	523	523	523	5.7E+04	5.7E+04	5.7E+04	9.2	3	1	1	0	0	CYTOPLASMIC DYNEIN 1 LIGHT INTERMEDIATE CHAIN 1.	A2RRG7; Q53HC8; Q53HK7; Q6MZE7; Q9Y6G9	A2RRG7_HUMAN; DC1L1_HUMAN; Q6MZE7_HUMAN
761	IPI00007682	ATP6V1A	617	617	617	6.8E+04	6.8E+04	6.8E+04	6.2	2	1	1	0	0	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS ISOFORM.		
762	IPI00008219	RAD23A	363	363	363	4.0E+04	4.0E+04	4.0E+04	14.1	3	0	1	0	0	UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG A.	P54725; Q59EU8; Q5M7Z1	Q59EU8_HUMAN; Q5M7Z1_HUMAN; RD23A_HUMAN
763	IPI00008223	RAD23B	409	409	409	4.3E+04	4.3E+04	4.3E+04	17.4	5	1	1	0	0	UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG B.	P54727; Q53F10; Q7Z5K8; Q8WUB0	Q53F10_HUMAN; Q7Z5K8_HUMAN; RD23B_HUMAN
764	IPI00009104	RUVBL2	463	463	463	5.1E+04	5.1E+04	5.1E+04	9.5	3	1	1	0	0	RUVB-LIKE 2.	Q6FIB9; Q6PK27; Q9Y230; Q9Y361	Q6FIB9_HUMAN; RUVB2_HUMAN
765	IPI00009634	SQRDL	450	450	450	5.0E+04	5.0E+04	5.0E+04	10.9	4	1	1	0	0	SULFIDE:QUINONE OXIDOREDUCTASE, MITOCHONDRIAL PRECURSOR.	Q53HW7; Q9UHS8; Q9UQM8; Q9Y6N5	Q53HW7_HUMAN; Q9UHS8_HUMAN; SQRD_HUMAN
766	IPI00010314; IPI00442121; IPI00790373	ALAD	330	359	343	3.6E+04	3.9E+04	3.8E+04	8.6	2	1	1	0	0	DELTA-AMINOLEVULINIC ACID DEHYDRATASE.; DELTA-AMINOLEVULINIC ACID DEHYDRATASE ISOFORM A.; DELTA-AMINOLEVULINIC ACID DEHYDRATASE ISOFORM B.	P13716; Q16870; Q16871; Q6ZMU0; Q9BVQ9	; HEM2_HUMAN; Q6ZMU0_HUMAN
767	IPI00010720	CCT5	541	541	541	6.0E+04	6.0E+04	6.0E+04	14.2	6	1	1	0	0	T-COMPLEX PROTEIN 1 SUBUNIT EPSILON.	P48643; Q96GI1; Q9BU08; Q9HB74	Q96GI1_HUMAN; Q9BU08_HUMAN; Q9HB74_HUMAN; TCPE_HUMAN
768	IPI00012442	G3BP1	466	466	466	5.2E+04	5.2E+04	5.2E+04	7.5	2	1	1	0	0	RAS GTPASE-ACTIVATING PROTEIN-BINDING PROTEIN 1.	Q13283; Q32P45; Q53HH4; Q5HYE9; Q5U0Q1; Q6FI03	G3BP1_HUMAN; Q32P45_HUMAN; Q53HH4_HUMAN; Q5HYE9_HUMAN; Q5U0Q1_HUMAN; Q6FI03_HUMAN
769	IPI00012578	KPNA4	521	521	521	5.8E+04	5.8E+04	5.8E+04	11.7	5	1	1	0	0	IMPORTIN ALPHA-4 SUBUNIT.	O00190; O00629	IMA4_HUMAN
770	IPI00013068	EIF3S6	445	445	445	5.2E+04	5.2E+04	5.2E+04	18.9	6	1	1	0	0	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 6.	O43902; P60228; Q64058; Q64059; Q64252; Q6FG33; Q6IAX5; Q8WVK4	IF36_HUMAN; Q6FG33_HUMAN; Q6IAX5_HUMAN; Q8WVK4_HUMAN
771	IPI00013122	CDC37	378	378	378	4.4E+04	4.4E+04	4.4E+04	18.8	5	1	1	0	0	HSP90 CO-CHAPERONE CDC37.	A1L0W4; Q16543; Q53YA2; Q6FG59	A1L0W4_HUMAN; CDC37_HUMAN; Q53YA2_HUMAN; Q6FG59_HUMAN
772	IPI00013219	ILK	452	452	452	5.1E+04	5.1E+04	5.1E+04	5.5	2	1	1	0	0	INTEGRIN-LINKED PROTEIN KINASE.	P57043; Q13418; Q68DZ3	ILK_HUMAN
773	IPI00013466; IPI00783136	ASNA1	348	363	356	3.9E+04	4.0E+04	4.0E+04	5.5	2	1	1	0	0	ARSA ARSENITE TRANSPORTER, ATP-BINDING, HOMOLOG 1 VARIANT.; ARSENICAL PUMP-DRIVING ATPASE.	O43681; Q53FC6; Q92849	ARSA1_HUMAN; Q53FC6_HUMAN
774	IPI00015856; IPI00029820; IPI00658188; IPI00658215	DNPEP	378	485	442	4.1E+04	5.3E+04	4.9E+04	11.1	3	1	1	0	0	HYPOTHETICAL PROTEIN DNPEP.; DNPEP PROTEIN (FRAGMENT).; 48 KDA PROTEIN.; 52 KDA PROTEIN.	Q53SB6; Q9BSS9	; Q53SB6_HUMAN; Q9BSS9_HUMAN
775	IPI00016249; IPI00554715	FXR1	539	621	580	6.1E+04	7.0E+04	6.5E+04	7.3	3	1	1	0	0	ISOFORM 1 OF FRAGILE X MENTAL RETARDATION SYNDROME-RELATED PROTEIN 1.; ISOFORM 2 OF FRAGILE X MENTAL RETARDATION SYNDROME-RELATED PROTEIN 1.	P51114; Q7Z450; Q8N6R8	FXR1_HUMAN
776	IPI00016405	OCIAD1	245	245	245	2.8E+04	2.8E+04	2.8E+04	11.8	2	1	1	0	0	OCIA DOMAIN CONTAINING 1 ISOFORM 1.	Q9NX40	Q9NX40_HUMAN
777	IPI00016458; IPI00029239	L2HGDH	441	463	452	4.9E+04	5.0E+04	4.9E+04	8.2	3	1	1	0	0	ISOFORM 1 OF L-2-HYDROXYGLUTARATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR.; ISOFORM 2 OF L-2-HYDROXYGLUTARATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR.	Q9BRR1; Q9H9P8	L2HDH_HUMAN
778	IPI00016610	PCBP1	356	356	356	3.7E+04	3.7E+04	3.7E+04	21.1	4	1	1	0	0	POLY(RC)-BINDING PROTEIN 1.	Q13157; Q14975; Q15365; Q53SS8	PCBP1_HUMAN; Q53SS8_HUMAN
779	IPI00016801	GLUD1	558	558	558	6.1E+04	6.1E+04	6.1E+04	21.3	9	1	1	0	0	GLUTAMATE DEHYDROGENASE 1, MITOCHONDRIAL PRECURSOR.	P00367; Q14400; Q53GW3; Q5TBU3; Q9UQV0	DHE3_HUMAN; Q14400_HUMAN; Q53GW3_HUMAN; Q9UQV0_HUMAN
780	IPI00017184	EHD1	534	534	534	6.1E+04	6.1E+04	6.1E+04	9.9	4	1	1	0	0	EH DOMAIN-CONTAINING PROTEIN 1.	O14611; Q2M3Q4; Q9H4M9; Q9UNR3	EHD1_HUMAN
781	IPI00017763	NAP1L4	377	377	377	4.3E+04	4.3E+04	4.3E+04	18.8	5	1	1	0	0	NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 4.		

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
782	IPI00017895; IPI00719611	GPD2	601	727	664	6.8E+04	8.1E+04	7.4E+04	21.6	9	1	1	0	0	ISOFORM 1 OF GLYCEROL-3-PHOSPHATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR.; ISOFORM 2 OF GLYCEROL-3-PHOSPHATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR.	P43304; Q53RD0; Q53T76; Q59FR1; Q8WUQ0; Q9HAP9	GPDM_HUMAN; Q53RD0_HUMAN; Q53T76_HUMAN; Q8WUQ0_HUMAN
783	IPI00018140; IPI00402183; IPI00402185	SYNCRIP	410	623	532	4.6E+04	7.0E+04	6.0E+04	4.2	2	1	1	0	0	ISOFORM 1 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN Q.; ISOFORM 3 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN Q.; ISOFORM 5 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN Q.	O60506; Q53H05; Q59GL1; Q5TCG2; Q5TCG3; Q8IW78; Q8N599; Q96LC1; Q96LC2; Q9Y583	HNRPQ_HUMAN; Q59GL1_HUMAN; Q5TCG3_HUMAN
784	IPI00018813; IPI00743825	COPS2	443	453	448	5.2E+04	5.3E+04	5.2E+04	17.9	7	1	1	0	0	ISOFORM 2 OF COP9 SIGNALOSOME COMPLEX SUBUNIT 2.; ISOFORM 1 OF COP9 SIGNALOSOME COMPLEX SUBUNIT 2.	O88950; P61201; Q15647; Q53HJ0; Q59EL2; Q6FGP4; Q9BY54; Q9R249; Q9UNI2; Q9UNQ5	CSN2_HUMAN; Q53HJ0_HUMAN; Q59EL2_HUMAN
785	IPI00018873; IPI00337370	PBEF1	368	491	430	4.2E+04	5.6E+04	4.9E+04	19.8	5	1	1	0	0	ISOFORM 1 OF NICOTINAMIDE PHOSPHORIBOSYLTRANSFERASE.; ISOFORM 2 OF NICOTINAMIDE PHOSPHORIBOSYLTRANSFERASE.	P43490; Q3KQV0; Q658Z1; Q8WW95	NAMPT_HUMAN; Q658Z1_HUMAN
786	IPI00018946	PANK4	773	773	773	8.6E+04	8.6E+04	8.6E+04	8.4	5	1	1	0	0	PANTOTHENATE KINASE 4.	Q53EU3; Q5TA84; Q7RTX2; Q7RTX3; Q9H3X5; Q9NVE7	PANK4_HUMAN; Q7RTX2_HUMAN
787	IPI00018968; IPI00479845; IPI00604652; IPI00604676; IPI00646350	APPBP1	445	537	516	5.1E+04	6.1E+04	5.8E+04	7.1	2	0	1	0	0	NEDD8-ACTIVATING ENZYME E1 REGULATORY SUBUNIT.; 60 KDA PROTEIN.; AMYLOID BETA PRECURSOR PROTEIN-BINDING PROTEIN 1 ISOFORM C.; AMYLOID BETA PRECURSOR PROTEIN-BINDING PROTEIN 1 ISOFORM B.; 61 KDA PROTEIN.	Q13564	; ULA1_HUMAN
788	IPI00019450; IPI00642416; IPI00646322; IPI00646813	TROVE2	518	538	529	5.8E+04	6.1E+04	6.0E+04	4.8	2	0	1	0	0	ISOFORM LONG OF 60 KDA SS-A/RO RIBONUCLEOPROTEIN.; TROVE DOMAIN FAMILY, MEMBER 2.; TROVE DOMAIN FAMILY, MEMBER 2.; 60KD RO/SSA AUTOANTIGEN ISOFORM 1.	P10155; Q5LJ98; Q5LJ99; Q5LJA0; Q86WL3; Q86WL4; Q92787; Q9H1W6	Q5LJ98_HUMAN; Q5LJ99_HUMAN; Q5LJA0_HUMAN; Q86WL3_HUMAN; Q86WL4_HUMAN; RO60_HUMAN
789	IPI00019912	HSD17B4	736	736	736	8.0E+04	8.0E+04	8.0E+04	3.9	2	1	1	0	0	PEROXISOMAL MULTIFUNCTIONAL ENZYME TYPE 2.	P51659; Q59H27; Q9UBA4	DHB4_HUMAN; Q59H27_HUMAN; Q9UBA4_HUMAN
790	IPI00008943; IPI00019918; IPI00027599; IPI00155054	DDX19A; DDX19B	447	479	463	5.0E+04	5.4E+04	5.2E+04	9.0	3	1	1	0	0	ISOFORM 1 OF ATP-DEPENDENT RNA HELICASE DDX19B.; ATP-DEPENDENT RNA HELICASE DDX19A.; ISOFORM 2 OF ATP-DEPENDENT RNA HELICASE DDX19B.; HYPOTHETICAL PROTEIN DKFZP686C21137.	Q2NL95; Q53FM0; Q53G16; Q68DY7; Q69YM2; Q6FIB7; Q6IAE0; Q7Z4W5; Q9H0U0; Q9HBZ9; Q9NUU7; Q9UMR2	DD19A_HUMAN; DD19B_HUMAN; Q2NL95_HUMAN; Q53G16_HUMAN; Q68DY7_HUMAN; Q69YM2_HUMAN; Q7Z4W5_HUMAN; Q9H0U0_HUMAN; Q9HBZ9_HUMAN
791	IPI00019927	PSMD7	324	324	324	3.7E+04	3.7E+04	3.7E+04	16.4	3	0	1	0	0	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 7.	P51665; Q6PKI2; Q96E97	PSD7_HUMAN
792	IPI00020042; IPI00738042	LOC652826; PSMC4	414	418	416	4.7E+04	4.7E+04	4.7E+04	28.7	9	1	1	0	0	ISOFORM 1 OF 26S PROTEASE REGULATORY SUBUNIT 6B.; SIMILAR TO 26S PROTEASE REGULATORY SUBUNIT 6B.	P43686; Q96FV5; Q9UBM3; Q9UEX3	; PRS6B_HUMAN
793	IPI00020672	BBS1; DPP3	737	737	737	8.3E+04	8.3E+04	8.3E+04	7.2	3	1	1	0	0	ISOFORM 1 OF DIPEPTIDYL-PEPTIDASE 3.	O95748; Q53GT4; Q53HL4; Q5JPB8; Q969H2; Q9BV67; Q9HAL6; Q9NY33	DPP3_HUMAN; Q53GT4_HUMAN; Q53HL4_HUMAN; Q5JPB8_HUMAN
794	IPI00021728; IPI00176637; IPI00793912	EIF2S2; LOC728350	327	333	330	3.8E+04	3.8E+04	3.8E+04	14.1	3	1	1	0	0	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 SUBUNIT 2.; SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR 2 SUBUNIT 2.; EIF2S2 PROTEIN.	P20042; Q3B7I9; Q6IBR8; Q96I16; Q9BVU0; Q9UJE4	; IF2B_HUMAN; Q3B7I9_HUMAN; Q6IBR8_HUMAN; Q96I16_HUMAN
795	IPI00021891; IPI00219713; IPI00411626	FGG	406	453	432	4.6E+04	5.2E+04	4.9E+04	15.9	5	1	1	0	0	ISOFORM GAMMA-B OF FIBRINOGEN GAMMA CHAIN PRECURSOR.; ISOFORM GAMMA-A OF FIBRINOGEN GAMMA CHAIN PRECURSOR.; HYPOTHETICAL PROTEIN DKFZP779N0926.	P02679; P04469; P04470; Q53Y18; Q7Z664; Q96A14; Q96KJ3	FIBG_HUMAN; Q53Y18_HUMAN; Q7Z664_HUMAN
796	IPI00021926	PSMC6	389	389	389	4.4E+04	4.4E+04	4.4E+04	7.5	2	1	1	0	0	26S PROTEASE REGULATORY SUBUNIT S10B.	P49719; P62333; Q6IBU3; Q92524	PRS10_HUMAN
797	IPI00022395	C9	559	559	559	6.3E+04	6.3E+04	6.3E+04	4.1	2	0	1	0	0	COMPLEMENT COMPONENT C9 PRECURSOR.	P02748; Q9UGI4	CO9_HUMAN; Q9UGI4_HUMAN
798	IPI00022538	GENX-3414	358	358	358	3.9E+04	3.9E+04	3.9E+04	14.3	3	0	1	0	0	GENETHONIN-1.	O95210	GET1_HUMAN
799	IPI00022648	EIF5	431	431	431	4.9E+04	4.9E+04	4.9E+04	10.4	4	1	1	0	0	EUKARYOTIC TRANSLATION INITIATION FACTOR 5.	P55010; Q05DF3; Q32Q19; Q53XB3; Q6IBU0; Q9H5N2; Q9UG48	IF5_HUMAN; Q05DF3_HUMAN; Q32Q19_HUMAN; Q53XB3_HUMAN; Q6IBU0_HUMAN
800	IPI00022694	PSMD4	377	377	377	4.1E+04	4.1E+04	4.1E+04	9.3	2	0	1	0	0	ISOFORM RPN10A OF 26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 4.	P55036; Q5VWC5; Q9NS92	PSMD4_HUMAN
801	IPI00022895	A1BG	495	495	495	5.4E+04	5.4E+04	5.4E+04	8.9	3	1	1	0	0	ALPHA-1B-GLYCOPROTEIN PRECURSOR.	P04217; Q8IYJ6; Q96P39	A1BG_HUMAN
802	IPI00023919; IPI00745502	PSMC5	402	406	404	4.5E+04	4.6E+04	4.5E+04	29.8	8	1	1	0	0	26S PROTEASE REGULATORY SUBUNIT 8.; 45 KDA PROTEIN.	O35051; O43208; P47210; P52915; P52916; P62195	; PRS8_HUMAN
803	IPI00024317	GCDH	438	438	438	4.8E+04	4.8E+04	4.8E+04	6.6	2	0	1	0	0	ISOFORM LONG OF GLUTARYL-COA DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.	O14719; Q92947	GCDH_HUMAN
804	IPI00024403	CPNE3	537	537	537	6.0E+04	6.0E+04	6.0E+04	7.3	3	1	1	0	0	COPINE-3.	O75131; Q05DL8; Q8IYA1	CPNE3_HUMAN; Q05DL8_HUMAN
805	IPI00024580; IPI00789136; IPI00792499	MCCC1	434	725	592	4.8E+04	8.0E+04	6.6E+04	11.1	3	0	1	0	0	METHYLCROTONOYL-COA CARBOXYLASE SUBUNIT ALPHA, MITOCHONDRIALPRECURSOR.; 48 KDA PROTEIN.; HYPOTHETICAL PROTEIN DKFZP686B20267.	Q59ES4; Q68D27; Q96RQ3; Q9H959; Q9NS97	; MCCA_HUMAN; Q68D27_HUMAN
806	IPI00024623	ACADSB	432	432	432	4.7E+04	4.7E+04	4.7E+04	11.6	3	1	1	0	0	SHORT/BRANCHED CHAIN SPECIFIC ACYL-COA DEHYDROGENASE, MITOCHONDRIALPRECURSOR.	P45954; Q5SQN6; Q96CX7	ACDSB_HUMAN; Q5SQN6_HUMAN
807	IPI00024934	MUT	750	750	750	8.3E+04	8.3E+04	8.3E+04	9.3	6	1	1	0	0	METHYLMALONYL-COA MUTASE, MITOCHONDRIAL PRECURSOR.	P22033; Q59HB4; Q5SYZ3; Q96B11; Q9UD64	MUTA_HUMAN; Q59HB4_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
808	IPI00026813; IPI00607601; IPI00607790	FNTA	288	379	326	3.5E+04	4.4E+04	3.9E+04	11.2	3	1	1	0	0	PROTEIN FARNESYLTRANSFERASE/GERANYLGERANYLTRANSFERASE TYPE I ALPHASUBUNIT.; FARNESYLTRANSFERASE, CAAX BOX, ALPHA ISOFORM C.; FARNESYLTRANSFERASE, CAAX BOX, ALPHA ISOFORM B.	P49354; Q53XJ9; Q9UDC1	; PFTA_HUMAN; Q53XJ9_HUMAN
809	IPI00028091	ACTR3	418	418	418	4.7E+04	4.7E+04	4.7E+04	16.8	4	1	1	0	0	ACTIN-LIKE PROTEIN 3.	P32391; P61158; Q53QM2; Q59FV6	ARP3_HUMAN; Q53QM2_HUMAN; Q59FV6_HUMAN
810	IPI00028366	SETD7	366	366	366	4.1E+04	4.1E+04	4.1E+04	11.2	3	1	1	0	0	HISTONE-LYSINE N-METHYLTRANSFERASE, H3 LYSINE-4 SPECIFIC SET7.	Q0VAH3; Q4W5A9; Q8WTS6; Q9C0E6	Q4W5A9_HUMAN; SETD7_HUMAN
811	IPI00028369; IPI00784901; IPI00785171	KIAA1715	305	428	385	3.3E+04	4.8E+04	4.3E+04	6.1	2	0	1	0	0	ISOFORM 1 OF PROTEIN LUNAPARK.; ISOFORM 3 OF PROTEIN LUNAPARK.; ISOFORM 2 OF PROTEIN LUNAPARK.	Q2M2V8; Q2YD99; Q658W8; Q8N5V9; Q96MS5; Q9C0E8	LNP_HUMAN
812	IPI00029012	EIF3S10	1382	1382	1382	1.7E+05	1.7E+05	1.7E+05	2.0	2	0	1	0	0	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10.	O00653; Q05BS0; Q14152; Q15778; Q24JU4; Q3B770; Q5T5X0; Q6P1R0; Q7Z5T5	IF3A_HUMAN; Q05BS0_HUMAN; Q24JU4_HUMAN; Q3B770_HUMAN; Q5T5X0_HUMAN; Q6P1R0_HUMAN; Q7Z5T5_HUMAN
813	IPI00029643	ZAK	455	455	455	5.2E+04	5.2E+04	5.2E+04	8.4	3	1	1	0	0	ISOFORM 2 OF MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE MLT.	Q53SX1; Q580W8; Q59GY5; Q86YW8; Q9HCC4; Q9HCC5; Q9HDD2; Q9NYE9; Q9NYL2	MLTK_HUMAN
814	IPI00030320	DDX6	483	483	483	5.4E+04	5.4E+04	5.4E+04	7.5	2	0	1	0	0	PROBABLE ATP-DEPENDENT RNA HELICASE DDX6.	P26196; Q5D048; Q8IV96	DDX6_HUMAN; Q8IV96_HUMAN
815	IPI00031708; IPI00793664	FAH	295	419	357	3.3E+04	4.6E+04	4.0E+04	12.2	4	1	1	0	0	FUMARYLACETOACETASE.; 33 KDA PROTEIN.	P16930; Q53XA7	; FAAA_HUMAN; Q53XA7_HUMAN
816	IPI00031812; IPI00385699; IPI00643351	YBX1	315	374	338	3.5E+04	4.2E+04	3.8E+04	27.5	4	1	1	0	0	NUCLEASE SENSITIVE ELEMENT-BINDING PROTEIN 1.; 35 KDA PROTEIN.; PROTEIN.	A0JLU4; P16990; P16991; P67809; Q05D43; Q14972; Q15325; Q5FVF0; Q6PKI6	; A0JLU4_HUMAN; Q05D43_HUMAN; Q6PKI6_HUMAN; YBOX1_HUMAN
817	IPI00031820	FARSA	508	508	508	5.8E+04	5.8E+04	5.8E+04	5.5	2	0	1	0	0	PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN.	Q6IBR2; Q9NSD8; Q9Y285; Q9Y4W8	Q6IBR2_HUMAN; SYFA_HUMAN
818	IPI00032179	SERPINC1	465	465	465	5.3E+04	5.3E+04	5.3E+04	18.5	5	1	1	0	0	ANTITHROMBIN III VARIANT.	Q5TC78; Q7KYQ5; Q7KYY4; Q7KZ97; Q8IZZ8; Q8IZZ9; Q8J000; Q8J001; Q8TCE1; Q9UBW9; Q9UE54	Q5TC78_HUMAN; Q7KYQ5_HUMAN; Q7KYY4_HUMAN; Q7KZ97_HUMAN; Q8IZZ8_HUMAN; Q8IZZ9_HUMAN; Q8J000_HUMAN; Q8J001_HUMAN; Q8TCE1_HUMAN; Q9UBW9_HUMAN; Q9UE54_HUMAN
819	IPI00033025; IPI00552502; IPI00816201	SEPT7	418	438	431	4.9E+04	5.1E+04	5.0E+04	4.3	2	0	1	0	0	ISOFORM 1 OF SEPTIN-7.; CELL DIVISION CYCLE 10 ISOFORM 2.; ISOFORM 2 OF SEPTIN-7.	Q16181; Q309B3; Q3B7A3; Q3LIE9; Q52M76; Q59EY4; Q5JXL7; Q6NX50; Q8TC62	Q3B7A3_HUMAN; Q3LIE9_HUMAN; Q59EY4_HUMAN; Q5JXL7_HUMAN; Q8TC62_HUMAN; SEPT7_HUMAN
820	IPI00043073; IPI00178745; IPI00298800; IPI00384414	GYPA	85	150	115	9.3E+03	1.6E+04	1.2E+04	29.5	2	1	1	0	0	GLYCOPHORIN ERIK (STA) PRECURSOR.; GLYCOPHORIN MZ II-V.; GLYCOPHORIN A PRECURSOR.; GLYCOPHORIN ERIK I-IV PRECURSOR.	P02724; Q03867; Q03870; Q13030; Q14419; Q14420; Q14421; Q14423; Q14424; Q14438; Q14440; Q14446; Q16308; Q16336; Q58HE6; Q58HE7; Q6WBG7; Q7KZ29; Q8WTS2; Q8WWP1; Q8WWP2; Q8WWP3; Q8WWP4; Q9BS51; Q9BZD9; Q9UM93	GLPA_HUMAN; Q03867_HUMAN; Q03870_HUMAN; Q13030_HUMAN; Q14419_HUMAN; Q14420_HUMAN; Q14421_HUMAN; Q14423_HUMAN; Q14424_HUMAN; Q14438_HUMAN; Q14440_HUMAN; Q14446_HUMAN; Q16308_HUMAN; Q16336_HUMAN; Q58HE6_HUMAN; Q58HE7_HUMAN; Q6WBG7_HUMAN; Q7KZ29_HUMAN; Q8WTS2_HUMAN; Q8WWP1_HUMAN; Q8WWP2_HUMAN; Q8WWP3_HUMAN; Q8WWP4_HUMAN; Q9BZD9_HUMAN; Q9UM93_HUMAN
821	IPI00065491; IPI00748058	STAC3	325	364	345	3.7E+04	4.2E+04	3.9E+04	13.2	5	1	1	0	0	ISOFORM 1 OF SH3 AND CYSTEINE-RICH DOMAIN-CONTAINING PROTEIN 3.; ISOFORM 2 OF SH3 AND CYSTEINE-RICH DOMAIN-CONTAINING PROTEIN 3.	Q96HU5; Q96MF2	STAC3_HUMAN
822	IPI00075080; IPI00219941	OSBPL1A	437	950	694	5.0E+04	1.1E+05	7.9E+04	7.6	3	1	1	0	0	ISOFORM B OF OXYSTEROL-BINDING PROTEIN-RELATED PROTEIN 1.; ISOFORM A OF OXYSTEROL-BINDING PROTEIN-RELATED PROTEIN 1.	Q6DKJ0; Q6GSK5; Q96IZ3; Q9BXW6; Q9BZF5; Q9NW87	OSBL1_HUMAN; Q6DKJ0_HUMAN; Q6GSK5_HUMAN; Q96IZ3_HUMAN
823	IPI00096066	SUCLG2	432	432	432	4.7E+04	4.7E+04	4.7E+04	11.8	5	1	1	0	0	SUCCINYL-COA LIGASE [GDP-FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR.	O95195; Q3ZCW5; Q6NUH7; Q86VX8; Q8WUQ1; Q96I99	Q3ZCW5_HUMAN; SUCB2_HUMAN
824	IPI00100247	TXNDC13	349	349	349	3.9E+04	3.9E+04	3.9E+04	7.2	2	0	1	0	0	THIOREDOXIN DOMAIN-CONTAINING PROTEIN 13 PRECURSOR.	Q8N4P7; Q8NCC1; Q9H1E5; Q9UJA1; Q9ULQ8	TXD13_HUMAN
825	IPI00100292; IPI00168532; IPI00252412; IPI00744937; IPI00746278	NPEPL1; STX16	412	523	487	4.4E+04	5.6E+04	5.2E+04	5.2	2	0	1	0	0	ISOFORM 1 OF PROBABLE AMINOPEPTIDASE NPEPL1.; ISOFORM 3 OF PROBABLE AMINOPEPTIDASE NPEPL1.; ISOFORM 2 OF PROBABLE AMINOPEPTIDASE NPEPL1.; 52 KDA PROTEIN.; 56 KDA PROTEIN.	Q53G37; Q5W083; Q8NDH3; Q8TF28; Q8WUI2; Q9H1T6; Q9HAI5	; PEPL1_HUMAN
826	IPI00101405; IPI00797614	FDPS	353	419	386	4.1E+04	4.8E+04	4.4E+04	7.9	2	0	1	0	0	FARNESYL DIPHOSPHATE SYNTHASE.; FARNESYL PYROPHOSPHATE SYNTHETASE.	P14324; Q96G29	FPPS_HUMAN; Q96G29_HUMAN
827	IPI00105598	PSMD11	423	423	423	4.8E+04	4.8E+04	4.8E+04	18.7	6	1	1	0	0	PROTEASOME 26S NON-ATPASE SUBUNIT 11 VARIANT (FRAGMENT).	Q53FT5	Q53FT5_HUMAN
828	IPI00156689	VAT1	393	393	393	4.2E+04	4.2E+04	4.2E+04	7.9	2	1	1	0	0	SYNAPTIC VESICLE MEMBRANE PROTEIN VAT-1 HOMOLOG.	Q13035; Q5BKZ7; Q96A39; Q99536; Q9BUT8	VAT1_HUMAN
829	IPI00163230	COPS6	327	327	327	3.6E+04	3.6E+04	3.6E+04	9.5	2	1	1	0	0	COP9 SIGNALOSOME COMPLEX SUBUNIT 6.	O15387; Q7L5N1	CSN6_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
830	IPI00164528	SNTA1	505	505	505	5.4E+04	5.4E+04	5.4E+04	11.1	3	0	1	0	0	ALPHA-1-SYNTROPHIN.	Q13424; Q16438; Q29RY0	Q29RY0_HUMAN; SNTA1_HUMAN
831	IPI00165261; IPI00374338; IPI00794956	SCFD1	575	642	620	6.5E+04	7.2E+04	7.0E+04	10.1	4	1	1	0	0	SEC1 FAMILY DOMAIN-CONTAINING PROTEIN 1.; VESICLE TRANSPORT-RELATED PROTEIN ISOFORM B.; VESICLE TRANSPORT-RELATED PROTEIN ISOFORM A VARIANT (FRAGMENT).	O60754; O94990; Q53GW1; Q7Z529; Q8WVM8; Q9BZI3; Q9UNL3; Q9Y6A8	; Q53GW1_HUMAN; SCFD1_HUMAN
832	IPI00166866; IPI00386879	IGHA1	494	499	497	5.3E+04	5.3E+04	5.3E+04	12.6	4	0	1	0	0	IGHA1 PROTEIN.; CDNA FLJ14473 FIS, CLONE MAMMA1001080, HIGHLY SIMILAR TO HOMO SAPIENSSNC73 PROTEIN (SNC73) MRNA.	Q8N5K4; Q96K68	Q8N5K4_HUMAN; Q96K68_HUMAN
833	IPI00167515; IPI00745895	ZADH1	287	351	319	3.2E+04	3.8E+04	3.5E+04	22.3	4	1	1	0	0	ISOFORM 1 OF ZINC-BINDING ALCOHOL DEHYDROGENASE DOMAIN-CONTAININGPROTEIN 1.; SIMILAR TO ZINC BINDING ALCOHOL DEHYDROGENASE, DOMAIN CONTAINING 1.	Q3L8A4; Q6MZH8; Q8N8N7	; Q3L8A4_HUMAN; ZADH1_HUMAN
834	IPI00168407	PDPR	879	879	879	9.9E+04	9.9E+04	9.9E+04	3.4	2	0	1	0	0	HYPOTHETICAL PROTEIN DKFZP686J1643.	Q6AI20; Q6AWC9; Q8NCN5	Q6AI20_HUMAN; Q6AWC9_HUMAN; Q8NCN5_HUMAN
835	IPI00172450; IPI00172452; IPI00216378; IPI00296678; IPI00334344; IPI00336118; IPI00556423; IPI00646849	CAMK2G	495	558	526	5.6E+04	6.3E+04	5.9E+04	12.5	5	1	1	0	0	ISOFORM 4 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II GAMMACHAIN.; CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II GAMMA ISOFORM 6.; CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II GAMMA ISOFORM 1.; CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II GAMMA ISOFORM 2.; ISOFORM 1 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II GAMMACHAIN.; CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II GAMMA ISOFORM 4.; ISOFORM 3 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II GAMMACHAIN.; CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE (CAM KINASE) II GAMMA.	O00561; O15378; Q13279; Q13280; Q13282; Q13555; Q13556; Q5SQZ3; Q5SQZ4; Q5SWX3; Q5SWX4; Q7KYX5; Q8N4I3; Q8NIA4	; KCC2G_HUMAN; O00561_HUMAN; Q13279_HUMAN; Q13280_HUMAN; Q13282_HUMAN; Q5SQZ3_HUMAN; Q5SWX3_HUMAN; Q5SWX4_HUMAN; Q7KYX5_HUMAN; Q8N4I3_HUMAN; Q8NIA4_HUMAN
836	IPI00172636; IPI00430291; IPI00827573; IPI00827606; IPI00827625; IPI00827717; IPI00828081; IPI00828139; IPI00828178	CAMK2D	478	518	499	5.4E+04	5.8E+04	5.6E+04	15.0	5	1	1	0	0	ISOFORM DELTA 6 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IIDELTA CHAIN.; ISOFORM DELTA 2 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IIDELTA CHAIN.; ISOFORM DELTA 10 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPEII DELTA CHAIN.; ISOFORM DELTA 7 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IIDELTA CHAIN.; ISOFORM DELTA 11 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPEII DELTA CHAIN.; ISOFORM DELTA 3 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IIDELTA CHAIN.; ISOFORM DELTA 4 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IIDELTA CHAIN.; ISOFORM DELTA 8 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IIDELTA CHAIN.; ISOFORM DELTA 9 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IIDELTA CHAIN.	Q13557; Q52PK4; Q59G21; Q8N553; Q9UGH6; Q9UQE9	KCC2D_HUMAN
837	IPI00179057; IPI00480142; IPI00643885; IPI00644450	CUL4B	234	917	737	2.8E+04	1.0E+05	8.4E+04	2.1	2	0	1	0	0	ISOFORM 1 OF CULLIN-4B.; ISOFORM 2 OF CULLIN-4B.; 103 KDA PROTEIN.; 28 KDA PROTEIN.	Q13620; Q5JRZ4; Q6PIE4; Q6UP07; Q7Z673; Q9BY37; Q9UEB7; Q9UED7	; CUL4B_HUMAN; Q5JRZ4_HUMAN
838	IPI00179415; IPI00747748	PPP3CA	511	521	516	5.8E+04	5.9E+04	5.8E+04	7.5	3	1	1	0	0	ISOFORM 1 OF SERINE/THREONINE-PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNITALPHA ISOFORM.; ISOFORM 2 OF SERINE/THREONINE-PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNITALPHA ISOFORM.	A1A441; Q08209; Q8TAW9; Q9UMM5	A1A441_HUMAN; PP2BA_HUMAN; Q9UMM5_HUMAN
839	IPI00180675	TUBA1A	451	451	451	5.0E+04	5.0E+04	5.0E+04	41.9	13	1	1	0	0	TUBULIN ALPHA-3 CHAIN.	P04687; P05209; Q71U36; Q9UQM3	Q9UQM3_HUMAN; TBA3_HUMAN
840	IPI00181231; IPI00783302	PTCD3	689	690	690	7.9E+04	7.9E+04	7.9E+04	6.0	3	1	1	0	0	79 KDA PROTEIN.; PENTATRICOPEPTIDE REPEAT DOMAIN 3.	Q597H0; Q658Y9; Q96EY7; Q9BUZ8; Q9NWL0	; Q597H0_HUMAN; Q658Y9_HUMAN; Q96EY7_HUMAN; Q9BUZ8_HUMAN; Q9NWL0_HUMAN
841	IPI00185374; IPI00335069; IPI00787055	PSMD12	397	456	430	4.6E+04	5.3E+04	5.0E+04	14.9	6	1	1	0	0	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 12.; SIMILAR TO PROTEASOME 26S NON-ATPASE SUBUNIT 12 ISOFORM 2.; SIMILAR TO 26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 12.	O00232; Q53HA2; Q6P053	; PSD12_HUMAN
842	IPI00216003	CUL5	837	837	837	9.7E+04	9.7E+04	9.7E+04	11.3	8	1	1	0	0	CULLIN HOMOLOG 5.		
843	IPI00216470	PIP5K2B	416	416	416	4.7E+04	4.7E+04	4.7E+04	5.5	2	0	1	0	0	ISOFORM 1 OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE TYPE-2 BETA.	P78356; Q5U0E8; Q8TBP2	PI52B_HUMAN
844	IPI00216694	PLS3	630	630	630	7.1E+04	7.1E+04	7.1E+04	3.5	2	0	1	0	0	PLASTIN 3.	Q53GY0; Q5JRN9; Q96HI1	Q53GY0_HUMAN; Q5JRN9_HUMAN; Q96HI1_HUMAN
845	IPI00216951	DARS	501	501	501	5.7E+04	5.7E+04	5.7E+04	8.2	3	0	1	0	0	ASPARTYL-TRNA SYNTHETASE, CYTOPLASMIC.	P14868; Q2TNI3; Q32Q69; Q53HV4; Q53R85; Q53T60; Q53YC5; Q68CR9; Q9BW52	Q53R85_HUMAN; Q53T60_HUMAN; Q68CR9_HUMAN; SYDC_HUMAN
846	IPI00218015; IPI00329133	LDHD	484	507	496	5.2E+04	5.5E+04	5.4E+04	5.6	2	1	1	0	0	ISOFORM 2 OF PROBABLE D-LACTATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR.; ISOFORM 1 OF PROBABLE D-LACTATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR.	Q86WU2; Q8IZK5	LDHD_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
847	IPI00218971; IPI00788806; IPI00790255; IPI00794806	PPM2C	537	588	565	6.1E+04	6.7E+04	6.4E+04	10.6	4	0	1	0	0	[PYRUVATE DEHYDROGENASE [LIPOAMIDE]]-PHOSPHATASE 1, MITOCHONDRIALPRECURSOR.; PYRUVATE DEHYDROGENASE PHOSPHATASE PRECURSOR.; 65 KDA PROTEIN.; 67 KDA PROTEIN.	Q5U5K1; Q6P1N1; Q9P0J1	; PDP1_HUMAN; Q6P1N1_HUMAN
848	IPI00219575; IPI00794082	BLMH	279	455	367	3.2E+04	5.3E+04	4.2E+04	10.0	2	1	1	0	0	BLEOMYCIN HYDROLASE.; 32 KDA PROTEIN.	Q13867; Q53F86; Q9UER9	; BLMH_HUMAN
849	IPI00219613; IPI00787827	PITRM1	1037	1038	1038	1.2E+05	1.2E+05	1.2E+05	3.2	2	0	1	0	0	ISOFORM 1 OF PRESEQUENCE PROTEASE, MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF PRESEQUENCE PROTEASE, MITOCHONDRIAL PRECURSOR.	O95204; Q2M2G6; Q4VBR1; Q5JRW7; Q5JRX3; Q7L5Z7; Q9BSI6; Q9BVJ5; Q9UPP8	PREP_HUMAN
850	IPI00220150	IDH3G	393	393	393	4.3E+04	4.3E+04	4.3E+04	21.4	4	1	1	0	0	ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT GAMMA, MITOCHONDRIAL PRECURSOR.	P51553; Q9BUU5	IDH3G_HUMAN
851	IPI00220396	PHKG1	390	390	390	4.5E+04	4.5E+04	4.5E+04	15.6	4	1	1	0	0	PFKFB2 PROTEIN.	Q6NSZ4; Q75LP5	Q6NSZ4_HUMAN; Q75LP5_HUMAN
852	IPI00220637; IPI00514587	SARS	514	536	525	5.9E+04	6.1E+04	6.0E+04	8.0	3	0	1	0	0	SERYL-TRNA SYNTHETASE, CYTOPLASMIC.; SERYL-TRNA SYNTHETASE.	P49591; Q0VGA5; Q53HA4; Q5T5C7; Q5T5C8; Q9NSE3	Q0VGA5_HUMAN; Q53HA4_HUMAN; Q5T5C7_HUMAN; Q5T5C8_HUMAN; SYSC_HUMAN
853	IPI00249656	LOC347273	364	364	364	4.2E+04	4.2E+04	4.2E+04	5.8	2	1	1	0	0	HYPOTHETICAL PROTEIN LOC347273.	Q5BKX8	Q5BKX8_HUMAN
854	IPI00257508	DPYSL2	572	572	572	6.2E+04	6.2E+04	6.2E+04	20.6	6	1	1	0	0	DIHYDROPYRIMIDINASE-RELATED PROTEIN 2.	O00424; Q16555; Q53ET2; Q59GB4; Q8NAN9	DPYL2_HUMAN; Q53ET2_HUMAN; Q59GB4_HUMAN; Q8NAN9_HUMAN
855	IPI00291016	NDUFV3	473	473	473	5.1E+04	5.1E+04	5.1E+04	7.0	2	0	1	0	0	NADH-UBIQUINONE OXIDOREDUCTASE FLAVOPROTEIN 3 ISOFORM A PRECURSOR.	Q8WU60; Q96DP0	Q8WU60_HUMAN; Q96DP0_HUMAN
856	IPI00291262; IPI00400826; IPI00795633	CLU	448	501	466	5.2E+04	5.8E+04	5.4E+04	10.2	3	0	1	0	0	CLUSTERIN PRECURSOR.; CLUSTERIN ISOFORM 1.; 52 KDA PROTEIN.	P10909; P11380; P11381; Q2TU75; Q5HYC1; Q7Z5B9	; CLUS_HUMAN; Q2TU75_HUMAN
857	IPI00291510	IMPDH2	514	514	514	5.6E+04	5.6E+04	5.6E+04	17.1	6	1	1	0	0	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 2.	P12268; Q6LEF3	IMDH2_HUMAN
858	IPI00291972	RTN4IP1	396	396	396	4.4E+04	4.4E+04	4.4E+04	5.6	2	0	1	0	0	ISOFORM 1 OF RETICULON-4-INTERACTING PROTEIN 1, MITOCHONDRIALPRECURSOR.	Q8N9B3; Q8WWV3; Q8WZ66; Q9BRA4	RT4I1_HUMAN
859	IPI00293307	ADFP	437	437	437	4.8E+04	4.8E+04	4.8E+04	11.2	3	1	1	0	0	ADIPOPHILIN.	Q6FHZ7; Q99541; Q9BSC3	ADFP_HUMAN; Q6FHZ7_HUMAN
860	IPI00293616	DDX3Y	660	660	660	7.3E+04	7.3E+04	7.3E+04	5.2	2	0	1	0	0	ATP-DEPENDENT RNA HELICASE DDX3Y.	O15523; Q8IYV7	DDX3Y_HUMAN
861	IPI00293655	DDX1	740	740	740	8.2E+04	8.2E+04	8.2E+04	11.2	5	1	1	0	0	ATP-DEPENDENT RNA HELICASE DDX1.	Q92499	DDX1_HUMAN
862	IPI00294158	BLVRA	296	296	296	3.3E+04	3.3E+04	3.3E+04	17.6	4	1	1	0	0	BILIVERDIN REDUCTASE A PRECURSOR.	O95019; P53004; Q86UX0; Q96QL4; Q9BRW8	BIEA_HUMAN
863	IPI00295992; IPI00643435; IPI00646144	ATAD3A	572	634	597	6.4E+04	7.1E+04	6.7E+04	5.3	3	0	1	0	0	ISOFORM 2 OF ATPASE FAMILY AAA DOMAIN-CONTAINING PROTEIN 3A.; ISOFORM 1 OF ATPASE FAMILY AAA DOMAIN-CONTAINING PROTEIN 3A.; ATPASE FAMILY, AAA DOMAIN CONTAINING 3A.	Q5SV23; Q5SV24; Q8N275; Q96A50; Q9NVI7	ATD3A_HUMAN; Q5SV24_HUMAN
864	IPI00297982	EIF2S3	472	472	472	5.1E+04	5.1E+04	5.1E+04	8.7	2	1	1	0	0	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 SUBUNIT 3.	P41091; Q2VIR3; Q53HK3	IF2G_HUMAN; Q2VIR3_HUMAN; Q53HK3_HUMAN
865	IPI00298887; IPI00306436; IPI00412752; IPI00784414	STAT3	722	773	759	8.3E+04	8.8E+04	8.7E+04	5.1	2	1	1	0	0	88 KDA PROTEIN.; ISOFORM DEL-701 OF SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 3.; SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 3 ISOFORM 3.; ISOFORM 1 OF SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 3.	O14916; P40763; Q9BW54; Q9BXH2	; Q9BXH2_HUMAN; STAT3_HUMAN
866	IPI00299240; IPI00514837; IPI00642897	CACNA1S	1856	1875	1868	2.1E+05	2.1E+05	2.1E+05	1.7	2	0	1	0	0	VOLTAGE-DEPENDENT L-TYPE CALCIUM CHANNEL SUBUNIT ALPHA-1S.; CALCIUM CHANNEL, VOLTAGE-DEPENDENT, L TYPE, ALPHA 1S SUBUNIT.; CALCIUM CHANNEL, VOLTAGE-DEPENDENT, L TYPE, ALPHA 1S SUBUNIT.	Q12966; Q13062; Q5T4J6; Q5T4J7	; Q12966_HUMAN; Q13062_HUMAN; Q5T4J6_HUMAN; Q5T4J7_HUMAN
867	IPI00299571; IPI00644989	PDIA6	440	492	466	4.8E+04	5.4E+04	5.1E+04	16.1	5	1	1	0	0	ISOFORM 2 OF PROTEIN DISULFIDE-ISOMERASE A6 PRECURSOR.; ISOFORM 1 OF PROTEIN DISULFIDE-ISOMERASE A6 PRECURSOR.	Q15084; Q53RC7; Q6ZSH5; Q99778	PDIA6_HUMAN; Q53RC7_HUMAN
868	IPI00303120	TMEM143	459	459	459	5.2E+04	5.2E+04	5.2E+04	17.2	6	1	1	0	0	TRANSMEMBRANE PROTEIN 143.	Q96AN5	Q96AN5_HUMAN
869	IPI00303200	TMOD4	345	345	345	3.9E+04	3.9E+04	3.9E+04	24.1	6	1	1	0	0	TROPOMODULIN-4.	Q5JR83; Q8WVL3; Q9NZQ9; Q9UKH2	Q5JR83_HUMAN; TMOD4_HUMAN
870	IPI00304803	GMPR	345	345	345	3.7E+04	3.7E+04	3.7E+04	9.9	3	1	1	0	0	GMP REDUCTASE 1.	P36959; Q96HQ6	GMPR1_HUMAN
871	IPI00329600; IPI00641681	SCCPDH	241	429	335	2.6E+04	4.7E+04	3.7E+04	11.6	3	1	1	0	0	PROBABLE SACCHAROPINE DEHYDROGENASE.; SACCHAROPINE DEHYDROGENASE.	Q5VTK4; Q8NBX0; Q8TAR0; Q9Y363	Q5VTK4_HUMAN; SCPDH_HUMAN
872	IPI00329633	TARS	723	723	723	8.3E+04	8.3E+04	8.3E+04	3.2	2	0	1	0	0	THREONYL-TRNA SYNTHETASE, CYTOPLASMIC.	P26639; Q53GX7; Q5M7Z9; Q96FP5; Q9BWA6	Q53GX7_HUMAN; Q5M7Z9_HUMAN; SYTC_HUMAN
873	IPI00329653; IPI00384529; IPI00807589; IPI00807621; IPI00807645	COBL	379	1343	933	4.2E+04	1.4E+05	1.0E+05	3.5	3	1	1	0	0	ISOFORM 5 OF PROTEIN CORDON-BLEU.; ISOFORM 1 OF PROTEIN CORDON-BLEU.; ISOFORM 2 OF PROTEIN CORDON-BLEU.; ISOFORM 3 OF PROTEIN CORDON-BLEU.; ISOFORM 4 OF PROTEIN CORDON-BLEU.	O75128; Q2T9J3; Q504Y4; Q86XA7; Q8N304; Q8TCM1	COBL_HUMAN; Q8TCM1_HUMAN
874	IPI00333619; IPI00394758	ALDH3A2	485	508	497	5.5E+04	5.8E+04	5.6E+04	11.6	4	1	1	0	0	ISOFORM 1 OF FATTY ALDEHYDE DEHYDROGENASE.; ISOFORM 2 OF FATTY ALDEHYDE DEHYDROGENASE.	P51648; Q59H65; Q68D64; Q6I9T3; Q93011; Q96J37	AL3A2_HUMAN; Q59H65_HUMAN; Q68D64_HUMAN; Q6I9T3_HUMAN
875	IPI00383947	KBTBD5	621	621	621	6.9E+04	6.9E+04	6.9E+04	5.8	3	1	1	0	0	ISOFORM 1 OF KELCH REPEAT AND BTB DOMAIN-CONTAINING PROTEIN 5.	Q2TBA0; Q86SI1; Q96MR2	KBTB5_HUMAN

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
876	IPI00396485; IPI00472724	EEF1A1	462	462	462	5.0E+04	5.0E+04	5.0E+04	23.6	9	1	1	0	0	ELONGATION FACTOR 1-ALPHA 1.; EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 ALPHA-LIKE 3.	P04719; P04720; P68104; Q16577; Q53G85; Q53G89; Q53GA1; Q53GE9; Q53HM9; Q53HQ7; Q53HR1; Q53HR5; Q5VTE0; Q6IPN6; Q6IPS9; Q6IPT9; Q6IQ15; Q6P082; Q6P4C9; Q8IUB0; Q8TBL1; Q96C29; Q96CD8; Q96EB3; Q96RE1; Q9H2I7; Q9NZS6	EF1A1_HUMAN; Q16577_HUMAN; Q53G85_HUMAN; Q53G89_HUMAN; Q53GA1_HUMAN; Q53GE9_HUMAN; Q53HM9_HUMAN; Q53HQ7_HUMAN; Q53HR1_HUMAN; Q53HR5_HUMAN; Q5VTE0_HUMAN; Q6IPN6_HUMAN; Q6IPS9_HUMAN; Q6IPT9_HUMAN; Q6IQ15_HUMAN; Q6P082_HUMAN; Q6P4C9_HUMAN; Q8IUB0_HUMAN; Q8TBL1_HUMAN; Q96C29_HUMAN; Q96CD8_HUMAN; Q96EB3_HUMAN; Q96RE1_HUMAN; Q9H2I7_HUMAN; Q9NZS6_HUMAN
877	IPI00399036; IPI00411639; IPI00413108; IPI00553164; IPI00790580	LOC388524; RPSA; RPSAP15; hCG_1984468	147	300	266	1.6E+04	3.3E+04	3.0E+04	19.0	5	1	1	0	0	SIMILAR TO 40S RIBOSOMAL PROTEIN SA (P40) (34/67 KDA LAMININ RECEPTOR)(COLON CARCINOMA LAMININ-BINDING PROTEIN) (NEM/1CHD4) (MULTIDRUGRESISTANCE-ASSOCIATED PROTEIN MGR1-AG) ISOFORM 1.; LAMININ RECEPTOR-LIKE PROTEIN LAMRL5.; RIBOSOMAL PROTEIN SA.; 40S RIBOSOMAL PROTEIN SA.; 16 KDA PROTEIN.	P08865; P11085; P12030; Q16471; Q6IPD1; Q6IPD2; Q6NSD1; Q6NXQ8; Q86VC0; Q96RS2	; Q6NSD1_HUMAN; Q6NXQ8_HUMAN; Q86VC0_HUMAN; Q96RS2_HUMAN; RSSA_HUMAN
878	IPI00413451	SERPINB6	409	409	409	4.6E+04	4.6E+04	4.6E+04	21.5	6	1	1	0	0	HYPOTHETICAL PROTEIN DKFZP686I04222.	Q59F97; Q7Z2Y7	Q59F97_HUMAN; Q7Z2Y7_HUMAN
879	IPI00418497; IPI00656071	TIMM50	353	456	405	4.0E+04	5.0E+04	4.5E+04	8.1	3	1	1	0	0	ISOFORM 2 OF IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM50,MITOCHONDRIAL PRECURSOR.; ISOFORM 1 OF IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM50,MITOCHONDRIAL PRECURSOR.	Q0VAB1; Q330K1; Q3ZCQ8; Q6QA00; Q96FJ5; Q96GY2; Q9H370	Q0VAB1_HUMAN; Q330K1_HUMAN; TIM50_HUMAN
880	IPI00419237; IPI00789806	LAP3	488	519	504	5.3E+04	5.6E+04	5.4E+04	20.4	8	1	1	0	0	ISOFORM 1 OF CYTOSOL AMINOPEPTIDASE.; ISOFORM 2 OF CYTOSOL AMINOPEPTIDASE.	P28838; Q6IAM6; Q6P0L6; Q9UQE3	AMPL_HUMAN
881	IPI00419263; IPI00639841; IPI00827665	PECI	195	394	316	2.2E+04	4.4E+04	3.5E+04	18.1	4	1	1	0	0	PEROXISOMAL 3,2-TRANS-ENOYL-COA ISOMERASE.; PEROXISOMAL 3,2-TRANS-ENOYL-COA ISOMERASE.; 22 KDA PROTEIN.	O75521; Q53GC8; Q53HG3; Q59E94; Q5JYK5; Q5JYK7; Q6IBN4; Q7L124; Q8N0X0; Q9BUE9; Q9H0T9; Q9NQH1; Q9NYD2; Q9NYH7; Q9UN55	; PECI_HUMAN; Q53GC8_HUMAN; Q53HG3_HUMAN; Q59E94_HUMAN; Q5JYK7_HUMAN; Q6IBN4_HUMAN; Q7L124_HUMAN; Q9NYD2_HUMAN
882	IPI00423426; IPI00423430	EPM2A	331	331	331	3.7E+04	3.7E+04	3.7E+04	9.7	2	1	1	0	0	ISOFORM 1 OF LAFORIN.; ISOFORM 3 OF LAFORIN.	O95278; O95483; Q5THQ4; Q6IS15; Q8IU96; Q8IX24; Q8IX25; Q9BS66; Q9UEN2	EPM2A_HUMAN; Q5THQ4_HUMAN; Q6IS15_HUMAN
883	IPI00427586; IPI00436355	PRKG1	671	686	679	7.6E+04	7.8E+04	7.7E+04	7.0	3	1	1	0	0	CGMP-DEPENDENT PROTEIN KINASE 1, ALPHA ISOZYME.; CGMP-DEPENDENT PROTEIN KINASE 1, BETA ISOZYME.	P14619; Q13976; Q5JSJ6; Q5SQU3; Q6P5T7	KGP1A_HUMAN; KGP1B_HUMAN; Q5SQU3_HUMAN; Q6P5T7_HUMAN
884	IPI00444179; IPI00787636	LSDP5	463	524	494	5.1E+04	5.7E+04	5.4E+04	6.3	2	0	1	0	0	LIPID STORAGE DROPLET PROTEIN 5.; LIPID STORAGE DROPLET PROTEIN 5.	A2RRC1; Q00G26	; A2RRC1_HUMAN; Q00G26_HUMAN
885	IPI00449049	PARP1	1014	1014	1014	1.1E+05	1.1E+05	1.1E+05	2.8	2	1	1	0	0	POLY [ADP-RIBOSE] POLYMERASE 1.	P09874; Q05D33; Q5VX86; Q6PJL0; Q8IUZ9; Q96P95	PARP1_HUMAN; Q05D33_HUMAN; Q5VX86_HUMAN; Q6PJL0_HUMAN; Q96P95_HUMAN
886	IPI00465233; IPI00745266	EIF3S6IP	564	607	586	6.7E+04	7.1E+04	6.9E+04	5.1	2	0	1	0	0	DJ1014D13.1 PROTEIN.; EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 6-INTERACTINGPROTEIN.	Q53HQ1; Q53HT4; Q5QTR1; Q5TI15; Q6ICD2; Q7Z5X3; Q8N7H0; Q9Y262	IF3I_HUMAN; Q53HQ1_HUMAN; Q53HT4_HUMAN; Q5QTR1_HUMAN; Q5TI15_HUMAN; Q6ICD2_HUMAN; Q7Z5X3_HUMAN; Q8N7H0_HUMAN
887	IPI00465430; IPI00644712	XRCC6	609	609	609	7.0E+04	7.0E+04	7.0E+04	11.2	5	1	1	0	0	70 KDA PROTEIN.; ATP-DEPENDENT DNA HELICASE 2 SUBUNIT 1.	P12956; Q6FG89; Q6IC76; Q9UCQ2; Q9UCQ3	; KU70_HUMAN; Q6FG89_HUMAN; Q6IC76_HUMAN
888	IPI00477616	PPP2R4	373	373	373	4.2E+04	4.2E+04	4.2E+04	6.2	2	1	1	0	0	REGULATORY SUBUNIT PR 53 OF PROTEIN PHOSPHATASE 2A ISOFORM B.		
889	IPI00479186	PKM2	531	531	531	5.8E+04	5.8E+04	5.8E+04	63.7	46	1	1	0	0	ISOFORM M2 OF PYRUVATE KINASE ISOZYMES M1/M2.	P14618; P14786; Q53GK4; Q8WUW7; Q96E76; Q9BWB5; Q9NYI7; Q9UK31; Q9UKK4; Q9UPF2	KPYM_HUMAN; Q53GK4_HUMAN; Q8WUW7_HUMAN; Q9NYI7_HUMAN; Q9UK31_HUMAN; Q9UKK4_HUMAN
890	IPI00479217; IPI00644079; IPI00644224	HNRPU	549	825	727	6.2E+04	9.1E+04	8.0E+04	6.1	3	0	1	0	0	ISOFORM SHORT OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN U.; HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN U ISOFORM A.; HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN U.	O75507; Q00839; Q5RI17; Q5RI19; Q7Z4Q5; Q8N174; Q96BA7; Q96HY9;	HNRPU_HUMAN; Q5RI17_HUMAN; Q5RI19_HUMAN; Q7Z4Q5_HUMAN; Q96BA7_HUMAN; Q9UEL2_HUMAN
891	IPI00549672	PSMD13	377	377	377	4.3E+04	4.3E+04	4.3E+04	19.1	5	1	1	0	0	HSPC027.	Q53GN6; Q53XU2; Q9Y6E3	Q53GN6_HUMAN; Q53XU2_HUMAN; Q9Y6E3_HUMAN
892	IPI00550689	C22orf28	505	505	505	5.5E+04	5.5E+04	5.5E+04	5.0	2	0	1	0	0	UPF0027 PROTEIN C22ORF28.	Q6IAI0; Q9BWL4; Q9NTH1; Q9P037; Q9P0J3; Q9Y3I0	CV028_HUMAN
893	IPI00550852	DCTN4	460	460	460	5.2E+04	5.2E+04	5.2E+04	5.9	2	0	1	0	0	DYNACTIN SUBUNIT 4.	Q8TAN8; Q9NSJ5; Q9UJW0	DCTN4_HUMAN; Q9NSJ5_HUMAN
894	IPI00641829	ATP6V1G2; BAT1	443	443	443	5.1E+04	5.1E+04	5.1E+04	7.7	3	1	1	0	0	BAT1 PROTEIN.	Q0EFA1; Q2L6F9; Q53GL9	Q0EFA1_HUMAN; Q2L6F9_HUMAN; Q53GL9_HUMAN
895	IPI00643525	C4A	1744	1744	1744	1.9E+05	1.9E+05	1.9E+05	13.1	15	1	1	0	0	COMPLEMENT COMPONENT 4A.	Q5JNX2; Q6U2F6	Q5JNX2_HUMAN; Q6U2F6_HUMAN
896	IPI00643920; IPI00788802; IPI00789310; IPI00792641; IPI00793119	TKT	339	623	497	3.7E+04	6.8E+04	5.4E+04	6.4	2	0	1	0	0	TRANSKETOLASE.; TRANSKETOLASE VARIANT (FRAGMENT).; 37 KDA PROTEIN.; HYPOTHETICAL PROTEIN DKFZP686J13123.; 39 KDA PROTEIN.	P29401; Q53EM5; Q6MZE3; Q8TBA3; Q96HH3	; Q53EM5_HUMAN; Q6MZE3_HUMAN; TKT_HUMAN
897	IPI00646909; IPI00791613	TUBA8	449	467	458	5.0E+04	5.2E+04	5.1E+04	37.6	12	1	1	0	0	TUBULIN ALPHA-8 CHAIN.; 52 KDA PROTEIN.	Q2M3N4; Q9NY65	; TBA8_HUMAN

Protein Group[2]	IPI ID	IPI gene name	Amino Acids in Sequence[1]			Protein Molecular Weight[1]			Seq. Cov. (max)	Unique Peptides (max)	Detection				Protein name	Uniprot Id	Uniprot Entry Name
			Min.	Max.	Mean	Min.	Max.	Mean			Expt. I-1	Expt. I-2	Expt. II	Expt. iii			
898	IPI00647400	RNPEP	611	611	611	6.8E+04	6.8E+04	6.8E+04	6.4	3	0	1	0	0	68 KDA PROTEIN.		
899	IPI00654777	EIF3S5	372	372	372	3.9E+04	3.9E+04	3.9E+04	23.1	7	1	1	0	0	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 5.	Q6IB45	Q6IB45_HUMAN
900	IPI00742905	DHX9	1315	1315	1315	1.5E+05	1.5E+05	1.5E+05	2.4	2	0	1	0	0	ATP-DEPENDENT RNA HELICASE A.	Q05CI5; Q12803; Q32Q22; Q58F26; Q6PJK6	Q05CI5_HUMAN; Q12803_HUMAN; Q32Q22_HUMAN; Q58F26_HUMAN; Q6PJK6_HUMAN
901	IPI00743654	NEB	3007	3007	3007	3.5E+05	3.5E+05	3.5E+05	2.2	5	0	1	0	0	NEBULIN (FRAGMENT).	Q14215	Q14215_HUMAN
902	IPI00747849; IPI00816734	ATP1B1	301	305	303	3.5E+04	3.5E+04	3.5E+04	8.3	2	1	1	0	0	ISOFORM 1 OF SODIUM/POTASSIUM-TRANSPORTING ATPASE SUBUNIT BETA-1.; ISOFORM 2 OF SODIUM/POTASSIUM-TRANSPORTING ATPASE SUBUNIT BETA-1.	P05026; Q58I20; Q5TGZ3; Q6LEU2	AT1B1_HUMAN; Q58I20_HUMAN; Q6LEU2_HUMAN
903	IPI00791485	CORO6	542	542	542	6.0E+04	6.0E+04	6.0E+04	6.6	3	1	1	0	0	ISOFORM 1 OF CORONIN-6.		
904	IPI00007247; IPI00387103	PCCB	302	539	421	3.3E+04	5.8E+04	4.6E+04	6.1	2	1	0	0	0	PROPIONYL-COA CARBOXYLASE BETA CHAIN, MITOCHONDRIAL PRECURSOR.; HYPOTHETICAL PROTEIN.	P05166; Q16813; Q59GV0; Q8WVH4; Q96CX0; Q9HBR7	PCCB_HUMAN; Q59GV0_HUMAN; Q8WVH4_HUMAN; Q9HBR7_HUMAN
905	IPI00008483	MAOA	527	527	527	6.0E+04	6.0E+04	6.0E+04	7.0	2	1	0	0	0	AMINE OXIDASE [FLAVIN-CONTAINING] A.	P21397; Q16426; Q49A63; Q53EZ0; Q5HYP1; Q5UL91; Q5UL94; Q5ULA3; Q5ULA9	AOFA_HUMAN; Q49A63_HUMAN; Q53EZ0_HUMAN; Q5HYP1_HUMAN; Q5UL91_HUMAN; Q5UL94_HUMAN; Q5ULA3_HUMAN; Q5ULA9_HUMAN
906	IPI00009771	LMNB2	620	620	620	7.0E+04	7.0E+04	7.0E+04	3.4	2	1	0	0	0	LAMIN B2.		
907	IPI00010346	NLN	704	704	704	8.1E+04	8.1E+04	8.1E+04	5.5	3	1	0	0	0	NEUROLYSIN, MITOCHONDRIAL PRECURSOR.	Q8NDD9; Q96K48; Q9BYT8; Q9ULJ4	NEUL_HUMAN; Q8NDD9_HUMAN; Q96K48_HUMAN
908	IPI00011916	JTV1	320	320	320	3.5E+04	3.5E+04	3.5E+04	10.6	2	1	0	0	0	MULTISYNTHETASE COMPLEX AUXILIARY COMPONENT P38.	Q13155; Q75MR1; Q96CZ5; Q9P1L2	MCA2_HUMAN; Q75MR1_HUMAN
909	IPI00013881; IPI00026230; IPI00479191	HNRPH1; HNRPH2	449	472	457	4.9E+04	5.1E+04	5.0E+04	7.4	2	1	0	0	0	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H.; HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H'.; HNRPH1 PROTEIN.	A1L400; P31943; P55795; Q68DG4; Q6IBM4; Q9HHA7	A1L400_HUMAN; HNRH1_HUMAN; HNRH2_HUMAN; Q68DG4_HUMAN; Q6IBM4_HUMAN
910	IPI00019502	MYH9	1960	1960	1960	2.3E+05	2.3E+05	2.3E+05	1.7	2	1	0	0	0	MYOSIN-9.	O60805; P35579; Q60FE2; Q86XU5; Q99529	MYH9_HUMAN; Q60FE2_HUMAN; Q86XU5_HUMAN; Q99529_HUMAN
911	IPI00019568; IPI00784409	F2	622	622	622	7.0E+04	7.0E+04	7.0E+04	3.7	2	1	0	0	0	PROTHROMBIN PRECURSOR (FRAGMENT).; 70 KDA PROTEIN.	P00734; Q15253; Q4QZ40; Q53H04; Q53H06; Q69EZ8; Q7Z7P3; Q86WA1; Q8TD58	; Q15253_HUMAN; Q4QZ40_HUMAN; Q53H04_HUMAN; Q53H06_HUMAN; Q69EZ8_HUMAN; Q7Z7P3_HUMAN; Q86WA1_HUMAN; Q8TD58_HUMAN; THRB_HUMAN
912	IPI00020567	ARHGAP1	439	439	439	5.0E+04	5.0E+04	5.0E+04	6.8	2	1	0	0	0	RHO GTPASE-ACTIVATING PROTEIN 1.	Q07960	RHG01_HUMAN
913	IPI00021301; IPI00790886	ASPA	260	313	287	3.0E+04	3.6E+04	3.3E+04	8.0	2	1	0	0	0	ASPARTOACYLASE.; 30 KDA PROTEIN.	P45381; Q6FH48	; ACY2_HUMAN; Q6FH48_HUMAN
914	IPI00022371	HRG	525	525	525	6.0E+04	6.0E+04	6.0E+04	7.4	3	1	0	0	0	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.	P04196; Q68DR3	HRG_HUMAN; Q68DR3_HUMAN
915	IPI00022697; IPI00794194; IPI00794224; IPI00797141	DRG2	172	364	281	1.8E+04	4.1E+04	3.1E+04	8.5	2	1	0	0	0	DEVELOPMENTALLY-REGULATED GTP-BINDING PROTEIN 2.; 38 KDA PROTEIN.; 18 KDA PROTEIN.; 27 KDA PROTEIN.	P55039; Q53Y50; Q9BWB2	; DRG2_HUMAN; Q53Y50_HUMAN
916	IPI00023006	ACTC1	377	377	377	4.2E+04	4.2E+04	4.2E+04	65.0	33	1	0	0	0	ACTIN, ALPHA CARDIAC MUSCLE 1.	P04270; P68032	ACTC_HUMAN
917	IPI00024990	ALDH6A1	535	535	535	5.8E+04	5.8E+04	5.8E+04	5.8	2	1	0	0	0	METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE [ACYLATING], MITOCHONDRIALPRECURSOR.	O43573; Q02252; Q53FN8; Q53H94; Q9UKM8	MMSA_HUMAN; O43573_HUMAN; Q53FN8_HUMAN; Q53H94_HUMAN
918	IPI00025721	COPS3	423	423	423	4.8E+04	4.8E+04	4.8E+04	9.5	2	1	0	0	0	COP9 SIGNALOSOME COMPLEX SUBUNIT 3.	O43191; Q7LDR6; Q9UNS2	CSN3_HUMAN
919	IPI00026516	OXCT1	520	520	520	5.6E+04	5.6E+04	5.6E+04	9.0	3	1	0	0	0	SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE 1, MITOCHONDRIALPRECURSOR.	A1E286; P55809; Q6IAV5	A1E286_HUMAN; Q6IAV5_HUMAN; SCOT_HUMAN
920	IPI00026942	ERLIN2	347	347	347	3.9E+04	3.9E+04	3.9E+04	8.4	2	1	0	0	0	SPFH2 PROTEIN (FRAGMENT).	A0JLQ1	A0JLQ1_HUMAN
921	IPI00027258; IPI00413058; IPI00413060	SYNPO	685	929	839	7.4E+04	9.9E+04	9.0E+04	3.5	2	1	0	0	0	ISOFORM 2 OF SYNAPTOPODIN.; ISOFORM 1 OF SYNAPTOPODIN.; ISOFORM 3 OF SYNAPTOPODIN.	O15271; Q71HJ6; Q8N3V7; Q9UPX1	Q71HJ6_HUMAN; SYNPO_HUMAN
922	IPI00027444	SERPINB1	379	379	379	4.3E+04	4.3E+04	4.3E+04	7.7	2	1	0	0	0	LEUKOCYTE ELASTASE INHIBITOR.	P30740; Q53FB9; Q5W0E1	ILEU_HUMAN
923	IPI00028635; IPI00383680; IPI00552307; IPI00552972; IPI00789816	RPN2	506	647	603	5.6E+04	7.1E+04	6.6E+04	5.1	2	1	0	0	0	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 63 KDASUBUNIT PRECURSOR.; RIBOPHORIN II.; RIBOPHORIN II.; 56 KDA PROTEIN.; 71 KDA PROTEIN.	Q5JYR3; Q5JYR6	; Q5JYR3_HUMAN; Q5JYR6_HUMAN
924	IPI00029485	DCTN1	1278	1278	1278	1.4E+05	1.4E+05	1.4E+05	4.5	3	1	0	0	0	ISOFORM P150 OF DYNACTIN-1.	O95296; Q14203; Q6MZZ3; Q9BRM9; Q9UIU1; Q9UIU2	DYNA_HUMAN; Q6MZZ3_HUMAN
925	IPI00031618; IPI00796836	DDI2; RSC1A1	419	1022	721	4.7E+04	1.1E+05	7.9E+04	7.9	2	1	0	0	0	PROTEIN DDI1 HOMOLOG 2.; 112 KDA PROTEIN.	Q5TDH0; Q7RTZ0; Q9BRT1	; Q5TDH0_HUMAN; Q7RTZ0_HUMAN; Q9BRT1_HUMAN
926	IPI00166642	D2HGDH	521	521	521	5.6E+04	5.6E+04	5.6E+04	3.5	2	1	0	0	0	ISOFORM 1 OF D-2-HYDROXYGLUTARATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR.	Q6IQ24; Q8N465; Q8N5Q8	D2HDH_HUMAN
927	IPI00179291; IPI00645898; IPI00793375	XPNPEP1	552	666	614	6.2E+04	7.5E+04	6.9E+04	5.0	2	1	0	0	0	ISOFORM 1 OF XAA-PRO AMINOPEPTIDASE 1.; X-PROLYL AMINOPEPTIDASE (AMINOPEPTIDASE P) 1, SOLUBLE.; CYTOSOLIC AMINOPEPTIDASE P.	O15250; Q53EX6; Q5T6H7; Q8N3Q0; Q96D23; Q9NQW7	; Q5T6H7_HUMAN; XPP1_HUMAN
928	IPI00215610	MPP1	466	466	466	5.2E+04	5.2E+04	5.2E+04	6.4	2	1	0	0	0	55 KDA ERYTHROCYTE MEMBRANE PROTEIN.	Q00013; Q2TSB6; Q53F93; Q5J7V5	EM55_HUMAN; Q2TSB6_HUMAN; Q53F93_HUMAN; Q5J7V5_HUMAN
929	IPI00215637	DDX3X	662	662	662	7.3E+04	7.3E+04	7.3E+04	5.4	3	1	0	0	0	ATP-DEPENDENT RNA HELICASE DDX3X.	O00571; O15536; Q59GX6; Q5JSI3; Q5S4N1	DDX3X_HUMAN; Q59GX6_HUMAN; Q5JSI3_HUMAN; Q5S4N1_HUMAN
930	IPI00218857; IPI00218858; IPI00220438	MAP2K3	318	352	339	3.6E+04	4.0E+04	3.8E+04	8.0	2	1	0	0	0	ISOFORM 1 OF DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE3.; ISOFORM 2 OF DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE3.; ISOFORM 3 OF DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE3.	P46734; Q53EZ9; Q6FHG1; Q6FI23; Q99441; Q9UE71; Q9UE72	MP2K3_HUMAN; Q53EZ9_HUMAN; Q6FHG1_HUMAN; Q6FI23_HUMAN
931	IPI00220271	AKR1A1	325	325	325	3.7E+04	3.7E+04	3.7E+04	18.8	4	1	0	0	0	ALCOHOL DEHYDROGENASE.	P14550; Q6IAZ4	AK1A1_HUMAN; Q6IAZ4_HUMAN
932	IPI00221234; IPI00786942	ALDH7A1	539	549	544	5.8E+04	5.9E+04	5.9E+04	7.8	3	1	0	0	0	SIMILAR TO ALDEHYDE DEHYDROGENASE FAMILY 7 MEMBER A1.; SIMILAR TO ANTIQUITIN.		

			Amino Acids in Sequence[1]			Protein Molecular Weight[1]					Detection						
Protein Group[2]	IPI ID	IPI gene name	Min.	Max.	Mean	Min.	Max.	Mean	Seq. Cov. (max)	Unique Peptides (max)	Expt. I-1	Expt. I-2	Expt. II	Expt. iii	Protein name	Uniprot Id	Uniprot Entry Name
933	IPI00291165; IPI00744711	PNPT1	783	785	784	8.6E+04	8.6E+04	8.6E+04	3.4	2	1	0	0	0	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE 1, MITOCHONDRIAL PRECURSOR.; 86 KDA PROTEIN.	Q53SU0; Q68CN1; Q7Z7D1; Q8IWX1; Q8TCS8; Q96T05; Q9BRU3; Q9BVX0	; PNPT1_HUMAN
934	IPI00294578	TGM2	687	687	687	7.7E+04	7.7E+04	7.7E+04	4.2	2	1	0	0	0	ISOFORM 1 OF PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE 2.	P21980; Q16436; Q6B838; Q6DKH2; Q6ZTL3; Q9BTN7; Q9UH35	Q6B838_HUMAN; Q6DKH2_HUMAN; Q6ZTL3_HUMAN; TGM2_HUMAN
935	IPI00296283	MAPK12	367	367	367	4.2E+04	4.2E+04	4.2E+04	10.6	3	1	0	0	0	MITOGEN-ACTIVATED PROTEIN KINASE 12.	P53778; Q14260; Q6IC53; Q6N076; Q99588; Q99672	MK12_HUMAN; Q6IC53_HUMAN; Q6N076_HUMAN
936	IPI00298237; IPI00554538; IPI00554617	TPP1	320	563	480	3.4E+04	6.1E+04	5.2E+04	5.0	2	1	0	0	0	ISOFORM 1 OF TRIPEPTIDYL-PEPTIDASE 1 PRECURSOR.; ISOFORM 3 OF TRIPEPTIDYL-PEPTIDASE 1 PRECURSOR.; ISOFORM 2 OF TRIPEPTIDYL-PEPTIDASE 1 PRECURSOR.	O14773; Q53HP2; Q53HT1; Q5JAK6; Q6UX56; Q96C37	Q53HP2_HUMAN; TPP1_HUMAN
937	IPI00298520; IPI00514053	ARCN1	511	552	532	5.7E+04	6.2E+04	5.9E+04	4.2	2	1	0	0	0	HYPOTHETICAL PROTEIN DKFZP686M09245.; COATOMER SUBUNIT DELTA.	P48444; Q52M80; Q6MZV5	COPD_HUMAN; Q6MZV5_HUMAN
938	IPI00298971	VTN	478	478	478	5.4E+04	5.4E+04	5.4E+04	5.7	2	1	0	0	0	VITRONECTIN PRECURSOR.	P01141; P04004; Q9BSH7	VTNC_HUMAN
939	IPI00299063	STIM1	685	685	685	7.7E+04	7.7E+04	7.7E+04	3.7	2	1	0	0	0	STROMAL INTERACTION MOLECULE 1 PRECURSOR.	Q13586; Q8N382	Q8N382_HUMAN; STIM1_HUMAN
940	IPI00301280	TMEM43	400	400	400	4.5E+04	4.5E+04	4.5E+04	11.8	2	1	0	0	0	TRANSMEMBRANE PROTEIN 43.		
941	IPI00302329	MYH8	1937	1937	1937	2.2E+05	2.2E+05	2.2E+05	38.4	135	1	0	0	0	MYOSIN-8.	P13535; Q14910	MYH8_HUMAN
942	IPI00303335	NEB	6669	6669	6669	7.7E+05	7.7E+05	7.7E+05	0.6	3	1	0	0	0	NEBULIN.	P20929; Q05C45; Q14214; Q14918; Q15346; Q53QQ2; Q53TG8; Q6PJ54; Q7Z2R0; Q96MF8; Q9Y5Z1	NEBU_HUMAN; Q05C45_HUMAN; Q14214_HUMAN; Q14918_HUMAN; Q53QQ2_HUMAN; Q53TG8_HUMAN; Q6PJ54_HUMAN; Q7Z2R0_HUMAN; Q96MF8_HUMAN; Q9Y5Z1_HUMAN
943	IPI00304071	FLJ20920	615	615	615	6.8E+04	6.8E+04	6.8E+04	7.5	2	1	0	0	0	HYPOTHETICAL PROTEIN FLJ20920.	Q96CM8; Q9H7G2	Q96CM8_HUMAN; Q9H7G2_HUMAN
944	IPI00334190	STOML2	356	356	356	3.9E+04	3.9E+04	3.9E+04	8.7	2	1	0	0	0	STOMATIN-LIKE PROTEIN 2.	O60376; Q53G29; Q96FY2; Q9P042; Q9UJZ1	STML2_HUMAN
945	IPI00375333	RRAD	308	308	308	3.3E+04	3.3E+04	3.3E+04	10.1	2	1	0	0	0	GTP-BINDING PROTEIN RAD.	P55042; Q92788; Q96F39	Q92788_HUMAN; RAD_HUMAN
946	IPI00396370; IPI00719752; IPI00747447	EIF3S9	814	874	854	9.2E+04	9.9E+04	9.7E+04	3.6	2	1	0	0	0	ISOFORM 1 OF EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9.; ISOFORM 2 OF EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9.; 99 KDA PROTEIN.	P55884; Q2NL77; Q59FS8; Q86UM1; Q96G38; Q9UMF9	; IF39_HUMAN; Q59FS8_HUMAN; Q86UM1_HUMAN; Q96G38_HUMAN
947	IPI00410693; IPI00412714; IPI00470497; IPI00470498	SERBP1	387	408	398	4.2E+04	4.5E+04	4.4E+04	8.7	2	1	0	0	0	ISOFORM 1 OF PLASMINOGEN ACTIVATOR INHIBITOR 1 RNA-BINDING PROTEIN.; ISOFORM 4 OF PLASMINOGEN ACTIVATOR INHIBITOR 1 RNA-BINDING PROTEIN.; ISOFORM 2 OF PLASMINOGEN ACTIVATOR INHIBITOR 1 RNA-BINDING PROTEIN.; ISOFORM 3 OF PLASMINOGEN ACTIVATOR INHIBITOR 1 RNA-BINDING PROTEIN.	Q5VU19; Q5VU20; Q5VU21; Q5VU22; Q63HR1; Q8NC51; Q8WUH0; Q96SE2; Q9BTY3; Q9BUM4; Q9Y367; Q9Y4S3	PAIRB_HUMAN; Q5VU19_HUMAN; Q5VU20_HUMAN; Q5VU21_HUMAN; Q5VU22_HUMAN; Q63HR1_HUMAN
948	IPI00465260	GARS	751	751	751	8.5E+04	8.5E+04	8.5E+04	3.2	2	1	0	0	0	GARS PROTEIN.		
949	IPI00604624	NIF3L1	377	377	377	4.2E+04	4.2E+04	4.2E+04	10.3	2	1	0	0	0	HYPOTHETICAL PROTEIN NIF3L1.	Q53TX4; Q658J0	Q53TX4_HUMAN; Q658J0_HUMAN
950	IPI00642211	RNPEP	658	658	658	7.3E+04	7.3E+04	7.3E+04	5.3	2	1	0	0	0	AMINOPEPTIDASE B.	Q7RU04	Q7RU04_HUMAN
951	IPI00748490; IPI00827636	AARSD1	412	586	499	4.5E+04	6.6E+04	5.6E+04	7.3	2	1	0	0	0	ALANYL-TRANSFER RNA SYNTHETASE FAMILY PROTEIN.; ISOFORM 1 OF ALANYL-TRNA SYNTHETASE DOMAIN-CONTAINING PROTEIN 1.	Q9BTE6	; AASD1_HUMAN
952	IPI00791835	ANK1	1040	1040	1040	1.2E+05	1.2E+05	1.2E+05	3.1	2	1	0	0	0	PROTEIN.		
953	IPI00828062		238	238	238	2.5E+04	2.5E+04	2.5E+04	19.3	3	1	0	0	0	ANTI-(ED-B) SCFV (FRAGMENT).	A2KBB9; A2KBC0; A2KBC1; A2KBC2; A2KBC3; A2KBC4; A2KBC5; A2KBC6; A2KBC7; A2KBC8	A2KBB9_HUMAN; A2KBC0_HUMAN; A2KBC1_HUMAN; A2KBC2_HUMAN; A2KBC3_HUMAN; A2KBC4_HUMAN; A2KBC5_HUMAN; A2KBC6_HUMAN; A2KBC7_HUMAN; A2KBC8_HUMAN
954	IPI00830047		106	106	106	1.1E+04	1.1E+04	1.1E+04	32.1	2	1	0	0	0	PROTEIN.		

[1] Values for min (minimum), max (maximum) and mean are for the proteins in each group

[2] Proteins that share the same group of assigned peptides

Type of file:	table
Label:	Table 2
Filename:	PubMed_17911086_Hojlund_Table2.pdf

M700304-MCP 2

Supplemental Table 2. Peptides identified in human muscle biopsy tissue

Protien group[1]	IPI ID	IPI gene name	Protein name	Sequence	Prev. amino acid	Next amino acid	Peptide identification probability	Mascot ions score	Modification	Observed m/z	Precursor charge state	Mass error (ppm)'	First amino acid	Last amino acid	Shared[2]
1	IPI00000690; IPI00157908	AIFM1	ISOFORM 1 OF APOPTOSIS-INDUCING FACTOR 1, MITOCHONDRIAL PRECURSOR.; ISOFORM 3 OF APOPTOSIS-INDUCING FACTOR 1, MITOCHONDRIAL PRECURSOR.	AALSASEGEEVPQDK	K	A	95.00%	71		765.8689	2	0.7	113	127	No
				ALGTEVIQLFPEK	R	G	95.00%	84		722.9114	2	6.7	321	333	No
				ALGTEVIQLFPEKGNMGK	R	I	95.00%	33	M16: Oxidation	650.0184	3	9.1	325	342	No
				APSHVPFLLIGGGTAAFAAAR	K	S	95.00%	80		1012.5640	2	5.6	128	148	No
				APSHVPFLLIGGGTAAFAAAR	K	S	95.00%	74		675.3788	3	6.2	124	144	No
				ELWFSDDPNVTK	K	T	95.00%	63		725.8503	2	5.0	174	185	No
				GVIFYLR	K	D	95.00%	36		434.2602	2	3.7	559	565	No
				ILPEYLSNWTMEK	K	V	95.00%	60	M11: Oxidation	820.4120	2	7.3	343	355	No
				ISGLGLTPEQK	R	Q	95.00%	59		571.8262	2	1.8	99	109	No
				KAALSASEGEEVPQDK	K	A	95.00%	79		829.9232	2	8.8	112	127	No
				KVETDHIVAAVGLEPNVELAK	R	T	95.00%	64		744.7514	3	6.6	384	404	No
				KVETDHIVAAVGLEPNVELAK	R	T	95.00%	34		558.8163	4	8.0	388	408	No
				LNDGSQITYEK	K	C	95.00%	63		634.3160	2	5.6	245	255	No
				TGGLEIDSDFGGFR	K	V	95.00%	79		735.8522	2	6.7	405	418	No
				VLIVSEDPELPYMRPPLSK	R	E	95.00%	46	M13: Oxidation	733.7342	3	6.0	155	173	No
				VMPNAIVQSVGVSSGK	K	L	95.00%	102	M2: Oxidation	794.9280	2	7.2	359	374	No
				VMPNAIVQSVGVSSGK	K	L	95.00%	52	M2: Oxidation	530.2852	3	2.1	363	378	No
2	IPI00000792; IPI00641565; IPI00642016; IPI00647366	CRYZ	QUINONE OXIDOREDUCTASE.; 26 KDA PROTEIN.; 22 KDA PROTEIN.; 32 KDA PROTEIN.	DLSLLSHGGR	K	V	95.00%	33		527.7882	2	3.7	233	242	No
				KPLLPYTPGSDVAGVIEAVGDNASAFK	R	K	95.00%	58		906.1515	3	7.0	62	88	No
				SDIAVPIPK	R	D	95.00%	61		470.2830	2	7.0	26	34	No
				VAEAHENIIHGSGATGK	K	M	95.00%	77		845.9377	2	9.5	308	324	No
				VFEFGGPEVLK	R	L	95.00%	52		611.3336	2	6.0	13	23	No
3	IPI00000811; IPI00789119; IPI00796198	PSMB6	PROTEASOME SUBUNIT BETA TYPE 6 PRECURSOR.; 20 KDA PROTEIN.; 12 KDA PROTEIN.	LAAIAESGVER	R	Q	95.00%	72		558.3111	2	7.3	210	220	No
				QVLLGDQIPK	R	F	95.00%	31		555.8340	2	6.8	221	230	No
				VTDKLTPIHDR	R	I	95.00%	32		647.8652	2	8.0	64	74	No
4	IPI00000816	YWHAE	14-3-3 PROTEIN EPSILON.	AAFDDAIAELDTLSEESYK	K	D	95.00%	110		1044.4970	2	9.5	197	215	No
				AAFDDAIAELDTLSEESYK	K	D	95.00%	80		696.6644	3	5.4	197	215	No
				AASDIAMTELPPTHPIR	K	L	95.00%	45	M7: Oxidation	918.4792	2	9.6	154	170	No
				AASDIAMTELPPTHPIR	K	L	95.00%	81	M7: Oxidation	612.6551	3	9.1	154	170	No
				DSTLIMQLLR	K	D	95.00%	65	M6: Oxidation	603.3372	2	8.2	216	225	Yes
				DSTLIMQLLR	K	D	95.00%	63		595.3373	2	4.3	216	225	No
				EAAENSLVAYK	K	A	95.00%	59		597.8077	2	5.8	143	153	No
				KVAGMDVELTVEER	K	N	95.00%	84	M5: Oxidation	796.4111	2	8.9	29	42	No
				KVAGMDVELTVEER	K	N	95.00%	31	M5: Oxidation	531.2753	3	6.4	29	42	No
				NLLSVAYK	R	N	95.00%	33		907.5325	1	7.9	43	50	Yes
				NLLSVAYK	R	N	95.00%	39		454.2683	2	3.9	43	50	Yes
				QMVETELK	R	L	95.00%	45	M2: Oxidation	497.2534	2	6.2	87	94	No
				VAGMDVELTVEER	K	N	95.00%	99	M4: Oxidation	732.3632	2	9.1	30	42	No
				YDEMVESMK	R	K	95.00%	59	M4: Oxidation, M8: Oxidation	582.2376	2	6.3	20	28	No
				YLAEFATGNDR	R	K	95.00%	42		628.8040	2	7.1	131	141	No
5	IPI00000874; IPI00640741	PRDX1	PEROXIREDOXIN-1.; 19 KDA PROTEIN.	ADEGISFR	K	G	95.00%	56		447.7229	2	6.5	121	128	No
				ATAVMPDGQFK	K	D	95.00%	37	M5: Oxidation	1180.5790	1	9.6	17	27	No
				ATAVMPDGQFK	K	D	95.00%	55	M5: Oxidation	590.7916	2	6.7	17	27	No
				DISLSDYK	K	G	95.00%	65		940.4717	1	9.5	28	35	No
				DISLSDYK	K	G	95.00%	39		470.7386	2	6.9	28	35	No
				GLFIIDDK	R	G	95.00%	39		920.5165	1	7.5	129	136	No
				GLFIIDDK	R	G	95.00%	53		460.7613	2	5.6	129	136	No
				IGHPAPNFK	K	A	95.00%	32		980.5358	1	3.9	8	16	No
				IGHPAPNFK	K	A	95.00%	28		490.7730	2	6.4	8	16	No
				KQGGLGPMNIPLVSDPK	K	R	95.00%	33	M8: Oxidation	883.9849	2	8.0	93	109	No
				KQGGLGPMNIPLVSDPK	K	R	95.00%	39	M8: Oxidation	589.6590	3	7.6	93	109	No
				KQGGLGPMNIPLVSDPKR	K	T	95.00%	36	M8: Oxidation	481.5211	4	6.2	93	110	No
				LVQAFQFTDK	R	H	95.00%	70		598.8239	2	6.9	159	168	No
				QGGLGPMNIPLVSDPK	K	R	95.00%	54	M7: Oxidation	819.9382	2	9.6	94	109	No
				QGGLGPMNIPLVSDPKR	K	T	95.00%	29	M7: Oxidation	598.9940	3	6.8	94	110	No

				QITVNDLPVGR	R	S	95.00%	73		606.3436	2	3.6	141	151	Yes
				QITVNDLPVGR	R	S	95.00%	28		404.5660	3	6.1	141	151	Yes
				TIAQDYGVLK	R	A	95.00%	31		1107.6140	1	8.2	111	120	No
				TIAQDYGVLK	R	A	95.00%	73		554.3098	2	6.0	111	120	No
6	IPI00000875; IPI00747497	EEF1G	ELONGATION FACTOR 1-GAMMA.; 50 KDA PROTEIN.	ALIAAQYSGAQVR	K	V	95.00%	94		674.3751	2	3.0	18	30	No
				EYFSWEGAFQHVGK	R	A	95.00%	54		842.9003	2	9.9	415	428	No
				ILGLLDAYLK	R	T	95.00%	81		559.8497	2	7.7	138	147	No
				KLDPGSEETQTLVR	R	E	95.00%	46		786.9181	2	3.0	401	414	No
				KLDPGSEETQTLVR	R	E	95.00%	32		524.9486	3	4.2	401	414	No
				LDPGSEETQTLVR	K	E	95.00%	34		722.8750	2	9.4	402	414	No
				STFVLDEFKR	K	K	95.00%	61		621.3339	2	5.6	286	295	No
				STFVLDEFKR	K	K	95.00%	42		414.5581	3	4.5	286	295	No
7	IPI00001091	AFG3L2	AFG3-LIKE PROTEIN 2.	GLGYAQYLPK	K	E	95.00%	42		555.3058	2	3.7	602	611	No
				GMGGLFSVGETTAK	R	V	95.00%	75	M2: Oxidation	685.8368	2	2.1	284	297	No
				HFEQAIER	K	V	95.00%	32		515.2620	2	4.2	544	551	No
				NLETLQQELGIEGENR	R	V	95.00%	126		921.9710	2	7.8	225	240	No
				NLETLQQELGIEGENR	R	V	95.00%	43		614.9824	3	6.4	225	240	No
				VALLLLEK	K	E	95.00%	54		449.8041	2	2.8	726	733	No
				VGQISFDLPR	K	Q	95.00%	59		566.3138	2	3.0	670	679	No
				VSEEIFFGR	R	I	95.00%	56		542.2803	2	4.8	633	641	No
				VTQSAYAQIVQFGMNEK	K	V	95.00%	89	M14: Oxidation	965.4816	2	9.0	653	669	No
8	IPI00001539	ACAA2	3-KETOACYL-COA THIOLASE, MITOCHONDRIAL.	AANDAGYFNDEMAPIEVK	K	T	95.00%	100	M12: Oxidation	985.9534	2	9.2	192	209	No
				AANDAGYFNDEMAPIEVK	K	T	95.00%	37	M12: Oxidation	657.6349	3	4.2	192	209	No
				DFTATDLSEFAAK	K	A	95.00%	77		708.3437	2	7.1	26	38	No
				DGTVTAGNASGVADGAGAVIIASEDAVK	K	K	95.00%	80		839.4294	3	9.6	242	269	No
				DGTVTAGNASGVADGAGAVIIASEDAVKK	K	H	95.00%	65		882.1277	3	9.1	242	270	No
				DMDLVEVNEAFAPQYLAVER	K	S	95.00%	94	M2: Oxidation	1163.0680	2	9.2	313	332	No
				ETPALTINR	K	L	95.00%	31		507.7844	2	2.5	82	90	No
				GVFVVAAK	R	R	95.00%	32		790.4889	1	7.8	6	13	No
				ITAHLVHELR	R	R	95.00%	29		594.8503	2	6.2	361	370	No
				RTPFGAYGGLLK	K	D	95.00%	36		640.3659	2	5.9	14	25	No
				SLDLDISK	R	T	95.00%	56		445.7487	2	6.7	333	340	No
				TNVNGGAIALGHPLGGSGSR	K	I	95.00%	113		917.9863	2	6.7	341	360	No
				TNVNGGAIALGHPLGGSGSR	K	I	95.00%	63		612.3249	3	3.7	341	360	No
				TPFGAYGGLLK	R	D	95.00%	39		1123.6250	1	8.9	15	25	No
				TPFGAYGGLLK	R	D	95.00%	70		562.3151	2	6.3	15	25	No
				VSPETVDSVIMGNVLQSSSDAIYLAR	K	H	95.00%	50	M11: Oxidation	923.1413	3	9.5	46	71	No
9	IPI00001589	TIMM13	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM13.	LDPGLIMEQVK	K	V	95.00%	32	M7: Oxidation	629.8458	2	9.4	17	27	No
				VQIAVANAQELLQR	K	M	95.00%	52		776.9520	2	9.6	28	41	No
10	IPI00001639	KPNB1	IMPORTIN BETA-1 SUBUNIT.	AAVENLPTFLVELSR	R	V	95.00%	95		829.9642	2	5.3	28	42	No
				AAVENLPTFLVELSR	R	V	95.00%	48		553.6446	3	3.8	28	42	No
				GALQYLVPILTQTLTK	K	Q	95.00%	81		880.0279	2	6.1	317	332	No
				GALQYLVPILTQTLTK	K	Q	95.00%	79		587.0220	3	7.4	317	332	No
				LAATNALLNSLEFTK	K	A	95.00%	103		803.4517	2	6.5	192	206	No
				LQQVLQMESHIQSTSDR	R	I	95.00%	38	M7: Oxidation	672.6670	3	1.7	558	574	No
				SNEILTAIIQGMR	K	K	95.00%	47	M12: Oxidation	731.3964	2	7.7	170	182	No
				TTLVIMER	K	L	95.00%	33	M6: Oxidation	489.7711	2	5.1	550	557	No
				TVSPDRLELEAAQK	K	F	95.00%	45		778.9223	2	5.3	10	23	No
				VAALQNLVK	R	I	95.00%	37		478.3020	2	2.3	235	243	No
				VLANPGNSQVAR	R	V	95.00%	44		613.3404	2	6.4	43	54	No
11	IPI00001730	FHOD1	FH1/FH2 DOMAIN-CONTAINING PROTEIN.	AALLNFDEFAVSK	K	D	95.00%	77		712.8802	2	7.1	718	730	No
				AEPIWELPTR	K	A	95.00%	51		606.3265	2	2.1	526	535	No
				AETLAGAMPNEAGGHPDAR	R	Q	95.00%	69	M8: Oxidation	940.9390	2	7.3	463	481	No
				AETLAGAMPNEAGGHPDAR	R	Q	95.00%	34	M8: Oxidation	627.6254	3	2.3	463	481	No
				EIAEPLFDLK	R	V	95.00%	43		587.8243	2	3.9	796	805	No
				FLENVAAAETEK	R	Q	95.00%	74		661.3381	2	3.3	443	454	No
				FSGVAGEAPSNPSVPVAVSSGPGR	K	G	95.00%	45		1113.5720	2	9.3	1021	1044	No
				HLGTAGTDVDLR	R	T	95.00%	55		627.8314	2	8.5	313	324	No
				LYSSSGPELR	K	R	95.00%	47		554.7885	2	4.8	127	136	No
				SGLGDDLVQALGLSK	K	G	95.00%	96		736.9078	2	7.7	1144	1158	No
				SNAINIGLTTLPPVHVIK	R	A	95.00%	21		629.7100	3	3.9	700	717	No
				TQLVLYENALK	R	L	95.00%	39		646.3712	2	6.4	325	335	No
				VDFEQLTENLGQLER	K	R	95.00%	103		895.9567	2	7.2	890	904	No

				VGMEQLVQNATFR	K	C	95.00%	40	M3: Oxidation	754.8852	2	6.2	806	818	No
12	IPI00002149	SAR1B	GTP-BINDING PROTEIN SAR1B.	IDRPEAISEER	K	L	95.00%	32		657.8417	2	7.6	136	146	No
				LLESKEELDSLMTDETIANVPILILGNK	R	I	95.00%	63	M12: Oxidation	1038.8930	3	4.8	108	135	No
				LVFLGLDNAGK	K	T	95.00%	60		573.8346	2	7.8	28	38	No
13	IPI00002352	MYLPF	MYOSIN LIGHT CHAIN 2.	DGIIDKEDLR	R	D	95.00%	46		1173.6210	1	7.6	43	52	No
				DGIIDKEDLR	R	D	95.00%	66		587.3118	2	3.2	43	52	No
				DGIIDKEDLRDTFAAMGR	R	L	95.00%	37	M16: Oxidation	1020.0070	2	9.7	43	60	No
				DTFAAMGR	R	L	95.00%	44	M6: Oxidation	442.7033	2	5.9	53	60	No
				DTFAAMGR	R	L	95.00%	32		868.4038	1	5.8	53	60	No
				DTFAAMGR	R	L	95.00%	46		434.7052	2	4.5	53	60	No
				EAFTVIDQNR	K	D	95.00%	77		1192.6040	1	6.3	33	42	No
				EAFTVIDQNR	K	D	95.00%	91		596.8051	2	5.1	33	42	No
				EAFTVIDQNRDGIIDK	K	E	95.00%	55		917.4791	2	8.5	33	48	No
				EAFTVIDQNRDGIIDK	K	E	95.00%	34		611.9881	3	7.5	33	48	No
				EAFTVIDQNRDGIIDKEDLR	K	D	95.00%	42		1174.1090	2	9.0	33	52	No
				EAFTVIDQNRDGIIDKEDLR	K	D	95.00%	57		783.0724	3	5.2	33	52	No
				EASGPINFTVFLTMFGEK	K	L	95.00%	116	M14: Oxidation	1002.5000	2	7.0	74	91	No
				EASGPINFTVFLTMFGEK	K	L	95.00%	63	M14: Oxidation	668.6692	3	6.5	74	91	No
				EASGPINFTVFLTMFGEK	K	L	95.00%	116		994.5029	2	7.0	74	91	No
				EASGPINFTVFLTMFGEK	K	L	95.00%	71		663.3384	3	7.9	74	91	No
				EDLRDTFAAMGR	K	L	95.00%	31	M10: Oxidation	466.5565	3	4.0	49	60	No
				FSQEEIK	R	N	95.00%	52		440.7258	2	2.3	132	138	No
				GADPEDVITGAFK	K	V	95.00%	107		660.3326	2	6.8	94	106	No
				GADPEDVITGAFK	K	V	95.00%	66		440.5567	3	4.5	94	106	No
				GADPEDVITGAFKVLDPEGK	K	G	95.00%	42		686.6912	3	8.8	94	113	No
				LKGADPEDVITGAFK	K	V	95.00%	90		780.9232	2	6.9	92	106	No
				LKGADPEDVITGAFK	K	V	95.00%	50		520.9510	3	6.1	92	106	No
				LNVKNEELDAMMK	R	E	95.00%	69	M11: Oxidation	775.8879	2	7.7	61	73	No
				LNVKNEELDAMMK	R	E	95.00%	61	M11: Oxidation	783.8856	2	7.9	61	73	No
				LNVKNEELDAMMK	R	E	95.00%	64	M11: Oxidation, M12: Oxidation	783.8760	2	-4.4	61	73	No
				LNVKNEELDAMMK	R	E	95.00%	47	M11: Oxidation, M12: Oxidation	522.9226	3	0.6	61	73	No
				LNVKNEELDAMMK	R	E	95.00%	60	M12: Oxidation	775.8878	2	7.5	61	73	No
				LNVKNEELDAMMK	R	E	95.00%	45	M12: Oxidation	517.5928	3	4.3	61	73	No
				LNVKNEELDAMMK	R	E	95.00%	80		767.8875	2	3.9	61	73	No
				NEELDAMMK	K	E	95.00%	59	M7: Oxidation	548.7391	2	4.5	65	73	No
				NEELDAMMK	K	E	95.00%	68	M7: Oxidation	556.7370	2	5.2	65	73	No
				NEELDAMMK	K	E	95.00%	68	M7: Oxidation, M8: Oxidation	556.7370	2	5.2	65	73	No
				NEELDAMMK	K	E	95.00%	38	M8: Oxidation	1096.4730	1	7.1	65	73	No
				NEELDAMMK	K	E	95.00%	58	M8: Oxidation	548.7397	2	5.5	65	73	No
				NEELDAMMK	K	E	95.00%	63		1080.4810	1	9.5	65	73	No
				NEELDAMMK	K	E	95.00%	62		540.7403	2	1.9	65	73	No
				NICYVITHGDAK	K	D	95.00%	84		667.3389	2	9.2	156	167	No
				NMWAAFPPDVGGNVDYK	K	N	95.00%	89	M2: Oxidation	948.9410	2	8.0	139	155	No
				NMWAAFPPDVGGNVDYK	K	N	95.00%	44	M2: Oxidation	632.9595	3	2.0	139	155	No
				NMWAAFPPDVGGNVDYK	K	N	95.00%	118		940.9445	2	9.0	139	155	No
14	IPI00002459; IPI00221226	ANXA6	ANNEXIN VI ISOFORM 2.; ANNEXIN A6.	ALIEILATR	K	T	95.00%	28		999.6271	1	6.8	457	465	No
				ALIEILATR	K	T	95.00%	70		500.3157	2	3.2	457	465	No
				DAFVAIVQSVK	R	N	95.00%	54		1176.6690	1	5.0	588	598	No
				DAFVAIVQSVK	R	N	95.00%	75		588.8383	2	5.1	588	598	No
				DAISGIGTDEK	K	C	95.00%	32		553.2738	2	1.7	103	113	No
				DAYERDLEADIIGDTSGHFQK	K	M	95.00%	57		794.0455	3	6.3	136	156	No
				DLEADIIGDTSGHFQK	R	M	95.00%	113		873.4283	2	8.0	141	156	No
				DLEADIIGDTSGHFQK	R	M	95.00%	56		582.6213	3	7.8	141	156	No
				DLIADLK	K	Y	95.00%	45		787.4626	1	7.4	69	75	No
				DLIADLKYELTGK	K	F	95.00%	77		739.9139	2	6.2	69	81	No
				DLIADLKYELTGK	K	F	95.00%	33		493.6115	3	5.4	69	81	No
				DLMTDLK	R	S	95.00%	29	M3: Oxidation	426.2160	2	6.5	412	418	No
				DLMTDLKSEISGDLAR	R	L	95.00%	62	M3: Oxidation	890.4506	2	7.5	412	427	No
				DLMTDLKSEISGDLAR	R	L	95.00%	55	M3: Oxidation	593.9691	3	6.4	412	427	No
				DLMTDLKSEISGDLAR	R	L	95.00%	50		882.4510	2	5.1	412	427	No
				EAILDIITSR	K	S	95.00%	90		565.8278	2	4.8	41	50	No
				EDAQVAAEILEIADTPSGDK	R	T	95.00%	127		1036.5100	2	4.0	521	540	No
				EDAQVAAEILEIADTPSGDK	R	T	95.00%	38		691.3428	3	4.2	521	540	No
				EDAQVAAEILEIADTPSGDKTSLETR	R	F	95.00%	87		920.4633	3	5.6	521	546	No

				EEDDVVSEDLVQQDVQDLYEAGELK	R	W	95.00%	77		955.7836	3	6.6	167	191	No
				EIKDAISGIGTDEK	K	C	95.00%	61		738.3869	2	4.3	100	113	No
				GELSGDFEK	R	L	95.00%	34		981.4618	1	8.9	232	240	No
				GELSGDFEK	R	L	95.00%	30		491.2329	2	4.9	232	240	No
				GFGSDKEAILDIITSR	K	S	95.00%	126		861.4648	2	8.2	35	50	No
				GFGSDKEAILDIITSR	K	S	95.00%	49		574.6442	3	5.5	35	50	No
				GLGTDEDTIIDIITHR	K	S	95.00%	137		884.9638	2	6.3	378	393	No
				GLGTDEDTIIDIITHR	K	S	95.00%	68		590.3097	3	2.8	378	393	No
				GSIHDFPGFDPNQDAEALYTAMK	R	G	95.00%	80	M22: Oxidation	847.3928	3	8.7	12	34	No
				GSIHDFPGFDPNQDAEALYTAMK	R	G	95.00%	74		842.0593	3	6.6	12	34	No
				GTVRPANDFNPDADAK	K	A	95.00%	81		844.4081	2	2.5	355	370	No
				GTVRPANDFNPDADAK	K	A	95.00%	42		563.2758	3	4.4	355	370	No
				ILISLATGHR	R	E	95.00%	71		540.8348	2	8.0	500	509	No
				ILISLATGHREEGGENLDQAR	R	E	95.00%	45		1140.0950	2	3.7	500	520	No
				ILISLATGHREEGGENLDQAR	R	E	95.00%	46		760.3997	3	3.9	500	520	No
				LILGLMMPPAHYDAK	R	Q	95.00%	67	M6: Oxidation, M7: Oxidation	851.4465	2	8.2	428	442	No
				LILGLMMPPAHYDAK	R	Q	95.00%	38	M6: Oxidation, M7: Oxidation	567.9654	3	5.7	428	442	No
				LVFDEYLK	R	T	95.00%	33		513.7831	2	6.8	213	220	No
				MLVVLLQGTR	K	E	95.00%	42	M1: Oxidation	573.3452	2	9.5	157	166	No
				MTNYDVEHTIK	K	K	95.00%	32	M1: Oxidation	683.8223	2	4.0	569	579	No
				MTNYDVEHTIKK	K	E	95.00%	54	M1: Oxidation	747.8688	2	2.3	569	580	No
				NKPLFFADK	K	L	95.00%	31		540.3007	2	4.2	599	607	No
				SEIDLLNIR	R	R	95.00%	47		1072.6090	1	7.7	630	638	No
				SEIDLLNIR	R	R	95.00%	77		536.8068	2	5.0	630	638	No
				SEISGDLAR	K	L	95.00%	30		474.2463	2	5.3	419	427	No
				SELDMLDIR	R	E	95.00%	51	M5: Oxidation	554.2735	2	3.1	282	290	No
				SLEDALSSDTSGHFR	K	R	95.00%	114		811.3804	2	4.4	484	498	No
				SLEDALSSDTSGHFR	K	R	95.00%	75		541.2559	3	4.0	484	498	No
				SLEDALSSDTSGHFRR	K	I	95.00%	33		593.2896	3	3.6	484	499	No
				SLHQAIEGDTSGDFLK	K	A	95.00%	107		859.4302	2	7.5	648	663	No
				SLHQAIEGDTSGDFLK	K	A	95.00%	44		573.2879	3	4.8	648	663	No
				STPEYFAER	R	L	95.00%	38		550.2575	2	1.0	251	259	No
				TNEQMHQLVAAYK	R	D	95.00%	67	M5: Oxidation	774.8798	2	2.3	123	135	No
				TNEQMHQLVAAYK	R	D	95.00%	39	M5: Oxidation	516.9223	3	2.0	123	135	No
				TNEQMHQLVAAYK	R	D	95.00%	51		766.8835	2	3.8	123	135	No
				TTGKPIEASIR	K	G	95.00%	36		586.8393	2	5.7	221	231	No
				VFQEFIK	R	M	95.00%	49		455.7576	2	3.9	556	562	No
				WGTDEAQFIYILGNR	K	S	95.00%	106		891.9508	2	6.8	192	206	No
				WGTDEAQFIYILGNR	K	S	95.00%	48		594.9695	3	6.3	192	206	No
15	IPI00002460; IPI00021771; IPI00514510	ANXA7	ISOFORM 1 OF ANNEXIN A7.; ISOFORM 2 OF ANNEXIN A7.; ANNEXIN VII ISOFORM 2.	DENQSINHQMAQEDAQR	R	L	95.00%	31	M10: Oxidation	677.2989	3	8.6	332	348	No
				EFSGYVESGLK	R	T	95.00%	38		608.3019	2	5.1	376	386	No
				GAGTDDSTLVR	K	I	95.00%	52		546.2749	2	7.7	431	441	No
				GFGTDEQAIVDVVANR	K	S	95.00%	91		845.9281	2	4.9	178	193	No
				GFGTDEQAIVDVVANR	K	S	95.00%	48		564.2881	3	5.1	178	193	No
				PAANFDAIR	R	D	95.00%	37		487.7599	2	6.1	181	189	No
				SEIDLVQIK	R	Q	95.00%	63		522.8027	2	3.2	425	433	No
				TLGTMIAGDTSGDYR	K	R	95.00%	45	M5: Oxidation	787.3667	2	5.5	443	457	No
16	IPI00002521; IPI00456008	ATP5J	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR.; ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F0 COMPLEX, SUBUNIT F6ISOFORM B PRECURSOR.	FEDPKFEVIEKPQA	K	-	95.00%	71		838.9382	2	8.8	95	108	No
				FEDPKFEVIEKPQA	K	-	95.00%	44		559.6267	3	6.3	95	108	No
				FEVIEKPQA	K	-	95.00%	48		530.7900	2	4.0	100	108	No
				LKQMFGNADMNTFPTFK	K	F	95.00%	41	M4: Oxidation, M10: Oxidation	674.6592	3	7.7	86	102	No
				QMFGNADMNTFPTFK	K	F	95.00%	61	M2: Oxidation, M8: Oxidation	890.8957	2	9.0	80	94	No
				QTSGGPVDASSEYQQELER	R	E	95.00%	49		694.3261	3	9.7	63	81	No
				RQTSGGPVDASSEYQQELER	K	E	95.00%	58		746.3577	3	6.4	62	81	No
17	IPI00002536; IPI00216155; IPI00216156	SESN1	ISOFORM T2 OF SESTRIN-1.; ISOFORM T1 OF SESTRIN-1.; ISOFORM T3 OF SESTRIN-1.	ESMFVFSSDDEEVTPAR	R	A	95.00%	47	M3: Oxidation	981.4337	2	8.0	307	323	No
				LYPDVGQLIDEK	R	F	95.00%	31		695.3741	2	9.7	367	378	No
18	IPI00002966	HSPA4	HEAT SHOCK 70 KDA PROTEIN 4.	AFSDPFVEAEK	R	S	95.00%	44		620.3022	2	5.4	74	84	No

				AGGIETIANEYSDR	R	C	95.00%	62		748.3599	2	6.0	20	33	No
				EDIYAVEIVGGATR	K	I	95.00%	68		746.8933	2	9.2	333	346	No
				EFSITDVVPYPISLR	R	W	95.00%	70		868.4728	2	6.1	391	405	No
				ELSTTLNADEAVTR	K	G	95.00%	62		760.3884	2	5.6	361	374	No
				LKETAESVLK	K	K	95.00%	35		559.3285	2	1.9	125	134	No
				MQVDQEEPHVEEQQQQTPAENK	K	A	95.00%	52	M1: Oxidation	880.0652	3	4.1	522	543	No
				NFTTEQVTAMLLSK	R	L	95.00%	98	M10: Oxidation	799.9130	2	5.1	111	124	No
				SNLAYDIVQLPTGLTGIK	K	V	95.00%	83		952.0374	2	6.6	85	102	No
				SNLAYDIVQLPTGLTGIK	K	V	95.00%	66		635.0279	3	7.1	85	102	No
				VLATAFDTTLGGR	K	K	95.00%	88		661.3635	2	5.5	222	234	No
19	IPI00003021; IPI00640401	ATP1A2	SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-2 CHAIN PRECURSOR.; CATION-TRANSPORTING ATPASE.	ADIGIAMGISGSDVSK	K	Q	95.00%	73	M7: Oxidation	768.8896	2	8.7	725	740	No
				DMTSEQLDEILK	K	N	95.00%	60	M2: Oxidation	719.3482	2	7.0	669	680	No
				DTAGDASESALLK	R	C	95.00%	66		639.3187	2	5.4	444	456	No
				FDTDELNFPTEK	K	L	95.00%	35		728.3406	2	6.0	568	579	No
				GVGIISEGNETVEDIAAR	K	L	95.00%	116		915.4734	2	7.8	627	644	No
				IATLASGLEVGR	R	T	95.00%	107		593.8454	2	2.8	268	279	No
				LNIPMSQVNPR	R	E	95.00%	52	M5: Oxidation	642.8454	2	7.4	645	655	No
				NHTEIVFAR	K	T	95.00%	30		543.7916	2	5.2	681	689	No
				NMVPQQALVIR	K	E	95.00%	41	M2: Oxidation	642.8618	2	4.7	161	171	No
				QGAIVAVTGDGVNDSPALK	R	K	95.00%	112		906.4850	2	6.5	705	723	No
				SPEFTHENPLETR	R	N	95.00%	63		778.8776	2	8.2	226	238	No
				VAEIPFNSTNK	K	Y	95.00%	34		610.3238	2	6.2	475	485	No
				VDNSSLTGESEPQTR	K	S	95.00%	85		810.3841	2	5.5	211	225	No
				VIMVTGDHPITAK	K	A	95.00%	62	M3: Oxidation	699.3825	2	7.7	610	622	No
20	IPI00003362	HSPA5	HSPA5 PROTEIN.	AKFEELNMDLFR	R	S	95.00%	63	M8: Oxidation	764.8805	2	4.0	326	337	No
				AKFEELNMDLFR	R	S	95.00%	39	M8: Oxidation	510.2559	3	3.2	326	337	No
				DAGTIAGLNVMR	K	I	95.00%	54	M11: Oxidation	617.3226	2	8.9	187	198	No
				DNHLLGTFDLTGIPPAPR	K	G	95.00%	48		645.3473	3	6.4	476	493	No
				ELEEIVQPIISK	K	L	95.00%	68		699.4017	2	4.4	623	634	No
				IEWLESHQDADIEDFK	K	A	95.00%	40		658.9782	3	5.2	603	618	No
				IEWLESHQDADIEDFKAK	K	K	95.00%	39		725.3547	3	3.5	603	620	No
				IINEPTAAAIAYGLDK	R	R	95.00%	122		830.4572	2	6.3	199	214	No
				IINEPTAAAIAYGLDK	R	R	95.00%	68		553.9742	3	6.5	199	214	No
				IINEPTAAAIAYGLDKR	R	E	95.00%	112		908.5094	2	7.6	199	215	No
				IINEPTAAAIAYGLDKR	R	E	95.00%	55		606.0097	3	8.9	199	215	No
				ITPSYVAFTPEGER	R	L	95.00%	78		783.8976	2	4.3	62	75	No
				KKELEEIVQPIISK	K	L	95.00%	38		827.4983	2	5.7	621	634	No
				KKELEEIVQPIISK	K	L	95.00%	31		552.0007	3	4.3	621	634	No
				KSDIDEIVLVGGSTR	K	I	95.00%	117		794.9345	2	4.0	354	368	No
				KSDIDEIVLVGGSTR	K	I	95.00%	33		530.2916	3	2.8	354	368	No
				KVTHAVVTVPAYFNDAQR	K	Q	95.00%	54		672.6971	3	4.6	165	182	No
				NELESYAYSLK	R	N	95.00%	81		658.8268	2	6.4	564	574	No
				NQLTSNPENTVFDAK	K	R	95.00%	112		839.4127	2	5.5	83	97	No
				SDIDEIVLVGGSTR	K	I	95.00%	50		730.8892	2	7.3	355	368	No
				SQIFSTASDNQPTVTIK	K	V	95.00%	106		918.9733	2	2.4	449	465	No
				SQIFSTASDNQPTVTIK	K	V	95.00%	38		612.9861	3	4.6	449	465	No
				TFAPEEISAMVLTK	K	M	95.00%	78	M10: Oxidation	776.9043	2	4.8	140	153	No
				TKPYIQVDIGGGQTK	K	T	95.00%	91		802.9398	2	4.2	125	139	No
				TKPYIQVDIGGGQTK	K	T	95.00%	48		535.6284	3	2.8	125	139	No
				TWNDPSVQQDIK	R	F	95.00%	82		715.8525	2	3.8	103	114	No
				VEIIANDQGNR	R	I	95.00%	52		1228.6370	1	7.0	51	61	No
				VEIIANDQGNR	R	I	95.00%	81		614.8218	2	5.9	51	61	No
				VTHAVVTVPAYFNDAQR	K	Q	95.00%	83		944.4955	2	6.2	166	182	No
				VTHAVVTVPAYFNDAQR	K	Q	95.00%	38		629.9987	3	4.7	166	182	No
				VYEGERPLTK	K	D	95.00%	48		596.3259	2	5.4	466	475	No
21	IPI00003482	DECR1	2,4-DIENOYL-COA REDUCTASE, MITOCHONDRIAL PRECURSOR.	AMLPPNSFQGK	K	V	95.00%	42	M2: Oxidation	603.3060	2	4.4	50	60	No
				ATAEQISSQTGNK	K	V	95.00%	52		667.8370	2	8.2	98	110	No
				EQWDTIEELIR	K	K	95.00%	59		716.3656	2	7.8	320	330	No
				FNVIQPGPIK	R	T	95.00%	35		556.8318	2	7.9	235	244	No
				VAFITGGGTGLGK	K	G	95.00%	67		589.3372	2	6.9	61	73	No
				VAGHPNIVINNAAGNFISPTER	K	L	95.00%	73		764.4065	3	6.2	134	155	No
22	IPI00003814	MAP2K6	ISOFORM 1 OF DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE6.	ADDLEPIMELGR	K	G	95.00%	51	M8: Oxidation	687.8363	2	5.2	50	61	No
				DVKPSNVLINALGQVK	R	M	95.00%	43		848.0018	2	8.9	179	194	No
				DVKPSNVLINALGQVK	R	M	95.00%	44		565.6689	3	6.1	179	194	No
				EAFEQPQTSSTPPR	K	D	95.00%	47		787.8737	2	-3.7	18	31	No

				GTDVASFVK	K	L	95.00%	32		462.2486	2	5.9	321	329	No
				QVVEEPSPQLPADK	K	F	95.00%	32		768.9023	2	3.7	269	282	No
23	IPI00003815; IPI00794402; IPI00796541	ARHGDIA	RHO GDP-DISSOCIATION INHIBITOR 1.; 28 KDA PROTEIN.; 26 KDA PROTEIN.	IDKTDYMVGSYGPR	K	A	95.00%	64	M7: Oxidation	809.3879	2	5.8	139	152	No
				SIQEIQELDKDDESLR	K	K	95.00%	41		639.9910	3	8.7	34	49	No
				SIQEIQELDKDDESLRK	K	Y	95.00%	43		682.6899	3	9.0	34	50	No
				TDYMVGSYGPR	K	A	95.00%	32	M4: Oxidation	631.2843	2	6.7	142	152	No
24	IPI00003833	MTCH2	MITOCHONDRIAL CARRIER HOMOLOG 2.	EVSSSFDHVIK	K	E	95.00%	33		624.3213	2	6.1	112	122	No
				GLFTGLTPR	R	L	95.00%	43		481.2806	2	6.3	69	77	No
				SAATLITHPFHVITLR	R	S	95.00%	36		593.0146	3	8.8	132	147	No
				VLIQVGYEPLPPTIGR	K	N	95.00%	56		876.5143	2	8.3	26	41	No
				VLQHYQESDKGEELGPGNVQK	K	E	95.00%	61		785.7311	3	8.3	91	111	No
25	IPI00003865	HSPA8	ISOFORM 1 OF HEAT SHOCK COGNATE 71 KDA PROTEIN.	ARFEELNADLFR	R	G	95.00%	63		740.8885	2	9.6	300	311	Yes
				ARFEELNADLFR	R	G	95.00%	51		494.2596	3	5.6	300	311	Yes
				DAGTIAGLNVLR	K	I	95.00%	54		1199.6850	1	8.2	160	171	No
				DAGTIAGLNVLR	K	I	95.00%	105		600.3444	2	4.9	160	171	No
				EIAEAYLGK	K	T	95.00%	38		993.5342	1	8.4	129	137	No
				EIAEAYLGK	K	T	95.00%	33		497.2662	2	-1.2	129	137	No
				FDDAVVQSDMK	R	H	95.00%	48	M10: Oxidation	635.7892	2	6.3	78	88	No
				FEELNADLFR	R	G	95.00%	69		627.3177	2	8.7	302	311	Yes
				IINEPTAAAIAYGLDK	R	K	95.00%	122		830.4572	2	6.3	172	187	Yes
				IINEPTAAAIAYGLDK	R	K	95.00%	68		553.9742	3	6.5	172	187	Yes
				IINEPTAAAIAYGLDKK	R	V	95.00%	112		894.5021	2	2.9	172	188	No
				IINEPTAAAIAYGLDKK	R	V	95.00%	55		596.6706	3	2.9	172	188	No
				LDKSQIHDIVLVGGSTR	K	I	95.00%	77		919.5145	2	4.1	326	342	No
				LDKSQIHDIVLVGGSTR	K	I	95.00%	65		613.3461	3	4.8	326	342	No
				LDKSQIHDIVLVGGSTR	K	I	95.00%	28		460.2613	4	4.3	326	342	No
				LLQDFFNGK	K	E	95.00%	49		1081.5780	1	8.5	349	357	Yes
				LLQDFFNGK	K	E	95.00%	68		541.2897	2	2.9	349	357	Yes
				LYQSAGGMPGGMPGGFPGGGAPPSGGASSGPTIEEVD	K	-	95.00%	61	M8: Oxidation, M12: Oxidation	1126.8420	3	6.3	610	646	No
				MKEIAEAYLGK	K	T	95.00%	66	M1: Oxidation	634.8339	2	3.1	127	137	No
				MKEIAEAYLGK	K	T	95.00%	32	M1: Oxidation	423.5583	3	2.6	127	137	No
				MKEIAEAYLGK	K	T	95.00%	51		626.8364	2	3.0	127	137	No
				MVNHFIAEFK	R	R	95.00%	41	M1: Oxidation	626.3170	2	5.2	237	246	No
				MVNHFIAEFK	R	R	95.00%	57		618.3194	2	5.0	237	246	No
				NQTAEKEEFEHQQK	K	E	95.00%	37		582.6132	3	8.3	584	597	No
				NQVAMNPTNTVFDAK	K	R	95.00%	118	M5: Oxidation	833.3993	2	0.1	57	71	No
				NSLESYAFNMK	K	A	95.00%	73	M10: Oxidation	660.3025	2	2.3	540	550	No
				NSLESYAFNMK	K	A	95.00%	49		652.3066	2	4.7	540	550	No
				QTQTFTTYSDNQPGVLIQVYEGER	K	A	95.00%	78		925.4553	3	8.3	424	447	No
				RFDDAVVQSDMK	R	H	95.00%	59	M11: Oxidation	713.8381	2	3.2	77	88	No
				RFDDAVVQSDMK	R	H	95.00%	39	M11: Oxidation	476.2284	3	4.1	77	88	No
				SFYPEEVSSMVLTK	K	M	95.00%	108	M10: Oxidation	816.9008	2	6.5	113	126	No
				SFYPEEVSSMVLTK	K	M	95.00%	39	M10: Oxidation	544.9362	3	6.0	113	126	No
				SINPDEAVAYGAAVQAAILSGDK	K	S	95.00%	132		1130.5860	2	7.9	362	384	No
				SINPDEAVAYGAAVQAAILSGDK	K	S	95.00%	82		754.0588	3	6.5	362	384	No
				SQIHDIVLVGGSTR	K	I	95.00%	98		741.4109	2	4.2	329	342	No
				SQIHDIVLVGGSTR	K	I	95.00%	40		494.6086	3	1.5	329	342	No
				STAGDTHLGGEDFDNR	K	M	95.00%	77		846.3690	2	2.2	221	236	Yes
				STAGDTHLGGEDFDNR	K	M	95.00%	48		564.5830	3	4.2	221	236	Yes
				TTPSYVAFTDTER	R	L	95.00%	100		744.3601	2	7.1	37	49	Yes
				TVTNAVVTVPAYFNDSQR	K	Q	95.00%	73		991.5108	2	7.9	138	155	No
				TVTNAVVTVPAYFNDSQR	K	Q	95.00%	65		661.3413	3	5.1	138	155	No
				VEIIANDQGNR	K	T	95.00%	52		1228.6370	1	7.0	26	36	Yes
				VEIIANDQGNR	K	T	95.00%	81		614.8218	2	5.9	26	36	Yes
26	IPI00003933; IPI00745553	HAGH	HYDROXYACYL GLUTATHIONE HYDROLASE ISOFORM 1.; HYDROXYACYLGLUTATHIONE HYDROLASE.	ALLEVLGR	K	L	95.00%	33		435.7768	2	5.1	203	210	No
				EAAIVDPVQPQK	K	V	95.00%	75		647.8584	2	6.2	72	83	No
				EKTVQQHAGETDPVTTMR	R	A	95.00%	50	M17: Oxidation	682.0040	3	9.3	277	294	No
				ITHLSTLQVGSLNVK	K	C	95.00%	93		805.4750	2	8.9	137	151	No
				ITHLSTLQVGSLNVK	K	C	95.00%	35		537.3192	3	8.8	137	151	No
				TVQQHAGETDPVTTMR	K	A	95.00%	58	M15: Oxidation	893.9311	2	8.3	279	294	No
				TVQQHAGETDPVTTMR	K	A	95.00%	42	M15: Oxidation	596.2883	3	5.5	279	294	No

27	IPI00003949	UBE2N	UBIQUITIN-CONJUGATING ENZYME E2 N.	LELFLPEEYPMAAPK	K	V	95.00%	37	M11: Oxidation	882.4575	2	7.8	54	68	No
				LLAEPVPGIK	R	A	95.00%	38		518.8259	2	2.8	15	24	No
				TNEAQAIETAR	K	A	95.00%	79		602.3068	2	7.3	131	141	No
				YFHVVIAGPQDSPFEGGTFK	R	L	95.00%	48		732.7042	3	9.2	34	53	No
28	IPI00003968	NDUFA9	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 9,MITOCHONDRIAL PRECURSOR.	DAFPEAIIVKPSDIFGR	R	E	95.00%	58		938.0119	2	7.5	193	209	No
				FGPIPLGSLGWK	R	T	95.00%	39		636.3655	2	6.1	223	234	No
				GIVNAVKDPDANGK	K	S	95.00%	45		699.3778	2	6.4	248	261	No
				IPQAIAQLSK	K	E	95.00%	69		534.8287	2	7.1	148	157	No
				LFLPFPLPLFAYR	R	W	95.00%	47		797.4714	2	9.5	287	299	No
				LPHLPGLEDLGIQATPLELK	K	A	95.00%	46		718.7512	3	9.2	329	348	No
				MGSQVIIPYR	R	C	95.00%	51	M1: Oxidation	590.3167	2	5.1	76	85	No
				NFDFEDVFVK	K	I	95.00%	35		630.3072	2	9.3	138	147	No
				SFAFVGPSR	K	Y	95.00%	36		484.2582	2	8.8	262	270	No
				SSVSGIVATVFGATGFLGR	R	Y	95.00%	90		609.3368	3	7.4	49	67	No
				TVKQPVYVVDVSK	K	G	95.00%	72		731.4244	2	6.3	235	247	No
				VFEISPFEPWITR	R	D	95.00%	53		810.9326	2	9.0	304	316	No
				WLSAEIEDVKPAK	R	T	95.00%	30		495.9396	3	5.2	361	373	No
				YLLFHLVK	R	Y	95.00%	25		516.8208	2	8.7	271	278	No
29	IPI00004247; IPI00216725; IPI00446678	PHKA1	ISOFORM 1 OF PHOSPHORYLASE B KINASE REGULATORY SUBUNIT ALPHA, SKELETALMUSCLE ISOFORM.; ISOFORM 2 OF PHOSPHORYLASE B KINASE REGULATORY SUBUNIT ALPHA, SKELETALMUSCLE ISOFORM.; 133 KDA PROTEIN.	AALEALDELDLFGVK	K	G	95.00%	112		802.4367	2	4.4	207	221	No
				AALEALDELDLFGVK	K	G	95.00%	48		535.2941	3	5.2	207	221	No
				AYELEQSVVK	K	L	95.00%	47		583.3111	2	3.2	74	83	No
				EALEAVLIK	K	G	95.00%	32		985.6016	1	8.1	353	361	No
				EALEAVLIK	K	G	95.00%	76		493.3024	2	3.4	353	361	No
				ELLTELYGK	R	V	95.00%	54		533.2987	2	5.7	808	816	No
				FSVHVESVLNR	K	V	95.00%	54		643.8506	2	6.1	1107	1117	No
				FSVHVESVLNR	K	V	95.00%	52		429.5686	3	3.7	1107	1117	No
				GDKTNQGISELNASSVGMAK	R	A	95.00%	62	M18: Oxidation	675.0006	3	4.7	187	206	No
				GIYVETIAEVYPIR	K	V	95.00%	43		811.9513	2	9.4	459	472	No
				GPDWNTELYNER	K	S	95.00%	86		747.3419	2	6.5	791	802	No
				HLTVGLPPEPR	K	E	95.00%	46		608.3510	2	7.4	853	863	No
				IVHIANDLFLQEQK	K	T	95.00%	29		556.6458	3	5.7	1154	1167	No
				MTGQPTITFPISHSMLDEDGTSLNSSILAALR	R	K	95.00%	51	M1: Oxidation, M15: Oxidation	1145.9080	3	9.3	556	587	No
				NLLHHILSGK	K	E	95.00%	28		566.3400	2	7.2	956	965	No
				PSFNLLDSPHPR	R	Q	95.00%	79		690.3618	2	6.1	728	739	No
				PSFNLLDSPHPR	R	Q	95.00%	71		460.5760	3	3.6	728	739	No
				SVRPTDSNVSPAISIHEIGAVGATK	R	T	95.00%	43	S1: Phospho	862.7750	3	6.4	972	996	No
				SVRPTDSNVSPAISIHEIGAVGATK	R	T	95.00%	43		836.1158	3	2.1	972	996	No
				SVRPTDSNVSPAISIHEIGAVGATK	R	T	95.00%	28		627.3412	4	5.9	972	996	No
				TADFGIWER	K	G	95.00%	74		547.7700	2	4.6	178	186	No
				TLGADDTMLAK	K	D	95.00%	37	M8: Oxidation	576.2892	2	7.4	1168	1178	No
				TNQGISELNASSVGMAK	K	A	95.00%	115	M15: Oxidation	861.9260	2	6.4	190	206	No
				TQPGLFAEMFR	R	L	95.00%	35	M9: Oxidation	656.8278	2	8.9	907	917	No
				VEIHLPR	R	D	95.00%	45		432.2608	2	4.0	749	755	No
				VPVGFYQK	R	V	95.00%	32		469.2625	2	2.6	1067	1074	No
				YISGILR	R	K	95.00%	26		411.2505	2	5.6	828	834	No
30	IPI00004471	PDLIM3	ISOFORM 1 OF PDZ AND LIM DOMAIN PROTEIN 3.	GETHLWSPQVSEDGK	R	A	95.00%	83		835.3967	2	1.9	83	97	No
				GETHLWSPQVSEDGK	R	A	95.00%	64		557.2685	3	4.5	83	97	No
				IDRGETHLWSPQVSEDGK	K	A	95.00%	117		1027.5090	2	7.5	80	97	No
				IDRGETHLWSPQVSEDGK	K	A	95.00%	53		685.3398	3	4.6	80	97	No
				INLESEPQDGNYFEHK	K	H	95.00%	91		960.4468	2	4.3	103	118	No
				INLESEPQDGNYFEHK	K	H	95.00%	41		640.6357	3	7.3	103	118	No
				LAPNIPLEMELPGVK	K	I	95.00%	46	M9: Oxidation	818.9584	2	6.3	170	184	No
				LAPNIPLEMELPGVK	K	I	95.00%	29		810.9626	2	8.4	170	184	No
				LSGGIDFNQPLVITR	R	I	95.00%	93		815.4554	2	3.8	17	31	No
				PQTVILPGPAPWGFR	M	L	95.00%	76		818.4614	2	8.4	2	16	No
				PQTVILPGPAPWGFR	M	L	95.00%	42		545.9756	3	6.1	2	16	No
				TKPPEGYDTVTLYPK	R	-	95.00%	67		854.9520	2	9.4	349	363	No
				TKPPEGYDTVTLYPK	R	-	95.00%	43		570.3002	3	2.8	349	363	No

				VLQGMVDDGSDDRPAGTR	R	S	95.00%	73	M5: Oxidation	952.9459	2	3.3	255	272	No
				VLQGMVDDGSDDRPAGTR	R	S	95.00%	74	M5: Oxidation	635.6345	3	5.4	255	272	No
				VLQGMVDDGSDDRPAGTR	R	S	95.00%	63		944.9504	2	5.4	255	272	No
				VLQGMVDDGSDDRPAGTR	R	S	95.00%	59		630.3015	3	3.3	255	272	No
31	IPI00004860; IPI00759723	RARS	ISOFORM COMPLEXED OF ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC.; ISOFORM MONOMERIC OF ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC.	IYDALDVSLIER	K	G	95.00%	82		703.8864	2	8.2	322	333	No
				VEIAGPGFINVHLR	K	K	95.00%	33		507.9596	3	5.9	154	167	No
32	IPI00004902; IPI00556451	ETFB	ISOFORM 1 OF ELECTRON TRANSFER FLAVOPROTEIN SUBUNIT BETA.; ISOFORM 2 OF ELECTRON TRANSFER FLAVOPROTEIN SUBUNIT BETA.	EIDGGLETLR	R	L	95.00%	33		551.7964	2	9.3	165	174	No
				GIHVEVPPAEAER	R	L	95.00%	43		702.3734	2	7.5	86	98	No
				GIHVEVPPAEAER	R	L	95.00%	42		468.5836	3	4.7	86	98	No
				IEVIKPGDLGVDLTSK	K	L	95.00%	43		561.9945	3	8.5	206	221	No
				LGPLQVAR	R	V	95.00%	42		427.2685	2	3.6	99	106	No
				LKLPAVVTADLR	R	L	95.00%	52		648.4110	2	6.9	175	186	No
				LKLPAVVTADLR	R	L	95.00%	40		432.6097	3	6.4	175	186	No
				LPAVVTADLR	K	L	95.00%	38		527.8155	2	-2.9	177	186	No
				LSVISVEDPPQR	K	T	95.00%	37		670.3710	2	8.8	222	233	No
				TAGVKVETTEDLVAK	R	L	95.00%	58		780.9316	2	4.3	234	248	No
				VDLVLLGK	K	Q	95.00%	37		428.7810	2	3.8	117	124	No
				VETTEDLVAK	K	L	95.00%	31		552.7960	2	4.6	239	248	No
33	IPI00005040; IPI00513827	ACADM	MEDIUM-CHAIN SPECIFIC ACYL-COA DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.; HYPOTHETICAL PROTEIN DKFZP686M24262.	AFAGDIANQLATDAVQILGGNGFNTEYPVEK	K	L	95.00%	46		1075.2130	3	9.6	359	389	No
				AFAGDIANQLATDAVQILGGNGFNTEYPVEK	K	L	95.00%	43		806.6610	4	9.1	359	389	No
				AFTGFIVEADTPGIQIGR	K	K	95.00%	114		946.5075	2	7.9	218	235	No
				AFTGFIVEADTPGIQIGR	K	K	95.00%	70		631.3387	3	4.4	218	235	No
				ANWYFLLAR	K	S	95.00%	68		577.3157	2	6.7	198	206	No
				EEIIPVAAEYDK	R	T	95.00%	57		688.8541	2	3.9	58	69	No
				EEIIPVAAEYDKTGEYPVPLIR	R	R	95.00%	60		834.7807	3	5.3	58	79	No
				ENVLIGDGAGFK	K	V	95.00%	49		610.3227	2	4.2	260	271	No
				GIVFEDVKVPK	R	E	95.00%	65		615.8628	2	6.4	249	259	No
				GIVFEDVKVPK	R	E	95.00%	30		410.9098	3	3.0	249	259	No
				IYQIYEGTSQIQR	K	L	95.00%	100		799.9183	2	6.8	396	408	No
				IYQIYEGTSQIQR	K	L	95.00%	63		533.6135	3	4.2	396	408	No
				QREPGLGFSFEFTEQQK	R	E	95.00%	46		676.6697	3	5.2	30	46	No
				TGEYPVPLIR	K	R	95.00%	42		572.8240	2	2.9	70	79	No
				TRPVVAAGAVGLAQR	K	A	95.00%	64		733.4404	2	8.7	280	294	No
				TRPVVAAGAVGLAQR	K	A	95.00%	40		489.2924	3	0.7	280	294	No
				VAMGAFDK	K	T	95.00%	36	M3: Oxidation	427.7100	2	4.6	272	279	No
34	IPI00005158; IPI00334291	LONP1	LON PROTEASE HOMOLOG, MITOCHONDRIAL PRECURSOR.; CDNA FLJ39307 FIS, CLONE OCBBF2013208, HIGHLY SIMILAR TO MITOCHONDRIALLON PROTEASE.	DIIALNPLYR	R	E	95.00%	45		594.3467	2	5.6	239	248	No
				ELGLEKDDKDAIEEK	K	F	95.00%	53		866.4290	2	-8.9	343	357	No
				FSVGGMTDVAEIK	R	G	95.00%	64	M6: Oxidation	685.3388	2	1.7	547	559	No
				HVMDVVDEELSK	K	L	95.00%	67	M3: Oxidation	708.8423	2	6.0	433	444	No
				ILEFIAVSQLR	R	G	95.00%	68		644.8915	2	9.4	438	448	No
				LGLLDNHSSEFNVTR	K	N	95.00%	55		851.4385	2	7.8	382	396	No
				LGLLDNHSSEFNVTR	K	N	95.00%	49		567.9595	3	4.0	445	459	No
				LKELVVPK	R	H	95.00%	35		463.3107	2	5.1	362	369	No
				LSSDVLTLLIK	K	Q	95.00%	88		601.3763	2	3.3	691	701	No
				MEMINVSGYVAQEK	R	L	95.00%	68	M1: Oxidation, M3: Oxidation	815.8840	2	8.9	590	603	No
				QNLAMTGEVSLTGK	R	I	95.00%	57	M5: Oxidation	732.8784	2	8.1	875	888	No
				TENPLILIDEVDK	K	I	95.00%	68		749.9109	2	8.8	582	594	No
				TENPLILIDEVDKIGR	K	G	95.00%	69		913.0115	2	4.2	582	597	No
				TENPLILIDEVDKIGR	K	G	95.00%	48		609.0118	3	6.8	582	597	No
				TKTENPLILIDEVDKIGR	K	G	95.00%	37		685.3940	3	8.1	580	597	No
				YSNENLDLAR	K	A	95.00%	45		597.7964	2	7.9	410	419	No

35	IPI00005668; IPI00029733; IPI00289524; IPI00291483; IPI00394704; IPI00455167; IPI00514814; IPI00736657	AKR1C1; AKR1C2; AKR1C3; AKR1C4; LOC648517	ALDO-KETO REDUCTASE FAMILY 1 MEMBER C2.; ALDO-KETO REDUCTASE FAMILY 1 MEMBER C1.; ALDO-KETO REDUCTASE FAMILY 1 MEMBER C4.; ALDO-KETO REDUCTASE FAMILY 1 MEMBER C3.; DIHYDRODIOL DEHYDROGENASE DD1 (FRAGMENT).; DIHYDRODIOL DEHYDROGENASE DD2.; ALDO-KETO REDUCTASE FAMILY 1, MEMBER C1.; SIMILAR TO ALDO-KETO REDUCTASE FAMILY 1 MEMBER C1 (20-ALPHA-HYDROXYSTEROID DEHYDROGENASE) (20-ALPHA-HSD) (TRANS-1,2-DIHYDROBENZENE-1,2-DIOL DEHYDROGENASE) (HIGH-AFFINITY HEPATIC BILEACID-BINDING PROTEIN) (HBAB) (CHLORDECONE REDUCTASE HOMOLOG HAKRC...ISOFORM 1.	LLEMILNKPGLK	R	Y	95.00%	37	M4: Oxidation	692.9191	2	4.5	172	183	No
				LLEMILNKPGLK	R	Y	95.00%	33	M4: Oxidation	462.2837	3	8.1	172	183	No
				LNDGHFMPVLGFGTYAPAEVPK	K	S	95.00%	52	M7: Oxidation	792.7331	3	5.8	10	31	No
				REDIFYTSK	K	L	95.00%	43		579.7971	2	5.9	76	84	No
				TPALIALR	R	Y	95.00%	60		427.7782	2	2.5	251	258	No
36	IPI00005957	SMPX	SMALL MUSCLE PROTEIN, X-LINKED.	AIQANINIPMGAFRPGAGQPPR	R	R	95.00%	57	M10: Oxidation	764.7466	3	9.1	13	34	No
				KLPGPAVNLSEIQNIK	K	S	95.00%	49		574.3426	3	9.2	62	77	No
37	IPI00006091; IPI00304639; IPI00375141; IPI00472316	DMD	ISOFORM 4 OF DYSTROPHIN.; ISOFORM 3 OF DYSTROPHIN.; DYSTROPHIN DP427L ISOFORM.; DYSTROPHIN DP427P1 ISOFORM.	AKQPDLAPGLTTIGASPTQTVTLVTQPVVTK	R	E	95.00%	76		1044.9300	3	7.4	2422	2452	No
				EEAEQVLGQAR	K	A	95.00%	55		615.3122	2	3.2	2590	2600	No
				EGPYTVDAIQK	K	K	95.00%	31		610.8154	2	5.3	2608	2618	No
				ELEQFNSDIQK	K	L	95.00%	42		675.8360	2	7.3	1782	1792	No
				LLEQSIQSAQETEK	K	S	95.00%	103		802.4192	2	7.8	1364	1377	No
				LLQQFPLDLEK	R	F	95.00%	29		672.3892	2	9.4	2690	2700	No
				LLVEELPLR	K	Q	95.00%	64		541.3390	2	7.3	2255	2263	No
				LQELQEATDELDLK	R	L	95.00%	90		822.9285	2	9.4	2936	2949	No
				NILSEFQR	K	D	95.00%	37		503.7730	2	6.0	2211	2218	No
				NIMAGLQQTNSEK	K	I	95.00%	80	M3: Oxidation	725.3581	2	5.3	126	138	No
				RPQLEELITAAQNLK	R	N	95.00%	34		575.3316	3	4.8	2524	2538	No
				TLNATGEEIIQQSSK	R	T	95.00%	95		809.9248	2	7.9	2161	2175	No
				VGNILQLGSK	R	L	95.00%	40		514.8099	2	1.3	396	405	No
				VLSQIDVAQK	R	K	95.00%	67		550.8223	2	4.5	1440	1449	No
				VMVGDLEDINEMIIK	R	Q	95.00%	30	M2: Oxidation, M12: Oxidation	875.9424	2	9.2	2498	2512	No
38	IPI00006211	VAPB	ISOFORM 1 OF VESICLE-ASSOCIATED MEMBRANE PROTEIN-ASSOCIATED PROTEINB/C.	FRGPFTDVVTTNLK	K	L	95.00%	61		797.9407	2	8.8	18	31	No
				GPFTDVVTTNLK	R	L	95.00%	83		646.3526	2	5.7	20	31	No
				TVQSNSPISALAPTGK	K	E	95.00%	61		785.9321	2	7.8	201	216	No
				VEQVLSLEPQHELK	K	F	95.00%	38		550.3066	3	7.9	4	17	No
39	IPI00006579	COX4I1	CYTOCHROME C OXIDASE SUBUNIT 4 ISOFORM 1, MITOCHONDRIAL PRECURSOR.	ASWSSLSMDEK	K	V	95.00%	39	M8: Oxidation	628.7833	2	9.6	68	78	No
				ASWSSLSMDEK	K	V	95.00%	69		620.7830	2	5.1	68	78	No
				ASWSSLSMDEKVELYR	K	I	95.00%	36	M8: Oxidation	639.6445	3	6.2	68	83	No
				DHPLPEVAHVK	R	H	95.00%	51		621.3398	2	6.0	43	53	No
				DHPLPEVAHVK	R	H	95.00%	53		414.5619	3	4.6	43	53	No
				ESFAEMNR	K	G	95.00%	36	M6: Oxidation	500.2191	2	9.8	88	95	No
				FKESFAEMNR	K	G	95.00%	40	M8: Oxidation	637.7996	2	5.8	86	95	No
				HYVYGPLPQSFDK	K	E	95.00%	31		775.8921	2	7.7	123	135	No
				HYVYGPLPQSFDKEWVAK	K	Q	95.00%	51		722.0394	3	7.3	123	140	No
				RDHPLPEVAHVK	R	H	95.00%	54		699.3906	2	5.6	42	53	No
				SEDFSLPAYMDR	K	R	95.00%	89	M10: Oxidation	723.8199	2	7.6	30	41	No
				SEDFSLPAYMDR	K	R	95.00%	95		715.8189	2	2.6	30	41	No
				VNPIQGLASK	K	W	95.00%	67		513.8034	2	4.0	150	159	No
40	IPI00006663; IPI00792207	ALDH2	ALDEHYDE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.; MITOCHONDRIAL ALDEHYDE DEHYDROGENASE 2 VARIANT (FRAGMENT).	ANNSTYGLAAAVFTK	R	D	95.00%	116		764.4007	2	8.5	437	451	No
				EEIFGPVMQILK	K	F	95.00%	41	M8: Oxidation	710.3872	2	7.5	415	426	No
				ELGEYGLQAYTEVK	R	T	95.00%	91		800.4062	2	8.7	493	506	No
				LGPALATGNVVVMK	K	V	95.00%	78	M13: Oxidation	693.3989	2	5.1	196	209	No

				TEQGPQVDETQFK	K	K	95.00%	81		753.8607	2	3.8	356	368	No
				TFVQEDIYDEFVER	R	S	95.00%	96		895.4269	2	9.8	325	338	No
				TFVQEDIYDEFVER	R	S	95.00%	45		597.2854	3	6.8	325	338	No
				TIPIDGDFFSYTR	K	H	95.00%	63		766.3818	2	8.0	160	172	No
				TVTVK	K	V	95.00%	29		547.3508	1	9.6	507	511	No
				VAEQTPLTALYVANLIK	K	E	95.00%	89		922.5360	2	5.8	210	226	No
				VAEQTPLTALYVANLIK	K	E	95.00%	47		615.3605	3	6.8	210	226	No
				VAFTGSTEIGR	K	V	95.00%	56		569.2983	2	-1.4	258	268	No
				VIQVAAGSSNLK	R	R	95.00%	62		593.8466	2	4.8	269	280	No
				VIQVAAGSSNLKR	R	V	95.00%	47		671.9005	2	9.4	269	281	No
				VVGNPFDSK	R	T	95.00%	29		481.7527	2	3.0	347	355	No
41	IPI00007052	FIS1	MITOCHONDRIAL FISSION 1 PROTEIN.	GIVLLEELLPK	K	G	95.00%	70		612.3880	2	5.2	54	64	No
				GLLQTEPQNNQAK	R	E	95.00%	72		720.8804	2	5.7	96	108	No
42	IPI00007402; IPI00784008	IPO7	120 KDA PROTEIN.; IMPORTIN-7.	AFAVGVQQVLLK	K	V	95.00%	83		636.8916	2	5.8	297	308	No
				AIFQTIQNR	K	N	95.00%	35		545.8077	2	6.0	966	974	No
				ENIVEAIIHSPELIR	R	V	95.00%	52		578.3284	3	5.5	95	109	No
				EYNEFAEVFLK	K	A	95.00%	48		694.8472	2	9.1	286	296	No
				FIQLLSDQSDQSVLIQK	R	Q	95.00%	40		981.5355	2	4.2	187	203	No
				KEVLQK	R	T	95.00%	31		744.4678	1	7.7	407	412	No
43	IPI00007611	ATP5O	ATP SYNTHASE O SUBUNIT, MITOCHONDRIAL PRECURSOR.	FSPLTTNLINLLAENGR	R	L	95.00%	104		937.0219	2	9.3	101	117	No
				FSPLTTNLINLLAENGR	R	L	95.00%	69		625.0157	3	6.8	101	117	No
				LSNTQGVVSAFSTMMSVHR	R	G	95.00%	69	M14: Oxidation, M15: Oxidation	1042.5070	2	7.4	118	136	No
				LSNTQGVVSAFSTMMSVHR	R	G	95.00%	36	M14: Oxidation, M15: Oxidation	695.3404	3	7.4	118	136	No
				LSNTQGVVSAFSTMMSVHR	R	G	95.00%	42		684.6764	3	6.4	118	136	No
				LVRPPVQVYGIEGR	K	Y	95.00%	43		791.9626	2	6.6	27	40	No
				LVRPPVQVYGIEGR	K	Y	95.00%	47		528.3086	3	1.9	27	40	No
				SFLSQGQVLK	K	L	95.00%	51		553.8165	2	3.6	163	172	No
				TDPSILGGMIVR	K	I	95.00%	74	M9: Oxidation	637.8462	2	5.3	177	188	No
				TDPSILGGMIVR	K	I	95.00%	33		629.8492	2	5.9	177	188	No
				VAASVLNPYVK	K	R	95.00%	63		580.8416	2	6.4	74	84	No
				VAQILKEPK	R	V	95.00%	38		513.3242	2	4.4	65	73	No
				YATALYSAASK	R	Q	95.00%	56		573.3000	2	7.0	41	51	No
44	IPI00007673; IPI00401259	CHCHD2; CHCHD9	COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN-CONTAINING PROTEIN 2.; COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN-CONTAINING PROTEIN 9.	AAPRPAPVAQPPAAAPPSAVGSSAAAPR	R	Q	95.00%	64		845.1323	3	6.8	24	51	No
				PAPVAQPPAAAPPSAVGSSAAAPR	R	Q	95.00%	36		713.3902	3	8.9	28	51	No
45	IPI00007702	HSPA2	HEAT SHOCK-RELATED 70 KDA PROTEIN 2.	ARFEELNADLFR	R	G	95.00%	63		740.8885	2	9.6	303	314	Yes
				ARFEELNADLFR	R	G	95.00%	51		494.2596	3	5.6	303	314	Yes
				DAGTITGLNVLR	K	I	95.00%	65		615.3499	2	5.2	161	172	No
				EIAEAYLGGK	K	V	95.00%	34		525.7799	2	4.3	130	139	No
				FDLTGIPPAPR	K	G	95.00%	55		592.3301	2	3.9	462	472	No
				FEELNADLFR	R	G	95.00%	69		627.3177	2	8.7	305	314	Yes
				GQIQEIVLVGGSTR	K	I	95.00%	67		728.9127	2	3.4	332	345	No
				IINEPTAAAIAYGLDK	R	K	95.00%	122		830.4572	2	6.3	173	188	Yes
				IINEPTAAAIAYGLDK	R	K	95.00%	68		553.9742	3	6.5	173	188	Yes
				IINEPTAAAIAYGLDKK	R	G	95.00%	112		894.5021	2	2.9	173	189	No
				IINEPTAAAIAYGLDKK	R	G	95.00%	55		596.6706	3	2.9	173	189	No
				KFEDATVQSDMK	R	H	95.00%	69	M11: Oxidation	707.8348	2	6.6	78	89	No
				LDKGQIQEIVLVGGSTR	K	I	95.00%	92		907.0199	2	7.4	329	345	No
				LDKGQIQEIVLVGGSTR	K	I	95.00%	52		605.0132	3	3.0	329	345	No
				LLQDFFNGK	K	E	95.00%	49		1081.5780	1	8.5	352	360	Yes
				LLQDFFNGK	K	E	95.00%	68		541.2897	2	2.9	352	360	Yes
				MKEIAEAYLGGK	K	V	95.00%	71	M1: Oxidation	663.3439	2	1.8	128	139	No
				MVSHLAEEFK	R	R	95.00%	30	M1: Oxidation	603.7944	2	-1.6	240	249	No
				MVSHLAEEFKR	R	K	95.00%	58	M1: Oxidation	681.8475	2	2.3	240	250	No
				MVSHLAEEFKR	R	K	95.00%	35	M1: Oxidation	454.9012	3	3.0	240	250	No
				NALESYTYNIK	K	Q	95.00%	78		658.3336	2	4.5	543	553	No
				NQVAMNPTNTIFDAK	K	R	95.00%	108	M5: Oxidation	840.4150	2	9.4	58	72	No
				SINPDEAVAYGAAVQAAILIGDK	K	S	95.00%	49		762.7451	3	9.4	365	387	No
				STAGDTHLGGEDFDNR	K	M	95.00%	77		846.3690	2	2.2	224	239	Yes
				STAGDTHLGGEDFDNR	K	M	95.00%	48		564.5830	3	4.2	224	239	Yes
				TFFPEEISSMVLTK	K	M	95.00%	91	M10: Oxidation	822.9188	2	6.2	114	127	No
				TFFPEEISSMVLTK	K	M	95.00%	36	M10: Oxidation	548.9471	3	3.8	114	127	No
				TTPSYVAFTDTER	R	L	95.00%	100		744.3601	2	7.1	38	50	Yes

				VEIIANDQGNR	K	T	95.00%	52		1228.6370	1	7.0	27	37	Yes
				VEIIANDQGNR	K	T	95.00%	81		614.8218	2	5.9	27	37	Yes
				VHSAVITVPAYFNDSQR	K	Q	95.00%	97		952.4949	2	8.2	140	156	No
				VHSAVITVPAYFNDSQR	K	Q	95.00%	53		635.3296	3	3.6	140	156	No
46	IPI00007750; IPI00794663	TUBA4A	TUBULIN ALPHA-1 CHAIN.; 48 KDA PROTEIN.	AFVHWYVGEGMEEGEFSEAR	R	E	95.00%	47	M11: Oxidation	782.6827	3	8.1	403	422	Yes
				AVFVDLEPTVIDEIR	R	N	95.00%	114		858.4703	2	6.3	65	79	No
				AVFVDLEPTVIDEIR	R	N	95.00%	94		572.6498	3	6.9	65	79	No
				DVNAAIAAIK	K	T	95.00%	39		985.5715	1	3.2	327	336	No
				DVNAAIAAIK	K	T	95.00%	91		493.2895	2	2.8	327	336	No
				EIIDPVLDR	K	I	95.00%	43		1069.5950	1	5.3	113	121	No
				EIIDPVLDR	K	I	95.00%	48		535.3010	2	4.2	113	121	No
				FDGALNVDLTEFQTNLVPYPR	R	I	95.00%	128		1205.1200	2	9.5	244	264	Yes
				FDGALNVDLTEFQTNLVPYPR	R	I	95.00%	64		803.7485	3	8.6	244	264	Yes
				FDLMYAK	K	R	95.00%	33	M4: Oxidation	452.2205	2	5.0	395	401	Yes
				IHFPLATYAPVISAEK	R	A	95.00%	94		878.9923	2	7.4	265	280	Yes
				IHFPLATYAPVISAEK	R	A	95.00%	78		586.3296	3	5.4	265	280	Yes
				LDHKFDLMYAK	R	R	95.00%	38	M8: Oxidation	698.8528	2	3.0	391	401	Yes
				LISQIVSSITASLR	R	F	95.00%	98		744.4507	2	9.3	230	243	Yes
				LISQIVSSITASLR	R	F	95.00%	83		496.6353	3	7.1	230	243	Yes
				NLDIERPTYTNLNR	R	L	95.00%	60		859.9495	2	4.9	216	229	Yes
				NLDIERPTYTNLNR	R	L	95.00%	50		573.6350	3	3.9	216	229	Yes
				QLFHPEQLITGK	R	E	95.00%	45		705.8943	2	4.2	85	96	Yes
				QLFHPEQLITGK	R	E	95.00%	44		470.9336	3	7.3	85	96	Yes
				QLFHPEQLITGKEDAANNYAR	R	G	95.00%	73		805.7444	3	5.1	85	105	Yes
				VGINYQPPTVVPGGDLAK	K	V	95.00%	84		912.9996	2	2.8	353	370	Yes
47	IPI00007752	TUBB2C	TUBULIN BETA-2C CHAIN.	ALTVPELTQQMFDAK	R	N	95.00%	102	M11: Oxidation	854.4418	2	7.5	283	297	No
				AVLVDLEPGTMDSVR	R	S	95.00%	102	M11: Oxidation	809.4167	2	6.0	63	77	No
				EVDEQMLNVQNK	K	N	95.00%	79	M6: Oxidation	731.8483	2	2.7	325	336	Yes
				EVDEQMLNVQNK	K	N	95.00%	55		723.8522	2	4.6	325	336	Yes
				FPGQLNADLR	R	K	95.00%	59		565.8047	2	4.9	242	251	Yes
				FWEVISDEHGIDPTGTYHGDSDLQLER	K	I	95.00%	58		1039.4860	3	5.4	20	46	No
				GHYTEGAELVDSVLDVVR	K	K	95.00%	168		980.0037	2	8.8	104	121	Yes
				GHYTEGAELVDSVLDVVR	K	K	95.00%	68		653.6696	3	5.5	104	121	Yes
				GHYTEGAELVDSVLDVVRK	K	E	95.00%	82		696.3701	3	8.4	104	122	Yes
				GHYTEGAELVDSVLDVVRK	K	E	95.00%	47		522.5282	4	5.8	104	122	Yes
				IMNTFSVVPSPK	R	V	95.00%	88	M2: Oxidation	668.3550	2	2.9	163	174	Yes
				INVYYNEATGGK	R	Y	95.00%	97		664.8307	2	3.7	47	58	No
				ISEQFTAMFR	R	R	95.00%	76	M8: Oxidation	623.3034	2	4.2	381	390	Yes
				KLAVNMVPFPR	R	L	95.00%	56	M6: Oxidation	644.3694	2	4.7	252	262	Yes
				LAVNMVPFPR	K	L	95.00%	77	M5: Oxidation	580.3237	2	8.4	253	262	Yes
				LHFFMPGFAPLTSR	R	G	95.00%	43	M5: Oxidation	818.9237	2	5.1	263	276	Yes
				LHFFMPGFAPLTSR	R	G	95.00%	57	M5: Oxidation	546.2853	3	5.5	263	276	Yes
				MSATFIGNSTAIQELFK	K	R	95.00%	125	M1: Oxidation	937.4791	2	7.1	363	379	No
				MSATFIGNSTAIQELFKR	K	I	95.00%	38	M1: Oxidation	677.3540	3	4.1	363	380	No
				MSMKEVDEQMLNVQNK	R	N	95.00%	67	M1: Oxidation, M3: Oxidation, M10: Oxidation	986.4527	2	7.6	321	336	Yes
				MSMKEVDEQMLNVQNK	R	N	95.00%	48	M1: Oxidation, M3: Oxidation, M10: Oxidation	657.9688	3	4.1	321	336	Yes
				NSSYFVEWIPNNVK	K	T	95.00%	53		848.9281	2	8.9	337	350	Yes
				SGPFGQIFRPDNFVFGQSGAGNNWAK	R	G	95.00%	81		933.4605	3	7.9	78	103	Yes
				YLTVAAVFR	R	G	95.00%	81		520.3027	2	3.3	310	318	Yes
48	IPI00007765	HSPA9	STRESS-70 PROTEIN, MITOCHONDRIAL PRECURSOR.	AQFEGIVTDLIR	R	R	95.00%	88		681.3818	2	9.3	349	360	No
				AQFEGIVTDLIR	R	R	95.00%	61		454.5884	3	4.7	349	360	No
				DAGQISGLNVLR	K	V	95.00%	80		621.8463	2	3.2	207	218	No
				EQQIVIQSSGGLSK	R	D	95.00%	87		737.4028	2	4.2	542	555	No
				EQQIVIQSSGGLSKDDIENMVK	R	N	95.00%	67	M20: Oxidation	812.0825	3	7.4	542	563	No
				ERVEAVNMAEGIIHDTETK	K	M	95.00%	56	M8: Oxidation	720.0254	3	7.2	577	595	No
				ETGVDLTKDNMALQR	R	V	95.00%	64	M11: Oxidation	853.9250	2	2.1	293	307	No
				LLGQFTLIGIPPAPR	K	G	95.00%	74		796.9855	2	6.1	499	513	No
				LLGQFTLIGIPPAPR	K	G	95.00%	40		531.6602	3	7.3	499	513	No
				LYSPSQIGAFVLMK	K	M	95.00%	83	M13: Oxidation	785.4260	2	5.8	160	173	No
				LYSPSQIGAFVLMK	K	M	95.00%	60	M13: Oxidation	523.9528	3	4.9	160	173	No
				MKETAENYLGHTAK	K	N	95.00%	82	M1: Oxidation	804.8928	2	5.3	174	187	No
				MKETAENYLGHTAK	K	N	95.00%	55	M1: Oxidation	536.9300	3	3.2	174	187	No

				NAVITVPAYFNDSQR	K	Q	95.00%	66		847.9360	2	8.3	188	202	No
				QAASSLQQASLK	R	L	95.00%	41		616.3398	2	5.8	635	646	No
				QAVTNPNNTFYATK	R	R	95.00%	96		784.8916	2	2.8	108	121	No
				RYDDPEVQKDIK	R	N	95.00%	53		753.3890	2	6.6	127	138	No
				SDIGEVILVGGMTR	K	M	95.00%	97	M12: Oxidation	731.8890	2	8.3	378	391	No
				SQVFSTAADGQTQVEIK	K	V	95.00%	121		904.9600	2	4.9	469	485	No
				STNGDTFLGGEDFDQALLR	K	H	95.00%	115		1028.4940	2	8.1	266	284	No
				STNGDTFLGGEDFDQALLR	K	H	95.00%	54		685.9959	3	4.6	266	284	No
				TTPSVVAFTADGER	R	L	95.00%	90		725.8657	2	4.0	86	99	No
				VEAVNMAEGIIHDTETK	R	M	95.00%	85	M6: Oxidation	936.9606	2	6.4	579	595	No
				VEAVNMAEGIIHDTETK	R	M	95.00%	52	M6: Oxidation	624.9737	3	2.1	579	595	No
				VINEPTAAALAYGLDK	R	S	95.00%	109		823.4509	2	8.4	219	234	No
				VINEPTAAALAYGLDK	R	S	95.00%	61		549.3010	3	4.3	219	234	No
				VQQTVQDLFGR	K	A	95.00%	93		645.8470	2	4.3	395	405	No
49	IPI00007856	MYH2	MYOSIN-2.	AAYLQSLNSADLLK	K	A	95.00%	105		753.9156	2	4.3	387	400	Yes
				AAYLQSLNSADLLK	K	A	95.00%	74		502.9464	3	4.4	387	400	Yes
				ADIAESQVNK	R	L	95.00%	52		1074.5510	1	7.4	1916	1925	Yes
				ADIAESQVNK	R	L	95.00%	81		537.7761	2	1.1	1916	1925	Yes
				ADIAESQVNKLR	R	V	95.00%	34		448.5825	3	2.7	1916	1927	Yes
				AEAHFALIHYAGVVDYNITGWLEK	K	N	95.00%	109		906.4701	3	8.2	576	599	No
				AEAHFALIHYAGVVDYNITGWLEK	K	N	95.00%	58		680.1039	4	7.3	576	599	No
				AEDEEEINAELTAK	R	K	95.00%	117		781.3685	2	3.7	932	945	Yes
				AEDEEEINAELTAK	R	K	95.00%	73		521.2471	3	1.3	932	945	Yes
				AGLLGLLEEMR	K	D	95.00%	88	M10: Oxidation	609.3355	2	5.4	773	783	Yes
				AGLLGLLEEMR	K	D	95.00%	58	M10: Oxidation	406.5597	3	5.7	773	783	Yes
				AGLLGLLEEMR	K	D	95.00%	62		1201.6510	1	-9.1	773	783	Yes
				AGLLGLLEEMR	K	D	95.00%	94		601.3371	2	3.9	773	783	Yes
				AGLLGLLEEMRDDK	K	L	95.00%	72	M10: Oxidation	788.4116	2	6.3	773	786	No
				AGLLGLLEEMRDDK	K	L	95.00%	44	M10: Oxidation	525.9426	3	4.1	773	786	No
				AGLLGLLEEMRDDK	K	L	95.00%	76		780.4151	2	7.5	773	786	No
				AGLLGLLEEMRDDK	K	L	95.00%	47		520.6109	3	4.1	773	786	No
				AGLLGLLEEMRDDKLAQLITR	K	T	95.00%	56	M10: Oxidation	791.1098	3	4.9	773	793	No
				AGLLGLLEEMRDDKLAQLITR	K	T	95.00%	32	M10: Oxidation	593.5849	4	6.0	773	793	No
				AGLLGLLEEMRDDKLAQLITR	K	T	95.00%	66		785.7807	3	8.2	773	793	No
				AGLLGLLEEMRDDKLAQLITR	K	T	95.00%	24		589.5864	4	6.3	773	793	No
				AITDAAMMAEELK	K	K	95.00%	86	M7: Oxidation, M8: Oxidation	713.3404	2	8.6	1764	1776	Yes
				AITDAAMMAEELK	K	K	95.00%	45	M7: Oxidation, M8: Oxidation	475.8937	3	3.3	1764	1776	Yes
				AITDAAMMAEELKK	K	E	95.00%	102	M7: Oxidation	769.3866	2	3.0	1764	1777	Yes
				AITDAAMMAEELKK	K	E	95.00%	44	M7: Oxidation	513.2606	3	3.4	1764	1777	Yes
				AITDAAMMAEELKK	K	E	95.00%	83	M7: Oxidation	777.3852	2	4.5	1764	1777	Yes
				AITDAAMMAEELKK	K	E	95.00%	52	M7: Oxidation	518.5913	3	1.7	1764	1777	Yes
				AITDAAMMAEELKK	K	E	95.00%	83	M7: Oxidation, M8: Oxidation	777.3852	2	4.5	1764	1777	Yes
				AITDAAMMAEELKK	K	E	95.00%	52	M7: Oxidation, M8: Oxidation	518.5913	3	1.7	1764	1777	Yes
				AITDAAMMAEELKK	K	E	95.00%	97	M8: Oxidation	769.3875	2	4.2	1764	1777	Yes
				AITDAAMMAEELKK	K	E	95.00%	52	M8: Oxidation	513.2598	3	1.9	1764	1777	Yes
				AITDAAMMAEELKK	K	E	95.00%	111		761.3883	2	1.9	1764	1777	Yes
				AITDAAMMAEELKK	K	E	95.00%	77		507.9281	3	1.8	1764	1777	Yes
				AITDAAMMAEELKKEQDTSAHLER	K	M	95.00%	37	M7: Oxidation, M8: Oxidation	907.4404	3	6.9	1764	1787	Yes
				ALQEAHQQTLDDLQAEEDK	K	V	95.00%	52		728.0195	3	7.4	1004	1022	Yes
				ALQEAHQQTLDDLQAEEDKVNTLTK	K	A	95.00%	100		946.8147	3	5.8	1004	1028	Yes
				ALQEAHQQTLDDLQAEEDKVNTLTK	K	A	95.00%	63		710.3631	4	5.9	1004	1028	Yes
				ANLLQAEIEELR	R	A	95.00%	105		699.8846	2	1.4	1684	1695	Yes
				ANLLQAEIEELR	R	A	95.00%	108		466.9276	3	5.6	1684	1695	Yes
				ANLLQAEIEELRATLEQTER	R	S	95.00%	46		1164.1250	2	9.2	1684	1703	Yes
				ANLLQAEIEELRATLEQTER	R	S	95.00%	73		776.4185	3	8.2	1684	1703	Yes
				ANTEVAQWR	K	T	95.00%	61		1074.5350	1	2.0	1370	1378	No
				ANTEVAQWR	K	T	95.00%	81		537.7719	2	2.6	1370	1378	No
				ATLEQTER	R	S	95.00%	72		474.2453	2	3.0	1696	1703	Yes
				CELQAALEEAEASLEHEEGK	K	I	95.00%	44		1093.5080	2	7.6	1544	1563	No
				CELQAALEEAEASLEHEEGK	K	I	95.00%	45		729.3390	3	4.1	1544	1563	No
				DDKLAQLITR	R	T	95.00%	69		586.8381	2	3.5	784	793	No

DDQVFPMNPPK	K	Y	95.00%	90	M7: Oxidation	652.3057	2	3.1	74	84	Yes
DDQVFPMNPPK	K	Y	95.00%	84		644.3124	2	9.6	74	84	Yes
DDQVFPMNPPKYDK	K	I	95.00%	47	M7: Oxidation	855.4003	2	4.7	74	87	Yes
DIDDLELTLAK	K	V	95.00%	54		1245.6670	1	7.2	959	969	Yes
DIDDLELTLAK	K	V	95.00%	99		623.3293	2	-5.9	959	969	Yes
DLEEATLQHEATAATLR	R	K	95.00%	159		934.9748	2	3.3	1183	1199	Yes
DLEEATLQHEATAATLR	R	K	95.00%	65		623.6530	3	4.2	1183	1199	Yes
DLEEATLQHEATAATLRK	R	K	95.00%	120		999.0282	2	9.0	1183	1200	Yes
DLEEATLQHEATAATLRK	R	K	95.00%	83		666.3520	3	4.8	1183	1200	Yes
DPLNETVVGLYQK	K	S	95.00%	91		738.3958	2	6.1	602	614	Yes
DTQIHLDDALR	K	S	95.00%	86		648.8323	2	1.4	1658	1668	No
DTQIHLDDALR	K	S	95.00%	38		432.8916	3	3.3	1658	1668	No
EAEFQK	R	M	95.00%	32		751.3677	1	6.7	1174	1179	Yes
EALVSQLSR	K	G	95.00%	52		1002.5580	1	-0.4	1301	1309	No
EALVSQLSR	K	G	95.00%	74		501.7846	2	3.0	1301	1309	No
EEQAEPDGTEVADK	R	A	95.00%	98		759.3368	2	3.3	373	386	Yes
EEQAEPDGTEVADKAAYLQSLNSADLLK	R	A	95.00%	84		1002.4970	3	5.4	373	400	Yes
EFEISNLQSK	K	I	95.00%	59		1194.6090	1	6.5	1090	1099	No
EFEISNLQSK	K	I	95.00%	74		597.8066	2	3.9	1090	1099	No
EKNDLQLQVQAEAEGLADAEER	K	C	95.00%	167		1228.6090	2	7.7	889	910	No
EKNDLQLQVQAEAEGLADAEER	K	C	95.00%	113		819.4094	3	8.9	889	910	No
EKSEMKMEIDDLASNVETVSK	K	A	95.00%	50	M5: Oxidation	800.3869	3	5.4	1226	1246	No
EKSEMKMEIDDLASNVETVSK	K	A	95.00%	99	M5: Oxidation	1208.0750	2	6.7	1226	1246	No
EKSEMKMEIDDLASNVETVSK	K	A	95.00%	72	M5: Oxidation	805.7170	3	3.5	1226	1246	No
EKSEMKMEIDDLASNVETVSK	K	A	95.00%	99	M5: Oxidation, M7: Oxidation	1208.0750	2	6.7	1226	1246	No
EKSEMKMEIDDLASNVETVSK	K	A	95.00%	72	M5: Oxidation, M7: Oxidation	805.7170	3	3.5	1226	1246	No
EKSEMKMEIDDLASNVETVSK	K	A	95.00%	58	M7: Oxidation	800.3870	3	5.5	1226	1246	No
ELEEISER	R	L	95.00%	49		1004.4910	1	0.9	1148	1155	Yes
ELEEISER	R	L	95.00%	42		502.7503	2	2.7	1148	1155	Yes
ELEEISERLEEAGGATSAQIEMNK	R	K	95.00%	100	M22: Oxidation	1325.6430	2	9.9	1148	1171	Yes
ELEEISERLEEAGGATSAQIEMNK	R	K	95.00%	95	M22: Oxidation	884.0965	3	8.4	1148	1171	Yes
ELEEISERLEEAGGATSAQIEMNK	R	K	95.00%	76	M22: Oxidation	663.3228	4	6.1	1148	1171	Yes
ELEEISERLEEAGGATSAQIEMNK	R	K	95.00%	120		1317.6430	2	7.9	1148	1171	Yes
ELEEISERLEEAGGATSAQIEMNK	R	K	95.00%	84		878.7634	3	6.7	1148	1171	Yes
ELEEISERLEEAGGATSAQIEMNK	R	K	95.00%	51		659.3240	4	5.9	1148	1171	Yes
ELEEISERLEEAGGATSAQIEMNKK	R	R	95.00%	70	M22: Oxidation	926.7932	3	6.2	1148	1172	Yes
ELEEISERLEEAGGATSAQIEMNKK	R	R	95.00%	37	M22: Oxidation	695.3460	4	5.0	1148	1172	Yes
ELEEISERLEEAGGATSAQIEMNKK	R	R	95.00%	47		921.4638	3	8.7	1148	1172	Yes
ELEGEVESEQK	R	R	95.00%	49		638.8011	2	2.7	1827	1837	Yes
ELEGEVESEQKR	R	N	95.00%	74		716.8548	2	6.8	1827	1838	Yes
ELEGEVESEQKR	R	N	95.00%	38		478.2381	3	4.6	1827	1838	Yes
ELTYQTEEDR	K	K	95.00%	51		642.2961	2	6.8	1855	1864	Yes
ELTYQTEEDRK	K	N	95.00%	70		706.3410	2	2.5	1855	1865	Yes
ELTYQTEEDRK	K	N	95.00%	42		471.2320	3	6.8	1855	1865	Yes
ELTYQTEEDRKNILR	K	L	95.00%	46		954.5008	2	5.8	1855	1869	Yes
ELTYQTEEDRKNILR	K	L	95.00%	39		636.6688	3	4.2	1855	1869	Yes
EMATMKEEFQK	K	I	95.00%	41	M2: Oxidation	694.3182	2	3.5	854	864	No
EMATMKEEFQK	K	I	95.00%	45	M2: Oxidation	702.3162	2	4.3	854	864	No
EMATMKEEFQK	K	I	95.00%	34	M2: Oxidation	468.5471	3	5.0	854	864	No
EMATMKEEFQK	K	I	95.00%	45	M2: Oxidation, M5: Oxidation	702.3162	2	4.3	854	864	No
EMATMKEEFQK	K	I	95.00%	35	M2: Oxidation, M5: Oxidation	468.5475	3	5.8	854	864	No
EMATMKEEFQK	K	I	95.00%	48	M5: Oxidation	694.3182	2	3.5	854	864	No
EMATMKEEFQK	K	I	95.00%	56		686.3207	2	3.4	854	864	No
ENKNLQQEISDLTEQIAEGGK	R	R	95.00%	56		782.0655	3	7.4	1507	1527	Yes

ENKNLQQEISDLTEQIAEGGKR	R	I	95.00%	59		834.1010	3	9.1	1507	1528	Yes
ENKNLQQEISDLTEQIAEGGKR	R	I	95.00%	50		625.8258	4	6.1	1507	1528	Yes
ENQSILITGESGAGK	R	T	95.00%	118		752.3882	2	1.9	171	185	Yes
ENQSILITGESGAGK	R	T	95.00%	46		501.9288	3	3.5	171	185	Yes
EQDTSAHLER	K	M	95.00%	69		593.2841	2	8.6	1778	1787	Yes
EQLAMVER	K	R	95.00%	54	M5: Oxidation	496.2496	2	3.0	1675	1682	Yes
EQLAMVER	K	R	95.00%	41		488.2543	2	7.4	1675	1682	Yes
EQYEEEQESK	R	A	95.00%	54		649.7764	2	4.7	1351	1360	No
EQYEEEQESKAELQR	R	A	95.00%	113		948.4391	2	4.3	1351	1365	No
EQYEEEQESKAELQR	R	A	95.00%	47		632.6265	3	0.8	1351	1365	No
ERIEAQNRPFDAK	R	T	95.00%	34		787.4102	2	2.3	23	35	No
EVTERAEDEEEINAELTAK	K	K	95.00%	123		1088.5220	2	4.6	927	945	Yes
EVTERAEDEEEINAELTAK	K	K	95.00%	64		726.0180	3	5.7	927	945	Yes
GFLAR	R	V	95.00%	24		563.3323	1	3.0	800	804	Yes
GKAEAHFALIHYAGVVDYNITGWLEK	K	N	95.00%	83		968.1733	3	5.4	574	599	No
GKAEAHFALIHYAGVVDYNITGWLEK	K	N	95.00%	33		726.3828	4	6.6	574	599	No
GKQAFTQQIEELKR	R	Q	95.00%	103		838.4631	2	2.9	1310	1323	Yes
GKQAFTQQIEELKR	R	Q	95.00%	75		559.3111	3	2.5	1310	1323	Yes
GKQAFTQQIEELKR	R	Q	95.00%	35		419.7347	4	1.2	1310	1323	Yes
GQTVEQVSNAVGALAK	K	A	95.00%	128		786.4274	2	4.9	417	432	No
GQTVEQVSNAVGALAK	K	A	95.00%	86		524.6203	3	3.7	417	432	No
GRLQTESGEFSR	R	Q	95.00%	54		683.8425	2	4.1	1284	1295	No
GRLQTESGEFSR	R	Q	95.00%	77		456.2314	3	5.3	1284	1295	No
GSSFQTVSALFR	K	E	95.00%	46		1299.6800	1	7.8	647	658	Yes
GSSFQTVSALFR	K	E	95.00%	99		650.3406	2	2.9	647	658	Yes
GSSFQTVSALFR	K	E	95.00%	47		433.8970	3	4.3	647	658	Yes
HADSVAELGEQIDNLQR	K	V	95.00%	166		947.9739	2	7.4	1202	1218	Yes
HADSVAELGEQIDNLQR	K	V	95.00%	85		632.3179	3	6.4	1202	1218	Yes
IAEKDEEIDQLK	K	R	95.00%	92		715.8789	2	8.2	1582	1593	Yes
IAEKDEEIDQLK	K	R	95.00%	50		477.5868	3	4.6	1582	1593	Yes
IAEKDEEIDQLKR	K	N	95.00%	95		793.9271	2	4.4	1582	1594	Yes
IAEKDEEIDQLKR	K	N	95.00%	79		529.6197	3	2.6	1582	1594	Yes
IAEQELLDASER	K	V	95.00%	87		687.3516	2	2.9	1707	1718	Yes
IAEQELLDASER	K	V	95.00%	37		458.5717	3	6.0	1707	1718	Yes
IEAQNRPFDAK	R	T	95.00%	71		644.8393	2	4.4	25	35	No
IEDEQALGIQLQK	K	K	95.00%	131		742.9053	2	4.3	1100	1112	No
IEDEQALGIQLQK	K	K	95.00%	88		495.6058	3	3.7	1100	1112	No
IEDEQALGIQLQKK	K	I	95.00%	81		806.9530	2	4.2	1100	1113	No
IEDEQALGIQLQKK	K	I	95.00%	34		538.3045	3	4.0	1100	1113	No
IEDMAMMTHLHEPAVLYNLK	K	E	95.00%	43	M4: Oxidation, M6: Oxidation, M7: Oxidation	802.0569	3	8.3	88	107	Yes
IEDMAMMTHLHEPAVLYNLK	K	E	95.00%	35	M4: Oxidation, M6: Oxidation, M7: Oxidation	601.7939	4	7.0	88	107	Yes
IEDMAMMTHLHEPAVLYNLK	K	E	95.00%	58	M6: Oxidation	791.3938	3	8.5	88	107	Yes
IEDMAMMTHLHEPAVLYNLK	K	E	95.00%	39	M6: Oxidation	796.7230	3	5.4	88	107	Yes
IEDMAMMTHLHEPAVLYNLK	K	E	95.00%	39	M6: Oxidation, M7: Oxidation	796.7230	3	5.4	88	107	Yes
IEDMAMMTHLHEPAVLYNLK	K	E	95.00%	46	M7: Oxidation	791.3921	3	6.4	88	107	Yes
IEDMAMMTHLHEPAVLYNLK	K	E	95.00%	58		786.0606	3	6.6	88	107	Yes
IEELEEEIEAER	R	A	95.00%	103		744.8617	2	5.7	1121	1132	Yes
IEELEEEIEAER	R	A	95.00%	67		496.9096	3	4.0	1121	1132	Yes
IHFGTTGK	R	L	95.00%	46		860.4694	1	7.2	253	260	Yes
IHFGTTGK	R	L	95.00%	29		430.7379	2	5.7	253	260	Yes
IKDELAK	K	S	95.00%	32		408.7472	2	3.9	865	871	No
IKELQAR	K	I	95.00%	31		429.2654	2	2.3	1114	1120	Yes
IKEVTER	K	A	95.00%	35		437.7546	2	1.7	925	931	Yes
IKEVTERAEDEEEINAELTAK	K	K	95.00%	115		1209.1170	2	9.3	925	945	Yes
IKEVTERAEDEEEINAELTAK	K	K	95.00%	82		806.4095	3	3.4	925	945	Yes
IKEVTERAEDEEEINAELTAK	K	K	95.00%	50		605.0596	4	4.3	925	945	Yes
IKLEQQVDDLEGSLEQEK	K	K	95.00%	166		1051.0440	2	6.2	1031	1048	Yes
IKLEQQVDDLEGSLEQEK	K	K	95.00%	72		701.0316	3	5.8	1031	1048	Yes
IKLEQQVDDLEGSLEQEKK	K	L	95.00%	137		1115.0950	2	9.1	1031	1049	No
IKLEQQVDDLEGSLEQEKK	K	L	95.00%	82		743.7285	3	3.6	1031	1049	No
IKLEQQVDDLEGSLEQEKK	K	L	95.00%	45		558.0484	4	3.7	1031	1049	No
IKNAYEESLDQLETLK	K	R	95.00%	115		947.5031	2	9.1	1490	1505	Yes
IKNAYEESLDQLETLK	K	R	95.00%	64		632.0006	3	2.6	1490	1505	Yes

IKNAYEESLDQLETLKR	K	E	95.00%	144		1025.5530	2	7.5	1490	1506	Yes
IKNAYEESLDQLETLKR	K	E	95.00%	88		684.0358	3	4.6	1490	1506	Yes
IKNAYEESLDQLETLKR	K	E	95.00%	74		513.2789	4	4.8	1490	1506	Yes
ILAEWK	K	Q	95.00%	33		759.4422	1	2.1	1458	1463	Yes
ILYADFK	R	Q	95.00%	47		869.4793	1	2.2	719	725	Yes
ILYADFK	R	Q	95.00%	55		435.2437	2	2.5	719	725	Yes
INQQLDTK	R	Q	95.00%	55		480.2638	2	3.6	446	453	Yes
INQQLDTKQPR	R	Q	95.00%	60		670.8722	2	5.7	446	456	Yes
INQQLDTKQPR	R	Q	95.00%	37		447.5833	3	4.1	446	456	Yes
IQGTLEDQIISANPLLEAFGNAK	K	T	95.00%	129		1221.6510	2	2.6	215	237	No
IQGTLEDQIISANPLLEAFGNAK	K	T	95.00%	121		814.7736	3	6.9	215	237	No
IQLEAK	K	I	95.00%	37		701.4219	1	2.9	919	924	Yes
IQLELNQVK	R	S	95.00%	46		1084.6430	1	5.9	1567	1575	Yes
IQLELNQVK	R	S	95.00%	74		542.8235	2	2.1	1567	1575	Yes
IQLELNQVKSEVDR	R	K	95.00%	62		835.9645	2	8.0	1567	1580	Yes
IQLELNQVKSEVDRK	R	I	95.00%	28		450.5092	4	5.9	1567	1581	Yes
IVESMQSTLDAEIR	R	S	95.00%	129	M5: Oxidation	804.4081	2	8.2	1599	1612	Yes
IVESMQSTLDAEIR	R	S	95.00%	55	M5: Oxidation	536.6071	3	6.6	1599	1612	Yes
IVESMQSTLDAEIR	R	S	95.00%	114		796.4084	2	5.4	1599	1612	Yes
IVESMQSTLDAEIR	R	S	95.00%	65		531.2747	3	5.1	1599	1612	Yes
KAITDAAMMAEELKK	K	E	95.00%	101	M8: Oxidation	833.4363	2	5.3	1763	1777	Yes
KAITDAAMMAEELKK	K	E	95.00%	81	M8: Oxidation	555.9587	3	2.7	1763	1777	Yes
KAITDAAMMAEELKK	K	E	95.00%	35	M8: Oxidation	417.2235	4	8.8	1763	1777	Yes
KAITDAAMMAEELKK	K	E	95.00%	80	M8: Oxidation	841.4315	2	2.7	1763	1777	Yes
KAITDAAMMAEELKK	K	E	95.00%	64	M8: Oxidation	561.2909	3	3.8	1763	1777	Yes
KAITDAAMMAEELKK	K	E	95.00%	80	M8: Oxidation, M9: Oxidation	841.4315	2	2.7	1763	1777	Yes
KAITDAAMMAEELKK	K	E	95.00%	64	M8: Oxidation, M9: Oxidation	561.2909	3	3.8	1763	1777	Yes
KAITDAAMMAEELKK	K	E	95.00%	103	M9: Oxidation	833.4359	2	4.9	1763	1777	Yes
KAITDAAMMAEELKK	K	E	95.00%	63	M9: Oxidation	555.9584	3	2.3	1763	1777	Yes
KAITDAAMMAEELKK	K	E	95.00%	37	M9: Oxidation	417.2219	4	5.0	1763	1777	Yes
KAITDAAMMAEELKK	K	E	95.00%	107		825.4387	2	5.2	1763	1777	Yes
KAITDAAMMAEELKK	K	E	95.00%	92		550.6276	3	3.8	1763	1777	Yes
KAITDAAMMAEELKK	K	E	95.00%	42		413.2216	4	1.3	1763	1777	Yes
KALQEAHQQTLDDLQAEEDKVNTLTK	K	A	95.00%	112		989.5156	3	8.1	1003	1028	Yes
KALQEAHQQTLDDLQAEEDKVNTLTK	K	A	95.00%	62		742.3849	4	3.0	1003	1028	Yes
KALQEAHQQTLDDLQAEEDKVNTLTK	K	A	95.00%	35		594.1111	5	5.8	1003	1028	Yes
KDIDDLELTLAK	K	V	95.00%	109		687.3849	2	6.4	958	969	Yes
KDIDDLELTLAK	K	V	95.00%	46		458.5916	3	4.3	958	969	Yes
KEFEISNLQSK	K	I	95.00%	69		661.8563	2	6.9	1089	1099	No
KEFEISNLQSK	K	I	95.00%	38		441.5729	3	5.6	1089	1099	No
KGSSFQTVSALFR	K	E	95.00%	125		714.3884	2	3.1	646	658	Yes
KGSSFQTVSALFR	K	E	95.00%	57		476.5949	3	3.2	646	658	Yes
KHADSVAELGEQIDNLQR	K	V	95.00%	137		1012.0210	2	6.5	1201	1218	Yes
KHADSVAELGEQIDNLQR	K	V	95.00%	93		675.0148	3	3.8	1201	1218	Yes
KHADSVAELGEQIDNLQR	K	V	95.00%	66		506.5136	4	4.9	1201	1218	Yes
KIAEKDEEIDQLK	R	R	95.00%	31		520.2861	3	6.2	1581	1593	No
KIAEQELLDASER	R	V	95.00%	123		751.3984	2	1.7	1706	1718	Yes
KIAEQELLDASER	R	V	95.00%	64		501.2686	3	2.5	1706	1718	Yes
KKEEITSGK	K	I	95.00%	39		510.2911	2	0.6	206	214	No
KKEFEISNLQSK	K	I	95.00%	96		725.9011	2	2.5	1088	1099	No
KKEFEISNLQSK	K	I	95.00%	57		484.2698	3	2.2	1088	1099	No
KKGSSFQTVSALFR	K	E	95.00%	66		778.4344	2	0.8	645	658	Yes
KKGSSFQTVSALFR	K	E	95.00%	49		519.2949	3	6.0	645	658	Yes
KKHADSVAELGEQIDNLQR	R	V	95.00%	89		717.7142	3	5.1	1200	1218	Yes
KKHADSVAELGEQIDNLQR	R	V	95.00%	53		538.5365	4	3.1	1200	1218	Yes
KKLETDISQMQGEMEDILQEAR	K	N	95.00%	90	M10: Oxidation	870.0991	3	8.1	1734	1755	No
KKLETDISQMQGEMEDILQEAR	K	N	95.00%	35	M10: Oxidation	652.8235	4	4.0	1734	1755	No
KKLETDISQMQGEMEDILQEAR	K	N	95.00%	93	M10: Oxidation	875.4277	3	4.7	1734	1755	No
KKLETDISQMQGEMEDILQEAR	K	N	95.00%	41	M10: Oxidation	656.8224	4	4.3	1734	1755	No
KKLETDISQMQGEMEDILQEAR	K	N	95.00%	93	M10: Oxidation, M14: Oxidation	875.4277	3	4.7	1734	1755	No

KKLETDISQMQGEMEDILQEAR	K	N	95.00%	41	M10: Oxidation, M14: Oxidation	656.8224	4	4.3	1734	1755	No
KKLETDISQMQGEMEDILQEAR	K	N	95.00%	62	M14: Oxidation	870.0975	3	6.4	1734	1755	No
KKLETDISQMQGEMEDILQEAR	K	N	95.00%	96		864.7649	3	5.4	1734	1755	No
KKLETDISQMQGEMEDILQEAR	K	N	95.00%	56		648.8265	4	6.7	1734	1755	No
KKMEGDLNEMEIQLNHANR	K	M	95.00%	39	M10: Oxidation	762.7066	3	3.1	1622	1640	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	39	M10: Oxidation	572.2825	4	4.2	1622	1640	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	70	M3: Oxidation	762.7060	3	2.4	1622	1640	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	77	M3: Oxidation	572.2819	4	3.1	1622	1640	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	58	M3: Oxidation	768.0369	3	1.3	1622	1640	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	54	M3: Oxidation	576.2810	4	3.7	1622	1640	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	58	M3: Oxidation, M10: Oxidation	768.0369	3	1.3	1622	1640	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	54	M3: Oxidation, M10: Oxidation	576.2810	4	3.7	1622	1640	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	53		757.3764	3	4.9	1622	1640	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	79		568.2838	4	4.2	1622	1640	Yes
KLEGDLK	R	L	95.00%	39		401.7396	2	4.6	1060	1066	Yes
KLETDISQMQGEMEDILQEAR	K	N	95.00%	67	M13: Oxidation	827.3995	3	7.2	1735	1755	No
KLETDISQMQGEMEDILQEAR	K	N	95.00%	99	M9: Oxidation	1240.5960	2	7.7	1735	1755	No
KLETDISQMQGEMEDILQEAR	K	N	95.00%	75	M9: Oxidation	827.3989	3	6.5	1735	1755	No
KLETDISQMQGEMEDILQEAR	K	N	95.00%	80	M9: Oxidation	1248.5950	2	9.1	1735	1755	No
KLETDISQMQGEMEDILQEAR	K	N	95.00%	92	M9: Oxidation	832.7300	3	5.8	1735	1755	No
KLETDISQMQGEMEDILQEAR	K	N	95.00%	93	M9: Oxidation, M13: Oxidation	1248.5890	2	4.2	1735	1755	No
KLETDISQMQGEMEDILQEAR	K	N	95.00%	92	M9: Oxidation, M13: Oxidation	832.7300	3	5.8	1735	1755	No
KLETDISQMQGEMEDILQEAR	K	N	95.00%	122		1232.6010	2	9.3	1735	1755	No
KLETDISQMQGEMEDILQEAR	K	N	95.00%	72		822.0666	3	5.6	1735	1755	No
KLQHELEEAEER	R	A	95.00%	84		755.8823	2	4.3	1904	1915	Yes
KLQHELEEAEER	R	A	95.00%	64		504.2562	3	1.7	1904	1915	Yes
KLQHELEEAEERADIAESQVNK	R	L	95.00%	93		1283.6470	2	4.3	1904	1925	Yes
KLQHELEEAEERADIAESQVNK	R	L	95.00%	46		856.0989	3	2.3	1904	1925	Yes
KLQHELEEAEERADIAESQVNK	R	L	95.00%	69		642.3272	4	4.0	1904	1925	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	46	M2: Oxidation	1079.5140	2	8.4	1623	1640	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	76	M2: Oxidation	720.0093	3	4.8	1623	1640	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	53	M2: Oxidation	540.2613	4	9.1	1623	1640	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	90	M2: Oxidation	1087.5110	2	8.1	1623	1640	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	57	M2: Oxidation	725.3447	3	9.9	1623	1640	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	50	M2: Oxidation	544.2559	4	1.3	1623	1640	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	90	M2: Oxidation, M9: Oxidation	1087.5110	2	8.1	1623	1640	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	57	M2: Oxidation, M9: Oxidation	725.3447	3	9.9	1623	1640	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	50	M2: Oxidation, M9: Oxidation	544.2559	4	1.3	1623	1640	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	69	M9: Oxidation	1079.5140	2	8.5	1623	1640	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	67	M9: Oxidation	720.0086	3	3.7	1623	1640	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	36	M9: Oxidation	540.2574	4	1.8	1623	1640	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	115		1071.5170	2	8.7	1623	1640	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	89		714.6783	3	5.6	1623	1640	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	59		536.2598	4	4.0	1623	1640	Yes
KRQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	89	M20: Oxidation	960.8171	3	8.9	147	170	Yes
KRQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	97		955.4839	3	7.2	147	170	Yes
LAQESIMDIENEK	K	Q	95.00%	105	M7: Oxidation	768.3721	2	6.5	1067	1079	No
LAQESIMDIENEK	K	Q	95.00%	95		760.3719	2	3.0	1067	1079	No
LAQESIMDIENEKQQLDEK	K	L	95.00%	95	M7: Oxidation	1139.0580	2	7.1	1067	1085	No
LAQESIMDIENEKQQLDEK	K	L	95.00%	66	M7: Oxidation	759.7066	3	5.4	1067	1085	No
LAQESIMDIENEKQQLDEK	K	L	95.00%	97		1131.0620	2	8.2	1067	1085	No
LAQESIMDIENEKQQLDEK	K	L	95.00%	61		754.3740	3	4.1	1067	1085	No
LAQESIMDIENEKQQLDEKLK	K	K	95.00%	36	M7: Oxidation	840.1025	3	8.3	1067	1087	No
LAQLITR	K	T	95.00%	37		814.5181	1	3.6	787	793	Yes

LAQLITR	K	T	95.00%	59		407.7621	2	1.4	787	793	Yes
LASADIETYLLEK	K	S	95.00%	129		733.3926	2	-1.2	261	273	Yes
LASADIETYLLEK	K	S	95.00%	66		489.2671	3	4.5	261	273	Yes
LDEAEQLALK	R	G	95.00%	51		1129.6220	1	9.6	1803	1812	Yes
LDEAEQLALK	R	G	95.00%	97		565.3107	2	2.5	1803	1812	Yes
LDEAEQLALKGGK	R	K	95.00%	66		686.3813	2	4.5	1803	1815	Yes
LDEAEQLALKGGK	R	K	95.00%	42		457.9226	3	2.6	1803	1815	Yes
LDEAEQLALKGGKK	R	Q	95.00%	81		750.4314	2	7.6	1803	1816	Yes
LDEAEQLALKGGKK	R	Q	95.00%	45		500.6212	3	2.9	1803	1816	Yes
LEEAGGATSAQIEMNK	R	K	95.00%	157	M14: Oxidation	832.8970	2	3.6	1156	1171	Yes
LEEAGGATSAQIEMNK	R	K	95.00%	68	M14: Oxidation	555.6020	3	6.1	1156	1171	Yes
LEEAGGATSAQIEMNK	R	K	95.00%	134		824.8989	2	2.7	1156	1171	Yes
LEEAGGATSAQIEMNKK	R	R	95.00%	88	M14: Oxidation	896.9449	2	3.7	1156	1172	Yes
LEEAGGATSAQIEMNKK	R	R	95.00%	37	M14: Oxidation	598.2982	3	2.0	1156	1172	Yes
LEEAGGATSAQIEMNKK	R	R	95.00%	105		888.9479	2	4.3	1156	1172	Yes
LEQQVDDLEGSLEQEK	K	K	95.00%	144		930.4526	2	5.2	1033	1048	Yes
LEQQVDDLEGSLEQEK	K	K	95.00%	113		620.6381	3	5.9	1033	1048	Yes
LEQQVDDLEGSLEQEKK	K	L	95.00%	116		994.5015	2	6.3	1033	1049	Yes
LEQQVDDLEGSLEQEKK	K	L	95.00%	69		663.3355	3	4.1	1033	1049	Yes
LETDISQMQGEMEDILQEAR	K	N	95.00%	36	M12: Oxidation	784.6980	3	3.4	1736	1755	No
LETDISQMQGEMEDILQEAR	K	N	95.00%	68	M8: Oxidation, M12: Oxidation	1184.5460	2	8.1	1736	1755	No
LETDISQMQGEMEDILQEAR	K	N	95.00%	55	M8: Oxidation, M12: Oxidation	790.0312	3	5.4	1736	1755	No
LETDISQMQGEMEDILQEAR	K	N	95.00%	135		1168.5530	2	9.7	1736	1755	No
LETDISQMQGEMEDILQEAR	K	N	95.00%	45		779.3713	3	9.7	1736	1755	No
LINDLTAQR	R	G	95.00%	51		1043.5890	1	3.4	1275	1283	No
LINDLTAQR	R	G	95.00%	89		522.2970	2	1.1	1275	1283	No
LQAAEEHVEAVNAK	R	C	95.00%	118		754.8915	2	2.8	1403	1416	No
LQAAEEHVEAVNAK	R	C	95.00%	48		503.5963	3	1.6	1403	1416	No
LQDLVDK	R	L	95.00%	35		830.4684	1	7.0	1870	1876	Yes
LQDLVDK	R	L	95.00%	42		415.7369	2	4.1	1870	1876	Yes
LQDLVDKLQAK	R	V	95.00%	88		635.8749	2	3.6	1870	1880	Yes
LQDLVDKLQAK	R	V	95.00%	55		424.2524	3	3.4	1870	1880	Yes
LQHELEEAEER	K	A	95.00%	69		691.8343	2	4.1	1905	1915	Yes
LQHELEEAEER	K	A	95.00%	59		461.5593	3	5.1	1905	1915	Yes
LQHELEEAEERADIAESQVNK	K	L	95.00%	114		1219.6040	2	8.0	1905	1925	Yes
LQHELEEAEERADIAESQVNK	K	L	95.00%	59		813.4023	3	4.6	1905	1925	Yes
LQHELEEAEERADIAESQVNK	K	L	95.00%	59		610.3048	4	6.5	1905	1925	Yes
LQNEVEDLMLDVER	R	T	95.00%	122	M9: Oxidation	859.9229	2	6.3	1427	1440	No
LQNEVEDLMLDVER	R	T	95.00%	86	M9: Oxidation	573.6165	3	3.8	1427	1440	No
LQNEVEDLMLDVER	R	T	95.00%	115		851.9251	2	5.9	1427	1440	No
LQNEVEDLMLDVER	R	T	95.00%	75		568.2850	3	4.2	1427	1440	No
LQQFFNHHMFVLEQEEYK	K	K	95.00%	58	M9: Oxidation	795.0480	3	4.4	488	505	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	35	M9: Oxidation	596.5412	4	9.8	488	505	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	43		789.7178	3	6.2	488	505	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	42		592.5402	4	6.1	488	505	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	68	M9: Oxidation	1256.1180	2	5.7	488	506	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	51	M9: Oxidation	837.7500	3	8.6	488	506	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	103		1248.1230	2	8.3	488	506	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	57		832.4158	3	5.6	488	506	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	42		499.8525	5	5.4	488	506	Yes
LQTESGEFSR	R	Q	95.00%	59		1153.5580	1	7.4	1286	1295	No
LQTESGEFSR	R	Q	95.00%	77		577.2810	2	4.4	1286	1295	No
LTGAVMHYGNLK	K	F	95.00%	81	M6: Oxidation	660.3458	2	4.2	355	366	No
LTGAVMHYGNLK	K	F	95.00%	36	M6: Oxidation	440.5658	3	2.8	355	366	No
LTGAVMHYGNLK	K	F	95.00%	85		652.3475	2	2.9	355	366	No
LYDQHLGK	K	S	95.00%	55		487.2609	2	3.1	555	562	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	108	M1: Oxidation	1015.4620	2	4.8	1624	1640	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	73	M1: Oxidation	677.3097	3	3.1	1624	1640	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	98	M1: Oxidation	1023.4620	2	6.9	1624	1640	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	71	M1: Oxidation	682.6416	3	3.5	1624	1640	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	98	M1: Oxidation, M8: Oxidation	1023.4620	2	6.9	1624	1640	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	71	M1: Oxidation, M8: Oxidation	682.6416	3	3.5	1624	1640	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	90	M8: Oxidation	1015.4650	2	7.0	1624	1640	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	49	M8: Oxidation	677.3115	3	5.7	1624	1640	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	124		1007.4680	2	8.1	1624	1640	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	77		671.9785	3	3.8	1624	1640	Yes

MEIDDLASNVETVSK	K	A	95.00%	137	M1: Oxidation	833.8993	2	3.7	1232	1246	No
MEIDDLASNVETVSK	K	A	95.00%	73	M1: Oxidation	556.2673	3	1.0	1232	1246	No
MEIDDLASNVETVSK	K	A	95.00%	150		825.9019	2	3.7	1232	1246	No
MEIDDLASNVETVSK	K	A	95.00%	51		550.9376	3	4.5	1232	1246	No
MFLWMVAR	K	I	95.00%	44	M1: Oxidation	535.2735	2	6.0	438	445	No
MFLWMVAR	K	I	95.00%	60	M1: Oxidation	543.2704	2	4.9	438	445	No
MFLWMVAR	K	I	95.00%	60	M1: Oxidation, M5: Oxidation	543.2704	2	4.9	438	445	No
MFLWMVAR	K	I	95.00%	54	M5: Oxidation	535.2723	2	3.9	438	445	No
MFLWMVAR	K	I	95.00%	54		527.2748	2	3.8	438	445	No
MVTLLK	K	E	95.00%	27	M1: Oxidation	720.4358	1	3.7	883	888	No
MVTLLK	K	E	95.00%	37		704.4404	1	3.2	883	888	Yes
NALAHALQSSR	K	H	95.00%	52		1167.6270	1	3.0	1333	1343	Yes
NALAHALQSSR	K	H	95.00%	94		584.3176	2	3.3	1333	1343	Yes
NAYEESLDQLETLK	K	R	95.00%	111		826.9099	2	6.0	1492	1505	Yes
NAYEESLDQLETLK	K	R	95.00%	61		551.6096	3	6.6	1492	1505	Yes
NAYEESLDQLETLKR	K	E	95.00%	138		904.9635	2	8.8	1492	1506	Yes
NAYEESLDQLETLKR	K	E	95.00%	53		603.6429	3	5.5	1492	1506	Yes
NDLQLQVQAEAEGLADAEER	K	C	95.00%	159		1100.0410	2	9.5	891	910	No
NDLQLQVQAEAEGLADAEER	K	C	95.00%	63		733.6920	3	3.2	891	910	No
NFDKILAEWK	R	Q	95.00%	40		632.3444	2	5.5	1454	1463	Yes
NFDKILAEWK	R	Q	95.00%	30		421.8982	3	4.0	1454	1463	Yes
NKDPLNETVVGLYQK	K	S	95.00%	121		859.4654	2	6.0	600	614	Yes
NKDPLNETVVGLYQK	K	S	95.00%	75		573.3107	3	2.1	600	614	Yes
NLQQEISDLTEQIAEGGK	K	R	95.00%	163		987.0017	2	6.4	1510	1527	Yes
NLQQEISDLTEQIAEGGK	K	R	95.00%	98		658.3360	3	4.8	1510	1527	Yes
NLQQEISDLTEQIAEGGKR	K	I	95.00%	145		1065.0560	2	9.5	1510	1528	Yes
NLQQEISDLTEQIAEGGKR	K	I	95.00%	53		710.3688	3	3.2	1510	1528	Yes
NLQQEISDLTEQIAEGGKR	K	I	95.00%	75		533.0291	4	4.1	1510	1528	Yes
NLTEEMAGLDETIAK	K	L	95.00%	124	M6: Oxidation	825.9053	2	7.8	983	997	Yes
NLTEEMAGLDETIAK	K	L	95.00%	71	M6: Oxidation	550.9387	3	6.4	983	997	Yes
NLTEEMAGLDETIAK	K	L	95.00%	131		817.9079	2	7.9	983	997	Yes
NLTEEMAGLDETIAK	K	L	95.00%	77		545.6058	3	4.2	983	997	Yes
NMEQTVK	K	D	95.00%	36	M2: Oxidation	433.2104	2	4.5	1791	1797	No
NMEQTVK	K	D	95.00%	34		425.2119	2	2.2	1791	1797	No
NTQGILK	R	D	95.00%	34		773.4569	1	5.9	1651	1657	No
NTQGILKDTQIHLDDALR	R	S	95.00%	97		1026.0540	2	5.0	1651	1668	No
NTQGILKDTQIHLDDALR	R	S	95.00%	59		684.3727	3	6.7	1651	1668	No
QAEEAEEQSNTNLAK	R	F	95.00%	100		831.3815	2	-4.0	1887	1901	No
QAEEAEEQSNTNLAK	R	F	95.00%	59		554.5954	3	5.3	1887	1901	No
QAFTQQIEELK	K	R	95.00%	37		667.8544	2	3.8	1312	1322	Yes
QAFTQQIEELKR	K	Q	95.00%	90		745.9052	2	3.8	1312	1323	Yes
QAFTQQIEELKR	K	Q	95.00%	61		497.6067	3	5.1	1312	1323	Yes
QEAPPHIFSISDNAYQFMLTDR	R	E	95.00%	103	M18: Oxidation	866.0826	3	7.0	149	170	Yes
QEAPPHIFSISDNAYQFMLTDR	R	E	95.00%	81		860.7453	3	0.4	149	170	Yes
QKQREEQAEPDGTEVADK	K	A	95.00%	33		686.6686	3	7.7	369	386	Yes
QLDEKEALVSQLSR	R	G	95.00%	101		808.4416	2	6.0	1296	1309	No
QLDEKEALVSQLSR	R	G	95.00%	67		539.2956	3	3.3	1296	1309	No
QLEEEIK	R	A	95.00%	50		444.7393	2	3.2	1324	1330	Yes
QREEQAEPDGTEVADK	K	A	95.00%	104		901.4207	2	7.2	371	386	Yes
QREEQAEPDGTEVADK	K	A	95.00%	62		601.2809	3	3.6	371	386	Yes
QREEQAEPDGTEVADKAAYLQSLNSADLLK	K	A	95.00%	96		1097.2200	3	7.7	371	400	Yes
QRLQNEVEDLMLDVER	K	T	95.00%	44	M11: Oxidation	668.3357	3	2.3	1425	1440	No
QRLQNEVEDLMLDVER	K	T	95.00%	64		663.0079	3	8.0	1425	1440	No
QVEQEKCELQAALEEAEASLEHEEGK	K	I	95.00%	90		976.4582	3	0.4	1538	1563	No
RANLLQAEIEELR	R	A	95.00%	86		777.9383	2	5.3	1683	1695	Yes
RANLLQAEIEELR	R	A	95.00%	90		518.9605	3	3.5	1683	1695	Yes
RANLLQAEIEELRATLEQTER	R	S	95.00%	41		828.4529	3	8.5	1683	1703	Yes
RANLLQAEIEELRATLEQTER	R	S	95.00%	79		621.5908	4	7.2	1683	1703	Yes
RDLEEATLQHEATAATLR	R	K	95.00%	113		1013.0270	2	4.5	1182	1199	Yes
RDLEEATLQHEATAATLR	R	K	95.00%	81		675.6859	3	2.7	1182	1199	Yes
RDLEEATLQHEATAATLR	R	K	95.00%	61		507.0161	4	2.1	1182	1199	Yes
RDLEEATLQHEATAATLRK	R	K	95.00%	41		539.0399	4	2.2	1182	1200	Yes
RQAEEAEEQSNTNLAK	K	F	95.00%	68		909.4431	2	8.5	1886	1901	No
RQAEEAEEQSNTNLAK	K	F	95.00%	45		606.6308	3	7.6	1886	1901	No
RQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	106	M19: Oxidation	918.1165	3	6.7	148	170	Yes

RQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	34	M19: Oxidation	688.8396	4	7.2	148	170	Yes
RQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	114		912.7863	3	8.4	148	170	Yes
RQEAPPHIFSISDNAYQFMLTDRENQSILITGESGAGK	K	T	95.00%	70	M19: Oxidation	1060.0320	4	9.5	148	185	Yes
RVIQYFATIAVTGEK	K	K	95.00%	106		848.4809	2	6.2	191	205	Yes
RVIQYFATIAVTGEK	K	K	95.00%	71		565.9888	3	4.3	191	205	Yes
SAETEKEMATMK	K	E	95.00%	40	M11: Oxidation	686.3135	2	4.0	848	859	Yes
SAETEKEMATMK	K	E	95.00%	34	M11: Oxidation	457.8794	3	6.5	848	859	Yes
SAETEKEMATMK	K	E	95.00%	37	M8: Oxidation, M11: Oxidation	694.3143	2	8.8	848	859	Yes
SAETEKEMATMK	K	E	95.00%	68		678.3158	2	3.6	848	859	Yes
SAETEKEMATMK	K	E	95.00%	41		452.5479	3	6.8	848	859	Yes
SAETEKEMATMKEEFQK	K	I	95.00%	83	M11: Oxidation	1016.9680	2	4.0	848	864	No
SAETEKEMATMKEEFQK	K	I	95.00%	47	M11: Oxidation	678.3137	3	2.3	848	864	No
SAETEKEMATMKEEFQK	K	I	95.00%	75	M8: Oxidation	1016.9690	2	4.3	848	864	No
SAETEKEMATMKEEFQK	K	I	95.00%	33	M8: Oxidation	678.3148	3	3.8	848	864	No
SAETEKEMATMKEEFQK	K	I	95.00%	75	M8: Oxidation	1024.9670	2	5.5	848	864	No
SAETEKEMATMKEEFQK	K	I	95.00%	51	M8: Oxidation	683.6451	3	1.9	848	864	No
SAETEKEMATMKEEFQK	K	I	95.00%	75	M8: Oxidation, M11: Oxidation	1024.9670	2	5.5	848	864	No
SAETEKEMATMKEEFQK	K	I	95.00%	51	M8: Oxidation, M11: Oxidation	683.6451	3	1.9	848	864	No
SAETEKEMATMKEEFQK	K	I	95.00%	96		1008.9730	2	6.2	848	864	No
SAETEKEMATMKEEFQK	K	I	95.00%	53		672.9824	3	2.8	848	864	No
SAMKTLAQLFSGAQTAEGEGAGGGAK	K	K	95.00%	94	M3: Oxidation	818.7440	3	9.3	615	640	No
SANFQKPK	K	V	95.00%	43		460.2563	2	4.9	563	570	Yes
SEMKMEIDDLASNVETVSK	K	A	95.00%	41	M3: Oxidation	714.6738	3	5.2	1228	1246	No
SEMKMEIDDLASNVETVSK	K	A	95.00%	129	M3: Oxidation	1079.5080	2	8.4	1228	1246	No
SEMKMEIDDLASNVETVSK	K	A	95.00%	77	M3: Oxidation	720.0056	3	5.4	1228	1246	No
SEMKMEIDDLASNVETVSK	K	A	95.00%	129	M3: Oxidation, M5: Oxidation	1079.5080	2	8.4	1228	1246	No
SEMKMEIDDLASNVETVSK	K	A	95.00%	86	M3: Oxidation, M5: Oxidation	720.0066	3	6.9	1228	1246	No
SEMKMEIDDLASNVETVSK	K	A	95.00%	102	M5: Oxidation	1071.5100	2	8.3	1228	1246	No
SEMKMEIDDLASNVETVSK	K	A	95.00%	52	M5: Oxidation	714.6751	3	7.1	1228	1246	No
SKEEEQQR	K	L	95.00%	51		517.2525	2	5.4	1267	1274	No
SLGTELFK	R	I	95.00%	34		894.4965	1	3.1	1482	1489	No
SLGTELFK	R	I	95.00%	73		447.7524	2	3.6	1482	1489	No
SQEDLKEQLAMVER	R	R	95.00%	98	M11: Oxidation	846.4202	2	3.0	1669	1682	Yes
SQEDLKEQLAMVER	R	R	95.00%	65	M11: Oxidation	564.6167	3	4.1	1669	1682	Yes
SQEDLKEQLAMVER	R	R	95.00%	117		838.4244	2	5.0	1669	1682	Yes
SQEDLKEQLAMVER	R	R	95.00%	65		559.2847	3	3.5	1669	1682	Yes
STHPHFVR	R	C	95.00%	32		490.7590	2	3.7	670	677	Yes
SYHIFYQITSNK	R	K	95.00%	87		750.8779	2	-0.5	285	296	Yes
SYHIFYQITSNK	R	K	95.00%	43		500.9233	3	3.7	285	296	Yes
TEELEEAK	R	K	95.00%	33		948.4558	1	3.3	1389	1396	Yes
TEELEEAK	R	K	95.00%	39		474.7330	2	5.9	1389	1396	Yes
TEELEEAKK	R	K	95.00%	40		538.7797	2	3.5	1389	1397	Yes
TEGGATLTVK	K	D	95.00%	54		488.7739	2	8.4	64	73	No
TEGGATLTVKDDQVFPMNPPK	K	Y	95.00%	79	M17: Oxidation	1131.0700	2	8.4	64	84	No
TEGGATLTVKDDQVFPMNPPK	K	Y	95.00%	91	M17: Oxidation	754.3829	3	9.0	64	84	No
TEGGATLTVKDDQVFPMNPPK	K	Y	95.00%	96		1123.0720	2	7.7	64	84	No
TEGGATLTVKDDQVFPMNPPK	K	Y	95.00%	79		749.0500	3	7.4	64	84	No
TEGGATLTVKDDQVFPMNPPKYDK	K	I	95.00%	67	M17: Oxidation	889.7742	3	3.3	64	87	No
TEGGATLTVKDDQVFPMNPPKYDK	K	I	95.00%	51		884.4431	3	4.0	64	87	No
TKYETDAIQR	R	T	95.00%	69		612.8171	2	3.2	1379	1388	Yes
TKYETDAIQR	R	T	95.00%	55		408.8806	3	3.1	1379	1388	Yes
TKYETDAIQRTEELEEAK	R	K	95.00%	74		1077.5420	2	8.6	1379	1396	Yes
TKYETDAIQRTEELEEAK	R	K	95.00%	38		718.6949	3	5.7	1379	1396	Yes
TKYETDAIQRTEELEEAK	R	K	95.00%	31		539.2729	4	5.3	1379	1396	Yes
TLAQLFSGAQTAEGEGAGGGAK	K	K	95.00%	170		1011.0050	2	3.9	619	640	No
TLAQLFSGAQTAEGEGAGGGAK	K	K	95.00%	109		674.3394	3	4.1	619	640	No

TLAQLFSGAQTAEGEGAGGGAKK	K	G	95.00%	41		717.0399	3	6.9	619	641	No
TLEDQLSELK	R	S	95.00%	44		1175.6260	1	8.0	1257	1266	No
TLEDQLSELK	R	S	95.00%	72		588.3142	2	3.7	1257	1266	No
TLEDQLSELKSKEEEQQR	R	L	95.00%	60		730.7078	3	8.5	1257	1274	No
TNAACAALDKK	R	Q	95.00%	39		553.2895	2	3.1	1441	1451	Yes
TPGAMEHELVLHQLR	K	C	95.00%	68	M5: Oxidation	873.9575	2	6.3	686	700	Yes
TPGAMEHELVLHQLR	K	C	95.00%	75	M5: Oxidation	582.9732	3	4.5	686	700	Yes
TPGAMEHELVLHQLR	K	C	95.00%	35	M5: Oxidation	437.4808	4	2.1	686	700	Yes
TPGAMEHELVLHQLR	K	C	95.00%	109		865.9571	2	2.9	686	700	Yes
TPGAMEHELVLHQLR	K	C	95.00%	77		577.6414	3	4.2	686	700	Yes
TPGAMEHELVLHQLR	K	C	95.00%	45		433.4824	4	2.8	686	700	Yes
TSVFVAEPK	K	E	95.00%	36		977.5336	1	2.9	36	44	Yes
TSVFVAEPK	K	E	95.00%	71		489.2706	2	2.6	36	44	Yes
TVNTKRVIQYFATIAVTGEK	K	K	95.00%	35		747.0939	3	9.4	186	205	Yes
VGNEYVTK	K	G	95.00%	69		455.2391	2	2.3	409	416	Yes
VIQYFATIAVTGEK	R	K	95.00%	132		770.4273	2	2.9	192	205	Yes
VIQYFATIAVTGEK	R	K	95.00%	82		513.9557	3	6.0	192	205	Yes
VKELTYQTEEDR	R	K	95.00%	71		755.8765	2	4.1	1853	1864	No
VKELTYQTEEDRK	R	N	95.00%	86		819.9239	2	3.7	1853	1865	Yes
VKELTYQTEEDRK	R	N	95.00%	58		546.9517	3	3.3	1853	1865	Yes
VKELTYQTEEDRK	R	N	95.00%	40		410.4650	4	1.6	1853	1865	Yes
VKNLTEEMAGLDETIAK	K	L	95.00%	107	M8: Oxidation	939.4888	2	8.8	981	997	Yes
VKNLTEEMAGLDETIAK	K	L	95.00%	57	M8: Oxidation	626.6605	3	6.7	981	997	Yes
VKNLTEEMAGLDETIAK	K	L	95.00%	140		931.4891	2	6.4	981	997	Yes
VKNLTEEMAGLDETIAK	K	L	95.00%	63		621.3273	3	4.2	981	997	Yes
VKVGNEYVTK	R	G	95.00%	59		568.8224	2	4.7	407	416	Yes
VLNASAIPEGQFIDSK	K	K	95.00%	115		844.9546	2	9.1	730	745	Yes
VLNASAIPEGQFIDSK	K	K	95.00%	76		563.6365	3	4.6	730	745	Yes
VLNASAIPEGQFIDSKK	K	A	95.00%	88		909.0018	2	8.1	730	746	Yes
VLNASAIPEGQFIDSKK	K	A	95.00%	54		606.3343	3	3.4	730	746	Yes
VQLLHTQNTSLINTK	R	K	95.00%	116		855.4858	2	5.1	1719	1733	Yes
VQLLHTQNTSLINTK	R	K	95.00%	74		570.6585	3	2.8	1719	1733	Yes
VQLLHTQNTSLINTKK	R	K	95.00%	102		919.5307	2	1.9	1719	1734	Yes
VQLLHTQNTSLINTKK	R	K	95.00%	62		613.3572	3	3.3	1719	1734	Yes
VQLLHTQNTSLINTKK	R	K	95.00%	34		460.2692	4	1.7	1719	1734	Yes
VRELEGEVESEQK	R	R	95.00%	79		766.3853	2	1.5	1825	1837	Yes
VRELEGEVESEQK	R	R	95.00%	42		511.2623	3	7.0	1825	1837	Yes
VRELEGEVESEQKR	R	N	95.00%	95		844.4380	2	3.9	1825	1838	Yes
VRELEGEVESEQKR	R	N	95.00%	87		563.2943	3	3.4	1825	1838	Yes
VRELEGEVESEQKR	R	N	95.00%	57		422.7220	4	1.9	1825	1838	Yes
VVFQLK	R	A	95.00%	28		733.4636	1	3.2	276	281	No
VVFQLKAER	R	S	95.00%	35		545.3275	2	4.7	276	284	No
YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	39	M10: Oxidation	695.3429	4	6.3	85	107	Yes
YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	51	M7: Oxidation	695.3415	4	4.3	85	107	Yes
YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	44	M7: Oxidation	932.1197	3	6.5	85	107	Yes
YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	41	M7: Oxidation	699.3425	4	7.5	85	107	Yes
YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	38	M7: Oxidation	703.3388	4	4.1	85	107	Yes
YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	45	M7: Oxidation, M10: Oxidation	932.1219	3	8.8	85	107	Yes
YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	47	M7: Oxidation, M10: Oxidation	699.3423	4	7.3	85	107	Yes
YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	44	M7: Oxidation, M9: Oxidation	932.1197	3	6.5	85	107	Yes
YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	37	M7: Oxidation, M9: Oxidation	699.3398	4	3.7	85	107	Yes
YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	38	M7: Oxidation, M9: Oxidation	703.3388	4	4.1	85	107	Yes
YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	38	M7: Oxidation, M9: Oxidation, M10: Oxidation	703.3388	4	4.1	85	107	Yes
YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	37	M9: Oxidation	695.3418	4	4.7	85	107	Yes
YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	44	M9: Oxidation	932.1201	3	6.8	85	107	Yes

				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	42	M9: Oxidation	699.3422	4	7.2	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	44	M9: Oxidation, M10: Oxidation	932.1201	3	6.8	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	54	M9: Oxidation, M10: Oxidation	699.3412	4	5.7	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	48		691.3441	4	6.3	85	107	Yes
				YETDAIQR	K	T	95.00%	34		498.2464	2	5.1	1381	1388	Yes
				YKVLNASAIPEGQFIDSK	R	K	95.00%	110		990.5358	2	9.8	728	745	Yes
				YKVLNASAIPEGQFIDSK	R	K	95.00%	53		660.6901	3	5.3	728	745	Yes
				YKVLNASAIPEGQFIDSKK	R	A	95.00%	82		703.3906	3	8.1	728	746	Yes
				YKVLNASAIPEGQFIDSKK	R	A	95.00%	28		527.7926	4	3.7	728	746	Yes
50	IPI00007926	C6orf108	C-MYC-RESPONSIVE PROTEIN RCL.	FGTVLTEHVAAAELGAR	R	G	95.00%	29		871.4609	2	-5.6	49	65	No
				FGTVLTEHVAAAELGAR	R	G	95.00%	61		581.3182	3	8.8	49	65	No
				YFEADPPGQVAASPDPTT	R	-	95.00%	72		931.9316	2	5.4	157	174	No
51	IPI00008215	ME1	NADP-DEPENDENT MALIC ENZYME.	DLAFTLEER	K	Q	95.00%	35		547.2827	2	4.1	27	35	No
				DMAAFNERPIIFALSNPTSK	K	A	95.00%	56	M2: Oxidation	746.7180	3	6.8	393	412	No
				GHIASVLNAWPEDVIK	R	A	95.00%	66		874.9781	2	8.4	131	146	No
				GLFITIHDR	R	G	95.00%	37		536.3048	2	6.0	122	130	No
				GSEYDDFLDEFMEAVSSK	R	Y	95.00%	104	M12: Oxidation	1042.9440	2	7.4	218	235	No
				NFEHLNSDFDR	K	Y	95.00%	35		697.3160	2	7.6	61	71	No
				TATVYPEPQNK	K	E	95.00%	50		624.3223	2	7.6	526	536	No
52	IPI00008418; IPI00219865; IPI00789460; IPI00794003	DIABLO	ISOFORM 1 OF DIABLO HOMOLOG, MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF DIABLO HOMOLOG, MITOCHONDRIAL PRECURSOR.; 19 KDA PROTEIN.; 18 KDA PROTEIN.	AESEQEAYLRED	R	-	95.00%	62		720.3254	2	9.7	228	239	No
				AVYTLTSLYR	K	Q	95.00%	50		593.8289	2	2.3	53	62	No
				LAEAQIEELR	K	Q	95.00%	72		586.3259	2	9.8	208	217	No
				SEPHSLSSEALMR	K	R	95.00%	32	M12: Oxidation	487.2368	3	6.7	63	75	No
53	IPI00008485	ACO1	IRON-RESPONSIVE ELEMENT-BINDING PROTEIN 1.	ANYLASPPLVIAYAIAGTIR	R	I	95.00%	54		1037.5970	2	8.0	548	567	No
				FVEFFGPGVAQLSIADR	K	A	95.00%	81		926.9877	2	4.2	277	293	No
				GPFLLGIK	K	A	95.00%	39		422.7718	2	7.2	786	793	No
				IDFEKEPLGVNAK	R	G	95.00%	42		487.2677	3	5.1	568	580	No
				IETVNESWNALATPSDK	K	L	95.00%	87		937.9639	2	3.4	616	632	No
				QAPQTIHLPSGEILDVFDAAER	K	Y	95.00%	60		803.0839	3	4.3	737	758	No
				VILQDFTGVPAVVDFAAMR	R	D	95.00%	87	M18: Oxidation	1033.0510	2	6.9	83	101	No
				VILQDFTGVPAVVDFAAMR	R	D	95.00%	49	M18: Oxidation	689.0339	3	3.2	83	101	No
				VLLEAAIR	R	N	95.00%	35		442.7845	2	4.9	41	48	No
				YQQAGLPLIVLAGK	R	E	95.00%	58		735.9407	2	3.4	759	772	No
54	IPI00008530; IPI00556485; IPI00791188; IPI00792267; IPI00793002; IPI00793584; IPI00794884	RPLP0	60S ACIDIC RIBOSOMAL PROTEIN P0.; RPLP0 PROTEIN.; 18 KDA PROTEIN.; 16 KDA PROTEIN.; 19 KDA PROTEIN.; 23 KDA PROTEIN.; 24 KDA PROTEIN.	GHLENNPALEK	R	L	95.00%	47		611.3198	2	7.2	67	77	No
				GNVGFVFTK	R	E	95.00%	40		484.7666	2	5.0	84	92	No
				GTIEILSDVQLIK	R	T	95.00%	74		714.9258	2	8.5	150	162	No
				IIQLLDDYPK	K	C	95.00%	66		609.3489	2	9.4	17	26	No
				TSFFQALGITTK	K	I	95.00%	100		657.3638	2	6.9	135	146	No
				VLALSVETDYTFPLAEK	R	V	95.00%	56		948.5131	2	9.3	248	264	No
55	IPI00008994; IPI00218108; IPI00218109; IPI00382995	NDRG2	ISOFORM 1 OF PROTEIN NDRG2.; ISOFORM 2 OF PROTEIN NDRG2.; ISOFORM 3 OF PROTEIN NDRG2.; CYTOPLASMIC PROTEIN NDR1.	GWMDWAAHK	K	L	95.00%	31	M3: Oxidation	559.2505	2	3.7	177	185	No
				ILLDQGQTHSVETPYGSVTFTVYGTPKPK	R	R	95.00%	84		1055.2240	3	7.7	33	61	No
				LDPTQTSFLK	K	M	95.00%	48		575.3138	2	3.4	278	287	No
				LTGLTSSIPEMILGHLFSQEELSGNSELIQK	K	Y	95.00%	49	M11: Oxidation	1129.9280	3	9.9	186	216	No
				MADSGGQPQLTQPGK	K	L	95.00%	102	M1: Oxidation	765.8677	2	3.3	288	302	No
				MADSGGQPQLTQPGK	K	L	95.00%	39	M1: Oxidation	510.9159	3	6.2	288	302	No
				MADSGGQPQLTQPGK	K	L	95.00%	60		757.8745	2	8.9	288	302	No
				NIITHAPNLDNIELYWNSYNNR	R	R	95.00%	60		892.1123	3	7.4	219	240	No
				RPAILTYHDVGLNYK	K	S	95.00%	84		880.4828	2	4.7	62	76	No
				RPAILTYHDVGLNYK	K	S	95.00%	65		587.3244	3	4.6	62	76	No
				RPAILTYHDVGLNYK	K	S	95.00%	38		440.7449	4	3.7	62	76	No
				TASLTSAASVDGNR	R	S	95.00%	54		675.3409	2	5.9	330	343	No
				YALNHPDTVEGLVLINIDPNAK	R	G	95.00%	64		802.7676	3	8.3	155	176	No
56	IPI00009236	CAV1	ISOFORM ALPHA OF CAVEOLIN-1.	ASFTTFTVTK	K	Y	95.00%	27		551.7985	2	9.6	87	96	No
				YVDSEGHLYTVPIR	K	E	95.00%	42		550.2881	3	9.3	6	19	No

57	IPI00009253	NAPA	ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN.	AIAHYEQSADYYKGEESNSSANK	K	C	95.00%	51		854.7241	3	7.1	141	163	No
				EAEAMALLAEAER	K	K	95.00%	67	M5: Oxidation	710.3496	2	8.7	7	19	No
				TIQGDEEDLR	K	-	95.00%	43		588.2865	2	8.9	286	295	No
58	IPI00009550	APOBEC2	PROBABLE C-]U-EDITING ENZYME APOBEC-2.	AFQPWEDIQENFLYYEEK	K	L	95.00%	77		1175.0500	2	8.5	201	218	No
				ELIELPPFEIVTGER	K	L	95.00%	37		871.4792	2	7.2	32	46	No
				IMKPQDFEYVWQNFVEQEEGESK	R	A	95.00%	52		954.1160	3	6.5	178	200	No
				LFMWEEPEIQAALK	R	K	95.00%	33	M3: Oxidation	860.9426	2	8.8	154	167	No
				LFMWEEPEIQAALK	R	K	95.00%	37	M3: Oxidation	574.2978	3	9.2	154	167	No
				LFMWEEPEIQAALK	R	K	95.00%	73		852.9459	2	9.8	154	167	No
				LFMWEEPEIQAALKK	R	L	95.00%	50	M3: Oxidation	616.9964	3	8.8	154	168	No
				LKELIELPPFEIVTGER	K	L	95.00%	65		661.7144	3	5.3	30	46	No
				LPANFFK	R	F	95.00%	29		836.4724	1	6.3	47	53	No
				LPANFFK	R	F	95.00%	52		418.7393	2	4.5	47	53	No
59	IPI00009551	MYOT	MYOTILIN.	EALIQDLER	K	K	95.00%	54		543.7960	2	4.0	155	163	No
				FIQVPENMSIDEGR	R	F	95.00%	68	M8: Oxidation	825.8973	2	4.3	252	265	No
				FSASSTLSSHITMSSSAFPASPQQHAGSNPGQR	R	V	95.00%	78	M13: Oxidation	1126.2020	3	8.7	52	84	No
				GLHSLIFEVVR	K	A	95.00%	55		635.3716	2	2.7	304	314	No
				GLHSLIFEVVR	K	A	95.00%	43		423.9171	3	3.0	304	314	No
				LAAQSGLYESEEL	R	-	95.00%	82		705.3486	2	6.7	486	498	No
				LDVTARPNQTLPAPK	R	Q	95.00%	36		810.9630	2	6.5	438	452	No
				LLGPQNAAAVFQAQDDSGAQDSQQHNSEHAR	R	L	95.00%	54		823.3898	4	5.6	189	219	No
				LQPPGPETSSFSSQTK	R	Q	95.00%	47		845.9222	2	4.5	21	36	No
				LQVPTSQVR	R	S	95.00%	25		514.3010	2	3.9	220	228	No
				QAFNPEGEFQR	K	L	95.00%	74		661.8131	2	4.1	475	485	No
				QSSIIIQPR	K	Q	95.00%	52		521.3061	2	-1.4	37	45	No
				VSGLPAPDVSWYLNGR	K	T	95.00%	81		865.9545	2	8.5	273	288	No
60	IPI00009896	EPHX1	EPOXIDE HYDROLASE 1.	DVELLYPVK	R	E	95.00%	48		538.3082	2	4.2	278	286	No
				EDDSIRPFKVETSDEEIHDLHQR	R	I	95.00%	38		699.5888	4	2.9	44	66	No
				FLGLTER	R	D	95.00%	36		418.2389	2	2.7	271	277	No
				FLSVLER	K	-	95.00%	44		432.2550	2	3.5	448	454	No
				GGHFAAFEEPELLAQDIR	R	K	95.00%	115		1000.5080	2	9.7	429	446	No
				GGHFAAFEEPELLAQDIR	R	K	95.00%	48		667.3395	3	7.5	429	446	No
				GGHFAAFEEPELLAQDIRK	R	F	95.00%	57		710.0378	3	7.0	429	447	No
				IIPLLTDPK	K	N	95.00%	21		505.3224	2	6.8	160	168	No
				PLLMVHGWPGSFYEFYK	K	I	95.00%	34	M4: Oxidation	696.3471	3	7.5	143	159	No
				VFYSLMR	K	E	95.00%	29	M6: Oxidation	466.2422	2	5.8	289	295	No
				YLEDGGLER	R	K	95.00%	30		526.2600	2	5.7	339	347	No
61	IPI00009943; IPI00550900	TPT1	TUMOR PROTEIN, TRANSLATIONALLY-CONTROLLED 1.; TRANSLATIONALLY-CONTROLLED TUMOR PROTEIN.	HILANFK	K	N	95.00%	29		421.7501	2	4.1	124	130	No
				VKPFMTGAAEQIK	R	H	95.00%	42	M5: Oxidation	718.3907	2	8.1	111	123	No
				VKPFMTGAAEQIK	R	H	95.00%	55	M5: Oxidation	479.2604	3	2.5	111	123	No
62	IPI00010080	OXSR1	SERINE/THREONINE-PROTEIN KINASE OSR1.	DLVIVAANLQK	R	I	95.00%	62		592.3611	2	7.8	478	488	No
				DTAEGVSQELISAGLVDGR	R	D	95.00%	106		958.9902	2	8.3	459	477	No
				EVLEGLEYLHK	R	N	95.00%	76		665.3610	2	6.3	129	139	No
				IPISLVLR	K	L	95.00%	63		455.8107	2	5.0	432	439	No
				LLSGGSVLDIIK	K	H	95.00%	86		607.8758	2	6.2	94	105	No
				SGVLDESTIATILR	K	E	95.00%	108		737.9163	2	8.6	115	128	No
63	IPI00010182; IPI00218836; IPI00815745	DBI	ISOFORM A 1 OF ACYL-COA-BINDING PROTEIN.; ISOFORM 2 OF ACYL-COA-BINDING PROTEIN.; DIAZEPAM BINDING INHIBITOR ISOFORM 2.	AYINKVEELK	K	K	95.00%	41		603.8461	2	9.0	74	83	No
				PGMLDFTGK	R	A	95.00%	38	M3: Oxidation	491.2422	2	4.8	46	54	No
				QATVGDINTERPGMLDFTGK	K	A	95.00%	43	M14: Oxidation	722.6926	3	5.4	35	54	No
				TKPSDEEMLFIYGHYK	K	Q	95.00%	36	M8: Oxidation	658.6546	3	8.3	19	34	No
				TKPSDEEMLFIYGHYK	K	Q	95.00%	45	M8: Oxidation	494.2413	4	5.1	19	34	No
				WDAWNELK	K	G	95.00%	36		531.2601	2	6.2	57	64	No
64	IPI00010271; IPI00219675; IPI00394837	RAC1	ISOFORM A OF RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 PRECURSOR.; ISOFORM B OF RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 PRECURSOR.; RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 ISOFORM RAC1C.	KLTPITYPQGLAMAK	K	E	95.00%	48	M13: Oxidation	549.9803	3	6.4	152	166	No
				LTPITYPQGLAMAK	K	E	95.00%	37	M12: Oxidation	760.4208	2	9.3	153	166	No

65	IPI00010331; IPI00016807	SIRT5	ISOFORM 2 OF NAD-DEPENDENT DEACETYLASE SIRTUIN-5.; ISOFORM 1 OF NAD-DEPENDENT DEACETYLASE SIRTUIN-5.	GAPEPGTQDASIPVEK	K	L	95.00%	88		798.4052	2	6.7	188	203	No
				NLLEIHGSLFK	K	T	95.00%	33		635.8678	2	9.2	153	163	No
				RVVVITQNIDELHR	R	K	95.00%	60		564.6617	3	8.0	134	147	No
66	IPI00010414; IPI00798196	PDLIM1	PDZ AND LIM DOMAIN PROTEIN 1.; 29 KDA PROTEIN.	DFEQPLAISR	K	V	95.00%	41		588.3087	2	2.9	23	32	No
				MNLASEPQEVLHIGSAHNR	K	S	95.00%	48	M1: Oxidation	530.5186	4	7.3	104	122	No
				SAMPFTASPASSTTAR	R	V	95.00%	81	M3: Oxidation	799.8859	2	9.7	123	138	No
				VTPPEGYEVVTVFPK	R	-	95.00%	42		831.4498	2	7.6	315	329	No
67	IPI00010418; IPI00743335; IPI00829992	MYO1C	MYOSIN-IC.; MYOSIN IC ISOFORM A.; MYOSIN IC ISOFORM B.	DGTIDFTPGSELLITK	R	A	95.00%	68		853.9514	2	5.5	1032	1047	No
				GEELLSPLNLEQAAYAR	K	D	95.00%	92		937.4922	2	5.6	362	378	No
				LLQSNPVLEAFGNAK	R	T	95.00%	50		800.9434	2	5.6	139	153	No
				MSLLQLVEILQSK	K	E	95.00%	84	M1: Oxidation	759.4399	2	6.9	606	618	No
				NPQSYLYLVK	R	G	95.00%	45		612.8398	2	7.3	225	234	No
				TLFATEDALEVR	K	R	95.00%	52		682.8636	2	9.6	687	698	No
				TSFLLNLR	R	R	95.00%	59		482.2880	2	5.6	814	821	No
				VLQALGSEPIQYAVPVVK	R	Y	95.00%	95		956.0569	2	5.5	910	927	No
				YLGLLENLR	K	V	95.00%	43		545.8204	2	6.2	613	621	No
68	IPI00010796	P4HB	PROTEIN DISULFIDE-ISOMERASE PRECURSOR.	EADDIVNWLK	R	K	95.00%	51		601.8101	2	5.3	121	130	No
				ENLLDFIK	K	H	95.00%	49		496.2789	2	3.4	223	230	No
				HNQLPLVIEFTEQTAPK	K	I	95.00%	108		983.0319	2	5.6	231	247	No
				HNQLPLVIEFTEQTAPK	K	I	95.00%	74		655.6915	3	7.0	231	247	No
				IKPHLMSQELPEDWDKQPVK	K	V	95.00%	41	M6: Oxidation	812.0906	3	4.9	351	370	No
				IKPHLMSQELPEDWDKQPVK	K	V	95.00%	47	M6: Oxidation	609.3206	4	5.9	351	370	No
				ILEFFGLK	R	K	95.00%	27		966.5754	1	9.1	301	308	No
				ILEFFGLK	R	K	95.00%	57		483.7891	2	4.0	301	308	No
				ILFIFIDSDHTDNQR	K	I	95.00%	95		917.4669	2	6.7	286	300	No
				KSNFAEALAAHK	R	Y	95.00%	38		429.5694	3	5.3	31	42	No
				LGETYKDHENIVIAK	K	M	95.00%	70		865.4641	2	4.5	410	424	No
				LGETYKDHENIVIAK	K	M	95.00%	47		577.3116	3	3.8	410	424	No
				LITLEEEMTK	R	Y	95.00%	58	M8: Oxidation	611.8201	2	6.7	317	326	No
				MDSTANEVEAVK	K	V	95.00%	75	M1: Oxidation	655.3034	2	3.4	425	436	No
				NFEDVAFDEKK	K	N	95.00%	44		671.3231	2	4.1	376	386	No
				NNFEGEVTKENLLDFIK	R	H	95.00%	35		670.6835	3	8.2	214	230	No
				SNFAEALAAHK	K	Y	95.00%	70		579.8012	2	3.3	32	42	No
				TGPAATTLPDGAAAESLVESSEVAVIGFFK	R	D	95.00%	89		979.1789	3	9.3	133	162	No
				THILLFLPK	K	S	95.00%	58		541.3455	2	5.1	255	263	No
				VDATEESDLAQQYGVR	K	G	95.00%	102		890.9261	2	5.1	82	97	No
				YKPESEELTAER	K	I	95.00%	56		726.3579	2	4.2	327	338	No
				YKPESEELTAER	K	I	95.00%	34		484.5733	3	1.7	327	338	No
				YQLDKDGVVLFK	K	K	95.00%	72		712.8961	2	3.6	196	207	No
				YQLDKDGVVLFK	K	K	95.00%	60		475.6001	3	3.8	196	207	No
69	IPI00010810	ETFA	ELECTRON TRANSFER FLAVOPROTEIN SUBUNIT ALPHA, MITOCHONDRIAL PRECURSOR.	AAVDAGFVPNDMQVGQTGK	R	I	95.00%	69		952.9708	2	8.3	250	268	No
				ASSTSPVEISEWLDQK	K	L	95.00%	93		888.9456	2	9.9	188	203	No
				GLLPEELTPLILATQK	K	Q	95.00%	65		868.5226	2	9.2	86	101	No
				GLLPEELTPLILATQK	K	Q	95.00%	55		579.3498	3	7.2	86	101	No
				GTSFDAAATSGGSASSEK	R	A	95.00%	121		815.8692	2	6.7	170	187	No
				LEVAPISDIIAIK	K	S	95.00%	69		691.4261	2	9.8	127	139	No
				LLYDLADQLHAAVGASR	K	A	95.00%	119		906.9928	2	9.4	233	249	No
				LLYDLADQLHAAVGASR	K	A	95.00%	69		604.9961	3	6.5	233	249	No
				SPDTFVR	K	T	95.00%	45		411.2148	2	7.3	140	146	No
				TIVAINKDPEAPIFQVADYGIVADLFK	K	V	95.00%	66		983.2071	3	8.0	295	321	No
				VLVAQHDVYK	K	G	95.00%	62		586.3311	2	5.7	76	85	No
70	IPI00011107	IDH2	ISOCITRATE DEHYDROGENASE [NADP], MITOCHONDRIAL PRECURSOR.	ATDFVADR	K	A	95.00%	41		447.7214	2	3.1	181	188	No
				DIFQEIFDK	K	H	95.00%	41		1154.5800	1	5.8	264	272	No
				DIFQEIFDK	K	H	95.00%	55		577.7952	2	7.8	264	272	No
				DQTDDQVTIDSALATQK	R	Y	95.00%	159		924.9539	2	9.1	90	106	No
				DQTDDQVTIDSALATQK	R	Y	95.00%	60		616.9709	3	7.5	90	106	No
				EKLILPHVDIQLK	K	Y	95.00%	67		773.4772	2	6.1	68	80	No
				EKLILPHVDIQLK	K	Y	95.00%	30		515.9878	3	6.8	68	80	No
				FAQMLEK	R	V	95.00%	42	M4: Oxidation	441.7250	2	2.9	394	400	No
				FAQMLEK	R	V	95.00%	43		433.7271	2	2.1	394	400	No

				FKDIFQEIFDK	R	H	95.00%	78		715.3778	2	7.6	262	272	No
				FKDIFQEIFDK	R	H	95.00%	54		477.2538	3	6.1	262	272	No
				FKDIFQEIFDKHYK	R	T	95.00%	43		929.4889	2	8.7	262	275	No
				FKDIFQEIFDKHYK	R	T	95.00%	46		619.9929	3	4.9	262	275	No
				FKDIFQEIFDKHYK	R	T	95.00%	37		465.2470	4	5.7	262	275	No
				GKLDGNQDLIR	R	F	95.00%	77		614.8373	2	1.3	383	393	No
				GKLDGNQDLIR	R	F	95.00%	42		410.2280	3	2.5	383	393	No
				GRPTSTNPIASIFAWTR	K	G	95.00%	80		938.0064	2	9.1	361	377	No
				GRPTSTNPIASIFAWTR	K	G	95.00%	75		625.6714	3	5.7	361	377	No
				IIWQFIK	R	E	95.00%	46		474.2942	2	9.1	61	67	No
				LDGNQDLIR	K	F	95.00%	64		522.2833	2	9.6	385	393	No
				LIDDMVAQVLK	R	S	95.00%	37	M5: Oxidation	1260.6980	1	8.1	289	299	No
				LIDDMVAQVLK	R	S	95.00%	99	M5: Oxidation	630.8519	2	6.7	289	299	No
				LIDDMVAQVLK	R	S	95.00%	92		622.8544	2	6.7	289	299	No
				LILPHVDIQLK	K	Y	95.00%	68		644.9088	2	8.0	70	80	No
				LILPHVDIQLK	K	Y	95.00%	44		430.2731	3	3.2	70	80	No
				LNEHFLNTTDFLDTIK	K	S	95.00%	94		960.9984	2	9.3	427	442	No
				LNEHFLNTTDFLDTIK	K	S	95.00%	69		640.9986	3	4.8	427	442	No
				LVPGWTKPITIGR	R	H	95.00%	60		719.4380	2	6.8	160	172	No
				LVPGWTKPITIGR	R	H	95.00%	46		479.9597	3	3.6	160	172	No
				MVFTPK	K	D	95.00%	27		722.3978	1	9.1	194	199	No
				NILGGTVFR	R	E	95.00%	57		488.7877	2	9.7	141	149	Yes
				PTSTNPIASIFAWTR	R	G	95.00%	108		831.4431	2	7.9	363	377	No
				PVVEMDGDEMTR	K	I	95.00%	66	M10: Oxidation	697.8043	2	5.3	49	60	No
				PVVEMDGDEMTR	K	I	95.00%	55	M5: Oxidation	697.8019	2	1.8	49	60	No
				PVVEMDGDEMTR	K	I	95.00%	67	M5: Oxidation	705.8010	2	4.2	49	60	No
				PVVEMDGDEMTR	K	I	95.00%	67	M5: Oxidation, M10: Oxidation	705.8010	2	4.2	49	60	No
				TIEAEAAHGTVTR	K	H	95.00%	107		678.3520	2	3.2	341	353	No
				TIEAEAAHGTVTR	K	H	95.00%	58		452.5698	3	1.3	341	353	No
				VAKPVVEMDGDEMTR	K	I	95.00%	77	M8: Oxidation	846.9026	2	2.1	46	60	No
				VAKPVVEMDGDEMTR	K	I	95.00%	65	M8: Oxidation	564.9377	3	2.2	46	60	No
				VAKPVVEMDGDEMTR	K	I	95.00%	77	M8: Oxidation	854.9019	2	4.2	46	60	No
				VAKPVVEMDGDEMTR	K	I	95.00%	86	M8: Oxidation	570.2722	3	7.1	46	60	No
				VAKPVVEMDGDEMTR	K	I	95.00%	77	M8: Oxidation, M13: Oxidation	854.9019	2	4.2	46	60	No
				VAKPVVEMDGDEMTR	K	I	95.00%	86	M8: Oxidation, M13: Oxidation	570.2722	3	7.1	46	60	No
				VAKPVVEMDGDEMTR	K	I	95.00%	81		838.9076	2	5.1	46	60	No
				VAKPVVEMDGDEMTR	K	I	95.00%	52		559.6060	3	2.1	46	60	No
				YFDLGLPNR	K	D	95.00%	51		1094.5700	1	5.6	81	89	No
				YFDLGLPNR	K	D	95.00%	58		547.7892	2	6.4	81	89	No
				YFDLGLPNRDQTDDQVTIDSALATQK	K	Y	95.00%	90		975.4889	3	7.9	81	106	No
71	IPI00011126	PSMC1	26S PROTEASE REGULATORY SUBUNIT 4.	APQETYADIGGLDNQIQEIK	K	E	95.00%	70		1102.0590	2	9.6	179	198	No
				GVILYGPPGTGK	K	T	95.00%	39		579.8320	2	3.1	221	232	No
				IKDYLLMEEEFIR	R	N	95.00%	60	M7: Oxidation	572.3011	3	8.8	68	80	No
				MTLADDVTLDDLIMAK	R	D	95.00%	96	M1: Oxidation, M14: Oxidation	898.9439	2	7.5	372	387	No
				TMLELLNQLDGFDSR	R	G	95.00%	109	M2: Oxidation	884.4419	2	9.7	308	322	No
				VAEEHAPSIVFIDEIDAIGTK	R	R	95.00%	49		752.0656	3	9.0	273	293	No
				VVGSELIQK	R	Y	95.00%	30		486.7931	2	5.6	250	258	No
72	IPI00011201	ME2	NAD-DEPENDENT MALIC ENZYME, MITOCHONDRIAL PRECURSOR.	HISDSVFLEAAK	R	A	95.00%	39		658.8495	2	4.5	485	496	No
				IETQDIQALR	K	F	95.00%	47		593.8313	2	9.6	58	67	No
				LFTPDVIR	R	A	95.00%	30		480.7834	2	7.3	398	405	No
73	IPI00011229	CTSD	CATHEPSIN D PRECURSOR.	DPDAQPGGELMLGGTDSK	R	Y	95.00%	107	M11: Oxidation	902.4130	2	5.9	236	253	No
				FDGILGMAYPR	K	I	95.00%	28	M7: Oxidation	628.3166	2	8.7	195	205	No
				VSTLPAITLK	K	L	95.00%	37		521.8336	2	7.6	332	341	No
74	IPI00011250; IPI00647149	UCHL3	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L3.; 17 KDA PROTEIN.	FLEESVSMSPEER	K	A	95.00%	51	M8: Oxidation	778.3583	2	8.9	122	134	No
				SQGQDVTSSVYFMK	K	Q	95.00%	76	M13: Oxidation	796.8687	2	1.8	75	88	No
				VTHETSAHEGQTEAPSIDEK	R	V	95.00%	55		722.6761	3	8.0	146	165	No
				YLENYDAIR	R	V	95.00%	43		578.7897	2	6.5	137	145	No
75	IPI00011285	CAPN1	CALPAIN-1 CATALYTIC SUBUNIT.	APSDLYQIILK	K	A	95.00%	77		630.8695	2	8.4	230	240	No
				DFFLANASR	R	A	95.00%	34		520.7643	2	4.1	463	471	No
				DMETIGFAVYEVPPELVGQPAVHLK	R	R	95.00%	80	M2: Oxidation	919.1470	3	8.6	437	461	No
				KAPSDLYQIILK	R	A	95.00%	66		694.9148	2	4.5	229	240	No
				KLYELIITR	K	Y	95.00%	32		574.8592	2	5.3	654	662	No

				LDETDDPDDYGDR	R	E	95.00%	70		763.3061	2	7.3	401	413	No
				LPPGEYVVVPSTFEPNKEGDFVLR	R	F	95.00%	31		897.1423	3	8.7	489	512	No
				LVFVHSAEGNEFWSALLEK	K	A	95.00%	33		726.0479	3	9.4	175	193	No
				LYELIITR	K	Y	95.00%	49		510.8105	2	3.7	655	662	No
				NYLSIFR	R	K	95.00%	44		456.7530	2	4.2	619	625	No
				QLAGEDMEISVK	R	E	95.00%	40	M7: Oxidation	668.3284	2	1.6	553	564	No
				RPTELLSNPQFIVDGATR	K	T	95.00%	74		672.0342	3	7.4	87	104	No
				SEQFINLR	R	E	95.00%	43		503.7735	2	7.0	474	481	No
				TLDTDLDGVVTFDLFK	K	W	95.00%	132		899.9680	2	9.0	691	706	No
				WNTTLYEGTWR	K	R	95.00%	42		713.8479	2	8.6	366	376	No
				YLGQDYEQLR	K	V	95.00%	63		642.8206	2	8.5	37	46	No
76	IPI00011416		ECH1	DELTA(3,5)-DELTA(2,4)-DIENOYL-COA ISOMERASE, MITOCHONDRIAL PRECURSOR.											
				EVDVGLAADVGTLQR	K	L	95.00%	34		771.9180	2	9.7	197	211	No
				EVDVGLAADVGTLQR	K	L	95.00%	51		514.9453	3	4.7	197	211	No
				HVLHVQLNRPNK	K	R	95.00%	45		727.9257	2	6.3	66	77	No
				HVLHVQLNRPNK	K	R	95.00%	26		485.6189	3	4.6	66	77	No
				HVLHVQLNRPNKR	K	N	95.00%	28		805.9782	2	8.1	66	78	No
				ISWYLR	R	D	95.00%	42		419.2372	2	5.2	138	143	No
				KMMADEALGSGLVSR	R	V	95.00%	101	M2: Oxidation, M3: Oxidation	798.8948	2	5.7	231	245	No
				LTGSSAQEEASGVALGEAPDHSYESLR	R	V	95.00%	34		921.1038	3	1.6	33	59	No
				MFTAGIDLMDMASDILQPK	K	G	95.00%	60	M1: Oxidation, M9: Oxidation, M11: Oxidation	715.6747	3	7.6	113	131	No
				MMADEALGSGLVSR	K	V	95.00%	87	M1: Oxidation, M2: Oxidation	734.8492	2	8.8	232	245	No
				MMADEALGSGLVSR	K	V	95.00%	112		718.8513	2	4.8	232	245	No
				VFPDKEVMLDAALALAAEISSK	R	S	95.00%	40		773.4227	3	8.8	246	267	No
				VIGNQSLVNELAFTAR	K	K	95.00%	111		866.4772	2	4.1	215	230	No
				VIGNQSLVNELAFTAR	K	K	95.00%	65		577.9905	3	9.6	215	230	No
				VNLLYSR	K	D	95.00%	38		432.7525	2	3.4	277	283	No
				YQETFNVIER	R	C	95.00%	58		649.8269	2	6.1	149	158	No
77	IPI00011525		CASQ1	CALSEQUESTRIN 1.	AFEDAAEEFHPYIPFFATFDSK	K	V	95.00%	91		1290.1020	2	7.7	196	217	No
				AFEDAAEEFHPYIPFFATFDSK	K	V	95.00%	74		860.4022	3	5.3	196	217	No
				ELQAFENIEDEIK	R	L	95.00%	100		789.3923	2	4.2	169	181	No
				ELQAFENIEDEIK	R	L	95.00%	45		526.5987	3	6.6	169	181	No
				ELQAFENIEDEIKLIGYFK	R	S	95.00%	49		767.0740	3	8.7	169	187	No
				GVGFGLVDSEK	K	D	95.00%	67		1107.5730	1	3.9	103	113	No
				GVGFGLVDSEK	K	D	95.00%	65		554.2908	2	4.5	103	113	No
				GVGFGLVDSEKDAAVAK	K	K	95.00%	92		831.9419	2	3.3	103	119	No
				GVGFGLVDSEKDAAVAK	K	K	95.00%	41		554.9629	3	1.5	103	119	No
				GVGFGLVDSEKDAAVAKK	K	L	95.00%	99		895.9917	2	5.7	103	120	No
				GVGFGLVDSEKDAAVAKK	K	L	95.00%	52		597.6627	3	4.0	103	120	No
				GVGFGLVDSEKDAAVAKK	K	L	95.00%	45		448.4985	4	2.9	103	120	No
				KLGLTEVDSMYVFK	K	G	95.00%	88	M10: Oxidation	823.4346	2	6.2	120	133	No
				KLGLTEVDSMYVFK	K	G	95.00%	49	M10: Oxidation	549.2911	3	3.9	120	133	No
				KLGLTEVDSMYVFK	K	G	95.00%	68		815.4382	2	7.5	120	133	No
				KYEVLALLYHEPPEDDK	K	A	95.00%	57		687.0231	3	7.1	63	79	No
				KYEVLALLYHEPPEDDK	K	A	95.00%	34		515.5203	4	9.0	63	79	No
				KYEVLALLYHEPPEDDKASQR	K	Q	95.00%	121		1251.1490	2	8.8	63	83	No
				KYEVLALLYHEPPEDDKASQR	K	Q	95.00%	83		834.4307	3	3.5	63	83	No
				KYEVLALLYHEPPEDDKASQR	K	Q	95.00%	66		626.0768	4	6.3	63	83	No
				LGLTEVDSMYVFK	K	G	95.00%	91	M9: Oxidation	759.3861	2	5.4	121	133	No
				LGLTEVDSMYVFK	K	G	95.00%	75		751.3912	2	8.9	121	133	No
				QFEMEELILELAAQVLEDK	R	G	95.00%	140	M4: Oxidation	1132.5830	2	9.0	84	102	No
				QFEMEELILELAAQVLEDK	R	G	95.00%	90	M4: Oxidation	755.3885	3	5.5	84	102	No
				QFEMEELILELAAQVLEDK	R	G	95.00%	61		750.0582	3	7.3	84	102	No
				YEVLALLYHEPPEDDK	K	A	95.00%	62		965.9816	2	5.8	64	79	No
				YEVLALLYHEPPEDDK	K	A	95.00%	47		644.3240	3	6.4	64	79	No
				YEVLALLYHEPPEDDKASQR	K	Q	95.00%	113		1187.1010	2	9.3	64	83	No
				YEVLALLYHEPPEDDKASQR	K	Q	95.00%	79		791.7358	3	7.9	64	83	No
				YEVLALLYHEPPEDDKASQR	K	Q	95.00%	37		594.0515	4	4.1	64	83	No
78	IPI00011635		BCL2L13	ISOFORM 2 OF BCL-2-LIKE 13 PROTEIN.	ALQMLLSQPVTYQAFR	K	E	95.00%	74	M4: Oxidation	941.5052	2	6.9	122	137	No
				EESLVEELSPASEK	R	K	95.00%	63		773.8840	2	7.3	418	431	No
				ELQEALPEAPAPLLPHITATSLLGTR	R	E	95.00%	33		913.5142	3	6.4	333	358	No
				EPDTEVITVEK	R	S	95.00%	40		630.3254	2	4.6	359	369	No

				ILVPLVLLR	K	Q	95.00%	63		518.3710	2	4.4	153	161	No
				LSPAGEMKPMPLSEGK	R	S	95.00%	32	M7: Oxidation, M10: Oxidation	852.4273	2	7.0	443	458	No
				YVVLSYLGLLSQEK	K	L	95.00%	92		806.4565	2	3.4	17	30	No
79	IPI00011770	NDUFA4	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 4.	FYSVNVDYSK	K	L	95.00%	57		611.2986	2	8.5	64	73	No
				LGPNDQYK	K	F	95.00%	63		467.7371	2	3.1	56	63	No
80	IPI00012007; IPI00827743	AHCY	ADENOSYLHOMOCYSTEINASE.; 31 KDA PROTEIN.	GISEETTTGVHNLYK	R	M	95.00%	86		824.9156	2	3.0	152	166	No
				IILLAEGR	R	L	95.00%	55		442.7842	2	4.0	336	343	No
				VADIGLAAWGR	K	K	95.00%	66		564.8151	2	5.0	9	19	No
				VAVVAGYGDVGK	K	G	95.00%	51		567.8129	2	1.8	215	226	No
				VPAINVNDSVTK	K	S	95.00%	73		628.8481	2	2.7	175	186	No
				YPQLLPGIR	K	G	95.00%	55		528.8168	2	4.7	143	151	No
81	IPI00012048; IPI00375531	NME1	NUCLEOSIDE DIPHOSPHATE KINASE A.; NON-METASTATIC CELLS 1, PROTEIN (NM23A) EXPRESSED IN ISOFORM A.	DRPFFAGLVK	K	Y	95.00%	50		575.3287	2	6.3	57	66	No
				GLVGEIIK	R	R	95.00%	27		414.7665	2	6.6	19	26	No
				GLVGEIIKR	R	F	95.00%	54		492.8185	2	8.4	19	27	Yes
				NIIHGSDSVESAEK	R	E	95.00%	38		743.3703	2	9.6	115	128	No
				VMLGETNPADSKPGTIR	R	G	95.00%	49	M2: Oxidation	901.4667	2	7.5	89	105	Yes
82	IPI00012268	PSMD2	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 2.	APVQPQQSPAAAPGGTDEKPSGK	K	E	95.00%	51		740.0431	3	1.4	9	31	No
				AVPLALALISVSNPR	R	L	95.00%	24		760.9694	2	9.6	689	703	No
				AVPLALALISVSNPR	R	L	95.00%	77		507.6469	3	5.6	689	703	No
				ELDIMEPK	R	V	95.00%	29	M5: Oxidation	495.7480	2	6.1	336	343	No
				FGGSGSQVDSAR	R	M	95.00%	30		584.2764	2	4.8	358	369	No
				LAQGLTHLGK	R	G	95.00%	41		519.3112	2	3.4	764	773	No
				LLTDDGNKWLYK	K	N	95.00%	44		733.3956	2	9.6	390	401	No
				LNILDTLSK	R	F	95.00%	58		508.8060	2	4.8	704	712	No
				MLVTFDEELRPLPVSVR	R	V	95.00%	46	M1: Oxidation	673.0356	3	5.8	829	845	No
				SETELKDTYAR	K	W	95.00%	47		656.8272	2	6.1	546	556	No
				TITGFQTHTTPVLLAHGER	K	A	95.00%	62		693.7076	3	3.9	861	879	No
				VGQAVDVVGQAGKPK	R	T	95.00%	97		726.9166	2	5.3	846	860	No
				VGQAVDVVGQAGKPK	R	T	95.00%	34		484.9455	3	2.1	846	860	No
83	IPI00012726; IPI00555747; IPI00642904; IPI00642944	PABPC4	ISOFORM 1 OF POLYADENYLATE-BINDING PROTEIN 4.; ISOFORM 2 OF POLYADENYLATE-BINDING PROTEIN 4.; POLY(A) BINDING PROTEIN, CYTOPLASMIC 4.; POLY(A) BINDING PROTEIN, CYTOPLASMIC 4.	ALDTMNFDVIK	R	G	95.00%	66	M5: Oxidation	641.8240	2	3.6	68	78	No
				EFSPFGSITSAK	K	V	95.00%	34		635.8217	2	2.8	313	324	No
				FSPAGPVLSIR	K	V	95.00%	46		572.3324	2	3.7	31	41	No
				ITGMLLEIDNSELLHMLESPESLR	K	S	95.00%	50	M4: Oxidation, M16: Oxidation	924.8050	3	7.0	577	600	No
				IVGSKPLYVALAQR	R	K	95.00%	49		757.9620	2	6.7	357	370	No
				IVGSKPLYVALAQR	R	K	95.00%	33		505.6423	3	3.5	357	370	No
				SLGYAYVNFQQPADAER	R	A	95.00%	117		964.9683	2	7.5	51	67	No
84	IPI00012728	ACSL1	ISOFORM 1 OF LONG-CHAIN-FATTY-ACID--COA LIGASE 1.	AELSLVFVDKPEK	K	A	95.00%	79		737.9163	2	5.9	193	205	No
				AELSLVFVDKPEK	K	A	95.00%	53		492.2789	3	3.4	193	205	No
				AILEDMVR	K	L	95.00%	41	M6: Oxidation	481.7555	2	5.0	633	640	No
				DGWLHTGDIGK	K	W	95.00%	34		599.8013	2	7.4	533	543	No
				DSGLKPFEQVK	K	G	95.00%	35		624.3368	2	1.6	644	654	No
				GITLHPELFSIDNGLLTPTMK	K	A	95.00%	57	M20: Oxidation	1157.1210	2	7.8	655	675	No
				GITLHPELFSIDNGLLTPTMK	K	A	95.00%	63	M20: Oxidation	771.7495	3	7.0	655	675	No
				GPNVFQGYLK	K	D	95.00%	56		561.8044	2	5.3	512	521	No
				GPNVFQGYLKDPAK	K	T	95.00%	64		767.4094	2	2.6	512	525	No
				GPNVFQGYLKDPAK	K	T	95.00%	44		511.9424	3	3.0	512	525	No
				IENIYMR	K	S	95.00%	34	M6: Oxidation	477.7422	2	5.0	573	579	No
				IFGQANTTLKR	R	W	95.00%	54		624.8608	2	5.8	377	387	No
				IFGQANTTLKR	R	W	95.00%	25		416.9091	3	3.9	377	387	No
				IGFFQGDIR	K	L	95.00%	64		526.7827	2	4.2	341	349	No
				IIVVMDAYGSELVER	K	G	95.00%	108	M5: Oxidation	855.4506	2	8.8	223	237	No
				KPDQPYEWLSYK	R	Q	95.00%	73		777.3935	2	9.6	113	124	No
				LAQGEYIAPEK	K	I	95.00%	72		609.8270	2	7.3	562	572	No
				LAQGEYIAPEKIENIYMR	K	S	95.00%	49	M17: Oxidation	718.7056	3	4.9	562	579	No
				LIPGLK	K	I	95.00%	27		640.4440	1	6.3	217	222	No
				LLLEGVENK	K	L	95.00%	31		1014.5920	1	7.8	208	216	No
				LLLEGVENK	K	L	95.00%	57		507.7982	2	4.8	208	216	No
				LMVTGAAPVSATVLTFLR	R	A	95.00%	142	M2: Oxidation	932.0304	2	6.2	430	447	No

				LMVTGAAPVSATVLTFLR	R	A	95.00%	87	M2: Oxidation	621.6905	3	7.7	430	447	No
				MPELVDFR	R	Q	95.00%	56	M1: Oxidation	511.7558	2	5.5	12	19	No
				SQIDDLYSTIK	R	-	95.00%	54		641.8340	2	5.4	687	697	No
				SQIDDLYSTIKV	R	-	95.00%	79		691.3688	2	5.9	687	698	No
				TAEALDKDGWLHTGDIGK	K	W	95.00%	106		963.9886	2	6.7	526	543	No
				TAEALDKDGWLHTGDIGK	K	W	95.00%	53		642.9943	3	5.6	526	543	No
				VLQPTVFPVVPR	K	L	95.00%	58		676.4144	2	7.9	357	368	No
				WLLDFASK	R	R	95.00%	37		490.2692	2	5.3	388	395	No
85	IPI00012750; IPI00401105; IPI00478694; IPI00740757	RPS25; hCG_1640785	40S RIBOSOMAL PROTEIN S25.; SIMILAR TO 40S RIBOSOMAL PROTEIN S25.; 14 KDA PROTEIN.; SIMILAR TO 40S RIBOSOMAL PROTEIN S25.	AALQELLSK	R	G	95.00%	63		486.7945	2	8.4	86	94	No
				DKLNNLVLFDK	R	A	95.00%	54		659.8787	2	9.3	42	52	No
				LITPAVVSER	K	L	95.00%	29		542.8263	2	7.5	67	76	No
				LNNLVLFDK	K	A	95.00%	35		538.3151	2	6.6	43	51	No
86	IPI00012912	CPT2	CARNITINE O-PALMITOYLTRANSFERASE 2, MITOCHONDRIAL PRECURSOR.	AGLLEPEVFHLNPAK	R	S	95.00%	41		817.9565	2	8.7	168	182	No
				ALEDMFDALEGK	K	S	95.00%	50	M5: Oxidation	677.8198	2	8.6	643	654	No
				DGSTAVHFEHSWGDGVAVLR	K	F	95.00%	45		714.0176	3	7.4	363	382	No
				DSTQTPAVTPQSQPATTDSTVTVQK	K	L	95.00%	41		863.4359	3	8.7	390	414	No
				DSVVLNFNPFMAFNPDPK	R	S	95.00%	101	M11: Oxidation	1034.5040	2	7.1	125	142	No
				ELHEQLVALDK	K	Q	95.00%	37		647.8561	2	2.7	94	104	No
				FFNEVFK	R	D	95.00%	46		465.7423	2	4.7	383	389	No
				KGNFYIFDVLDQDGNIVSPSEIQAHLK	R	Y	95.00%	67		1016.5300	3	8.5	248	274	No
				LNFELTDALK	K	T	95.00%	70		582.3218	2	3.9	415	424	No
				SFNLIIAK	K	D	95.00%	28		905.5507	1	5.1	355	362	No
				SFNLIIAK	K	D	95.00%	35		453.2788	2	4.0	355	362	No
				SIVPTMHYQDSLPR	R	L	95.00%	47	M6: Oxidation	830.4202	2	9.6	38	51	No
				YLSAQKPLLNDGQFR	R	K	95.00%	43		583.9842	3	4.5	64	78	No
87	IPI00013459; IPI00556190; IPI00791036	NDUFB5	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 5,MITOCHONDRIAL PRECURSOR.; NDUFB5 PROTEIN.; 22 KDA PROTEIN.	LFVIRPSR	R	F	95.00%	22		494.3120	2	5.8	54	61	No
				TMAVLQIEAEK	R	A	95.00%	63	M2: Oxidation	624.8351	2	9.2	134	144	No
				TMAVLQIEAEKAELR	R	V	95.00%	64	M2: Oxidation	859.4701	2	9.7	134	148	No
				TMAVLQIEAEKAELR	R	V	95.00%	51	M2: Oxidation	573.3135	3	5.3	134	148	No
88	IPI00013723	PIN1	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA-INTERACTING 1.	GDLGAFSR	R	G	95.00%	28		411.7118	2	5.7	120	127	No
				GQMQKPFEDASFALR	R	T	95.00%	38	M3: Oxidation	580.9567	3	9.5	128	142	No
				TGEMSGPVFTDSGIHIILR	R	T	95.00%	41	M4: Oxidation	682.6887	3	8.4	143	161	No
89	IPI00013745	PLCD4	PHOSPHOLIPASE C DELTA 4.	AEVQELFESFSADGQK	R	L	95.00%	112		892.9255	2	4.9	207	222	No
				AQTLLIQVISGQQLPK	K	V	95.00%	82		869.0234	2	6.4	627	642	No
				AQTLLIQVISGQQLPK	K	V	95.00%	72		579.6860	3	8.4	627	642	No
				DIQSSFHPEKPISPFK	R	A	95.00%	32		928.9902	2	9.5	611	626	No
				DIQSSFHPEKPISPFK	R	A	95.00%	29		619.6602	3	5.5	611	626	No
				EGSIVDPLVK	K	V	95.00%	27		528.8030	2	3.6	648	657	No
				EHYHFYEISSFSETK	K	A	95.00%	40		635.2909	3	3.7	514	528	No
				GLQLLVDLVTSMDHQER	R	L	95.00%	44	M12: Oxidation	657.3442	3	7.6	118	134	No
				GSAKPSFSISDVETIR	R	N	95.00%	77		847.4455	2	4.1	55	70	No
				GSAKPSFSISDVETIR	R	N	95.00%	41		565.2995	3	3.9	55	70	No
				LTLLEFLDFLQEEQKER	K	D	95.00%	42		717.7219	3	7.5	223	239	No
				RAEVQELFESFSADGQK	K	L	95.00%	58		647.6539	3	5.5	206	222	No
				SLAEELPLEQGFTIVFHGR	R	R	95.00%	32		715.0513	3	9.1	80	98	No
				VLVPELAMLR	R	F	95.00%	27	M8: Oxidation	578.8450	2	4.9	692	701	No
90	IPI00013847	UQCRC1	UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN 1, MITOCHONDRIALPRECURSOR.	ADLTEYLSTHYK	R	A	95.00%	90		720.8578	2	4.7	214	225	No
				ADLTEYLSTHYK	R	A	95.00%	49		480.9071	3	3.3	214	225	No
				DVVFNYLHATAFQGTPLAQAVEGPSENVR	R	K	95.00%	84		1044.2020	3	9.7	181	209	No
				DVVFNYLHATAFQGTPLAQAVEGPSENVR	R	K	95.00%	50		783.4022	4	8.2	181	209	No
				EVESMGAHLNAYSTR	K	E	95.00%	81	M5: Oxidation	840.8907	2	5.0	112	126	No
				EVESMGAHLNAYSTR	K	E	95.00%	48	M5: Oxidation	560.9295	3	4.6	112	126	No
				IAEVDASVVR	R	E	95.00%	63		1058.5910	1	6.1	433	442	No
				IAEVDASVVR	R	E	95.00%	89		529.7981	2	3.5	433	442	No

				IDDMMFVLQGQWMR	K	L	95.00%	52	M4: Oxidation, M5: Oxidation, M13: Oxidation	909.4141	2	9.7	365	378	No
				MKIDDMMFVLQGQWMR	R	L	95.00%	35	M1: Oxidation, M6: Oxidation, M7: Oxidation, M15: Oxidation	698.3196	3	4.8	363	378	No
				MVLAAAGGVEHQQLLDLAQK	R	H	95.00%	143	M1: Oxidation	1054.5700	2	7.3	229	248	No
				MVLAAAGGVEHQQLLDLAQK	R	H	95.00%	62	M1: Oxidation	703.3809	3	4.5	229	248	No
				MVLAAAGGVEHQQLLDLAQK	R	H	95.00%	47		698.0505	3	6.3	229	248	No
				NNGAGYFLEHLAFK	K	G	95.00%	92		790.9034	2	8.1	86	99	No
				NNGAGYFLEHLAFK	K	G	95.00%	35		527.6042	3	6.8	86	99	No
				RIPLAEWESR	R	I	95.00%	52		628.8436	2	3.4	423	432	No
				RIPLAEWESR	R	I	95.00%	49		419.5649	3	3.1	423	432	No
				SGMFWLR	R	-	95.00%	55	M3: Oxidation	456.7257	2	3.7	473	479	No
91	IPI00013860; IPI00479966	HIBADH	3-HYDROXYISOBUTYRATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.; HYPOTHETICAL PROTEIN (FRAGMENT).	DLGLAQDSATSTK	K	S	95.00%	70		653.8339	2	8.2	285	297	No
				EFQDAGEQVVSSPADVAEK	K	A	95.00%	90		1003.4790	2	7.5	77	95	No
				GSLLIDSSTIDPAVSK	K	E	95.00%	72		801.9414	2	9.8	126	141	No
				KDFSSVFQFLR	K	E	95.00%	52		687.3704	2	8.2	321	331	No
				KDFSSVFQFLR	K	E	95.00%	33		458.5833	3	9.1	321	331	No
				MGAVFMDAPVSGGVGAAR	K	S	95.00%	48	M1: Oxidation, M6: Oxidation	862.9075	2	-1.6	150	167	No
				MGAVFMDAPVSGGVGAAR	K	S	95.00%	54		846.9213	2	8.7	150	167	No
				SPILLGSLAHQIYR	K	M	95.00%	101		784.4588	2	8.7	298	311	No
				SPILLGSLAHQIYR	K	M	95.00%	64		523.3036	3	-0.5	298	311	No
				TPVGFIGLGNMGNPMAK	K	N	95.00%	51		852.4396	2	5.8	40	56	No
92	IPI00013894	STIP1	STRESS-INDUCED-PHOSPHOPROTEIN 1.	AAALEFLNR	K	F	95.00%	59		502.7823	2	3.8	79	87	No
				AMADPEVQQIMSDPAMR	R	L	95.00%	84	M2: Oxidation, M11: Oxidation, M16: Oxidation	969.4329	2	8.8	489	505	No
				DPQALSEHLK	K	N	95.00%	32		569.3035	2	7.6	514	523	No
				DPQALSEHLKNPVIAQK	K	I	95.00%	41		944.5265	2	8.3	514	530	No
				DPQALSEHLKNPVIAQK	K	I	95.00%	48		630.0179	3	4.5	514	530	No
				ELIEQLR	R	N	95.00%	29		450.7643	2	5.8	154	160	No
				KAAALEFLNR	R	F	95.00%	63		566.8309	2	5.3	78	87	No
				LAYINPDLALEEK	R	N	95.00%	65		744.9058	2	5.7	352	364	No
				LLEFQLALK	K	D	95.00%	58		537.8347	2	4.7	407	415	No
				LMDVGLIAIR	K	-	95.00%	78	M2: Oxidation	558.8287	2	3.8	534	543	No
				RAMADPEVQQIMSDPAMR	R	L	95.00%	34	M3: Oxidation, M12: Oxidation, M17: Oxidation	698.6594	3	9.8	488	505	No
				TVDLKPDWGK	K	G	95.00%	33		579.8132	2	2.0	64	73	No
				TYEEGLKHEANNPQLK	R	E	95.00%	48		935.9753	2	6.9	94	109	No
				TYEEGLKHEANNPQLK	R	E	95.00%	31		624.3198	3	7.3	94	109	No
				YKDAIHFYNK	K	S	95.00%	45		649.8353	2	7.2	316	325	No
				YKDAIHFYNK	K	S	95.00%	32		433.5575	3	2.6	316	325	No
93	IPI00013933	DSP	ISOFORM DPI OF DESMOPLAKIN.	AELIVQPELK	R	Y	95.00%	50		570.3402	2	4.1	85	94	No
				IEVLEEELR	K	L	95.00%	46		565.3135	2	7.7	1034	1042	No
				ITNLTQQLEQASIVK	K	K	95.00%	68		843.4829	2	8.3	1612	1626	No
				LLEAQIATGGIIDPK	R	E	95.00%	22		769.9507	2	8.9	2367	2381	No
				QAELDGKSAK	R	Q	95.00%	30		523.7789	2	1.6	1085	1094	No
				QLQNIIQATSR	R	E	95.00%	50		636.3630	2	8.6	271	281	No
				YGDGIQLTR	K	S	95.00%	43		511.7681	2	1.1	95	103	No
94	IPI00013991	TPM2	ISOFORM 1 OF TROPOMYOSIN BETA CHAIN.	AADESER	K	G	95.00%	29		777.3453	1	9.6	119	125	Yes
				AEQAEADKK	R	Q	95.00%	53		495.2527	2	7.3	22	30	No
				AISEELDNALNDITSL	K	-	95.00%	109		859.4310	2	2.6	269	284	No
				AISEELDNALNDITSL	K	-	95.00%	49		573.2928	3	7.5	269	284	No
				AMKDEEKMELQEMQLK	R	E	95.00%	84	M2: Oxidation, M13: Oxidation	1006.9740	2	2.7	134	149	No
				AMKDEEKMELQEMQLK	R	E	95.00%	65	M2: Oxidation, M8: Oxidation	1006.9800	2	8.2	134	149	No
				AMKDEEKMELQEMQLK	R	E	95.00%	33	M2: Oxidation, M8: Oxidation	671.6506	3	0.8	134	149	No
				AMKDEEKMELQEMQLK	R	E	95.00%	77	M2: Oxidation, M8: Oxidation	1014.9720	2	2.9	134	149	No
				AMKDEEKMELQEMQLK	R	E	95.00%	67	M2: Oxidation, M8: Oxidation	676.9842	3	3.7	134	149	No

AMKDEEKMELQEMQLK	R	E	95.00%	77	M2: Oxidation, M8: Oxidation, M13: Oxidation	1014.9720	2	2.9	134	149	No
AMKDEEKMELQEMQLK	R	E	95.00%	67	M2: Oxidation, M8: Oxidation, M13: Oxidation	676.9842	3	3.7	134	149	No
AMKDEEKMELQEMQLK	R	E	95.00%	61	M8: Oxidation, M13: Oxidation	1006.9760	2	5.1	134	149	No
ATDAEADVASLNR	K	R	95.00%	69		666.8254	2	2.6	78	90	Yes
ATDAEADVASLNR	K	R	95.00%	41		444.8863	3	2.9	78	90	Yes
ATDAEADVASLNRR	K	I	95.00%	32		744.8780	2	5.2	78	91	Yes
ATDAEADVASLNRR	K	I	95.00%	46		496.9205	3	3.5	78	91	Yes
EAQEKLEQAEKK	K	A	95.00%	45		715.8844	2	8.2	66	77	No
EDKYEEEIK	K	L	95.00%	30		591.7847	2	7.0	218	226	No
EDKYEEEIKLLEEK	K	L	95.00%	82		897.9592	2	5.0	218	231	No
EDKYEEEIKLLEEK	K	L	95.00%	37		598.9751	3	4.5	218	231	No
ENAIDRAEQAEADKK	K	Q	95.00%	51		844.4244	2	9.3	16	30	No
ENAIDRAEQAEADKK	K	Q	95.00%	34		563.2828	3	4.5	16	30	No
GTEDEVEK	K	Y	95.00%	44		453.7086	2	3.8	52	59	No
GTEDEVEKYSESVK	K	E	95.00%	100		800.3806	2	9.0	52	65	No
GTEDEVEKYSESVK	K	E	95.00%	35		533.9196	3	2.7	52	65	No
GTEDEVEKYSESVKEAQEK	K	L	95.00%	48		729.0127	3	3.5	52	70	No
HIAEDSDR	K	K	95.00%	45		471.7206	2	5.6	153	160	No
IQLVEEELDR	R	A	95.00%	57		1243.6630	1	7.9	92	101	Yes
IQLVEEELDR	R	A	95.00%	95		622.3312	2	0.8	92	101	Yes
IQLVEEELDRAQER	R	L	95.00%	66		864.4579	2	8.8	92	105	Yes
IQLVEEELDRAQER	R	L	95.00%	52		576.6364	3	0.4	92	105	Yes
KATDAEADVASLNR	K	R	95.00%	134		730.8758	2	6.3	77	90	Yes
KATDAEADVASLNR	K	R	95.00%	48		487.5850	3	3.3	77	90	Yes
KATDAEADVASLNRR	K	I	95.00%	48		808.9189	2	-3.5	77	91	Yes
KATDAEADVASLNRR	K	I	95.00%	62		539.6207	3	6.6	77	91	Yes
KATDAEADVASLNRR	K	I	95.00%	33		404.9667	4	4.7	77	91	Yes
KLVILEGELER	R	S	95.00%	94		649.8893	2	1.6	168	178	No
KLVILEGELER	R	S	95.00%	72		433.5980	3	7.5	168	178	No
KLVILEGELERSEER	R	A	95.00%	37		600.6729	3	9.0	168	182	No
LATALQKLEEAEK	R	A	95.00%	87		722.4111	2	5.7	106	118	Yes
LATALQKLEEAEK	R	A	95.00%	38		481.9438	3	6.8	106	118	Yes
LATALQKLEEAEKAADESER	R	G	95.00%	71		734.7194	3	7.8	106	125	Yes
LATALQKLEEAEKAADESER	R	G	95.00%	30		551.2904	4	5.8	106	125	Yes
LDKENAIDR	K	A	95.00%	45		537.2878	2	8.0	13	21	No
LEEAEKAADESER	K	G	95.00%	94		738.8469	2	2.8	113	125	Yes
LEEAEKAADESER	K	G	95.00%	63		492.8999	3	1.4	113	125	Yes
LEEAEKAADESERGMK	K	V	95.00%	62	M15: Oxidation	904.9289	2	9.0	113	128	Yes
LEEAEKAADESERGMK	K	V	95.00%	37	M15: Oxidation	603.6193	3	4.7	113	128	Yes
LKEAETR	K	A	95.00%	32		423.7403	2	4.9	232	238	Yes
LKGTEDEVEKYSESVK	K	E	95.00%	108		920.9661	2	3.4	50	65	No
LKGTEDEVEKYSESVK	K	E	95.00%	50		614.3133	3	3.2	50	65	No
LKGTEDEVEKYSESVK	K	E	95.00%	37		460.9861	4	1.5	50	65	No
LVILEGELER	K	S	95.00%	42		1170.6820	1	7.1	169	178	No
LVILEGELER	K	S	95.00%	85		585.8433	2	4.4	169	178	No
MELQEMQLK	K	E	95.00%	33	M1: Oxidation	583.2861	2	3.8	141	149	No
MELQEMQLK	K	E	95.00%	41	M1: Oxidation	591.2838	2	4.2	141	149	No
MELQEMQLK	K	E	95.00%	41	M1: Oxidation, M6: Oxidation	591.2838	2	4.2	141	149	No
MELQEMQLK	K	E	95.00%	36	M6: Oxidation	583.2852	2	2.3	141	149	No
MELQEMQLK	K	E	95.00%	34		575.2895	2	5.3	141	149	No
MQMLKLDKENAIDR	K	A	95.00%	36	M1: Oxidation, M3: Oxidation	868.9426	2	5.6	8	21	No
QLEEEQQALQK	K	K	95.00%	88		672.3480	2	5.5	38	48	No
QLEEEQQALQKK	K	L	95.00%	79		736.3961	2	5.8	38	49	No
RIQLVEEELDR	R	A	95.00%	73		700.3859	2	6.7	91	101	Yes
RIQLVEEELDR	R	A	95.00%	60		467.2593	3	5.4	91	101	Yes
RIQLVEEELDRAQER	R	L	95.00%	41		628.6716	3	2.7	91	105	Yes
RIQLVEEELDRAQER	R	L	95.00%	48		471.7569	4	5.3	91	105	Yes
SEERAEVAESK	R	C	95.00%	39		617.8019	2	3.7	179	189	No
SLEAQADK	K	Y	95.00%	31		431.2221	2	5.2	206	213	No
SLEAQADKYSTK	K	E	95.00%	80		670.8419	2	4.6	206	217	No
SLEAQADKYSTK	K	E	95.00%	36		447.5639	3	4.6	206	217	No
TIDDLEDEVYAQK	K	M	95.00%	105		769.8696	2	5.6	252	264	No
TIDDLEDEVYAQK	K	M	95.00%	54		513.5820	3	4.8	252	264	No

				YSESVKEAQEKLEQAEK	K	K	95.00%	80		998.5045	2	6.9	60	76	No
				YSESVKEAQEKLEQAEK	K	K	95.00%	32		666.0038	3	4.2	60	76	No
				YSTKEDKYEEEIK	K	L	95.00%	67		831.4021	2	3.1	214	226	No
				YSTKEDKYEEEIK	K	L	95.00%	31		554.6056	3	6.0	214	226	No
95	IPI00014398	FHL1	FOUR AND A HALF LIM DOMAINS 1 VARIANT.	AIVAGDQNVEYK	K	G	95.00%	80		653.8383	2	3.4	123	134	No
				HSGPSSYK	R	V	95.00%	34		431.7105	2	8.6	6	13	No
				KPIGADSK	R	E	95.00%	30		408.2377	2	5.8	61	68	No
				KPIGADSKEVHYK	R	N	95.00%	57		736.4056	2	8.5	61	73	No
				NFVAK	K	K	95.00%	25		578.3353	1	9.0	231	235	No
				NPITGFGK	K	G	95.00%	56		833.4571	1	5.7	242	249	No
				NPITGFGK	K	G	95.00%	50		417.2305	2	1.1	242	249	No
				QVIGTGSFFPK	K	G	95.00%	44		1180.6460	1	8.1	150	160	No
				QVIGTGSFFPK	K	G	95.00%	74		590.8245	2	3.6	150	160	No
96	IPI00014399	FHL3	FOUR AND A HALF LIM DOMAINS PROTEIN 3.	ELFYEDR	R	H	95.00%	36		971.4569	1	9.7	53	59	No
				ELFYEDR	R	H	95.00%	55		486.2306	2	6.0	53	59	No
				RPIVGLGGGK	K	Y	95.00%	50		477.3007	2	3.9	226	235	No
97	IPI00014424	EEF1A2	ELONGATION FACTOR 1-ALPHA 2.	EGNASGVSLLEALDTILPPTRPTDK	K	P	95.00%	101		865.4687	3	8.6	220	244	No
				EGNASGVSLLEALDTILPPTRPTDKPLR	K	L	95.00%	94		987.5497	3	9.3	220	247	No
				EGNASGVSLLEALDTILPPTRPTDKPLR	K	L	95.00%	33		740.9122	4	6.6	220	247	No
				EHALLAYTLGVK	R	Q	95.00%	74		657.8776	2	3.8	135	146	Yes
				EHALLAYTLGVK	R	Q	95.00%	44		438.9220	3	6.0	135	146	Yes
				EVSAYIK	K	K	95.00%	27		809.4472	1	7.8	173	179	No
				IGGIGTVPVGR	K	V	95.00%	42		1025.6200	1	8.7	256	266	Yes
				IGGIGTVPVGR	K	V	95.00%	90		513.3107	2	2.6	256	266	Yes
				LPLQDVYK	R	I	95.00%	39		975.5573	1	5.8	248	255	Yes
				LPLQDVYK	R	I	95.00%	61		488.2806	2	1.8	248	255	Yes
				MDSTEPAYSEK	K	R	95.00%	56	M1: Oxidation	637.2691	2	3.5	155	165	No
				MDSTEPAYSEK	K	R	95.00%	56		629.2739	2	7.1	155	165	No
				PGMVVTFAPVNITTEVK	R	S	95.00%	62	M3: Oxidation	909.9955	2	8.5	274	290	No
				QLIVGVNK	K	M	95.00%	42		870.5441	1	3.1	147	154	Yes
				QLIVGVNK	K	M	95.00%	37		435.7753	2	1.6	147	154	Yes
				QLIVGVNKMDSTEPAYSEK	K	R	95.00%	37	M9: Oxidation	709.0242	3	3.8	147	165	No
				QTVAVGVIK	R	N	95.00%	38		914.5709	1	3.7	431	439	No
				QTVAVGVIK	R	N	95.00%	43		457.7881	2	0.9	431	439	No
				RYDEIVK	K	E	95.00%	34		461.7557	2	4.0	166	172	No
				STTTGHLIYK	K	C	95.00%	53		560.8058	2	3.1	21	30	Yes
				THINIVVIGHVDSGK	K	S	95.00%	58		530.3015	3	4.8	6	20	Yes
				VETGILRPGMVVTFAPVNITTEVK	R	S	95.00%	73	M10: Oxidation	863.1512	3	8.2	267	290	No
				VETGILRPGMVVTFAPVNITTEVK	R	S	95.00%	27		857.8209	3	9.8	267	290	No
				YYITIIDAPGHR	K	D	95.00%	79		709.8791	2	4.9	85	96	No
				YYITIIDAPGHR	K	D	95.00%	74		473.5880	3	3.5	85	96	No
98	IPI00014439	QDPR	DIHYDROPTERIDINE REDUCTASE.	AALDGTPGMIGYGMAK	K	G	95.00%	65	M9: Oxidation, M14: Oxidation	792.8792	2	6.5	139	154	No
				EGGLLTLAGAK	K	A	95.00%	91		515.3052	2	7.6	128	138	No
				MTDSFTEQADQVTAEVGK	K	L	95.00%	38	M1: Oxidation	658.3036	3	7.2	56	73	No
				NRPSSGSLIQVVTTEGR	K	T	95.00%	51		900.9895	2	8.0	220	236	No
				NRPSSGSLIQVVTTEGR	K	T	95.00%	52		600.9953	3	7.5	220	236	No
				NSGMPPGAAAIAVLPVTLDTPMNR	K	K	95.00%	59	M4: Oxidation, M22: Oxidation	809.0865	3	9.0	168	191	No
99	IPI00014581; IPI00296039	TPM1	ISOFORM 1 OF TROPOMYOSIN-1 ALPHA CHAIN.; ISOFORM 4 OF TROPOMYOSIN-1 ALPHA CHAIN.	AADESER	K	G	95.00%	29		777.3453	1	9.6	119	125	Yes
				AEQAEADKK	R	A	95.00%	53		495.2527	2	7.3	22	30	No
				AISEELDHALNDMTSI	K	-	95.00%	65	M13: Oxidation	887.9175	2	5.8	269	284	Yes
				AISEELDHALNDMTSI	K	-	95.00%	35	M13: Oxidation	592.2813	3	6.4	269	284	Yes
				AISEELDHALNDMTSI	K	-	95.00%	44		879.9221	2	8.1	269	284	Yes
				AQKDEEKMEIQEIQLK	R	E	95.00%	88	M8: Oxidation	988.5129	2	8.3	134	149	No
				AQKDEEKMEIQEIQLK	R	E	95.00%	48	M8: Oxidation	659.3420	3	4.6	134	149	No
				ATDAEADVASLNR	K	R	95.00%	69		666.8254	2	2.6	78	90	Yes
				ATDAEADVASLNR	K	R	95.00%	41		444.8863	3	2.9	78	90	Yes
				ATDAEADVASLNRR	K	I	95.00%	32		744.8780	2	5.2	78	91	Yes
				ATDAEADVASLNRR	K	I	95.00%	46		496.9205	3	3.5	78	91	Yes
				DAQEKLELAEK	K	K	95.00%	42		637.3395	2	5.5	66	76	Yes
				DAQEKLELAEK	K	K	95.00%	39		425.2288	3	5.1	66	76	Yes
				DEEKMEIQEIQLK	K	E	95.00%	62	M5: Oxidation	824.9155	2	7.6	137	149	No

				ENALDRAEQAEADKK	K	A	95.00%	51		844.4244	2	9.3	16	30	No
				ENALDRAEQAEADKK	K	A	95.00%	34		563.2828	3	4.5	16	30	No
				GTEDELDKYSEALK	K	D	95.00%	100		799.3884	2	5.7	52	65	Yes
				GTEDELDKYSEALKDAQEK	K	L	95.00%	69		723.6816	3	4.3	52	70	Yes
				HIAEDADR	K	K	95.00%	31		463.7247	2	9.0	153	160	No
				HIAEDADRKYEEVAR	K	K	95.00%	54		901.4524	2	7.6	153	167	No
				HIAEDADRKYEEVAR	K	K	95.00%	31		601.3011	3	2.4	153	167	No
				HIAEDADRKYEEVAR	K	K	95.00%	31		451.2280	4	2.8	153	167	No
				IQLVEEELDR	R	A	95.00%	57		1243.6630	1	7.9	92	101	Yes
				IQLVEEELDR	R	A	95.00%	95		622.3312	2	0.8	92	101	Yes
				IQLVEEELDRAQER	R	L	95.00%	66		864.4579	2	8.8	92	105	Yes
				IQLVEEELDRAQER	R	L	95.00%	52		576.6364	3	0.4	92	105	Yes
				KATDAEADVASLNR	K	R	95.00%	134		730.8758	2	6.3	77	90	Yes
				KATDAEADVASLNR	K	R	95.00%	48		487.5850	3	3.3	77	90	Yes
				KATDAEADVASLNRR	K	I	95.00%	48		808.9189	2	-3.5	77	91	Yes
				KATDAEADVASLNRR	K	I	95.00%	62		539.6207	3	6.6	77	91	Yes
				KATDAEADVASLNRR	K	I	95.00%	33		404.9667	4	4.7	77	91	Yes
				KLVIIESDLER	R	A	95.00%	89		657.8894	2	5.7	168	178	No
				KLVIIESDLER	R	A	95.00%	58		438.9276	3	2.9	168	178	No
				KLVIIESDLERAEER	R	A	95.00%	30		900.5045	2	7.9	168	182	No
				KLVIIESDLERAEER	R	A	95.00%	53		600.6713	3	6.2	168	182	No
				LATALQKLEEAEK	R	A	95.00%	87		722.4111	2	5.7	106	118	Yes
				LATALQKLEEAEK	R	A	95.00%	38		481.9438	3	6.8	106	118	Yes
				LATALQKLEEAEKAADESER	R	G	95.00%	71		734.7194	3	7.8	106	125	Yes
				LATALQKLEEAEKAADESER	R	G	95.00%	30		551.2904	4	5.8	106	125	Yes
				LDKENALDR	K	A	95.00%	45		537.2878	2	8.0	13	21	Yes
				LEEAEKAADESER	K	G	95.00%	94		738.8469	2	2.8	113	125	Yes
				LEEAEKAADESER	K	G	95.00%	63		492.8999	3	1.4	113	125	Yes
				LEEAEKAADESERGMK	K	V	95.00%	62	M15: Oxidation	904.9289	2	9.0	113	128	Yes
				LEEAEKAADESERGMK	K	V	95.00%	37	M15: Oxidation	603.6193	3	4.7	113	128	Yes
				LKEAETR	K	A	95.00%	32		423.7403	2	4.9	232	238	Yes
				LKGTEDELDKYSEALK	K	D	95.00%	100		919.9786	2	5.6	50	65	Yes
				LKGTEDELDKYSEALK	K	D	95.00%	54		613.6548	3	5.4	50	65	Yes
				LKGTEDELDKYSEALK	K	D	95.00%	40		460.4929	4	4.8	50	65	Yes
				LVIIESDLER	K	A	95.00%	64		593.8419	2	6.3	169	178	No
				LVIIESDLERAEER	K	A	95.00%	43		836.4561	2	7.5	169	182	No
				LVIIESDLERAEER	K	A	95.00%	35		557.9724	3	5.7	169	182	No
				MEIQEIQLK	K	E	95.00%	52	M1: Oxidation	574.3075	2	3.2	141	149	No
				MQMLKLDKENALDR	K	A	95.00%	36	M1: Oxidation, M3: Oxidation	868.9426	2	5.6	8	21	Yes
				QLEDELVSLQK	K	K	95.00%	83		651.3500	2	-2.4	38	48	No
				QLEDELVSLQKK	K	L	95.00%	70		715.4048	2	7.9	38	49	No
				RIQLVEEELDR	R	A	95.00%	73		700.3859	2	6.7	91	101	Yes
				RIQLVEEELDR	R	A	95.00%	60		467.2593	3	5.4	91	101	Yes
				RIQLVEEELDRAQER	R	L	95.00%	41		628.6716	3	2.7	91	105	Yes
				RIQLVEEELDRAQER	R	L	95.00%	48		471.7569	4	5.3	91	105	Yes
				SIDDLEDELYAQK	K	L	95.00%	104		769.8660	2	1.0	252	264	No
				SIDDLEDELYAQK	K	L	95.00%	61		513.5827	3	6.3	252	264	No
				SKQLEDELVSLQK	R	K	95.00%	113		758.9185	2	4.4	36	48	No
				SKQLEDELVSLQK	R	K	95.00%	62		506.2813	3	3.8	36	48	No
				SKQLEDELVSLQKK	R	L	95.00%	68		822.9703	2	9.3	36	49	No
				SKQLEDELVSLQKK	R	L	95.00%	65		548.9800	3	4.3	36	49	No
				SKQLEDELVSLQKK	R	L	95.00%	33		411.9867	4	3.5	36	49	No
				SLEAQAEK	K	Y	95.00%	43		438.2304	2	6.3	206	213	Yes
				VLSDKLKEAETR	K	A	95.00%	59		694.8957	2	6.1	227	238	No
				YSQKEDRYEEEIK	K	V	95.00%	62		858.9160	2	9.3	214	226	No
				YSQKEDRYEEEIK	K	V	95.00%	36		572.9430	3	3.0	214	226	No
100	IPI00014852	PGM5	PHOSPHOGLUCOMUTASE-LIKE PROTEIN 5.	DLEALVTDK	R	S	95.00%	50		502.2716	2	4.1	388	396	No
				FDYEGLDPK	R	T	95.00%	45		542.2562	2	4.1	372	380	No
				FFSNLMDSGR	R	C	95.00%	57	M6: Oxidation	595.2731	2	6.2	305	314	No
				FNVANGGPAPDVVSDK	K	I	95.00%	84		793.8935	2	-1.5	75	90	No
				GGEYGFGAAFDADGDR	K	Y	95.00%	41		802.8396	2	5.9	222	237	No
				GLLTGPSQLK	K	I	95.00%	36		507.3061	2	4.5	154	163	No
				SFIGQQFAVGSHVYSVAK	K	T	95.00%	106		963.0049	2	5.1	397	414	No
				SFIGQQFAVGSHVYSVAK	K	T	95.00%	45		642.3394	3	5.5	397	414	No
				TDSFEYVDPVDGTVTK	K	K	95.00%	76		886.9226	2	8.0	415	430	No
				TDSFEYVDPVDGTVTKK	K	Q	95.00%	46		950.9698	2	7.1	415	431	No
				VEIVDPVDIYLNLLR	R	T	95.00%	110		886.0109	2	7.4	130	144	No
				VPVYETPAGWR	K	F	95.00%	36		637.8357	2	8.0	294	304	No

101	IPI00015141	CKMT2	CREATINE KINASE, SARCOMERIC MITOCHONDRIAL PRECURSOR.	DWPDAR	R	G	95.00%	44		759.3495	1	8.9	244	249	Yes
				EVENVAITALEGLK	R	G	95.00%	109		743.4170	2	6.4	187	200	No
				EVENVAITALEGLK	R	G	95.00%	65		495.9463	3	4.4	187	200	No
				EVENVAITALEGLKGDLAGR	R	Y	95.00%	49		685.7143	3	8.9	187	206	No
				GIWHNYDK	R	T	95.00%	28		1032.4990	1	8.0	250	257	No
				GIWHNYDK	R	T	95.00%	41		516.7514	2	4.5	250	257	No
				GQDIKVPPPLPQFGK	R	-	95.00%	47		540.9775	3	3.2	404	418	No
				GTGGVDTAAVADVYDISNIDR	R	I	95.00%	157		1055.0190	2	9.1	355	375	No
				GTGGVDTAAVADVYDISNIDR	R	I	95.00%	90		703.6804	3	7.3	355	375	No
				GWEFMWNER	R	L	95.00%	74	M5: Oxidation	635.7739	2	6.7	302	310	No
				GWEFMWNER	R	L	95.00%	51		627.7744	2	3.5	302	310	No
				HTTDLDASK	K	I	95.00%	55		494.2451	2	7.6	141	149	No
				ILENLR	K	L	95.00%	31		757.4597	1	3.1	345	350	No
				ITQGQFDEHYVLSSR	K	V	95.00%	117		890.4412	2	4.5	150	164	No
				ITQGQFDEHYVLSSR	K	V	95.00%	56		593.9640	3	5.6	150	164	No
				LFPPSADYPDLR	R	K	95.00%	64		695.8595	2	7.4	47	58	No
				LFPPSADYPDLRK	R	H	95.00%	37		759.9048	2	3.9	47	59	No
				LIDDHFLFDK	R	P	95.00%	51		421.5542	3	3.5	221	230	No
				LSEMTEQDQQR	K	L	95.00%	80	M4: Oxidation	690.8138	2	9.6	210	220	No
				LSEMTEQDQQR	K	L	95.00%	81		682.8136	2	5.6	210	220	No
				REVENVAITALEGLK	R	G	95.00%	120		821.4691	2	7.7	186	200	No
				REVENVAITALEGLK	R	G	95.00%	58		547.9806	3	5.1	186	200	No
				RGTGGVDTAAVADVYDISNIDR	K	I	95.00%	96		755.7149	3	8.0	354	375	No
				TFLIWINEEDHTR	K	V	95.00%	89		837.4237	2	6.4	258	270	No
				TFLIWINEEDHTR	K	V	95.00%	44		558.6182	3	6.0	258	270	No
				TVGMVAGDEESYEVFADLFDPVIK	K	L	95.00%	112	M4: Oxidation	1324.1410	2	9.5	105	128	No
				TVGMVAGDEESYEVFADLFDPVIK	K	L	95.00%	98	M4: Oxidation	883.0949	3	7.7	105	128	No
				TVGMVAGDEESYEVFADLFDPVIK	K	L	95.00%	116		1316.1370	2	4.3	105	128	No
				TVGMVAGDEESYEVFADLFDPVIK	K	L	95.00%	85		877.7638	3	8.4	105	128	No
				VPPPLPQFGK	K	-	95.00%	39		1079.6320	1	5.4	409	418	No
				VPPPLPQFGK	K	-	95.00%	56		540.3202	2	6.4	409	418	No
				VPPPLPQFGKK	K	-	95.00%	26		604.3666	2	3.9	409	419	No
				VPPPLPQFGKK	K	-	95.00%	32		403.2463	3	2.2	409	419	No
102	IPI00015421	KLHL31	KELCH-LIKE PROTEIN 31.	VLVTGGYIANAYSR	R	S	95.00%	74		742.4028	2	4.6	468	481	No
				VYVMGGSQLGPR	R	G	95.00%	72	M4: Oxidation	640.3309	2	5.4	515	526	No
				YAADLLSNIR	K	F	95.00%	52		568.3119	2	4.3	250	259	No
103	IPI00015833	CHCHD3	COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN-CONTAINING PROTEIN 3.	LSENVIDR	R	M	95.00%	49		473.2579	2	7.9	28	35	No
				RVAEELALEQAKK	R	E	95.00%	45		495.6219	3	4.2	65	77	No
				VAEELALEQAK	R	K	95.00%	84		600.8314	2	6.0	66	76	No
				VAEELALEQAKK	R	E	95.00%	60		664.8806	2	8.1	66	77	No
				VAEELALEQAKK	R	E	95.00%	36		443.5868	3	1.5	66	77	No
				YSGAYGASVSDEELK	R	R	95.00%	115		788.3681	2	6.7	49	63	No
				YSGAYGASVSDEELKR	R	R	95.00%	98		866.4198	2	7.4	49	64	No
104	IPI00015865	ADPRHL2	POLY(ADP-RIBOSE) GLYCOHYDROLASE ARH3.	ALVQSLLAK	R	E	95.00%	45		471.8055	2	4.6	84	92	No
				GYGAGVVTVFK	R	K	95.00%	50		549.3073	2	6.6	115	125	No
				HVQSLEPDPGTPGSER	R	T	95.00%	55		853.4125	2	1.4	54	69	No
				IGELLDQASVTR	K	E	95.00%	78		651.3599	2	4.1	249	260	No
				TEALYYTDDTAMAR	R	A	95.00%	36	M12: Oxidation	818.8671	2	6.0	70	83	No
105	IPI00015911	DLD	DIHYDROLIPOYL DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.	ADGGTQVIDTK	K	N	95.00%	59		552.7858	2	8.8	167	177	No
				ALTGGIAHLFK	K	Q	95.00%	64		564.3355	2	4.7	133	143	No
				EANLAASFGK	R	S	95.00%	44		1007.5200	1	3.4	496	505	No
				EANLAASFGK	R	S	95.00%	64		504.2634	2	2.8	496	505	No
				GIEMSEVR	R	L	95.00%	47	M4: Oxidation	468.7291	2	4.4	110	117	No
				IDVSIEAASGGK	K	A	95.00%	52		1146.6090	1	6.8	289	300	No
				IDVSIEAASGGK	K	A	95.00%	93		573.8051	2	1.4	289	300	No
				IPNIYAIGDVVAGPMLAHK	K	A	95.00%	93	M15: Oxidation	998.0476	2	6.7	347	365	No
				IPNIYAIGDVVAGPMLAHK	K	A	95.00%	64	M15: Oxidation	665.6996	3	4.5	347	365	No
				LGADVTAVEFLGHVGGVGIDMEISK	R	N	95.00%	100	M21: Oxidation	844.1079	3	8.7	235	259	No
				LGADVTAVEFLGHVGGVGIDMEISK	R	N	95.00%	33	M21: Oxidation	633.3320	4	7.3	235	259	No
				NLGLEELGIELDPR	K	G	95.00%	93		784.4252	2	5.8	321	334	No

				NLGLEELGIELDPR	K	G	95.00%	47		523.2845	3	2.9	321	334	No
				SEEQLKEEGIEYK	K	V	95.00%	93		791.3902	2	4.8	405	417	No
				SEEQLKEEGIEYK	K	V	95.00%	42		527.9293	3	4.5	405	417	No
106	IPI00015972	COX6C	CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR.	AGIFQSVK	K	-	95.00%	37		849.4908	1	8.7	68	75	No
				AGIFQSVK	K	-	95.00%	58		425.2483	2	6.3	68	75	No
				AYADFYR	K	N	95.00%	40		453.2141	2	5.1	48	54	No
				KAGIFQSVK	R	-	95.00%	40		489.2972	2	8.3	67	75	No
				NYDVMKDFEEMR	R	K	95.00%	42	M5: Oxidation, M11: Oxidation	804.8406	2	3.6	55	66	No
				NYDVMKDFEEMRK	R	A	95.00%	40	M5: Oxidation, M11: Oxidation	868.8925	2	8.4	55	67	No
107	IPI00016006; IPI00184477; IPI00797784	GPHN	ISOFORM 1 OF GEPHYRIN.; ISOFORM 2 OF GEPHYRIN.; 41 KDA PROTEIN.	DLVQDPSLLGGTISAYK	K	I	95.00%	37		888.9811	2	8.9	41	57	No
				DTASLSTTPSESPR	R	A	95.00%	54		724.8532	2	8.0	259	272	No
108	IPI00016077	GBAS	PROTEIN NIPSNAP2.	KNQLLLEFSFWNEPVPR	R	S	95.00%	69		706.3832	3	7.4	165	181	No
				QDGNEAVGGFFSQIGQLYMVHHLWAYR	R	D	95.00%	57		781.6340	4	7.3	214	240	No
				SDMLLSR	R	K	95.00%	64	M3: Oxidation	419.2128	2	4.4	158	164	No
				SGPNIYELR	R	S	95.00%	85		524.7783	2	5.6	182	190	No
				SYQLRPGTMIEWGNYWAR	R	A	95.00%	55	M9: Oxidation	748.7005	3	8.9	191	208	No
				YEGGYPALTEVMNK	R	L	95.00%	91	M12: Oxidation	794.3779	2	7.2	130	143	No
				YEGGYPALTEVMNK	R	L	95.00%	79		786.3810	2	8.1	130	143	No
109	IPI00016342; IPI00791850; IPI00792578; IPI00795370	RAB7A	RAS-RELATED PROTEIN RAB-7.; 9 KDA PROTEIN.; 11 KDA PROTEIN.; 9 KDA PROTEIN.	ATIGADFLTK	K	E	95.00%	43		518.7886	2	1.2	39	48	No
				DPENFPFVVLGNK	R	I	95.00%	75		738.3811	2	0.6	114	126	No
				EAINVEQAFQTIAR	K	N	95.00%	43		530.6186	3	7.0	158	171	No
				VIILGDSGVGK	K	T	95.00%	44		529.3215	2	8.8	11	21	No
110	IPI00016346	PROSC	PROLINE SYNTHETASE CO-TRANSCRIBED BACTERIAL HOMOLOG PROTEIN.	TFGENYVQELLEK	R	A	95.00%	42		785.3999	2	7.5	64	76	No
				VMVQINTSGEESK	K	H	95.00%	77	M2: Oxidation	719.3541	2	7.6	141	153	No
111	IPI00016457; IPI00029140; IPI00514595	CRAT	ISOFORM 1 OF CARNITINE O-ACETYLTRANSFERASE.; ISOFORM 3 OF CARNITINE O-ACETYLTRANSFERASE.; ISOFORM 2 OF CARNITINE O-ACETYLTRANSFERASE.	ALQPIVSEEEWAHTK	K	Q	95.00%	92		869.4513	2	7.7	53	67	No
				AYNTLIK	K	D	95.00%	27		822.4748	1	2.7	262	268	No
				AYNTLIK	K	D	95.00%	33		411.7413	2	2.7	262	268	No
				FNITPEIK	R	S	95.00%	29		961.5443	1	8.7	383	390	No
				IWNSSLQTNKEPVGILTSNHR	K	N	95.00%	78		798.7612	3	6.2	236	256	No
				IWNSSLQTNKEPVGILTSNHR	K	N	95.00%	43		599.3227	4	6.0	236	256	No
				LIEGVLDFK	K	V	95.00%	46		1033.6010	1	7.4	121	129	No
				LIEGVLDFK	K	V	95.00%	54		517.3040	2	6.4	142	150	No
				LPVPPLQQSLDHYLK	R	A	95.00%	35		874.4987	2	8.4	38	52	No
				LPVPPLQQSLDHYLK	R	A	95.00%	54		583.3318	3	2.9	17	31	No
				LSPDAFIQMALQLAYYR	K	I	95.00%	134	M9: Oxidation	1008.5260	2	9.0	406	422	No
				LSPDAFIQMALQLAYYR	K	I	95.00%	59	M9: Oxidation	672.6858	3	7.7	427	443	No
				QDFVDLQGQLR	K	F	95.00%	59		659.8456	2	5.8	127	137	No
				QLVDEFQASGGVGER	K	L	95.00%	131		796.3930	2	4.1	68	82	No
				QPVVIYSSPGVMLPK	R	Q	95.00%	86	M12: Oxidation	815.9545	2	8.1	112	126	No
				SASMDSLTFVK	R	A	95.00%	57	M4: Oxidation	601.2963	2	6.0	470	480	No
				SHVAGQMLHGGGSR	R	L	95.00%	55		697.3472	2	7.6	302	315	No
				SPMVPLPMPK	R	K	95.00%	31	M3: Oxidation, M8: Oxidation	564.7971	2	5.8	370	379	No
				TENWLSEWWLK	K	T	95.00%	49		746.3747	2	9.5	94	104	No
				VMIDNETLPVEYLGGK	K	P	95.00%	72	M2: Oxidation	897.4612	2	8.4	130	145	No
112	IPI00016513	RAB10	RAS-RELATED PROTEIN RAB-10.	AFLTLAEDILR	K	K	95.00%	76		631.3678	2	9.5	162	172	No
				FHTITTSYYR	R	G	95.00%	35		644.8256	2	8.3	71	80	No
				LLLIGDSGVGK	K	T	95.00%	55		536.3286	2	7.2	12	22	No
				LQIWDTAGQER	K	F	95.00%	51		658.8402	2	9.5	60	70	Yes
				NIDEHANEDVER	R	M	95.00%	62		720.8284	2	9.2	106	117	No
				TPVKEPNSENVDISSGGGVTGWK	K	S	95.00%	35		786.7321	3	9.7	174	196	No
113	IPI00016862; IPI00759575	GSR	ISOFORM MITOCHONDRIAL OF GLUTATHIONE REDUCTASE, MITOCHONDRIALPRECURSOR.; ISOFORM CYTOPLASMIC OF GLUTATHIONE REDUCTASE, MITOCHONDRIAL PRECURSOR.	ADFDNTVAIHPTSSEELVTLR	K	-	95.00%	54		772.3939	3	6.0	502	522	No
				ALLTPVAIAAGR	K	K	95.00%	66		576.8621	2	5.0	380	391	No
				LGIQTDDKGHIIVDEFQNTNVK	K	G	95.00%	52		828.7673	3	5.1	347	368	No
				TLSGLEVSMVTAVPGR	K	L	95.00%	38	M9: Oxidation	816.9376	2	2.5	301	316	No

114	IPI00016910; IPI00646839	EIF3S8; LOC728689	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 8.; SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 8,110KDA ISOFORM 1.	DAHNALLDIQSSGR	K	A	95.00%	57		748.8801	2	4.4	628	641	No
				DFESHITSYK	R	Q	95.00%	36		613.7937	2	8.3	151	160	No
				ELLGQGLLLR	K	S	95.00%	28		556.3497	2	6.7	644	653	No
				FEELTNLIR	R	T	95.00%	58		567.8148	2	4.9	57	65	No
				GGVPLVK	R	E	95.00%	24		669.4353	1	7.8	306	312	No
				IQEESLR	K	T	95.00%	33		437.7324	2	-7.4	783	789	No
				TEPTAQQNLALQLAEK	R	L	95.00%	82		877.9736	2	5.9	847	862	No
115	IPI00017283	IARS2	ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR.	AVLEEGTDVVIK	K	M	95.00%	51		636.8583	2	2.8	434	445	No
				DSFLGSIPGK	R	N	95.00%	49		510.7749	2	5.1	887	896	No
				EAQNLSAMEIR	R	K	95.00%	31	M8: Oxidation	639.3149	2	4.8	171	181	No
				ELSNFYFSIIK	R	D	95.00%	65		680.8649	2	4.8	793	803	No
				FLINLEGGDIR	K	E	95.00%	58		623.8472	2	5.6	960	970	No
				FLINLEGGDIREESSYK	K	V	95.00%	48		657.3384	3	6.3	960	976	No
				QQPDTELEIQQK	R	C	95.00%	51		728.8741	2	8.0	79	90	No
				QWFINITDIK	K	T	95.00%	46		639.3508	2	3.3	480	489	No
				TALAEAELEYNPEHVSR	R	S	95.00%	111		964.9793	2	8.0	251	267	No
				TALAEAELEYNPEHVSR	R	S	95.00%	93		643.6534	3	4.7	251	267	No
				TKDEYLINSQTTEHIVK	K	L	95.00%	45		673.6877	3	3.6	539	555	No
				TVIVHGFTLGEK	K	G	95.00%	57		650.8697	2	3.8	650	661	No
116	IPI00017334; IPI00791634	PHB	PROHIBITIN.; PROHIBITIN VARIANT (FRAGMENT).	AAIISAEGDSK	K	A	95.00%	39		531.2806	2	5.2	209	219	No
				AATFGLILDDVSLTHLTFGK	R	E	95.00%	45		707.0593	3	8.5	158	177	No
				DLQNVNITLR	K	I	95.00%	51		593.3343	2	1.2	84	93	No
				FDAGELITQR	R	E	95.00%	81		575.3025	2	5.7	134	143	No
				IFTSIGEDYDER	R	V	95.00%	71		722.8407	2	9.5	106	117	No
				ILFRPVASQLPR	R	I	95.00%	23		698.9304	2	7.2	94	105	No
				ILFRPVASQLPR	R	I	95.00%	36		466.2883	3	4.5	94	105	No
				KLEAAEDIAYQLSR	R	S	95.00%	35		536.2900	3	6.3	240	253	No
				NITYLPAGQSVLLQLPQ	R	-	95.00%	42		928.0264	2	6.4	256	272	No
				VLPSITTEILK	R	S	95.00%	30		607.3773	2	4.6	118	128	No
117	IPI00017367	RDX	RADIXIN.	AFAAQEDLEK	K	T	95.00%	36		561.2786	2	1.3	449	458	No
				AFAAQEDLEKTKEELK	K	T	95.00%	32		617.3270	3	5.5	449	464	No
				APDFVFYAPR	K	L	95.00%	81		591.8027	2	2.3	264	273	Yes
				EVWFFGLQYVDSK	R	G	95.00%	76		809.4048	2	4.0	41	53	No
				FFPEDVSEELIQEITQR	K	L	95.00%	100		1040.5250	2	9.0	84	100	No
				FFPEDVSEELIQEITQR	K	L	95.00%	67		694.0181	3	7.0	84	100	No
				IAQDLEMYGVNYFEIK	K	N	95.00%	73	M7: Oxidation	974.9771	2	4.9	194	209	No
				IGFPWSEIR	K	N	95.00%	65		552.7990	2	5.2	238	246	Yes
				KAPDFVFYAPR	K	L	95.00%	47		655.8540	2	7.8	263	273	No
				KAPDFVFYAPR	K	L	95.00%	43		437.5703	3	4.2	263	273	No
				LFFLQVK	R	E	95.00%	44		447.7794	2	6.4	101	107	Yes
				NQEQLAAELAEFTAK	K	I	95.00%	133		831.9247	2	4.6	413	427	No
				NQEQLAAELAEFTAK	K	I	95.00%	58		554.9526	3	4.9	413	427	No
				QLFDQVVK	K	T	95.00%	42		488.7801	2	5.5	28	35	Yes
				QLQALSSELAQAR	K	D	95.00%	63		707.8934	2	9.5	527	539	No
				RKPDTIEVQQMK	R	A	95.00%	37	M11: Oxidation	744.9012	2	6.6	295	306	Yes
				RKPDTIEVQQMK	R	A	95.00%	33	M11: Oxidation	496.9362	3	5.4	295	306	Yes
				VTTMDAELEFAIQPNTTGK	R	Q	95.00%	133	M4: Oxidation	1041.5160	2	8.1	9	27	Yes
118	IPI00017510	COX2	CYTOCHROME C OXIDASE SUBUNIT 2.	IFEMGPVFTL	K	-	95.00%	31	M4: Oxidation	585.3054	2	9.5	218	227	No
				IFEMGPVFTL	K	-	95.00%	34		577.3055	2	5.5	218	227	No
				ILYMTDEVNDPSLTIK	R	S	95.00%	95	M4: Oxidation	934.4807	2	9.0	83	98	No
				ILYMTDEVNDPSLTIK	R	S	95.00%	97		926.4833	2	9.2	83	98	No
				LLDVDNR	R	V	95.00%	40		844.4611	1	9.7	135	141	No
				LLDVDNR	R	V	95.00%	41		422.7319	2	3.7	135	141	No
				LNQTTFTATR	R	P	95.00%	65		576.8094	2	8.3	179	188	No
				LTNTNISDAQEMETVWTILPAIILVLIALPSLR	K	I	95.00%	31		913.0215	4	9.4	50	82	No
				MMITSQDVLHSWAVPTLGLK	R	T	95.00%	49	M2: Oxidation	748.3959	3	6.7	152	171	No
				MMITSQDVLHSWAVPTLGLK	R	T	95.00%	65		743.0660	3	9.1	152	171	No
				VVLPIEAPIR	R	M	95.00%	36		1106.7010	1	6.5	142	151	No
				VVLPIEAPIR	R	M	95.00%	59		553.8561	2	9.5	142	151	No
119	IPI00017726; IPI00336094	HSD17B10	ISOFORM 1 OF 3-HYDROXYACYL-COA DEHYDROGENASE TYPE-2.; ISOFORM 2 OF 3-HYDROXYACYL-COA DEHYDROGENASE TYPE-2.	DLAPIGIR	R	V	95.00%	25		427.7598	2	1.9	185	192	No
				GGIVGMTLPIAR	K	D	95.00%	49	M6: Oxidation	600.8486	2	9.7	173	184	No

				GQTHTLEDFQR	K	V	95.00%	58		666.3260	2	7.2	106	116	No
				LVAGEMGQNEPDQGGQR	R	G	95.00%	41	M6: Oxidation	601.2804	3	6.4	131	147	No
				LVGQGASAVLLDLPNSGGEAQAK	R	K	95.00%	78		1098.0980	2	9.9	30	52	No
120	IPI00017855; IPI00790739	ACO2	ACONITATE HYDRATASE, MITOCHONDRIAL PRECURSOR.; ACONITASE 2, MITOCHONDRIAL.	AKDINQEVYNFLATAGAK	R	Y	95.00%	137		977.0128	2	4.9	143	160	No
				AKDINQEVYNFLATAGAK	R	Y	95.00%	70		651.6774	3	4.2	143	160	No
				ATIERDGYAQILR	R	D	95.00%	34		502.6116	3	7.5	450	462	No
				DGYAQILR	R	D	95.00%	50		935.4977	1	2.7	430	437	No
				DGYAQILR	R	D	95.00%	55		468.2527	2	2.7	455	462	No
				DINQEVYNFLATAGAK	K	Y	95.00%	128		877.4463	2	4.9	145	160	No
				DINQEVYNFLATAGAK	K	Y	95.00%	82		585.3013	3	6.9	145	160	No
				DLEDLQILIK	K	V	95.00%	81		600.3510	2	4.3	578	587	No
				DSSGQHVDVSPTSQR	K	L	95.00%	90		800.3758	2	4.6	575	589	No
				DSSGQHVDVSPTSQR	K	L	95.00%	69		533.9194	3	3.9	575	589	No
				EDIANLADEFK	R	D	95.00%	59		632.8101	2	4.8	313	323	No
				EGWPLDIR	K	V	95.00%	72		493.2605	2	2.5	396	403	No
				EHAALEPR	R	H	95.00%	28		461.7441	2	6.2	697	704	No
				FNPETDYLTGTDGK	K	K	95.00%	90		779.3619	2	5.5	507	520	No
				FNPETDYLTGTDGKK	K	F	95.00%	91		843.4083	2	3.8	532	546	No
				FNPETDYLTGTDGKK	K	F	95.00%	39		562.6083	3	4.1	532	546	No
				FRLEAPDADELPK	K	G	95.00%	57		750.8925	2	4.6	522	534	No
				FRLEAPDADELPK	K	G	95.00%	79		500.9310	3	4.9	547	559	No
				FRLEAPDADELPKGEFDPGQDTYQHPPK	K	D	95.00%	75		1066.5180	3	6.1	522	549	No
				FRLEAPDADELPKGEFDPGQDTYQHPPK	K	D	95.00%	52		800.1395	4	5.0	547	574	No
				FRLEAPDADELPKGEFDPGQDTYQHPPK	K	D	95.00%	37		640.3125	5	4.0	522	549	No
				GEFDPGQDTYQHPPK	K	D	95.00%	48		858.3895	2	2.5	535	549	No
				GHLDNISNNLLIGAINIENGK	R	A	95.00%	151		1110.1040	2	9.7	633	653	No
				GHLDNISNNLLIGAINIENGK	R	A	95.00%	72		740.4041	3	8.3	633	653	No
				HPNGTQETILLNHTFNETQIEWFR	K	A	95.00%	55		975.8236	3	9.2	769	792	No
				HPNGTQETILLNHTFNETQIEWFR	K	A	95.00%	54		732.1179	4	6.8	769	792	No
				IHPVDKLTIQGLK	K	D	95.00%	22		731.4466	2	3.8	743	755	No
				IHPVDKLTIQGLK	K	D	95.00%	41		487.9670	3	3.8	743	755	No
				IVYGHLDDPASQEIER	K	G	95.00%	93		921.4598	2	4.5	69	84	No
				IVYGHLDDPASQEIER	K	G	95.00%	70		614.6423	3	4.1	69	84	No
				KQGLLPLTFADPADYNK	K	I	95.00%	72		946.0107	2	8.9	726	742	No
				KQGLLPLTFADPADYNK	K	I	95.00%	53		631.0071	3	4.6	726	742	No
				LEAPDADELPK	R	G	95.00%	44		599.3057	2	2.4	524	534	No
				LEAPDADELPKGEFDPGQDTYQHPPK	R	D	95.00%	65		965.4617	3	7.3	549	574	No
				LNRPLTLSEK	R	I	95.00%	33		585.8486	2	3.9	59	68	No
				LQLLEPFDK	R	W	95.00%	47		551.8143	2	5.2	590	598	No
				LQLLEPFDKWDGK	R	D	95.00%	33		794.9290	2	7.7	590	602	No
				LQLLEPFDKWDGKDLEDLQILIK	R	V	95.00%	63		923.8500	3	9.5	590	612	No
				LTGSLSGWSSPK	K	D	95.00%	82		610.3224	2	3.9	234	245	No
				LTIQGLKDFTPGKPLK	K	C	95.00%	29		586.0201	3	4.0	749	764	No
				NAVTQEFGPVPDTAR	R	Y	95.00%	111		801.4012	2	1.3	634	648	No
				NAVTQEFGPVPDTAR	R	Y	95.00%	44		534.6039	3	2.3	634	648	No
				NDANPETHAFVTSPEIVTALAIAGTLK	R	F	95.00%	102		927.4931	3	6.1	480	506	No
				NDANPETHAFVTSPEIVTALAIAGTLK	R	F	95.00%	49		695.8743	4	9.7	505	531	No
				NTIVTSYNR	K	N	95.00%	44		1067.5550	1	6.3	491	499	No
				NTIVTSYNR	K	N	95.00%	49		534.2795	2	2.6	491	499	No
				QGLLPLTFADPADYNK	K	I	95.00%	85		881.9586	2	4.2	702	717	No
				QGLLPLTFADPADYNK	K	I	95.00%	43		588.3088	3	5.1	702	717	No
				RLNRPLTLSEK	K	I	95.00%	30		663.8987	2	2.8	58	68	No
				RLNRPLTLSEK	K	I	95.00%	26		442.9345	3	1.5	58	68	No
				SQFTITPGSEQIR	K	A	95.00%	84		732.3802	2	2.2	412	424	No
				TGREDIANLADEFK	K	D	95.00%	82		789.8954	2	4.2	310	323	No
				TGREDIANLADEFK	K	D	95.00%	35		526.9322	3	2.9	310	323	No
				VAEKEGWPLDIR	K	V	95.00%	52		706.8859	2	7.1	392	403	No
				VAEKEGWPLDIR	K	V	95.00%	52		471.5920	3	4.5	392	403	No

				VAGILTVK	K	G	95.00%	32		800.5273	1	3.2	251	258	No
				VAGILTVK	K	G	95.00%	65		400.7680	2	4.3	251	258	No
				VAMQDATAQMAMLQFISSGLSK	R	V	95.00%	38	M10: Oxidation, M12: Oxidation	787.3857	3	4.9	96	117	No
				VAMQDATAQMAMLQFISSGLSK	R	V	95.00%	70	M3: Oxidation, M10: Oxidation	787.3857	3	4.9	96	117	No
				VAMQDATAQMAMLQFISSGLSK	R	V	95.00%	115	M3: Oxidation, M10: Oxidation	1188.5750	2	7.0	96	117	No
				VAMQDATAQMAMLQFISSGLSK	R	V	95.00%	74	M3: Oxidation, M10: Oxidation	792.7177	3	5.3	96	117	No
				VAMQDATAQMAMLQFISSGLSK	R	V	95.00%	118	M3: Oxidation, M10: Oxidation, M12: Oxidation	1188.5750	2	7.5	96	117	No
				VAMQDATAQMAMLQFISSGLSK	R	V	95.00%	83	M3: Oxidation, M10: Oxidation, M12: Oxidation	792.7178	3	5.5	96	117	No
				VAMQDATAQMAMLQFISSGLSK	R	V	95.00%	49	M3: Oxidation, M12: Oxidation	787.3857	3	4.9	96	117	No
				VAMSHFEPNEYIHYDLLEK	K	N	95.00%	78	M3: Oxidation	1176.0660	2	9.3	32	50	No
				VAMSHFEPNEYIHYDLLEK	K	N	95.00%	70	M3: Oxidation	784.3799	3	9.6	32	50	No
				VAMSHFEPNEYIHYDLLEK	K	N	95.00%	59		779.0442	3	4.3	32	50	No
				WDGKDLEDLQILIK	K	V	95.00%	55		562.6464	3	7.0	599	612	No
				WVVIGDENYGEGSSR	R	E	95.00%	111		834.3922	2	6.0	682	696	No
				YGVGFWK	K	P	95.00%	30		428.7232	2	3.4	161	167	No
121	IPI00018206	GOT2	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR.	ASAELALGENSEVLK	K	S	95.00%	106		765.9072	2	3.2	108	122	No
				ASAELALGENSEVLK	K	S	95.00%	82		510.9415	3	4.8	108	122	No
				DAGMQLQGYR	R	Y	95.00%	36	M4: Oxidation	1154.5350	1	7.3	171	180	No
				DAGMQLQGYR	R	Y	95.00%	78	M4: Oxidation	577.7673	2	0.2	171	180	No
				DAGMQLQGYR	R	Y	95.00%	71		569.7708	2	1.8	171	180	No
				DDNGKPYVLPSVR	R	K	95.00%	52		730.3827	2	2.0	69	81	No
				DDNGKPYVLPSVR	R	K	95.00%	32		487.2585	3	3.6	69	81	No
				EFSIYMTK	K	D	95.00%	31	M6: Oxidation	1034.4900	1	3.3	397	404	No
				EFSIYMTK	K	D	95.00%	42	M6: Oxidation	517.7492	2	3.5	397	404	No
				EFSIYMTK	K	D	95.00%	35		509.7526	2	5.3	397	404	No
				FVTVQTISGTGALR	R	I	95.00%	114		725.4075	2	0.3	126	139	No
				FVTVQTISGTGALR	R	I	95.00%	48		483.9423	3	3.2	126	139	No
				IAAAILNTPDLR	R	K	95.00%	55		1267.7470	1	7.7	326	337	No
				IAAAILNTPDLR	R	K	95.00%	82		634.3755	2	4.5	326	337	No
				IAAAILNTPDLRK	R	Q	95.00%	75		698.4230	2	4.1	326	338	No
				IAAAILNTPDLRK	R	Q	95.00%	50		465.9505	3	2.4	326	338	No
				IGASFLQR	R	F	95.00%	31		891.5037	1	-1.8	140	147	No
				IGASFLQR	R	F	95.00%	77		446.2567	2	0.4	140	147	No
				ILIRPMYSNPPLNGAR	K	I	95.00%	35	M6: Oxidation	914.5048	2	6.1	310	325	No
				ILIRPMYSNPPLNGAR	K	I	95.00%	35	M6: Oxidation	610.0030	3	1.6	310	325	No
				ISVAGVTSSNVGYLAHAIHQVTK	R	-	95.00%	114		1176.6480	2	9.0	408	430	No
				ISVAGVTSSNVGYLAHAIHQVTK	R	-	95.00%	62		784.7670	3	7.6	408	430	No
				ISVAGVTSSNVGYLAHAIHQVTK	R	-	95.00%	43		588.8259	4	5.3	408	430	No
				KMNLGVGAYR	K	D	95.00%	48	M2: Oxidation	562.7993	2	1.7	59	68	No
				KQWLQEVK	R	G	95.00%	46		529.8041	2	0.3	338	345	No
				MNLGVGAYR	K	D	95.00%	87	M1: Oxidation	498.7522	2	2.9	60	68	No
				MNLGVGAYR	K	D	95.00%	61		490.7537	2	0.8	60	68	No
				MNLGVGAYRDDNGKPYVLPSVR	K	K	95.00%	52	M1: Oxidation	813.0864	3	5.7	60	81	No
				NLFAFFDMAYQGFASGDGDKDAWAVR	R	H	95.00%	113	M8: Oxidation	972.4512	3	9.6	237	262	No
				NMGLYGER	K	V	95.00%	62	M2: Oxidation	478.2204	2	2.4	280	287	No
				PMYSNPPLNGAR	R	I	95.00%	35	M2: Oxidation	666.8265	2	6.0	314	325	No
				PTWGNHTPIFR	K	D	95.00%	61		663.3451	2	5.1	160	170	No
				QWLQEVK	K	G	95.00%	35		465.7574	2	2.3	339	345	No
				TQLVSNLK	R	K	95.00%	35		451.7707	2	2.6	356	363	No
				TQLVSNLKK	R	E	95.00%	24		515.8180	2	1.9	356	364	No
122	IPI00018246; IPI00220663; IPI00220665; IPI00220667	HK1	ISOFORM 1 OF HEXOKINASE-1.; ISOFORM 2 OF HEXOKINASE-1.; ISOFORM 3 OF HEXOKINASE-1.; ISOFORM 4 OF HEXOKINASE-1.	AEMELGLR	R	K	95.00%	36	M3: Oxidation	467.7395	2	4.5	497	504	No
				ASGVEGADVVK	K	L	95.00%	34		516.2748	2	4.1	181	191	No

				DFNPTATVK	R	M	95.00%	29		992.5108	1	5.4	58	66	No
				DMLLEVK	K	K	95.00%	37	M2: Oxidation	432.2330	2	3.5	486	492	No
				FKASGVEGADVVK	R	L	95.00%	29		653.8574	2	4.8	179	191	No
				FLLSESGSGK	R	G	95.00%	41		1024.5370	1	5.5	446	455	No
				FLLSESGSGK	R	G	95.00%	64		512.7718	2	4.2	446	455	No
				FLSQIESDR	K	L	95.00%	60		547.7809	2	5.1	790	798	No
				FLSQIESDRLALLQVR	K	A	95.00%	31		630.0289	3	2.8	786	801	No
				FNTSDVSAIEK	K	N	95.00%	64		605.8042	2	4.1	334	344	No
				GAALITAVGVR	K	L	95.00%	84		514.3193	2	4.2	904	914	No
				GAAMVTAVAYR	K	L	95.00%	55	M4: Oxidation	563.2930	2	4.9	456	466	No
				GDFIALDLGGSSFR	K	I	95.00%	82		727.8703	2	3.2	78	91	No
				GKFNTSDVSAIEK	R	N	95.00%	62		698.3614	2	2.1	336	348	No
				HIDLVEGDEGR	R	M	95.00%	51		620.3043	2	2.9	248	258	No
				IDEAILITWTK	K	R	95.00%	48		651.8742	2	7.0	167	177	No
				LALLQVR	R	A	95.00%	45		406.7732	2	3.3	799	805	No
				LNVTVGVDGTLYK	R	L	95.00%	61		689.8885	2	7.9	858	870	No
				LSDETLIDIMTR	R	F	95.00%	88	M10: Oxidation	711.8637	2	3.0	31	42	No
				LSDETLIDIMTR	R	F	95.00%	45		703.8665	2	3.3	31	42	No
				LVDEYSLNAGK	R	Q	95.00%	72		604.8128	2	1.1	728	738	No
				MISGMYLGEIVR	K	N	95.00%	84	M1: Oxidation, M5: Oxidation	700.8550	2	7.4	748	759	No
				MVSGMYLGELVR	K	L	95.00%	70	M1: Oxidation, M5: Oxidation	693.8474	2	7.9	300	311	No
				NILIDFTK	R	K	95.00%	31		963.5584	1	7.0	760	767	No
				NILIDFTK	R	K	95.00%	39		482.2811	2	2.8	756	763	No
				SANLVAATLGAILNR	R	L	95.00%	91		742.4398	2	8.2	386	400	No
				SANLVAATLGAILNR	R	L	95.00%	90		495.2943	3	5.1	386	400	No
				TPDGTENGDFLALDLGGTNFR	R	V	95.00%	127		1105.5290	2	6.4	519	539	No
				TPDGTENGDFLALDLGGTNFR	R	V	95.00%	57		737.3536	3	3.8	523	543	No
123	IPI00018342; IPI00640817	AK1	ADENYLATE KINASE ISOENZYME 1.; ADENYLATE KINASE 1.	ATEPVIAFYEK	K	R	95.00%	80		634.3385	2	9.1	156	166	No
				ATEPVIAFYEKR	K	G	95.00%	43		712.3876	2	6.2	156	167	No
				ATEPVIAFYEKR	K	G	95.00%	49		475.2605	3	5.1	156	167	No
				EVQQGEEFER	R	R	95.00%	42		1250.5760	1	8.7	98	107	No
				EVQQGEEFER	R	R	95.00%	38		625.7917	2	8.2	98	107	No
				GETSGRVDDNEETIK	R	K	95.00%	59		825.3912	2	7.5	133	147	No
				GETSGRVDDNEETIKK	R	R	95.00%	34		889.4401	2	8.6	133	148	No
				GFLIDGYPR	K	E	95.00%	72		519.2772	2	4.2	89	97	No
				GQLVPLETVLDMLR	K	D	95.00%	101	M12: Oxidation	800.4493	2	7.9	64	77	No
				GQLVPLETVLDMLR	K	D	95.00%	71	M12: Oxidation	533.9672	3	4.8	64	77	No
				GQLVPLETVLDMLR	K	D	95.00%	96		792.4528	2	9.2	64	77	No
				GQLVPLETVLDMLR	K	D	95.00%	51		528.6359	3	5.5	64	77	No
				IGQPTLLLYVDAGPETMTQR	R	L	95.00%	73	M17: Oxidation	740.3899	3	7.0	109	128	No
				IGQPTLLLYVDAGPETMTQR	R	L	95.00%	104		1102.0860	2	9.3	109	128	No
				IGQPTLLLYVDAGPETMTQR	R	L	95.00%	68		735.0596	3	8.8	109	128	No
				IIFVVGGPGSGK	K	G	95.00%	50		1130.6660	1	7.7	10	21	No
				IIFVVGGPGSGK	K	G	95.00%	93		565.8331	2	0.6	10	21	No
				LSEIMEK	K	G	95.00%	32	M5: Oxidation	433.2236	2	6.1	57	63	No
				RIGQPTLLLYVDAGPETMTQR	R	L	95.00%	76	M18: Oxidation	792.4258	3	9.4	108	128	No
				RLETYYK	K	A	95.00%	41		486.7644	2	5.7	149	155	No
				SEVSSGSAR	R	G	95.00%	36		440.2156	2	7.3	45	53	No
				VDDNEETIK	R	K	95.00%	45		531.7561	2	8.2	139	147	No
				VDDNEETIKK	R	R	95.00%	47		595.8050	2	9.6	139	148	No
				YGYTHLSTGDLLR	K	S	95.00%	92		748.3867	2	7.3	32	44	No
				YGYTHLSTGDLLR	K	S	95.00%	59		499.2585	3	3.5	32	44	No
124	IPI00018398	PSMC3	26S PROTEASE REGULATORY SUBUNIT 6A.	AMEVDERPTEQYSDIGGLDK	K	Q	95.00%	48	M2: Oxidation	1135.0300	2	9.7	174	193	No
				AMEVDERPTEQYSDIGGLDK	K	Q	95.00%	70	M2: Oxidation	757.0187	3	4.8	174	193	No
				DSYLILETLPTEYDSR	K	V	95.00%	64		957.9783	2	7.8	156	171	No
				EKAPSIIFIDELDAIGTK	K	R	95.00%	63		654.0322	3	8.2	277	294	No
				GATELTHEDYMEGILEVQAK	R	K	95.00%	52	M11: Oxidation	1125.5390	2	4.9	411	430	No
				GATELTHEDYMEGILEVQAK	R	K	95.00%	64	M11: Oxidation	750.6966	3	6.3	411	430	No
				GVLMYGPPGTGK	K	T	95.00%	68	M4: Oxidation	596.8076	2	2.9	222	233	No
				KMNVSPDVNYEELAR	R	C	95.00%	65	M2: Oxidation	890.9378	2	7.7	372	386	No
				KMNVSPDVNYEELAR	R	C	95.00%	70	M2: Oxidation	594.2919	3	3.5	372	386	No
				LAGPQLVQMFIGDGAK	K	L	95.00%	58	M9: Oxidation	830.9458	2	6.2	251	266	No
				MSTEEIIQR	K	T	95.00%	35	M1: Oxidation	561.7796	2	4.2	36	44	No
				QIQELVEAIVLPMNHK	K	E	95.00%	48	M13: Oxidation	626.6811	3	6.2	194	209	No
				QTYFLPVIGLVDAEK	R	L	95.00%	82		846.9720	2	8.7	130	144	No
				TMLELLNQLDGFQPNTQVK	R	V	95.00%	124	M2: Oxidation	1103.0760	2	9.5	309	327	No
				TMLELLNQLDGFQPNTQVK	R	V	95.00%	112	M2: Oxidation	735.7193	3	8.9	309	327	No

				VDILDPALLR	R	S	95.00%	39		562.8411	2	5.4	335	344	No
				VIAATNRVDILDPALLR	K	S	95.00%	50		617.3708	3	5.5	328	344	No
125	IPI00018465	CCT7	T-COMPLEX PROTEIN 1 SUBUNIT ETA.	AIKNDSVVAGGGAIEMELSK	R	Y	95.00%	33	M16: Oxidation	669.0182	3	5.6	399	418	No
				ATISNDGATILK	K	L	95.00%	53		602.3354	2	3.7	56	67	No
				GGAEQFMEETER	R	S	95.00%	66	M7: Oxidation	700.2950	2	1.5	376	387	No
				IALLNVELELK	K	A	95.00%	25		627.8921	2	7.2	237	247	No
				LIVDGRGK	K	A	95.00%	37		429.2602	2	-10.0	48	55	No
				LPIGDVATQYFADR	K	D	95.00%	79		783.4083	2	7.7	293	306	No
				MVVDAVMMLDDLLQLK	K	M	95.00%	110	M1: Oxidation, M7: Oxidation, M8: Oxidation	941.4817	2	9.4	178	193	No
				MVVDAVMMLDDLLQLK	K	M	95.00%	45	M1: Oxidation, M7: Oxidation, M8: Oxidation	627.9886	3	6.6	178	193	No
				NDSVVAGGGAIEMELSK	K	Y	95.00%	71	M13: Oxidation	846.9149	2	6.1	402	418	No
				QQLLIGAYAK	K	A	95.00%	45		552.8265	2	3.0	431	440	No
				QVKPYVEEGLHPQIIIR	K	A	95.00%	39		673.7206	3	3.4	107	123	No
				QVKPYVEEGLHPQIIIR	K	A	95.00%	28		505.5418	4	2.2	107	123	No
				SQDAEVGDGTTSVTLLAAEFLK	K	Q	95.00%	159		1126.5800	2	9.5	85	106	No
				SQDAEVGDGTTSVTLLAAEFLK	K	Q	95.00%	69		751.3879	3	8.1	85	106	No
				TFSYAGFEMQPK	K	K	95.00%	64	M9: Oxidation	711.3267	2	3.0	219	230	No
				VQGGALEDSQLVAGVAFK	K	K	95.00%	97		894.9836	2	5.5	200	217	No
126	IPI00018671; IPI00790757	DUSP3	DUAL SPECIFICITY PROTEIN PHOSPHATASE 3.; 23 KDA PROTEIN.	AADFIDQALAQK	R	N	95.00%	72		645.8444	2	8.9	105	116	No
				DSGITYLGIK	K	A	95.00%	46		533.7960	2	5.2	80	89	No
				IYVGNASVAQDIPK	R	L	95.00%	95		737.9059	2	8.9	37	50	No
				LGITHVLNAAEGR	K	S	95.00%	46		675.8835	2	7.1	54	66	No
				LGITHVLNAAEGR	K	S	95.00%	54		450.9242	3	5.5	54	66	No
				SFMHVNTNANFYK	R	D	95.00%	39	M3: Oxidation	794.8725	2	9.8	67	79	No
				SFMHVNTNANFYK	R	D	95.00%	41	M3: Oxidation	530.2490	3	6.2	67	79	No
				SPTLVIAYLMMR	R	Q	95.00%	81	M10: Oxidation, M11: Oxidation	713.8823	2	9.1	131	142	No
				SPTLVIAYLMMR	R	Q	95.00%	61	M10: Oxidation, M11: Oxidation	476.2560	3	5.8	131	142	No
127	IPI00018740	IDI2	ISOPENTENYL-DIPHOSPHATE DELTA-ISOMERASE 2.	AFSVVLFNTK	R	N	95.00%	64		563.3247	2	9.5	53	62	No
				KNVTLNPDPSETK	R	S	95.00%	60		721.8834	2	6.8	157	169	No
				LEEMLIVVDENDK	R	V	95.00%	86	M4: Oxidation	781.8915	2	8.0	17	29	No
128	IPI00018755; IPI00335132; IPI00419258; IPI00644653; IPI00645948; IPI00742929; IPI00815806	HMG1L10; HMGB1	HIGH MOBILITY GROUP PROTEIN 1-LIKE 10.; 22 KDA PROTEIN.; HIGH MOBILITY GROUP PROTEIN B1.; HIGH-MOBILITY GROUP BOX 1.; HIGH-MOBILITY GROUP BOX 1.; SIMILAR TO HIGH MOBILITY GROUP PROTEIN 1.; HIGH-MOBILITY GROUP BOX 1 VARIANT (FRAGMENT).	IKGEHPGLSIGDVAK	K	K	95.00%	35		507.6233	3	6.7	113	127	No
				LGEMWNNTAADDKQPYEK	K	K	95.00%	45	M4: Oxidation	709.3274	3	7.8	129	146	No
129	IPI00018804; IPI00168849	TRIP10	ISOFORM 2 OF CDC42-INTERACTING PROTEIN 4.; ISOFORM 1 OF CDC42-INTERACTING PROTEIN 4.	EGGEGYVPTSYLR	K	V	95.00%	41		714.3481	2	5.2	585	597	No
				HARPPDPPASAPPDSSSNSASQDTK	R	E	95.00%	58		839.7281	3	3.2	486	510	No
				SGRDPLAILSEISK	R	S	95.00%	31		495.9495	3	3.4	354	367	No
				SHMAEESKNEYAAQLQR	R	F	95.00%	41	M3: Oxidation	669.9817	3	5.0	180	196	No
				TPQMGDPASLEPQIAETLSNIER	K	L	95.00%	62	M4: Oxidation	838.4155	3	4.7	434	456	No
130	IPI00018942; IPI00645172	FLJ10769	FLJ10769 PROTEIN.; HYPOTHETICAL PROTEIN LOC55739.	GPMDSDDSHGSVLR	R	L	95.00%	30	M3: Oxidation	744.8284	2	6.6	220	233	No
				LSQALGNVTVVQK	R	G	95.00%	73		678.9029	2	9.4	234	246	No
				NVQGILEVSK	R	A	95.00%	42		543.8123	2	0.6	163	172	No
131	IPI00019600	UBE2V2	UBIQUITIN-CONJUGATING ENZYME E2 VARIANT 2.	ENMKLPQPPEGQTYNN	K	-	95.00%	32	M3: Oxidation	938.4347	2	3.6	130	145	No
				LLEELEEGQK	R	G	95.00%	62		594.3162	2	7.1	15	24	No
				VVLQELR	K	R	95.00%	36		428.7682	2	3.5	117	123	No
				WTGMIIGPPR	R	T	95.00%	47	M4: Oxidation	572.3064	2	5.6	46	55	No
				YPEAPPSVR	K	F	95.00%	37		508.2669	2	4.7	73	81	No
132	IPI00019755; IPI00642936; IPI00797661	GSTO1	GLUTATHIONE TRANSFERASE OMEGA-1.; GLUTATHIONE S-TRANSFERASE OMEGA 1.; 17 KDA PROTEIN.	EFTKLEEVLTNK	K	K	95.00%	33		725.8998	2	8.4	149	160	No

				EFTKLEEVLTNKK	K	T	95.00%	31		526.9676	3	8.0	149	161	No
				MILELFSK	K	V	95.00%	33	M1: Oxidation	498.7807	2	9.5	115	122	No
				MILELFSK	K	V	95.00%	38		490.7812	2	5.7	87	94	No
				VPSLVGSFIR	K	S	95.00%	56		537.8225	2	5.6	123	132	No
133	IPI00019884	ACTN2	ALPHA-ACTININ-2.	AGTQIENIEEDFR	K	N	95.00%	78		761.3696	2	8.3	55	67	Yes
				ALDYIASK	K	G	95.00%	32		440.7440	2	2.5	103	110	No
				ASFNHFDR	R	R	95.00%	39		497.2327	2	3.5	760	767	No
				ASTHETWAYGK	K	E	95.00%	35		625.7995	2	8.5	410	420	No
				ASTHETWAYGKEQILLQK	K	D	95.00%	30		701.7066	3	7.9	410	427	No
				ATLPEADGER	K	Q	95.00%	46		529.7622	2	4.4	563	572	No
				ATLPEADGERQSIMAIQNEVEK	K	V	95.00%	42	M14: Oxidation	815.7425	3	7.7	563	584	No
				DQSLQEELAR	R	Q	95.00%	67		594.7998	2	4.6	622	631	No
				DYESASLTEVR	K	A	95.00%	74		635.3043	2	3.6	428	438	No
				ETADTDTAEQVIASFR	R	I	95.00%	126		877.4207	2	5.2	821	836	No
				ETADTDTAEQVIASFR	R	I	95.00%	38		585.2835	3	5.9	821	836	No
				FAIQDISVEETSAK	R	E	95.00%	89		769.3964	2	6.4	141	154	Yes
				GITQEQMNEFR	K	A	95.00%	67	M7: Oxidation	684.8176	2	3.9	749	759	No
				GYEEWLLNEIR	K	R	95.00%	67		711.3620	2	6.8	384	394	No
				HRPDLIDYSK	R	L	95.00%	44		622.3271	2	2.2	193	202	No
				HRPDLIDYSK	R	L	95.00%	50		415.2207	3	2.3	193	202	No
				ILASDKPYILAEELR	R	R	95.00%	92		865.9912	2	3.0	837	851	No
				ILASDKPYILAEELR	R	R	95.00%	60		577.6648	3	5.4	837	851	No
				ISNRPAFMPSEGK	R	M	95.00%	43	M8: Oxidation	725.3658	2	5.2	354	366	No
				ISNRPAFMPSEGK	R	M	95.00%	36	M8: Oxidation	483.9117	3	2.4	354	366	No
				ISSSNPYSTVTMDELR	R	T	95.00%	113	M12: Oxidation	908.4327	2	7.9	593	608	No
				KAGTQIENIEEDFR	R	N	95.00%	52		825.4128	2	2.5	54	67	Yes
				KAGTQIENIEEDFRNGLK	R	L	95.00%	38		688.0298	3	8.3	54	71	Yes
				KHEAFESDLAAHQDR	R	V	95.00%	58		585.2830	3	4.2	443	457	Yes
				KHEAFESDLAAHQDR	R	V	95.00%	48		439.2136	4	2.9	443	457	Yes
				LASELLEWIR	R	R	95.00%	93		615.3513	2	4.3	289	298	No
				LLETIDQLHLEFAK	K	R	95.00%	88		835.4643	2	2.4	510	523	No
				LLETIDQLHLEFAK	K	R	95.00%	51		557.3145	3	6.7	510	523	No
				LMEEYER	R	L	95.00%	30	M2: Oxidation	493.2221	2	6.4	282	288	No
				LMLLLEVISGER	K	L	95.00%	84	M2: Oxidation	694.9011	2	8.5	72	83	Yes
				LNKDDPIGNINLAMEIAEK	K	H	95.00%	86	M14: Oxidation	705.3670	3	2.3	203	221	No
				LVSIGAEEIVDGNVK	K	M	95.00%	107		771.9276	2	6.1	114	128	No
				MLDAEDIVNTPKPDER	K	A	95.00%	70	M1: Oxidation	929.9517	2	5.1	228	243	No
				MLDAEDIVNTPKPDER	K	A	95.00%	59	M1: Oxidation	620.3021	3	2.4	228	243	No
				MVSDIAGAWQR	K	L	95.00%	63	M1: Oxidation	625.3060	2	3.3	367	377	No
				NNIDKLEGDHQLIQEALVFDNK	K	H	95.00%	60		851.7722	3	2.2	690	711	No
				NVNIQNFHTSWK	R	D	95.00%	39		744.3690	2	-6.3	170	181	No
				QSIMAIQNEVEK	R	V	95.00%	78	M4: Oxidation	703.3589	2	7.3	573	584	No
				SSIQITGALEDQMNQLK	R	Q	95.00%	110	M13: Oxidation	946.4827	2	7.3	663	679	No
				SSIQITGALEDQMNQLK	R	Q	95.00%	29	M13: Oxidation	631.3221	3	3.6	663	679	No
				SSIQITGALEDQMNQLK	R	Q	95.00%	85		938.4833	2	5.3	663	679	No
				TINEVETQILTR	R	D	95.00%	79		708.8932	2	6.0	734	745	No
				TINEVETQILTR	R	D	95.00%	45		472.9306	3	4.3	734	745	No
				VEQIAAIAQELNELDYHDAVNVNDR	R	C	95.00%	76		947.1430	3	9.5	458	482	No
				VGWELLLTTIAR	R	T	95.00%	64		686.4095	2	7.9	722	733	No
				VIQSYNIR	K	I	95.00%	39		496.7821	2	3.4	585	592	No
				VLAVNQENER	K	L	95.00%	64		586.3094	2	3.2	272	281	No
134	IPI00019888; IPI00336008	ALDH5A1	SUCCINATE SEMIALDEHYDE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.; ALDEHYDE DEHYDROGENASE 5A1 PRECURSOR, ISOFORM 1.	AGGLVPASGPAPGPAQLR	R	C	95.00%	40		808.4523	2	2.8	28	45	No
				IITAESGKPLK	R	E	95.00%	41		578.8546	2	6.0	141	151	No
				LAGLSAALLR	R	T	95.00%	90		492.8167	2	4.9	51	60	No
				VGNGFEEGTTQGPLINEK	R	A	95.00%	91		945.4742	2	8.3	370	387	No
				YGIDEYLELK	K	Y	95.00%	83		621.8217	2	7.7	519	528	No
135	IPI00019987	SUOX	SULFITE OXIDASE.	DGETVESGEVTIK	R	G	95.00%	34		682.3398	2	9.1	434	446	No
				VAPTVETSDPYADDPVR	K	H	95.00%	67		916.4473	2	8.3	166	182	No
				VVVPGVVGAR	R	H	95.00%	21		476.8032	2	4.5	367	376	No
136	IPI00020035	NIPSNAP3B	PROTEIN NIPSNAP3B.	AINAHVNLGYTK	R	V	95.00%	30		434.2411	3	4.9	168	179	No
				IDKQETEITYLIPWSK	R	L	95.00%	88		982.5291	2	6.0	121	136	No
				PGGPALWGDAFER	K	A	95.00%	33		686.8427	2	9.1	155	167	No
				VHVLWWNESADSR	R	A	95.00%	34		533.5988	3	5.7	194	206	No
				VVGVFHTEYGELNR	K	V	95.00%	53		810.4203	2	9.0	180	193	No
				VVGVFHTEYGELNR	K	V	95.00%	41		540.6151	3	7.1	180	193	No

137	IPI00020210	DYSF	DYSFERLIN_V1.	AEDLPQMDDAVMDNVK	R	Q	95.00%	66	M7: Oxidation, M12: Oxidation	911.9008	2	5.4	389	404	No
				ALGRPGPPFNITPR	K	R	95.00%	43		498.2883	3	6.8	1794	1807	No
				DVILDDLSLTGEK	R	M	95.00%	79		709.3813	2	8.4	1823	1835	No
				EFTGFPDPYTELNTGK	R	G	95.00%	33		908.4313	2	5.6	532	547	No
				EVLATPSLSASFNAPLLDTK	R	K	95.00%	116		1037.5650	2	7.2	91	110	No
				IETQNQLLGIADR	R	L	95.00%	43		735.9067	2	9.4	673	685	No
				IGETVVDLENR	K	L	95.00%	70		622.8319	2	5.8	1660	1670	No
				ISAPGGEIEEEPAGAVKPSK	K	A	95.00%	53		656.0126	3	4.5	486	505	No
				LALHVLQQQGLVPEHVESRPLYSPLQPDIEQGK	R	L	95.00%	26		930.5105	4	7.1	1751	1783	No
				LGHSELPAALEQAEDWLLR	K	L	95.00%	48		716.7129	3	6.5	761	779	No
				LLLSLETK	R	L	95.00%	39		458.7926	2	5.9	557	564	No
				LQTIFLK	K	Y	95.00%	22		431.7778	2	8.6	832	838	No
				NLVDPFVEVSFAGK	K	M	95.00%	43		761.4075	2	7.7	415	428	No
				TAIEILAWGLR	R	N	95.00%	54		621.8696	2	8.3	1333	1343	No
				TDALLGEFR	R	M	95.00%	32		511.2740	2	8.1	295	303	No
				THHLSQITEAALALK	R	L	95.00%	55		544.9767	3	4.3	746	760	No
				VEDLPADDILR	K	V	95.00%	35		628.3352	2	7.1	573	583	No
138	IPI00020436; IPI00429190; IPI00790785; IPI00795676	RAB11A; RAB11B	RAS-RELATED PROTEIN RAB-11B.; RAS-RELATED PROTEIN RAB-11A.; 24 KDA PROTEIN.; 22 KDA PROTEIN.	GAVGALLVYDIAK	R	H	95.00%	76		645.3825	2	7.9	83	95	No
				STIGVEFATR	K	S	95.00%	43		540.7930	2	8.5	42	51	No
139	IPI00020495	MRPS36	MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S36.	SAGLPSHSSVISQHSK	R	G	95.00%	37		541.2857	3	7.2	42	57	No
				SPDLLMYQGPPDTAEIIK	K	T	95.00%	57	M6: Oxidation	1002.5020	2	-2.1	61	78	No
140	IPI00020510	ZCD1	ZINC FINGER CDGSH DOMAIN-CONTAINING PROTEIN 1.	AMINLHIQK	K	D	95.00%	43	M2: Oxidation	542.3077	2	8.2	43	51	No
				HNEETGDNVGPLIIK	K	K	95.00%	98		818.4281	2	8.4	90	104	No
				HNEETGDNVGPLIIK	K	K	95.00%	35		545.9542	3	7.5	90	104	No
				IVHAFDMEDLGDK	K	A	95.00%	64	M7: Oxidation	753.3584	2	9.4	56	68	No
				IVHAFDMEDLGDK	K	A	95.00%	47	M7: Oxidation	502.5733	3	6.2	56	68	No
141	IPI00020530	THEM2	THIOESTERASE SUPERFAMILY MEMBER 2.	ITLVSAAPGK	K	V	95.00%	53		478.7970	2	8.4	28	37	No
				LGEDIVITAHVLK	K	Q	95.00%	57		469.9488	3	6.8	96	108	No
				TLAFTSVDLTNK	K	A	95.00%	38		655.3577	2	5.4	112	123	No
142	IPI00020906	IMPA1	INOSITOL MONOPHOSPHATASE.	EIQVIPLQR	K	D	95.00%	23		548.3345	2	7.6	265	273	No
				EKYPSHSFIGEESVAAGEK	K	S	95.00%	56		689.0059	3	6.9	60	78	No
				LQVSQQEDITK	K	S	95.00%	59		644.8462	2	7.5	146	156	No
				SLLVTELGSSR	K	T	95.00%	56		581.3335	2	9.7	157	167	No
				SSPVDLVTATDQK	K	V	95.00%	55		680.8567	2	7.0	37	49	No
143	IPI00020984	CANX	CALNEXIN PRECURSOR.	AEEDEILNR	K	S	95.00%	30		544.7664	2	2.1	574	582	No
				APVPTGEVYFADSFDR	K	G	95.00%	106		885.9280	2	8.1	62	77	No
				APVPTGEVYFADSFDR	K	G	95.00%	35		590.9553	3	9.3	62	77	No
				GTLSGWILSK	R	A	95.00%	54		531.3071	2	6.2	78	87	No
				KIPNPDFFEDLEPFR	R	M	95.00%	78		932.4747	2	7.0	401	415	No
				KIPNPDFFEDLEPFR	R	M	95.00%	61		621.9855	3	6.6	401	415	No
				PVIDNPNYK	R	G	95.00%	37		530.2792	2	2.9	372	380	No
				SDAEEDGGTVSQEEEDRKPK	K	A	95.00%	45		736.0015	3	6.4	554	573	No
				TPELNLDQFHDK	K	T	95.00%	77		728.8632	2	7.5	171	182	No
				TPELNLDQFHDK	K	T	95.00%	45		486.2429	3	3.9	171	182	No
144	IPI00020986; IPI00794403; IPI00796888	LUM	LUMICAN PRECURSOR.; 23 KDA PROTEIN.; 26 KDA PROTEIN.	FNALQYLR	R	L	95.00%	60		512.7856	2	5.1	228	235	No
				ISNIPDEYFK	K	R	95.00%	49		613.3118	2	4.3	217	226	No
				LKEDAVSAAFK	R	G	95.00%	31		589.8265	2	2.6	171	181	No
				LPSGLPVSLLTLYLDNNK	R	I	95.00%	130		979.0618	2	7.4	199	216	No
				LPSGLPVSLLTLYLDNNK	R	I	95.00%	54		653.0441	3	7.9	199	216	No
				NIPTVNENLENYYLEVNQLEK	K	F	95.00%	48		846.0956	3	5.7	268	288	No
				RFNALQYLR	K	L	95.00%	45		590.8374	2	6.6	227	235	No
				SLEDLQLTHNK	K	I	95.00%	79		649.3464	2	7.4	138	148	No
				SLEDLQLTHNK	K	I	95.00%	34		433.2313	3	2.4	138	148	No
				SLEYLDLSFNQIAR	K	L	95.00%	78		834.9396	2	7.0	185	198	No
145	IPI00021263; IPI00790768	YWHAZ	14-3-3 PROTEIN ZETA/DELTA.; 26 KDA PROTEIN.	DSTLIMQLLR	K	D	95.00%	65	M6: Oxidation	603.3372	2	8.2	213	222	Yes
				GIVDQSQQAYQEAFEISK	K	K	95.00%	54		681.0065	3	7.8	140	157	No
				NLLSVAYK	R	N	95.00%	33		907.5325	1	7.9	42	49	Yes
				NLLSVAYK	R	N	95.00%	39		454.2683	2	3.9	42	49	Yes
				SVTEQGAELSNEER	K	N	95.00%	112		774.8660	2	6.5	28	41	No
				YLAEVAAGDDKK	R	G	95.00%	61		640.3357	2	7.9	128	139	No
				YLAEVAAGDDKK	R	G	95.00%	39		427.2254	3	5.4	128	139	No

146	IPI00021338	DLAT	DIHYDROLIPOYLLYSINE-RESIDUE ACETYLTRANSFERASE COMPONENT OF PYRUVATEDEHYDROGENASE COMPLEX, MITOCHONDRIAL PRECURSOR.	DIDSFVPSK	K	V	95.00%	29		504.2588	2	4.8	355	363	Yes
				GIDLTQVK	K	G	95.00%	31		437.2582	2	4.3	336	343	Yes
				GVETIANDVVSLATK	K	A	95.00%	81		506.2826	3	6.4	500	514	Yes
				ISVNDFIIK	K	A	95.00%	41		524.8099	2	7.2	441	449	Yes
				VPEANSSWMDTVIR	K	Q	95.00%	66	M9: Oxidation	810.8954	2	8.6	458	471	Yes
				VPLPSLSPTMQAGTIAR	K	W	95.00%	50	M10: Oxidation	877.9856	2	8.9	61	77	Yes
				YLEKPITMLL	K	-	95.00%	37	M8: Oxidation	618.8555	2	9.4	605	614	Yes
147	IPI00021347	UBE2L3	UBIQUITIN-CONJUGATING ENZYME E2 L3.	IEINFPAEYPFKPPK	R	I	95.00%	48		597.3284	3	9.1	53	67	No
				TDQVIQSLIALVNDPQPEHPLR	K	A	95.00%	81		828.4543	3	8.7	101	122	No
				TDQVIQSLIALVNDPQPEHPLR	K	A	95.00%	28		621.5934	4	9.8	101	122	No
148	IPI00021369	CRYAB	ALPHA CRYSTALLIN B CHAIN.	APSWFDTGLSEMR	R	L	95.00%	82	M12: Oxidation	756.8485	2	6.5	57	69	No
				APSWFDTGLSEMR	R	L	95.00%	39	M12: Oxidation	504.8957	3	-5.2	57	69	No
				APSWFDTGLSEMR	R	L	95.00%	92		748.8503	2	5.6	57	69	No
				DIAIHHPWIR	M	R	95.00%	62		629.3518	2	8.0	2	11	No
				DRFSVNLDVK	K	H	95.00%	40		596.8247	2	7.5	73	82	No
				FSVNLDVK	R	H	95.00%	60		461.2592	2	6.5	75	82	No
				HEERQDEHGFISR	K	E	95.00%	68		820.3892	2	7.8	104	116	No
				HEERQDEHGFISR	K	E	95.00%	46		547.2609	3	5.6	104	116	No
				HFSPEELK	K	V	95.00%	53		493.7541	2	5.6	83	90	No
				HFSPEELKVK	K	V	95.00%	28		405.2267	3	5.1	83	92	No
				IPADVDPLTITSSLSSDGVLTVNGPR	R	K	95.00%	73		875.4700	3	6.1	124	149	No
				QDEHGFISR	R	E	95.00%	38		544.7646	2	8.0	108	116	No
				RPFFPFHSPSR	R	L	95.00%	56		687.8613	2	5.6	12	22	No
				RPFFPFHSPSR	R	L	95.00%	51		458.9096	3	4.4	12	22	No
				VLGDVIEVHGK	K	H	95.00%	83		583.3348	2	3.0	93	103	No
				VLGDVIEVHGKHEER	K	Q	95.00%	52		858.9621	2	7.5	93	107	No
149	IPI00021405; IPI00216952; IPI00216953; IPI00514204; IPI00644087; IPI00655812	LMNA	ISOFORM A OF LAMIN-A/C.; ISOFORM C OF LAMIN-A/C.; ISOFORM ADELTA10 OF LAMIN-A/C.; LAMIN A/C.; PROGERIN.; RHABDOMYOSARCOMA ANTIGEN MU-RMS-40.12.	IDSLSAQLSQLQK	R	Q	95.00%	60		715.9004	2	5.1	299	311	No
				IRIDSLSAQLSQLQK	R	Q	95.00%	46		850.4954	2	7.1	297	311	No
				IRIDSLSAQLSQLQK	R	Q	95.00%	41		567.3304	3	2.7	297	311	No
				ITESEEVVSR	R	E	95.00%	42		574.7988	2	8.6	63	72	No
				LADALQELR	R	A	95.00%	71		514.7931	2	4.2	241	249	No
				LKDLEALLNSK	R	E	95.00%	32		415.2487	3	3.1	134	144	No
				MQQQLDEYQELLDIK	R	L	95.00%	113	M1: Oxidation	955.4732	2	8.6	352	366	No
				MQQQLDEYQELLDIK	R	L	95.00%	34	M1: Oxidation	637.3156	3	4.7	352	366	No
				NSNLVGAAHEELQQSR	R	I	95.00%	84		876.9406	2	6.0	281	296	No
				NSNLVGAAHEELQQSR	R	I	95.00%	46		584.9615	3	3.4	281	296	No
				SGAQASSTPLSPTR	R	I	95.00%	62		680.3489	2	2.3	12	25	No
				SVGGSGGGSFGDNLVTR	R	S	95.00%	107		783.8821	2	3.2	628	644	No
				TALINSTGEEVAMR	R	K	95.00%	39	M13: Oxidation	754.3778	2	3.4	528	541	No
				TLEGELHDLR	R	G	95.00%	62		591.8122	2	3.7	157	166	No
150	IPI00021428	ACTA1	ACTIN, ALPHA SKELETAL MUSCLE.	AGFAGDDAPR	K	A	95.00%	57		976.4520	1	3.2	21	30	Yes
				AGFAGDDAPR	K	A	95.00%	90		488.7286	2	0.4	21	30	Yes
				AVFPSIVGR	R	P	95.00%	78		473.2801	2	0.1	31	39	Yes
				AVFPSIVGRPR	R	H	95.00%	77		599.8580	2	1.6	31	41	Yes
				AVFPSIVGRPR	R	H	95.00%	29		400.2415	3	2.1	31	41	Yes
				DLTDYLMK	R	I	95.00%	45	M7: Oxidation	1014.4920	1	9.3	186	193	Yes
				DLTDYLMK	R	I	95.00%	56	M7: Oxidation	507.7452	2	0.5	186	193	Yes
				DLTDYLMK	R	I	95.00%	44		499.7504	2	5.9	186	193	Yes
				DLYANNVMSGGTTMYPGIADR	K	M	95.00%	139	M14: Oxidation	1131.5230	2	9.0	294	314	No
				DLYANNVMSGGTTMYPGIADR	K	M	95.00%	83	M14: Oxidation	754.6836	3	7.9	294	314	No
				DLYANNVMSGGTTMYPGIADR	K	M	95.00%	111	M8: Oxidation	1131.5230	2	9.2	294	314	No
				DLYANNVMSGGTTMYPGIADR	K	M	95.00%	58	M8: Oxidation	754.6824	3	6.4	294	314	No
				DLYANNVMSGGTTMYPGIADR	K	M	95.00%	130	M8: Oxidation	1139.5170	2	6.2	294	314	No
				DLYANNVMSGGTTMYPGIADR	K	M	95.00%	88	M8: Oxidation	760.0115	3	3.0	294	314	No
				DLYANNVMSGGTTMYPGIADR	K	M	95.00%	130	M8: Oxidation, M14: Oxidation	1139.5170	2	6.2	294	314	No
				DLYANNVMSGGTTMYPGIADR	K	M	95.00%	88	M8: Oxidation, M14: Oxidation	760.0115	3	3.0	294	314	No
				DLYANNVMSGGTTMYPGIADR	K	M	95.00%	105		1123.5260	2	9.8	294	314	No
				DSYVGDEAQSK	K	R	95.00%	85		599.7709	2	9.3	53	63	Yes
				DSYVGDEAQSKR	K	G	95.00%	65		677.8182	2	3.5	53	64	Yes
				DSYVGDEAQSKR	K	G	95.00%	36		452.2152	3	4.6	53	64	Yes

EITALAPSTMK	K	I	95.00%	71	M10: Oxidation	1177.6180	1	3.4	318	328	Yes
EITALAPSTMK	K	I	95.00%	91	M10: Oxidation	589.3099	2	-1.7	318	328	Yes
EITALAPSTMK	K	I	95.00%	58		1161.6240	1	4.3	318	328	Yes
EITALAPSTMK	K	I	95.00%	76		581.3145	2	1.8	318	328	Yes
EITALAPSTMKIK	K	I	95.00%	36	M10: Oxidation	709.9036	2	4.5	318	330	Yes
GILTLK	R	Y	95.00%	37		644.4368	1	3.0	65	70	Yes
GYSFVTTAER	R	E	95.00%	43		1130.5600	1	9.9	199	208	Yes
GYSFVTTAER	R	E	95.00%	80		565.7778	2	-0.4	199	208	Yes
GYSFVTTAEREIVR	R	D	95.00%	31		543.2880	3	2.4	199	212	No
HQGVMVGMGQK	R	D	95.00%	63	M5: Oxidation	594.2880	2	1.2	42	52	Yes
HQGVMVGMGQK	R	D	95.00%	62	M5: Oxidation	602.2896	2	8.2	42	52	Yes
HQGVMVGMGQK	R	D	95.00%	62	M5: Oxidation	401.8615	3	6.2	42	52	Yes
HQGVMVGMGQK	R	D	95.00%	62	M5: Oxidation, M8: Oxidation	602.2896	2	8.2	42	52	Yes
HQGVMVGMGQK	R	D	95.00%	62	M5: Oxidation, M8: Oxidation	401.8615	3	6.2	42	52	Yes
HQGVMVGMGQK	R	D	95.00%	61	M8: Oxidation	594.2899	2	4.4	42	52	Yes
HQGVMVGMGQK	R	D	95.00%	71		1171.5740	1	2.1	42	52	Yes
HQGVMVGMGQK	R	D	95.00%	85		586.2923	2	4.3	42	52	Yes
IIAPPERK	K	Y	95.00%	36		462.2889	2	2.3	331	338	Yes
IKIIAPPER	K	K	95.00%	32		518.8319	2	3.8	329	337	Yes
IKIIAPPERK	K	Y	95.00%	26		582.8785	2	1.9	329	338	Yes
IWHHTFYNELR	K	V	95.00%	70		758.3789	2	0.2	87	97	Yes
IWHHTFYNELR	K	V	95.00%	66		505.9227	3	1.9	87	97	Yes
KDLYANNVMSGGTTMYPGIADR	R	M	95.00%	89	M15: Oxidation	1195.5650	2	4.5	293	314	No
KDLYANNVMSGGTTMYPGIADR	R	M	95.00%	73	M15: Oxidation	797.3807	3	5.9	293	314	No
KDLYANNVMSGGTTMYPGIADR	R	M	95.00%	80	M9: Oxidation	797.3804	3	5.6	293	314	No
KDLYANNVMSGGTTMYPGIADR	R	M	95.00%	99	M9: Oxidation	1203.5660	2	7.1	293	314	No
KDLYANNVMSGGTTMYPGIADR	R	M	95.00%	101	M9: Oxidation	802.7129	3	6.7	293	314	No
KDLYANNVMSGGTTMYPGIADR	R	M	95.00%	99	M9: Oxidation, M15: Oxidation	1203.5660	2	7.1	293	314	No
KDLYANNVMSGGTTMYPGIADR	R	M	95.00%	101	M9: Oxidation, M15: Oxidation	802.7129	3	6.7	293	314	No
KDLYANNVMSGGTTMYPGIADR	R	M	95.00%	57		792.0503	3	7.5	293	314	No
KYSVWIGGSILASLSTFQQMWITK	R	Q	95.00%	52	M20: Oxidation	920.8272	3	8.1	338	361	No
KYSVWIGGSILASLSTFQQMWITK	R	Q	95.00%	34		915.4942	3	6.8	338	361	No
LDLAGRDLTDYLMK	R	I	95.00%	34	M13: Oxidation	547.2877	3	6.4	180	193	Yes
MQKEITALAPSTMK	R	I	95.00%	62	M1: Oxidation, M13: Oxidation	790.9117	2	8.0	315	328	Yes
MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	64	M1: Oxidation	1089.8870	3	6.0	121	149	Yes
MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	87	M1: Oxidation	1095.2200	3	7.4	121	149	Yes
MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	38	M1: Oxidation	821.6656	4	5.9	121	149	Yes
MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	63	M1: Oxidation	1100.5530	3	8.7	121	149	Yes
MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	87	M1: Oxidation, M5: Oxidation	1095.2200	3	7.4	121	149	Yes
MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	38	M1: Oxidation, M5: Oxidation	821.6656	4	5.9	121	149	Yes
MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	63	M1: Oxidation, M5: Oxidation	1100.5530	3	8.7	121	149	Yes
MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	63	M1: Oxidation, M5: Oxidation, M14: Oxidation	1100.5530	3	8.7	121	149	Yes
MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	91	M5: Oxidation	1089.8870	3	6.1	121	149	Yes
QEYDEAGPSIVHR	K	K	95.00%	88		750.8618	2	5.0	362	374	Yes
QEYDEAGPSIVHR	K	K	95.00%	63		500.9097	3	3.4	362	374	Yes
QEYDEAGPSIVHRK	K	C	95.00%	64		814.9073	2	2.1	362	375	Yes
QEYDEAGPSIVHRK	K	C	95.00%	39		543.6076	3	2.3	362	375	Yes

				RGILTLK	K	Y	95.00%	40		400.7732	2	3.4	64	70	Yes
				SYELPDGQVITIGNER	K	F	95.00%	132		895.9526	2	2.7	241	256	Yes
				SYELPDGQVITIGNER	K	F	95.00%	73		597.6398	3	6.2	241	256	Yes
				TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	R	L	95.00%	79	M29: Oxidation	1071.5480	3	6.9	150	179	Yes
				TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	R	L	95.00%	56	M29: Oxidation	643.3307	5	5.5	150	179	Yes
				TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	R	L	95.00%	72		1066.2180	3	9.2	150	179	Yes
				TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	R	L	95.00%	39		799.9139	4	7.0	150	179	Yes
				VAPEEHPTLLTEAPLNPK	R	A	95.00%	102		978.5344	2	8.3	98	115	Yes
				VAPEEHPTLLTEAPLNPK	R	A	95.00%	64		652.6884	3	2.6	98	115	Yes
				VAPEEHPTLLTEAPLNPKANR	R	E	95.00%	33		766.4174	3	4.8	98	118	No
				YPIEHGIITNWDDMEK	K	I	95.00%	42	M14: Oxidation	988.9642	2	7.1	71	86	Yes
				YSVWIGGSILASLSTFQQMWITK	K	Q	95.00%	118	M19: Oxidation	1316.6880	2	7.4	339	361	No
				YSVWIGGSILASLSTFQQMWITK	K	Q	95.00%	75	M19: Oxidation	878.1273	3	6.9	339	361	No
				YSVWIGGSILASLSTFQQMWITK	K	Q	95.00%	78		872.7983	3	9.9	339	361	No
151	IPI00021435	PSMC2	26S PROTEASE REGULATORY SUBUNIT 7.	ALDEGDIALLK	R	T	95.00%	83		579.3276	2	4.6	24	34	No
				FDDGAGGDNEVQR	R	T	95.00%	59		690.3010	2	8.1	285	297	No
				FVNLGIEPPK	R	G	95.00%	49		557.3231	2	6.5	201	210	No
				GVLLFGPPGTGK	K	T	95.00%	28		571.8361	2	5.9	211	222	No
				IATEKDFLEAVNK	K	V	95.00%	64		739.4018	2	3.7	403	415	No
				QTLQSEQPLQVAR	K	C	95.00%	70		749.4098	2	6.2	85	97	No
152	IPI00021785	COX5B	CYTOCHROME C OXIDASE SUBUNIT 5B, MITOCHONDRIAL PRECURSOR.	GLDPYNVLAPK	K	G	95.00%	47		593.8314	2	6.4	58	68	No
				KGLDPYNVLAPK	K	G	95.00%	53		657.8810	2	8.9	57	68	No
				KGLDPYNVLAPK	K	G	95.00%	48		438.9227	3	7.6	57	68	No
153	IPI00021812; IPI00555610	AHNAK	NEUROBLAST DIFFERENTIATION-ASSOCIATED PROTEIN AHNAK (FRAGMENT).; 313 KDA PROTEIN.	GEGPDVDVNLPK	K	A	95.00%	40		620.3199	2	7.8	1737	1748	No
				GEGPEVDVNLPK	K	A	95.00%	30		627.3245	2	2.5	894	905	No
				VDVEVPDVSLEGPEGK	K	L	95.00%	38		834.9283	2	9.1	1043	1058	No
154	IPI00021831	PRKAR1A	CAMP-DEPENDENT PROTEIN KINASE TYPE I-ALPHA REGULATORY SUBUNIT.	GAISAEVYTEEDAASYVR	R	K	95.00%	109		965.9646	2	9.3	98	115	No
				HNIQALLK	K	D	95.00%	36		468.7861	2	1.2	25	32	No
				ILMGSTLR	R	K	95.00%	32	M3: Oxidation	453.7595	2	3.2	234	241	No
				LGPSDYFGEIALLMNRPR	R	A	95.00%	33	M14: Oxidation	689.0267	3	5.0	318	335	No
				LTVADALEPVQFEDGQK	R	I	95.00%	118		930.4805	2	7.4	265	281	No
				LTVADALEPVQFEDGQK	R	I	95.00%	68		620.6557	3	6.5	265	281	No
				NIQQYNSFVSLSV	R	-	95.00%	60		749.8871	2	8.3	369	381	No
				NVLFSHLDDNER	K	S	95.00%	95		729.8559	2	4.3	135	146	No
				NVLFSHLDDNER	K	S	95.00%	36		486.9060	3	3.2	135	146	No
				RSENEEFVEVGR	R	L	95.00%	76		725.8531	2	4.0	306	317	No
				RSENEEFVEVGR	R	L	95.00%	63		484.2379	3	3.9	306	317	No
				SENEEFVEVGR	R	L	95.00%	81		647.8026	2	4.4	307	317	No
				TDSREDEISPPPPNPVVK	R	G	95.00%	36	S9: Phospho	686.3270	3	2.8	75	92	No
				TDSREDEISPPPPNPVVK	R	G	95.00%	53		989.0057	2	5.2	75	92	No
				VSILESLDK	K	W	95.00%	42		502.2894	2	3.2	253	261	No
				VSILESLDKWER	K	L	95.00%	56		737.9034	2	5.5	253	264	No
				VSILESLDKWER	K	L	95.00%	56		492.2717	3	6.0	253	264	No
155	IPI00021841	APOA1	APOLIPOPROTEIN A-I PRECURSOR.	AKPALEDLR	K	Q	95.00%	37		506.7962	2	5.2	231	239	No
				ATEHLSTLSEK	K	A	95.00%	60		608.3187	2	6.1	220	230	No
				DLATVYVDVLK	K	D	95.00%	87		618.3542	2	9.6	37	47	No
				DSGRDYVSQFEGSALGK	K	Q	95.00%	62		908.4341	2	4.9	48	64	No
				DSGRDYVSQFEGSALGK	K	Q	95.00%	45		605.9594	3	6.1	48	64	No
				DYVSQFEGSALGK	R	Q	95.00%	70		700.8445	2	8.2	52	64	No
				EQLGPVTQEFWDNLEK	R	E	95.00%	93		966.9803	2	9.4	86	101	No
				LLDNWDSVTSTFSK	K	L	95.00%	103		806.9048	2	9.8	70	83	No
				LREQLGPVTQEFWDNLEK	K	E	95.00%	54		734.7180	3	8.4	84	101	No
				LSPLGEEMR	K	D	95.00%	35	M8: Oxidation	524.2638	2	5.1	165	173	No
				QGLLPVLESFK	R	V	95.00%	50		615.8642	2	8.6	240	250	No
				QKVEPLRAELQEGAR	R	Q	95.00%	31		862.4835	2	7.9	141	155	No
				THLAPYSDELR	R	Q	95.00%	35		651.3331	2	7.2	185	195	No
				THLAPYSDELR	R	Q	95.00%	33		434.5575	3	6.1	185	195	No
				VEPLRAELQEGAR	K	Q	95.00%	28		734.4052	2	7.2	143	155	No
				VKDLATVYVDVLK	R	D	95.00%	76		731.9343	2	5.8	35	47	No

				VKDLATVYVDVLK	R	D	95.00%	41		488.2926	3	6.8	35	47	No
				VSFLSALEEYTK	K	K	95.00%	87		693.8683	2	9.3	251	262	No
156	IPI00021890; IPI00747151	HSD17B8	ESTRADIOL 17-BETA-DEHYDROGENASE 8.; 24 KDA PROTEIN.	AGVIGLTQTAAR	K	E	95.00%	47		579.3407	2	7.9	174	185	No
				GNHAAFQADVSEAR	R	A	95.00%	73		736.8537	2	7.7	67	80	No
				SALALVTGAGSGIGR	R	A	95.00%	85		665.3843	2	8.7	11	25	No
				VGNVGQTNYAASK	K	A	95.00%	47		654.8375	2	9.4	161	173	No
157	IPI00021925	CPT1B	CARNITINE O-PALMITOYLTRANSFERASE I, MUSCLE ISOFORM.	ALLDIADLFQVPK	K	A	95.00%	63		721.9199	2	4.1	828	840	No
				DTDVLQHLSDSR	K	H	95.00%	32		693.3437	2	9.7	393	404	No
				ILDDPSPPQPGEEK	R	L	95.00%	50		761.3801	2	5.4	438	451	No
				KALLDIADLFQVPK	R	A	95.00%	38		524.3168	3	8.7	827	840	No
				LLKPQDLEMQFQR	R	I	95.00%	55	M9: Oxidation	554.6282	3	0.1	425	437	No
				LSTSQIPQSQIR	R	M	95.00%	31		679.3818	2	8.5	755	766	No
				SFTLISFK	K	N	95.00%	35		471.7715	2	5.5	527	534	No
158	IPI00022143; IPI00746655	FAM62A	ISOFORM 1 OF PROTEIN FAM62A.; ISOFORM 2 OF PROTEIN FAM62A.	ALTLGALTLPLAR	R	L	95.00%	78		655.4168	2	3.7	561	573	No
				FFLQDPQSQELDVQVK	R	D	95.00%	33		960.9974	2	8.3	531	546	No
				GNKEPNPMVQLSIQDVTQESK	K	A	95.00%	42	M8: Oxidation	786.7332	3	9.7	495	515	No
				HLSPYATLTVGDSSHK	K	T	95.00%	46		571.6290	3	6.1	818	833	No
				LLAETVAPAVR	K	G	95.00%	50		570.3469	2	6.2	160	170	No
				LLVPLVPDLQDVAQLR	R	S	95.00%	76		895.0395	2	6.8	308	323	No
				LLVPLVPDLQDVAQLR	R	S	95.00%	55		597.0296	3	8.0	308	323	No
				LTHVDSPLEAPAGPLGQVK	R	L	95.00%	36		643.6923	3	8.5	958	976	No
				QLLDDEEQLTAK	R	T	95.00%	66		701.8596	2	3.1	107	118	No
				SAELAAALLSIYMER	K	A	95.00%	62	M13: Oxidation	827.4344	2	5.3	802	816	No
				VQLDLAETDLSQGVAR	K	W	95.00%	118		857.9568	2	4.8	1086	1101	No
159	IPI00022200; IPI00072917; IPI00072918; IPI00220701; IPI00376964	COL6A3	ALPHA 3 TYPE VI COLLAGEN ISOFORM 1 PRECURSOR.; ALPHA 3 TYPE VI COLLAGEN ISOFORM 3 PRECURSOR.; ALPHA 3 TYPE VI COLLAGEN ISOFORM 4 PRECURSOR.; ISOFORM 2 OF COLLAGEN ALPHA-3(VI) CHAIN PRECURSOR.; ALPHA 3 TYPE VI COLLAGEN ISOFORM 2 PRECURSOR.	LLTPITTLTSEQIQK	K	L	95.00%	69		843.4940	2	6.4	1204	1218	No
				LQPVLQPLPSPGVGGK	R	R	95.00%	38		793.9743	2	8.5	1016	1031	No
				SVEDAQDVSLALTQR	K	G	95.00%	79		816.4230	2	8.6	1755	1769	No
				VPQIAFVITGGK	R	S	95.00%	55		615.3719	2	8.0	1743	1754	No
160	IPI00022202; IPI00215777; IPI00788624; IPI00789657; IPI00790115; IPI00793177	SLC25A3	ISOFORM A OF PHOSPHATE CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR.; ISOFORM B OF PHOSPHATE CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR.; 31 KDA PROTEIN.; 36 KDA PROTEIN.; CDNA FLJ90278 FIS, CLONE NT2RP1000325, HIGHLY SIMILAR TO PHOSPHATECARRIER PROTEIN, MITOCHONDRIALPRECURSOR.; 24 KDA PROTEIN.	FGFYEVFK	K	V	95.00%	28		518.7650	2	7.3	138	145	No
				GIFNGFSVTLK	K	E	95.00%	65		591.8336	2	5.9	102	112	No
				GSSASLVLKR	K	L	95.00%	60		509.3076	2	1.7	296	305	No
				IQTQPGYANTLR	R	D	95.00%	78		681.3658	2	4.3	190	201	No
				LPRPPPPEMPESLK	R	K	95.00%	32	M9: Oxidation	535.2914	3	4.1	342	355	No
161	IPI00022305	BZW2	BASIC LEUCINE ZIPPER AND W2 DOMAIN-CONTAINING PROTEIN 2.	ADVLSEEAILK	K	W	95.00%	83		594.3327	2	4.3	370	380	No
				DTLVQGLNEAGDDLEAVAK	R	F	95.00%	113		979.4982	2	8.5	32	50	No
				LLELFPVNR	R	Q	95.00%	34		550.8317	2	7.9	216	224	No
162	IPI00022314	SOD2	SUPEROXIDE DISMUTASE [MN], MITOCHONDRIAL PRECURSOR.	AIWNVINWENVTER	K	Y	95.00%	79		872.4503	2	6.2	203	216	No
				AIWNVINWENVTER	K	Y	95.00%	71		581.9689	3	5.3	203	216	No
				DFGSFDK	R	F	95.00%	50		815.3646	1	8.6	124	130	No
				GDVTAQIALQPALK	K	F	95.00%	109		712.9128	2	4.4	76	89	No
				GDVTAQIALQPALK	K	F	95.00%	25		475.6118	3	5.8	76	89	No
				GELLEAIK	K	R	95.00%	28		872.5176	1	9.3	115	122	No
				GELLEAIK	K	R	95.00%	42		436.7610	2	5.5	115	122	No
				GELLEAIKR	K	D	95.00%	61		514.8114	2	4.3	115	123	No
				HHAAYVNNLNVTEEK	K	Y	95.00%	75		869.9321	2	3.0	54	68	No
				HHAAYVNNLNVTEEK	K	Y	95.00%	58		580.2930	3	7.0	54	68	No
				HHAAYVNNLNVTEEKYQEALAK	K	G	95.00%	43		848.1018	3	8.4	54	75	No
				HHAAYVNNLNVTEEKYQEALAK	K	G	95.00%	46		636.3286	4	8.8	54	75	No
				NVRPDYLK	K	A	95.00%	33		502.7837	2	6.6	195	202	No

163	IPI00022361; IPI00791534	SLC4A1	BAND 3 ANION TRANSPORT PROTEIN.; SOLUTE CARRIER FAMILY 4 ANION EXCHANGER MEMBER 1 VARIANT.	ADFLEQPVLGFVR	R	L	95.00%	76		745.9098	2	7.3	234	246	No
				ASTPGAAAQIQEVK	K	E	95.00%	69		685.8720	2	5.9	744	757	No
				ATFDEEEGRDEYDEVAMPV	K	-	95.00%	66	M17: Oxidation	1109.4700	2	8.7	893	911	No
				FLFVLLGPEAPHIDYTQLGR	R	A	95.00%	59		762.7523	3	5.4	264	283	No
				GWVIHPLGLR	R	S	95.00%	27		574.3448	2	6.7	647	656	No
				HSHAGELEALGGVKPAVLTR	K	S	95.00%	73		681.3821	3	7.8	161	180	No
				HSHAGELEALGGVKPAVLTR	K	S	95.00%	103		511.2863	4	3.3	161	180	No
				IDAYMAQSR	R	G	95.00%	35	M5: Oxidation	535.7534	2	4.7	296	304	No
				IPPDSEATLVLVGR	K	A	95.00%	110		733.9171	2	3.0	220	233	No
				IPPDSEATLVLVGR	K	A	95.00%	33		489.6136	3	2.1	220	233	No
				LQEAAELEAVELPVPIR	R	F	95.00%	126		939.0304	2	7.6	247	263	No
				LQEAAELEAVELPVPIR	R	F	95.00%	83		626.3553	3	6.1	247	263	No
				SVTHANALTVMGK	R	A	95.00%	60	M11: Oxidation	672.8539	2	4.0	731	743	No
				TYNYNVLMVPK	K	P	95.00%	36	M8: Oxidation	679.3481	2	4.3	552	562	No
				VLLPLIFR	R	N	95.00%	43		485.8283	2	3.5	872	879	No
				VYVELQELVMDEK	K	N	95.00%	100	M10: Oxidation	805.9091	2	7.1	57	69	No
				VYVELQELVMDEKNQELR	K	W	95.00%	62	M10: Oxidation	751.0538	3	7.9	57	74	No
				YQSSPAKPDSSFYK	R	G	95.00%	48		802.8889	2	6.5	347	360	No
164	IPI00022433	HSPB6	ALPHA CRYSTALLIN FAMILY PROTEIN.	APSVALPVAQVPTDPGHFSVLLDVK	R	H	95.00%	51		853.1479	3	9.7	72	96	No
				ASAPLPGLSAPGR	R	L	95.00%	52		597.3407	2	7.7	30	42	No
				HEERPDEHGFVAR	R	E	95.00%	42		526.9212	3	4.2	118	130	No
				HFSPEEIAVK	K	V	95.00%	36		1156.6100	1	8.7	97	106	No
				HFSPEEIAVK	K	V	95.00%	54		578.8068	2	4.7	97	106	No
				LPPGVDPAAVTSALSPEGVLSIQAAPASAQAPPPAAAK	R	-	95.00%	45		880.2362	4	8.7	138	175	No
				LPPGVDPAAVTSALSPEGVLSIQAAPASAQAPPPAAAK	R	-	95.00%	45		704.3876	5	4.5	138	175	No
				RASAPLPGLSAPGR	R	L	95.00%	62	S3: Phospho	715.3743	2	6.2	29	42	No
				RASAPLPGLSAPGR	R	L	95.00%	29	S3: Phospho	477.2516	3	5.1	29	42	No
				RASAPLPGLSAPGR	R	L	95.00%	54		675.3929	2	9.2	29	42	No
				RASAPLPGLSAPGR	R	L	95.00%	48		450.5959	3	4.8	29	42	No
				VVGEHVEVHAR	K	H	95.00%	51		616.3341	2	4.7	107	117	No
				VVGEHVEVHAR	K	H	95.00%	35		411.2250	3	3.9	107	117	No
165	IPI00022442	NDUFAB1	ACYL CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR.	LSVNSHFMK	K	D	95.00%	50	M8: Oxidation	539.7751	2	6.3	98	106	No
				LYDKIDPEK	K	L	95.00%	46		560.8010	2	4.4	89	97	No
				VLYVLK	R	L	95.00%	20		734.4867	1	6.9	83	88	No
166	IPI00022463; IPI00798430	TF	SEROTRANSFERRIN PRECURSOR.; TRANSFERRIN VARIANT (FRAGMENT).	AIAANEADAVTLDAGLVYDAYLAPNNLKPVVAEFYGSK	R	E	95.00%	29		989.2691	4	9.1	70	107	No
				DGAGDVAFVK	K	H	95.00%	51		489.7502	2	2.8	216	225	No
				DLLFK	K	D	95.00%	28		635.3814	1	6.8	311	315	No
				DSAHGFLK	K	V	95.00%	35		437.7263	2	2.7	316	323	No
				DSGFQMNQLR	K	G	95.00%	77	M6: Oxidation	606.2801	2	3.5	123	132	No
				DSGFQMNQLR	K	G	95.00%	53		598.2828	2	3.9	123	132	No
				EDPQTFYYAVAVVK	K	K	95.00%	77		815.4177	2	6.9	108	121	No
				EDPQTFYYAVAVVK	K	K	95.00%	35		543.9472	3	5.9	108	121	No
				EFQLFSSPHGK	K	D	95.00%	58		638.8234	2	4.9	300	310	No
				EFQLFSSPHGK	K	D	95.00%	37		426.2182	3	5.0	300	310	No
				EGYYGYTGAFR	K	C	95.00%	61		642.2933	2	7.2	531	541	No
				HSTIFENLANK	K	A	95.00%	72		637.3325	2	2.3	226	236	No
				HSTIFENLANK	K	A	95.00%	45		425.2240	3	1.8	226	236	No
				IMNGEADAMSLDGGFVYIAGK	K	C	95.00%	138	M2: Oxidation, M9: Oxidation	1096.0120	2	4.8	400	420	No
				IMNGEADAMSLDGGFVYIAGK	K	C	95.00%	76	M2: Oxidation, M9: Oxidation	731.0112	3	5.8	400	420	No
				KSASDLTWDNLK	K	G	95.00%	63		689.3575	2	4.1	453	464	No
				MYLGYEYVTAIR	K	N	95.00%	75	M1: Oxidation	747.8732	2	5.6	332	343	No
				MYLGYEYVTAIR	K	N	95.00%	38	M1: Oxidation	498.9185	3	6.4	332	343	No
				MYLGYEYVTAIR	K	N	95.00%	64		739.8743	2	3.6	332	343	No
				SASDLTWDNLK	K	G	95.00%	79		625.3092	2	3.2	454	464	No
				SKEFQLFSSPHGK	K	D	95.00%	73		746.3862	2	3.2	298	310	No
				SKEFQLFSSPHGK	K	D	95.00%	43		497.9273	3	4.3	298	310	No
				SMGGKEDLIWELLNQAQEHFGK	R	D	95.00%	41	M2: Oxidation	637.3181	4	5.5	274	295	No
				SMGGKEDLIWELLNQAQEHFGKDK	R	S	95.00%	33	M2: Oxidation	698.1014	4	9.0	274	297	No
				TAGWNIPMGLLYNK	R	I	95.00%	68	M8: Oxidation	797.4152	2	7.8	476	489	No

				YLGEEYVK	K	A	95.00%	41		500.7549	2	2.7	669	676	No
167	IPI00022744; IPI00219994	CSE1L	ISOFORM 1 OF EXPORTIN-2.; ISOFORM 3 OF EXPORTIN-2.	AADEEAFEDNSEEYIR	R	R	95.00%	90		944.4019	2	3.9	356	371	No
				ALTLPGSSENEYIMK	K	A	95.00%	36	M14: Oxidation	834.9199	2	9.9	560	574	No
				GSNTIASAAADKIPGLLGVFQK	R	L	95.00%	38		720.0691	3	1.9	715	736	No
				HKDAAIYLVTSLASK	K	A	95.00%	28		539.6414	3	4.4	426	440	No
				IIIPEIQK	K	V	95.00%	30		477.3079	2	4.6	825	832	No
				LLQAFLER	R	G	95.00%	56		495.2936	2	0.8	707	714	No
				LLQTDDEEEAGLLELLK	K	S	95.00%	117		965.0086	2	1.1	252	268	No
				LVLDAFALPLTNLFK	K	A	95.00%	53		838.0029	2	8.6	175	189	No
				QIFILLFQR	K	L	95.00%	45		589.3625	2	6.2	769	777	No
				QLSDAISIIGR	K	E	95.00%	64		586.8383	2	4.0	110	120	No
				SANVNEFPVLK	K	A	95.00%	46		609.3350	2	7.5	471	481	No
				TGNIPALVR	R	L	95.00%	34		470.7866	2	7.8	698	706	No
168	IPI00022774	VCP	TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE.	AHVIVMAATNRPNSIDPALR	R	R	95.00%	41	M6: Oxidation	721.3899	3	1.6	339	358	No
				AVANETGAFFFLINGPEIMSK	R	L	95.00%	121	M19: Oxidation	1136.5780	2	6.9	257	277	No
				AVANETGAFFFLINGPEIMSK	R	L	95.00%	55	M19: Oxidation	758.0562	3	9.0	257	277	No
				DHFEEAMR	R	F	95.00%	30	M7: Oxidation	525.7220	2	4.5	734	741	No
				DVDLEFLAK	K	M	95.00%	35		1049.5550	1	2.7	669	677	No
				DVDLEFLAK	K	M	95.00%	49		525.2847	2	8.8	669	677	No
				ELQELVQYPVEHPDK	R	F	95.00%	82		912.4667	2	4.0	488	502	No
				ELQELVQYPVEHPDK	R	F	95.00%	35		608.6469	3	3.7	488	502	No
				ELQELVQYPVEHPDKFLK	R	F	95.00%	48		738.0648	3	6.0	488	505	No
				ESIESEIR	R	R	95.00%	34		481.7457	2	4.2	701	708	No
				ETVVEVPQVTWEDIGGLEDVKR	R	E	95.00%	40		833.4382	3	8.4	466	487	No
				EVDIGIPDATGR	R	L	95.00%	59		621.8230	2	3.9	366	377	No
				EVDIGIPDATGRLEILQIHTK	R	N	95.00%	29		773.4324	3	4.0	366	386	No
				FDREVDIGIPDATGR	R	L	95.00%	48		830.9245	2	6.8	363	377	No
				GILLYGPPGTGK	R	T	95.00%	54		586.8423	2	7.3	240	251	No
				IVSQLLTLMDGLK	R	Q	95.00%	71	M9: Oxidation	723.9208	2	6.5	324	336	No
				IVSQLLTLMDGLK	R	Q	95.00%	47	M9: Oxidation	482.9494	3	5.7	324	336	No
				IVSQLLTLMDGLK	R	Q	95.00%	71		715.9224	2	5.1	324	336	No
				KGDIFLVR	R	G	95.00%	29		474.2890	2	2.3	148	155	No
				KYEMFAQTLQQSR	R	G	95.00%	100	M4: Oxidation	823.4111	2	8.2	754	766	No
				LAGESESNLR	K	K	95.00%	60		538.2746	2	2.7	278	287	No
				LDQLIYIPLPDEK	R	S	95.00%	93		778.9366	2	4.7	639	651	No
				LEILQIHTK	R	N	95.00%	56		547.8361	2	6.1	378	386	No
				LIVDEAINEDNSVVSLSQPK	R	M	95.00%	138		1085.5770	2	9.8	26	45	No
				LIVDEAINEDNSVVSLSQPK	R	M	95.00%	65		724.0522	3	7.7	26	45	No
				MDELQLFR	K	G	95.00%	59	M1: Oxidation	534.2659	2	3.9	46	53	No
				NAPAIIFIDELDAIAPK	K	R	95.00%	112		906.0078	2	6.5	296	312	No
				NAPAIIFIDELDAIAPK	K	R	95.00%	73		604.3400	3	4.7	296	312	No
				NVFIIGATNRPDIIDPAILRPGR	K	L	95.00%	40		840.1514	3	4.9	616	638	No
				QTNPSAMEVEEDDPVPEIR	R	R	95.00%	62	M7: Oxidation	1086.5010	2	7.6	714	732	No
				QTNPSAMEVEEDDPVPEIRR	R	D	95.00%	37	M7: Oxidation	776.7013	3	4.4	714	733	No
				VINQILTEMDGMSTK	R	K	95.00%	76	M9: Oxidation, M12: Oxidation	856.4212	2	5.7	600	614	No
				WALSQSNPSALR	R	E	95.00%	97		665.3519	2	3.4	454	465	No
169	IPI00022793	HADHB	TRIFUNCTIONAL ENZYME BETA SUBUNIT, MITOCHONDRIAL PRECURSOR.	AALTGLLHR	R	T	95.00%	83		476.2937	2	5.8	83	91	No
				ALAMGYKPK	K	A	95.00%	30	M4: Oxidation	497.7773	2	7.1	327	335	No
				AMDSDWFAENYMGR	K	K	95.00%	87	M2: Oxidation, M12: Oxidation	862.8467	2	10.0	393	406	No
				AQDEGLLSDVVPFK	K	V	95.00%	83		759.4033	2	8.8	256	269	No
				AQDEGLLSDVVPFKVPGK	K	D	95.00%	65		633.6846	3	7.9	256	273	No
				AQDEGLLSDVVPFKVPGKDTVTK	K	D	95.00%	46		815.1126	3	5.6	256	278	No
				AQDEGLLSDVVPFKVPGKDTVTK	K	D	95.00%	35		611.5851	4	3.4	256	278	No
				DFMYVSQDPK	R	D	95.00%	55	M3: Oxidation	623.2789	2	3.0	340	349	No
				DLMPHDLAR	K	A	95.00%	43	M3: Oxidation	542.2696	2	5.1	74	82	No
				DNGIRPSSLEQMAK	K	L	95.00%	44	M12: Oxidation	781.3884	2	2.8	279	292	No
				DQLLLGPTYATPK	K	V	95.00%	78		708.8956	2	6.5	350	362	No
				EAALGAGFSDK	R	T	95.00%	76		1065.5280	1	6.2	119	129	No
				EAALGAGFSDK	R	T	95.00%	47		533.2671	2	4.4	119	129	No
				EVVDYIIFGTVIQEVK	K	T	95.00%	121		926.5152	2	6.3	97	112	No
				EVVDYIIFGTVIQEVK	K	T	95.00%	75		618.0138	3	8.1	97	112	No
				KAQDEGLLSDVVPFK	K	V	95.00%	118		823.4510	2	8.5	255	269	No

				KAQDEGLLSDVVPFKVPGK	K	D	95.00%	88		1014.0720	2	8.6	255	273	No
				KAQDEGLLSDVVPFKVPGK	K	D	95.00%	63		676.3826	3	7.0	255	273	No
				KAQDEGLLSDVVPFKVPGK	K	D	95.00%	34		507.5377	4	4.5	255	273	No
				KLMLDLNK	R	A	95.00%	27	M3: Oxidation	495.7891	2	4.4	182	189	No
				LAAAFAVSR	R	L	95.00%	34		905.5255	1	5.2	231	239	No
				LAAAFAVSR	R	L	95.00%	71		453.2667	2	5.4	231	239	No
				LEQDEYALR	R	S	95.00%	58		568.7866	2	5.7	240	248	No
				LKPAFIKPYGTVTAANSSFLTDG ASAMLIMAEEK	K	A	95.00%	60	M27: Oxidation, M30: Oxidation	901.9706	4	8.5	293	326	No
				LMLDLNK	K	A	95.00%	38	M2: Oxidation	431.7403	2	2.0	183	189	No
				NVVVVDGVR	R	T	95.00%	49		956.5596	1	7.1	54	62	No
				NVVVVDGVR	R	T	95.00%	60		478.7828	2	5.2	54	62	No
				TPFLLSGTSYK	R	D	95.00%	38		1213.6570	1	8.7	63	73	No
				TPFLLSGTSYK	R	D	95.00%	74		607.3303	2	4.9	63	73	No
				TPFLLSGTSYKDLMPHDLAR	R	A	95.00%	33	M14: Oxidation	760.0622	3	7.3	63	82	No
				VGLPPLEK	K	F	95.00%	32		852.5231	1	4.0	410	417	No
				VGLPPLEK	K	F	95.00%	42		426.7653	2	3.7	410	417	No
170	IPI00022891	SLC25A4	ADP/ATP TRANSLOCASE 1.	AAYFGVYDTAK	R	G	95.00%	43		1205.5870	1	2.3	189	199	No
				AAYFGVYDTAK	R	G	95.00%	71		603.2985	2	3.9	189	199	No
				DFLAGGVAAAVSK	K	T	95.00%	53		1205.6620	1	7.4	11	23	No
				DFLAGGVAAAVSK	K	T	95.00%	108		603.3334	2	4.9	11	23	No
				DFLAGGVAAAVSK	K	T	95.00%	30		402.5585	3	5.5	11	23	No
				EQGFLSFWR	K	G	95.00%	56		585.2931	2	3.4	64	72	No
				GAWSNVLR	K	G	95.00%	56		451.7482	2	4.1	273	280	No
				GMGGAFVLVLYDEIKK	R	Y	95.00%	90	M2: Oxidation	878.4780	2	7.1	281	296	No
				GMGGAFVLVLYDEIKK	R	Y	95.00%	52	M2: Oxidation	585.9869	3	5.4	281	296	No
				GNLANVIR	R	Y	95.00%	56		428.7553	2	2.7	73	80	No
				LLLQVQHASK	K	Q	95.00%	50		568.8482	2	8.2	34	43	No
				QLFLGGVDR	K	H	95.00%	32		1004.5600	1	6.9	97	105	No
				QLFLGGVDR	K	H	95.00%	66		502.7817	2	2.5	97	105	No
				TAVAPIER	K	V	95.00%	42		428.7499	2	3.1	24	31	No
				YFPTQALNFAFK	R	D	95.00%	88		723.8805	2	7.6	81	92	No
171	IPI00023191	TOM1	TARGET OF MYB1.	AGLQSLEASGR	R	L	95.00%	40		544.7911	2	3.9	351	361	No
				EVKYEAPQATDGLAGALDAR	K	Q	95.00%	37		692.3565	3	6.2	383	402	No
				FHVLVASQDFVESVLVR	R	T	95.00%	50		649.0284	3	7.8	85	101	No
				LEDEFDMFALTR	R	G	95.00%	39	M7: Oxidation	751.8520	2	8.3	362	373	No
				SELEMVSGNVR	R	V	95.00%	40	M5: Oxidation	618.8022	2	5.8	222	232	No
				SSPDLTGVVTIYEDLR	R	R	95.00%	90		882.9630	2	9.0	130	145	No
				VLNLIQSWADAFR	K	S	95.00%	77		766.9226	2	9.7	117	129	No
				YEAPQATDGLAGALDAR	K	Q	95.00%	111		859.9270	2	6.4	386	402	No
172	IPI00023635; IPI00555726	IMPA2	ISOFORM 1 OF INOSITOL MONOPHOSPHATASE 2.; ISOFORM 2 OF INOSITOL MONOPHOSPHATASE 2.	ALVLTEIGPK	K	R	95.00%	58		520.8258	2	7.6	168	177	No
				FIAEEAAASGAK	R	C	95.00%	59		582.8025	2	6.1	78	89	No
173	IPI00023640	PDCD5	PROGRAMMED CELL DEATH PROTEIN 5.	LSNLALVKPEK	R	T	95.00%	40		606.3757	2	5.8	56	66	No
				LSNLALVKPEK	R	T	95.00%	29		404.5854	3	3.4	56	66	No
				NSILAQVLDQSAR	R	A	95.00%	77		707.8915	2	6.9	41	53	No
				VSEQGLIEILK	K	K	95.00%	31		614.8668	2	8.4	87	97	No
				VSEQGLIEILKK	K	V	95.00%	33		452.9439	3	4.1	87	98	No
174	IPI00024046	CDH13	CADHERIN-13 PRECURSOR.	DIQGSLQDIFK	K	F	95.00%	65		632.3358	2	4.1	116	126	No
				INENTGSVSVTR	R	T	95.00%	59		638.8330	2	6.6	190	201	No
				MTAFDADDPATDNALLR	R	Y	95.00%	122	M1: Oxidation	926.9323	2	9.7	267	283	No
				SIVVSPILIPENQR	R	Q	95.00%	36		782.9644	2	9.4	139	152	No
				TLEGPVPLEVIVIDQNDNRPIFR	K	E	95.00%	45		878.8210	3	8.2	224	246	No
175	IPI00024157	FKBP3	FK506-BINDING PROTEIN 3.	ARLEIEPEWAYGK	K	K	95.00%	44		781.4122	2	9.5	188	200	No
				DHLVTAYNHLFETK	K	R	95.00%	31		563.2921	3	9.6	57	70	No
				ETKSEETLDEGPPK	K	Y	95.00%	78		780.3796	2	4.5	97	110	No
				FLQEHGSDSFLAEHK	K	L	95.00%	87		872.9244	2	6.6	28	42	No
				FLQEHGSDSFLAEHK	K	L	95.00%	52		582.2857	3	6.9	28	42	No
				GWDEALLTMSK	R	G	95.00%	52	M9: Oxidation	633.8118	2	9.2	174	184	No
				SEETLDEGPPK	K	Y	95.00%	61		601.2867	2	5.4	100	110	No
				SEETLDEGPPKYTK	K	S	95.00%	50		797.3919	2	6.8	100	113	No
176	IPI00024175	PSMA7	ISOFORM 1 OF PROTEASOME SUBUNIT ALPHA TYPE 7.	ALLEVVQSGGK	K	N	95.00%	63		550.8232	2	6.3	194	204	No
				GRDIVVLGVEK	R	K	95.00%	48		592.8597	2	9.3	37	47	No
				LTVEDPVTVEYITR	R	Y	95.00%	93		817.9420	2	7.2	96	109	No
				NYTDEAIETDDLTIK	K	L	95.00%	94		870.9199	2	7.8	175	189	No
				YVAEIEKEKEENEK	K	K	95.00%	83		869.4390	2	8.9	228	241	No

177	IPI00024664; IPI00375145	USP5	ISOFORM LONG OF UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 5.; ISOFORM SHORT OF UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 5.	DGLGGLPDIVR	R	D	95.00%	35		556.3129	2	5.7	134	144	No
				DRVTSAVEALLSADSASR	R	K	95.00%	36		616.6563	3	3.7	145	162	No
				EEDPATGTGDPPR	K	K	95.00%	33		671.3005	2	0.5	81	93	No
				FASFPDYLVIQIK	R	K	95.00%	80		770.9304	2	7.4	562	574	No
				IFQNAPTDPTQDFSTQVAK	K	L	95.00%	107		1054.5290	2	10.0	361	379	No
				IFQNAPTDPTQDFSTQVAK	K	L	95.00%	53		703.3518	3	4.6	361	379	No
				IGEWELIQESGVPLKPLFGPGYTGIR	R	N	95.00%	45		952.8576	3	9.5	304	329	No
				IVILPDYLEIAR	K	D	95.00%	51		707.9214	2	2.7	122	133	No
				LGHGLLSGEYSKPVPESGDGERVPEQK	K	E	95.00%	30		717.1188	4	4.7	380	406	No
				SAADSISESVPVGPK	R	V	95.00%	59		722.3738	2	4.5	756	770	No
				VDYIMQLPVPMDAALNKEELLEYEEK	R	K	95.00%	34	M5: Oxidation, M11: Oxidation	1038.1850	3	8.9	483	508	No
				VTSAVEALLSADSASR	R	K	95.00%	64		788.9177	2	6.0	147	162	No
				YFDGSGGNNHAVEHYR	R	E	95.00%	40		608.2707	3	3.7	223	238	No
178	IPI00024670; IPI00744902	REEP5	RECEPTOR EXPRESSION-ENHANCING PROTEIN 5.; 21 KDA PROTEIN.	ATVNLLGEEK	K	K	95.00%	58		537.3001	2	7.4	177	186	No
				KATVNLLGEEKK	K	S	95.00%	31		665.3962	2	7.8	176	187	No
179	IPI00024804; IPI00396118; IPI00794585	ATP2A1	ISOFORM SERCA1B OF SARCOPLASMIC/ENDOPLASMIC RETICULUM CALCIUM ATPASE1.; ISOFORM SERCA1A OF SARCOPLASMIC/ENDOPLASMIC RETICULUM CALCIUM ATPASE1.; SIMILAR TO ATPASE, CA++ TRANSPORTING, CARDIAC MUSCLE, FAST TWITCH 1.	AEIGIAMGSGTAVAK	K	T	95.00%	109	M7: Oxidation	696.3662	2	2.9	714	728	Yes
				AEIGIAMGSGTAVAK	K	T	95.00%	94		688.3702	2	5.1	714	728	Yes
				ALDLTQWLMVLK	R	I	95.00%	85	M9: Oxidation	723.9096	2	5.7	961	972	No
				ALDLTQWLMVLK	R	I	95.00%	61	M9: Oxidation	482.9422	3	5.4	961	972	No
				ALDLTQWLMVLK	R	I	95.00%	83		715.9114	2	4.6	961	972	No
				ALGIVATTGVGTEIGK	K	I	95.00%	125		743.9348	2	9.0	219	234	No
				ALGIVATTGVGTEIGK	K	I	95.00%	65		496.2899	3	3.8	219	234	No
				ARDIVPGDIVEVAVGDK	K	V	95.00%	34		584.9923	3	6.5	142	158	No
				ARDIVPGDIVEVAVGDKVPADIR	K	I	95.00%	105		802.1172	3	6.7	142	164	No
				ARDIVPGDIVEVAVGDKVPADIR	K	I	95.00%	72		601.8405	4	7.7	142	164	No
				AYTGREFDDLPLAEQR	R	E	95.00%	38		627.6468	3	5.3	652	667	No
				DIVPGDIVEVAVGDK	R	V	95.00%	97		763.4149	2	6.8	144	158	No
				DIVPGDIVEVAVGDK	R	V	95.00%	54		509.2786	3	5.5	144	158	No
				DIVPGDIVEVAVGDKVPADIR	R	I	95.00%	113		1089.1030	2	7.7	144	164	No
				DIVPGDIVEVAVGDKVPADIR	R	I	95.00%	55		726.4043	3	7.0	144	164	No
				DQMAATEQDKTPLQQK	R	L	95.00%	83	M3: Oxidation	924.4524	2	8.5	237	252	No
				DQMAATEQDKTPLQQK	R	L	95.00%	70	M3: Oxidation	616.6353	3	4.9	237	252	No
				DTPPKREEMVLDDSAR	R	F	95.00%	38	M9: Oxidation	937.9523	2	2.6	568	583	No
				EEMVLDDSAR	R	F	95.00%	79	M3: Oxidation	590.7643	2	4.4	574	583	No
				EFDDLPLAEQR	R	E	95.00%	76		666.8281	2	3.4	657	667	No
				EFDDLPLAEQR	R	E	95.00%	44		444.8889	3	5.4	657	667	No
				EFTLEFSR	K	D	95.00%	42		1028.5150	1	9.6	482	489	Yes
				EFTLEFSR	K	D	95.00%	60		514.7578	2	2.4	482	489	Yes
				EPLISGWLFFR	K	Y	95.00%	63		682.8785	2	9.1	826	836	Yes
				FLEYETDLTFVGVVGMLDPPRK	R	E	95.00%	39	M16: Oxidation	848.1067	3	5.6	584	605	No
				GAPEGVIDR	K	C	95.00%	58		457.2430	2	4.2	516	524	Yes
				HTEPVPDPR	K	A	95.00%	39		524.2671	2	3.7	190	198	No
				IGIFGENEEVADR	R	A	95.00%	113		724.8589	2	5.4	639	651	No
				IMAVIKEWGTGR	K	D	95.00%	28	M2: Oxidation	688.8760	2	5.8	545	556	No
				IMAVIKEWGTGR	K	D	95.00%	31	M2: Oxidation	459.5858	3	4.0	545	556	No
				IRDQMAATEQDKTPLQQK	K	L	95.00%	61	M5: Oxidation	1059.0430	2	5.8	235	252	No
				IRDQMAATEQDKTPLQQK	K	L	95.00%	67	M5: Oxidation	706.3637	3	4.3	235	252	No
				IRDQMAATEQDKTPLQQK	K	L	95.00%	41	M5: Oxidation	530.0242	4	3.3	235	252	No
				IRDQMAATEQDKTPLQQK	K	L	95.00%	53		701.0312	3	3.0	235	252	No
				ISLPVIGLDEILK	K	F	95.00%	106		705.4386	2	5.1	973	985	No
				ISLPVIGLDEILK	K	F	95.00%	37		470.6285	3	5.5	973	985	No
				IVEYLQSYDEITAMTGDGVNDAPALK	K	K	95.00%	92	M14: Oxidation	943.7975	3	9.3	687	712	No

				IVEYLQSYDEITAMTGDGVNDAPALKK	K	A	95.00%	89	M14: Oxidation	986.4949	3	7.9	687	713	No
				IVEYLQSYDEITAMTGDGVNDAPALKK	K	A	95.00%	60		981.1616	3	6.2	687	713	No
				KAEIGIAMGSGTAVAK	K	T	95.00%	119	M8: Oxidation	760.4186	2	9.2	713	728	Yes
				KAEIGIAMGSGTAVAK	K	T	95.00%	71	M8: Oxidation	507.2777	3	1.2	713	728	Yes
				KAEIGIAMGSGTAVAK	K	T	95.00%	53		501.9464	3	1.9	713	728	Yes
				KEFTLEFSR	K	D	95.00%	50		578.8086	2	7.8	481	489	Yes
				KNMLFSGTNIAAGK	K	A	95.00%	40	M3: Oxidation	734.3868	2	1.8	205	218	Yes
				KNMLFSGTNIAAGK	K	A	95.00%	43	M3: Oxidation	489.9285	3	4.7	205	218	Yes
				LDEFGEQLSK	K	V	95.00%	42		1165.5850	1	9.3	253	262	Yes
				LDEFGEQLSK	K	V	95.00%	70		583.2954	2	7.4	253	262	Yes
				MFIIDK	K	V	95.00%	27	M1: Oxidation	782.4167	1	5.5	366	371	No
				MNVFNTDVR	K	S	95.00%	71	M1: Oxidation	556.2661	2	3.4	452	460	No
				MNVFNTDVR	K	S	95.00%	65		548.2691	2	4.2	452	460	No
				NAENAIEALK	R	E	95.00%	41		1072.5620	1	-1.5	111	120	Yes
				NAENAIEALK	R	E	95.00%	71		536.7884	2	4.8	111	120	Yes
				NAENAIEALKEYEPEMGK	R	V	95.00%	103	M16: Oxidation	1026.4930	2	8.7	111	128	Yes
				NAENAIEALKEYEPEMGK	R	V	95.00%	70	M16: Oxidation	684.6614	3	4.3	111	128	Yes
				NAENAIEALKEYEPEMGK	R	V	95.00%	95		1018.4920	2	5.9	111	128	Yes
				NAENAIEALKEYEPEMGK	R	V	95.00%	46		679.3293	3	3.7	111	128	Yes
				NMLFSGTNIAAGK	K	A	95.00%	98	M2: Oxidation	670.3395	2	2.5	206	218	Yes
				NMLFSGTNIAAGK	K	A	95.00%	84		662.3448	2	6.6	206	218	Yes
				NMLFSGTNIAAGKALGIVATTGVGTEIGK	K	I	95.00%	57	M2: Oxidation	936.5120	3	8.0	206	234	No
				REEMVLDDSAR	K	F	95.00%	37	M4: Oxidation	668.8165	2	6.2	573	583	No
				RIGIFGENEEVADR	R	A	95.00%	88		802.9083	2	3.3	638	651	No
				RIGIFGENEEVADR	R	A	95.00%	54		535.6076	3	2.3	638	651	No
				STTLRVDQSILTGESVSVIK	K	H	95.00%	45		711.7365	3	8.0	170	189	Yes
				TASEMVLADDNFSTIVAAVEEGR	K	A	95.00%	158	M5: Oxidation	1221.0910	2	9.7	729	751	Yes
				TASEMVLADDNFSTIVAAVEEGR	K	A	95.00%	100	M5: Oxidation	814.3936	3	6.1	729	751	Yes
				TASEMVLADDNFSTIVAAVEEGR	K	A	95.00%	61	M5: Oxidation	611.0388	4	-7.6	729	751	Yes
				VDQSILTGESVSVIK	R	H	95.00%	96		787.9398	2	4.8	175	189	Yes
				VDQSILTGESVSVIK	R	H	95.00%	75		525.6276	3	2.0	175	189	Yes
				VGEATETALTTLVEK	K	M	95.00%	141		781.4261	2	7.5	437	451	No
				VGEATETALTTLVEK	K	M	95.00%	62		521.2788	3	-7.7	437	451	No
				VGTTRVPLTGPVK	R	E	95.00%	32		662.9048	2	4.7	530	542	No
				VGTTRVPLTGPVK	R	E	95.00%	21		442.2718	3	3.2	530	542	No
				VIMITGDNK	R	G	95.00%	44	M3: Oxidation	1006.5330	1	8.2	621	629	Yes
				VIMITGDNK	R	G	95.00%	49	M3: Oxidation	503.7675	2	2.7	621	629	Yes
				VIMITGDNK	R	G	95.00%	39		495.7693	2	1.1	621	629	Yes
				VPLTGPVK	R	E	95.00%	53		810.5131	1	4.9	535	542	No
				VPLTGPVK	R	E	95.00%	47		405.7595	2	2.7	535	542	No
				VPLTGPVKEK	R	I	95.00%	65		534.3288	2	2.9	535	544	No
				YGLNELPAEEGK	K	T	95.00%	78		660.3310	2	4.3	36	47	No
180	IPI00024915; IPI00759663	PRDX5	ISOFORM MITOCHONDRIAL OF PEROXIREDOXIN-5, MITOCHONDRIAL PRECURSOR.; ISOFORM CYTOPLASMIC+PEROXISOMAL OF PEROXIREDOXIN-5, MITOCHONDRIALPRECURSOR.	ETDLLLDDSLVSIFGNR	K	R	95.00%	95		954.0004	2	8.7	108	124	No
				ETDLLLDDSLVSIFGNRR	K	L	95.00%	32		688.3702	3	8.5	108	125	No
				FSMVVQDGIVK	R	A	95.00%	66	M3: Oxidation	619.8318	2	8.3	129	139	No
				LLADPTGAFGK	R	E	95.00%	35		1089.6030	1	8.0	97	107	No
				THLPGFVEQAEALK	K	A	95.00%	46		770.4162	2	4.7	51	64	No
				THLPGFVEQAEALK	K	A	95.00%	52		513.9467	3	4.6	51	64	No
				VNLAELFK	K	G	95.00%	63		467.2790	2	9.7	76	83	No
181	IPI00024919; IPI00374151	PRDX3	THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE, MITOCHONDRIAL PRECURSOR.; PEROXIREDOXIN 3 ISOFORM B.	DLSLDDFK	K	G	95.00%	33		476.7379	2	5.2	84	91	No
				DYGVLLEGSGLALR	R	G	95.00%	128		731.9059	2	9.1	171	184	No
				GLFIIDPNGVIK	R	H	95.00%	55		643.3859	2	9.0	185	196	No
				GTAVVNGEFK	K	D	95.00%	35		511.2743	2	8.9	74	83	No
				HLSVNDLPVGR	K	S	95.00%	47		603.8374	2	6.2	197	207	No
				HLSVNDLPVGR	K	S	95.00%	42		402.8938	3	5.2	197	207	No
182	IPI00024920	ATP5D	ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR.	AQAELVGTADEATR	K	A	95.00%	111		716.3636	2	7.8	137	150	No

				IEANEALVK	R	A	95.00%	67		493.7823	2	4.5	157	165	No
				PGLVVVHAEDGTTSK	R	Y	95.00%	43		503.9388	3	6.2	82	96	No
183	IPI00024983; IPI00410134	RTN2	ISOFORM RTN2-A OF RETICULON-2.; ISOFORM RTN2-C OF RETICULON-2.	AKIPGTGALASAAAAVSGSK	R	A	95.00%	133		864.4949	2	9.4	522	541	No
				AKIPGTGALASAAAAVSGSK	R	A	95.00%	73		576.6643	3	6.7	522	541	No
				IPGTGALASAAAAVSGSK	K	A	95.00%	119		764.9278	2	9.3	524	541	No
				IPGTGALASAAAAVSGSK	K	A	95.00%	72		510.2858	3	5.4	524	541	No
				QHQAQIDQYVGLVTNQLSHIK	R	A	95.00%	46		605.8257	4	4.4	497	517	No
				VADLLYWK	K	D	95.00%	64		504.2856	2	6.7	345	352	No
				VVSAATQLR	R	H	95.00%	82		472.7828	2	5.1	439	447	No
184	IPI00024993	ECHS1	ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR.	EGMTAFVEK	K	R	95.00%	40	M3: Oxidation	514.2460	2	6.9	274	282	No
				ESVNAAFEMTLTEGSK	K	L	95.00%	91	M9: Oxidation	865.4100	2	9.7	242	257	No
				KLFYSTFATDDRK	K	E	95.00%	69		796.4158	2	7.4	261	273	No
				LFYSTFATDDRK	K	E	95.00%	50		732.3674	2	6.8	262	273	No
				NNTVGLIQLNRPK	K	A	95.00%	67		733.9313	2	7.1	44	56	No
				SLAMEMVLTGDR	K	I	95.00%	68	M4: Oxidation, M6: Oxidation	677.8255	2	6.2	186	197	No
185	IPI00025019	PSMB1	PROTEASOME SUBUNIT BETA TYPE 1 PRECURSOR.	DVFISAAER	K	D	95.00%	41		504.2642	2	4.5	205	213	No
				EGIREETVSLR	K	K	95.00%	43		644.8522	2	8.1	229	239	No
186	IPI00025084; IPI00794720	CAPNS1	CALPAIN SMALL SUBUNIT 1.; 34 KDA PROTEIN.	ILGGVISAISEAAAQYNPEPPPPR	R	T	95.00%	72		612.5834	4	6.9	61	84	No
				LGFEEFK	K	Y	95.00%	48		435.2269	2	5.8	159	165	No
				SMVAVMDSDTTGK	R	L	95.00%	41	M2: Oxidation, M6: Oxidation	687.3055	2	7.6	146	158	No
				THYSNIEANESEEVR	R	Q	95.00%	79		889.4095	2	6.7	85	99	No
				THYSNIEANESEEVR	R	Q	95.00%	56		593.2751	3	6.0	85	99	No
187	IPI00025086	COX5A	CYTOCHROME C OXIDASE SUBUNIT 5A, MITOCHONDRIAL PRECURSOR.	GINTLVTYDMVPEPK	K	I	95.00%	110	M10: Oxidation	846.9358	2	6.9	73	87	No
				ILEVVK	R	D	95.00%	40		700.4658	1	6.8	108	113	No
				ILEVVKDK	R	A	95.00%	37		472.2969	2	3.2	108	115	No
				KGINTLVTYDMVPEPK	R	I	95.00%	44	M11: Oxidation	607.6587	3	7.2	72	87	No
				WVTYFNKPDIDAWELR	R	K	95.00%	42		685.0149	3	5.1	56	71	No
188	IPI00025092; IPI00791650; IPI00797657	MYBPC1	MYOSIN-BINDING PROTEIN C, SLOW-TYPE.; 127 KDA PROTEIN.; MYOSIN BINDING PROTEIN C, SLOW TYPE ISOFORM 4.	ADAAEYSVMTTGGQSSAK	K	L	95.00%	139	M9: Oxidation	895.4062	2	7.3	408	425	Yes
				ADAAEYSVMTTGGQSSAK	K	L	95.00%	71	M9: Oxidation	597.2717	3	4.5	408	425	Yes
				ADAAEYSVMTTGGQSSAK	K	L	95.00%	123		887.4032	2	1.1	408	425	Yes
				ADAAEYSVMTTGGQSSAK	K	L	95.00%	76		591.9394	3	3.4	408	425	Yes
				AIMEGSGR	K	I	95.00%	50	M3: Oxidation	418.7039	2	7.5	565	572	Yes
				AKDNFAGNYR	K	C	95.00%	58		578.2838	2	4.3	132	141	Yes
				AVNAAGASEPK	K	Y	95.00%	63		507.7670	2	4.1	812	822	Yes
				AVNDLGTVEIECK	K	L	95.00%	96		695.8511	2	4.0	1121	1133	Yes
				DDGNAAITGYTIQK	K	A	95.00%	85		733.8652	2	6.5	957	970	Yes
				DDSGVYHINLK	R	N	95.00%	70		630.8180	2	4.6	592	602	Yes
				DGAEIDKNQINIR	K	N	95.00%	97		743.3899	2	3.8	876	888	Yes
				DGAEIDKNQINIR	K	N	95.00%	69		495.9286	3	2.5	876	888	Yes
				DNFAGNYR	K	C	95.00%	39		956.4313	1	9.2	134	141	Yes
				DNFAGNYR	K	C	95.00%	41		478.7162	2	2.2	134	141	Yes
				DWTLVETPPGEEQAK	K	Q	95.00%	71		850.4198	2	8.0	35	49	No
				EAGTTPAKDWTLVETPPGEEQAK	K	Q	95.00%	48		819.0774	3	7.0	27	49	No
				EENEVPAPAPPPEEPSKEK	K	E	95.00%	56		1037.5070	2	3.4	8	26	Yes
				EIIEPPK	K	I	95.00%	43		825.4747	1	2.8	832	838	Yes
				EIIEPPKIR	K	I	95.00%	26		547.8343	2	3.0	832	840	Yes
				EPPIMVTK	R	Q	95.00%	47	M5: Oxidation	465.7539	2	3.1	339	346	Yes
				EPPIMVTK	R	Q	95.00%	34		457.7560	2	2.0	339	346	Yes
				EVKQQEEEPQVDVWELLK	R	N	95.00%	33		742.7187	3	4.9	198	215	Yes
				FTITGLPTDAK	K	I	95.00%	27		1163.6410	1	8.1	795	805	Yes
				FTITGLPTDAK	K	I	95.00%	67		582.3214	2	3.0	795	805	Yes
				FVETASIDIQIIDRPGPPQIVK	K	I	95.00%	65		812.7964	3	9.4	918	939	Yes
				FVVELADPK	R	L	95.00%	68		509.2860	2	1.9	272	280	Yes
				FVVELADPKLEVK	R	W	95.00%	71		743.9330	2	3.9	272	284	Yes
				FVVELADPKLEVK	R	W	95.00%	66		496.2915	3	4.4	272	284	Yes
				GKWMDLASK	K	A	95.00%	34	M4: Oxidation	526.2684	2	3.9	97	105	Yes
				HILIIEGATK	K	A	95.00%	54		1094.6640	1	5.8	398	407	Yes
				HILIIEGATK	K	A	95.00%	66		547.8336	2	1.6	398	407	Yes
				IAFQYGITDLR	K	G	95.00%	78		648.8547	2	4.7	225	235	Yes
				IEDVWGENVALTWTPPK	K	D	95.00%	112		978.0048	2	5.1	940	956	Yes

IEDVWGENVALTWTPPKDDGNAAITGYTIQK	K	A	95.00%	56		1134.9090	3	7.6	940	970	Yes
IFAVNAIGISK	R	P	95.00%	48		1132.6820	1	8.1	694	704	Yes
IFAVNAIGISK	R	P	95.00%	112		566.8414	2	1.6	694	704	Yes
IFAVNAIGISKPSMPSR	R	P	95.00%	56	M14: Oxidation	902.5020	2	9.4	694	710	Yes
IFAVNAIGISKPSMPSR	R	P	95.00%	75	M14: Oxidation	602.0012	3	4.9	694	710	Yes
IFAVNAIGISKPSMPSR	R	P	95.00%	41		596.6678	3	2.0	694	710	Yes
IILDGLDADNTVTVIAGNK	K	L	95.00%	162		971.5355	2	6.8	524	542	Yes
IILDGLDADNTVTVIAGNK	K	L	95.00%	73		648.0248	3	4.7	524	542	Yes
ILDPAYQVDK	K	G	95.00%	37		1161.6200	1	3.4	257	266	Yes
ILDPAYQVDK	K	G	95.00%	87		581.3116	2	-0.4	257	266	Yes
ILDPAYQVDKGGR	K	V	95.00%	47		716.3871	2	4.6	257	269	Yes
ILTPLTDQTVNLGK	K	E	95.00%	96		756.9391	2	4.3	435	448	Yes
ILTPLTDQTVNLGK	K	E	95.00%	47		504.9620	3	4.2	435	448	Yes
IRTESYPDSSTLVIDIAER	R	D	95.00%	57		722.3801	3	7.1	573	591	Yes
IRTESYPDSSTLVIDIAERDDSGVYHINLK	R	N	95.00%	78		852.4421	4	9.4	573	602	Yes
KDGAEIDKNQINIR	K	N	95.00%	107		807.4402	2	7.0	857	870	Yes
KDGAEIDKNQINIR	K	N	95.00%	57		538.6268	3	2.1	875	888	Yes
KDGAEIDKNQINIR	K	N	95.00%	33		404.2223	4	2.9	875	888	Yes
KEENEVPAPAPPPEEPSK	K	E	95.00%	89		972.9900	2	8.3	7	24	Yes
KEENEVPAPAPPPEEPSKEK	K	E	95.00%	47		1101.5590	2	7.8	7	26	Yes
KEENEVPAPAPPPEEPSKEK	K	E	95.00%	57		734.7073	3	5.9	7	26	Yes
KHILIIEGATK	K	A	95.00%	53		611.8817	2	2.5	397	407	Yes
KHILIIEGATK	K	A	95.00%	59		408.2568	3	1.8	397	407	Yes
KMIEGVAYEVR	K	I	95.00%	74	M2: Oxidation	655.8452	2	3.6	683	693	Yes
KMIEGVAYEVR	K	I	95.00%	42	M2: Oxidation	437.5661	3	3.6	683	693	Yes
KMIEGVAYEVR	K	I	95.00%	90		647.8469	2	2.3	683	693	Yes
KMIEGVAYEVR	K	I	95.00%	50		432.2339	3	2.5	683	693	Yes
LEIPISGEPPPK	R	A	95.00%	64		638.8652	2	5.5	545	556	Yes
LEIPISGEPPPK	R	A	95.00%	42		426.2447	3	2.3	545	556	Yes
LRLEIPISGEPPPK	K	A	95.00%	66		773.4575	2	4.1	543	556	Yes
LRLEIPISGEPPPK	K	A	95.00%	64		515.9741	3	3.7	543	556	Yes
LSVDLKPLK	K	I	95.00%	41		1012.6450	1	3.6	426	434	Yes
LSVDLKPLK	K	I	95.00%	64		506.8260	2	3.1	426	434	Yes
LVIANALTEDEGDYVFAPDAYNVTLPAK	K	V	95.00%	49		1003.8520	3	10.0	488	515	Yes
LVIANALTEDEGDYVFAPDAYNVTLPAK	K	V	95.00%	55		753.1393	4	8.0	488	515	Yes
MFSNQGVCTLEIR	R	K	95.00%	43	M1: Oxidation	757.3683	2	9.5	1095	1107	Yes
MIEGVAYEVR	K	I	95.00%	39	M1: Oxidation	1182.5940	1	9.2	684	693	Yes
MIEGVAYEVR	K	I	95.00%	78	M1: Oxidation	591.7964	2	1.7	684	693	Yes
MIEGVAYEVR	K	I	95.00%	71		583.7996	2	2.7	684	693	Yes
NEAGEAHASIK	K	V	95.00%	61		563.7816	2	5.4	603	613	Yes
NGEEIIPGPK	K	S	95.00%	57		1053.5640	1	5.0	377	386	Yes
NGEEIIPGPK	K	S	95.00%	58		527.2845	2	2.8	377	386	Yes
NGLPVQESDR	K	L	95.00%	53		557.7797	2	2.1	467	476	Yes
NGLPVQESDRLK	K	V	95.00%	42		678.3714	2	4.9	467	478	Yes
NSETDTIIFIR	R	K	95.00%	79		654.8476	2	5.6	889	899	Yes
NSETDTIIFIR	R	K	95.00%	35		436.9025	3	9.0	889	899	Yes
PFVPLAVTSPPTLLTVDSVTDTTVTMR	R	W	95.00%	61	M26: Oxidation	958.8519	3	7.9	711	737	Yes
PRPELTWK	K	K	95.00%	32		513.7922	2	2.6	867	874	Yes
PSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMR	K	W	95.00%	97	M3: Oxidation, M32: Oxidation	1182.6250	3	9.8	705	737	Yes
PSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMR	K	W	95.00%	58	M3: Oxidation, M32: Oxidation	887.2193	4	8.5	705	737	Yes
QNANSQLSILFIEKPQGGTVK	K	V	95.00%	92		1136.6270	2	7.4	50	70	Yes
QNANSQLSILFIEKPQGGTVK	K	V	95.00%	77		758.0852	3	4.3	50	70	Yes
QQEEEPQVDVWELLK	K	N	95.00%	90		935.4717	2	6.4	201	215	Yes
QQEEEPQVDVWELLK	K	N	95.00%	57		623.9840	3	6.8	201	215	Yes
RSGEGQEDAGELDFSGLLK	K	R	95.00%	115		1004.4930	2	7.6	177	195	Yes
RSGEGQEDAGELDFSGLLK	K	R	95.00%	80		669.9971	3	6.6	177	195	Yes
RVGEAVNLVIPFQGK	R	P	95.00%	63		813.9752	2	5.6	852	866	Yes
RVGEAVNLVIPFQGK	R	P	95.00%	42		542.9863	3	6.0	852	866	Yes
RVGEAVNLVIPFQGKPR	R	P	95.00%	50		627.3699	3	3.6	852	868	Yes
RVGEAVNLVIPFQGKPR	R	P	95.00%	33		470.7787	4	2.3	852	868	Yes
SGEGQEDAGELDFSGLLK	R	R	95.00%	133		926.4421	2	8.0	178	195	Yes
SGEGQEDAGELDFSGLLK	R	R	95.00%	95		617.9633	3	6.9	178	195	Yes
SGEGQEDAGELDFSGLLKR	R	R	95.00%	81		1004.4940	2	8.9	178	196	Yes

				SGEGQEDAGELDFSGLLKR	R	R	95.00%	73		669.9985	3	8.7	178	196	Yes
				SHSGKYDLQVK	R	V	95.00%	37		631.3340	2	4.8	904	914	Yes
				SMEWFTVIEHYHR	K	T	95.00%	78	M2: Oxidation	875.9104	2	6.9	975	987	Yes
				SMEWFTVIEHYHR	K	T	95.00%	50	M2: Oxidation	584.2774	3	9.0	975	987	Yes
				SMEWFTVIEHYHR	K	T	95.00%	68		867.9137	2	7.8	975	987	Yes
				SMEWFTVIEHYHR	K	T	95.00%	45		578.9436	3	5.3	975	987	Yes
				TESYPDSSTLVIDIAER	R	D	95.00%	120		948.4720	2	6.4	575	591	Yes
				TESYPDSSTLVIDIAERDDSGVYHINLK	R	N	95.00%	72		1046.5220	3	7.5	575	602	Yes
				TESYPDSSTLVIDIAERDDSGVYHINLK	R	N	95.00%	54		785.1423	4	5.8	575	602	Yes
				TKFTITGLPTDAK	K	I	95.00%	81		696.8935	2	3.6	793	805	Yes
				TKFTITGLPTDAK	K	I	95.00%	41		464.9308	3	1.8	793	805	Yes
				TSATITELVIGNEYYFR	R	V	95.00%	111		989.0104	2	8.2	988	1004	Yes
				TSATITELVIGNEYYFR	R	V	95.00%	94		659.6745	3	5.6	988	1004	Yes
				VAIVDDPR	K	Y	95.00%	55		442.7470	2	2.1	1085	1092	Yes
				VDKFVETASIDIQIIDRPGPPQIVK	K	I	95.00%	51		926.8603	3	8.8	915	939	Yes
				VDKFVETASIDIQIIDRPGPPQIVK	K	I	95.00%	89		695.3967	4	8.1	915	939	Yes
				VGEAVNLVIPFQGK	R	P	95.00%	91		735.9244	2	6.0	853	866	Yes
				VGEAVNLVIPFQGK	R	P	95.00%	29		490.9518	3	5.1	853	866	Yes
				VGEAVNLVIPFQGKPR	R	P	95.00%	39		862.5040	2	8.2	853	868	Yes
				VGEAVNLVIPFQGKPR	R	P	95.00%	50		575.3367	3	5.0	853	868	Yes
				VGEAVNLVIPFQGKPRPELTWK	R	K	95.00%	43		826.8074	3	7.7	853	874	Yes
				VGEDITFIAK	K	V	95.00%	44		1092.6030	1	7.6	71	80	Yes
				VGEDITFIAK	K	V	95.00%	89		546.8023	2	2.2	71	80	Yes
				VHVIDPPK	K	I	95.00%	34		452.7675	2	1.6	516	523	Yes
				VHVIDPPKIILDGLDADNTVTVIAGNK	K	L	95.00%	67		943.1994	3	9.0	516	542	Yes
				VHVIDPPKIILDGLDADNTVTVIAGNK	K	L	95.00%	44		707.6511	4	8.4	516	542	Yes
				VKAEDLLR	K	K	95.00%	32		943.5627	1	5.2	81	88	Yes
				VKAEDLLR	K	K	95.00%	47		472.2841	2	2.7	81	88	Yes
				VKAVNAAGASEPK	R	Y	95.00%	42		621.3520	2	8.8	810	822	Yes
				VKAVNAAGASEPK	R	Y	95.00%	30		414.5682	3	2.9	810	822	Yes
				VYTFEMQIIK	R	A	95.00%	59	M6: Oxidation	644.3419	2	7.8	122	131	Yes
				VYTFEMQIIK	R	A	95.00%	52		636.3411	2	2.6	122	131	Yes
				WMDLASK	K	A	95.00%	31	M2: Oxidation	866.4106	1	2.6	99	105	Yes
				WMDLASK	K	A	95.00%	35	M2: Oxidation	433.7089	2	2.0	99	105	Yes
				YYSQPILVK	K	E	95.00%	64		555.8160	2	3.7	823	831	Yes
189	IPI00025239		NDUFS2	NADH DEHYDROGENASE [UBIQUINONE] IRON-SULFUR PROTEIN 2, MITOCHONDRIALPRECURSOR.	APGFAHLAGLDK	K	M	95.00%	55		598.8285	2	5.1	426	437	No
				GEFGVYLVSDGSSR	K	P	95.00%	97		736.8599	2	6.7	405	418	No
				GEFGVYLVSDGSSRPYR	K	C	95.00%	35		944.9672	2	3.8	405	421	No
				GHMLADVVAIIGTQDIVFGEVDR	K	-	95.00%	70	M3: Oxidation	824.4317	3	7.7	441	463	No
				IKAPGFAHLAGLDK	K	M	95.00%	49		719.4167	2	2.5	424	437	No
				IKAPGFAHLAGLDK	K	M	95.00%	59		479.9471	3	2.5	424	437	No
				LDELEELLTNNR	R	I	95.00%	73		729.8817	2	7.9	255	266	No
				LDELEELLTNNR	R	I	95.00%	35		486.9219	3	4.0	255	266	No
				LLNIRPPPR	K	A	95.00%	22		538.3418	2	1.5	158	166	No
				LVMELSGEMVR	R	K	95.00%	69	M3: Oxidation, M9: Oxidation	648.3224	2	2.4	97	107	No
				LVMELSGEMVR	R	K	95.00%	40	M9: Oxidation	640.3252	2	2.8	97	107	No
				LYTEGYQVPPGATYTAIEAPK	K	G	95.00%	62		1135.0820	2	7.1	384	404	No
				MHAAYIRPGGVHQDLPLGLMDDIYQFSK	R	N	95.00%	49	M1: Oxidation, M20: Oxidation	801.9029	4	8.4	222	249	No
				NITLNFGPQHPAAHGVLR	K	L	95.00%	80		971.5327	2	8.4	79	96	No
				NITLNFGPQHPAAHGVLR	K	L	95.00%	36		648.0224	3	5.3	79	96	No
				TIDIGVVTAEEALNYGFSGVMLR	R	G	95.00%	58	M21: Oxidation	824.4296	3	9.8	272	294	No
				TQPYDVYDQVEFDVPVGSR	K	G	95.00%	117		1107.5280	2	5.8	305	323	No
				TQPYDVYDQVEFDVPVGSR	K	G	95.00%	69		738.6876	3	5.3	305	323	No
				TSMESLIHHFK	K	L	95.00%	37	M3: Oxidation	673.3345	2	2.8	373	383	No
				TYLQALPYFDR	K	L	95.00%	61		693.8635	2	9.6	128	138	No
				VLFGEITR	R	L	95.00%	46		467.7734	2	2.9	172	179	No

190	IPI00025252; IPI00657680	PDIA3	PROTEIN DISULFIDE-ISOMERASE A3 PRECURSOR.; 55 KDA PROTEIN.	EATNPPVIQEEKPK	R	K	95.00%	77		790.4229	2	2.9	483	496	No
				ELSDFISYLQR	R	E	95.00%	57		685.8551	2	4.9	472	482	No
				FAHTNVESLVNEYDDNGEGIILFR	R	P	95.00%	38		918.1168	3	4.9	184	207	No
				FLQDYFDGNLKR	R	Y	95.00%	56		758.3887	2	6.4	352	363	No
				GFPTIYFSPANK	R	K	95.00%	49		671.3492	2	4.6	449	460	No
				LAPEYEAAATR	R	L	95.00%	36		596.3066	2	3.7	63	73	No
				MDATANDVPSPYEVR	K	G	95.00%	86	M1: Oxidation	840.8831	2	2.6	434	448	No
				TFSHELSDFGLESTAGEIPVVAIR	K	T	95.00%	43		859.1128	3	7.1	306	329	No
				VVVAENFDEIVNNENK	K	D	95.00%	84		916.9622	2	7.5	380	395	No
				YGVSGYPTLK	K	I	95.00%	39		542.7900	2	3.8	95	104	No
191	IPI00025366	CS	CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR.	AALPSHVVTMLDNFPTNLHPMSQLSAAVTALNSESNFAR	R	A	95.00%	43	M10: Oxidation, M21: Oxidation	1046.7780	4	7.6	145	183	No
				ALGFPLER	R	P	95.00%	34		451.7602	2	2.8	441	448	No
				ALGFPLERPK	R	S	95.00%	40		564.3351	2	4.0	441	450	No
				ALGVLAQLIWSR	R	A	95.00%	78		663.9038	2	7.5	429	440	No
				DILADLIPK	K	E	95.00%	39		997.6019	1	8.3	35	43	No
				DILADLIPK	K	E	95.00%	65		499.3032	2	4.9	35	43	No
				DYIWNTLNSGR	R	V	95.00%	59		669.8296	2	5.2	330	340	No
				GLVYETSVLDPDEGIR	K	F	95.00%	90		881.9537	2	7.3	77	92	No
				GLVYETSVLDPDEGIR	K	F	95.00%	59		588.3045	3	6.4	77	92	No
				IVPNVLLEQGK	K	A	95.00%	43		1209.7280	1	6.3	383	393	No
				IVPNVLLEQGK	K	A	95.00%	88		605.3660	2	2.6	383	393	No
				LRDYIWNTLNSGR	K	V	95.00%	83		804.4239	2	6.5	328	340	No
				LRDYIWNTLNSGR	K	V	95.00%	35		536.6179	3	5.2	328	340	No
				LVAQLYK	K	I	95.00%	28		834.5168	1	9.4	376	382	No
				LVAQLYK	K	I	95.00%	32		417.7594	2	2.5	376	382	No
				SMSTEGLMK	K	F	95.00%	43	M2: Oxidation, M8: Oxidation	508.2304	2	8.8	451	459	No
				TKYWELIYEDSMDLIAK	R	L	95.00%	48	M12: Oxidation	712.0246	3	7.6	192	208	No
				TKYWELIYEDSMDLIAK	R	L	95.00%	51		706.6943	3	9.5	192	208	No
				TVVGQITVDMMYGGMR	K	G	95.00%	105	M10: Oxidation, M11: Oxidation, M15: Oxidation	903.4210	2	5.8	58	73	No
				TVVGQITVDMMYGGMR	K	G	95.00%	39	M10: Oxidation, M11: Oxidation, M15: Oxidation	602.6150	3	3.2	58	73	No
				TVVGQITVDMMYGGMR	K	G	95.00%	36	M10: Oxidation, M15: Oxidation	895.4249	2	7.4	58	73	No
				VVPGYGHAVLR	R	K	95.00%	55		584.3379	2	3.6	341	351	No
192	IPI00025512	HSPB1	HEAT-SHOCK PROTEIN BETA-1.	AQLGGPEAAK	R	S	95.00%	53		471.2601	2	6.9	189	198	No
				AQLGGPEAAKSDETAAK	R	-	95.00%	86		822.4216	2	6.8	189	205	No
				DGVVEITGK	K	H	95.00%	52		917.5012	1	7.4	115	123	No
				DGVVEITGK	K	H	95.00%	48		459.2532	2	4.5	115	123	No
				DGVVEITGKHEER	K	Q	95.00%	69		734.8806	2	9.4	115	127	No
				DWYPHSR	R	L	95.00%	32		480.7235	2	6.6	21	27	No
				GPSWDPFR	R	D	95.00%	38		481.2330	2	5.1	13	20	No
				GPSWDPFRDWYPHSR	R	L	95.00%	37		634.9659	3	7.4	13	27	No
				KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK	R	L	95.00%	62	M29: Oxidation	1081.5640	3	7.6	141	171	No
				KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK	R	L	95.00%	27	M29: Oxidation	811.4248	4	7.8	141	171	No
				KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK	R	L	95.00%	90		1076.2330	3	8.6	141	171	No
				LATQSNEITIPVTFESR	K	A	95.00%	92		953.5092	2	9.5	172	188	No
				LATQSNEITIPVTFESR	K	A	95.00%	36		636.0084	3	9.1	172	188	No
				LFDQAFGLPR	R	L	95.00%	86		582.3166	2	3.3	28	37	No
				PLPPAAIESPAVAAPAYSR	R	A	95.00%	89		939.5185	2	8.8	57	75	No
				PLPPAAIESPAVAAPAYSR	R	A	95.00%	46		626.6817	3	9.0	57	75	No
				QLSSGVSEIR	R	H	95.00%	34	S3: Phospho	578.2777	2	5.5	80	89	No
				QLSSGVSEIR	R	H	95.00%	67		538.2945	2	5.9	80	89	No
				RVPFSLLR	R	G	95.00%	25		494.3115	2	4.9	5	12	No
				TKDGVVEITGK	K	H	95.00%	56		573.8265	2	6.8	113	123	No
				TKDGVVEITGKHEER	K	Q	95.00%	75		566.6353	3	4.7	113	127	No
				TKDGVVEITGKHEER	K	Q	95.00%	33		425.2281	4	3.7	113	127	No
				VPFSLLR	R	G	95.00%	48		416.2607	2	5.2	6	12	No
				VSLDVNHFAPDELTVK	R	T	95.00%	77		892.4739	2	9.4	97	112	No
				VSLDVNHFAPDELTVK	R	T	95.00%	44		595.3168	3	6.6	97	112	No

193	IPI00025753	DSG1	DESMOGLEIN-1 PRECURSOR.	ALNSMGQDLERPLELR	R	V	95.00%	29	M5: Oxidation	619.9927	3	7.1	129	144	No
				IIRQEPSDSPMFIINR	K	N	95.00%	37	M11: Oxidation	644.6776	3	8.2	198	213	No
				ISGVGIDQPPYGIFVINQK	R	T	95.00%	76		1023.0660	2	7.8	87	105	No
				QEPSDSPMFIINR	R	N	95.00%	39	M8: Oxidation	775.3764	2	8.3	201	213	No
				TMNNFLDREQYGQYALAVR	R	G	95.00%	51	M2: Oxidation	769.0458	3	7.9	220	238	No
				VGDFVATDLDTGRPSTTVR	K	Y	95.00%	38		669.6817	3	7.2	404	422	No
				YQGTILSIDDNLQR	K	T	95.00%	46		818.4271	2	7.4	460	473	No
				YVMGNNPADLLAVDSR	R	T	95.00%	73	M3: Oxidation	875.9324	2	7.8	423	438	No
194	IPI00025796	NDUFS3	NADH DEHYDROGENASE [UBIQUINONE] IRON-SULFUR PROTEIN 3, MITOCHONDRIALPRECURSOR.	DFPLSGYVELR	K	Y	95.00%	76		648.3408	2	7.7	201	211	No
				FEIVYNLLSLR	R	F	95.00%	52		683.8954	2	7.0	126	136	No
				ILTDYGFEGHPFR	R	K	95.00%	59		776.3881	2	5.6	187	199	No
				ILTDYGFEGHPFR	R	K	95.00%	30		517.9300	3	9.4	187	199	No
				KFDLNSPWEAFPVYR	R	Q	95.00%	35		623.6554	3	9.1	232	246	No
				QLSAFGEYVAEILPK	K	Y	95.00%	83		832.9564	2	8.9	57	71	No
				QNRFEIVYNLLSLR	R	F	95.00%	51		589.0018	3	7.7	123	136	No
				SLVDLTAVDVPTR	K	Q	95.00%	33		693.3901	2	5.9	110	122	No
				TYTDELTPIESAVSVFK	K	A	95.00%	71		950.4918	2	8.8	145	161	No
				VVAEPVELAQEFR	R	K	95.00%	88		743.9053	2	8.2	219	231	No
				VVAEPVELAQEFR	R	K	95.00%	34		496.2733	3	9.2	219	231	No
				VVAEPVELAQEFRK	R	F	95.00%	49		807.9543	2	9.4	219	232	No
195	IPI00025819	CAPN3	ISOFORM I OF CALPAIN-3.	AFHAFDKDGDGIIK	R	L	95.00%	44		511.9306	3	3.7	795	808	No
				DFFLYNASK	K	A	95.00%	41		552.7750	2	5.0	523	531	No
				FPIQFVWK	K	R	95.00%	42		532.8034	2	5.2	93	100	No
				GHAYSVTGLDEVPFKGEK	R	V	95.00%	102		967.4951	2	8.5	333	350	No
				GHAYSVTGLDEVPFKGEK	R	V	95.00%	59		645.3298	3	4.0	333	350	No
				HYDTDQSGTINSYEMR	K	N	95.00%	101	M15: Oxidation	966.9150	2	9.7	733	748	No
				HYDTDQSGTINSYEMR	K	N	95.00%	38	M15: Oxidation	644.9429	3	5.0	733	748	No
				LNLQEFHHLWNK	K	I	95.00%	40		526.9467	3	4.1	712	723	No
				NAVNDAGFHLNNQLYDIITMR	R	Y	95.00%	78	M20: Oxidation	812.4028	3	6.1	749	769	No
				NEFWSALLEK	R	A	95.00%	43		618.8230	2	9.4	198	207	No
				NFPDTFWTNPQYR	R	L	95.00%	36		843.3969	2	8.7	449	461	No
				NLSEEVENTISVDRPVK	R	K	95.00%	100		965.0080	2	7.9	579	595	No
				SMIALMDTDGSGK	R	L	95.00%	48	M2: Oxidation, M6: Oxidation	679.3083	2	7.9	699	711	No
				TKPIIFVSDR	K	A	95.00%	30		588.3466	2	5.4	599	608	No
196	IPI00025874	RPN1	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 67 KDASUBUNIT PRECURSOR.	ALTSEIALLQSR	K	L	95.00%	63		651.3801	2	7.1	564	575	No
				ATSFLLALEPELEAR	R	L	95.00%	63		830.4550	2	3.7	105	119	No
				FVDHVFDEQVIDSLTVK	R	I	95.00%	104		996.0162	2	5.9	394	410	No
				LPVALDPGAK	K	I	95.00%	30		490.7959	2	5.9	156	165	No
				NIEIDSPYEISR	K	A	95.00%	74		718.3624	2	6.9	419	430	No
				NLVEQHIQDIVVHYTFNK	K	V	95.00%	50		733.0564	3	6.0	454	471	No
				SEDLLDYGPFR	R	D	95.00%	49		656.3179	2	4.5	233	243	No
				TILPAAAQDVYYR	K	D	95.00%	32		740.8981	2	5.6	321	333	No
				VTAEVVLAHLGGGSTSR	K	A	95.00%	49		827.4531	2	3.6	88	104	No
				VTAEVVLAHLGGGSTSR	K	A	95.00%	67		551.9714	3	3.6	88	104	No
197	IPI00025879	MYH1	MYOSIN-1.	AAYLQNLNSADLLK	K	A	95.00%	90		767.4200	2	2.9	387	400	No
				AAYLQNLNSADLLK	K	A	95.00%	47		511.9507	3	5.7	387	400	No
				ADIAESQVNK	R	L	95.00%	52		1074.5510	1	7.4	1914	1923	Yes
				ADIAESQVNK	R	L	95.00%	81		537.7761	2	1.1	1914	1923	Yes
				ADIAESQVNKLR	R	V	95.00%	34		448.5825	3	2.7	1914	1925	Yes
				AEDEEEINAELTAK	R	K	95.00%	117		781.3685	2	3.7	930	943	Yes
				AEDEEEINAELTAK	R	K	95.00%	73		521.2471	3	1.3	930	943	Yes
				AGLLGLLEEMR	K	D	95.00%	88	M10: Oxidation	609.3355	2	5.4	771	781	Yes
				AGLLGLLEEMR	K	D	95.00%	58	M10: Oxidation	406.5597	3	5.7	771	781	Yes
				AGLLGLLEEMR	K	D	95.00%	62		1201.6510	1	-9.1	771	781	Yes
				AGLLGLLEEMR	K	D	95.00%	94		601.3371	2	3.9	771	781	Yes
				AGLLGLLEEMRDEK	K	L	95.00%	75	M10: Oxidation	795.4216	2	9.0	771	784	Yes
				AGLLGLLEEMRDEK	K	L	95.00%	48	M10: Oxidation	530.6150	3	5.1	771	784	Yes
				AGLLGLLEEMRDEK	K	L	95.00%	90		787.4214	2	5.6	771	784	Yes
				AGLLGLLEEMRDEK	K	L	95.00%	48		525.2841	3	6.6	771	784	Yes
				AITDAAMMAEELK	K	K	95.00%	86	M7: Oxidation, M8: Oxidation	713.3404	2	8.6	1762	1774	Yes
				AITDAAMMAEELK	K	K	95.00%	45	M7: Oxidation, M8: Oxidation	475.8937	3	3.3	1762	1774	Yes
				AITDAAMMAEELKK	K	E	95.00%	102	M7: Oxidation	769.3866	2	3.0	1762	1775	Yes
				AITDAAMMAEELKK	K	E	95.00%	44	M7: Oxidation	513.2606	3	3.4	1762	1775	Yes

AITDAAMMAEELKK	K	E	95.00%	83	M7: Oxidation	777.3852	2	4.5	1762	1775	Yes
AITDAAMMAEELKK	K	E	95.00%	52	M7: Oxidation	518.5913	3	1.7	1762	1775	Yes
AITDAAMMAEELKK	K	E	95.00%	83	M7: Oxidation, M8: Oxidation	777.3852	2	4.5	1762	1775	Yes
AITDAAMMAEELKK	K	E	95.00%	52	M7: Oxidation, M8: Oxidation	518.5913	3	1.7	1762	1775	Yes
AITDAAMMAEELKK	K	E	95.00%	97	M8: Oxidation	769.3875	2	4.2	1762	1775	Yes
AITDAAMMAEELKK	K	E	95.00%	52	M8: Oxidation	513.2598	3	1.9	1762	1775	Yes
AITDAAMMAEELKK	K	E	95.00%	111		761.3883	2	1.9	1762	1775	Yes
AITDAAMMAEELKK	K	E	95.00%	77		507.9281	3	1.8	1762	1775	Yes
AITDAAMMAEELKKEQDTSAHLER	K	M	95.00%	37	M7: Oxidation, M8: Oxidation	907.4404	3	6.9	1762	1785	Yes
ALEDQLSEIK	R	T	95.00%	51		1145.6110	1	4.7	1255	1264	No
ALEDQLSEIK	R	T	95.00%	85		573.3087	2	3.5	1255	1264	No
ALEDQLSEIKTKEEEQQR	R	L	95.00%	50		725.3740	3	5.5	1255	1272	No
ALQEAHQQTLDDLQAEEDK	K	V	95.00%	52		728.0195	3	7.4	1002	1020	Yes
ALQEAHQQTLDDLQAEEDKVNTLTK	K	A	95.00%	100		946.8147	3	5.8	1002	1026	Yes
ALQEAHQQTLDDLQAEEDKVNTLTK	K	A	95.00%	63		710.3631	4	5.9	1002	1026	Yes
ANLLQAEIEELR	R	A	95.00%	105		699.8846	2	1.4	1682	1693	Yes
ANLLQAEIEELR	R	A	95.00%	108		466.9276	3	5.6	1682	1693	Yes
ANLLQAEIEELRATLEQTER	R	S	95.00%	46		1164.1250	2	9.2	1682	1701	Yes
ANLLQAEIEELRATLEQTER	R	S	95.00%	73		776.4185	3	8.2	1682	1701	Yes
ANSEVAQWR	K	T	95.00%	51		1060.5270	1	9.1	1368	1376	Yes
ANSEVAQWR	K	T	95.00%	66		530.7642	2	2.9	1368	1376	Yes
ATLEQTER	R	S	95.00%	72		474.2453	2	3.0	1694	1701	Yes
DDQVFPMNPPK	K	Y	95.00%	90	M7: Oxidation	652.3057	2	3.1	74	84	Yes
DDQVFPMNPPK	K	Y	95.00%	84		644.3124	2	9.6	74	84	Yes
DDQVFPMNPPKYDK	K	I	95.00%	47	M7: Oxidation	855.4003	2	4.7	74	87	Yes
DIDDLELTLAK	K	V	95.00%	54		1245.6670	1	7.2	957	967	Yes
DIDDLELTLAK	K	V	95.00%	99		623.3293	2	-5.9	957	967	Yes
DLEEATLQHEATAATLR	R	K	95.00%	159		934.9748	2	3.3	1181	1197	Yes
DLEEATLQHEATAATLR	R	K	95.00%	65		623.6530	3	4.2	1181	1197	Yes
DLEEATLQHEATAATLRK	R	K	95.00%	120		999.0282	2	9.0	1181	1198	Yes
DLEEATLQHEATAATLRK	R	K	95.00%	83		666.3520	3	4.8	1181	1198	Yes
DLQHRLDEAEQLALK	K	G	95.00%	52		889.9805	2	7.1	1796	1810	Yes
DLQHRLDEAEQLALK	K	G	95.00%	58		593.6564	3	7.3	1796	1810	Yes
DPLNETVVGLYQK	K	S	95.00%	91		738.3958	2	6.1	602	614	Yes
DTLVSQLSR	K	G	95.00%	46		1018.5600	1	6.5	1299	1307	No
DTLVSQLSR	K	G	95.00%	59		509.7830	2	4.8	1299	1307	No
DTQLHLDDALR	K	S	95.00%	86		648.8323	2	1.4	1656	1666	No
DTQLHLDDALR	K	S	95.00%	38		432.8916	3	3.3	1656	1666	No
EAEFQK	R	M	95.00%	32		751.3677	1	6.7	1172	1177	Yes
EEQAEPDGTEVADK	R	A	95.00%	98		759.3368	2	3.3	373	386	Yes
EEQAEPDGTEVADKAAYLQNLNSADLLK	R	A	95.00%	36		1011.5030	3	7.6	373	400	No
EFEMSGLQSK	K	I	95.00%	54	M4: Oxidation	586.2726	2	5.8	1088	1097	No
EFEMSGLQSK	K	I	95.00%	54		1155.5410	1	5.0	1088	1097	No
EFEMSGLQSK	K	I	95.00%	44		578.2737	2	3.4	1088	1097	No
EKSEMKMEIDDLASNMETVSK	K	A	95.00%	54	M5: Oxidation, M7: Oxidation, M16: Oxidation	821.7071	3	4.8	1224	1244	No
ELEEISER	R	L	95.00%	49		1004.4910	1	0.9	1146	1153	Yes
ELEEISER	R	L	95.00%	42		502.7503	2	2.7	1146	1153	Yes
ELEEISERLEEAGGATSAQIEMNK	R	K	95.00%	100	M22: Oxidation	1325.6430	2	9.9	1146	1169	Yes
ELEEISERLEEAGGATSAQIEMNK	R	K	95.00%	95	M22: Oxidation	884.0965	3	8.4	1146	1169	Yes
ELEEISERLEEAGGATSAQIEMNK	R	K	95.00%	76	M22: Oxidation	663.3228	4	6.1	1146	1169	Yes
ELEEISERLEEAGGATSAQIEMNK	R	K	95.00%	120		1317.6430	2	7.9	1146	1169	Yes
ELEEISERLEEAGGATSAQIEMNK	R	K	95.00%	84		878.7634	3	6.7	1146	1169	Yes
ELEEISERLEEAGGATSAQIEMNK	R	K	95.00%	51		659.3240	4	5.9	1146	1169	Yes
ELEEISERLEEAGGATSAQIEMNKK	R	R	95.00%	70	M22: Oxidation	926.7932	3	6.2	1146	1170	Yes

ELEEISERLEEAGGATSAQIEMNKK	R	R	95.00%	37	M22: Oxidation	695.3460	4	5.0	1146	1170	Yes
ELEEISERLEEAGGATSAQIEMNKK	R	R	95.00%	47		921.4638	3	8.7	1146	1170	Yes
ELEGEVESEQK	R	R	95.00%	49		638.8011	2	2.7	1825	1835	Yes
ELEGEVESEQKR	R	N	95.00%	74		716.8548	2	6.8	1825	1836	Yes
ELEGEVESEQKR	R	N	95.00%	38		478.2381	3	4.6	1825	1836	Yes
ELTYQTEEDR	K	K	95.00%	51		642.2961	2	6.8	1853	1862	Yes
ELTYQTEEDRK	K	N	95.00%	70		706.3410	2	2.5	1853	1863	Yes
ELTYQTEEDRK	K	N	95.00%	42		471.2320	3	6.8	1853	1863	Yes
ELTYQTEEDRKNILR	K	L	95.00%	46		954.5008	2	5.8	1853	1867	Yes
ELTYQTEEDRKNILR	K	L	95.00%	39		636.6688	3	4.2	1853	1867	Yes
EMANMKEEFEK	K	T	95.00%	40	M2: Oxidation, M5: Oxidation	709.3088	2	8.4	852	862	No
ENKNLQQEISDLTEQIAEGGK	R	R	95.00%	56		782.0655	3	7.4	1505	1525	Yes
ENKNLQQEISDLTEQIAEGGKR	R	I	95.00%	59		834.1010	3	9.1	1505	1526	Yes
ENKNLQQEISDLTEQIAEGGKR	R	I	95.00%	50		625.8258	4	6.1	1505	1526	Yes
ENQSILITGESGAGK	R	T	95.00%	118		752.3882	2	1.9	171	185	Yes
ENQSILITGESGAGK	R	T	95.00%	46		501.9288	3	3.5	171	185	Yes
EQDTSAHLER	K	M	95.00%	69		593.2841	2	8.6	1776	1785	Yes
EQLAMVER	K	R	95.00%	54	M5: Oxidation	496.2496	2	3.0	1673	1680	Yes
EQLAMVER	K	R	95.00%	41		488.2543	2	7.4	1673	1680	Yes
EQYEEEQEAK	R	A	95.00%	45		641.7803	2	6.9	1349	1358	No
EQYEEEQEAKAELQR	R	A	95.00%	90		940.4437	2	6.4	1349	1363	No
EQYEEEQEAKAELQR	R	A	95.00%	34		627.2961	3	2.7	1349	1363	No
ERIEAQNKPFDAK	R	T	95.00%	48		773.4089	2	4.7	23	35	No
EVTERAEDEEEINAELTAK	K	K	95.00%	123		1088.5220	2	4.6	925	943	Yes
EVTERAEDEEEINAELTAK	K	K	95.00%	64		726.0180	3	5.7	925	943	Yes
GFLAR	R	V	95.00%	24		563.3323	1	3.0	798	802	Yes
GKPEAHFSLIHYAGTVDYNIAGWLDK	K	N	95.00%	92		968.1643	3	8.4	574	599	No
GKPEAHFSLIHYAGTVDYNIAGWLDK	K	N	95.00%	35		726.3738	4	6.5	574	599	No
GKQAFTQQIEELKR	R	Q	95.00%	103		838.4631	2	2.9	1308	1321	Yes
GKQAFTQQIEELKR	R	Q	95.00%	75		559.3111	3	2.5	1308	1321	Yes
GKQAFTQQIEELKR	R	Q	95.00%	35		419.7347	4	1.2	1308	1321	Yes
GQTVQQVYNAVGALAK	K	A	95.00%	138		823.9529	2	7.0	417	432	Yes
GQTVQQVYNAVGALAK	K	A	95.00%	75		549.6390	3	9.0	417	432	Yes
GSSFQTVSALFR	K	E	95.00%	46		1299.6800	1	7.8	645	656	Yes
GSSFQTVSALFR	K	E	95.00%	99		650.3406	2	2.9	645	656	Yes
GSSFQTVSALFR	K	E	95.00%	47		433.8970	3	4.3	645	656	Yes
HADSVAELGEQIDNLQR	K	V	95.00%	166		947.9739	2	7.4	1200	1216	Yes
HADSVAELGEQIDNLQR	K	V	95.00%	85		632.3179	3	6.4	1200	1216	Yes
IAEKDEEIDQMK	K	R	95.00%	55	M11: Oxidation	732.8539	2	7.2	1580	1591	No
IAEKDEEIDQMK	K	R	95.00%	38	M11: Oxidation	488.9042	3	5.0	1580	1591	No
IAEKDEEIDQMK	K	R	95.00%	74		724.8565	2	7.2	1580	1591	No
IAEKDEEIDQMKR	K	N	95.00%	58	M11: Oxidation	810.9055	2	7.7	1580	1592	No
IAEKDEEIDQMKR	K	N	95.00%	47	M11: Oxidation	540.9383	3	5.3	1580	1592	No
IAEKDEEIDQMKR	K	N	95.00%	73		802.9050	2	4.0	1580	1592	No
IAEKDEEIDQMKR	K	N	95.00%	68		535.6075	3	6.9	1580	1592	No
IAEQELLDASER	K	V	95.00%	87		687.3516	2	2.9	1705	1716	Yes
IAEQELLDASER	K	V	95.00%	37		458.5717	3	6.0	1705	1716	Yes
IEAQNKPFDAK	R	T	95.00%	40		630.8381	2	7.4	25	35	Yes
IEDEQALGMQLQK	K	K	95.00%	108	M9: Oxidation	759.8807	2	3.9	1098	1110	No
IEDEQALGMQLQK	K	K	95.00%	56	M9: Oxidation	506.9252	3	8.1	1098	1110	No
IEDEQALGMQLQK	K	K	95.00%	88		751.8838	2	4.7	1098	1110	No
IEDEQALGMQLQKK	K	I	95.00%	40	M9: Oxidation	549.6210	3	2.8	1098	1111	No
IEDMAMMTHLHEPAVLYNLK	K	E	95.00%	43	M4: Oxidation, M6: Oxidation, M7: Oxidation	802.0569	3	8.3	88	107	Yes
IEDMAMMTHLHEPAVLYNLK	K	E	95.00%	35	M4: Oxidation, M6: Oxidation, M7: Oxidation	601.7939	4	7.0	88	107	Yes
IEDMAMMTHLHEPAVLYNLK	K	E	95.00%	58	M6: Oxidation	791.3938	3	8.5	88	107	Yes
IEDMAMMTHLHEPAVLYNLK	K	E	95.00%	39	M6: Oxidation	796.7230	3	5.4	88	107	Yes
IEDMAMMTHLHEPAVLYNLK	K	E	95.00%	39	M6: Oxidation, M7: Oxidation	796.7230	3	5.4	88	107	Yes
IEDMAMMTHLHEPAVLYNLK	K	E	95.00%	46	M7: Oxidation	791.3921	3	6.4	88	107	Yes
IEDMAMMTHLHEPAVLYNLK	K	E	95.00%	58		786.0606	3	6.6	88	107	Yes
IEELEEEIEAER	R	A	95.00%	103		744.8617	2	5.7	1119	1130	Yes

IEELEEEIEAER	R	A	95.00%	67		496.9096	3	4.0	1119	1130	Yes
IHFGTTGK	R	L	95.00%	46		860.4694	1	7.2	253	260	Yes
IHFGTTGK	R	L	95.00%	29		430.7379	2	5.7	253	260	Yes
IKELQAR	K	I	95.00%	31		429.2654	2	2.3	1112	1118	Yes
IKEVTER	K	A	95.00%	35		437.7546	2	1.7	923	929	Yes
IKEVTERAEDEEEINAELTAK	K	K	95.00%	115		1209.1170	2	9.3	923	943	Yes
IKEVTERAEDEEEINAELTAK	K	K	95.00%	82		806.4095	3	3.4	923	943	Yes
IKEVTERAEDEEEINAELTAK	K	K	95.00%	50		605.0596	4	4.3	923	943	Yes
IKLEQQVDDLEGSLEQEK	K	K	95.00%	166		1051.0440	2	6.2	1029	1046	Yes
IKLEQQVDDLEGSLEQEK	K	K	95.00%	72		701.0316	3	5.8	1029	1046	Yes
IKLEQQVDDLEGSLEQEKK	K	I	95.00%	137		1115.0950	2	9.1	1029	1047	No
IKLEQQVDDLEGSLEQEKK	K	I	95.00%	82		743.7285	3	3.6	1029	1047	No
IKLEQQVDDLEGSLEQEKK	K	I	95.00%	45		558.0484	4	3.7	1029	1047	No
IKNAYEESLDQLETLK	K	R	95.00%	115		947.5031	2	9.1	1488	1503	Yes
IKNAYEESLDQLETLK	K	R	95.00%	64		632.0006	3	2.6	1488	1503	Yes
IKNAYEESLDQLETLKR	K	E	95.00%	144		1025.5530	2	7.5	1488	1504	Yes
IKNAYEESLDQLETLKR	K	E	95.00%	88		684.0358	3	4.6	1488	1504	Yes
IKNAYEESLDQLETLKR	K	E	95.00%	74		513.2789	4	4.8	1488	1504	Yes
ILAEWK	K	Q	95.00%	33		759.4422	1	2.1	1456	1461	Yes
ILYADFK	R	Q	95.00%	47		869.4793	1	2.2	717	723	Yes
ILYADFK	R	Q	95.00%	55		435.2437	2	2.5	717	723	Yes
INQQLDTK	R	Q	95.00%	55		480.2638	2	3.6	446	453	Yes
INQQLDTKQPR	R	Q	95.00%	60		670.8722	2	5.7	446	456	Yes
INQQLDTKQPR	R	Q	95.00%	37		447.5833	3	4.1	446	456	Yes
IQHELEEAEER	R	A	95.00%	69		691.8343	2	4.1	1903	1913	No
IQHELEEAEER	R	A	95.00%	59		461.5593	3	5.1	1903	1913	No
IQHELEEAEERADIAESQVNK	R	L	95.00%	114		1219.6040	2	8.0	1903	1923	No
IQHELEEAEERADIAESQVNK	R	L	95.00%	59		813.4023	3	4.6	1903	1923	No
IQHELEEAEERADIAESQVNK	R	L	95.00%	59		610.3048	4	6.5	1903	1923	No
IQLEAK	K	I	95.00%	37		701.4219	1	2.9	917	922	Yes
IQLELNQVK	R	S	95.00%	46		1084.6430	1	5.9	1565	1573	Yes
IQLELNQVK	R	S	95.00%	74		542.8235	2	2.1	1565	1573	Yes
IQLELNQVKSEVDR	R	K	95.00%	62		835.9645	2	8.0	1565	1578	Yes
IQLELNQVKSEVDRK	R	I	95.00%	28		450.5092	4	5.9	1565	1579	Yes
IVESMQSTLDAEIR	R	S	95.00%	129	M5: Oxidation	804.4081	2	8.2	1597	1610	Yes
IVESMQSTLDAEIR	R	S	95.00%	55	M5: Oxidation	536.6071	3	6.6	1597	1610	Yes
IVESMQSTLDAEIR	R	S	95.00%	114		796.4084	2	5.4	1597	1610	Yes
IVESMQSTLDAEIR	R	S	95.00%	65		531.2747	3	5.1	1597	1610	Yes
KAITDAAMMAEELKK	K	E	95.00%	101	M8: Oxidation	833.4363	2	5.3	1761	1775	Yes
KAITDAAMMAEELKK	K	E	95.00%	81	M8: Oxidation	555.9587	3	2.7	1761	1775	Yes
KAITDAAMMAEELKK	K	E	95.00%	35	M8: Oxidation	417.2235	4	8.8	1761	1775	Yes
KAITDAAMMAEELKK	K	E	95.00%	80	M8: Oxidation	841.4315	2	2.7	1761	1775	Yes
KAITDAAMMAEELKK	K	E	95.00%	64	M8: Oxidation	561.2909	3	3.8	1761	1775	Yes
KAITDAAMMAEELKK	K	E	95.00%	80	M8: Oxidation, M9: Oxidation	841.4315	2	2.7	1761	1775	Yes
KAITDAAMMAEELKK	K	E	95.00%	64	M8: Oxidation, M9: Oxidation	561.2909	3	3.8	1761	1775	Yes
KAITDAAMMAEELKK	K	E	95.00%	103	M9: Oxidation	833.4359	2	4.9	1761	1775	Yes
KAITDAAMMAEELKK	K	E	95.00%	63	M9: Oxidation	555.9584	3	2.3	1761	1775	Yes
KAITDAAMMAEELKK	K	E	95.00%	37	M9: Oxidation	417.2219	4	5.0	1761	1775	Yes
KAITDAAMMAEELKK	K	E	95.00%	107		825.4387	2	5.2	1761	1775	Yes
KAITDAAMMAEELKK	K	E	95.00%	92		550.6276	3	3.8	1761	1775	Yes
KAITDAAMMAEELKK	K	E	95.00%	42		413.2216	4	1.3	1761	1775	Yes
KALQEAHQQTLDDLQAEEDKVNTLTK	K	A	95.00%	112		989.5156	3	8.1	1001	1026	Yes
KALQEAHQQTLDDLQAEEDKVNTLTK	K	A	95.00%	62		742.3849	4	3.0	1001	1026	Yes
KALQEAHQQTLDDLQAEEDKVNTLTK	K	A	95.00%	35		594.1111	5	5.8	1001	1026	Yes
KDIDDLELTLAK	K	V	95.00%	109		687.3849	2	6.4	956	967	Yes
KDIDDLELTLAK	K	V	95.00%	46		458.5916	3	4.3	956	967	Yes
KEFEMSGLQSK	K	I	95.00%	45	M5: Oxidation	650.3223	2	8.7	1087	1097	No
KGSSFQTVSALFR	K	E	95.00%	125		714.3884	2	3.1	644	656	Yes
KGSSFQTVSALFR	K	E	95.00%	57		476.5949	3	3.2	644	656	Yes
KHADSVAELGEQIDNLQR	K	V	95.00%	137		1012.0210	2	6.5	1199	1216	Yes
KHADSVAELGEQIDNLQR	K	V	95.00%	93		675.0148	3	3.8	1199	1216	Yes
KHADSVAELGEQIDNLQR	K	V	95.00%	66		506.5136	4	4.9	1199	1216	Yes
KIAEQELLDASER	R	V	95.00%	123		751.3984	2	1.7	1704	1716	Yes
KIAEQELLDASER	R	V	95.00%	64		501.2686	3	2.5	1704	1716	Yes
KKEFEMSGLQSK	K	I	95.00%	60	M6: Oxidation	714.3638	2	-0.6	1086	1097	No

KKEFEMSGLQSK	K	I	95.00%	32	M6: Oxidation	476.5830	3	9.0	1086	1097	No
KKEFEMSGLQSK	K	I	95.00%	53		706.3683	2	2.2	1086	1097	No
KKGSSFQTVSALFR	K	E	95.00%	66		778.4344	2	0.8	643	656	Yes
KKGSSFQTVSALFR	K	E	95.00%	49		519.2949	3	6.0	643	656	Yes
KKHADSVAELGEQIDNLQR	R	V	95.00%	89		717.7142	3	5.1	1198	1216	Yes
KKHADSVAELGEQIDNLQR	R	V	95.00%	53		538.5365	4	3.1	1198	1216	Yes
KKLETDISQIQGEMEDIIQEAR	K	N	95.00%	80	M14: Oxidation	864.1106	3	4.8	1732	1753	No
KKLETDISQIQGEMEDIIQEAR	K	N	95.00%	33	M14: Oxidation	648.3342	4	3.8	1732	1753	No
KKLETDISQIQGEMEDIIQEAR	K	N	95.00%	88		858.7822	3	8.5	1732	1753	No
KKLETDISQIQGEMEDIIQEAR	K	N	95.00%	54		644.3368	4	5.9	1732	1753	No
KKMEGDLNEMEIQLNHANR	K	M	95.00%	39	M10: Oxidation	762.7066	3	3.1	1620	1638	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	39	M10: Oxidation	572.2825	4	4.2	1620	1638	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	70	M3: Oxidation	762.7060	3	2.4	1620	1638	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	77	M3: Oxidation	572.2819	4	3.1	1620	1638	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	58	M3: Oxidation	768.0369	3	1.3	1620	1638	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	54	M3: Oxidation	576.2810	4	3.7	1620	1638	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	58	M3: Oxidation, M10: Oxidation	768.0369	3	1.3	1620	1638	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	54	M3: Oxidation, M10: Oxidation	576.2810	4	3.7	1620	1638	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	53		757.3764	3	4.9	1620	1638	Yes
KKMEGDLNEMEIQLNHANR	K	M	95.00%	79		568.2838	4	4.2	1620	1638	Yes
KLEGDLK	R	L	95.00%	39		401.7396	2	4.6	1058	1064	Yes
KLETDISQIQGEMEDIIQEAR	K	N	95.00%	80	M13: Oxidation	821.4150	3	8.4	1733	1753	No
KLETDISQIQGEMEDIIQEAR	K	N	95.00%	148		1223.6210	2	8.7	1733	1753	No
KLETDISQIQGEMEDIIQEAR	K	N	95.00%	72		816.0828	3	7.8	1733	1753	No
KMEGDLNEMEIQLNHANR	K	M	95.00%	46	M2: Oxidation	1079.5140	2	8.4	1621	1638	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	76	M2: Oxidation	720.0093	3	4.8	1621	1638	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	53	M2: Oxidation	540.2613	4	9.1	1621	1638	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	90	M2: Oxidation	1087.5110	2	8.1	1621	1638	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	57	M2: Oxidation	725.3447	3	9.9	1621	1638	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	50	M2: Oxidation	544.2559	4	1.3	1621	1638	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	90	M2: Oxidation, M9: Oxidation	1087.5110	2	8.1	1621	1638	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	57	M2: Oxidation, M9: Oxidation	725.3447	3	9.9	1621	1638	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	50	M2: Oxidation, M9: Oxidation	544.2559	4	1.3	1621	1638	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	69	M9: Oxidation	1079.5140	2	8.5	1621	1638	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	67	M9: Oxidation	720.0086	3	3.7	1621	1638	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	36	M9: Oxidation	540.2574	4	1.8	1621	1638	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	115		1071.5170	2	8.7	1621	1638	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	89		714.6783	3	5.6	1621	1638	Yes
KMEGDLNEMEIQLNHANR	K	M	95.00%	59		536.2598	4	4.0	1621	1638	Yes
KQVEQEKSELQAALEEAEASLEHEEGK	K	I	95.00%	57		760.6304	4	7.4	1535	1561	No
KRQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	89	M20: Oxidation	960.8171	3	8.9	147	170	Yes
KRQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	97		955.4839	3	7.2	147	170	Yes
LAQLITR	K	T	95.00%	37		814.5181	1	3.6	785	791	Yes
LAQLITR	K	T	95.00%	59		407.7621	2	1.4	785	791	Yes
LASADIETYLLEK	K	S	95.00%	129		733.3926	2	-1.2	261	273	Yes
LASADIETYLLEK	K	S	95.00%	66		489.2671	3	4.5	261	273	Yes
LDEAEQLALK	R	G	95.00%	51		1129.6220	1	9.6	1801	1810	Yes
LDEAEQLALK	R	G	95.00%	97		565.3107	2	2.5	1801	1810	Yes
LDEAEQLALKGGK	R	K	95.00%	66		686.3813	2	4.5	1801	1813	Yes
LDEAEQLALKGGK	R	K	95.00%	42		457.9226	3	2.6	1801	1813	Yes
LDEAEQLALKGGKK	R	Q	95.00%	81		750.4314	2	7.6	1801	1814	Yes
LDEAEQLALKGGKK	R	Q	95.00%	45		500.6212	3	2.9	1801	1814	Yes
LEEAGGATSAQIEMNK	R	K	95.00%	157	M14: Oxidation	832.8970	2	3.6	1154	1169	Yes
LEEAGGATSAQIEMNK	R	K	95.00%	68	M14: Oxidation	555.6020	3	6.1	1154	1169	Yes
LEEAGGATSAQIEMNK	R	K	95.00%	134		824.8989	2	2.7	1154	1169	Yes
LEEAGGATSAQIEMNKK	R	R	95.00%	88	M14: Oxidation	896.9449	2	3.7	1154	1170	Yes
LEEAGGATSAQIEMNKK	R	R	95.00%	37	M14: Oxidation	598.2982	3	2.0	1154	1170	Yes
LEEAGGATSAQIEMNKK	R	R	95.00%	105		888.9479	2	4.3	1154	1170	Yes
LEQQVDDLEGSLEQEK	K	K	95.00%	144		930.4526	2	5.2	1031	1046	Yes
LEQQVDDLEGSLEQEK	K	K	95.00%	113		620.6381	3	5.9	1031	1046	Yes
LEQQVDDLEGSLEQEKK	K	I	95.00%	116		994.5015	2	6.3	1031	1047	No
LEQQVDDLEGSLEQEKK	K	I	95.00%	69		663.3355	3	4.1	1031	1047	No

LETDISQIQGEMEDIIQEAR	K	N	95.00%	109	M12: Oxidation	1167.5700	2	7.7	1734	1753	No
LETDISQIQGEMEDIIQEAR	K	N	95.00%	139		1159.5730	2	8.4	1734	1753	No
LETDISQIQGEMEDIIQEAR	K	N	95.00%	73		773.3831	3	6.4	1734	1753	No
LINDLTAQR	R	A	95.00%	51		1043.5890	1	3.4	1273	1281	Yes
LINDLTAQR	R	A	95.00%	89		522.2970	2	1.1	1273	1281	Yes
LQDAEEHVEAVNAK	R	C	95.00%	124		776.8860	2	2.2	1401	1414	No
LQDAEEHVEAVNAK	R	C	95.00%	47		518.2609	3	4.2	1401	1414	No
LQDLVDK	R	L	95.00%	35		830.4684	1	7.0	1868	1874	Yes
LQDLVDK	R	L	95.00%	42		415.7369	2	4.1	1868	1874	Yes
LQDLVDKLQAK	R	V	95.00%	88		635.8749	2	3.6	1868	1878	Yes
LQDLVDKLQAK	R	V	95.00%	55		424.2524	3	3.4	1868	1878	Yes
LQNEVEDLMIDVER	R	T	95.00%	122	M9: Oxidation	859.9229	2	6.3	1425	1438	No
LQNEVEDLMIDVER	R	T	95.00%	86	M9: Oxidation	573.6165	3	3.8	1425	1438	No
LQNEVEDLMIDVER	R	T	95.00%	115		851.9251	2	5.9	1425	1438	No
LQNEVEDLMIDVER	R	T	95.00%	75		568.2850	3	4.2	1425	1438	No
LQQFFNHHMFVLEQEEYK	K	K	95.00%	58	M9: Oxidation	795.0480	3	4.4	488	505	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	35	M9: Oxidation	596.5412	4	9.8	488	505	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	43		789.7178	3	6.2	488	505	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	42		592.5402	4	6.1	488	505	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	68	M9: Oxidation	1256.1180	2	5.7	488	506	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	51	M9: Oxidation	837.7500	3	8.6	488	506	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	103		1248.1230	2	8.3	488	506	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	57		832.4158	3	5.6	488	506	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	42		499.8525	5	5.4	488	506	Yes
LQTESGEYSR	R	Q	95.00%	58		585.2775	2	2.8	1284	1293	No
LTGAVMHYGNMK	K	F	95.00%	72	M11: Oxidation	669.3234	2	3.3	355	366	Yes
LTGAVMHYGNMK	K	F	95.00%	75	M6: Oxidation	669.3235	2	3.5	355	366	Yes
LTGAVMHYGNMK	K	F	95.00%	62	M6: Oxidation	677.3207	2	3.1	355	366	Yes
LTGAVMHYGNMK	K	F	95.00%	62	M6: Oxidation, M11: Oxidation	677.3207	2	3.1	355	366	Yes
LTGAVMHYGNMK	K	F	95.00%	61		661.3256	2	2.7	355	366	Yes
LYEQHLGK	K	S	95.00%	47		494.2697	2	5.2	555	562	No
MEGDLNEMEIQLNHANR	K	M	95.00%	108	M1: Oxidation	1015.4620	2	4.8	1622	1638	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	73	M1: Oxidation	677.3097	3	3.1	1622	1638	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	98	M1: Oxidation	1023.4620	2	6.9	1622	1638	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	71	M1: Oxidation	682.6416	3	3.5	1622	1638	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	98	M1: Oxidation, M8: Oxidation	1023.4620	2	6.9	1622	1638	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	71	M1: Oxidation, M8: Oxidation	682.6416	3	3.5	1622	1638	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	90	M8: Oxidation	1015.4650	2	7.0	1622	1638	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	49	M8: Oxidation	677.3115	3	5.7	1622	1638	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	124		1007.4680	2	8.1	1622	1638	Yes
MEGDLNEMEIQLNHANR	K	M	95.00%	77		671.9785	3	3.8	1622	1638	Yes
MEIDDLASNMETVSK	K	A	95.00%	141	M1: Oxidation	849.8865	2	5.0	1230	1244	No
MEIDDLASNMETVSK	K	A	95.00%	133	M1: Oxidation	857.8880	2	9.7	1230	1244	No
MEIDDLASNMETVSK	K	A	95.00%	133	M1: Oxidation, M10: Oxidation	857.8880	2	9.7	1230	1244	No
MEIDDLASNMETVSK	K	A	95.00%	119	M10: Oxidation	849.8866	2	5.1	1230	1244	No
MEIDDLASNMETVSK	K	A	95.00%	136		841.8904	2	6.6	1230	1244	No
MFLWMVTR	K	I	95.00%	43	M1: Oxidation	550.2784	2	5.2	438	445	Yes
MFLWMVTR	K	I	95.00%	55	M1: Oxidation	558.2754	2	4.5	438	445	Yes
MFLWMVTR	K	I	95.00%	55	M1: Oxidation, M5: Oxidation	558.2754	2	4.5	438	445	Yes
MFLWMVTR	K	I	95.00%	50	M5: Oxidation	550.2784	2	5.2	438	445	Yes
MFLWMVTR	K	I	95.00%	47		542.2820	2	7.2	438	445	Yes
MQGTLEDQIISANPLLEAFGNAK	K	T	95.00%	129	M1: Oxidation	1238.6320	2	6.9	215	237	Yes
MQGTLEDQIISANPLLEAFGNAK	K	T	95.00%	107	M1: Oxidation	826.0911	3	7.3	215	237	Yes
MVTLMQEK	K	N	95.00%	47	M1: Oxidation, M5: Oxidation	506.2481	2	2.7	881	888	No
MVTLMQEK	K	N	95.00%	48	M5: Oxidation	498.2505	2	2.5	881	888	No
NAYEESLDQLETLK	K	R	95.00%	111		826.9099	2	6.0	1490	1503	Yes
NAYEESLDQLETLK	K	R	95.00%	61		551.6096	3	6.6	1490	1503	Yes
NAYEESLDQLETLKR	K	E	95.00%	138		904.9635	2	8.8	1490	1504	Yes
NAYEESLDQLETLKR	K	E	95.00%	53		603.6429	3	5.5	1490	1504	Yes
NDLQLQVQAEADSLADAEER	K	C	95.00%	164		1108.0340	2	5.5	889	908	No
NDLQLQVQAEADSLADAEER	K	C	95.00%	101		739.0232	3	2.8	889	908	No
NFDKILAEWK	R	Q	95.00%	40		632.3444	2	5.5	1452	1461	Yes

NFDKILAEWK	R	Q	95.00%	30		421.8982	3	4.0	1452	1461	Yes
NKDPLNETVVGLYQK	K	S	95.00%	121		859.4654	2	6.0	600	614	Yes
NKDPLNETVVGLYQK	K	S	95.00%	75		573.3107	3	2.1	600	614	Yes
NLQQEISDLTEQIAEGGK	K	R	95.00%	163		987.0017	2	6.4	1508	1525	Yes
NLQQEISDLTEQIAEGGK	K	R	95.00%	98		658.3360	3	4.8	1508	1525	Yes
NLQQEISDLTEQIAEGGKR	K	I	95.00%	145		1065.0560	2	9.5	1508	1526	Yes
NLQQEISDLTEQIAEGGKR	K	I	95.00%	53		710.3688	3	3.2	1508	1526	Yes
NLQQEISDLTEQIAEGGKR	K	I	95.00%	75		533.0291	4	4.1	1508	1526	Yes
NLTEEMAGLDETIAK	K	L	95.00%	124	M6: Oxidation	825.9053	2	7.8	981	995	Yes
NLTEEMAGLDETIAK	K	L	95.00%	71	M6: Oxidation	550.9387	3	6.4	981	995	Yes
NLTEEMAGLDETIAK	K	L	95.00%	131		817.9079	2	7.9	981	995	Yes
NLTEEMAGLDETIAK	K	L	95.00%	77		545.6058	3	4.2	981	995	Yes
NTQAILKDTQLHLDDALR	R	S	95.00%	51		689.0440	3	5.7	1649	1666	No
QAEEAEEQSNVNLSK	R	F	95.00%	117		838.3944	2	2.2	1885	1899	No
QAEEAEEQSNVNLSK	R	F	95.00%	64		559.2686	3	7.6	1885	1899	No
QAFTQQIEELK	K	R	95.00%	37		667.8544	2	3.8	1310	1320	Yes
QAFTQQIEELKR	K	Q	95.00%	90		745.9052	2	3.8	1310	1321	Yes
QAFTQQIEELKR	K	Q	95.00%	61		497.6067	3	5.1	1310	1321	Yes
QEAPPHIFSISDNAYQFMLTDR	R	E	95.00%	103	M18: Oxidation	866.0826	3	7.0	149	170	Yes
QEAPPHIFSISDNAYQFMLTDR	R	E	95.00%	81		860.7453	3	0.4	149	170	Yes
QKQREEQAEPDGTEVADK	K	A	95.00%	33		686.6686	3	7.7	369	386	Yes
QLDEKDTLVSQLSR	R	G	95.00%	107		816.4401	2	7.3	1294	1307	No
QLDEKDTLVSQLSR	R	G	95.00%	66		544.6294	3	7.3	1294	1307	No
QLEEEIK	R	A	95.00%	50		444.7393	2	3.2	1322	1328	Yes
QREEQAEPDGTEVADK	K	A	95.00%	104		901.4207	2	7.2	371	386	Yes
QREEQAEPDGTEVADK	K	A	95.00%	62		601.2809	3	3.6	371	386	Yes
QRLQNEVEDLMIDVER	K	T	95.00%	44	M11: Oxidation	668.3357	3	2.3	1423	1438	No
QRLQNEVEDLMIDVER	K	T	95.00%	64		663.0079	3	8.0	1423	1438	No
QVEQEKSELQAALEEAEASLEHEEGK	K	I	95.00%	94		971.1387	3	6.7	1536	1561	No
QVEQEKSELQAALEEAEASLEHEEGK	K	I	95.00%	60		728.6054	4	6.0	1536	1561	No
RANLLQAEIEELR	R	A	95.00%	86		777.9383	2	5.3	1681	1693	Yes
RANLLQAEIEELR	R	A	95.00%	90		518.9605	3	3.5	1681	1693	Yes
RANLLQAEIEELRATLEQTER	R	S	95.00%	41		828.4529	3	8.5	1681	1701	Yes
RANLLQAEIEELRATLEQTER	R	S	95.00%	79		621.5908	4	7.2	1681	1701	Yes
RDLEEATLQHEATAATLR	R	K	95.00%	113		1013.0270	2	4.5	1180	1197	Yes
RDLEEATLQHEATAATLR	R	K	95.00%	81		675.6859	3	2.7	1180	1197	Yes
RDLEEATLQHEATAATLR	R	K	95.00%	61		507.0161	4	2.1	1180	1197	Yes
RDLEEATLQHEATAATLRK	R	K	95.00%	41		539.0399	4	2.2	1180	1198	Yes
RIQHELEEAEER	R	A	95.00%	76		769.8843	2	2.9	1902	1913	No
RIQHELEEAEER	R	A	95.00%	60		513.5924	3	3.2	1902	1913	No
RIQHELEEAEERADIAESQVNK	R	L	95.00%	87		865.4377	3	6.2	1902	1923	No
RIQHELEEAEERADIAESQVNK	R	L	95.00%	82		649.3293	4	4.8	1902	1923	No
RQAEEAEEQSNVNLSK	K	F	95.00%	43		611.3019	3	6.5	1884	1899	No
RQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	106	M19: Oxidation	918.1165	3	6.7	148	170	Yes
RQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	34	M19: Oxidation	688.8396	4	7.2	148	170	Yes
RQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	114		912.7863	3	8.4	148	170	Yes
RQEAPPHIFSISDNAYQFMLTDRENQSILITGESGAGK	K	T	95.00%	70	M19: Oxidation	1060.0320	4	9.5	148	185	Yes
RVIQYFATIAVTGEK	K	K	95.00%	106		848.4809	2	6.2	191	205	Yes
RVIQYFATIAVTGEK	K	K	95.00%	71		565.9888	3	4.3	191	205	Yes
SAETEKEMANMKEEFEK	K	T	95.00%	40	M8: Oxidation	682.9747	3	4.1	846	862	No
SAETEKEMANMKEEFEK	K	T	95.00%	57	M8: Oxidation	1031.9570	2	5.8	846	862	No
SAETEKEMANMKEEFEK	K	T	95.00%	59	M8: Oxidation, M11: Oxidation	1031.9570	2	5.6	846	862	No
SAETEKEMANMKEEFEK	K	T	95.00%	40	M8: Oxidation, M11: Oxidation	688.3063	3	4.1	846	862	No
SAETEKEMANMKEEFEK	K	T	95.00%	57		1015.9640	2	7.6	846	862	No
SAETEKEMANMKEEFEK	K	T	95.00%	34		677.6425	3	3.2	846	862	No
SALAHALQSSR	K	H	95.00%	84		570.8121	2	3.4	1331	1341	No
SELQAALEEAEASLEHEEGK	K	I	95.00%	136		1085.5170	2	4.6	1542	1561	No
SELQAALEEAEASLEHEEGK	K	I	95.00%	68		724.0146	3	6.1	1542	1561	No
SEMKMEIDDLASNMETVSK	K	A	95.00%	47	M3: Oxidation, M5: Oxidation	730.6620	3	4.0	1226	1244	No

SEMKMEIDDLASNMETVSK	K	A	95.00%	46	M3: Oxidation, M5: Oxidation, M14: Oxidation	735.9954	3	6.3	1226	1244	No
SLSTELFK	R	I	95.00%	34		924.5075	1	3.4	1480	1487	No
SLSTELFK	R	I	95.00%	68		462.7583	2	4.8	1480	1487	No
SQEDLKEQLAMVER	R	R	95.00%	98	M11: Oxidation	846.4202	2	3.0	1667	1680	Yes
SQEDLKEQLAMVER	R	R	95.00%	65	M11: Oxidation	564.6167	3	4.1	1667	1680	Yes
SQEDLKEQLAMVER	R	R	95.00%	117		838.4244	2	5.0	1667	1680	Yes
SQEDLKEQLAMVER	R	R	95.00%	65		559.2847	3	3.5	1667	1680	Yes
STHPHFVR	R	C	95.00%	32		490.7590	2	3.7	668	675	Yes
SYHIFYQIMSNK	R	K	95.00%	85	M9: Oxidation	773.8758	2	4.9	285	296	No
SYHIFYQIMSNK	R	K	95.00%	35	M9: Oxidation	516.2546	3	7.7	285	296	No
SYHIFYQIMSNK	R	K	95.00%	83		765.8785	2	5.1	285	296	No
TEAGATVTVK	K	D	95.00%	50		488.7727	2	6.1	64	73	No
TEAGATVTVKDDQVFPMNPPK	K	Y	95.00%	76	M17: Oxidation	1131.0660	2	4.9	64	84	No
TEAGATVTVKDDQVFPMNPPK	K	Y	95.00%	84	M17: Oxidation	754.3827	3	8.9	64	84	No
TEAGATVTVKDDQVFPMNPPK	K	Y	95.00%	39		749.0489	3	6.0	64	84	No
TEAGATVTVKDDQVFPMNPPKYDK	K	I	95.00%	71	M17: Oxidation	889.7745	3	3.8	64	87	No
TEAGATVTVKDDQVFPMNPPKYDK	K	I	95.00%	55		884.4412	3	1.8	64	87	No
TEELEEAK	R	K	95.00%	33		948.4558	1	3.3	1387	1394	Yes
TEELEEAK	R	K	95.00%	39		474.7330	2	5.9	1387	1394	Yes
TEELEEAKK	R	K	95.00%	40		538.7797	2	3.5	1387	1395	Yes
TKYETDAIQR	R	T	95.00%	69		612.8171	2	3.2	1377	1386	Yes
TKYETDAIQR	R	T	95.00%	55		408.8806	3	3.1	1377	1386	Yes
TKYETDAIQRTEELEEAK	R	K	95.00%	74		1077.5420	2	8.6	1377	1394	Yes
TKYETDAIQRTEELEEAK	R	K	95.00%	38		718.6949	3	5.7	1377	1394	Yes
TKYETDAIQRTEELEEAK	R	K	95.00%	31		539.2729	4	5.3	1377	1394	Yes
TLALLFVGATGAEAEAGGGK	K	K	95.00%	171		916.9958	2	4.2	619	638	No
TLALLFVGATGAEAEAGGGK	K	K	95.00%	102		611.6674	3	5.7	619	638	No
TLALLFVGATGAEAEAGGGKK	K	G	95.00%	122		981.0455	2	6.2	619	639	No
TLALLFVGATGAEAEAGGGKK	K	G	95.00%	51		654.3675	3	8.1	619	639	No
TNAACAALDKK	R	Q	95.00%	39		553.2895	2	3.1	1439	1449	Yes
TPGAMEHELVLHQLR	K	C	95.00%	68	M5: Oxidation	873.9575	2	6.3	684	698	Yes
TPGAMEHELVLHQLR	K	C	95.00%	75	M5: Oxidation	582.9732	3	4.5	684	698	Yes
TPGAMEHELVLHQLR	K	C	95.00%	35	M5: Oxidation	437.4808	4	2.1	684	698	Yes
TPGAMEHELVLHQLR	K	C	95.00%	109		865.9571	2	2.9	684	698	Yes
TPGAMEHELVLHQLR	K	C	95.00%	77		577.6414	3	4.2	684	698	Yes
TPGAMEHELVLHQLR	K	C	95.00%	45		433.4824	4	2.8	684	698	Yes
TSVFVVDPK	K	E	95.00%	29		991.5532	1	6.8	36	44	No
TSVFVVDPK	K	E	95.00%	72		496.2798	2	5.5	36	44	No
TVNTKRVIQYFATIAVTGEK	K	K	95.00%	35		747.0939	3	9.4	186	205	Yes
VGNEYVTK	K	G	95.00%	69		455.2391	2	2.3	409	416	Yes
VIQYFATIAVTGEK	R	K	95.00%	132		770.4273	2	2.9	192	205	Yes
VIQYFATIAVTGEK	R	K	95.00%	82		513.9557	3	6.0	192	205	Yes
VKELTYQTEEDR	K	K	95.00%	71		755.8765	2	4.1	1851	1862	No
VKELTYQTEEDRK	K	N	95.00%	86		819.9239	2	3.7	1851	1863	No
VKELTYQTEEDRK	K	N	95.00%	58		546.9517	3	3.3	1851	1863	No
VKELTYQTEEDRK	K	N	95.00%	40		410.4650	4	1.6	1851	1863	No
VKNLTEEMAGLDETIAK	K	L	95.00%	107	M8: Oxidation	939.4888	2	8.8	979	995	Yes
VKNLTEEMAGLDETIAK	K	L	95.00%	57	M8: Oxidation	626.6605	3	6.7	979	995	Yes
VKNLTEEMAGLDETIAK	K	L	95.00%	140		931.4891	2	6.4	979	995	Yes
VKNLTEEMAGLDETIAK	K	L	95.00%	63		621.3273	3	4.2	979	995	Yes
VKVGNEYVTK	R	G	95.00%	59		568.8224	2	4.7	407	416	Yes
VLNASAIPEGQFIDSK	K	K	95.00%	115		844.9546	2	9.1	728	743	Yes
VLNASAIPEGQFIDSK	K	K	95.00%	76		563.6365	3	4.6	728	743	Yes
VLNASAIPEGQFIDSKK	K	A	95.00%	88		909.0018	2	8.1	728	744	Yes
VLNASAIPEGQFIDSKK	K	A	95.00%	54		606.3343	3	3.4	728	744	Yes
VQLLHTQNTSLINTK	R	K	95.00%	116		855.4858	2	5.1	1717	1731	Yes
VQLLHTQNTSLINTK	R	K	95.00%	74		570.6585	3	2.8	1717	1731	Yes
VQLLHTQNTSLINTKK	R	K	95.00%	102		919.5307	2	1.9	1717	1732	Yes
VQLLHTQNTSLINTKK	R	K	95.00%	62		613.3572	3	3.3	1717	1732	Yes
VQLLHTQNTSLINTKK	R	K	95.00%	34		460.2692	4	1.7	1717	1732	Yes
VRELEGEVESEQK	R	R	95.00%	79		766.3853	2	1.5	1823	1835	Yes
VRELEGEVESEQK	R	R	95.00%	42		511.2623	3	7.0	1823	1835	Yes
VRELEGEVESEQKR	R	N	95.00%	95		844.4380	2	3.9	1823	1836	Yes

				VRELEGEVESEQKR	R	N	95.00%	87		563.2943	3	3.4	1823	1836	Yes
				VRELEGEVESEQKR	R	N	95.00%	57		422.7220	4	1.9	1823	1836	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	39	M10: Oxidation	695.3429	4	6.3	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	51	M7: Oxidation	695.3415	4	4.3	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	44	M7: Oxidation	932.1197	3	6.5	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	41	M7: Oxidation	699.3425	4	7.5	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	38	M7: Oxidation	703.3388	4	4.1	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	45	M7: Oxidation, M10: Oxidation	932.1219	3	8.8	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	47	M7: Oxidation, M10: Oxidation	699.3423	4	7.3	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	44	M7: Oxidation, M9: Oxidation	932.1197	3	6.5	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	37	M7: Oxidation, M9: Oxidation	699.3398	4	3.7	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	38	M7: Oxidation, M9: Oxidation	703.3388	4	4.1	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	38	M7: Oxidation, M9: Oxidation, M10: Oxidation	703.3388	4	4.1	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	37	M9: Oxidation	695.3418	4	4.7	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	44	M9: Oxidation	932.1201	3	6.8	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	42	M9: Oxidation	699.3422	4	7.2	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	44	M9: Oxidation, M10: Oxidation	932.1201	3	6.8	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	54	M9: Oxidation, M10: Oxidation	699.3412	4	5.7	85	107	Yes
				YDKIEDMAMMTHLHEPAVLYNLK	K	E	95.00%	48		691.3441	4	6.3	85	107	Yes
				YETDAIQR	K	T	95.00%	34		498.2464	2	5.1	1379	1386	Yes
				YKVLNASAIPEGQFIDSK	R	K	95.00%	110		990.5358	2	9.8	726	743	Yes
				YKVLNASAIPEGQFIDSK	R	K	95.00%	53		660.6901	3	5.3	726	743	Yes
				YKVLNASAIPEGQFIDSKK	R	A	95.00%	82		703.3906	3	8.1	726	744	Yes
				YKVLNASAIPEGQFIDSKK	R	A	95.00%	28		527.7926	4	3.7	726	744	Yes
198	IPI00025880	MYH7	MYOSIN-7.	ADIAESQVNK	R	L	95.00%	52		1074.5510	1	7.4	1910	1919	Yes
				ADIAESQVNK	R	L	95.00%	81		537.7761	2	1.1	1910	1919	Yes
				ADIAESQVNKLR	R	A	95.00%	34		448.5825	3	2.7	1910	1921	Yes
				AERDYHIFYQILSNK	K	K	95.00%	79		948.9874	2	3.2	279	293	No
				AERDYHIFYQILSNK	K	K	95.00%	45		632.9952	3	4.8	279	293	No
				AGLLGLLEEMR	K	D	95.00%	88	M10: Oxidation	609.3355	2	5.4	767	777	Yes
				AGLLGLLEEMR	K	D	95.00%	58	M10: Oxidation	406.5597	3	5.7	767	777	Yes
				AGLLGLLEEMR	K	D	95.00%	62		1201.6510	1	-9.1	767	777	Yes
				AGLLGLLEEMR	K	D	95.00%	94		601.3371	2	3.9	767	777	Yes
				AGLLGLLEEMRDER	K	L	95.00%	50	M10: Oxidation	809.4238	2	7.7	767	780	Yes
				AGLLGLLEEMRDER	K	L	95.00%	68	M10: Oxidation	539.9509	3	6.0	767	780	Yes
				AGLLGLLEEMRDER	K	L	95.00%	46		801.4236	2	4.3	767	780	Yes
				AGLLGLLEEMRDER	K	L	95.00%	54		534.6177	3	3.2	767	780	Yes
				AITDAAMMAEELK	K	K	95.00%	86	M7: Oxidation, M8: Oxidation	713.3404	2	8.6	1758	1770	Yes
				AITDAAMMAEELK	K	K	95.00%	45	M7: Oxidation, M8: Oxidation	475.8937	3	3.3	1758	1770	Yes
				AITDAAMMAEELKK	K	E	95.00%	102	M7: Oxidation	769.3866	2	3.0	1758	1771	Yes
				AITDAAMMAEELKK	K	E	95.00%	44	M7: Oxidation	513.2606	3	3.4	1758	1771	Yes
				AITDAAMMAEELKK	K	E	95.00%	83	M7: Oxidation	777.3852	2	4.5	1758	1771	Yes
				AITDAAMMAEELKK	K	E	95.00%	52	M7: Oxidation	518.5913	3	1.7	1758	1771	Yes
				AITDAAMMAEELKK	K	E	95.00%	83	M7: Oxidation, M8: Oxidation	777.3852	2	4.5	1758	1771	Yes
				AITDAAMMAEELKK	K	E	95.00%	52	M7: Oxidation, M8: Oxidation	518.5913	3	1.7	1758	1771	Yes
				AITDAAMMAEELKK	K	E	95.00%	97	M8: Oxidation	769.3875	2	4.2	1758	1771	Yes
				AITDAAMMAEELKK	K	E	95.00%	52	M8: Oxidation	513.2598	3	1.9	1758	1771	Yes
				AITDAAMMAEELKK	K	E	95.00%	111		761.3883	2	1.9	1758	1771	Yes

AITDAAMMAEELKK	K	E	95.00%	77		507.9281	3	1.8	1758	1771	Yes
AITDAAMMAEELKKEQDTSAHLER	K	M	95.00%	37	M7: Oxidation, M8: Oxidation	907.4404	3	6.9	1758	1781	Yes
AKLQTENGELSR	R	Q	95.00%	58		673.3601	2	3.5	1278	1289	No
ALQEAHQQALDDLQAEEDK	K	V	95.00%	48		718.0157	3	7.1	998	1016	Yes
ALQEAHQQALDDLQAEEDKVNTLTK	K	A	95.00%	100		936.8147	3	9.6	998	1022	No
ALQEAHQQALDDLQAEEDKVNTLTK	K	A	95.00%	55		702.8597	4	5.0	998	1022	No
ANDDLKENIAIVER	R	R	95.00%	120		800.4223	2	1.5	1663	1676	Yes
ANDDLKENIAIVER	R	R	95.00%	75		533.9528	3	5.3	1663	1676	Yes
ANDDLKENIAIVERR	R	N	95.00%	58		878.4757	2	4.6	1663	1677	Yes
ANDDLKENIAIVERR	R	N	95.00%	70		585.9875	3	6.6	1663	1677	Yes
ANDDLKENIAIVERR	R	N	95.00%	28		439.7414	4	3.9	1663	1677	Yes
ANSEVAQWR	K	T	95.00%	51		1060.5270	1	9.1	1364	1372	Yes
ANSEVAQWR	K	T	95.00%	66		530.7642	2	2.9	1364	1372	Yes
AQLEFNQIK	R	A	95.00%	43		1090.5980	1	7.5	1561	1569	Yes
AQLEFNQIK	R	A	95.00%	75		545.8014	2	4.7	1561	1569	Yes
AQLEFNQIKAEIER	R	K	95.00%	91		844.9600	2	8.7	1561	1574	Yes
AVVEQTER	R	S	95.00%	72		466.2471	2	1.7	1690	1697	Yes
DFELNALNAR	K	I	95.00%	64		1162.5970	1	9.8	1084	1093	No
DFELNALNAR	K	I	95.00%	82		581.7988	2	3.4	1084	1093	No
DIDDLELTLAK	R	V	95.00%	54		1245.6670	1	7.2	953	963	No
DIDDLELTLAK	R	V	95.00%	99		623.3293	2	-5.9	953	963	No
DLEEATLQHEATAAALR	R	K	95.00%	138		919.9714	2	5.4	1177	1193	Yes
DLEEATLQHEATAAALR	R	K	95.00%	67		613.6491	3	3.6	1177	1193	Yes
DLEEATLQHEATAAALRK	R	K	95.00%	119		984.0176	2	3.8	1177	1194	Yes
DLEEATLQHEATAAALRK	R	K	95.00%	75		656.3477	3	3.8	1177	1194	Yes
DLQHRLDEAEQIALK	K	G	95.00%	52		889.9805	2	7.1	1792	1806	Yes
DLQHRLDEAEQIALK	K	G	95.00%	58		593.6564	3	7.3	1792	1806	Yes
DPLNETVVGLYQK	K	S	95.00%	91		738.3958	2	6.1	599	611	Yes
DQSPGKGTLEDQIIQANPALEAFGNAK	K	T	95.00%	89		938.1507	3	8.7	208	234	No
DQSPGKGTLEDQIIQANPALEAFGNAK	K	T	95.00%	46		703.8649	4	8.6	208	234	No
DSLLVIQWNIR	R	A	95.00%	80		678.8918	2	8.7	809	819	No
DTQIQLDDAVR	K	A	95.00%	55		1273.6480	1	6.6	1652	1662	Yes
DTQIQLDDAVR	K	A	95.00%	94		637.3256	2	3.5	1652	1662	Yes
DVFVPDDK	K	Q	95.00%	31		934.4548	1	2.6	36	43	No
DVFVPDDKQEFVK	K	A	95.00%	72		783.3995	2	3.7	36	48	No
DVFVPDDKQEFVK	K	A	95.00%	37		522.6016	3	2.5	36	48	No
DYHIFYQILSNK	R	K	95.00%	81		770.8994	2	7.1	282	293	No
DYHIFYQILSNK	R	K	95.00%	45		514.2679	3	5.3	282	293	No
EAEFQK	R	M	95.00%	32		751.3677	1	6.7	1168	1173	Yes
EALISQLTR	K	G	95.00%	46		1030.5930	1	2.7	1295	1303	Yes
EALISQLTR	K	G	95.00%	61		515.8003	2	2.8	1295	1303	Yes
EDQVMQQNPPK	K	F	95.00%	67	M5: Oxidation	665.3156	2	9.3	73	83	No
EDQVMQQNPPK	K	F	95.00%	64		657.3140	2	3.0	73	83	No
EDQVMQQNPPKFDK	K	I	95.00%	73	M5: Oxidation	860.4100	2	6.3	73	86	No
EDQVMQQNPPKFDK	K	I	95.00%	40	M5: Oxidation	573.9413	3	4.1	73	86	No
EDQVMQQNPPKFDK	K	I	95.00%	81		852.4096	2	2.9	73	86	No
EDQVMQQNPPKFDK	K	I	95.00%	57		568.6121	3	8.2	73	86	No
EEQAEPDGTEEADKSAYLMGLNSADLLK	R	G	95.00%	100	M19: Oxidation	1014.1410	3	4.1	370	397	No
EEQAEPDGTEEADKSAYLMGLNSADLLK	R	G	95.00%	76		1008.8120	3	7.2	370	397	No
EGGKVTAETEYGK	R	T	95.00%	52		684.8429	2	9.5	55	67	No
EKEMASMKEEFTR	R	L	95.00%	67	M4: Oxidation	816.3773	2	3.6	846	858	No
EKEMASMKEEFTR	R	L	95.00%	43	M4: Oxidation	544.5875	3	3.5	846	858	No
EKEMASMKEEFTR	R	L	95.00%	65	M4: Oxidation	824.3760	2	5.1	846	858	No
EKEMASMKEEFTR	R	L	95.00%	45	M4: Oxidation	549.9203	3	5.7	846	858	No
EKEMASMKEEFTR	R	L	95.00%	37	M4: Oxidation	412.6902	4	1.0	846	858	No
EKEMASMKEEFTR	R	L	95.00%	65	M4: Oxidation, M7: Oxidation	824.3760	2	5.1	846	858	No
EKEMASMKEEFTR	R	L	95.00%	45	M4: Oxidation, M7: Oxidation	549.9203	3	5.7	846	858	No
EKEMASMKEEFTR	R	L	95.00%	37	M4: Oxidation, M7: Oxidation	412.6902	4	1.0	846	858	No
EKEMASMKEEFTR	R	L	95.00%	67	M7: Oxidation	816.3780	2	4.4	846	858	No
EKEMASMKEEFTR	R	L	95.00%	39	M7: Oxidation	544.5877	3	4.0	846	858	No

EKEMASMKEEFTR	R	L	95.00%	77		808.3791	2	2.7	846	858	No
EKSEFKLELDDVTSNMEQIIK	K	A	95.00%	79	M16: Oxidation	838.0959	3	9.1	1220	1240	Yes
EKSEFKLELDDVTSNMEQIIK	K	A	95.00%	33	M16: Oxidation	628.8243	4	9.7	1220	1240	Yes
EKSEFKLELDDVTSNMEQIIK	K	A	95.00%	84		832.7598	3	3.7	1220	1240	Yes
EKSEFKLELDDVTSNMEQIIK	K	A	95.00%	35		624.8219	4	3.9	1220	1240	Yes
ELEEISER	R	L	95.00%	49		1004.4910	1	0.9	1142	1149	Yes
ELEEISER	R	L	95.00%	42		502.7503	2	2.7	1142	1149	Yes
ELEEISERLEEAGGATSVQIEMNK	R	K	95.00%	82	M22: Oxidation	893.4395	3	7.5	1142	1165	Yes
ELEEISERLEEAGGATSVQIEMNK	R	K	95.00%	56	M22: Oxidation	670.3314	4	7.1	1142	1165	Yes
ELEEISERLEEAGGATSVQIEMNK	R	K	95.00%	69		888.1052	3	4.4	1142	1165	Yes
ELEEISERLEEAGGATSVQIEMNKK	R	R	95.00%	68	M22: Oxidation	936.1401	3	9.5	1142	1166	Yes
ELENELEAEQK	R	R	95.00%	85		666.3235	2	4.5	1821	1831	No
ELENELEAEQKR	R	N	95.00%	81		744.3724	2	1.9	1821	1832	No
ELENELEAEQKR	R	N	95.00%	47		496.5846	3	2.7	1821	1832	No
ELTYQTEEDR	K	K	95.00%	51		642.2961	2	6.8	1849	1858	Yes
ELTYQTEEDRK	K	N	95.00%	70		706.3410	2	2.5	1849	1859	Yes
ELTYQTEEDRK	K	N	95.00%	42		471.2320	3	6.8	1849	1859	Yes
ELTYQTEEDRKNLLR	K	L	95.00%	46		954.5008	2	5.8	1849	1863	No
ELTYQTEEDRKNLLR	K	L	95.00%	39		636.6688	3	4.2	1849	1863	No
EMASMKEEFTR	K	L	95.00%	47	M2: Oxidation	687.8074	2	2.7	848	858	No
EMASMKEEFTR	K	L	95.00%	41	M2: Oxidation	458.8740	3	2.2	848	858	No
EMASMKEEFTR	K	L	95.00%	65	M2: Oxidation	695.8058	2	4.0	848	858	No
EMASMKEEFTR	K	L	95.00%	45	M2: Oxidation	464.2057	3	2.4	848	858	No
EMASMKEEFTR	K	L	95.00%	65	M2: Oxidation, M5: Oxidation	695.8058	2	4.0	848	858	No
EMASMKEEFTR	K	L	95.00%	45	M2: Oxidation, M5: Oxidation	464.2057	3	2.4	848	858	No
EMASMKEEFTR	K	L	95.00%	34	M5: Oxidation	687.8076	2	2.9	848	858	No
EMASMKEEFTR	K	L	95.00%	44		679.8142	2	8.9	848	858	No
EMASMKEEFTR	K	L	95.00%	36		453.5437	3	5.2	848	858	No
EMNERLEDEEEMNAELTAK	K	K	95.00%	70	M12: Oxidation	766.3376	3	2.6	921	939	Yes
EMNERLEDEEEMNAELTAK	K	K	95.00%	73	M2: Oxidation, M12: Oxidation	771.6697	3	3.2	921	939	Yes
ENIAIVER	K	R	95.00%	43		472.2666	2	4.3	1669	1676	Yes
ENKNLQEEISDLTEQLGSSGK	R	T	95.00%	125		1160.0780	2	6.9	1501	1521	No
ENKNLQEEISDLTEQLGSSGK	R	T	95.00%	84		773.7184	3	3.4	1501	1521	No
ENQSILITGESGAGK	R	T	95.00%	118		752.3882	2	1.9	170	184	Yes
ENQSILITGESGAGK	R	T	95.00%	46		501.9288	3	3.5	170	184	Yes
EQDTSAHLER	K	M	95.00%	69		593.2841	2	8.6	1772	1781	Yes
EQYEEETEAK	R	A	95.00%	52		628.2742	2	5.9	1345	1354	Yes
EQYEEETEAKAELQR	R	V	95.00%	104		926.9355	2	3.6	1345	1359	Yes
EQYEEETEAKAELQR	R	V	95.00%	39		618.2937	3	4.8	1345	1359	Yes
FDKIEDMAMLTFLHEPAVLYNLK	K	D	95.00%	58	M7: Oxidation	689.3574	4	6.3	84	106	No
FDKIEDMAMLTFLHEPAVLYNLK	K	D	95.00%	49	M7: Oxidation	924.1385	3	5.9	84	106	No
FDKIEDMAMLTFLHEPAVLYNLK	K	D	95.00%	65	M7: Oxidation	693.3564	4	6.7	84	106	No
FDKIEDMAMLTFLHEPAVLYNLK	K	D	95.00%	49	M7: Oxidation, M9: Oxidation	924.1385	3	5.9	84	106	No
FDKIEDMAMLTFLHEPAVLYNLK	K	D	95.00%	65	M7: Oxidation, M9: Oxidation	693.3564	4	6.7	84	106	No
FDKIEDMAMLTFLHEPAVLYNLK	K	D	95.00%	67	M9: Oxidation	689.3573	4	6.2	84	106	No
FDKIEDMAMLTFLHEPAVLYNLK	K	D	95.00%	49		913.4783	3	9.4	84	106	No
FDKIEDMAMLTFLHEPAVLYNLK	K	D	95.00%	71		685.3597	4	7.9	84	106	No
GKLTYTQQLEDLK	R	R	95.00%	40		768.9211	2	4.4	1304	1316	No
GKLTYTQQLEDLK	R	R	95.00%	32		512.9494	3	3.3	1304	1316	No
GKLTYTQQLEDLKR	R	Q	95.00%	93		846.9693	2	1.2	1304	1317	No
GKLTYTQQLEDLKR	R	Q	95.00%	84		564.9838	3	4.2	1304	1317	No
GKLTYTQQLEDLKR	R	Q	95.00%	34		423.9901	4	4.8	1304	1317	No
GKPEAHFSLIHYAGIVDYNIIGWLQK	K	N	95.00%	98		990.5364	3	8.7	571	596	No
GQNVQQVIYATGALAK	K	A	95.00%	149		830.9611	2	7.2	414	429	No

GQNVQQVIYATGALAK	K	A	95.00%	62		554.3097	3	6.6	414	429	No
GSSFQTVSALHR	K	E	95.00%	78		645.3373	2	5.1	641	652	Yes
GSSFQTVSALHRENLNK	K	L	95.00%	60		944.4929	2	5.4	641	657	Yes
GTLEDQIIQANPALEAFGNAK	K	T	95.00%	143		1100.5760	2	8.4	214	234	Yes
GTLEDQIIQANPALEAFGNAK	K	T	95.00%	96		734.0500	3	4.2	214	234	Yes
HADSVAELGEQIDNLQR	K	V	95.00%	166		947.9739	2	7.4	1196	1212	Yes
HADSVAELGEQIDNLQR	K	V	95.00%	85		632.3179	3	6.4	1196	1212	Yes
HRLQNEIEDLMVDVER	K	S	95.00%	86	M11: Oxidation	671.3367	3	3.6	1419	1434	Yes
HRLQNEIEDLMVDVER	K	S	95.00%	79		998.5089	2	8.8	1419	1434	Yes
HRLQNEIEDLMVDVER	K	S	95.00%	88		666.0065	3	5.7	1419	1434	Yes
HRLQNEIEDLMVDVER	K	S	95.00%	34		499.7565	4	5.1	1419	1434	Yes
IEDEQALGSQLQK	R	K	95.00%	135		729.8759	2	-0.2	1094	1106	No
IEDEQALGSQLQK	R	K	95.00%	59		486.9212	3	2.6	1094	1106	No
IEDEQALGSQLQKK	R	L	95.00%	73		793.9267	2	4.0	1094	1107	No
IEDMAMLTFLHEPAVLYNLK	K	D	95.00%	70	M4: Oxidation	788.7446	3	8.3	87	106	No
IEDMAMLTFLHEPAVLYNLK	K	D	95.00%	65	M4: Oxidation	1190.6100	2	8.0	87	106	No
IEDMAMLTFLHEPAVLYNLK	K	D	95.00%	71	M4: Oxidation	794.0759	3	7.9	87	106	No
IEDMAMLTFLHEPAVLYNLK	K	D	95.00%	65	M4: Oxidation, M6: Oxidation	1190.6100	2	8.0	87	106	No
IEDMAMLTFLHEPAVLYNLK	K	D	95.00%	71	M4: Oxidation, M6: Oxidation	794.0759	3	7.9	87	106	No
IEDMAMLTFLHEPAVLYNLK	K	D	95.00%	57	M6: Oxidation	788.7410	3	3.8	87	106	No
IEDMAMLTFLHEPAVLYNLK	K	D	95.00%	48		783.4089	3	3.1	87	106	No
IEELEEELEAER	R	T	95.00%	103		744.8617	2	5.7	1115	1126	Yes
IEELEEELEAER	R	T	95.00%	67		496.9096	3	4.0	1115	1126	Yes
IKELTYQTEEDR	R	K	95.00%	67		762.8881	2	9.0	1847	1858	No
IKELTYQTEEDR	R	K	95.00%	33		508.9268	3	6.6	1847	1858	No
IKELTYQTEEDRK	R	N	95.00%	91		826.9315	2	3.3	1847	1859	No
IKELTYQTEEDRK	R	N	95.00%	68		551.6251	3	6.1	1847	1859	No
IKELTYQTEEDRK	R	N	95.00%	44		413.9694	4	2.7	1847	1859	No
ILAEWK	K	Q	95.00%	33		759.4422	1	2.1	1452	1457	Yes
ILNPAAIPEGQFIDSR	R	K	95.00%	102		870.9727	2	5.1	724	739	No
ILNPAAIPEGQFIDSR	R	K	95.00%	85		580.9843	3	5.0	724	739	No
ILYGDFR	R	Q	95.00%	43		442.2399	2	4.6	713	719	Yes
INATLETK	R	Q	95.00%	34		889.5071	1	8.5	443	450	No
INATLETK	R	Q	95.00%	52		445.2545	2	1.9	443	450	Yes
INATLETKQPR	R	Q	95.00%	51		635.8622	2	3.6	443	453	Yes
IQLEAK	K	V	95.00%	37		701.4219	1	2.9	913	918	Yes
KAITDAAMMAEELKK	K	E	95.00%	101	M8: Oxidation	833.4363	2	5.3	1757	1771	Yes
KAITDAAMMAEELKK	K	E	95.00%	81	M8: Oxidation	555.9587	3	2.7	1757	1771	Yes
KAITDAAMMAEELKK	K	E	95.00%	35	M8: Oxidation	417.2235	4	8.8	1757	1771	Yes
KAITDAAMMAEELKK	K	E	95.00%	80	M8: Oxidation	841.4315	2	2.7	1757	1771	Yes
KAITDAAMMAEELKK	K	E	95.00%	64	M8: Oxidation	561.2909	3	3.8	1757	1771	Yes
KAITDAAMMAEELKK	K	E	95.00%	80	M8: Oxidation, M9: Oxidation	841.4315	2	2.7	1757	1771	Yes
KAITDAAMMAEELKK	K	E	95.00%	64	M8: Oxidation, M9: Oxidation	561.2909	3	3.8	1757	1771	Yes
KAITDAAMMAEELKK	K	E	95.00%	103	M9: Oxidation	833.4359	2	4.9	1757	1771	Yes
KAITDAAMMAEELKK	K	E	95.00%	63	M9: Oxidation	555.9584	3	2.3	1757	1771	Yes
KAITDAAMMAEELKK	K	E	95.00%	37	M9: Oxidation	417.2219	4	5.0	1757	1771	Yes
KAITDAAMMAEELKK	K	E	95.00%	107		825.4387	2	5.2	1757	1771	Yes
KAITDAAMMAEELKK	K	E	95.00%	92		550.6276	3	3.8	1757	1771	Yes
KAITDAAMMAEELKK	K	E	95.00%	42		413.2216	4	1.3	1757	1771	Yes
KALQEAHQQALDDLQAEEDKVNTLTK	K	A	95.00%	103		979.5103	3	6.4	997	1022	No
KALQEAHQQALDDLQAEEDKVNTLTK	K	A	95.00%	65		734.8832	4	4.3	997	1022	No
KALQEAHQQALDDLQAEEDKVNTLTK	K	A	95.00%	49		588.1085	5	5.1	997	1022	No
KDFELNALNAR	K	I	95.00%	76		645.8459	2	2.6	1083	1093	No
KDFELNALNAR	K	I	95.00%	33		430.9003	3	3.4	1083	1093	No
KDQSPGKGTLEDQIIQANPALEAFGNAK	K	T	95.00%	97		980.8472	3	6.6	207	234	No
KDQSPGKGTLEDQIIQANPALEAFGNAK	K	T	95.00%	41		735.8881	4	7.5	207	234	No
KDVFVPDDKQEFVK	K	A	95.00%	44		847.4459	2	2.2	35	48	No
KDVFVPDDKQEFVK	K	A	95.00%	32		565.3014	3	5.0	35	48	No
KGSSFQTVSALHR	K	E	95.00%	101		709.3837	2	3.0	640	652	Yes
KGSSFQTVSALHR	K	E	95.00%	69		473.2583	3	2.9	640	652	Yes
KHADSVAELGEQIDNLQR	K	V	95.00%	137		1012.0210	2	6.5	1195	1212	Yes

KHADSVAELGEQIDNLQR	K	V	95.00%	93		675.0148	3	3.8	1195	1212	Yes
KHADSVAELGEQIDNLQR	K	V	95.00%	66		506.5136	4	4.9	1195	1212	Yes
KKDFELNALNAR	K	I	95.00%	98		709.8933	2	2.2	1082	1093	No
KKDFELNALNAR	K	I	95.00%	55		473.5987	3	3.4	1082	1093	No
KKHADSVAELGEQIDNLQR	R	V	95.00%	89		717.7142	3	5.1	1194	1212	Yes
KKHADSVAELGEQIDNLQR	R	V	95.00%	53		538.5365	4	3.1	1194	1212	Yes
KKMDADLSQLQTEVEEAVQECR	K	N	95.00%	42	M3: Oxidation	856.0825	3	7.3	1728	1749	No
KKMEGDLNEMEIQLSHANR	K	M	95.00%	48	M10: Oxidation	565.5286	4	2.1	1616	1634	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	54	M3: Oxidation	753.7057	3	6.7	1616	1634	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	42	M3: Oxidation	565.5287	4	2.2	1616	1634	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	60	M3: Oxidation	759.0351	3	3.6	1616	1634	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	69	M3: Oxidation	569.5274	4	2.1	1616	1634	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	60	M3: Oxidation, M10: Oxidation	759.0351	3	3.6	1616	1634	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	69	M3: Oxidation, M10: Oxidation	569.5274	4	2.1	1616	1634	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	61		748.3721	3	4.1	1616	1634	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	69		561.5313	4	4.5	1616	1634	Yes
KLAEQELIETSER	R	V	95.00%	113		773.4159	2	7.4	1700	1712	Yes
KLAEQELIETSER	R	V	95.00%	66		515.9439	3	2.1	1700	1712	Yes
KLEGDLK	R	L	95.00%	39		401.7396	2	4.6	1054	1060	Yes
KMDADLSQLQTEVEEAVQECR	K	N	95.00%	85	M2: Oxidation	813.3857	3	9.6	1729	1749	No
KMEGDLNEMEIQLSHANR	K	M	95.00%	83	M2: Oxidation	711.0037	3	2.1	1617	1634	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	49	M2: Oxidation	533.5064	4	5.2	1617	1634	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	90	M2: Oxidation	1074.0030	2	6.0	1617	1634	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	59	M2: Oxidation	716.3382	3	6.0	1617	1634	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	47	M2: Oxidation	537.5055	4	5.9	1617	1634	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	90	M2: Oxidation, M9: Oxidation	1074.0030	2	6.0	1617	1634	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	59	M2: Oxidation, M9: Oxidation	716.3382	3	6.0	1617	1634	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	47	M2: Oxidation, M9: Oxidation	537.5055	4	5.9	1617	1634	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	52	M9: Oxidation	711.0025	3	0.3	1617	1634	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	37	M9: Oxidation	533.5066	4	5.5	1617	1634	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	107		1058.0130	2	9.9	1617	1634	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	87		705.6741	3	4.8	1617	1634	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	46		529.5076	4	5.0	1617	1634	Yes
KQLEAEKMELQSALEEAEASLEHEEGK	R	I	95.00%	103	M8: Oxidation	1024.8380	3	9.3	1531	1557	No
KQLEAEKMELQSALEEAEASLEHEEGK	R	I	95.00%	62	M8: Oxidation	768.8776	4	6.0	1531	1557	No
KQLEAEKMELQSALEEAEASLEHEEGK	R	I	95.00%	57	M8: Oxidation	615.3052	5	8.6	1531	1557	No
KVQHELDEAEER	R	A	95.00%	64		741.8678	2	5.9	1898	1909	Yes
KVQHELDEAEER	R	A	95.00%	62		494.9157	3	8.4	1898	1909	Yes
KVQHELDEAEERADIAESQVNK	R	L	95.00%	97		1269.6380	2	9.4	1898	1919	Yes
KVQHELDEAEERADIAESQVNK	R	L	95.00%	58		846.7584	3	6.3	1898	1919	Yes
KVQHELDEAEERADIAESQVNK	R	L	95.00%	67		635.3188	4	3.2	1898	1919	Yes
LAEKDEEMEQAKR	K	N	95.00%	50	M8: Oxidation	531.5968	3	9.8	1576	1588	Yes
LAEKDEEMEQAKR	K	N	95.00%	46		526.2601	3	0.3	1576	1588	Yes
LAEQELIETSER	K	V	95.00%	115		709.3655	2	3.9	1701	1712	Yes
LAEQELIETSER	K	V	95.00%	41		473.2462	3	3.9	1701	1712	Yes
LASADIETYLLEK	K	S	95.00%	129		733.3926	2	-1.2	258	270	Yes
LASADIETYLLEK	K	S	95.00%	66		489.2671	3	4.5	258	270	Yes
LDEAEQIALK	R	G	95.00%	51		1129.6220	1	9.6	1797	1806	Yes
LDEAEQIALK	R	G	95.00%	97		565.3107	2	2.5	1797	1806	Yes
LDEAEQIALKGGK	R	K	95.00%	66		686.3813	2	4.5	1797	1809	Yes
LDEAEQIALKGGK	R	K	95.00%	42		457.9226	3	2.6	1797	1809	Yes
LDEAEQIALKGGKK	R	Q	95.00%	81		750.4314	2	7.6	1797	1810	Yes
LDEAEQIALKGGKK	R	Q	95.00%	45		500.6212	3	2.9	1797	1810	Yes
LEAQTRPFDLK	R	K	95.00%	60		659.3650	2	4.0	24	34	No
LEAQTRPFDLKK	R	D	95.00%	57		723.4115	2	2.3	24	35	No
LEAQTRPFDLKK	R	D	95.00%	41		482.6107	3	3.2	24	35	No
LEDEEEMNAELTAK	R	K	95.00%	117	M7: Oxidation	819.3672	2	2.9	926	939	Yes

LEDEEEMNAELTAK	R	K	95.00%	124		811.3694	2	2.5	926	939	Yes
LEEAGGATSVQIEMNK	R	K	95.00%	146	M14: Oxidation	846.9111	2	1.7	1150	1165	Yes
LEEAGGATSVQIEMNK	R	K	95.00%	50	M14: Oxidation	564.9460	3	6.3	1150	1165	Yes
LEEAGGATSVQIEMNK	R	K	95.00%	132		838.9142	2	2.4	1150	1165	Yes
LEEAGGATSVQIEMNKK	R	R	95.00%	71	M14: Oxidation	910.9600	2	3.2	1150	1166	Yes
LEEAGGATSVQIEMNKK	R	R	95.00%	34	M14: Oxidation	607.6447	3	6.6	1150	1166	No
LELDDVTSNMEQIIK	K	A	95.00%	104	M10: Oxidation	882.4473	2	7.3	1226	1240	Yes
LELDDVTSNMEQIIK	K	A	95.00%	32	M10: Oxidation	588.6335	3	6.1	1226	1240	No
LELDDVTSNMEQIIK	K	A	95.00%	97		874.4501	2	7.5	1226	1240	Yes
LELDDVTSNMEQIIK	K	A	95.00%	72		583.3007	3	4.2	1226	1240	Yes
LEQQVDDLEGSLEQEK	K	K	95.00%	144		930.4526	2	5.2	1027	1042	Yes
LEQQVDDLEGSLEQEK	K	K	95.00%	113		620.6381	3	5.9	1027	1042	Yes
LEQQVDDLEGSLEQEKK	K	V	95.00%	116		994.5015	2	6.3	1027	1043	Yes
LEQQVDDLEGSLEQEKK	K	V	95.00%	69		663.3355	3	4.1	1027	1043	Yes
LFDNHLGK	K	S	95.00%	31		943.5037	1	3.6	552	559	No
LFDNHLGK	K	S	95.00%	55		472.2547	2	1.4	552	559	No
LKEALEK	R	S	95.00%	30		415.7544	2	2.6	859	865	No
LKELQAR	K	I	95.00%	31		429.2654	2	2.3	1108	1114	No
LKNAYEESLEHLETFK	K	R	95.00%	133		976.0031	2	8.7	1484	1499	Yes
LKNAYEESLEHLETFK	K	R	95.00%	75		651.0009	3	2.9	1484	1499	Yes
LKNAYEESLEHLETFK	K	R	95.00%	45		488.5031	4	3.9	1484	1499	Yes
LKNAYEESLEHLETFKR	K	E	95.00%	113		1054.0520	2	6.0	1484	1500	Yes
LKNAYEESLEHLETFKR	K	E	95.00%	59		703.0364	3	5.3	1484	1500	Yes
LKNAYEESLEHLETFKR	K	E	95.00%	53		527.5279	4	2.8	1484	1500	Yes
LKQREEQAEPDGTEEADK	K	S	95.00%	39		691.6658	3	3.8	366	383	No
LLSSLDIDHNQYK	K	F	95.00%	105		773.4031	2	4.5	745	757	Yes
LLSSLDIDHNQYK	K	F	95.00%	34		515.9373	3	3.2	745	757	Yes
LLSTLFANYAGADAPIEK	K	G	95.00%	140		947.5093	2	7.5	616	633	No
LLSTLFANYAGADAPIEK	K	G	95.00%	91		632.0070	3	4.6	616	633	No
LQDLVDK	R	L	95.00%	35		830.4684	1	7.0	1864	1870	Yes
LQDLVDK	R	L	95.00%	42		415.7369	2	4.1	1864	1870	Yes
LQDLVDKLQLK	R	V	95.00%	85		656.8982	2	3.2	1864	1874	Yes
LQDLVDKLQLK	R	V	95.00%	64		438.2683	3	3.7	1864	1874	Yes
LQEAEEAVEAVNAK	R	C	95.00%	131		750.8849	2	5.0	1397	1410	No
LQEAEEAVEAVNAK	R	C	95.00%	68		500.9250	3	3.3	1397	1410	No
LQEAEEAVEAVNAKCSSLEK	R	T	95.00%	74		716.6912	3	4.1	1397	1416	No
LQNEIEDLMVDVER	R	S	95.00%	123	M9: Oxidation	859.9257	2	9.6	1421	1434	Yes
LQNEIEDLMVDVER	R	S	95.00%	92	M9: Oxidation	573.6166	3	4.1	1421	1434	Yes
LQNEIEDLMVDVER	R	S	95.00%	109		851.9232	2	3.7	1421	1434	Yes
LQNEIEDLMVDVER	R	S	95.00%	79		568.2845	3	3.2	1421	1434	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	58	M9: Oxidation	795.0480	3	4.4	485	502	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	35	M9: Oxidation	596.5412	4	9.8	485	502	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	43		789.7178	3	6.2	485	502	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	42		592.5402	4	6.1	485	502	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	68	M9: Oxidation	1256.1180	2	5.7	485	503	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	51	M9: Oxidation	837.7500	3	8.6	485	503	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	103		1248.1230	2	8.3	485	503	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	57		832.4158	3	5.6	485	503	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	42		499.8525	5	5.4	485	503	Yes
LQTENGELSR	K	Q	95.00%	49		573.7955	2	6.7	1280	1289	No
LTGAIMHFGNMK	K	F	95.00%	67	M11: Oxidation	668.3349	2	4.8	352	363	Yes
LTGAIMHFGNMK	K	F	95.00%	78	M6: Oxidation	668.3349	2	4.8	352	363	No
LTGAIMHFGNMK	K	F	95.00%	64	M6: Oxidation	676.3300	2	1.4	352	363	No
LTGAIMHFGNMK	K	F	95.00%	67	M6: Oxidation, M11: Oxidation	676.3319	2	4.2	352	363	Yes
LTGAIMHFGNMK	K	F	95.00%	95		660.3377	2	5.3	352	363	Yes
LTQESIMDLENDK	K	Q	95.00%	86	M7: Oxidation	776.3684	2	4.9	1061	1073	No
LTQESIMDLENDK	K	Q	95.00%	58		768.3713	2	5.4	1061	1073	No
LTQESIMDLENDKQQLDER	K	L	95.00%	107	M7: Oxidation	1161.0610	2	8.9	1061	1079	No
LTQESIMDLENDKQQLDER	K	L	95.00%	78	M7: Oxidation	774.3716	3	2.6	1061	1079	No
LTQESIMDLENDKQQLDER	K	L	95.00%	41	M7: Oxidation	581.0270	4	-3.7	1061	1079	No
LTQESIMDLENDKQQLDER	K	L	95.00%	118		1153.0620	2	7.3	1061	1079	No
LTQESIMDLENDKQQLDER	K	L	95.00%	73		769.0417	3	4.8	1061	1079	No
LTYTQQLEDLK	K	R	95.00%	85		676.3633	2	5.6	1306	1316	No
LTYTQQLEDLKR	K	Q	95.00%	85		754.4125	2	3.2	1306	1317	No
LTYTQQLEDLKR	K	Q	95.00%	64		503.2791	3	6.2	1306	1317	No
MDADLSQLQTEVEEAVQECR	K	N	95.00%	73	M1: Oxidation	1155.5250	2	8.2	1730	1749	No
MEGDLNEMEIQLSHANR	K	M	95.00%	106	M1: Oxidation	1001.9560	2	4.1	1618	1634	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	68	M1: Oxidation	668.3069	3	4.4	1618	1634	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	88	M1: Oxidation	1009.9510	2	1.6	1618	1634	Yes

MEGDLNEMEIQLSHANR	K	M	95.00%	68	M1: Oxidation	673.6376	3	3.0	1618	1634	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	88	M1: Oxidation, M8: Oxidation	1009.9510	2	1.6	1618	1634	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	68	M1: Oxidation, M8: Oxidation	673.6376	3	3.0	1618	1634	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	83	M8: Oxidation	1001.9580	2	6.4	1618	1634	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	45	M8: Oxidation	668.3068	3	4.3	1618	1634	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	148		993.9626	2	8.0	1618	1634	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	83		662.9764	3	6.1	1618	1634	Yes
MELQSALEEAEASLEHEEGK	K	I	95.00%	143	M1: Oxidation	1123.5220	2	9.7	1538	1557	No
MELQSALEEAEASLEHEEGK	K	I	95.00%	73	M1: Oxidation	749.3466	3	4.8	1538	1557	No
MELQSALEEAEASLEHEEGK	K	I	95.00%	129		1115.5240	2	10.0	1538	1557	No
MELQSALEEAEASLEHEEGK	K	I	95.00%	70		744.0148	3	4.6	1538	1557	No
MFNWMVTR	R	I	95.00%	47	M1: Oxidation	550.7566	2	3.1	435	442	No
MFNWMVTR	R	I	95.00%	56	M1: Oxidation	558.7542	2	3.2	435	442	No
MFNWMVTR	R	I	95.00%	56	M1: Oxidation, M5: Oxidation	558.7542	2	3.2	435	442	No
MFNWMVTR	R	I	95.00%	54	M5: Oxidation	550.7580	2	5.5	435	442	No
MFNWMVTR	R	I	95.00%	35		1084.5120	1	4.2	435	442	No
MFNWMVTR	R	I	95.00%	52		542.7602	2	5.1	435	442	No
MVSLLQEK	K	N	95.00%	53	M1: Oxidation	963.5215	1	3.1	877	884	Yes
MVSLLQEK	K	N	95.00%	53	M1: Oxidation	482.2638	2	1.3	877	884	Yes
MVSLLQEK	K	N	95.00%	48		947.5253	1	1.7	877	884	Yes
MVSLLQEK	K	N	95.00%	55		474.2693	2	7.7	877	884	Yes
NALAHALQSAR	K	H	95.00%	47		1151.6330	1	4.3	1327	1337	Yes
NALAHALQSAR	K	H	95.00%	80		576.3195	2	2.2	1327	1337	Yes
NAYEESLEHLETFK	K	R	95.00%	112		855.4108	2	6.8	1486	1499	Yes
NAYEESLEHLETFK	K	R	95.00%	47		570.6091	3	5.5	1486	1499	Yes
NAYEESLEHLETFKR	K	E	95.00%	102		933.4626	2	7.5	1486	1500	Yes
NAYEESLEHLETFKR	K	E	95.00%	51		622.6431	3	5.5	1486	1500	Yes
NDLQLQVQAEQDNLADAEER	K	C	95.00%	169		1150.0540	2	8.4	885	904	No
NDLQLQVQAEQDNLADAEER	K	C	95.00%	106		767.0347	3	3.6	885	904	No
NFDKILAEWK	R	Q	95.00%	40		632.3444	2	5.5	1448	1457	Yes
NFDKILAEWK	R	Q	95.00%	30		421.8982	3	4.0	1448	1457	Yes
NKDPLNETVVGLYQK	K	S	95.00%	121		859.4654	2	6.0	597	611	Yes
NKDPLNETVVGLYQK	K	S	95.00%	75		573.3107	3	2.1	597	611	Yes
NLQEEISDLTEQLGSSGK	K	T	95.00%	163		974.4875	2	8.1	1504	1521	No
NLQEEISDLTEQLGSSGK	K	T	95.00%	90		649.9916	3	4.1	1504	1521	No
NLTEEMAGLDEIIAK	K	L	95.00%	114	M6: Oxidation	831.9211	2	4.9	977	991	Yes
NLTEEMAGLDEIIAK	K	L	95.00%	71	M6: Oxidation	554.9494	3	3.8	977	991	Yes
NLTEEMAGLDEIIAK	K	L	95.00%	117		823.9225	2	3.6	977	991	Yes
NLTEEMAGLDEIIAK	K	L	95.00%	84		549.6174	3	3.1	977	991	Yes
NMEQTIK	K	D	95.00%	32	M2: Oxidation	440.2186	2	5.4	1785	1791	Yes
NMEQTIKDLQHR	K	L	95.00%	39	M2: Oxidation	764.8834	2	3.0	1785	1796	Yes
NNLLQAELEELR	R	A	95.00%	115		721.3893	2	3.9	1678	1689	Yes
NNLLQAELEELR	R	A	95.00%	96		481.2624	3	4.5	1678	1689	Yes
NNLLQAELEELRAVVEQTER	R	S	95.00%	72		785.4218	3	7.7	1678	1697	Yes
NWPWMK	K	L	95.00%	29		431.2093	2	3.1	826	831	Yes
QAEEAEEQANTNLSK	R	F	95.00%	117		831.3911	2	7.6	1881	1895	Yes
QAEEAEEQANTNLSK	R	F	95.00%	64		554.5937	3	2.1	1881	1895	Yes
QKYEESQSELESSQK	K	E	95.00%	99		900.4216	2	3.0	1458	1472	Yes
QKYEESQSELESSQK	K	E	95.00%	59		600.6168	3	2.6	1458	1472	Yes
QLDEKEALISQLTR	R	G	95.00%	112		822.4584	2	7.2	1290	1303	No
QLDEKEALISQLTR	R	G	95.00%	73		548.6397	3	3.9	1290	1303	No
QLEAEKMELQSALEEAEASLEHEEGK	K	I	95.00%	91	M7: Oxidation	982.1372	3	7.7	1532	1557	No
QLEAEKMELQSALEEAEASLEHEEGK	K	I	95.00%	61	M7: Oxidation	736.8535	4	5.9	1532	1557	No
QLEEEVK	R	A	95.00%	37		437.7308	2	1.7	1318	1324	No
QREEQAEPDGTEEADK	K	S	95.00%	47		916.4064	2	5.5	368	383	No
QREEQAEPDGTEEADK	K	S	95.00%	40		611.2758	3	9.2	368	383	No
QREEQAEPDGTEEADKSAYLMGLNSADLLK	K	G	95.00%	81	M21: Oxidation	1108.8660	3	8.2	368	397	No
QREEQAEPDGTEEADKSAYLMGLNSADLLK	K	G	95.00%	62		1103.5350	3	9.4	368	397	No
QREEQAEPDGTEEADKSAYLMGLNSADLLK	K	G	95.00%	40		827.9004	4	5.7	368	397	No
RDLEEATLQHEATAAALR	R	K	95.00%	119		998.0237	2	6.8	1176	1193	Yes
RDLEEATLQHEATAAALR	R	K	95.00%	84		665.6832	3	3.9	1176	1193	Yes
RDLEEATLQHEATAAALR	R	K	95.00%	65		499.5138	4	2.9	1176	1193	Yes

RDSLLVIQWNIR	R	A	95.00%	53		756.9397	2	4.2	808	819	No
RDSLLVIQWNIR	R	A	95.00%	46		504.9620	3	3.5	808	819	No
RNNLLQAELEELR	R	A	95.00%	81		799.4423	2	6.6	1677	1689	Yes
RNNLLQAELEELR	R	A	95.00%	88		533.2958	3	3.4	1677	1689	Yes
RQAEEAEEQANTNLSK	K	F	95.00%	75		909.4435	2	9.0	1880	1895	Yes
RQAEEAEEQANTNLSK	K	F	95.00%	47		606.6296	3	5.7	1880	1895	Yes
RSEAPPHIFSISDNAYQYMLTDR	K	E	95.00%	118	M19: Oxidation	909.7731	3	7.4	147	169	Yes
RSEAPPHIFSISDNAYQYMLTDR	K	E	95.00%	50	M19: Oxidation	682.5812	4	6.5	147	169	Yes
RSEAPPHIFSISDNAYQYMLTDR	K	E	95.00%	125		904.4421	3	8.1	147	169	Yes
RSEAPPHIFSISDNAYQYMLTDR	K	E	95.00%	45		678.5836	4	8.3	147	169	Yes
RSEAPPHIFSISDNAYQYMLTDRENQSILITGESGAGK	K	T	95.00%	56	M19: Oxidation	1053.7730	4	8.6	147	184	Yes
RSEAPPHIFSISDNAYQYMLTDRENQSILITGESGAGK	K	T	95.00%	77		1049.7750	4	9.3	147	184	Yes
RVIQYFAVIAAIGDR	K	S	95.00%	86		846.4896	2	6.9	190	204	No
RVIQYFAVIAAIGDR	K	S	95.00%	60		564.6616	3	5.4	190	204	No
SAYLMGLNSADLLK	K	G	95.00%	105	M5: Oxidation	756.3973	2	5.7	384	397	Yes
SAYLMGLNSADLLK	K	G	95.00%	88		748.3988	2	4.4	384	397	Yes
SEAPPHIFSISDNAYQYMLTDR	R	E	95.00%	84	M18: Oxidation	857.7385	3	6.8	148	169	Yes
SEAPPHIFSISDNAYQYMLTDR	R	E	95.00%	78		852.4084	3	8.7	148	169	Yes
SEAPPHIFSISDNAYQYMLTDRENQSILITGESGAGK	R	T	95.00%	37	M18: Oxidation	1014.7450	4	6.5	148	184	Yes
SEFKLELDDVTSNMEQIIK	K	A	95.00%	127	M14: Oxidation	1128.0700	2	9.4	1222	1240	Yes
SEFKLELDDVTSNMEQIIK	K	A	95.00%	57	M14: Oxidation	752.3806	3	6.4	1222	1240	Yes
SEFKLELDDVTSNMEQIIK	K	A	95.00%	146		1120.0710	2	7.3	1222	1240	Yes
SEFKLELDDVTSNMEQIIK	K	A	95.00%	61		747.0488	3	6.1	1222	1240	Yes
SKAEETQR	R	S	95.00%	37		474.7449	2	7.4	1261	1268	No
SLQSLLKDTQIQLDDAVR	K	A	95.00%	54		681.7121	3	5.8	1645	1662	Yes
SLSTELFK	R	L	95.00%	34		924.5075	1	3.4	1476	1483	Yes
SLSTELFK	R	L	95.00%	68		462.7583	2	4.8	1476	1483	Yes
SNAAAAALDK	R	K	95.00%	41		466.2493	2	6.2	1435	1444	Yes
SNAAAAALDKK	R	Q	95.00%	81		530.2949	2	2.0	1435	1445	Yes
SPGVMDNPLVMHQLR	K	C	95.00%	70	M11: Oxidation	855.4329	2	6.4	680	694	No
SPGVMDNPLVMHQLR	K	C	95.00%	59	M11: Oxidation	570.6229	3	3.6	680	694	No
SPGVMDNPLVMHQLR	K	C	95.00%	64	M5: Oxidation	855.4329	2	6.4	680	694	No
SPGVMDNPLVMHQLR	K	C	95.00%	64	M5: Oxidation	570.6230	3	3.7	680	694	No
SPGVMDNPLVMHQLR	K	C	95.00%	77	M5: Oxidation	863.4288	2	4.6	680	694	No
SPGVMDNPLVMHQLR	K	C	95.00%	69	M5: Oxidation	575.9540	3	2.8	680	694	No
SPGVMDNPLVMHQLR	K	C	95.00%	77	M5: Oxidation, M11: Oxidation	863.4288	2	4.6	680	694	No
SPGVMDNPLVMHQLR	K	C	95.00%	69	M5: Oxidation, M11: Oxidation	575.9540	3	2.8	680	694	No
SPGVMDNPLVMHQLR	K	C	95.00%	91		847.4324	2	3.0	680	694	No
SPGVMDNPLVMHQLR	K	C	95.00%	70		565.2923	3	5.5	680	694	No
SRVIFQLK	K	A	95.00%	30		495.8115	2	5.2	271	278	Yes
STHPHFVR	R	C	95.00%	32		490.7590	2	3.7	664	671	Yes
SVNDLTSQR	R	A	95.00%	58		510.2636	2	7.2	1269	1277	No
TEELEEAK	R	K	95.00%	33		948.4558	1	3.3	1383	1390	Yes
TEELEEAK	R	K	95.00%	39		474.7330	2	5.9	1383	1390	Yes
TEELEEAKK	R	K	95.00%	40		538.7797	2	3.5	1383	1391	Yes
TIHELEK	K	V	95.00%	31		435.2440	2	7.9	1522	1528	No
TKYETDAIQR	R	T	95.00%	69		612.8171	2	3.2	1373	1382	Yes
TKYETDAIQR	R	T	95.00%	55		408.8806	3	3.1	1373	1382	Yes
TKYETDAIQRTEELEEAK	R	K	95.00%	74		1077.5420	2	8.6	1373	1390	Yes
TKYETDAIQRTEELEEAK	R	K	95.00%	38		718.6949	3	5.7	1373	1390	Yes
TKYETDAIQRTEELEEAK	R	K	95.00%	31		539.2729	4	5.3	1373	1390	Yes
TLEDQMNEHR	R	S	95.00%	59	M6: Oxidation	644.7856	2	3.2	1251	1260	No
TLEDQMNEHR	R	S	95.00%	65		636.7876	2	2.3	1251	1260	No
TLEDQMNEHR	R	S	95.00%	33		424.8611	3	2.4	1251	1260	No
TVTVK	K	E	95.00%	29		547.3508	1	9.6	68	72	No
TVTVKEDQVMQQNPPK	K	F	95.00%	85	M10: Oxidation	929.4758	2	3.0	68	83	No
TVTVKEDQVMQQNPPK	K	F	95.00%	61	M10: Oxidation	619.9860	3	2.3	68	83	No
TVTVKEDQVMQQNPPK	K	F	95.00%	99		921.4797	2	4.4	68	83	No
TVTVKEDQVMQQNPPK	K	F	95.00%	50		614.6577	3	7.6	68	83	No
TVTVKEDQVMQQNPPKFDK	K	I	95.00%	48	M10: Oxidation	750.0507	3	3.6	68	86	No
TVTVKEDQVMQQNPPKFDK	K	I	95.00%	53		744.7178	3	2.0	68	86	No

				VGNEYVTK	K	G	95.00%	69		455.2391	2	2.3	406	413	Yes
				VGNEYVTKGQNVQQVIYATGALAK	K	A	95.00%	61		851.1287	3	7.3	406	429	No
				VIFQLK	R	A	95.00%	31		747.4807	1	5.0	273	278	Yes
				VIQYFAVIAAIGDR	R	S	95.00%	129		768.4374	2	5.4	191	204	No
				VIQYFAVIAAIGDR	R	S	95.00%	65		512.6281	3	6.6	191	204	No
				VKEMNERLEDEEEMNAELTAK	K	K	95.00%	69	M14: Oxidation	842.0610	3	5.1	919	939	Yes
				VKEMNERLEDEEEMNAELTAK	K	K	95.00%	40	M14: Oxidation	631.7974	4	4.5	919	939	Yes
				VKEMNERLEDEEEMNAELTAK	K	K	95.00%	63	M4: Oxidation	842.0579	3	1.5	919	939	Yes
				VKEMNERLEDEEEMNAELTAK	K	K	95.00%	37	M4: Oxidation	635.7957	4	3.9	919	939	Yes
				VKEMNERLEDEEEMNAELTAK	K	K	95.00%	50	M4: Oxidation, M14: Oxidation	847.3940	3	6.7	919	939	Yes
				VKEMNERLEDEEEMNAELTAK	K	K	95.00%	37	M4: Oxidation, M14: Oxidation	635.7957	4	3.9	919	939	Yes
				VKEMNERLEDEEEMNAELTAK	K	K	95.00%	57		836.7292	3	5.0	919	939	Yes
				VKLEQQVDDLEGSLEQEK	K	K	95.00%	157		1044.0380	2	8.1	1025	1042	Yes
				VKLEQQVDDLEGSLEQEK	K	K	95.00%	68		696.3594	3	5.5	1025	1042	Yes
				VKLEQQVDDLEGSLEQEKK	K	V	95.00%	136		1108.0860	2	8.3	1025	1043	Yes
				VKLEQQVDDLEGSLEQEKK	K	V	95.00%	87		739.0583	3	6.1	1025	1043	Yes
				VKLEQQVDDLEGSLEQEKK	K	V	95.00%	47		554.5450	4	4.7	1025	1043	Yes
				VKNLTEEMAGLDEIIAK	K	L	95.00%	77	M8: Oxidation	945.5076	2	9.3	975	991	Yes
				VKNLTEEMAGLDEIIAK	K	L	95.00%	32	M8: Oxidation	630.6721	3	5.7	975	991	Yes
				VKNLTEEMAGLDEIIAK	K	L	95.00%	121		937.5083	2	7.4	975	991	Yes
				VKNLTEEMAGLDEIIAK	K	L	95.00%	54		625.3402	3	5.4	975	991	Yes
				VKVGNEYVTK	R	G	95.00%	59		568.8224	2	4.7	404	413	Yes
				VQHELDEAEER	K	A	95.00%	52		677.8201	2	6.2	1899	1909	Yes
				VQHELDEAEER	K	A	95.00%	35		452.2151	3	4.1	1899	1909	Yes
				VQHELDEAEERADIAESQVNK	K	L	95.00%	119		1205.5860	2	6.5	1899	1919	Yes
				VQHELDEAEERADIAESQVNK	K	L	95.00%	67		804.0601	3	6.6	1899	1919	Yes
				VQHELDEAEERADIAESQVNK	K	L	95.00%	61		603.2958	4	4.6	1899	1919	Yes
				VQLLHSQNTSLINQK	R	K	95.00%	119		861.9822	2	3.7	1713	1727	Yes
				VQLLHSQNTSLINQK	R	K	95.00%	59		574.9913	3	4.7	1713	1727	Yes
				VQLLHSQNTSLINQKK	R	K	95.00%	37		617.6885	3	2.4	1713	1728	Yes
				VRELENELEAEQK	R	R	95.00%	86		793.9081	2	3.5	1819	1831	No
				VRELENELEAEQK	R	R	95.00%	42		529.6079	3	3.4	1819	1831	No
				VRELENELEAEQKR	R	N	95.00%	101		871.9578	2	2.3	1819	1832	No
				VRELENELEAEQKR	R	N	95.00%	78		581.6412	3	2.4	1819	1832	No
				VRELENELEAEQKR	R	N	95.00%	41		436.4836	4	4.0	1819	1832	No
				VTAETEYGK	K	T	95.00%	50		499.2475	2	2.9	59	67	No
				VVDSLQTSLDAETR	R	S	95.00%	138		767.3948	2	3.7	1593	1606	Yes
				VVDSLQTSLDAETR	R	S	95.00%	72		511.9321	3	2.9	1593	1606	Yes
				YEESQSELESSQK	K	E	95.00%	113		772.3474	2	6.9	1460	1472	Yes
				YETDAIQR	K	T	95.00%	34		498.2464	2	5.1	1375	1382	Yes
199	IPI00025974	CHMP4B	CHARGED MULTIVESICULAR BODY PROTEIN 4B.	EALENANTNTEVLK	R	N	95.00%	75		773.3981	2	8.0	94	107	No
				GGPTPQEAIQR	K	L	95.00%	48		577.3055	2	5.5	18	28	No
				KIEQELTAAK	K	K	95.00%	30		565.8277	2	4.6	46	55	No
				QLAQIDGTLSTIEFQR	K	E	95.00%	108		910.4897	2	8.7	78	93	No
				QLAQIDGTLSTIEFQR	K	E	95.00%	34		607.3263	3	4.2	78	93	No
200	IPI00026154; IPI00792916; IPI00829824	PRKCSH	GLUCOSIDASE 2 SUBUNIT BETA PRECURSOR.; GLUCOSIDASE II BETA SUBUNIT PRECURSOR.; HAPLN4 PROTEIN (FRAGMENT).	AQQEQELAADAFK	K	E	95.00%	61		724.8562	2	1.6	207	219	No
				ESLQQMAEVTR	R	E	95.00%	31	M6: Oxidation	654.3234	2	9.4	125	135	No
				LWEEQLAAAK	K	A	95.00%	42		579.8146	2	4.5	197	206	No
				SLEDQVEMLR	K	T	95.00%	60	M8: Oxidation	618.3043	2	5.3	168	177	No
201	IPI00026185	CAPZB	ISOFORM 1 OF F-ACTIN CAPPING PROTEIN SUBUNIT BETA.	SGSGTMNLGGSLTR	K	Q	95.00%	47	M6: Oxidation	677.3315	2	8.8	182	195	No
				STLNEIYFGK	R	T	95.00%	56		586.3090	2	8.6	226	235	No
202	IPI00026216	NPEPPS	PUROMYCIN-SENSITIVE AMINOPEPTIDASE.	AGIISTVEVLK	R	V	95.00%	80		565.3500	2	7.8	628	638	No
				AQELDALDNSHPIEVSVGHPSEVDEIFDAISYSK	R	G	95.00%	51		928.7051	4	8.2	407	440	No
				ATFDISLVVPK	K	D	95.00%	76		595.3480	2	4.0	198	208	No
				DAESIHQYLLQR	R	K	95.00%	85		736.8814	2	3.5	901	912	No
				DAESIHQYLLQR	R	K	95.00%	56		491.5903	3	3.7	901	912	No

				DLSLPPVDR	R	L	95.00%	33		506.2807	2	5.9	607	615	No
				DNWEELYNR	K	Y	95.00%	50		619.7789	2	4.6	833	841	No
				DVFSPIGER	K	L	95.00%	31		510.2636	2	3.0	681	689	No
				DYFNVPYPLPK	K	I	95.00%	71		676.8511	2	3.8	294	304	No
				ETALLIDPK	R	N	95.00%	27		999.5811	1	8.3	328	336	No
				ETALLIDPK	R	N	95.00%	43		500.2929	2	5.2	328	336	No
				FIKDNWEELYNR	K	Y	95.00%	56		813.9037	2	4.8	830	841	No
				FIKDNWEELYNR	K	Y	95.00%	44		542.9380	3	4.1	830	841	No
				HGDGTTLDIMLK	K	L	95.00%	62	M10: Oxidation	658.8336	2	5.4	754	765	No
				HGDGTTLDIMLK	K	L	95.00%	31	M10: Oxidation	439.5586	3	5.8	754	765	No
				IDFVGELNDK	K	M	95.00%	61		575.2957	2	3.6	146	155	No
				ILMDKPEMNVVLK	K	N	95.00%	48	M3: Oxidation, M8: Oxidation	781.4236	2	3.9	559	571	No
				KPYPDDENLVEVK	R	F	95.00%	59		773.3987	2	6.2	222	234	No
				LGLQNDLFSLAR	R	A	95.00%	95		673.8774	2	2.7	616	627	No
				LGWDPKPGEGHLDALLR	R	G	95.00%	49		625.3381	3	3.0	690	706	No
				LGWDPKPGEGHLDALLR	R	G	95.00%	33		469.2571	4	6.3	690	706	No
				LNLGTVGFYR	K	T	95.00%	76		570.3176	2	5.2	581	590	No
				LSVEGFAVDK	K	M	95.00%	53		1064.5720	1	8.3	854	863	No
				LSVEGFAVDK	K	M	95.00%	71		532.7872	2	3.3	854	863	No
				LSVEGFAVDKMAGEVK	K	A	95.00%	32	M11: Oxidation	848.4360	2	0.7	854	869	No
				MLHDYIGDKDFK	R	K	95.00%	41	M1: Oxidation	749.3592	2	3.8	447	458	No
				MLHDYIGDKDFKK	R	G	95.00%	44	M1: Oxidation	813.4092	2	6.5	447	459	No
				NAATEDLWESLENASGKPIAAVMNTWTK	K	Q	95.00%	89	M23: Oxidation	1021.8380	3	8.2	472	499	No
				QILSADLR	K	S	95.00%	47		458.2695	2	5.2	737	744	No
				QMGFPLIYVEAEQVEDDRLLR	K	L	95.00%	60	M2: Oxidation	846.4355	3	7.9	500	520	No
				SKYTTPSGEVR	R	Y	95.00%	30		612.8193	2	6.9	162	172	No
				SPVYLTVLK	R	H	95.00%	56		510.3117	2	1.4	745	753	No
				TQYSSAMLESLLPGIR	R	D	95.00%	88	M7: Oxidation	891.4648	2	6.1	591	606	No
				TQYSSAMLESLLPGIR	R	D	95.00%	63	M7: Oxidation	594.6458	3	6.2	591	606	No
				VALSNMNVIDR	R	K	95.00%	58	M6: Oxidation	624.3263	2	2.3	211	221	No
				VLGATLLPDLIQK	R	V	95.00%	117		690.9291	2	2.6	782	794	No
				VLGATLLPDLIQK	R	V	95.00%	51		460.9568	3	5.7	782	794	No
				VLTFALSEEVRPQDTVSVIGGVAGGSK	K	H	95.00%	59		906.1621	3	6.8	795	821	No
				VTLSFPSTLQTGTGTLK	K	I	95.00%	78		875.9905	2	7.8	129	145	No
				YAAVTQFEATDAR	R	R	95.00%	105		721.8515	2	2.5	173	185	No
				YAAVTQFEATDARR	R	A	95.00%	34		799.9039	2	4.5	173	186	No
				YQGGFLISR	R	L	95.00%	63		520.7816	2	2.3	842	850	No
203	IPI00026271	RPS14	40S RIBOSOMAL PROTEIN S14.	ELGITALHIK	K	L	95.00%	33		547.8379	2	9.4	87	96	No
				IEDVTPIPSDSTR	R	R	95.00%	42		715.3674	2	6.6	129	141	No
204	IPI00026272; IPI00031562; IPI00081836; IPI00102165; IPI00216456; IPI00216457; IPI00220855; IPI00255316; IPI00291764; IPI00339274; IPI00552873	H2AFJ; HIST1H2AB; HIST1H2AC; HIST1H2AD; HIST1H2AE; HIST1H2AG; HIST1H2AH; HIST1H2AI; HIST1H2AJ; HIST1H2AK; HIST1H2AL; HIST1H2AM; HIST2H2AA3; HIST2H2AA4; HIST2H2AC; HIST3H2A	HISTONE H2A TYPE 1-B.; HISTONE H2A TYPE 3.; HISTONE H2A TYPE 1-H.; H2A HISTONE FAMILY, MEMBER J ISOFORM 1.; HISTONE H2A TYPE 1-C.; HISTONE H2A TYPE 2-A.; H2A HISTONE FAMILY, MEMBER J ISOFORM 2.; HISTONE H2A TYPE 1-D.; HISTONE H2A TYPE 1.; HISTONE H2A TYPE 2-C.; HISTONE H2A TYPE 1-J.	AGLQFPVGR	R	V	95.00%	65		472.7710	2	2.3	22	30	No
				HLQLAIR	R	N	95.00%	31		425.7682	2	2.7	83	89	No
				NDEELNKLLGK	R	V	95.00%	38		636.8498	2	9.1	90	100	No
				VTIAQGGVLPNIQAVLLPK	K	K	95.00%	75		966.0951	2	6.6	101	119	No
				VTIAQGGVLPNIQAVLLPK	K	K	95.00%	54		644.3995	3	6.9	101	119	No
205	IPI00026314; IPI00646773	GSN	ISOFORM 1 OF GELSOLIN PRECURSOR.; ISOFORM 2 OF GELSOLIN PRECURSOR.	AGALNSNDAFVLK	K	T	95.00%	79		660.3563	2	6.7	534	546	No
				AGKEPGLQIWR	K	V	95.00%	36		418.9048	3	2.0	62	72	No
				AQPVQVAEGSEPDGFWEALGGK	R	A	95.00%	108		1136.5570	2	7.7	627	648	No
				AQPVQVAEGSEPDGFWEALGGK	R	A	95.00%	65		758.0375	3	3.5	627	648	No

				DPDQTDGLGLSYLSSHIANVER	R	V	95.00%	59		796.3912	3	4.1	398	419	No
				DSQEEEKTEALTSAK	K	R	95.00%	77		833.4009	2	7.1	714	728	No
				DSQEEEKTEALTSAK	K	R	95.00%	39		555.9323	3	-0.4	714	728	No
				EVQGFESATFLGYFK	R	S	95.00%	109		861.9281	2	6.0	148	162	No
				HVVPNEVVVQR	K	L	95.00%	37		638.3663	2	5.8	127	137	No
				HVVPNEVVVQR	K	L	95.00%	37		425.9117	3	1.6	178	188	No
				NWRDPDQTDGLGLSYLSSHIANVER	K	V	95.00%	61		711.6028	4	5.8	395	419	No
				PALPAGTEDTAKEDAANRK	K	L	95.00%	40		489.5034	4	3.2	227	245	No
				QTQVSVLPEGGETPLFK	K	Q	95.00%	92		915.4939	2	8.1	374	390	No
				QTQVSVLPEGGETPLFK	K	Q	95.00%	42		610.6624	3	3.5	374	390	No
				TGAQELLR	K	V	95.00%	48		444.2542	2	6.0	565	572	No
				TPSAAYLWVGTGASEAEK	K	T	95.00%	110		919.4580	2	5.9	598	615	No
				VHVSEEGTEPEAMLQVLGPK	R	P	95.00%	35	M13: Oxidation	722.6987	3	2.4	258	277	No
				VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK	R	E	95.00%	30	M13: Oxidation	830.1764	4	7.4	207	238	No
				VPFDAATLHTSTAMAAQHGMDDDGTGQK	R	Q	95.00%	55	M14: Oxidation, M20: Oxidation	969.1024	3	6.1	420	447	No
				VPVDPATYGQFYGGDSYIILYNYR	K	H	95.00%	67		924.4556	3	5.7	458	481	No
				YIETDPANR	R	D	95.00%	31		539.7648	2	4.3	679	687	No
206	IPI00026538		SH3BGR	SH3 DOMAIN-BINDING GLUTAMIC ACID-RICH PROTEIN.	EGSEDAGNLPEAQEK	K	N	95.00%	75		787.3604	2	9.2	183	197	No
				ELDIAGDEDNRR	K	W	95.00%	34		701.8375	2	7.7	99	110	No
				KQQEVVGFLEANKIDFK	K	E	95.00%	30		665.0334	3	4.3	82	98	No
				VFVATSSGSIAIR	K	K	95.00%	74		654.3755	2	8.3	68	80	No
207	IPI00026665	QARS	GLUTAMINYL-TRNA SYNTHETASE.	ATGILLYGLASR	K	L	95.00%	72		617.8670	2	8.2	69	80	No
				EAATQAQQTLGSTIDK	R	A	95.00%	98		831.4259	2	5.5	53	68	No
				HTGYVIELQHVVK	R	G	95.00%	29		508.2865	3	3.6	658	670	No
				ILQLVATGAVR	K	D	95.00%	36		570.8636	2	7.6	517	527	No
				KIHTEPQLSAALEYVR	K	S	95.00%	40		619.0100	3	3.5	98	113	No
				LAWGQPVGLR	R	H	95.00%	42		548.8203	2	5.2	648	657	No
				LFTLTALR	R	R	95.00%	46		467.7921	2	4.0	534	541	No
				SHPLDPIDTVDFER	R	E	95.00%	44		547.6056	3	5.6	114	127	No
				SLDIQVPNFPADETK	K	G	95.00%	51		837.4274	2	4.8	605	619	No
208	IPI00026904	ADSL	ISOFORM 1 OF ADENYLOSUCCINATE LYASE.	AFIITGQTYTR	R	K	95.00%	73		635.8461	2	3.7	235	245	No
				FLEEEVYPLLKPYESVMK	R	V	95.00%	57	M17: Oxidation	744.0563	3	8.0	460	477	No
				HLMTLVMDPLQTASVQWFER	R	T	95.00%	48	M3: Oxidation, M7: Oxidation	812.0755	3	8.5	310	329	No
				IQVDAYFSPIHSQLDHLLDPSSFTGR	R	A	95.00%	56		981.8359	3	9.5	427	452	No
				IRQELPFMATENIIMAMVK	R	A	95.00%	65	M8: Oxidation, M15: Oxidation, M17: Oxidation	761.7288	3	6.7	373	391	No
				KVDIEVLSVLASLGASVHK	R	I	95.00%	75		655.7227	3	7.1	246	264	No
				KVDIEVLSVLASLGASVHK	R	I	95.00%	50		492.0431	4	5.3	246	264	No
				LLANLKEMEEPFEK	R	Q	95.00%	39	M8: Oxidation	853.9447	2	8.2	271	284	No
				LLANLKEMEEPFEK	R	Q	95.00%	33	M8: Oxidation	569.6295	3	3.1	271	284	No
				NALDLLLPK	R	L	95.00%	66		498.8114	2	5.5	126	134	No
				SNLENIDFK	K	M	95.00%	52		540.2734	2	1.5	67	75	No
				VLSQQAASVVK	R	Q	95.00%	82		565.3350	2	3.5	405	415	No
209	IPI00026964	UQCRFS1	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIALPRECURSOR.	EIEQEAAVELSQLR	K	D	95.00%	95		807.9277	2	8.5	183	196	No
				EIEQEAAVELSQLR	K	D	95.00%	48		538.9542	3	8.0	183	196	No
				GKPLFVR	R	H	95.00%	25		408.7602	2	3.6	171	177	No
				NAVTQFVSSMSASADVLALAK	K	I	95.00%	77	M10: Oxidation	709.3713	3	8.5	131	151	No
				NAVTQFVSSMSASADVLALAK	K	I	95.00%	64		704.0403	3	9.5	131	151	No
				RLEVLDSTK	R	S	95.00%	46		530.8086	2	8.5	93	101	No
				SGPFAPVLSATSR	R	G	95.00%	75		645.3519	2	8.2	8	20	No
				VPDFSEYR	K	R	95.00%	39		506.7457	2	9.6	85	92	No
210	IPI00027107	TUFM	TU TRANSLATION ELONGATION FACTOR, MITOCHONDRIAL.	ADAVQDSEMVELVELEIR	K	E	95.00%	77	M9: Oxidation	1031.5130	2	7.7	186	203	No
				ADAVQDSEMVELVELEIR	K	E	95.00%	48	M9: Oxidation	688.0081	3	3.4	186	203	No
				AEAGDNLGALVR	R	G	95.00%	114		593.3166	2	2.1	319	330	No
				DKPHVNVGTIGHVDHGK	R	T	95.00%	65		905.4784	2	6.9	57	73	No
				DKPHVNVGTIGHVDHGK	R	T	95.00%	43		603.9855	3	2.4	57	73	No
				DLEKPFLLPVEAVYSVPGR	R	G	95.00%	50		1065.0950	2	7.8	256	274	No
				DLEKPFLLPVEAVYSVPGR	R	G	95.00%	34		710.3994	3	8.4	256	274	No

				EHLLLAR	R	Q	95.00%	31		426.2608	2	3.9	166	172	No
				ELLTEFGYK	R	G	95.00%	50		550.2902	2	4.4	204	212	No
				GITINAAHVEYSTAAR	R	H	95.00%	111		837.4401	2	6.7	108	123	No
				GITINAAHVEYSTAAR	R	H	95.00%	60		558.6275	3	3.4	108	123	No
				GLVMVKPGSIKPHQK	R	V	95.00%	50	M4: Oxidation	817.9752	2	0.5	340	354	No
				GLVMVKPGSIKPHQK	R	V	95.00%	25	M4: Oxidation	545.6544	3	3.4	340	354	No
				GTVVTGTLER	R	G	95.00%	52		516.7916	2	6.1	275	284	No
				IILPPEKELAMPGEDLK	R	F	95.00%	41	M11: Oxidation	637.0228	3	8.8	392	408	No
				KYEEIDNAPEER	K	A	95.00%	76		746.8543	2	5.8	94	105	No
				KYEEIDNAPEER	K	A	95.00%	34		498.2376	3	3.4	94	105	No
				LLDAVDTYIPVPAR	K	D	95.00%	88		771.9351	2	5.9	242	255	No
				QIGVEHVVVYVNK	R	A	95.00%	84		742.4208	2	4.4	173	185	No
				QIGVEHVVVYVNK	R	A	95.00%	29		495.2830	3	4.2	173	185	No
				TIGTGLVTNTLAMTEEEK	R	N	95.00%	97	M13: Oxidation	962.4916	2	8.6	433	450	No
				TTLTAAITK	K	I	95.00%	23		460.2793	2	4.5	74	82	No
				TVVTGIEMFHK	R	S	95.00%	57	M8: Oxidation	639.3346	2	3.8	304	314	No
				YEEIDNAPEER	K	A	95.00%	34		682.8063	2	5.5	95	105	No
211	IPI00027146	GLUD2	GLUTAMATE DEHYDROGENASE 2, MITOCHONDRIAL PRECURSOR.	MVEGFFDR	K	G	95.00%	35	M1: Oxidation	508.7330	2	6.9	69	76	Yes
				YSTDVSVDEVK	R	A	95.00%	39		621.3024	2	5.4	152	162	Yes
212	IPI00027230	HSP90B1	ENDOPLASMIN PRECURSOR.	EEASDYLELDTIK	K	N	95.00%	76		763.3747	2	9.2	253	265	No
				ELISNASDALDK	R	I	95.00%	57		638.3295	2	6.1	103	114	Yes
				ELISNASDALDKIR	R	L	95.00%	83		772.9214	2	4.1	103	116	No
				FAFQAEVNR	K	M	95.00%	42		541.2779	2	4.5	76	84	No
				FQSSHHPTDITSLDQYVER	R	M	95.00%	58		754.0334	3	9.5	512	530	No
				GVVDSDDLPLNVSR	K	E	95.00%	91		743.3837	2	3.1	435	448	No
				LIINSLYK	K	N	95.00%	24		482.3006	2	5.6	88	95	No
				NLLHVTDTGVGMTR	K	E	95.00%	54	M12: Oxidation	765.3953	2	5.3	143	156	No
				SILFVPTSAPR	K	G	95.00%	57		594.3465	2	5.2	385	395	No
213	IPI00027252	PHB2	PROHIBITIN-2.	AQVSLLIR	R	R	95.00%	45		450.2911	2	7.2	158	165	No
				DLQMVNISLR	K	V	95.00%	34	M4: Oxidation	602.8278	2	9.7	98	107	No
				ESVFTVEGGHR	R	A	95.00%	53		609.3030	2	5.4	38	48	No
				FNASQLITQR	K	A	95.00%	65		589.3260	2	9.4	148	157	No
				IGGVQQDTILAEGLHFR	R	I	95.00%	83		618.6728	3	8.2	55	71	No
				IVQAEGEAEAAK	K	M	95.00%	97		608.3185	2	5.7	225	236	No
				LGLDYEER	R	V	95.00%	41		497.7501	2	7.8	124	131	No
				LLLGAGAVAYGVR	K	E	95.00%	60		630.3833	2	8.8	25	37	No
				MLGEALSKNPGYIK	K	L	95.00%	56	M1: Oxidation	768.9159	2	9.2	237	250	No
				QKIVQAEGEAEAAK	R	M	95.00%	59		736.3964	2	6.2	223	236	No
				VLPSIVNEVLK	R	S	95.00%	32		605.8784	2	6.5	132	142	No
				VLSRPNAQELPSMYQR	R	L	95.00%	35	M13: Oxidation	952.9957	2	9.5	108	123	No
				VLSRPNAQELPSMYQR	R	L	95.00%	30	M13: Oxidation	635.6640	3	5.7	108	123	No
214	IPI00027255	MYL6; MYL6B	MYOSIN LIGHT POLYPEPTIDE 6B.	AEPAVPQAPQK	K	T	95.00%	41		568.3130	2	6.0	36	46	No
				ALGQNPTNAEVLK	R	V	95.00%	56		677.8733	2	4.1	95	107	No
				EAFELFDR	K	V	95.00%	54		513.7520	2	6.3	71	78	No
				GQGTYEDYLEGFR	R	V	95.00%	77		767.8478	2	4.1	139	151	No
				HVLTTLGEK	R	M	95.00%	51		499.2902	2	4.4	168	176	No
				KPAGPSISKPAAK	K	P	95.00%	32		417.9218	3	5.8	11	23	No
				RVDFETFLPMLQAVAK	R	N	95.00%	47	M10: Oxidation	627.6759	3	9.3	121	136	No
				RVDFETFLPMLQAVAK	R	N	95.00%	56		933.0126	2	9.4	121	136	No
				RVDFETFLPMLQAVAK	R	N	95.00%	32		622.3420	3	5.8	121	136	No
				TKAEPAVPQAPQK	K	T	95.00%	34		682.8859	2	7.3	34	46	No
				TQEPPVDLSK	K	V	95.00%	32		1113.5890	1	8.8	47	56	No
				TQEPPVDLSK	K	V	95.00%	51		557.2965	2	5.2	47	56	No
215	IPI00027350; IPI00375400	PRDX2	PEROXIREDOXIN-2.; 16 KDA PROTEIN.	ATAVVDGAFK	K	E	95.00%	53		978.5338	1	7.9	17	26	No
				ATAVVDGAFK	K	E	95.00%	70		489.7701	2	6.5	17	26	No
				ATAVVDGAFKEVK	K	L	95.00%	28		667.8749	2	7.5	17	29	No
				ATAVVDGAFKEVK	K	L	95.00%	31		445.5846	3	4.7	17	29	No
				EGGLGPLNIPLLADVTR	K	R	95.00%	96		867.9982	2	7.4	93	109	No
				EGGLGPLNIPLLADVTR	K	R	95.00%	71		579.0018	3	8.0	93	109	No
				GLFIIDGK	R	G	95.00%	35		862.5106	1	7.5	128	135	No
				GLFIIDGK	R	G	95.00%	33		431.7568	2	1.9	128	135	No
				IGKPAPDFK	R	A	95.00%	35		972.5594	1	7.5	8	16	No
				IGKPAPDFK	R	A	95.00%	39		486.7812	2	2.6	8	16	No
				KEGGLGPLNIPLLADVTR	R	R	95.00%	97		932.0461	2	7.3	92	109	No
				KEGGLGPLNIPLLADVTR	R	R	95.00%	49		621.7010	3	8.8	42	59	No
				KEGGLGPLNIPLLADVTRR	R	L	95.00%	37		673.7346	3	8.1	92	110	No
				LSEDYGVLK	R	T	95.00%	49		512.2748	2	5.2	61	69	No
				PGSDTIKPNVDDSK	K	E	95.00%	33		491.5830	3	6.6	128	141	No
				QITVNDLPVGR	R	S	95.00%	73		606.3436	2	3.6	140	150	Yes

				QITVNDLPVGR	R	S	95.00%	28		404.5660	3	6.1	90	100	Yes
				RLSEDYGVLK	R	T	95.00%	36		590.3271	2	7.6	110	119	No
				TDEGIAYR	K	G	95.00%	44		462.7273	2	4.3	120	127	No
216	IPI00027448	ATP5L	ATP SYNTHASE SUBUNIT G, MITOCHONDRIAL.	GIIGYDV	R	-	95.00%	27		736.3925	1	5.8	97	103	No
				IVNSAQTGSFK	K	Q	95.00%	40		1151.6170	1	9.5	56	66	No
				IVNSAQTGSFK	K	Q	95.00%	85		576.3100	2	5.2	56	66	No
				KIVNSAQTGSFK	K	Q	95.00%	69		640.3586	2	6.5	55	66	No
				LATFWYYAK	R	V	95.00%	56		581.8049	2	7.0	27	35	No
				TPALVNAAVTYSK	K	P	95.00%	76		667.8753	2	8.0	12	24	No
				TPALVNAAVTYSKPR	K	L	95.00%	102		794.4506	2	4.6	12	26	No
				TPALVNAAVTYSKPR	K	L	95.00%	75		529.9712	3	7.6	12	26	No
				VELVPPTPAEIPR	K	A	95.00%	86		709.4097	2	4.1	36	48	No
217	IPI00027487	CKM	CREATINE KINASE M-TYPE.	AVEKLSVEALNSLTGEFK	R	G	95.00%	46		645.6905	3	6.1	153	170	No
				AVEKLSVEALNSLTGEFKGK	R	Y	95.00%	63		530.7983	4	4.5	153	172	No
				DWPDAR	R	G	95.00%	44		759.3495	1	8.9	210	215	Yes
				ELFDPIISDR	K	H	95.00%	57		1204.6290	1	5.9	87	96	No
				ELFDPIISDR	K	H	95.00%	65		602.8179	2	5.3	87	96	No
				EQQQLIDDHFLFDK	K	P	95.00%	92		888.4376	2	3.8	183	196	No
				EQQQLIDDHFLFDK	K	P	95.00%	34		592.6297	3	7.1	183	196	No
				EQQQLIDDHFLFDKPVSPLLLASGMAR	K	D	95.00%	88	M25: Oxidation	1028.8750	3	8.5	183	209	No
				EQQQLIDDHFLFDKPVSPLLLASGMAR	K	D	95.00%	55	M25: Oxidation	771.9068	4	6.8	183	209	No
				EQQQLIDDHFLFDKPVSPLLLASGMAR	K	D	95.00%	90		1023.5450	3	9.8	183	209	No
				EQQQLIDDHFLFDKPVSPLLLASGMAR	K	D	95.00%	29		767.9084	4	7.3	183	209	No
				FEEILTR	K	L	95.00%	44		907.4909	1	2.2	308	314	No
				FEEILTR	K	L	95.00%	46		454.2489	2	1.2	308	314	No
				FKLNYKPEEEYPDLSK	K	H	95.00%	94		1000.5140	2	8.9	10	25	No
				FKLNYKPEEEYPDLSK	K	H	95.00%	52		667.3423	3	4.8	10	25	No
				GGDDLDPNYVLSSR	K	V	95.00%	118		754.3567	2	1.6	117	130	No
				GQSIDDMIPAQK	K	-	95.00%	43	M7: Oxidation	1318.6410	1	7.5	370	381	No
				GQSIDDMIPAQK	K	-	95.00%	95	M7: Oxidation	659.8216	2	3.0	370	381	No
				GQSIDDMIPAQK	K	-	95.00%	87		651.8228	2	0.9	370	381	No
				GTGGVDTAAVGSVFDVSNADR	R	L	95.00%	76	S12: Phospho	1037.9630	2	4.8	321	341	No
				GTGGVDTAAVGSVFDVSNADR	R	L	95.00%	74	T2: Phospho	1037.9630	2	4.8	321	341	No
				GTGGVDTAAVGSVFDVSNADR	R	L	95.00%	76	T7: Phospho	1037.9660	2	7.4	321	341	No
				GTGGVDTAAVGSVFDVSNADR	R	L	95.00%	170		997.9805	2	5.7	321	341	No
				GTGGVDTAAVGSVFDVSNADR	R	L	95.00%	95		665.6560	3	5.3	321	341	No
				GTGGVDTAAVGSVFDVSNADRLGSSEVEQVQLVVDGVK	R	L	95.00%	148		1254.6440	3	8.9	321	358	No
				HGGYKPTDK	R	H	95.00%	54		501.7590	2	9.1	97	105	No
				HKTDLNHENLK	K	G	95.00%	40		674.8575	2	7.2	106	116	No
				HKTDLNHENLK	K	G	95.00%	46		450.2399	3	4.9	106	116	No
				HKTDLNHENLKGGDDLDPNYVLSSR	K	V	95.00%	92		946.4742	3	8.9	106	130	No
				HKTDLNHENLKGGDDLDPNYVLSSR	K	V	95.00%	44		710.1038	4	3.5	106	130	No
				HPKFEEILTR	K	L	95.00%	43		635.3544	2	4.1	305	314	No
				HPKFEEILTR	K	L	95.00%	68		423.9051	3	3.2	305	314	No
				IEEIFK	K	K	95.00%	44		778.4367	1	1.9	260	265	No
				IEEIFKK	K	A	95.00%	36		906.5304	1	0.2	260	266	No
				IEEIFKK	K	A	95.00%	49		453.7707	2	3.8	260	266	No
				LAHLSK	K	H	95.00%	24		668.4150	1	8.1	299	304	No
				LEKGQSIDDMIPAQK	K	-	95.00%	58	M10: Oxidation	844.9381	2	9.0	367	381	No
				LGSSEVEQVQLVVDGVK	R	L	95.00%	134		893.4904	2	7.3	342	358	No
				LGSSEVEQVQLVVDGVK	R	L	95.00%	105		595.9958	3	6.8	342	358	No
				LMVEMEK	K	K	95.00%	34	M2: Oxidation	895.4282	1	1.3	359	365	No
				LMVEMEK	K	K	95.00%	41	M2: Oxidation	448.2198	2	5.3	359	365	No
				LMVEMEK	K	K	95.00%	40	M2: Oxidation	456.2175	2	5.8	359	365	No
				LMVEMEK	K	K	95.00%	40	M2: Oxidation, M5: Oxidation	456.2175	2	5.8	359	365	No
				LMVEMEK	K	K	95.00%	30	M5: Oxidation	895.4301	1	3.5	359	365	No
				LMVEMEK	K	K	95.00%	43	M5: Oxidation	448.2186	2	2.7	359	365	No

				LMVEMEK	K	K	95.00%	41		879.4347	1	3.0	359	365	No
				LMVEMEK	K	K	95.00%	42		440.2214	2	3.3	359	365	No
				LNYKPEEEYPDLSK	K	H	95.00%	89		862.9278	2	5.4	12	25	No
				LNYKPEEEYPDLSK	K	H	95.00%	60		575.6235	3	9.6	12	25	No
				LSVEALNSLTGEFK	K	G	95.00%	41	S8: Phospho	794.3953	2	9.9	157	170	No
				LSVEALNSLTGEFK	K	G	95.00%	130		754.4084	2	5.5	157	170	No
				LSVEALNSLTGEFK	K	G	95.00%	47		503.2740	3	3.8	157	170	No
				LSVEALNSLTGEFKGK	K	Y	95.00%	91		846.9675	2	5.9	157	172	No
				LSVEALNSLTGEFKGK	K	Y	95.00%	46		564.9821	3	7.9	157	172	No
				LSVEALNSLTGEFKGKYYPLK	K	S	95.00%	57		786.4371	3	8.6	157	177	No
				PFGNTHNK	M	F	95.00%	46		457.7312	2	6.8	2	9	No
				PVSPLLLASGMAR	K	D	95.00%	77	M11: Oxidation	664.3789	2	6.9	197	209	Yes
				PVSPLLLASGMAR	K	D	95.00%	88		656.3820	2	7.7	197	209	Yes
				RAVEKLSVEALNSLTGEFK	R	G	95.00%	59		697.7241	3	5.5	152	170	No
				RGTGGVDTAAVGSVFDVSNADR	K	L	95.00%	130		1076.0330	2	6.8	320	341	No
				RGTGGVDTAAVGSVFDVSNADR	K	L	95.00%	96		717.6882	3	2.7	320	341	No
				SFLVWVNEEDHLR	K	V	95.00%	100		822.4178	2	5.7	224	236	No
				SFLVWVNEEDHLR	K	V	95.00%	62		548.6142	3	5.3	224	236	No
				SMTEKEQQQLIDDHFLFDK	K	P	95.00%	50	M2: Oxidation	790.0471	3	5.1	178	196	No
				SMTEKEQQQLIDDHFLFDKPVSPLLLASGMAR	K	D	95.00%	36	M2: Oxidation	915.9737	4	8.4	178	209	No
				SMTEKEQQQLIDDHFLFDKPVSPLLLASGMAR	K	D	95.00%	58	M2: Oxidation	1226.2950	3	9.4	178	209	No
				SMTEKEQQQLIDDHFLFDKPVSPLLLASGMAR	K	D	95.00%	47	M2: Oxidation	919.9714	4	7.2	178	209	No
				SMTEKEQQQLIDDHFLFDKPVSPLLLASGMAR	K	D	95.00%	43	M2: Oxidation	736.1796	5	8.6	178	209	No
				SMTEKEQQQLIDDHFLFDKPVSPLLLASGMAR	K	D	95.00%	58	M2: Oxidation, M30: Oxidation	1226.2950	3	9.4	178	209	No
				SMTEKEQQQLIDDHFLFDKPVSPLLLASGMAR	K	D	95.00%	47	M2: Oxidation, M30: Oxidation	919.9714	4	7.2	178	209	No
				SMTEKEQQQLIDDHFLFDKPVSPLLLASGMAR	K	D	95.00%	43	M2: Oxidation, M30: Oxidation	736.1796	5	8.6	178	209	No
				SMTEKEQQQLIDDHFLFDKPVSPLLLASGMAR	K	D	95.00%	37	M30: Oxidation	915.9711	4	5.6	178	209	No
				SMTEKEQQQLIDDHFLFDKPVSPLLLASGMAR	K	D	95.00%	39		911.9637	4	-4.0	178	209	No
				TDLNHENLK	K	G	95.00%	67		542.2785	2	5.1	108	116	No
				TDLNHENLKGGDDLDPNYVLSSR	K	V	95.00%	72		1286.6250	2	5.3	108	130	No
				TDLNHENLKGGDDLDPNYVLSSR	K	V	95.00%	67		858.0884	3	8.4	108	130	No
				VLTLELYK	K	K	95.00%	36		978.5928	1	5.2	33	40	No
				VLTLELYK	K	K	95.00%	71		489.7987	2	2.0	33	40	No
				VLTLELYKK	K	L	95.00%	24		1106.6840	1	0.8	33	41	No
				VLTLELYKK	K	L	95.00%	57		553.8461	2	1.4	33	41	No
218	IPI00027497	GPI	GLUCOSE-6-PHOSPHATE ISOMERASE.	AVLHVALR	R	N	95.00%	32		878.5596	1	2.3	97	104	No
				AVLHVALR	R	N	95.00%	59		439.7833	2	1.3	97	104	No
				DVMPEVNK	K	V	95.00%	28	M3: Oxidation	474.2321	2	5.8	117	124	No
				EWFLQAAK	K	D	95.00%	49		992.5262	1	5.7	227	234	No
				EWFLQAAK	K	D	95.00%	68		496.7655	2	2.6	227	234	No
				FAAYFQQGDMESNGK	R	Y	95.00%	94	M10: Oxidation	854.8713	2	4.1	348	362	No
				HFVALSTNTTK	K	V	95.00%	71		1218.6540	1	4.7	242	252	No
				HFVALSTNTTK	K	V	95.00%	72		609.8294	2	2.2	242	252	No
				ILLANFLAQTEALMR	K	G	95.00%	108	M14: Oxidation	860.4825	2	6.0	424	438	No
				ILLANFLAQTEALMR	K	G	95.00%	84	M14: Oxidation	573.9922	3	8.2	424	438	No
				ILLANFLAQTEALMR	K	G	95.00%	104		852.4860	2	7.1	424	438	No
				ILLANFLAQTEALMR	K	G	95.00%	74		568.6587	3	4.9	424	438	No
				INYTEGR	K	A	95.00%	40		426.7170	2	5.5	90	96	No
				KIEPELDGSAQVTSHDASTNGLINFIK	K	Q	95.00%	67		962.1692	3	8.0	524	550	No
				KIEPELDGSAQVTSHDASTNGLINFIK	K	Q	95.00%	48		721.8798	4	9.2	524	550	No
				LQQWYR	K	E	95.00%	33		447.2375	2	4.2	13	18	No
				LTPFMLGALVAMYEHK	K	I	95.00%	51	M5: Oxidation, M12: Oxidation	926.9774	2	6.9	482	497	No
				LTPFMLGALVAMYEHK	K	I	95.00%	41	M5: Oxidation, M12: Oxidation	618.3197	3	5.0	482	497	No

				LTPFMLGALVAMYEHK	K	I	95.00%	86		910.9822	2	6.7	482	497	No
				MLVDLAK	R	S	95.00%	31	M1: Oxidation	805.4500	1	0.7	67	73	No
				MLVDLAK	R	S	95.00%	37	M1: Oxidation	403.2295	2	2.0	67	73	No
				NLVTEDVMR	K	M	95.00%	33	M8: Oxidation	1092.5440	1	7.6	58	66	No
				NLVTEDVMR	K	M	95.00%	71	M8: Oxidation	546.7750	2	5.6	58	66	No
				NLVTEDVMR	K	M	95.00%	43		538.7761	2	3.1	58	66	No
				SNTPILVDGK	R	D	95.00%	36		1043.5800	1	5.5	107	116	No
				SNTPILVDGK	R	D	95.00%	67		522.2918	2	1.8	107	116	No
				SNTPILVDGKDVMPEVNK	R	V	95.00%	88	M13: Oxidation	986.5128	2	5.9	107	124	No
				SNTPILVDGKDVMPEVNK	R	V	95.00%	62	M13: Oxidation	658.0087	3	2.1	107	124	No
				SNTPILVDGKDVMPEVNK	R	V	95.00%	69		978.5147	2	5.2	107	124	No
				SPEDLER	K	L	95.00%	43		423.2082	2	9.4	455	461	No
				TFTTQETITNAETAK	K	E	95.00%	134		828.4122	2	2.1	212	226	No
				TFTTQETITNAETAK	K	E	95.00%	47		552.6110	3	2.7	212	226	No
				TFTTQETITNAETAKEWFLQAAK	K	D	95.00%	65		877.1159	3	6.4	212	234	No
				TITDVINIGIGGSDLGPLMVTEALKPYSSGGPR	K	V	95.00%	122	M19: Oxidation	1115.5950	3	8.8	148	180	No
				TITDVINIGIGGSDLGPLMVTEALKPYSSGGPR	K	V	95.00%	30	M19: Oxidation	836.9495	4	9.9	148	180	No
				TITDVINIGIGGSDLGPLMVTEALKPYSSGGPR	K	V	95.00%	34		1110.2640	3	8.9	148	180	No
				TLAQLNPESSLFIIASK	K	T	95.00%	137		916.5075	2	-5.4	195	211	No
				TLAQLNPESSLFIIASK	K	T	95.00%	81		611.3486	3	7.1	195	211	No
				VFEGNRPTNSIVFTK	K	L	95.00%	57		854.9586	2	4.1	467	481	No
				VFEGNRPTNSIVFTK	K	L	95.00%	44		570.3085	3	4.4	467	481	No
				VKEFGIDPQNMFEFWDWVGGR	K	Y	95.00%	64	M11: Oxidation	858.4082	3	6.5	253	273	No
				VWYVSNIDGTHIAK	R	T	95.00%	88		801.9222	2	5.3	181	194	No
				VWYVSNIDGTHIAK	R	T	95.00%	49		534.9507	3	5.3	181	194	No
219	IPI00027547	DCD	DERMCIDIN PRECURSOR.	DAVEDLESVGK	K	G	95.00%	41		1161.5740	1	8.1	86	96	No
				DAVEDLESVGK	K	G	95.00%	62		581.2897	2	6.5	86	96	No
				ENAGEDPGLAR	K	Q	95.00%	72		564.7712	2	5.2	43	53	No
				LGKDAVEDLESVGK	K	G	95.00%	49		487.2620	3	3.8	83	96	No
220	IPI00027809; IPI00181738; IPI00218862; IPI00748557	PPP3CB	PROTEIN PHOSPHATASE 3 (FORMERLY 2B), CATALYTIC SUBUNIT, BETA ISOFORM.; ISOFORM 3 OF SERINE/THREONINE-PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNITBETA ISOFORM.; ISOFORM 2 OF SERINE/THREONINE-PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNITBETA ISOFORM.; SERINE/THREONINE PROTEIN PHOSPHATASE.	GLTPTGMLPSGVLAGGR	K	Q	95.00%	75	M7: Oxidation	800.4377	2	9.1	435	451	No
				HLTEYFTFK	R	Q	95.00%	39		593.3068	2	9.6	164	172	No
				IINEGAAILR	R	R	95.00%	57		535.3246	2	3.9	73	82	No
				LFEVGGSPANTR	K	Y	95.00%	69		624.3240	2	1.5	110	121	Yes
				LTSEEVFDLDGIPR	R	V	95.00%	79		795.9076	2	3.5	38	51	No
				QTLQSATVEAIEAEK	R	A	95.00%	36		809.4277	2	8.5	452	466	No
221	IPI00028004; IPI00788896; IPI00789577	PSMB3	PROTEASOME SUBUNIT BETA TYPE 3.; 13 KDA PROTEIN.; 12 KDA PROTEIN.	FGIQAQMVTTDFQK	R	I	95.00%	82	M7: Oxidation	815.4073	2	7.4	28	41	No
				LNLYELK	R	E	95.00%	32		446.7625	2	3.1	71	77	No
				LYIGLAGLATDVQTVAQR	R	L	95.00%	80		630.3611	3	9.6	49	66	No
222	IPI00028520; IPI00221298	NDUFV1	ISOFORM 1 OF NADH DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN 1,MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF NADH DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN 1,MITOCHONDRIAL PRECURSOR.	AAYIYIR	R	G	95.00%	46		435.2495	2	3.1	153	159	No
				EAYEAGLIGK	R	N	95.00%	51		1050.5520	1	4.6	175	184	No
				EAYEAGLIGK	R	N	95.00%	49		525.7791	2	2.9	175	184	No
				GDARPAEIDSLWEISK	R	Q	95.00%	33		893.9592	2	7.2	402	417	No
				GDARPAEIDSLWEISK	R	Q	95.00%	59		596.3077	3	5.5	402	417	No
				GEFYNEASNLQVAIR	R	E	95.00%	97		855.9335	2	8.3	160	174	No
				GEFYNEASNLQVAIR	R	E	95.00%	57		570.9564	3	5.0	160	174	No
				GGAGFPTGLK	R	W	95.00%	40		452.7507	2	4.6	89	98	No
				GGTWFAGFGR	R	E	95.00%	56		528.2587	2	3.0	258	267	No
				GPDWILGEIK	K	T	95.00%	55		564.3106	2	2.6	72	81	No
				HFRPELEER	R	M	95.00%	54		606.8124	2	3.5	441	449	No
				HFRPELEER	R	M	95.00%	43		404.8772	3	2.8	441	449	No
				IFTNLYGR	R	H	95.00%	42		492.2717	2	4.2	41	48	No

				LIEFYK	R	H	95.00%	28		406.7328	2	2.4	370	375	No
				PAEIDSLWEISK	R	Q	95.00%	86		694.3638	2	6.3	406	417	No
				TSFGSLKDEDR	K	I	95.00%	52		627.8049	2	4.2	30	40	No
223	IPI00029111	DPYSL3	DPYSL3 PROTEIN.	AALAGGTTMIIDHVVPEPESSLT EAYEK	K	W	95.00%	40	M9: Oxidation	982.4958	3	9.0	209	236	No
				DNFTAIPEGTNGVEER	K	M	95.00%	67		874.9136	2	5.8	460	475	No
				GMTTVDDFFQGTK	K	A	95.00%	63	M2: Oxidation	731.8337	2	4.8	196	208	No
				GMYDGPVFDLTTTPK	R	G	95.00%	75	M2: Oxidation	829.3978	2	5.4	611	625	No
				IFNLYPR	K	K	95.00%	47		461.7646	2	6.8	505	511	No
				ISVGSDSDLVIWDPDAVK	R	I	95.00%	61		958.4952	2	8.9	515	532	No
				IVNDDQSFYADIYMEDGLIK	R	Q	95.00%	99	M14: Oxidation	1183.0590	2	7.9	138	157	No
				MDENQFVAVTSTNAAK	K	I	95.00%	98	M1: Oxidation	871.4132	2	6.7	489	504	No
				NHQSAAEYNIFEGMELR	K	G	95.00%	34	M14: Oxidation	675.6497	3	9.8	538	554	No
				NLHQSGFSLSGTQVDEGVR	R	S	95.00%	82		1016.0080	2	8.8	646	664	No
				NLHQSGFSLSGTQVDEGVR	R	S	95.00%	43		677.6709	3	3.7	646	664	No
				QEVQNLIK	K	D	95.00%	27		486.2822	2	4.0	264	271	No
				QIGDNLIVPGGVK	K	T	95.00%	31		655.3825	2	6.8	158	170	No
				SAADLISQAR	K	K	95.00%	84		516.2810	2	5.4	373	382	No
224	IPI00029133; IPI00456747	ATP5F1	ATP SYNTHASE B CHAIN, MITOCHONDRIAL PRECURSOR.; ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F0 COMPLEX, SUBUNIT B1.	EQEHMINWVEK	K	H	95.00%	41	M5: Oxidation	729.8453	2	9.6	211	221	No
				HVVQSISTQQEK	K	E	95.00%	75		692.3701	2	6.5	222	233	No
				HVVQSISTQQEKETIAK	K	C	95.00%	116		963.5268	2	8.3	222	238	No
				HVVQSISTQQEKETIAK	K	C	95.00%	46		642.6860	3	6.5	222	238	No
				HYLFDVQR	R	N	95.00%	37		539.2826	2	8.5	164	171	No
				LAQLEEAK	K	Q	95.00%	37		451.2557	2	4.4	132	139	No
				LDYHISVQNMMR	R	R	95.00%	45	M10: Oxidation, M11: Oxidation	769.8623	2	4.7	197	208	No
				LDYHISVQNMMR	R	R	95.00%	41	M10: Oxidation, M11: Oxidation	513.5770	3	3.8	197	208	No
				LDYHISVQNMMR	R	R	95.00%	33		753.8697	2	7.8	197	208	No
				LDYHISVQNMMR	R	R	95.00%	49		502.9147	3	5.8	197	208	No
				NNIAMALEVTYR	R	E	95.00%	86	M5: Oxidation	705.8628	2	8.9	172	183	No
				QASIQHIQNAIDTEK	K	S	95.00%	96		848.4421	2	5.7	140	154	No
				YGLIPEEFFQFLYPK	R	T	95.00%	48		945.9957	2	7.9	56	70	No
				YGPFVADFADK	K	L	95.00%	71		615.3011	2	8.0	116	126	No
				YGPFVADFADKLNEQK	K	L	95.00%	84		921.4667	2	9.7	116	131	No
				YGPFVADFADKLNEQK	K	L	95.00%	62		614.6461	3	8.2	116	131	No
225	IPI00029264	CYC1	CYTOCHROME C1 HEME PROTEIN, MITOCHONDRIAL PRECURSOR.	ELAAEVEVQDGPNEDGEMFMR PGK	K	L	95.00%	104	M18: Oxidation, M20: Oxidation	894.0748	3	8.0	147	170	No
				GLLSSLDHTSIR	R	R	95.00%	80		649.8622	2	7.4	100	111	No
				GLLSSLDHTSIR	R	R	95.00%	43		433.5775	3	7.8	100	111	No
				GLLSSLDHTSIRR	R	G	95.00%	34		485.6098	3	3.9	100	112	No
				LFDYFPK	K	P	95.00%	27		465.2449	2	5.0	171	177	No
				LFDYFPKPYPNSEAAR	K	A	95.00%	50		638.9910	3	9.6	171	186	No
226	IPI00029558	NDUFC2	NADH DEHYDROGENASE [UBIQUINONE] 1 SUBUNIT C2.	EDYLYAVR	R	D	95.00%	36		514.7610	2	8.5	78	85	No
				LHPEDFPEEDKK	K	T	95.00%	38		742.3630	2	7.5	95	106	No
				LHPEDFPEEDKK	K	T	95.00%	32		495.2417	3	1.5	95	106	No
				TYGEIFEK	K	F	95.00%	30		493.7483	2	5.3	107	114	No
227	IPI00029561	NDUFA10	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 10,MITOCHONDRIAL PRECURSOR.	ITSAYLQDIENAYK	K	K	95.00%	96		814.9180	2	6.7	229	242	No
				ITSAYLQDIENAYKK	K	T	95.00%	91		878.9680	2	9.0	229	243	No
				ITSAYLQDIENAYKK	K	T	95.00%	33		586.3134	3	7.0	229	243	No
				KVVEDIEYLK	K	F	95.00%	61		618.3508	2	4.0	268	277	No
				KYSPGYNTEVGDK	R	W	95.00%	36		729.3553	2	7.9	338	350	No
				LLQYSDALEHLLTTGQGVVLER	R	S	95.00%	69		819.1183	3	8.1	140	161	No
				LLQYSDALEHLLTTGQGVVLER	R	S	95.00%	46		614.5908	4	8.2	140	161	No
				LQSWLYSSR	R	L	95.00%	50		570.2997	2	5.9	131	139	No
				VVEDIEYLK	K	F	95.00%	40		1107.6010	1	6.6	269	277	No
				VVEDIEYLK	K	F	95.00%	38		554.3051	2	7.7	269	277	No
228	IPI00029623	PSMA6	PROTEASOME SUBUNIT ALPHA TYPE 6.	AINQGGLTSVAVR	K	G	95.00%	97		643.3694	2	6.3	31	43	No
				HITIFSPEGR	R	L	95.00%	31		578.8127	2	5.3	12	21	No
				LLDSSTVTHLFK	K	I	95.00%	79		680.8838	2	9.0	60	71	No
				LLDSSTVTHLFK	K	I	95.00%	49		454.2566	3	4.7	60	71	No
				LYQVEYAFK	R	A	95.00%	51		580.8082	2	8.0	22	30	No

229	IPI00029722	KIF5A	KINESIN HEAVY CHAIN ISOFORM 5A.	ISFLENNLEQLTK	K	V	95.00%	62		774.9250	2	9.5	830	842	No
				TGAEGAVLDEAK	K	N	95.00%	41		580.7980	2	6.8	242	253	No
230	IPI00030104	MYBPC2	MYOSIN-BINDING PROTEIN C, FAST-TYPE.	AGPPINVMVK	K	E	95.00%	84	M8: Oxidation	521.2938	2	2.7	934	943	No
				ASEQAVFK	K	C	95.00%	44		440.2342	2	3.5	452	459	No
				AVNELGEALAECK	R	L	95.00%	88		673.8409	2	8.4	1123	1135	No
				DDGNSEIMGYFVQK	K	A	95.00%	97	M8: Oxidation	809.8613	2	5.4	959	972	No
				DDGNSEIMGYFVQK	K	A	95.00%	77		801.8635	2	5.1	959	972	No
				DGVELTREDSFK	K	A	95.00%	64		698.3447	2	4.3	381	392	No
				DGVELTREDSFK	K	A	95.00%	40		465.8989	3	3.9	381	392	No
				EAPAEAPKEAPPEDQSPTAEEPTGVFLK	K	K	95.00%	67		979.1553	3	9.9	29	56	No
				EAPPEDQSPTAEEPTGVFLK	K	K	95.00%	50	S8: Phospho	1111.5040	2	4.6	37	56	No
				EAPPEDQSPTAEEPTGVFLK	K	K	95.00%	99		1071.5230	2	6.2	37	56	No
				EAPPEDQSPTAEEPTGVFLK	K	K	95.00%	38		714.6819	3	2.7	37	56	No
				EAPPKEAPAEAPK	K	E	95.00%	59		667.8566	2	7.2	24	36	No
				EAPPKEAPAEAPK	K	E	95.00%	43		445.5719	3	3.2	24	36	No
				EPPVLIVTPLEDQQVFVGDR	K	V	95.00%	94		1126.1100	2	6.8	343	362	No
				EPPVLIVTPLEDQQVFVGDR	K	V	95.00%	51		751.0766	3	7.4	343	362	No
				ESHNSASNVYTVELHIGK	K	V	95.00%	99		992.9898	2	-0.6	108	125	No
				ESHNSASNVYTVELHIGK	K	V	95.00%	62		662.3326	3	4.7	108	125	No
				EVWGTNALVEWQAPK	K	D	95.00%	79		864.4479	2	7.0	944	958	No
				FLITNYQGVLTLNIR	K	R	95.00%	95		883.0123	2	8.8	1095	1109	No
				FLTPLIDR	K	V	95.00%	48		487.7895	2	3.5	1051	1058	No
				GDEVFTTTEGR	K	T	95.00%	53		1211.5660	1	9.3	582	592	No
				GDEVFTTTEGR	K	T	95.00%	71		606.2844	2	5.1	582	592	No
				HILIFSDVVQEDR	R	G	95.00%	110		785.9206	2	6.6	404	416	No
				HILIFSDVVQEDR	R	G	95.00%	70		524.2827	3	5.8	404	416	No
				IAFQYGITDLR	K	G	95.00%	78		648.8547	2	4.7	229	239	Yes
				IKLMVEISDPDLTLK	K	W	95.00%	36	M4: Oxidation	865.9922	2	8.5	274	288	No
				IKLMVEISDPDLTLK	K	W	95.00%	48	M4: Oxidation	577.6629	3	6.4	274	288	No
				KDDDDLGIPPEIWELLK	K	G	95.00%	97		998.5277	2	9.5	203	219	No
				KKDDDDLGIPPEIWELLK	K	G	95.00%	83		1062.5750	2	9.1	202	219	No
				KKDDDDLGIPPEIWELLK	K	G	95.00%	49		708.7167	3	5.2	202	219	No
				KKDDDDLGIPPEIWELLK	K	G	95.00%	62		531.7889	4	4.0	202	219	No
				KLDPAYQVDR	K	G	95.00%	57		602.8245	2	6.9	261	270	No
				KLDPAYQVDR	K	G	95.00%	44		402.2178	3	4.2	261	270	No
				KPDSVSVETGKDAVVVAK	K	V	95.00%	140		915.0111	2	6.7	57	74	No
				KPDSVSVETGKDAVVVAK	K	V	95.00%	72		610.3418	3	4.2	57	74	No
				KPDSVSVETGKDAVVVAK	K	V	95.00%	64		458.0073	4	1.9	57	74	No
				KSDTAGELDFSGLLK	K	K	95.00%	112		790.9169	2	5.3	175	189	No
				KSDTAGELDFSGLLK	K	K	95.00%	57		527.6132	3	4.1	175	189	No
				KVGEQLNLVVPFQGK	R	P	95.00%	99		828.4804	2	2.6	854	868	No
				KVGEQLNLVVPFQGK	R	P	95.00%	41		552.6580	3	5.9	854	868	No
				KVGEQLNLVVPFQGKPR	R	P	95.00%	104		955.0633	2	8.4	854	870	No
				KVGEQLNLVVPFQGKPR	R	P	95.00%	70		637.0428	3	5.2	854	870	No
				KVGEQLNLVVPFQGKPR	R	P	95.00%	34		478.0330	4	3.1	854	870	No
				LDVSITGEPPPVATWLK	R	G	95.00%	63		912.0061	2	4.7	565	581	No
				LMVEISDPDLTLK	K	W	95.00%	65	M2: Oxidation	745.3996	2	5.9	276	288	No
				LMVEISDPDLTLK	K	W	95.00%	103		737.4012	2	4.7	276	288	No
				LNFEVFTETTYESTK	K	M	95.00%	120		904.9426	2	9.9	689	703	No
				LNFLEIK	K	V	95.00%	61		438.7655	2	4.1	524	530	No
				LNFLEIKVEYVPK	K	Q	95.00%	41		796.4658	2	8.5	524	536	No
				LNFLEIKVEYVPK	K	Q	95.00%	29		531.3115	3	5.4	524	536	No
				MIEGILYEMR	K	V	95.00%	59	M1: Oxidation	635.8143	2	2.5	704	713	No
				MIEGILYEMR	K	V	95.00%	64	M1: Oxidation	643.8119	2	2.8	704	713	No
				MIEGILYEMR	K	V	95.00%	67	M1: Oxidation, M9: Oxidation	643.8129	2	4.3	704	713	No
				MIEGILYEMR	K	V	95.00%	60	M9: Oxidation	635.8143	2	2.5	704	713	No
				MIEGILYEMR	K	V	95.00%	75		627.8180	2	4.4	704	713	No
				PFMPIAPTSEPLHLIVEDVTDTTTTLK	K	W	95.00%	63	M3: Oxidation	994.8582	3	7.0	731	757	No
				PQVVWTK	R	G	95.00%	30		429.2496	2	3.3	871	877	No
				QDASGQSLESFK	R	R	95.00%	67		648.8117	2	6.3	158	169	No
				QDASGQSLESFKR	R	T	95.00%	43		726.8595	2	1.9	158	170	No
				QDASGQSLESFKR	R	T	95.00%	49		484.9096	3	3.4	158	170	No
				QLEVLQDIADLTVK	K	A	95.00%	126		792.9480	2	1.9	438	451	No
				QLEVLQDIADLTVK	K	A	95.00%	75		528.9690	3	3.9	438	451	No
				RHILIFSDVVQEDR	K	G	95.00%	74		576.3157	3	4.2	403	416	No
				SDSGEYELSVQIENMK	R	D	95.00%	88	M15: Oxidation	922.9238	2	9.5	906	921	No
				SDSGEYELSVQIENMK	R	D	95.00%	99		914.9232	2	6.1	906	921	No

				SDSGEYELSVQIENMKDTATIR	R	I	95.00%	86	M15: Oxidation	834.7315	3	4.9	906	927	No
				SDTAGELDFSGLLK	K	K	95.00%	108		726.8718	2	9.1	176	189	No
				SDTAGELDFSGLLKK	K	R	95.00%	51		790.9183	2	7.2	176	190	No
				TGITFKPFEYK	K	E	95.00%	51		665.8602	2	5.7	1031	1041	No
				TGITFKPFEYK	K	E	95.00%	36		444.2413	3	2.5	1031	1041	No
				TGITFKPFEYKEHDFR	K	M	95.00%	35		672.3436	3	6.1	1031	1046	No
				TMEWFNVYER	K	N	95.00%	66	M2: Oxidation	695.8127	2	5.4	977	986	No
				TSDFDTVFFVR	R	Q	95.00%	86		667.3277	2	3.6	891	901	No
				TSENAIVVVAGNK	K	L	95.00%	113		651.3600	2	4.3	550	562	No
				VFAVNAIGVSQPSMNTK	R	P	95.00%	93	M14: Oxidation	889.9654	2	6.7	714	730	No
				VFAVNAIGVSQPSMNTK	R	P	95.00%	41	M14: Oxidation	593.6458	3	6.0	714	730	No
				VFAVNAIGVSQPSMNTK	R	P	95.00%	112		881.9672	2	5.8	714	730	No
				VGEQLNLVVPFQGK	K	P	95.00%	66		764.4358	2	6.6	855	868	No
				VGEQLNLVVPFQGKPR	K	P	95.00%	66		891.0132	2	6.1	855	870	No
				VGEQLNLVVPFQGKPR	K	P	95.00%	68		594.3434	3	3.8	855	870	No
				VVGVNIAGR	R	T	95.00%	64		442.7708	2	2.2	812	820	No
				WLELGSK	K	S	95.00%	48		832.4630	1	7.3	93	99	No
				YVFENVGK	K	K	95.00%	37		955.4952	1	6.7	302	309	No
				YVFENVGK	K	K	95.00%	34		478.2501	2	3.8	302	309	No
231	IPI00030182	GAMT	GUANIDINOACETATE N-METHYLTRANSFERASE.	VLEVGFGMAIAASK	R	V	95.00%	68	M8: Oxidation	704.8863	2	9.7	64	77	No
				WETPYMHALAAAASSK	R	G	95.00%	40	M6: Oxidation	875.4223	2	5.7	45	60	No
				YYAFPQMITPLVTK	R	-	95.00%	41	M7: Oxidation	844.4495	2	8.2	222	235	No
232	IPI00030275	TRAP1	HEAT SHOCK PROTEIN 75 KDA, MITOCHONDRIAL PRECURSOR.	AFLDALQNQAEASSK	K	I	95.00%	91		796.9044	2	5.5	182	196	No
				AQLLQPTLEINPR	R	H	95.00%	62		746.9305	2	2.9	635	647	No
				EGIVTATEQEVKEDIAK	R	L	95.00%	80		930.4894	2	5.6	450	466	No
				EGIVTATEQEVKEDIAK	R	L	95.00%	33		620.6636	3	7.9	450	466	No
				ELGSSVALYSR	R	K	95.00%	36		591.3135	2	2.2	358	368	No
				ELISNASDALEK	R	L	95.00%	59		645.3383	2	7.5	115	126	No
				ELLQESALIR	R	K	95.00%	65		586.3403	2	3.3	403	412	No
				GVVDSEDIPLNLSR	R	E	95.00%	96		757.4001	2	4.0	389	402	No
				GVVDSEDIPLNLSR	R	E	95.00%	51		505.2707	3	6.7	389	402	No
				LVSDGQALPEMEIHLQTNAEK	K	G	95.00%	40	M11: Oxidation	780.3938	3	4.4	131	151	No
				YESSALPSGQLTSLSEYASR	R	M	95.00%	107		1073.5260	2	6.4	470	489	No
233	IPI00030363	ACAT1	ACETYL-COA ACETYLTRANSFERASE, MITOCHONDRIAL PRECURSOR.	DGLTDVYNK	K	I	95.00%	49		1024.5000	1	4.9	182	190	No
				DGLTDVYNK	K	I	95.00%	51		512.7523	2	1.4	182	190	No
				EAYMGNVLQGGEGQAPTR	K	Q	95.00%	116	M4: Oxidation	947.4491	2	7.2	88	105	No
				EAYMGNVLQGGEGQAPTR	K	Q	95.00%	44	M4: Oxidation	631.9655	3	2.2	88	105	No
				EAYMGNVLQGGEGQAPTR	K	Q	95.00%	106		939.4515	2	7.1	88	105	No
				EAYMGNVLQGGEGQAPTR	K	Q	95.00%	51		626.6345	3	3.1	88	105	No
				EEVKEAYMGNVLQGGEGQAPTR	K	Q	95.00%	68	M8: Oxidation	793.7146	3	1.3	84	105	No
				EEVKEAYMGNVLQGGEGQAPTR	K	Q	95.00%	44		788.3854	3	4.4	84	105	No
				ENGTVTAANASTLNDGAAALVLMTADAAK	K	R	95.00%	71	M23: Oxidation	926.4673	3	8.5	274	302	No
				EVVIVSATR	K	T	95.00%	43		973.5734	1	5.4	41	49	No
				EVVIVSATR	K	T	95.00%	74		487.2895	2	3.1	41	49	No
				FGNEVIPVTVTVK	K	G	95.00%	68		701.9080	2	9.7	231	243	No
				GQPDVVVKEDEEYK	K	R	95.00%	87		817.9016	2	2.3	244	257	No
				GQPDVVVKEDEEYKR	K	V	95.00%	77		895.9568	2	7.4	244	258	No
				GQPDVVVKEDEEYKR	K	V	95.00%	67		597.6381	3	3.3	244	258	No
				GSTPYGGVKLEDLIVK	R	D	95.00%	48		838.4734	2	6.9	166	181	No
				IVAFADAAVEPIDFPIAPVYAASMVLK	R	D	95.00%	89	M24: Oxidation	945.5136	3	7.0	312	338	No
				IVAFADAAVEPIDFPIAPVYAASMVLK	R	D	95.00%	53	M24: Oxidation	709.3882	4	8.5	312	338	No
				IVAFADAAVEPIDFPIAPVYAASMVLK	R	D	95.00%	71		940.1846	3	9.9	312	338	No
				IVGHLTHALK	R	Q	95.00%	61		544.8383	2	9.5	394	403	No
				LEDLIVK	K	D	95.00%	41		829.5062	1	3.0	175	181	No
				LEDLIVK	K	D	95.00%	42		415.2560	2	0.7	175	181	No
				LEDLIVKDGLTDVYNK	K	I	95.00%	97		918.0016	2	8.2	175	190	No
				LEDLIVKDGLTDVYNK	K	I	95.00%	62		612.3361	3	6.7	175	190	No
				LGSIAIQGAIEK	K	A	95.00%	51		1199.7100	1	8.3	67	78	No
				LGSIAIQGAIEK	K	A	95.00%	89		600.3565	2	4.2	67	78	No
				LNVTPLAR	R	I	95.00%	42		442.2726	2	1.0	304	311	No
				MLEIDPQK	K	V	95.00%	37	M1: Oxidation	989.5072	1	9.3	366	373	No

				MLEIDPQKVNINGGAVSLGHPIGMSGAR	K	I	95.00%	54	M1: Oxidation, M24: Oxidation	965.1663	3	5.9	366	393	No
				MLEIDPQKVNINGGAVSLGHPIGMSGAR	K	I	95.00%	56	M1: Oxidation, M24: Oxidation	724.1282	4	8.0	366	393	No
				NEQDAYAINSYTR	R	S	95.00%	123		772.8562	2	4.1	209	221	No
				RLNVTPLAR	K	I	95.00%	37		520.3253	2	4.8	303	311	No
				TPIGSFLGSLSLLPATK	R	L	95.00%	131		851.4998	2	7.2	50	66	No
				TPIGSFLGSLSLLPATK	R	L	95.00%	88		568.0012	3	5.0	50	66	No
				TPIGSFLGSLSLLPATKLGSIAIQGAIEK	R	A	95.00%	28		961.5647	3	6.2	50	78	No
				VNINGGAVSLGHPIGMSGAR	K	I	95.00%	84	M16: Oxidation	962.0015	2	4.1	374	393	No
				VNINGGAVSLGHPIGMSGAR	K	I	95.00%	49	M16: Oxidation	641.6728	3	8.2	374	393	No
234	IPI00030405	HSPB3	HEAT-SHOCK PROTEIN BETA-3.	AAQSPPVDSAAETPPR	R	E	95.00%	50		797.4003	2	3.3	50	65	No
				HLIEIPVR	R	Y	95.00%	31		488.8049	2	7.6	8	15	No
235	IPI00030702; IPI00607898; IPI00792971; IPI00795359; IPI00795821	IDH3A	ISOFORM 1 OF ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT ALPHA,MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT ALPHA,MITOCHONDRIAL PRECURSOR.; ISOCITRATE DEHYDROGENASE 3 (NAD+) ALPHA VARIANT (FRAGMENT).; 28 KDA PROTEIN.; 23 KDA PROTEIN.	DMANPTALLLSAVMMLR	K	H	95.00%	57	M2: Oxidation, M14: Oxidation	626.9926	3	6.8	300	316	No
				DMANPTALLLSAVMMLR	K	H	95.00%	68	M2: Oxidation, M14: Oxidation	947.9850	2	9.5	300	316	No
				DMANPTALLLSAVMMLR	K	H	95.00%	78	M2: Oxidation, M14: Oxidation	632.3248	3	7.7	300	316	No
				DMANPTALLLSAVMMLR	K	H	95.00%	99	M2: Oxidation, M14: Oxidation, M15: Oxidation	947.9850	2	9.5	300	316	No
				DMANPTALLLSAVMMLR	K	H	95.00%	86	M2: Oxidation, M14: Oxidation, M15: Oxidation	632.3235	3	5.7	300	316	No
				ENTEGEYSGIEHVIVDGVVQSIK	R	L	95.00%	97		1251.6290	2	5.9	147	169	No
				ENTEGEYSGIEHVIVDGVVQSIK	R	L	95.00%	63		834.7587	3	9.8	147	169	No
				IAEFAFEYAR	R	N	95.00%	81		608.8056	2	2.6	179	188	No
				TPIAAGHPSMNLLLR	K	K	95.00%	50	M10: Oxidation	803.9474	2	8.1	101	115	No
				TPIAAGHPSMNLLLR	K	K	95.00%	40	M10: Oxidation	536.2982	3	3.0	101	115	No
				TPYTDVNIVTIR	K	E	95.00%	88		696.3827	2	2.8	135	146	No
236	IPI00030828; IPI00607861	H6PD	90 KDA PROTEIN.; GDH/6PGL ENDOPLASMIC BIFUNCTIONAL PROTEIN PRECURSOR.	GSAVVGQYQSYSEQVR	R	R	95.00%	108		879.4323	2	6.3	317	332	No
				LANDIEATAVR	K	A	95.00%	61		586.8215	2	6.5	578	588	No
				MSLSLPLINR	R	A	95.00%	49	M1: Oxidation	580.3337	2	7.4	740	749	No
237	IPI00030986; IPI00220297	KBTBD10	ISOFORM LONG OF KELCH REPEAT AND BTB DOMAIN-CONTAINING PROTEIN 10.; ISOFORM SHORT OF KELCH REPEAT AND BTB DOMAIN-CONTAINING PROTEIN 10.	EFAPTEVNDIWK	K	Y	95.00%	73		724.8621	2	6.9	559	570	No
				EVVLDNVDPAILDLIIK	K	Y	95.00%	112		940.0509	2	7.7	73	89	No
				EVVLDNVDPAILDLIIK	K	Y	95.00%	88		627.0357	3	6.3	73	89	No
				EYFLSEIDEAK	R	K	95.00%	91		672.3248	2	3.4	60	70	No
				LYQSTLLQDGLK	R	D	95.00%	86		689.8868	2	5.4	13	24	No
				LYQSTLLQDGLKDLLDEK	R	K	95.00%	102		1046.5710	2	7.5	13	30	No
				LYQSTLLQDGLKDLLDEK	R	K	95.00%	51		698.0478	3	4.7	13	30	No
				LYQSTLLQDGLKDLLDEKK	R	F	95.00%	45		740.7468	3	5.3	13	31	No
				LYQSTLLQDGLKDLLDEKK	R	F	95.00%	28		555.8124	4	5.9	13	31	No
				TGAGEVNGDVGDEDLLPGYLNDIPR	K	H	95.00%	33		862.7568	3	8.5	273	297	No
				VFIFNPK	R	K	95.00%	29		432.7563	2	7.3	465	471	No
				VYGHNVISHK	K	G	95.00%	34		577.3135	2	6.5	437	446	No
				WDVMTEFPQER	K	S	95.00%	61	M4: Oxidation	727.3299	2	6.6	522	532	No
				YFKDHVEKDDIIK	K	S	95.00%	36		825.4362	2	6.2	231	243	No
238	IPI00031107; IPI00414384	HSDL2	HSDL2 PROTEIN.; HYDROXYSTEROID DEHYDROGENASE-LIKE PROTEIN.	DGANIVIAAK	K	T	95.00%	31		971.5601	1	7.7	33	42	No
				DGANIVIAAK	K	T	95.00%	67		486.2815	2	2.6	33	42	No
				GGNVGYGEPSDQADVVMSMTTDDFVK	K	M	95.00%	57	M17: Oxidation, M19: Oxidation	917.7344	3	4.0	353	378	No
				KVDIIADAAYSIFQKPK	R	S	95.00%	58		636.3653	3	8.3	220	236	No
				KVDIIADAAYSIFQKPK	R	S	95.00%	36		477.5236	4	3.5	220	236	No

				KVESTGAVPEFKEEK	K	L	95.00%	39		559.9636	3	3.1	284	298	No
				LDLMMNVNTR	R	G	95.00%	54	M4: Oxidation, M5: Oxidation	619.7998	2	3.5	118	127	No
				LLGTIYTAAEEIEAVGGK	K	A	95.00%	134		918.0021	2	8.7	50	67	No
				LLGTIYTAAEEIEAVGGK	K	A	95.00%	65		612.3376	3	9.0	50	67	No
				SGAVEETFR	R	I	95.00%	49		498.2470	2	6.4	307	315	No
				VAHILNISPPLNLNPVWFK	K	Q	95.00%	42		724.7547	3	7.0	145	163	No
				VDIIADAAYSIFQKPK	K	S	95.00%	62		889.9972	2	9.7	221	236	No
				VDIIADAAYSIFQKPK	K	S	95.00%	29		593.6661	3	7.5	221	236	No
				VESTGAVPEFKEEK	K	L	95.00%	50		775.3945	2	3.9	285	298	No
239	IPI00031169	RAB2A	RAS-RELATED PROTEIN RAB-2A.	FQPVHDLTIGVEFGAR	R	M	95.00%	43		595.9855	3	6.6	31	46	No
				GAAGALLVYDITR	R	R	95.00%	41		660.3742	2	6.0	78	90	No
				TASNVEEAFINTAK	K	E	95.00%	95		747.8809	2	6.6	152	165	No
				YIIIGDTGVGK	K	S	95.00%	36		568.3267	2	8.0	9	19	No
240	IPI00031397	ACSL3	LONG-CHAIN-FATTY-ACID--COA LIGASE 3.	GEILIGGQSVTMGYYK	R	N	95.00%	76	M12: Oxidation	866.4407	2	6.1	526	541	No
				GIIVHTMAAVEALGAK	K	A	95.00%	41	M7: Oxidation	798.9466	2	4.2	250	265	No
				IGYSSPQTLADQSSK	R	I	95.00%	88		791.3944	2	3.1	349	363	No
				LKDIVSLVPR	K	L	95.00%	42		570.3647	2	5.5	221	230	No
				LSPEPWTPETGLVTDAFK	R	L	95.00%	71		994.5131	2	8.3	682	699	No
				VLSEAAISASLEK	K	F	95.00%	107		659.3702	2	4.6	661	673	No
241	IPI00031461	GDI2	RAB GDP DISSOCIATION INHIBITOR BETA.	DLGTESQIFISR	K	T	95.00%	70		683.3589	2	6.2	391	402	No
				EIRPALELLEPIEQK	K	F	95.00%	29		593.3450	3	7.2	365	379	No
				FDLGQDVIDFTGHALALYR	K	T	95.00%	64		717.7064	3	7.4	175	193	Yes
				FKIPGSPPESMGR	R	G	95.00%	33	M11: Oxidation	709.8660	2	9.7	56	68	No
				FLVYVANFDEKDPR	K	T	95.00%	44		571.6295	3	4.6	143	156	No
				FVSISDLLVPK	K	D	95.00%	61		609.3646	2	5.5	380	390	No
				IPGSPPESMGR	K	G	95.00%	40	M9: Oxidation	572.2790	2	2.9	58	68	No
				KFDLGQDVIDFTGHALALYR	K	T	95.00%	81		760.4036	3	5.6	174	193	No
				KFDLGQDVIDFTGHALALYR	K	T	95.00%	53		570.5549	4	6.0	174	193	No
				MLLYTEVTR	K	Y	95.00%	37	M1: Oxidation	571.3029	2	4.6	90	98	Yes
				MTGSEFDFEEMKR	R	K	95.00%	44	M1: Oxidation, M11: Oxidation	819.8509	2	9.8	424	436	No
				NPYYGGESASITPLEDLYKR	R	F	95.00%	56		758.3799	3	6.6	36	55	No
				PALELLEPIEQK	R	F	95.00%	60		690.3978	2	6.4	368	379	No
				SPYLYPLYGLGELPQGFAR	K	L	95.00%	116		1071.0660	2	7.8	222	240	Yes
				SPYLYPLYGLGELPQGFAR	K	L	95.00%	72		714.3803	3	8.3	222	240	Yes
				VPSTEAEALASSLMGLFEK	K	R	95.00%	47	M14: Oxidation	998.5020	2	0.6	119	137	No
				VPSTEAEALASSLMGLFEK	K	R	95.00%	52	M14: Oxidation	666.0092	3	8.6	119	137	No
				YIAIVSTTVETK	K	E	95.00%	32		662.8764	2	6.4	349	360	No
242	IPI00031522	HADHA	TRIFUNCTIONAL ENZYME SUBUNIT ALPHA, MITOCHONDRIAL PRECURSOR.	ADMVIEAVFEDLSLK	K	H	95.00%	101	M3: Oxidation	848.4337	2	4.7	441	455	No
				ADMVIEAVFEDLSLK	K	H	95.00%	63	M3: Oxidation	565.9576	3	3.3	441	455	No
				ADMVIEAVFEDLSLK	K	H	95.00%	90		840.4381	2	6.9	441	455	No
				ALTSFER	K	D	95.00%	33		412.2203	2	1.8	416	422	No
				DATLTALDR	K	G	95.00%	53		975.5149	1	3.7	391	399	No
				DATLTALDR	K	G	95.00%	76		488.2610	2	2.9	391	399	No
				DGPGFYTTR	K	C	95.00%	36		1013.4780	1	8.3	541	549	No
				DGPGFYTTR	K	C	95.00%	57		507.2406	2	4.0	541	549	No
				DLNSDMDSILASLK	K	L	95.00%	113	M6: Oxidation	769.3784	2	4.4	647	660	No
				DLNSDMDSILASLK	K	L	95.00%	57	M6: Oxidation	513.2557	3	6.1	647	660	No
				DLNSDMDSILASLK	K	L	95.00%	105		761.3812	2	4.8	647	660	No
				DLNSDMDSILASLK	K	L	95.00%	59		507.9231	3	4.2	647	660	No
				DSIFSNLTGQLDYQGFEK	R	A	95.00%	121		1031.4990	2	6.7	423	440	No
				DSIFSNLTGQLDYQGFEK	R	A	95.00%	84		688.0021	3	6.6	423	440	No
				DTSASAVAVGLK	K	Q	95.00%	60		1118.6160	1	8.8	520	531	No
				DTSASAVAVGLK	K	Q	95.00%	82		559.8080	2	2.2	520	531	No
				ELHSEFSEVMNEIWASDQIR	K	S	95.00%	63	M10: Oxidation	812.7144	3	5.7	67	86	No
				FGELVMTK	K	E	95.00%	49	M6: Oxidation	940.4883	1	7.2	327	334	No
				FGELVMTK	K	E	95.00%	52	M6: Oxidation	470.7458	2	2.3	327	334	No
				FGGGNPELLTQMVSK	R	G	95.00%	98	M12: Oxidation	797.4069	2	7.0	611	625	No
				FGGGNPELLTQMVSK	R	G	95.00%	50	M12: Oxidation	531.9395	3	5.1	611	625	No
				FGGGNPELLTQMVSK	R	G	95.00%	86		789.4082	2	5.5	611	625	No
				FVDLYGAQK	R	I	95.00%	51		1040.5510	1	8.9	720	728	No
				FVDLYGAQK	R	I	95.00%	52		520.7754	2	1.1	720	728	No
				GFYIYQEGVK	K	R	95.00%	48		1203.6110	1	4.6	635	644	No
				GFYIYQEGVK	K	R	95.00%	69		602.3083	2	3.0	635	644	No
				HLAILGAGLMGAGIAQVSVDK	K	G	95.00%	96	M10: Oxidation	1019.0670	2	4.7	363	383	No
				HLAILGAGLMGAGIAQVSVDK	K	G	95.00%	60	M10: Oxidation	679.7164	3	8.2	363	383	No
				ILQEGVDPK	R	K	95.00%	30		998.5596	1	7.2	561	569	No
				ILQEGVDPK	R	K	95.00%	56		499.7807	2	1.2	561	569	No

				KLDSLTTSFGFPVGAATLVDEVGVDVAK	K	H	95.00%	80		946.1796	3	8.6	570	597	No
				KLDSLTTSFGFPVGAATLVDEVGVDVAK	K	H	95.00%	65		709.8870	4	9.0	570	597	No
				KMGLVDQLVEPLGPGLKPPEER	K	T	95.00%	42	M2: Oxidation	806.7791	3	6.1	214	235	No
				KMGLVDQLVEPLGPGLKPPEER	K	T	95.00%	45	M2: Oxidation	605.3366	4	6.6	214	235	No
				KTVLGTPEVLLGALPGAGGTQR	R	L	95.00%	129		1068.1220	2	7.4	166	187	No
				KTVLGTPEVLLGALPGAGGTQR	R	L	95.00%	34		712.4163	3	6.5	166	187	No
				LDSLTTSFGFPVGAATLVDEVGVDVAK	K	H	95.00%	61		903.4802	3	7.8	571	597	No
				LPPKSEVSSDEDIQFR	K	L	95.00%	102		923.9692	2	6.3	661	676	No
				LPPKSEVSSDEDIQFR	K	L	95.00%	65		616.3142	3	4.4	661	676	No
				LTAYAMTIPFVR	K	Q	95.00%	74	M6: Oxidation	699.8790	2	3.2	268	279	No
				LTAYAMTIPFVR	K	Q	95.00%	51		691.8826	2	4.8	268	279	No
				MGLVDQLVEPLGPGLKPPEER	K	T	95.00%	100	M1: Oxidation	1145.6190	2	7.7	215	235	No
				MGLVDQLVEPLGPGLKPPEER	K	T	95.00%	74	M1: Oxidation	764.0822	3	8.2	215	235	No
				MGLVDQLVEPLGPGLKPPEER	K	T	95.00%	64		758.7476	3	4.3	215	235	No
				MQLLEIITTEK	K	T	95.00%	84	M1: Oxidation	667.8709	2	7.1	506	516	No
				MQLLEIITTEK	K	T	95.00%	63		659.8718	2	4.7	506	516	No
				MVGVPAALDMMLTGR	K	S	95.00%	108	M1: Oxidation, M10: Oxidation, M11: Oxidation	805.3978	2	7.7	191	205	No
				MVGVPAALDMMLTGR	K	S	95.00%	56	M1: Oxidation, M10: Oxidation, M11: Oxidation	537.2660	3	4.6	191	205	No
				SEVSSDEDIQFR	K	L	95.00%	87		706.3259	2	7.0	665	676	No
				TGIEQGSDAGYLCESQK	K	F	95.00%	39		893.4078	2	6.2	310	326	No
				TIEYLEEVAITFAK	R	G	95.00%	97		813.9430	2	9.2	236	249	No
				TIEYLEEVAITFAK	R	G	95.00%	59		542.9640	3	8.2	236	249	No
				TILKDATLTALDR	K	G	95.00%	68		715.9180	2	4.2	387	399	No
				TLQEVTQLSQEAQR	K	I	95.00%	103		815.9302	2	7.6	112	125	No
				TLQEVTQLSQEAQR	K	I	95.00%	73		544.2877	3	4.4	112	125	No
				TSKDTSASAVAVGLK	K	Q	95.00%	87		717.8961	2	2.6	517	531	No
				TSKDTSASAVAVGLK	K	Q	95.00%	44		478.9336	3	3.3	517	531	No
				TVLGTPEVLLGALPGAGGTQR	K	L	95.00%	149		1004.0730	2	6.8	167	187	No
				TVLGTPEVLLGALPGAGGTQR	K	L	95.00%	99		669.7178	3	6.8	167	187	No
				VIGMHYFSPVDK	K	M	95.00%	62	M4: Oxidation	704.8523	2	2.3	494	505	No
				VIGMHYFSPVDK	K	M	95.00%	40	M4: Oxidation	470.2374	3	2.2	494	505	No
				VIGMHYFSPVDK	K	M	95.00%	51		696.8553	2	2.9	494	505	No
				VIGMHYFSPVDKMQLLEIITTEK	K	T	95.00%	34	M4: Oxidation, M13: Oxidation	908.8138	3	9.9	494	516	No
				VIIVVK	K	D	95.00%	35		670.4890	1	3.4	535	540	No
243	IPI00031697	TMEM109	TRANSMEMBRANE PROTEIN 109 PRECURSOR.	EAPVDVLTQIGR	R	S	95.00%	56		649.3661	2	9.7	48	59	No
				REAPVDVLTQIGR	K	S	95.00%	27		485.2794	3	6.6	47	59	No
244	IPI00031804; IPI00294779	VDAC3	ISOFORM 1 OF VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 3.; ISOFORM 2 OF VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 3.	AADFQLHTHVNDGTEFGGSIYQK	K	V	95.00%	92		845.7434	3	9.5	175	197	No
				LSQNNFALGYK	K	A	95.00%	62		627.8326	2	7.3	164	174	No
				LTLDTIFVPNTGK	K	K	95.00%	99		709.9039	2	7.1	97	109	No
				LTLDTIFVPNTGKK	K	S	95.00%	37		773.9529	2	8.5	97	110	No
				LTLDTIFVPNTGKK	K	S	95.00%	56		516.3027	3	4.8	97	110	No
				LTLSALIDGK	K	N	95.00%	36		1030.6240	1	8.5	257	266	No
				LTLSALIDGK	K	N	95.00%	88		515.8147	2	6.3	257	266	No
				SKLSQNNFALGYK	K	A	95.00%	30		490.6004	3	7.0	162	174	No
				VNNASLIGLGYTQTLRPGVK	K	L	95.00%	89		1051.1010	2	8.3	237	256	No
				VNNASLIGLGYTQTLRPGVK	K	L	95.00%	41		701.0676	3	4.8	237	256	No
245	IPI00032137	ACTN3	ALPHA-ACTININ-3.	AGTQIENIEEDFR	K	N	95.00%	78		761.3696	2	8.3	62	74	Yes
				ASFNHFDR	R	K	95.00%	39		497.2327	2	3.5	767	774	No
				DDPIGNLNTAFEVAEK	K	Y	95.00%	62		866.9304	2	7.7	213	228	No
				DQTLQEELAR	R	Q	95.00%	54		601.8091	2	7.0	629	638	No
				DYDSALLQEVR	R	A	95.00%	73		654.8300	2	6.5	435	445	No

				FAIQDISVEETSAK	R	E	95.00%	89		769.3964	2	6.4	148	161	Yes
				GLSQEQLNEFR	K	A	95.00%	46		660.8351	2	5.6	756	766	No
				KAGTQIENIEEDFR	R	N	95.00%	52		825.4128	2	2.5	61	74	Yes
				KAGTQIENIEEDFRNGLK	R	L	95.00%	38		688.0298	3	8.3	61	78	Yes
				LAAGLAGSLEEQMAGLR	R	Q	95.00%	106	M13: Oxidation	851.9486	2	5.5	670	686	No
				LASELLEWIR	K	R	95.00%	80		615.3546	2	9.7	296	305	No
				LMLLLEVISGER	K	L	95.00%	84	M2: Oxidation	694.9011	2	8.5	79	90	Yes
				LRKDDPIGNLNTAFEVAEK	K	Y	95.00%	40		710.7184	3	9.4	210	228	No
				LVSIGAEEIVDGNLK	K	M	95.00%	64		778.9373	2	8.3	121	135	No
				MLDAEDIVNTPKPDEK	K	A	95.00%	38	M1: Oxidation	610.9661	3	1.5	235	250	No
				TINEVENQVLTR	R	D	95.00%	61		708.3817	2	4.3	741	752	No
246	IPI00032195	HSPB2	HEAT-SHOCK PROTEIN BETA-2.	AALSHDGILNLEAPR	R	G	95.00%	40		526.2911	3	8.1	259	273	No
				FGEGLLPEEILTPTLYHGYYVRPR	R	A	95.00%	33		705.8809	4	9.9	154	177	No
				TVDNLLEVSAR	R	H	95.00%	57		608.8362	2	8.9	217	227	No
				TYVLPADVDPWR	R	V	95.00%	39		716.3744	2	9.5	245	256	No
247	IPI00032450; IPI00783617	ASPH	ASPARTATE BETA-HYDROXYLASE ISOFORM D.; ASPARTATE BETA-HYDROXYLASE ISOFORM E.	LGIYDADGDGDFDVDDAK	K	V	95.00%	92		950.9173	2	9.2	73	90	No
				VLLEGPSGVAK	K	R	95.00%	26		1069.6300	1	3.9	91	101	No
				VLLEGPSGVAK	K	R	95.00%	42		535.3195	2	4.9	91	101	No
248	IPI00032561	CAB39	CALCIUM-BINDING PROTEIN 39.	DVAQIFNNILR	K	R	95.00%	80		651.8668	2	6.6	97	107	No
				LIEFLSK	K	F	95.00%	38		425.2620	2	8.7	302	308	No
				LLGELLLDR	K	H	95.00%	69		521.3223	2	5.4	232	240	No
				LLSAEFLEQHYDR	K	F	95.00%	47		810.9115	2	8.0	197	209	No
				LLSAEFLEQHYDR	K	F	95.00%	61		540.9422	3	5.3	197	209	No
				NIQFEAFHVFK	R	V	95.00%	56		690.3643	2	6.9	269	279	No
				TQPILDILLK	K	N	95.00%	30		577.3691	2	9.0	288	297	No
249	IPI00032826; IPI00168839	FAM10A5; ST13	HSC70-INTERACTING PROTEIN.; PROTEIN FAM10A5.	AIDLFTDAIK	K	L	95.00%	63		553.8119	2	5.4	133	142	No
				AIEINPDSAQPYK	R	W	95.00%	67		723.3704	2	3.5	174	186	No
				LDYDEDASAMLK	K	E	95.00%	93	M10: Oxidation	693.8123	2	4.8	211	222	No
				QDPSVLHTEEMR	K	F	95.00%	41	M11: Oxidation	729.3459	2	9.8	18	29	No
				VAAIEALNDGELQK	K	A	95.00%	111		735.8984	2	5.7	119	132	No
				VAAIEALNDGELQK	K	A	95.00%	67		490.9343	3	4.6	119	132	No
250	IPI00032875; IPI00455179	ETFDH	ISOFORM 1 OF ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE,MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE,MITOCHONDRIAL PRECURSOR.	ALNEGGFQSIPK	R	L	95.00%	88		630.8357	2	3.6	365	376	No
				ELWVIDEK	K	N	95.00%	34		516.2775	2	5.4	277	284	No
				FAEEADVVIVGAGPAGLSAAVR	R	L	95.00%	111		1050.0690	2	7.8	65	86	No
				GAPLNTPVTEDR	K	F	95.00%	44		635.3275	2	2.3	135	146	No
				GIATNDVGIQK	K	D	95.00%	52		558.3084	2	2.4	213	223	No
				ITTHYTIYPR	R	D	95.00%	37		632.8398	2	2.1	42	51	No
				NLSIYDGPEQR	R	F	95.00%	56		646.3226	2	7.1	549	559	No
				SGILAAESIFNQLTSENLQSK	K	T	95.00%	95		750.7310	3	6.9	406	426	No
				TIGLHVTEYEDNLK	K	N	95.00%	94		816.4222	2	5.0	427	440	No
				TIGLHVTEYEDNLK	K	N	95.00%	39		544.6181	3	6.4	427	440	No
251	IPI00032959	GPD1L	GLYCEROL-3-PHOSPHATE DEHYDROGENASE 1-LIKE.	ALGITLIK	K	G	95.00%	38		414.7852	2	7.9	115	122	No
				ELLQTPNFR	K	I	95.00%	30		559.3081	2	6.8	181	189	No
				KALGITLIK	K	G	95.00%	30		478.8323	2	6.0	114	122	No
				KLTDIINNDHENVK	R	Y	95.00%	75		826.9416	2	8.8	51	64	No
				KLTDIINNDHENVK	R	Y	95.00%	36		551.6292	3	6.6	51	64	No
				LISDIIR	K	E	95.00%	35		415.2644	2	7.4	133	139	No
				LQGPQTSAEVYR	K	I	95.00%	51		674.8524	2	8.0	299	310	No
				LTDIINNDHENVK	K	Y	95.00%	62		762.8935	2	8.6	52	64	No
				VMENGLLFK	K	E	95.00%	31	M2: Oxidation	533.7873	2	5.6	172	180	No
252	IPI00033022; IPI00181352; IPI00218889; IPI00477431; IPI00514550; IPI00743573; IPI00794575	DNM2	ISOFORM 1 OF DYNAMIN-2.; DYNAMIN 2 ISOFORM 4.; ISOFORM 2 OF DYNAMIN-2.; 98 KDA PROTEIN.; DYNAMIN 2 ISOFORM 2.; 98 KDA PROTEIN.; 98 KDA PROTEIN.	GISPVPINLR	K	V	95.00%	37		533.3280	2	5.6	114	123	No
				GMEELIPLVNK	R	L	95.00%	48	M2: Oxidation	629.8420	2	3.5	5	15	No
				VPVGDQPPDIEYQIK	K	D	95.00%	72		849.4485	2	8.1	143	157	No
				VYSPHVLNLTLIDLPGITK	R	V	95.00%	43		698.4109	3	7.6	124	142	No

253	IPI00033036	METAP2	METHIONINE AMINOPEPTIDASE 2.	GPSAAGEQEPDKESGASVDEVAR	K	Q	95.00%	56		762.6946	3	8.7	47	69	No
				NFDVGHVPIR	K	L	95.00%	61		577.3135	2	6.2	386	395	No
				SKGPSAAGEQEPDKESGASVDEVAR	K	Q	95.00%	31		626.0546	4	7.7	45	69	No
254	IPI00033494; IPI00220573; IPI00604523; IPI00719669	MRCL3; MRLC2	MYOSIN REGULATORY LIGHT CHAIN.; MYOSIN REGULATORY LIGHT CHAIN 2, NONSARCOMERIC.; MYOSIN REGULATORY LIGHT CHAIN MRCL3 VARIANT.; SIMILAR TO MYOSIN REGULATORY LIGHT CHAIN MRCL2.	EAFNMIDQNR	K	D	95.00%	36	M5: Oxidation	627.2884	2	8.5	36	45	Yes
				GNFNYIEFTR	K	I	95.00%	56		630.8105	2	9.5	152	161	No
255	IPI00037283; IPI00146935; IPI00235412; IPI00473085; IPI00555883	DNM1L	ISOFORM 5 OF DYNAMIN-1-LIKE PROTEIN.; ISOFORM 1 OF DYNAMIN-1-LIKE PROTEIN.; ISOFORM 3 OF DYNAMIN-1-LIKE PROTEIN.; ISOFORM 4 OF DYNAMIN-1-LIKE PROTEIN.; ISOFORM 2 OF DYNAMIN-1-LIKE PROTEIN.	ALQGASQIIAEIR	K	E	95.00%	44		685.3979	2	5.5	693	705	No
				DTLQSELVGQLYK	K	S	95.00%	68		747.4003	2	4.8	654	666	No
				FISNPNSIILAVTAANTDMATSEALK	R	I	95.00%	56	M19: Oxidation	903.4680	3	2.4	173	198	No
				GHAVNLLDVPVPVAR	K	K	95.00%	66		778.9562	2	8.5	594	608	No
				IFSPNVVNLTLVDLPGMTK	K	V	95.00%	124	M17: Oxidation	1037.5720	2	4.7	134	152	No
				LDLMDAGTDAMDVLMGR	K	V	95.00%	77	M4: Oxidation, M11: Oxidation, M15: Oxidation	936.4215	2	8.5	217	233	No
				LGIIGVVNR	K	S	95.00%	72		470.8040	2	5.9	239	247	No
				LYTDFDEIRQEIENETER	K	I	95.00%	55		767.3665	3	6.7	100	117	No
				RPLILQLVHVSQEDK	R	R	95.00%	50		592.3489	3	7.3	61	75	No
				SATLLQLITK	K	F	95.00%	47		544.3442	2	7.1	330	339	No
				SSLLDDLLTESEDMAQR	K	R	95.00%	105	M14: Oxidation	969.9600	2	7.9	667	683	No
				SSVLESLVGR	K	D	95.00%	43		523.7976	2	2.6	39	48	No
				SVTDSIRDEYAFLQK	K	K	95.00%	42		886.4529	2	6.4	257	271	No
				SVTDSIRDEYAFLQK	K	K	95.00%	38		591.3030	3	3.7	257	271	No
				TLESVDPLGGLNTIDILTAIR	R	N	95.00%	121		1106.1270	2	9.6	377	397	No
256	IPI00044608	KIAA1881	PLASMA MEMBRANE ASSOCIATED PROTEIN, S3-12.	AKDAVSSGVASVVDVAK	R	G	95.00%	32		534.9666	3	8.6	88	104	Yes
				DAVSTGLTGAVNLAK	K	G	95.00%	87		708.8907	2	2.6	882	896	Yes
				DAVSTGLTGAVNVAK	K	G	95.00%	80		701.8852	2	6.0	486	500	Yes
				DAVSTGLTGAVNVAR	K	G	95.00%	89		715.8887	2	6.4	222	236	Yes
				DAVTTGVTGAVNVAK	K	G	95.00%	80		701.8811	2	0.1	948	962	Yes
				DTIYSGVTSAVNVAK	K	G	95.00%	106		762.9060	2	8.7	618	632	Yes
				DTMSTGLTGAANVAK	K	G	95.00%	57	M3: Oxidation	726.8597	2	7.6	387	401	Yes
				DTVFSGVTGAMSMAK	K	G	95.00%	70	M11: Oxidation, M13: Oxidation	767.3548	2	5.7	981	995	Yes
				DTVSTGLTGAVNVAK	K	G	95.00%	94		716.8876	2	1.8	156	170	No
				DTVTTGLMGAVNVAK	K	G	95.00%	71	M8: Oxidation	746.8900	2	2.7	684	698	Yes
				DTVTTGLVGAVNVAK	K	G	95.00%	68		722.9054	2	1.2	585	599	Yes
				EVVSSGVTGAMDMAK	K	G	95.00%	56	M11: Oxidation, M13: Oxidation	757.3540	2	8.1	123	137	No
				GAMQTGLNTTQNIATGTK	K	D	95.00%	84	M3: Oxidation	911.9589	2	7.0	402	419	No
				GVVQGGLDTTR	K	S	95.00%	48		551.7995	2	4.8	105	115	Yes
				LDQGSGASAEDAAVQEER	R	D	95.00%	110		916.9190	2	2.1	1234	1251	Yes
				LGDLGPSFR	R	Q	95.00%	47		481.2621	2	5.7	1181	1189	Yes
				VLSAEQGSYFVR	K	L	95.00%	37		678.3524	2	0.8	1169	1180	Yes
257	IPI00062037	DYNLL2	DYNEIN LIGHT CHAIN 2, CYTOPLASMIC.	DIAAYIK	K	K	95.00%	37		793.4537	1	9.5	37	43	No
				NFGSYVTHETK	R	H	95.00%	52		641.8128	2	8.5	61	71	No
258	IPI00063234; IPI00219774	PRKAR2A	PRKAR2A PROTEIN.; CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY SUBUNIT.	AATIVATSEGSLWGLDR	R	V	95.00%	106		873.9622	2	8.0	218	234	No
				ADEHVIDQGDDGDNFYVIER	K	G	95.00%	102		1154.0190	2	6.2	162	181	No
				ADEHVIDQGDDGDNFYVIER	K	G	95.00%	80		769.6830	3	7.3	162	181	No
				APASVLPAATPR	R	Q	95.00%	67		575.8351	2	3.4	45	56	No
				DGGNQEVEIAR	K	C	95.00%	48		594.2887	2	3.1	297	307	No
				GQYFGELALVTNKPR	K	A	95.00%	90		846.9622	2	5.3	311	325	No
				GQYFGELALVTNKPR	K	A	95.00%	42		564.9763	3	3.3	311	325	No
				GSFGELALMYNTPR	R	A	95.00%	63	M9: Oxidation	786.3848	2	5.6	204	217	No
				GTYDILVTK	R	D	95.00%	53		505.2834	2	1.8	182	190	No
				MFESFIESVPLLK	K	S	95.00%	68	M1: Oxidation	778.4148	2	8.6	251	263	No
				MFGSSVDLGNLGQ	K	-	95.00%	85	M1: Oxidation	670.8157	2	5.8	370	382	No
				NISHYEEQLVK	R	M	95.00%	58		680.3518	2	3.7	359	369	No
				NLDQEQLSQVLDAMFER	K	I	95.00%	41	M14: Oxidation	684.6680	3	8.6	142	158	No

				QQPPDLVEFAVEYFTR	R	L	95.00%	85		969.9925	2	8.8	24	39	No
				QQPPDLVEFAVEYFTR	R	L	95.00%	62		646.9969	3	7.7	24	39	No
				QSLGHPPPEPGPDR	R	V	95.00%	42		495.2503	3	3.7	57	70	No
259	IPI00063827	ABHD14B	ISOFORM 1 OF ABHYDROLASE DOMAIN-CONTAINING PROTEIN 14B.	AVAIDLPGLGHSK	R	E	95.00%	31		426.5818	3	5.9	64	76	No
				FSSETWQNLGTLHR	R	L	95.00%	62		838.4217	2	9.8	43	56	No
				FSSETWQNLGTLHR	R	L	95.00%	37		559.2835	3	9.4	43	56	No
				FSVLLLHGIR	R	F	95.00%	34		577.8599	2	5.9	33	42	No
260	IPI00063903; IPI00640630	USMG5	UP-REGULATED DURING SKELETAL MUSCLE GROWTH PROTEIN 5.; 7 KDA PROTEIN.	AGPESDAQYQFTGIK	M	K	95.00%	111		806.3893	2	3.2	2	16	No
				AGPESDAQYQFTGIK	M	K	95.00%	43		537.9315	3	8.2	2	16	No
				AGPESDAQYQFTGIKK	M	Y	95.00%	88		870.4426	2	9.6	2	17	No
				KYFNSYTLTGR	K	M	95.00%	48		675.3519	2	7.8	17	27	No
				YFNSYTLTGR	K	M	95.00%	58		611.3041	2	8.2	18	27	No
261	IPI00065501	JSRP1	JUNCTIONAL SARCOPLASMIC RETICULUM PROTEIN 1.	DAVPGEAALQAR	R	V	95.00%	39		599.3174	2	3.4	146	157	No
				EAAENDEEEPGEATGEAVR	R	E	95.00%	84		1001.9360	2	8.3	206	224	No
				EAAENDEEEPGEATGEAVREDR	R	V	95.00%	70		801.6811	3	3.8	206	227	No
				FEAQAPPSAPPAPR	K	A	95.00%	39		718.3737	2	4.1	179	192	No
				LADSGSVPHDSQVAEGPSVDTRPK	R	K	95.00%	70		817.0757	3	6.5	41	64	No
262	IPI00069693		SIMILAR TO RIBOSOMAL PROTEIN L14.	GTAAAAAAAAAAK	K	V	95.00%	40		508.2827	2	3.9	148	160	No
				LVAIVDVIDQNR	K	A	95.00%	35		677.8943	2	8.4	24	35	No
263	IPI00075248; IPI00386621; IPI00794543	CALM1; CALM2; CALM3	CALMODULIN.; CALM3 PROTEIN.; 17 KDA PROTEIN.	EADIDGDGQVNYEEFVQMMTAK	R	-	95.00%	42	M18: Oxidation, M19: Oxidation	841.3704	3	10.0	128	149	No
				EAFSLFDK	K	D	95.00%	36		478.7440	2	7.7	15	22	No
				EAFSLFDKDGDGTITTK	K	E	95.00%	74		922.9575	2	8.1	15	31	No
				EAFSLFDKDGDGTITTK	K	E	95.00%	39		615.6412	3	8.6	15	31	No
				ELGTVMR	K	S	95.00%	39	M6: Oxidation	411.2155	2	4.9	32	38	No
				VFDKDGNGYISAAELR	R	H	95.00%	102		877.9471	2	8.5	92	107	No
				VFDKDGNGYISAAELR	R	H	95.00%	51		585.6325	3	5.9	92	107	No
264	IPI00098902	OGDH	OXOGLUTARATE (ALPHA-KETOGLUTARATE) DEHYDROGENASE (LIPOAMIDE) ISOFORM 1PRECURSOR.	ARDMVGQVAITR	K	I	95.00%	29	M4: Oxidation	666.8592	2	3.6	918	929	No
				DMVGQVAITR	R	I	95.00%	47	M2: Oxidation	553.2885	2	1.3	920	929	No
				FEEFLQR	R	K	95.00%	46		484.7482	2	4.5	264	270	No
				FETPGIMQFTNEEK	K	R	95.00%	46	M7: Oxidation	843.8931	2	5.8	238	251	No
				GHHVAQLDPLGILDADLDSSVPADIISSTDK	R	L	95.00%	92		1067.2180	3	8.0	141	171	No
				GHHVAQLDPLGILDADLDSSVPADIISSTDK	R	L	95.00%	64		800.6661	4	9.0	141	171	No
				GRLNVLANVIR	R	K	95.00%	72		612.8830	2	3.3	313	323	No
				GSLAAVAHAQSLVEAQPNVDK	R	L	95.00%	109		1053.0610	2	6.8	102	122	No
				GSLAAVAHAQSLVEAQPNVDK	R	L	95.00%	50		702.3732	3	2.3	102	122	No
				GSLAAVAHAQSLVEAQPNVDKLVEDHLAVQSLIR	R	A	95.00%	58		1193.6550	3	5.9	102	135	No
				GSLAAVAHAQSLVEAQPNVDKLVEDHLAVQSLIR	R	A	95.00%	42		895.4962	4	9.0	102	135	No
				GSLAAVAHAQSLVEAQPNVDKLVEDHLAVQSLIR	R	A	95.00%	26		716.5979	5	8.1	102	135	No
				HWLDSPWPGFFTLDGQPR	K	S	95.00%	39		719.3552	3	6.7	583	600	No
				IEQLSPFPFDLLLK	R	E	95.00%	80		830.4777	2	6.7	930	943	No
				KPLIIFTPK	R	S	95.00%	58		528.8497	2	8.7	852	860	No
				LEAADEGSGDVK	K	Y	95.00%	50		595.7836	2	4.3	337	348	No
				LGFYGLDESDLDK	K	V	95.00%	90		736.3547	2	3.9	172	184	No
				LLDTAFDLDVFK	R	N	95.00%	117		698.8746	2	3.5	1009	1020	No
				LNVLANVIR	R	K	95.00%	67		506.3211	2	2.9	315	323	No
				LNVLANVIRK	R	E	95.00%	44		570.3682	2	1.7	315	324	No
				LVEDHLAVQSLIR	K	A	95.00%	88		746.9318	2	4.6	123	135	No
				LVEDHLAVQSLIR	K	A	95.00%	63		498.2903	3	4.2	123	135	No
				NGHNEMDEPMFTQPLMYK	R	Q	95.00%	44	M6: Oxidation, M10: Oxidation, M16: Oxidation	743.9853	3	6.7	511	528	No
				NITLSLVANPSHLEAADPVVMGK	R	T	95.00%	103	M21: Oxidation	1196.6390	2	6.7	365	387	No
				NITLSLVANPSHLEAADPVVMGK	R	T	95.00%	73	M21: Oxidation	798.0937	3	4.6	365	387	No

				NQGYYDYVKPR	K	L	95.00%	49		701.8465	2	6.8	962	972	No
				NTNAGAPPGTAYQSPLPLSR	R	G	95.00%	132		1006.5230	2	8.6	82	101	No
				NTNAGAPPGTAYQSPLPLSR	R	G	95.00%	34		671.3489	3	5.3	82	101	No
				QILLPFR	R	K	95.00%	34		443.7822	2	5.6	845	851	No
				RQILLPFR	R	K	95.00%	25		521.8318	2	2.9	844	851	No
				SSENGVDYVIMGMPHR	K	G	95.00%	51	M11: Oxidation, M13: Oxidation	912.4134	2	7.3	297	312	No
				SSENGVDYVIMGMPHR	K	G	95.00%	52	M11: Oxidation, M13: Oxidation	608.6092	3	3.4	297	312	No
				SSFDEMLPGTHFQR	R	V	95.00%	66	M6: Oxidation	834.3832	2	5.9	870	883	No
				SSFDEMLPGTHFQR	R	V	95.00%	36	M6: Oxidation	556.5915	3	5.9	870	883	No
				SSPYPTDVAR	R	V	95.00%	33		1092.5390	1	5.5	457	466	No
				SSPYPTDVAR	R	V	95.00%	45		546.7717	2	2.7	457	466	No
				STRFEEFLQR	R	K	95.00%	40		656.8389	2	3.8	261	270	No
				STRFEEFLQR	R	K	95.00%	30		438.2292	3	5.2	261	270	No
				SWDIFFR	K	N	95.00%	46		485.7460	2	5.7	75	81	No
				TIIDKSSENGVDYVIMGMPHR	K	G	95.00%	51	M16: Oxidation, M18: Oxidation	798.7261	3	8.2	292	312	No
				TVDWALAEYMAFGSLLK	R	E	95.00%	65	M10: Oxidation	644.3314	3	8.3	650	666	No
				VFHLPTTTFIGGQESALPLR	K	E	95.00%	57		728.7372	3	6.4	185	204	No
				VIPEDGPAAQNPENVK	R	R	95.00%	69		839.4296	2	3.9	884	899	No
				VIPEDGPAAQNPENVKR	R	L	95.00%	108		917.4762	2	-0.8	884	900	No
				VYYDLTR	K	E	95.00%	38		465.2418	2	2.8	908	914	No
				YAELLVSQGVVNQPEYEEEISK	K	Y	95.00%	61		842.0941	3	8.2	540	561	No
				YAELLVSQGVVNQPEYEEEISKYDK	K	I	95.00%	83		977.4916	3	9.6	540	564	No
265	IPI00100160; IPI00746694	CAND1	ISOFORM 1 OF CULLIN-ASSOCIATED NEDD8-DISSOCIATED PROTEIN 1.; SIMILAR TO TIP120.	ALTLIAGSPLK	K	I	95.00%	65		542.3453	2	4.4	631	641	No
				EGPAVVGQFIQDVK	K	N	95.00%	47		743.9058	2	8.8	813	826	No
				FMATNDLMTELQK	R	D	95.00%	58	M2: Oxidation, M8: Oxidation	787.3693	2	4.1	24	36	No
				IDLRPVLGEGVPILASFLR	K	K	95.00%	56		689.0827	3	7.1	642	660	No
				ISGSILNELIGLVR	K	S	95.00%	105		742.4510	2	6.3	730	743	No
				ITSEALLVTQQLVK	K	V	95.00%	26		771.9644	2	6.6	535	548	No
				LGTLSALDILIK	K	N	95.00%	87		628.9011	2	8.8	668	679	No
				LTLIDPETLLPR	K	L	95.00%	49		690.9141	2	7.1	958	969	No
				SVILEAFSSPSEEVK	K	S	95.00%	76		811.4266	2	8.0	859	873	No
				VIRPLDQPSSFDATPYIK	K	D	95.00%	27		683.0386	3	6.6	549	566	No
266	IPI00100192; IPI00619911; IPI00647805; IPI00807412	NT5C3	ISOFORM 3 OF CYTOSOLIC 5'-NUCLEOTIDASE III.; ISOFORM 1 OF CYTOSOLIC 5'-NUCLEOTIDASE III.; ISOFORM 4 OF CYTOSOLIC 5'-NUCLEOTIDASE III.; ISOFORM 2 OF CYTOSOLIC 5'-NUCLEOTIDASE III.	EIVAESDVMLK	K	E	95.00%	39	M9: Oxidation	625.3227	2	2.1	122	132	No
				GFKGELIHVFNK	K	H	95.00%	37		463.5975	3	5.5	191	202	No
				LKEIVAESDVMLK	K	E	95.00%	60	M11: Oxidation	745.9176	2	8.8	120	132	No
				MADGVANVEHILK	R	I	95.00%	59	M1: Oxidation	706.8702	2	8.4	234	246	No
				MADGVANVEHILK	R	I	95.00%	43	M1: Oxidation	471.5823	3	7.4	234	246	No
				NTEYFNQLK	R	D	95.00%	32		578.7886	2	4.6	209	217	No
				SHGLLVQQALPK	K	A	95.00%	70		645.8850	2	6.6	106	117	No
				SHGLLVQQALPK	K	A	95.00%	30		430.9259	3	6.6	106	117	No
267	IPI00100775	C11orf67	ISOFORM 1 OF UPF0366 PROTEIN C11ORF67.	ETGTEHSPGVQPADVK	R	E	95.00%	46		826.4044	2	4.8	40	55	No
				EYNALVAQGVR	K	V	95.00%	38		1219.6540	1	8.9	103	113	No
				EYNALVAQGVR	K	V	95.00%	88		610.3295	2	6.2	103	113	No
				GVQTLVIGR	K	G	95.00%	27		942.5825	1	9.3	61	69	No
				GVQTLVIGR	K	G	95.00%	79		471.7934	2	5.6	61	69	No
				VLQTEQAVK	R	E	95.00%	46		508.2966	2	6.4	94	102	No
				VPSSTVEYLK	K	K	95.00%	48		561.8071	2	1.5	77	86	No
				VPSSTVEYLKK	K	H	95.00%	44		625.8583	2	7.2	77	87	No
268	IPI00100980	EHD2	EH DOMAIN-CONTAINING PROTEIN 2.	ADMVETQQLMR	K	V	95.00%	42	M3: Oxidation, M10: Oxidation	677.3160	2	7.3	221	231	No
				FGAFHSPALEDADFDGKPMVLVAGQYSTGK	R	T	95.00%	33	M19: Oxidation	1057.8490	3	6.9	42	71	No
				FGAFHSPALEDADFDGKPMVLVAGQYSTGK	R	T	95.00%	62	M19: Oxidation	793.6395	4	7.9	42	71	No
				GYDFPAVLR	R	W	95.00%	46		519.2769	2	3.6	168	176	No
				KLNPFGNTFLNR	R	F	95.00%	44		710.8920	2	4.2	124	135	No
				KLNPFGNTFLNR	R	F	95.00%	41		474.2649	3	6.3	124	135	No
				LEGHGLPANLPR	K	R	95.00%	50		637.3573	2	3.8	517	528	No
				LEGHGLPANLPR	K	R	95.00%	54		425.2403	3	2.6	517	528	No

				LEISDEFSEAIGALR	K	G	95.00%	110		825.4290	2	7.0	194	208	No
				LFELEEQDLFR	R	D	95.00%	94		719.8681	2	4.5	270	280	No
				LLEALDEMLTHDIAK	K	L	95.00%	65	M8: Oxidation	864.4544	2	6.8	378	392	No
				LLEALDEMLTHDIAK	K	L	95.00%	30	M8: Oxidation	576.6404	3	9.5	378	392	No
				LLPLEEHYR	K	F	95.00%	27		585.3249	2	8.6	33	41	No
				LNPFGNTFLNR	K	F	95.00%	44		646.8452	2	5.6	125	135	No
				LPNSVLGR	K	I	95.00%	49		428.2573	2	1.9	481	488	No
				QEELESTEVGVQGGAFEGTHMGPFVER	R	G	95.00%	112	M21: Oxidation	979.4581	3	7.4	399	425	No
				RLFELEEQDLFR	R	D	95.00%	41		532.2822	3	4.9	269	280	No
				SKYDEIFYNLAPADGK	K	L	95.00%	111		915.9584	2	9.5	451	466	No
				SKYDEIFYNLAPADGK	K	L	95.00%	43		610.9717	3	4.3	451	466	No
				TSFIQYLLEQEVPGSR	K	V	95.00%	38		933.9910	2	7.4	72	87	No
				TSFIQYLLEQEVPGSR	K	V	95.00%	60		622.9960	3	6.4	72	87	No
				VHAYIISYLK	R	K	95.00%	45		603.8539	2	9.5	306	315	No
				VYIGSFWSQPLLVPDNR	R	R	95.00%	42		996.0312	2	7.8	252	268	No
269	IPI00007935; IPI00103146; IPI00552367; IPI00553102	PDLIM5	PDZ AND LIM DOMAIN PROTEIN 5.; PDZ AND LIM DOMAIN 5 ISOFORM E.; PDZ AND LIM DOMAIN 5 ISOFORM D.; PDZ AND LIM DOMAIN 5 ISOFORM B.	ASAAPKPEPVPVQK	R	G	95.00%	39		709.9066	2	3.2	84	97	No
				ASAAPKPEPVPVQK	R	G	95.00%	39		473.6076	3	4.5	84	97	No
				ASAAPKPEPVPVQK	R	K	95.00%	47		709.9100	2	8.0	84	97	No
				ASAAPKPEPVPVQK	R	K	95.00%	52		473.6085	3	6.3	84	97	No
				ASAAPKPEPVPVQKK	R	T	95.00%	33		516.3064	3	5.0	84	98	No
				DFNMPLTISSLK	K	D	95.00%	68	M4: Oxidation	691.3614	2	8.0	23	34	No
				DFNMPLTISSLK	K	D	95.00%	69		683.3624	2	5.9	23	34	No
				EKIPLHVFSPK	K	Y	95.00%	31		647.8818	2	2.5	185	195	No
				IGDVVLSIDGINAQGMTHLEAQNK	R	I	95.00%	66	M16: Oxidation	847.1074	3	9.3	46	69	No
				IGDVVLSIDGINAQGMTHLEAQNK	R	I	95.00%	64		841.7740	3	7.4	46	69	No
				ILAQITGTEHLK	R	E	95.00%	56		662.3886	2	4.2	285	296	No
				ILAQITGTEHLK	R	E	95.00%	54		441.9292	3	6.0	162	173	No
				ILAQITGTEHLKESEADNTK	R	K	95.00%	37		733.3893	3	9.9	162	181	No
				IPLHVFSPK	K	Y	95.00%	50		519.3143	2	5.6	187	195	No
				LIEDTEDWRPR	R	T	95.00%	35		715.3622	2	6.1	141	151	No
				LRDWHHEVSAR	K	A	95.00%	46		703.3637	2	7.6	199	209	No
				YTEFYHVPTHSDASK	R	K	95.00%	59		891.4181	2	8.4	124	138	No
				YTEFYHVPTHSDASK	R	K	95.00%	39		594.6151	3	9.1	124	138	No
270	IPI00103467	ALDH1B1	ALDEHYDE DEHYDROGENASE X, MITOCHONDRIAL PRECURSOR.	EEIFGPVQPLFK	K	F	95.00%	29		702.3871	2	6.3	415	426	No
				GFFIKPTVFGGVQDDMR	R	I	95.00%	38	M16: Oxidation	643.9926	3	4.5	395	411	No
				IAKEEIFGPVQPLFK	R	F	95.00%	34		858.4968	2	7.0	412	426	No
				IAKEEIFGPVQPLFK	R	F	95.00%	44		572.6659	3	4.8	412	426	No
				KTFPTVNPTTGEVIGHVAEGDRADVDR	K	A	95.00%	53		721.1223	4	7.3	52	78	No
				KVGNPFELDTQQGPQVDKEQFER	R	V	95.00%	46		897.1192	3	7.3	347	369	No
				KVGNPFELDTQQGPQVDKEQFER	R	V	95.00%	38		673.0890	4	3.7	347	369	No
				LAPALATGNTVVMK	K	V	95.00%	90	M13: Oxidation	701.3948	2	3.0	196	209	No
				LLNLLADLVER	R	D	95.00%	73		634.8891	2	9.8	104	114	No
				TFVEESIYNEFLER	R	T	95.00%	98		888.4343	2	6.6	325	338	No
				VAEQTPLSALYLASLIK	K	E	95.00%	100		909.0339	2	9.6	210	226	No
				VAFTGSTEVGHLIQK	K	A	95.00%	96		793.9348	2	4.7	258	272	No
				VGNPFELDTQQGPQVDKEQFER	K	V	95.00%	58		854.4218	3	8.8	348	369	No
				VLGYIQLGQK	R	E	95.00%	60		559.8356	2	5.1	370	379	No
				YGLAAAVFTR	R	D	95.00%	64		534.7987	2	5.0	442	451	No
271	IPI00103994	LARS	LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC.	SFITTDVNPYYDSFVR	R	W	95.00%	73		962.4697	2	9.8	204	219	No
				STGNFLTLTQAIDK	K	F	95.00%	54		754.9084	2	8.3	720	733	No
				TGFFEFQAAK	K	D	95.00%	44		573.2889	2	5.9	823	832	No
				VDIGDTIIYLVH	R	-	95.00%	79		679.3766	2	6.2	1165	1176	No
				VFASELNAGIIK	R	T	95.00%	94		631.3652	2	5.4	796	807	No
				VFEVNASNLEK	R	Q	95.00%	55		625.3274	2	3.3	29	39	No
272	IPI00152330; IPI00647802	LRRC20	ISOFORM 1 OF LEUCINE-RICH REPEAT-CONTAINING PROTEIN 20.; 20 KDA PROTEIN.	ELHLEGNFLHR	R	L	95.00%	41		455.5773	3	6.3	78	88	No
				FDMLMSPEGAR	K	A	95.00%	34	M3: Oxidation, M5: Oxidation	643.2866	2	7.5	170	180	No
				FMTTFSQLR	K	E	95.00%	53	M2: Oxidation	573.7893	2	7.9	69	77	No

				FNPLNAEVR	R	V	95.00%	47		530.2862	2	5.5	153	161	No
				LPSEVSALQHLK	R	A	95.00%	57		441.2567	3	4.9	89	100	No
				LVSFPIGIYK	K	V	95.00%	47		568.8453	2	9.3	34	43	No
				NVSGQIHLITLANNELK	R	S	95.00%	32		622.0185	3	5.6	47	63	No
				VIAPPLIK	R	F	95.00%	20		425.7953	2	7.2	162	169	No
273	IPI00155601	LRP16	PROTEIN LRP16.	VDLSTSTDWK	K	E	95.00%	43		576.2880	2	8.3	87	96	No
				YVIHTVGPIAYGEPSASQAAELR	K	S	95.00%	75		810.4283	3	9.4	222	244	No
274	IPI00156282; IPI00414289	GPS1	G PROTEIN PATHWAY SUPPRESSOR 1 ISOFORM 2.; G PROTEIN PATHWAY SUPPRESSOR 1 ISOFORM 1.	AESTPEIAEQR	K	G	95.00%	47		615.8065	2	6.8	225	235	No
				DIIFK	R	F	95.00%	28		635.3814	1	6.8	364	368	No
				EGSQGELTPANSQSR	R	M	95.00%	56		780.8709	2	5.5	472	486	No
				LFLELEPQVR	K	D	95.00%	39		622.3596	2	4.9	318	327	No
275	IPI00157144; IPI00303868	GYS1	GYS1 PROTEIN.; GLYCOGEN [STARCH] SYNTHASE, MUSCLE.	AFPEHFTYEPNEADAAQGYR	K	Y	95.00%	65		771.6860	3	9.3	552	571	No
				FSAMHEFQNLHAQSK	K	A	95.00%	46	M4: Oxidation	895.9219	2	4.2	223	237	No
				FSAMHEFQNLHAQSK	K	A	95.00%	35	M4: Oxidation	597.6184	3	6.2	223	237	No
				GADVFLEALAR	K	L	95.00%	112		581.3194	2	3.5	274	284	No
				IGLFNSSADR	R	V	95.00%	59		540.2794	2	2.1	399	408	No
				KFSAMHEFQNLHAQSK	K	A	95.00%	41	M5: Oxidation	640.3160	3	4.7	222	237	No
				KLYESLLVGSLPDMNK	R	M	95.00%	75	M14: Oxidation	911.9900	2	5.2	339	354	No
				KLYESLLVGSLPDMNK	R	M	95.00%	34	M14: Oxidation	608.3287	3	4.2	339	354	No
				KPDIVTPNGLNVK	R	K	95.00%	65		697.9066	2	3.2	209	221	No
				LPVATIFTTHATLLGR	R	Y	95.00%	102		856.0027	2	3.9	132	147	No
				LPVATIFTTHATLLGR	R	Y	95.00%	84		571.0042	3	3.5	132	147	No
				LSDLLDWK	R	Y	95.00%	35		989.5361	1	5.2	528	535	No
				LSDLLDWK	R	Y	95.00%	51		495.2732	2	7.6	528	535	No
				LYESLLVGSLPDMNK	K	M	95.00%	63	M13: Oxidation	847.9415	2	4.4	340	354	No
				QLWDTANTVK	K	E	95.00%	30		588.3121	2	8.7	324	333	No
				RKPDIVTPNGLNVK	K	K	95.00%	47		775.9575	2	3.4	208	221	No
				RKPDIVTPNGLNVK	K	K	95.00%	32		517.6412	3	3.9	208	221	No
				RLPVATIFTTHATLLGR	R	Y	95.00%	96		623.0392	3	5.3	131	147	No
				RNSVDTATSSSLSTPSEPLSPTSSLGEERN	K	-	95.00%	53	S3: Phospho	1062.8270	3	6.5	644	673	No
				TLYFFIAGR	K	Y	95.00%	47		544.3056	2	8.5	259	267	No
				TNNFNVETLK	R	G	95.00%	32		590.3061	2	2.8	308	317	No
				TQVELLEAPTPALK	R	R	95.00%	85		755.4355	2	6.7	75	88	No
				TQVELLEAPTPALKR	R	T	95.00%	73		833.4830	2	2.4	75	89	No
				TQVELLEAPTPALKR	R	T	95.00%	76		555.9918	3	3.4	75	89	No
				VGGIYTVLQTK	K	A	95.00%	78		589.8458	2	4.2	40	50	No
				VIFHPEFLSSTSPLLPVDYEEFVR	K	G	95.00%	49		941.1623	3	9.3	411	434	No
				VNGSEQTVVAFFIMPAR	R	T	95.00%	84	M14: Oxidation	941.4891	2	9.0	291	307	No
276	IPI00164623; IPI00783987	C3	187 KDA PROTEIN.; COMPLEMENT C3 PRECURSOR (FRAGMENT).	AAVYHHFISDGVR	K	K	95.00%	56		736.3776	2	2.0	914	926	No
				AGDFLEANYMNLQR	K	S	95.00%	77	M10: Oxidation	829.3912	2	6.2	1172	1185	No
				AGDFLEANYMNLQR	K	S	95.00%	48	M10: Oxidation	553.2636	3	6.6	1172	1185	No
				AYYENSPQQVFSTEFEVK	R	E	95.00%	84		1083.5160	2	9.4	208	225	No
				DAPDHQELNLDVSLQLPSR	K	S	95.00%	34		716.3680	3	6.9	1285	1303	No
				DFDFVPPVVR	K	W	95.00%	48		595.8180	2	5.9	1245	1254	No
				EGVQKEDIPPADLSDQVPDTESETR	R	I	95.00%	91		919.1057	3	3.5	955	979	No
				EPGQDLVVLPLSITTDFIPSFR	R	L	95.00%	31		815.4487	3	9.1	509	530	No
				EVVADSVWVDVK	R	D	95.00%	65		673.3599	2	8.7	545	556	No
				GQGTLSVVTMYHAK	K	A	95.00%	57	M10: Oxidation	754.3867	2	5.0	1340	1353	No
				GYTQQLAFR	K	Q	95.00%	50		542.2856	2	4.3	1052	1060	No
				HQQTVTIPPK	R	S	95.00%	40		574.8293	2	6.8	882	891	No
				IHWESASLLR	R	S	95.00%	43		404.5583	3	4.7	1311	1320	No
				ILLQGTPVAQMTEDAVDAER	R	L	95.00%	114	M11: Oxidation	1087.0540	2	8.2	980	999	No
				ILLQGTPVAQMTEDAVDAER	R	L	95.00%	53	M11: Oxidation	725.0374	3	7.1	980	999	No
				IPIEDGSGEVVLSR	R	K	95.00%	104		735.8981	2	5.3	291	304	No
				KQELSEAEQATR	K	T	95.00%	52		695.3575	2	7.0	428	439	No
				KVLLDGVQNPR	R	A	95.00%	54		619.8687	2	5.8	305	315	No
				LSINTHPSQKPLSITVR	K	T	95.00%	39		631.0333	3	4.0	409	425	No
				LVAYYTLIGASGQR	R	E	95.00%	57		756.4221	2	9.3	531	544	No
				NTLIIYLDK	R	V	95.00%	34		546.8213	2	3.8	1442	1450	No
				QKPDGVFQEDAPVIHQEMIGGLR	K	N	95.00%	37	M18: Oxidation	645.8318	4	6.2	1112	1134	No
				SEETKENEGFTVTAEGK	R	G	95.00%	109		928.4355	2	3.7	1323	1339	No

				SEETKENEGFTVTAEGK	R	G	95.00%	50		619.2930	3	3.7	1321	1337	No
				SGIPIVTSPYQIHFTK	R	T	95.00%	49		894.4963	2	8.5	344	359	No
				SNLDEDIIAEENIVSR	R	S	95.00%	107		908.9568	2	7.1	749	764	No
				SNLDEDIIAEENIVSR	R	S	95.00%	69		606.3067	3	6.3	749	764	No
				SSLSVPYVIVPLK	K	T	95.00%	43		701.4260	2	5.9	892	904	No
				SYTVAIAGYALAQMGR	R	L	95.00%	53	M14: Oxidation	844.4336	2	6.9	1186	1201	No
				TELRPGETLNVNFLLR	R	M	95.00%	44		624.6869	3	5.9	463	478	No
				TGLQEVEVK	K	A	95.00%	44		501.7787	2	2.3	905	913	No
				TKKQELSEAEQATR	R	T	95.00%	40		540.2894	3	7.5	426	439	No
				TMQALPYSTVGNSNNYLHLSVLR	R	T	95.00%	53	M2: Oxidation	865.4445	3	5.7	440	462	No
				TVMVNIENPEGIPVK	R	Q	95.00%	42	M3: Oxidation	828.4436	2	6.9	162	176	No
				VHQYFNVELIQPGAVK	K	V	95.00%	70		921.5056	2	6.4	1463	1478	No
				VHQYFNVELIQPGAVK	K	V	95.00%	44		614.6723	3	5.3	1463	1478	No
				VLLDGVQNPR	K	A	95.00%	29		555.8182	2	1.1	306	315	No
				VPVAVQGEDTVQSLTQGDGVAK	R	L	95.00%	130		1099.5780	2	8.4	387	408	No
				VPVAVQGEDTVQSLTQGDGVAK	R	L	95.00%	55		733.3855	3	4.8	387	408	No
				VQLSNDFDEYIMAIEQTIK	K	S	95.00%	148	M12: Oxidation	1137.0660	2	10.0	1552	1570	No
				VQLSNDFDEYIMAIEQTIK	K	S	95.00%	63	M12: Oxidation	758.3779	3	7.4	1552	1570	No
				VTIKPAPETEK	K	R	95.00%	30		404.9018	3	4.6	1367	1377	No
				YRGDQDATMSILDISMMTGFAPDTDDLK	R	Q	95.00%	56	M9: Oxidation, M16: Oxidation, M17: Oxidation	1052.4770	3	9.4	1392	1419	No
				YYGGGYGSTQATFMVFQALAQYQK	R	D	95.00%	59	M14: Oxidation	899.0958	3	8.1	1261	1284	No
277	IPI00168081; IPI00784073	SMYD1	57 KDA PROTEIN.; SET AND MYND DOMAIN-CONTAINING PROTEIN 1.	AYAILLVTHGPSHPITK	K	D	95.00%	109		909.5248	2	7.4	419	435	No
				AYAILLVTHGPSHPITK	K	D	95.00%	61		606.6841	3	4.6	419	435	No
				AYAILLVTHGPSHPITK	K	D	95.00%	40		455.2658	4	6.2	419	435	No
				EAALNNQPMQVMAEPSNEPSPALFHK	R	K	95.00%	90	M9: Oxidation, M12: Oxidation	961.4626	3	9.5	466	491	No
				EFWAADIIFAER	K	A	95.00%	84		734.3729	2	7.2	26	37	No
				ISEGEELTVSYIDFLNVSEER	K	K	95.00%	125		1215.1000	2	7.9	242	262	No
				KLKDDLFLGVK	K	D	95.00%	55		638.3933	2	8.4	282	292	No
				KLKDDLFLGVK	K	D	95.00%	53		425.9289	3	2.4	282	292	No
				LKDDLFLGVK	K	D	95.00%	46		574.3414	2	1.7	283	292	No
				LYHPNNAQLGMAVMR	K	A	95.00%	48	M11: Oxidation, M14: Oxidation	873.9313	2	7.4	384	398	No
				LYHPNNAQLGMAVMR	K	A	95.00%	52	M11: Oxidation, M14: Oxidation	582.9546	3	3.6	384	398	No
				MENVEVFTAEGK	R	G	95.00%	47	M1: Oxidation	685.3217	2	3.4	6	17	No
				QEPVFADTNIYMLR	K	M	95.00%	62	M12: Oxidation	856.9281	2	9.7	339	352	No
				QEPVFADTNIYMLR	K	M	95.00%	41	M12: Oxidation	571.6193	3	6.2	339	352	No
				SEGLYHEVVK	R	L	95.00%	66		580.8041	2	4.3	321	330	No
				VQTEMELR	R	M	95.00%	42	M5: Oxidation	511.2561	2	5.3	445	452	No
278	IPI00169383	PGK1	PHOSPHOGLYCERATE KINASE 1.	AEPAKIEAFR	K	A	95.00%	59		566.3130	2	1.6	142	151	No
				AHSSMVGVNLPQK	R	A	95.00%	84	M5: Oxidation	692.3569	2	0.4	172	184	No
				AHSSMVGVNLPQK	R	A	95.00%	50	M5: Oxidation	461.9099	3	6.3	172	184	No
				AHSSMVGVNLPQK	R	A	95.00%	57		684.3634	2	6.2	172	184	No
				AHSSMVGVNLPQK	R	A	95.00%	41		456.5756	3	0.4	172	184	No
				ALESPERPFLAILGGAK	K	V	95.00%	84		885.0073	2	5.8	200	216	No
				ALESPERPFLAILGGAK	K	V	95.00%	64		590.3392	3	3.1	200	216	No
				ALMDEVVK	K	A	95.00%	55	M3: Oxidation	460.7427	2	1.2	354	361	No
				ALMDEVVK	K	A	95.00%	35		452.7463	2	3.6	354	361	No
				DVLFLK	K	D	95.00%	34		734.4485	1	4.2	92	97	No
				ELNYFAK	K	A	95.00%	33		884.4600	1	9.2	193	199	No
				FHVEEEGK	R	G	95.00%	33		487.7369	2	8.0	124	131	No
				FHVEEEGKGK	R	D	95.00%	40		580.2921	2	1.4	124	133	No
				IQLINNMLDK	K	V	95.00%	33	M7: Oxidation	1217.6610	1	4.0	221	230	No
				IQLINNMLDK	K	V	95.00%	59	M7: Oxidation	609.3342	2	3.3	221	230	No
				IQLINNMLDK	K	V	95.00%	57		601.3370	2	3.8	221	230	No
				IQLINNMLDKVNEMIIGGGMAFTFLK	K	V	95.00%	35	M7: Oxidation, M14: Oxidation, M20: Oxidation	986.8494	3	6.2	221	246	No
				ITLPVDFVTADKFDENAK	K	T	95.00%	132		1012.0330	2	9.6	280	297	No
				ITLPVDFVTADKFDENAK	K	T	95.00%	66		675.0224	3	6.3	280	297	No
				LGDVYVNDAFGTAHR	K	A	95.00%	117		817.9061	2	7.1	157	171	No
				LGDVYVNDAFGTAHR	K	A	95.00%	85		545.6070	3	7.6	157	171	No

				LTLDKLDVK	K	G	95.00%	46		522.8218	2	4.7	7	15	No
				NNQITNNQR	K	I	95.00%	33		551.2781	2	7.5	31	39	No
				PDGVPMPDKYSLEPVAVELK	R	S	95.00%	33	M6: Oxidation	734.0520	3	8.7	67	86	No
				PFLAILGGAK	R	V	95.00%	60		493.8100	2	8.2	207	216	No
				QIVWNGPVGVFEWEAFAR	K	G	95.00%	129		1053.0450	2	9.9	333	350	No
				QIVWNGPVGVFEWEAFAR	K	G	95.00%	59		702.3635	3	6.7	333	350	No
				SLLGKDVLFLK	K	D	95.00%	41		616.8878	2	4.7	87	97	No
				SLLGKDVLFLK	K	D	95.00%	32		411.5919	3	-1.5	87	97	No
				SVVLMSHLGRPDGVPMPDK	K	Y	95.00%	37	M16: Oxidation	684.3558	3	4.8	57	75	No
				SVVLMSHLGRPDGVPMPDK	K	Y	95.00%	34	M5: Oxidation, M16: Oxidation	689.6885	3	6.3	57	75	No
				SVVLMSHLGRPDGVPMPDKYSLEPVAVELK	K	S	95.00%	50	M5: Oxidation, M16: Oxidation	1099.2510	3	9.0	57	86	No
				VADKIQLINNMLDK	K	V	95.00%	80	M11: Oxidation	815.9503	2	5.3	217	230	No
				VADKIQLINNMLDK	K	V	95.00%	36	M11: Oxidation	544.3022	3	4.3	217	230	No
				VADKIQLINNMLDKVNEMIIGGGMAFTFLK	K	V	95.00%	38	M11: Oxidation, M18: Oxidation, M24: Oxidation	843.6982	4	8.3	217	246	No
				VDFNVPMK	R	N	95.00%	32	M7: Oxidation	965.4813	1	4.8	23	30	No
				VDFNVPMK	R	N	95.00%	53	M7: Oxidation	483.2447	2	5.0	23	30	No
				VDFNVPMK	R	N	95.00%	36		475.2458	2	2.1	23	30	No
				VKAEPAKIEAFR	K	A	95.00%	50		679.8961	2	3.5	140	151	No
				VLNNMEIGTSLFDEEGAK	K	I	95.00%	115	M5: Oxidation	991.9822	2	9.2	247	264	No
				VLNNMEIGTSLFDEEGAK	K	I	95.00%	61	M5: Oxidation	661.6550	3	5.7	247	264	No
				VLNNMEIGTSLFDEEGAK	K	I	95.00%	92		983.9847	2	9.3	247	264	No
				VLPGVDALSNI	K	-	95.00%	35		1097.6290	1	7.1	407	417	No
				VLPGVDALSNI	K	-	95.00%	68		549.3152	2	1.6	407	417	No
				VNEMIIGGGMAFTFLK	K	V	95.00%	79	M4: Oxidation, M10: Oxidation	880.4496	2	8.6	231	246	No
				VNEMIIGGGMAFTFLK	K	V	95.00%	78	M4: Oxidation, M10: Oxidation	587.3025	3	8.8	231	246	No
				VSHVSTGGGASLELLEGK	K	V	95.00%	141		870.9640	2	3.9	389	406	No
				VSHVSTGGGASLELLEGK	K	V	95.00%	50		580.9791	3	4.8	389	406	No
				WNTEDKVSHVSTGGGASLELLEGK	K	V	95.00%	82		838.7604	3	7.2	383	406	No
				YAEAVTR	K	A	95.00%	45		405.2141	2	5.8	324	330	No
				YSLEPVAVELK	K	S	95.00%	39		1247.6890	1	0.4	76	86	No
				YSLEPVAVELK	K	S	95.00%	76		624.3534	2	8.1	76	86	No
279	IPI00170914	ADSSL1	ISOFORM 1 OF ADENYLOSUCCINATE SYNTHETASE ISOZYME 1.	AHLVFDFHQAVDGLQEVQR	R	Q	95.00%	96		1105.0690	2	6.5	134	152	No
				AHLVFDFHQAVDGLQEVQR	R	Q	95.00%	81		737.0491	3	7.4	134	152	No
				AHLVFDFHQAVDGLQEVQR	R	Q	95.00%	32		553.0376	4	5.2	134	152	No
				AVSFIGNGVVIHLPGLFEEAEK	K	N	95.00%	32		776.0941	3	9.4	94	115	No
				AVSFIGNGVVIHLPGLFEEAEKNEK	K	K	95.00%	54		899.8224	3	9.8	94	118	No
				DGVYFMYEALHGPPK	R	K	95.00%	55	M6: Oxidation	870.4142	2	5.8	234	248	No
				EYDFHLLPSGIINTK	K	A	95.00%	69		873.9642	2	7.8	79	93	No
				EYDFHLLPSGIINTK	K	A	95.00%	52		582.9799	3	9.8	79	93	No
				FVENHVGVAVK	R	W	95.00%	59		599.8372	2	6.7	432	442	No
				FVENHVGVAVK	R	W	95.00%	28		400.2262	3	3.9	432	442	No
				GHEWGVTTGR	R	K	95.00%	54		550.2709	2	4.9	326	335	No
				IPYFPANQEMLQK	R	V	95.00%	47	M10: Oxidation	797.9050	2	5.0	386	398	No
				LDILDVLGEVK	K	V	95.00%	109		607.3601	2	6.2	364	374	No
				NLAHQHQSMFPTLEIDIEGQLKR	K	L	95.00%	31	M9: Oxidation	907.8049	3	7.6	198	220	No
				NLAHQHQSMFPTLEIDIEGQLKR	K	L	95.00%	47	M9: Oxidation	681.1047	4	6.4	198	220	No
				RIPYFPANQEMLQK	K	V	95.00%	48	M11: Oxidation	875.9597	2	9.3	385	398	No
				RIPYFPANQEMLQK	K	V	95.00%	54	M11: Oxidation	584.3055	3	3.3	385	398	No
				RWEDLPPQAQNYIR	R	F	95.00%	58		893.4630	2	8.0	418	431	No
				RWEDLPPQAQNYIR	R	F	95.00%	55		595.9774	3	7.1	418	431	No
				VEVEYETLPGWK	K	A	95.00%	75		725.3718	2	6.1	399	410	No
				VGIGAFPTEQINEIGGLLQTR	R	G	95.00%	121		1107.1090	2	7.7	305	325	No
				VGIGAFPTEQINEIGGLLQTR	R	G	95.00%	72		738.4080	3	6.7	305	325	No
				VTVVLGAQWGDEGK	R	G	95.00%	109		729.8902	2	9.0	33	46	No
				VTVVLGAQWGDEGKGK	R	V	95.00%	72		822.4472	2	6.5	33	48	No
				VTVVLGAQWGDEGKGK	R	V	95.00%	34		548.6340	3	6.5	33	48	No
				VVDLLATDADIISR	K	C	95.00%	110		750.9233	2	7.6	49	62	No
				VVDLLATDADIISR	K	C	95.00%	93		500.9495	3	3.6	49	62	No
				WEDLPPQAQNYIR	R	F	95.00%	45		815.4078	2	3.1	419	431	No

				YAHMVNGFTALALTK	R	L	95.00%	40	M4: Oxidation	551.6235	3	4.7	349	363	No
280	IPI00170935	LRRC47	LEUCINE-RICH REPEAT-CONTAINING PROTEIN 47.	ADLATAPPHVTVVR	K	-	95.00%	41		723.9108	2	4.7	570	583	No
				ADLATAPPHVTVVR	K	-	95.00%	28		482.9429	3	4.3	570	583	No
				APGPGLAQGLPQLHSLVLR	R	R	95.00%	33		642.0461	3	4.8	65	83	No
				ELLLTGPGLEER	R	V	95.00%	61		663.8718	2	6.4	23	34	No
				NALGPGLSPELGPLPALR	R	V	95.00%	77		886.5146	2	7.9	85	102	No
				SILEYLR	R	V	95.00%	29		447.2598	2	2.3	253	259	No
				TAATLATHELR	R	A	95.00%	84		592.3290	2	5.6	371	381	No
				VLHVSENPVPLTVR	R	V	95.00%	56		780.4542	2	6.2	311	324	No
281	IPI00171199; IPI00419249	PSMA3	ISOFORM 2 OF PROTEASOME SUBUNIT ALPHA TYPE 3.; ISOFORM 1 OF PROTEASOME SUBUNIT ALPHA TYPE 3.	AVENSSTAIGIR	K	C	95.00%	36		609.3321	2	6.0	30	41	No
				IIYIVHDEVK	K	D	95.00%	34		614.8565	2	8.8	190	199	No
				SNFGYNIPLK	R	H	95.00%	57		576.8107	2	7.0	101	110	No
282	IPI00171573; IPI00185975	CCDC109A	COILED-COIL DOMAIN CONTAINING 109A.; CCDC109A PROTEIN.	DLLSHENAATLNDVK	R	T	95.00%	69		820.4255	2	8.6	166	180	No
				LEDLKEQLAPLEK	R	V	95.00%	36		509.2922	3	8.4	207	219	No
				LRDPLQVHLPLR	R	Q	95.00%	54		486.3000	3	5.9	334	345	No
				VAIYSPDGVR	R	V	95.00%	34		538.7944	2	6.5	125	134	No
283	IPI00171761; IPI00171769; IPI00552881	FUNDC2	21 KDA PROTEIN.; FUN14 DOMAIN CONTAINING 2.; FUN14 DOMAIN CONTAINING 2.	AEEVVSFVK	K	K	95.00%	55		504.2796	2	9.9	162	170	No
				KLFGQESGPSAEK	R	Y	95.00%	48		689.3603	2	8.2	68	80	No
				LFGQESGPSAEK	K	Y	95.00%	72		625.3107	2	5.7	69	80	No
				SKAEEVVSFVK	R	K	95.00%	30		408.2312	3	8.0	160	170	No
284	IPI00173461	JPH1	JUNCTOPHILIN-1.	ADAADQAALAAR	K	Q	95.00%	64		572.2938	2	3.3	388	399	No
				AKADAADQAALAAR	R	Q	95.00%	90		671.8617	2	5.6	386	399	No
				ELSPDFYQPGPDYVK	R	Q	95.00%	79		877.9223	2	5.0	411	425	No
				QSVPYGMATVIR	R	S	95.00%	82	M7: Oxidation	669.3497	2	2.1	145	156	No
				SVADEQVTAIVNKPLMSK	R	A	95.00%	31	M16: Oxidation	973.5242	2	7.0	500	517	No
285	IPI00173549; IPI00735855; IPI00737694; IPI00742098	SYNPO2	SYNAPTOPODIN 2.; SYNAPTOPODIN-2.; SIMILAR TO SYNAPTOPODIN 2 ISOFORM 3.; SIMILAR TO SYNAPTOPODIN 2 ISOFORM 2.	HQPYQLNASLFTFQPPDAK	K	D	95.00%	38		734.7083	3	5.0	967	985	No
				IAQPSYPPARPASTLNVAGPFK	K	G	95.00%	26		761.4221	3	9.1	808	829	No
				PASTLNVAGPFK	R	G	95.00%	41		601.3367	2	6.2	818	829	No
				QESASSSYFVAPR	K	P	95.00%	52		714.8475	2	7.9	1059	1071	No
				TAKPFPGSVNQPATPFSPTR	R	N	95.00%	45		700.7076	3	9.1	588	607	No
				VSPNPELLSLLQNSEGK	K	R	95.00%	119		912.9939	2	5.0	704	720	No
				YVVDSDTVQAHAAR	K	A	95.00%	34		511.2583	3	5.7	886	899	No
286	IPI00176469; IPI00641178; IPI00644715; IPI00645029	CABC1	ISOFORM 1 OF CHAPERONE-ACTIVITY OF BC1 COMPLEX-LIKE, MITOCHONDRIALPRECURSOR.; ISOFORM 3 OF CHAPERONE-ACTIVITY OF BC1 COMPLEX-LIKE, MITOCHONDRIALPRECURSOR.; CHAPERONE, ABC1 ACTIVITY OF BC1 COMPLEX HOMOLOG.; CHAPERONE, ABC1 ACTIVITY OF BC1 COMPLEX HOMOLOG.	ALQSTAVEQIGMFLGK	R	V	95.00%	58	M12: Oxidation	570.3090	3	9.8	42	57	No
				ALQSTAVEQIGMFLGK	R	V	95.00%	63		846.9589	2	6.1	42	57	No
				AVLGSSPFLSEANAER	K	I	95.00%	122		824.4258	2	5.9	195	210	No
				DKLEYFEERPFAAASIGQVHLAR	R	M	95.00%	59		883.1349	3	9.9	274	296	No
				DKLEYFEERPFAAASIGQVHLAR	R	M	95.00%	41		662.6013	4	7.0	274	296	No
				EAGFPGQASSPLGR	R	A	95.00%	58		687.3482	2	5.2	127	140	No
				FLTGYEVK	K	V	95.00%	31		478.7604	2	3.8	546	553	No
				IHNLIPVMLR	K	H	95.00%	36	M8: Oxidation	611.3641	2	5.0	587	596	No
				KAVLGSSPFLSEANAER	K	I	95.00%	109		888.4742	2	6.5	246	262	No
				LANFGGLAVGLGFGALAEVAK	R	K	95.00%	139		988.0641	2	9.4	162	182	No
				LANFGGLAVGLGFGALAEVAK	R	K	95.00%	101		659.0440	3	7.3	162	182	No
				LANFGGLAVGLGFGALAEVAKK	R	S	95.00%	64		701.7436	3	8.8	214	235	No
				LGQMLSIQDDAFINPHLAK	K	I	95.00%	106	M4: Oxidation	1064.0580	2	8.0	225	243	No
				LGQMLSIQDDAFINPHLAK	K	I	95.00%	79	M4: Oxidation	709.7084	3	8.7	277	295	No
				SFTDLYIQIIR	R	A	95.00%	73		684.8854	2	7.3	465	475	No
				TLNNDLGPNWR	K	D	95.00%	63		650.3289	2	4.0	315	325	No
				VALLDFGATR	K	E	95.00%	33		1062.6040	1	8.3	503	512	No
				VALLDFGATR	K	E	95.00%	83		531.8034	2	3.8	503	512	No
287	IPI00176532	JPH2	ISOFORM 1 OF JUNCTOPHILIN-2.	AEAAEQAALAANQESNIAR	K	T	95.00%	102		964.4835	2	6.2	398	416	No

				AKAEAAEQAALAANQESNIAR	K	T	95.00%	54		709.7004	3	2.9	396	416	No
				ELAPDFYQPGPEYQK	R	R	95.00%	44		891.4319	2	9.5	421	435	No
				GGFALSLLANAEAAAR	R	A	95.00%	72		766.4188	2	4.1	198	213	No
				LLQEILENSESLLEPPDR	R	G	95.00%	57		699.0407	3	6.5	438	455	No
				MAIEALQAPPAPSREPEVALYQGYHSYAVR	R	T	95.00%	83	M1: Oxidation	1110.9000	3	8.0	543	572	No
				QSVPYGMAVVVR	R	S	95.00%	61	M7: Oxidation	661.3560	2	7.9	145	156	No
288	IPI00176903	PTRF	ISOFORM 1 OF POLYMERASE I AND TRANSCRIPT RELEASE FACTOR.	ATEMVEVGADDDEGGAER	K	G	95.00%	132	M4: Oxidation	933.8901	2	3.1	338	355	No
				ATEMVEVGADDDEGGAERGEAGDLR	K	R	95.00%	55	M4: Oxidation	855.7086	3	3.4	338	362	No
				IIGAVDQIQLTQAQLEER	K	Q	95.00%	140		1013.0610	2	7.4	61	78	No
				IIGAVDQIQLTQAQLEER	K	Q	95.00%	74		675.7079	3	4.8	61	78	No
				KLEVNEAELLR	K	R	95.00%	63		657.3771	2	2.6	137	147	No
				KLEVNEAELLR	K	R	95.00%	55		438.5873	3	2.5	137	147	No
				KSFTPDHVVYAR	R	S	95.00%	49		710.3751	2	2.8	299	310	No
				LEVNEAELLR	K	R	95.00%	70		593.3309	2	5.0	138	147	No
				MEKTK	K	V	95.00%	24	M1: Oxidation	652.3343	1	0.4	241	245	No
				QAEMEGAVQSIQGELSK	R	L	95.00%	98	M4: Oxidation	910.9468	2	8.5	79	95	No
				QAEMEGAVQSIQGELSK	R	L	95.00%	48		902.9349	2	-7.4	79	95	No
				SDQVNGVLVLSLLDK	K	I	95.00%	114		800.4590	2	8.9	46	60	No
				SFTPDHVVYAR	K	S	95.00%	53		646.3262	2	0.9	300	310	No
				VMIYQDEVKLPAK	K	L	95.00%	53	M2: Oxidation	775.4219	2	3.7	153	165	No
289	IPI00177817	ATP2A2	ISOFORM SERCA2A OF SARCOPLASMIC/ENDOPLASMIC RETICULUM CALCIUM ATPASE2.	AEIGIAMGSGTAVAK	K	T	95.00%	109	M7: Oxidation	696.3662	2	2.9	713	727	Yes
				AEIGIAMGSGTAVAK	K	T	95.00%	94		688.3702	2	5.1	713	727	Yes
				AFTGREFDELNPSAQR	K	D	95.00%	43		919.4520	2	7.0	651	666	No
				AKDIVPGDIVEIAVGDK	K	V	95.00%	41		869.9888	2	6.0	142	158	No
				AKDIVPGDIVEIAVGDK	K	V	95.00%	50		580.3287	3	6.3	142	158	No
				AKDIVPGDIVEIAVGDKVPADIR	K	L	95.00%	54		797.4560	3	9.5	142	164	No
				AKDIVPGDIVEIAVGDKVPADIR	K	L	95.00%	57		598.3425	4	6.9	142	164	No
				AMGVVVATGVNTEIGK	K	I	95.00%	108	M2: Oxidation	781.4196	2	3.4	219	234	No
				AMGVVVATGVNTEIGK	K	I	95.00%	62	M2: Oxidation	521.2828	3	4.3	219	234	No
				DIVPGDIVEIAVGDK	K	V	95.00%	118		770.4250	2	9.7	144	158	No
				DIVPGDIVEIAVGDKVPADIR	K	L	95.00%	106		1096.1100	2	6.4	144	164	No
				DIVPGDIVEIAVGDKVPADIR	K	L	95.00%	34		731.0744	3	4.5	144	164	No
				EEMHLEDSANFIK	R	Y	95.00%	67	M3: Oxidation	789.8639	2	5.8	573	585	No
				EEMHLEDSANFIK	R	Y	95.00%	41		781.8655	2	4.5	573	585	No
				EFDELNPSAQR	R	D	95.00%	70		653.3090	2	1.9	656	666	No
				EFTLEFSR	K	D	95.00%	42		1028.5150	1	9.6	482	489	Yes
				EFTLEFSR	K	D	95.00%	60		514.7578	2	2.4	482	489	Yes
				EPLISGWLFFR	K	Y	95.00%	63		682.8785	2	9.1	825	835	Yes
				EWGSGSDTLR	R	C	95.00%	32		1107.5150	1	7.4	550	559	No
				EWGSGSDTLR	R	C	95.00%	36		554.2611	2	6.6	550	559	No
				GAPEGVIDR	K	C	95.00%	58		457.2430	2	4.2	515	523	Yes
				HTDPVPDPR	K	A	95.00%	35		517.2593	2	3.8	190	198	No
				IGIFGQDEDVTSK	R	A	95.00%	108		704.8568	2	6.8	638	650	No
				IRDEMVATEQER	K	T	95.00%	59	M5: Oxidation	746.8613	2	5.5	235	246	No
				IRDEMVATEQER	K	T	95.00%	38	M5: Oxidation	498.2436	3	5.8	235	246	No
				ISLPVILMDETLK	K	F	95.00%	91	M8: Oxidation	744.4288	2	6.7	972	984	No
				ISLPVILMDETLK	K	F	95.00%	39	M8: Oxidation	496.6219	3	7.0	972	984	No
				ISLPVILMDETLK	K	F	95.00%	70		736.4296	2	4.5	972	984	No
				IVEFLQSFDEITAMTGDGVNDAPALK	K	K	95.00%	82	M14: Oxidation	933.1315	3	6.5	686	711	No
				IVEFLQSFDEITAMTGDGVNDAPALKK	K	A	95.00%	50	M14: Oxidation	975.8299	3	6.3	686	712	No
				KAEIGIAMGSGTAVAK	K	T	95.00%	119	M8: Oxidation	760.4186	2	9.2	712	727	Yes
				KAEIGIAMGSGTAVAK	K	T	95.00%	71	M8: Oxidation	507.2777	3	1.2	712	727	Yes
				KAEIGIAMGSGTAVAK	K	T	95.00%	53		501.9464	3	1.9	712	727	Yes
				KEFTLEFSR	K	D	95.00%	50		578.8086	2	7.8	481	489	Yes
				KNMLFSGTNIAAGK	K	A	95.00%	40	M3: Oxidation	734.3868	2	1.8	205	218	Yes
				KNMLFSGTNIAAGK	K	A	95.00%	43	M3: Oxidation	489.9285	3	4.7	205	218	Yes
				LDEFGEQLSK	K	V	95.00%	42		1165.5850	1	9.3	253	262	Yes
				LDEFGEQLSK	K	V	95.00%	70		583.2954	2	7.4	253	262	Yes
				MNVFDTELK	K	G	95.00%	42	M1: Oxidation	1112.5410	1	9.5	452	460	No
				MNVFDTELK	K	G	95.00%	59	M1: Oxidation	556.7715	2	4.7	452	460	No
				MNVFDTELK	K	G	95.00%	56		548.7729	2	2.7	452	460	No
				MNVFDTELKGLSK	K	I	95.00%	44	M1: Oxidation	749.3846	2	-0.7	452	464	No
				MNVFDTELKGLSK	K	I	95.00%	35	M1: Oxidation	499.9281	3	4.2	452	464	No

				NAENAIEALK	R	E	95.00%	41		1072.5620	1	-1.5	111	120	Yes
				NAENAIEALK	R	E	95.00%	71		536.7884	2	4.8	111	120	Yes
				NAENAIEALKEYEPEMGK	R	V	95.00%	103	M16: Oxidation	1026.4930	2	8.7	111	128	Yes
				NAENAIEALKEYEPEMGK	R	V	95.00%	70	M16: Oxidation	684.6614	3	4.3	111	128	Yes
				NAENAIEALKEYEPEMGK	R	V	95.00%	95		1018.4920	2	5.9	111	128	Yes
				NAENAIEALKEYEPEMGK	R	V	95.00%	46		679.3293	3	3.7	111	128	Yes
				NMLFSGTNIAAGK	K	A	95.00%	98	M2: Oxidation	670.3395	2	2.5	206	218	Yes
				NMLFSGTNIAAGK	K	A	95.00%	84		662.3448	2	6.6	206	218	Yes
				NYLEPAILE	R	-	95.00%	46		1061.5620	1	9.7	989	997	No
				NYLEPAILE	R	-	95.00%	49		531.2823	2	4.5	989	997	No
				REEMHLEDSANFIK	R	Y	95.00%	38	M4: Oxidation	578.9455	3	5.1	572	585	No
				RIGIFGQDEDVTSK	R	A	95.00%	71		782.9078	2	6.6	637	650	No
				RIGIFGQDEDVTSK	R	A	95.00%	48		522.2734	3	4.6	637	650	No
				STTLRVDQSILTGESVSVIK	K	H	95.00%	45		711.7365	3	8.0	170	189	Yes
				TASEMVLADDNFSTIVAAVEEGR	K	A	95.00%	158	M5: Oxidation	1221.0910	2	9.7	728	750	Yes
				TASEMVLADDNFSTIVAAVEEGR	K	A	95.00%	100	M5: Oxidation	814.3936	3	6.1	728	750	Yes
				TASEMVLADDNFSTIVAAVEEGR	K	A	95.00%	61	M5: Oxidation	611.0388	4	-7.6	728	750	Yes
				TVEEVLGHFGVNESTGLSLEQVK	K	K	95.00%	53		824.7639	3	5.6	8	30	No
				TVEEVLGHFGVNESTGLSLEQVKK	K	L	95.00%	86		867.4625	3	5.6	8	31	No
				VDQSILTGESVSVIK	R	H	95.00%	96		787.9398	2	4.8	175	189	Yes
				VDQSILTGESVSVIK	R	H	95.00%	75		525.6276	3	2.0	175	189	Yes
				VGEATETALTCLVEK	K	M	95.00%	87		782.4081	2	9.1	437	451	No
				VGSTKVPMTSGVK	R	Q	95.00%	33	M8: Oxidation	653.8603	2	6.7	529	541	No
				VIMITGDNK	R	G	95.00%	44	M3: Oxidation	1006.5330	1	8.2	620	628	Yes
				VIMITGDNK	R	G	95.00%	49	M3: Oxidation	503.7675	2	2.7	620	628	Yes
				VIMITGDNK	R	G	95.00%	39		495.7693	2	1.1	620	628	Yes
				WGSNELPAEEGK	R	T	95.00%	80		658.8126	2	3.7	36	47	No
290	IPI00028031; IPI00178744	ACADVL	ISOFORM 1 OF VERY-LONG-CHAIN SPECIFIC ACYL-COA DEHYDROGENASE,MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF VERY-LONG-CHAIN SPECIFIC ACYL-COA DEHYDROGENASE,MITOCHONDRIAL PRECURSOR.	AGLGSGLSLSGLVHPELSR	R	S	95.00%	116		925.5169	2	6.7	559	577	No
				AGLGSGLSLSGLVHPELSR	R	S	95.00%	72		617.3464	3	5.3	559	577	No
				ALEQFATVVEAK	R	L	95.00%	54		1305.7170	1	8.8	585	596	No
				ALEQFATVVEAK	R	L	95.00%	104		653.3574	2	1.1	585	596	No
				ALEQFATVVEAK	R	L	95.00%	29		435.9088	3	4.0	585	596	No
				ASNTAEVFFDGVR	K	V	95.00%	87		706.8473	2	4.1	350	362	No
				ASNTAEVFFDGVR	K	V	95.00%	53		471.5678	3	4.8	350	362	No
				EGMAALQSDPWQQELYR	R	N	95.00%	99	M3: Oxidation	1019.4780	2	7.2	662	678	No
				EKITAFVVER	K	G	95.00%	53		596.3431	2	3.8	323	332	No
				ELSGLGSALK	K	N	95.00%	51		974.5566	1	4.4	529	538	No
				ELSGLGSALK	K	N	95.00%	60		487.7812	2	2.3	529	538	No
				ELVEPVSR	K	F	95.00%	36		928.5120	1	1.6	150	157	No
				ELVEPVSR	K	F	95.00%	36		464.7605	2	2.9	150	157	No
				FFEEVNDPAK	R	N	95.00%	58		598.2877	2	3.4	158	167	No
				FFEEVNDPAKNDALEMVEETTWQGLK	R	E	95.00%	70	M16: Oxidation	1019.4860	3	7.0	158	183	No
				FGMAAALAGTMR	R	G	95.00%	51	M11: Oxidation	606.8000	2	4.3	388	399	No
				FGMAAALAGTMR	R	G	95.00%	35	M3: Oxidation	606.7992	2	2.9	388	399	No
				FGMAAALAGTMR	R	G	95.00%	92	M3: Oxidation	614.7960	2	1.8	388	399	No
				FGMAAALAGTMR	R	G	95.00%	92	M3: Oxidation, M11: Oxidation	614.7960	2	1.8	388	399	No
				GFGGITHGPPEK	R	K	95.00%	70		598.8099	2	4.6	333	344	No
				GFGGITHGPPEKK	R	M	95.00%	54		662.8566	2	2.9	333	345	No
				GFGGITHGPPEKK	R	M	95.00%	45		442.2397	3	1.4	333	345	No
				GGVVTSNPLGF	R	-	95.00%	38		1047.5540	1	6.4	691	701	No
				GGVVTSNPLGF	R	-	95.00%	62		524.2798	2	4.0	691	701	No
				GILLFGTK	K	A	95.00%	33		848.5312	1	7.7	234	241	No
				GILLFGTK	K	A	95.00%	54		424.7680	2	4.0	234	241	No
				GIVNEQFLLQR	K	L	95.00%	76		658.8741	2	5.7	603	613	No
				GIVNEQFLLQR	K	L	95.00%	43		439.5842	3	3.2	603	613	No
				GKELSGLGSALK	K	N	95.00%	53		580.3402	2	3.2	527	538	No

				GQLTTDQVFPYPSVLNEEQTQFLK	K	E	95.00%	74		928.1445	3	8.7	126	149	No
				IFEGTNDILR	R	L	95.00%	44		1177.6290	1	5.7	506	515	No
				IFEGTNDILR	R	L	95.00%	75		589.3185	2	6.2	484	493	No
				IFGSEAAWK	K	V	95.00%	34		1008.5230	1	7.7	466	474	No
				IFGSEAAWK	K	V	95.00%	59		504.7631	2	2.9	466	474	No
				IHNFGLIQEK	K	L	95.00%	61		599.8354	2	3.7	419	428	No
				IHNFGLIQEK	K	L	95.00%	40		400.2260	3	3.3	419	428	No
				IREGMAALQSDPWQQELYR	R	N	95.00%	43	M5: Oxidation	769.7158	3	5.4	660	678	No
				ITAFVVER	K	G	95.00%	53		467.7750	2	6.5	303	310	No
				KGIVNEQFLLQR	K	L	95.00%	73		722.9214	2	5.1	602	613	No
				KGIVNEQFLLQR	K	L	95.00%	39		482.2826	3	3.0	602	613	No
				LWISNGGLADIFTVFAK	K	T	95.00%	127		926.5102	2	6.3	294	310	No
				LWISNGGLADIFTVFAK	K	T	95.00%	51		618.0093	3	6.2	294	310	No
				NDALEMVEETTWQGLK	K	E	95.00%	83	M6: Oxidation	940.4473	2	6.2	168	183	No
				NPFGNAGLLLGEAGK	K	Q	95.00%	97		729.3953	2	4.9	539	553	No
				NPFGNAGLLLGEAGK	K	Q	95.00%	56		486.5990	3	3.9	539	553	No
				RAGLGSGLSLSGLVHPELSR	R	S	95.00%	74		669.3805	3	5.5	558	577	No
				RAGLGSGLSLSGLVHPELSR	R	S	95.00%	51		502.2878	4	6.3	536	555	No
				SFAVGMFK	K	G	95.00%	31	M6: Oxidation	902.4482	1	3.9	118	125	No
				TPVTDPATGAVK	K	E	95.00%	40		1156.6290	1	6.5	311	322	No
				TPVTDPATGAVK	K	E	95.00%	69		578.8167	2	3.3	289	300	No
				VAMHILNNGR	K	F	95.00%	54	M3: Oxidation	570.8036	2	4.0	356	365	No
				VPSENVLGEVGSGFK	R	V	95.00%	116		759.8988	2	6.1	363	377	No
				VPSENVLGEVGSGFK	R	V	95.00%	59		506.9349	3	5.6	363	377	No
291	IPI00179330; IPI00418813; IPI00456429; IPI00719280; IPI00743241; IPI00743650; IPI00744274; IPI00783060; IPI00784990; IPI00789107; IPI00789823; IPI00790633; IPI00792712	RPS27A; UBA52; UBB; UBC	UBIQUITIN AND RIBOSOMAL PROTEIN S27A PRECURSOR.; CDNA FLJ46113 FIS, CLONE TESTI2036285, HIGHLY SIMILAR TO RATTUSNORVEGICUS UBIQUITIN C.; UBIQUITIN AND RIBOSOMAL PROTEIN L40 PRECURSOR.; UBIQUITIN B PRECURSOR.; 44 KDA PROTEIN.; 44 KDA PROTEIN.; 44 KDA PROTEIN.; UBIQUITIN.; UBIQUITIN C SPLICE VARIANT.; 30 KDA PROTEIN.; 16 KDA PROTEIN.; 25 KDA PROTEIN.; 39 KDA PROTEIN.	EGIPPDQQR	K	L	95.00%	36		520.2674	2	9.2	34	42	No
				ESTLHLVLR	K	L	95.00%	36		1067.6300	1	8.0	111	119	No
				ESTLHLVLR	K	L	95.00%	49		534.3167	2	3.8	64	72	No
				ESTLHLVLR	K	R	95.00%	57		534.3159	2	2.3	64	72	No
				IQDKEGIPPDQQR	K	L	95.00%	67		762.4022	2	9.4	30	42	No
				LIFAGK	R	Q	95.00%	32		648.4127	1	6.3	43	48	No
				TITLEVEPSDTIENVK	K	A	95.00%	112		894.4747	2	7.6	12	27	No
				TITLEVEPSDTIENVK	K	A	95.00%	34		596.6525	3	7.6	12	27	No
				TLSDYNIQK	R	D	95.00%	62		541.2828	2	4.3	55	63	No
				TLSDYNIQK	R	E	95.00%	44		541.2824	2	3.5	55	63	No
292	IPI00183968	TPM3	TROPOMYOSIN 3 ISOFORM 1.	AADAEAEVASLNR	K	R	95.00%	49		658.8294	2	4.9	79	91	No
				AADAEAEVASLNR	K	R	95.00%	38		439.5562	3	6.5	79	91	No
				AADAEAEVASLNRR	K	I	95.00%	43		491.5894	3	4.8	79	92	No
				AADESER	K	G	95.00%	29		777.3453	1	9.6	120	126	Yes
				AISEELDHALNDMTSI	K	-	95.00%	65	M13: Oxidation	887.9175	2	5.8	270	285	Yes
				AISEELDHALNDMTSI	K	-	95.00%	35	M13: Oxidation	592.2813	3	6.4	270	285	Yes
				AISEELDHALNDMTSI	K	-	95.00%	44		879.9221	2	8.1	270	285	Yes
				ALKDEEKMELQEIQLK	R	E	95.00%	107	M8: Oxidation	981.0223	2	5.1	135	150	Yes
				ALKDEEKMELQEIQLK	R	E	95.00%	46	M8: Oxidation	654.3511	3	5.5	135	150	Yes
				ALKDEEKMELQEIQLK	R	E	95.00%	38	M8: Oxidation	491.0146	4	4.2	135	150	Yes
				DAQEKLELAEK	K	K	95.00%	42		637.3395	2	5.5	67	77	Yes
				DAQEKLELAEK	K	K	95.00%	39		425.2288	3	5.1	67	77	Yes
				DEEKMELQEIQLK	K	E	95.00%	62	M5: Oxidation	824.9155	2	7.6	138	150	Yes
				EDKYEEEIK	K	I	95.00%	30		591.7847	2	7.0	219	227	Yes
				GTEDELDKYSEALK	K	D	95.00%	100		799.3884	2	5.7	53	66	Yes
				GTEDELDKYSEALKDAQEK	K	L	95.00%	69		723.6816	3	4.3	53	71	Yes
				HIAEEADRKYEEVAR	K	K	95.00%	53		908.4615	2	8.9	154	168	Yes
				ILTDKLKEAETR	K	A	95.00%	56		708.9106	2	4.8	228	239	Yes
				IQLVEEELDR	R	A	95.00%	57		1243.6630	1	7.9	93	102	Yes
				IQLVEEELDR	R	A	95.00%	95		622.3312	2	0.8	93	102	Yes
				IQLVEEELDRAQER	R	L	95.00%	66		864.4579	2	8.8	93	106	Yes
				IQLVEEELDRAQER	R	L	95.00%	52		576.6364	3	0.4	93	106	Yes
				KAADAEAEVASLNR	K	R	95.00%	117		722.8766	2	4.1	78	91	No
				KAADAEAEVASLNR	K	R	95.00%	49		482.2543	3	5.2	78	91	No
				KAADAEAEVASLNRR	K	I	95.00%	43		800.9291	2	6.0	78	92	No
				KAADAEAEVASLNRR	K	I	95.00%	44		534.2871	3	3.1	78	92	No

				KLVIIEGDLER	R	T	95.00%	69		642.8843	2	6.0	169	179	Yes
				KLVIIEGDLER	R	T	95.00%	75		428.9243	3	3.3	169	179	Yes
				KLVIIEGDLERTEER	R	A	95.00%	31		900.5034	2	6.6	169	183	Yes
				KLVIIEGDLERTEER	R	A	95.00%	40		600.6729	3	8.9	169	183	Yes
				LATALQKLEEAEK	R	A	95.00%	87		722.4111	2	5.7	107	119	Yes
				LATALQKLEEAEK	R	A	95.00%	38		481.9438	3	6.8	107	119	Yes
				LATALQKLEEAEKAADESER	R	G	95.00%	71		734.7194	3	7.8	107	126	Yes
				LATALQKLEEAEKAADESER	R	G	95.00%	30		551.2904	4	5.8	107	126	Yes
				LDKENALDR	K	A	95.00%	45		537.2878	2	8.0	14	22	Yes
				LDKENALDRAEQAEAEQK	K	Q	95.00%	85		1029.5180	2	8.5	14	31	No
				LDKENALDRAEQAEAEQK	K	Q	95.00%	42		686.6797	3	6.3	14	31	No
				LDKENALDRAEQAEAEQK	K	Q	95.00%	35		515.2603	4	3.6	14	31	No
				LEEAEKAADESER	K	G	95.00%	94		738.8469	2	2.8	114	126	Yes
				LEEAEKAADESER	K	G	95.00%	63		492.8999	3	1.4	114	126	Yes
				LEEAEKAADESERGMK	K	V	95.00%	62	M15: Oxidation	904.9289	2	9.0	114	129	Yes
				LEEAEKAADESERGMK	K	V	95.00%	37	M15: Oxidation	603.6193	3	4.7	114	129	Yes
				LKEAETR	K	A	95.00%	32		423.7403	2	4.9	233	239	Yes
				LKGTEDELDKYSEALK	K	D	95.00%	100		919.9786	2	5.6	51	66	Yes
				LKGTEDELDKYSEALK	K	D	95.00%	54		613.6548	3	5.4	51	66	Yes
				LKGTEDELDKYSEALK	K	D	95.00%	40		460.4929	4	4.8	51	66	Yes
				LVIIEGDLER	K	T	95.00%	69		578.8371	2	7.3	170	179	Yes
				MELQEIQLK	K	E	95.00%	52	M1: Oxidation	574.3075	2	3.2	142	150	Yes
				MQMLKLDKENALDR	K	A	95.00%	36	M1: Oxidation, M3: Oxidation	868.9426	2	5.6	9	22	Yes
				QLEDELAAMQK	K	K	95.00%	85	M9: Oxidation	646.3175	2	5.1	39	49	No
				QLEDELAAMQK	K	K	95.00%	41		638.3215	2	7.4	39	49	No
				RIQLVEEELDR	R	A	95.00%	73		700.3859	2	6.7	92	102	Yes
				RIQLVEEELDR	R	A	95.00%	60		467.2593	3	5.4	92	102	Yes
				RIQLVEEELDRAQER	R	L	95.00%	41		628.6716	3	2.7	92	106	Yes
				RIQLVEEELDRAQER	R	L	95.00%	48		471.7569	4	5.3	92	106	Yes
				SKQLEDELAAMQK	R	K	95.00%	75	M11: Oxidation	753.8845	2	9.1	37	49	No
				SKQLEDELAAMQK	R	K	95.00%	37	M11: Oxidation	502.9246	3	7.0	37	49	No
				SKQLEDELAAMQKK	R	L	95.00%	70	M11: Oxidation	817.9311	2	7.3	37	50	No
				SKQLEDELAAMQKK	R	L	95.00%	56	M11: Oxidation	545.6226	3	6.0	37	50	No
				SLEAQAEK	K	Y	95.00%	43		438.2304	2	6.3	207	214	Yes
				TIDDLEDELYAQK	K	L	95.00%	100		776.8774	2	5.3	253	265	Yes
				TIDDLEDELYAQK	K	L	95.00%	52		518.2546	3	6.2	253	265	Yes
				YSQKEDKYEEEIK	K	I	95.00%	78		844.9086	2	4.3	215	227	Yes
				YSQKEDKYEEEIK	K	I	95.00%	31		563.6105	3	8.1	215	227	Yes
293	IPI00185631; IPI00448879; IPI00794112	AMPD1	ADENOSINE MONOPHOSPHATE DEAMINASE 1.; AMP DEAMINASE 1.; 90 KDA PROTEIN.	DGVVYVYPNEAAVSK	K	D	95.00%	66		805.9095	2	3.0	241	255	No
				EPLMEEYAIAAQVFK	K	L	95.00%	108	M4: Oxidation	877.9415	2	4.4	688	702	No
				EPLMEEYAIAAQVFK	K	L	95.00%	54	M4: Oxidation	585.6287	3	1.8	688	702	No
				EPLMEEYAIAAQVFK	K	L	95.00%	65		869.9458	2	6.5	688	702	No
				EVGADLVEAK	K	Y	95.00%	46		1030.5500	1	7.5	438	447	No
				EVGADLVEAK	K	Y	95.00%	64		515.7759	2	1.7	438	447	No
				FDKFNDKYNPVGASELR	R	D	95.00%	111		1000.5020	2	3.9	401	417	No
				FDKFNDKYNPVGASELR	R	D	95.00%	42		667.3371	3	3.9	401	417	No
				FDKFNDKYNPVGASELR	R	D	95.00%	42		500.7548	4	3.9	401	417	No
				FLGDNYLEEGPAGNDIR	K	R	95.00%	122		940.4519	2	6.9	729	745	No
				FLGDNYLEEGPAGNDIR	K	R	95.00%	46		627.3019	3	3.8	729	745	No
				FLGDNYLEEGPAGNDIRR	K	T	95.00%	47		1018.5040	2	7.6	729	746	No
				FLGDNYLEEGPAGNDIRR	K	T	95.00%	60		679.3348	3	2.4	729	746	No
				FQVHQMLNEMDELK	K	E	95.00%	51	M6: Oxidation, M10: Oxidation	897.4174	2	3.7	300	313	No
				GEDPFRTDNLPENLGYHLK	K	M	95.00%	38		739.0356	3	5.7	220	238	No
				GLMISLSTDDPMQFHFTK	K	E	95.00%	49	M3: Oxidation, M12: Oxidation	1050.5030	2	9.1	670	687	No
				HITGFDSVDDESK	K	H	95.00%	91		725.3334	2	6.1	534	546	No
				HITGFDSVDDESKHSGHMFSSK	K	S	95.00%	37	M18: Oxidation	616.7782	4	2.3	534	555	No
				IYDVFR	R	S	95.00%	34		406.7198	2	1.2	491	496	No
				KGEDPFRTDNLPENLGYHLK	K	M	95.00%	52		781.7360	3	8.1	219	238	No
				KTVNLSIPLSETSSTK	R	L	95.00%	115		852.9775	2	5.1	109	124	No
				KTVNLSIPLSETSSTK	R	L	95.00%	45		568.9858	3	2.0	109	124	No
				LKMHPYDLTVDSLDVHAGR	K	Q	95.00%	54	M3: Oxidation	728.3726	3	4.7	377	395	No
				LKMHPYDLTVDSLDVHAGR	K	Q	95.00%	60	M3: Oxidation	546.5320	4	5.9	377	395	No
				MHPYDLTVDSLDVHAGR	K	Q	95.00%	76	M1: Oxidation	971.4633	2	3.0	379	395	No
				MHPYDLTVDSLDVHAGR	K	Q	95.00%	83	M1: Oxidation	647.9794	3	5.0	379	395	No
				MHPYDLTVDSLDVHAGR	K	Q	95.00%	54	M1: Oxidation	486.2379	4	7.9	379	395	No

				MKDGVVYVYPNEAAVSK	K	D	95.00%	86	M1: Oxidation	943.4770	2	4.9	239	255	No
				MKDGVVYVYPNEAAVSK	K	D	95.00%	45	M1: Oxidation	629.3194	3	3.0	239	255	No
				NFLPHFGK	K	M	95.00%	42		480.2604	2	2.7	499	506	No
				NIDGEAWVANESFYPVFTPPVK	R	K	95.00%	98		1240.6200	2	7.3	197	218	No
				NIDGEAWVANESFYPVFTPPVK	R	K	95.00%	33		827.4100	3	0.3	197	218	No
				NIDGEAWVANESFYPVFTPPVKK	R	G	95.00%	36		870.1155	3	8.6	197	219	No
				NPFLDFLQK	K	G	95.00%	64		561.3070	2	5.8	661	669	No
				SYQIDADRVVYSTK	K	E	95.00%	89		822.9183	2	3.3	351	364	No
				TDNLPENLGYHLK	R	M	95.00%	70		757.3906	2	5.3	226	238	No
				TDNLPENLGYHLK	R	M	95.00%	42		505.2619	3	3.1	226	238	No
				TDNYINGEYFATIIK	K	E	95.00%	81		881.4460	2	8.0	423	437	No
				TDNYINGEYFATIIK	K	E	95.00%	40		587.9643	3	4.0	423	437	No
				TVNLSIPLSETSSTK	K	L	95.00%	90		788.9325	2	8.7	110	124	No
				VFASEVKDEGGR	K	Q	95.00%	43		647.3273	2	2.2	53	64	No
				YNPVGASELR	K	D	95.00%	53		553.2887	2	4.9	379	388	No
294	IPI00186290	EEF2	ELONGATION FACTOR 2.	ALLELQLEPEELYQTFQR	R	I	95.00%	120		1110.5890	2	6.5	163	180	No
				ALLELQLEPEELYQTFQR	R	I	95.00%	65		740.7281	3	5.9	163	180	No
				ARPFPDGLAEDIDKGEVSAR	K	Q	95.00%	85		715.0383	3	9.7	606	625	No
				ARPFPDGLAEDIDKGEVSAR	K	Q	95.00%	80		536.5266	4	2.2	606	625	No
				AYLPVNESFGFTADLR	K	S	95.00%	108		900.4604	2	8.9	786	801	No
				AYLPVNESFGFTADLR	K	S	95.00%	61		600.6414	3	6.4	786	801	No
				EDLYLKPIQR	K	T	95.00%	28		637.8618	2	3.6	440	449	No
				EGIPALDNFLDKL	K	-	95.00%	67		722.8897	2	1.8	846	858	No
				ETVSEESNVLCLSK	R	S	95.00%	60		769.3807	2	7.6	581	594	No
				FSVSPVVR	K	V	95.00%	35		445.7594	2	1.2	499	506	No
				GEGQLGPAER	K	A	95.00%	40		507.2577	2	5.8	240	249	No
				GGGQIIPTAR	R	R	95.00%	35		485.2806	2	5.2	717	726	No
				GHVFEESQVAGTPMFVVK	R	A	95.00%	152	M14: Oxidation	989.4997	2	8.6	768	785	No
				GHVFEESQVAGTPMFVVK	R	A	95.00%	51	M14: Oxidation	660.0015	3	7.3	768	785	No
				GLKEGIPALDNFLDKL	K	-	95.00%	58		871.9944	2	6.6	843	858	No
				GLKEGIPALDNFLDKL	K	-	95.00%	51		581.6636	3	3.2	843	858	No
				GPLMMYISK	K	M	95.00%	32	M4: Oxidation, M5: Oxidation	536.2681	2	5.9	392	400	No
				IMGPNYTPGK	R	K	95.00%	36	M2: Oxidation	547.2743	2	5.0	429	438	No
				IMGPNYTPGKK	R	E	95.00%	30	M2: Oxidation	611.3243	2	8.5	429	439	No
				KEDLYLKPIQR	K	T	95.00%	40		701.9109	2	5.7	439	449	No
				KEDLYLKPIQR	K	T	95.00%	55		468.2763	3	5.2	439	449	No
				NMSVIAHVDHGK	R	S	95.00%	56	M2: Oxidation	662.3318	2	5.9	21	32	No
				RGHVFEESQVAGTPMFVVK	K	A	95.00%	32	M15: Oxidation	712.0337	3	4.8	767	785	No
				SDPVVSYR	K	E	95.00%	31		461.7376	2	4.4	573	580	No
				STAISLFYELSENDLNFIK	K	Q	95.00%	118		1102.5710	2	9.9	72	90	No
				STAISLFYELSENDLNFIK	K	Q	95.00%	90		735.3810	3	6.8	72	90	No
				TGTITTFEHAHNMR	K	V	95.00%	51	M13: Oxidation	816.3865	2	3.2	482	495	No
				TGTITTFEHAHNMR	K	V	95.00%	40	M13: Oxidation	544.5942	3	4.3	482	495	No
				TILMMGR	R	Y	95.00%	37	M4: Oxidation, M5: Oxidation	427.2191	2	3.1	450	456	No
				VFDAIMNFK	K	K	95.00%	42	M6: Oxidation	550.7786	2	3.9	300	308	No
				VFSGLVSTGLK	R	V	95.00%	27		1107.6480	1	5.8	416	426	No
				VFSGLVSTGLK	R	V	95.00%	80		554.3258	2	2.1	416	426	No
				VNFTVDQIR	M	A	95.00%	35		1091.5870	1	1.5	2	10	No
				VNFTVDQIR	M	A	95.00%	74		546.2989	2	4.6	2	10	No
				WLPAGDALLQMITIHLPSPVTAQK	R	Y	95.00%	72		867.4881	3	8.1	343	366	No
				YEWDVAEAR	K	K	95.00%	64		569.7638	2	2.5	639	647	No

295	IPI00186966; IPI00220586; IPI00220587; IPI00220996; IPI00220997; IPI00220998; IPI00220999; IPI00221000; IPI00221001; IPI00329733; IPI00395680	BIN1	ISOFORM IIA OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM BIN1-13 OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM BIN1+12A OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM IIB OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM IIC1 OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM II2 OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM II3 OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM BIN1 OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM BIN1-10-13 OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM IIC2 OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.; ISOFORM IID OF MYC BOX-DEPENDENT-INTERACTING PROTEIN 1.	AGDVVLVIPFQNPEEQDEGWLMGVK	K	E	95.00%	35	M22: Oxidation	929.4709	3	9.4	447	471	No
				GVFPENFTER	R	V	95.00%	64		598.2952	2	6.4	582	591	No
				GVFPENFTERVP	R	-	95.00%	41		696.3561	2	6.1	486	497	No
				HHYESLQTAK	R	K	95.00%	39		405.2067	3	6.4	155	164	No
				IAENNDLLWMDYHQK	K	L	95.00%	63	M10: Oxidation	953.4498	2	5.8	103	117	No
				IAENNDLLWMDYHQK	K	L	95.00%	48	M10: Oxidation	635.9683	3	4.4	103	117	No
				LDLPPGFMFK	R	V	95.00%	49	M8: Oxidation	590.8127	2	8.3	515	524	No
				LNQNLNDVLVGLEK	K	Q	95.00%	114		784.9399	2	4.5	228	241	No
				LNQNLNDVLVGLEK	K	Q	95.00%	66		523.6304	3	6.7	228	241	No
				LVDQALLTMDTYLGQFPDIK	K	S	95.00%	74	M9: Oxidation	1149.1020	2	9.1	118	137	No
				LVDQALLTMDTYLGQFPDIK	K	S	95.00%	62	M9: Oxidation	766.4013	3	6.1	118	137	No
				LVDQALLTMDTYLGQFPDIK	K	S	95.00%	66		761.0688	3	5.0	118	137	No
				SPSPPDGSPAATPEIR	K	V	95.00%	54	S3: Phospho	829.8832	2	9.4	296	311	No
				SPSPPDGSPAATPEIR	K	V	95.00%	91		789.8975	2	6.6	296	311	No
				VFEEMNVDLQEELPSLWNSR	K	V	95.00%	35	M5: Oxidation	817.7297	3	9.6	184	203	No
				VGFYVNTFQSIAGLEENFHK	R	E	95.00%	57		1150.5820	2	9.3	204	223	No
				VGFYVNTFQSIAGLEENFHK	R	E	95.00%	48		767.3894	3	7.6	204	223	No
				VGFYVNTFQSIAGLEENFHKEMSK	R	L	95.00%	38	M22: Oxidation	698.5947	4	5.6	204	227	No
				VNHEPEPAGGATPGATLPK	R	S	95.00%	89		921.9734	2	1.9	296	314	No
				VNHEPEPAGGATPGATLPK	R	S	95.00%	53		614.9858	3	3.4	296	314	No
				VQAQHDYTATDTDELQLK	K	A	95.00%	155		1038.5030	2	4.9	356	373	No
				VQAQHDYTATDTDELQLK	K	A	95.00%	78		692.6704	3	3.3	356	373	No
296	IPI00215715; IPI00745082	CAMK2A	ISOFORM A OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II ALPHACHAIN.; CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE IIA ISOFORM 2.	AGAYDFPSPEWDTVTPEAK	K	D	95.00%	54		1040.9850	2	5.7	227	245	Yes
				DLKPENLLLASK	R	L	95.00%	31		670.8993	2	8.7	135	146	No
				DLKPENLLLASK	R	L	95.00%	40		447.6011	3	6.4	135	146	No
				ESSESTNTTIEDEDTK	K	V	95.00%	86		893.3875	2	8.8	329	344	No
				ITQYLDAGGIPR	R	T	95.00%	96		652.3597	2	7.9	434	445	No
				VTEQLIEAISNGDFESYTK	K	M	95.00%	50		715.3572	3	7.4	353	371	No
				WQIVHFHR	K	S	95.00%	33		561.8018	2	-0.4	462	469	No
297	IPI00215746	FABP4	FATTY ACID-BINDING PROTEIN, ADIPOCYTE.	EVGVGFATR	K	K	95.00%	50		468.2539	2	5.3	23	31	No
				LVSSENFDDYMK	K	E	95.00%	70	M11: Oxidation	732.3262	2	5.5	11	22	No
				VAGMAKPNMIISVNGDVITIK	K	S	95.00%	28	M4: Oxidation, M9: Oxidation	735.0734	3	9.8	33	53	No
298	IPI00215780	RPS19	40S RIBOSOMAL PROTEIN S19.	DVNQQEFVR	K	A	95.00%	40		567.7835	2	4.2	8	16	No
				LKVPEWVDTVK	K	L	95.00%	26		657.3836	2	9.4	28	38	No
299	IPI00215790	RPL38	60S RIBOSOMAL PROTEIN L38.	IEEIKDFLLTAR	K	R	95.00%	34		483.2801	3	5.7	5	16	No
				KIEEIKDFLLTAR	R	R	95.00%	26		788.4665	2	8.8	4	16	No
				KIEEIKDFLLTAR	R	R	95.00%	43		525.9786	3	5.6	4	16	No
				QSLPPGLAVK	K	E	95.00%	45		505.3093	2	6.0	58	67	No
				YLYTLVITDKEK	R	A	95.00%	50		743.4194	2	7.0	41	52	No
300	IPI00215901; IPI00218988	AK2	ISOFORM 1 OF ADENYLATE KINASE ISOENZYME 2, MITOCHONDRIAL.; ISOFORM 2 OF ADENYLATE KINASE ISOENZYME 2, MITOCHONDRIAL.	AVLLGPPGAGK	R	G	95.00%	34		490.3038	2	5.7	18	28	No
				LVSDEMVVELIEK	K	N	95.00%	40	M6: Oxidation	760.4075	2	9.2	73	85	No
301	IPI00215914; IPI00215917; IPI00797941	ARF1; ARF3	ADP-RIBOSYLATION FACTOR 1.; ADP-RIBOSYLATION FACTOR 3.; 14 KDA PROTEIN.	DAVLLVFANK	R	Q	95.00%	59		545.3237	2	8.0	118	127	No
				ILMVGLDAAGK	R	T	95.00%	76	M3: Oxidation	552.3135	2	5.0	20	30	No
				MLAEDELR	R	D	95.00%	31	M1: Oxidation	496.7422	2	4.1	110	117	No

				QDLPNAMNAAEITDK	K	L	95.00%	84	M7: Oxidation	823.8947	2	7.2	128	142	No
302	IPI00215920	ARF6	ADP-RIBOSYLATION FACTOR 6.	DAIILIFANK	R	Q	95.00%	57		559.3385	2	6.1	114	123	No
				FNVWDVGGQDK	K	I	95.00%	30		632.8047	2	4.2	59	69	No
				ILMLGLDAAGK	R	T	95.00%	57	M3: Oxidation	559.3232	2	8.2	16	26	No
303	IPI00215983	CA1	CARBONIC ANHYDRASE 1.	ADGLAVIGVLMK	K	V	95.00%	93	M11: Oxidation	601.8507	2	9.5	139	150	No
				ADGLAVIGVLMK	K	V	95.00%	100		593.8514	2	6.6	139	150	No
				EIINVGHSFHVNFEDNDNR	K	S	95.00%	39		752.6901	3	5.2	59	77	No
				ESISVSSEQLAQFR	K	S	95.00%	84		790.9055	2	7.2	215	228	No
				GGPFSDSYR	K	L	95.00%	54		493.2258	2	5.9	82	90	No
				HDTSLKPISVSYNPATAK	K	E	95.00%	122		965.0136	2	5.8	41	58	No
				HDTSLKPISVSYNPATAK	K	E	95.00%	62		643.6764	3	2.8	41	58	No
				HDTSLKPISVSYNPATAK	K	E	95.00%	35		483.0108	4	5.9	41	58	No
				LFQFHFHWGSTNEHGSEHTVDGVK	R	Y	95.00%	66		932.7776	3	9.2	91	114	No
				LYPIANGNNQSPVDIK	K	T	95.00%	68		871.9626	2	5.5	20	35	No
				TSETKHDTSLKPISVSYNPATAK	K	E	95.00%	47		825.7691	3	7.6	36	58	No
				VLDALQAIK	K	T	95.00%	38		970.5989	1	5.1	161	169	No
				VLDALQAIK	K	T	95.00%	79		485.8031	2	4.7	161	169	No
				YSAELHVAHWNSAK	K	Y	95.00%	78		806.9012	2	4.7	115	128	No
				YSAELHVAHWNSAK	K	Y	95.00%	31		538.2705	3	5.3	115	128	No
				YSSLAEAASK	K	A	95.00%	64		513.7616	2	4.5	129	138	No
304	IPI00024145; IPI00216024; IPI00216026; IPI00216027; IPI00411815; IPI00455531; IPI00718908; IPI00737171	LOC647153; LOC729317; VDAC2	ISOFORM 1 OF VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2.; ISOFORM 2 OF VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2.; ISOFORM 3 OF VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2.; ISOFORM 4 OF VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2.; ISOFORM 5 OF VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2.; SIMILAR TO VOLTAGE-DEPENDENT ANION CHANNEL 2.; ISOFORM 6 OF VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2.; SIMILAR TO VOLTAGE-DEPENDENT ANION CHANNEL 2.	GFGFGLVK	K	L	95.00%	39		412.7397	2	5.3	47	54	No
				LTFDTTFSPNTGK	K	K	95.00%	90		714.8581	2	5.0	123	135	No
				LTFDTTFSPNTGKK	K	S	95.00%	61		778.9078	2	7.4	123	136	No
				LTLSALVDGK	K	S	95.00%	35		1016.6080	1	8.5	267	276	No
				LTLSALVDGK	K	S	95.00%	82		508.8065	2	5.7	267	276	No
				NNFAVGYR	R	T	95.00%	39		470.7397	2	8.0	193	200	No
				TGDFQLHTNVNDGTEFGGSIYQK	R	V	95.00%	63		843.4011	3	7.2	201	223	No
				VNNSSLIGVGYTQTLRPGVK	K	L	95.00%	116		1052.0920	2	9.2	263	282	No
				VNNSSLIGVGYTQTLRPGVK	K	L	95.00%	47		701.7303	3	9.1	263	282	No
				YQLDPTASISAK	K	V	95.00%	88		647.3431	2	7.2	251	262	No
305	IPI00216049; IPI00216746; IPI00514561; IPI00647717; IPI00807545	HNRPK	ISOFORM 1 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K.; ISOFORM 2 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K.; HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K.; HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K.; ISOFORM 3 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K.	GSYGDLGGPIITTQVTIPK	R	D	95.00%	87		959.0291	2	8.7	378	396	No
				IDEPLEGSEDR	K	I	95.00%	79		630.2971	2	8.4	423	433	No
				IILDLISESPIK	K	G	95.00%	86		670.9098	2	5.6	208	219	No
				IITITGTQDQIQNAQYLLQNSVK	R	Q	95.00%	70		863.8082	3	7.7	434	456	No
				ILSISADIETIGEILKK	R	I	95.00%	36		615.0361	3	7.1	87	103	No
				LLIHQSLAGGIIGVK	R	G	95.00%	48		759.9764	2	5.0	149	163	No
				LLIHQSLAGGIIGVK	R	G	95.00%	59		506.9865	3	4.3	149	163	No
				RPAEDMEEEQAFKR	K	S	95.00%	60	M6: Oxidation	584.6085	3	4.2	22	35	No
				TDYNASVSVPDSSGPER	R	I	95.00%	76		890.9101	2	7.5	70	86	No
				VVLIGGKPDR	R	V	95.00%	28		527.3275	2	4.5	168	177	No
306	IPI00216070	MYL1	MYOSIN LIGHT CHAIN 1, SKELETAL MUSCLE ISOFORM.	ALGTNPTNAEVR	R	K	95.00%	35		1242.6530	1	7.3	81	92	No
				ALGTNPTNAEVR	R	K	95.00%	85		621.8251	2	-1.7	81	92	No
				ALGTNPTNAEVRK	R	V	95.00%	75		685.8757	2	3.1	81	93	No
				DQATYEDFVEGLR	K	V	95.00%	108		771.8641	2	8.2	125	137	No
				DQATYEDFVEGLR	K	V	95.00%	68		514.9119	3	8.1	125	137	No

				EAFLLFDR	K	T	95.00%	39		1010.5390	1	8.2	57	64	No
				EAFLLFDR	K	T	95.00%	75		505.7735	2	7.9	57	64	No
				EEKIDLSAIK	K	I	95.00%	28		573.3279	2	5.1	35	44	No
				EGNGTVMGAELR	K	H	95.00%	46	M7: Oxidation	625.2998	2	5.7	142	153	Yes
				EGNGTVMGAELR	K	H	95.00%	67		617.3024	2	5.8	142	153	Yes
				EQQDEFK	K	E	95.00%	34		462.2131	2	7.7	50	56	No
				EQQDEFKEAFLLFDR	K	T	95.00%	117		957.9739	2	8.4	50	64	No
				EQQDEFKEAFLLFDR	K	T	95.00%	41		638.9857	3	9.2	50	64	No
				HIMSI	K	-	95.00%	25		600.3215	1	5.9	190	194	No
				HVLATLGEK	R	M	95.00%	71		967.5673	1	9.8	154	162	No
				HVLATLGEK	R	M	95.00%	69		484.2849	2	4.3	154	162	No
				IDLSAIK	K	I	95.00%	32		759.4660	1	5.6	38	44	No
				IDLSAIKIEFSK	K	E	95.00%	55		682.4017	2	8.7	38	49	No
				IDLSAIKIEFSK	K	E	95.00%	42		455.2685	3	4.5	38	49	No
				IEFEQFLPMMQAISNNK	K	D	95.00%	35	M9: Oxidation, M10: Oxidation	691.3395	3	9.5	108	124	No
				IEFEQFLPMMQAISNNK	K	D	95.00%	84		1020.5090	2	8.3	108	124	No
				IEFEQFLPMMQAISNNK	K	D	95.00%	49		680.6741	3	6.5	108	124	No
				IEFSK	K	E	95.00%	25		623.3444	1	6.3	45	49	No
				IEFSKEQQDEFK	K	E	95.00%	54		764.3753	2	6.2	45	56	No
				IEFSKEQQDEFKEAFLLFDR	K	T	95.00%	53		840.4285	3	9.6	45	64	No
				ITLSQVGDVLR	K	A	95.00%	44		1200.7050	1	8.1	70	80	No
				ITLSQVGDVLR	K	A	95.00%	113		600.8545	2	4.8	70	80	No
				ITLSQVGDVLR	K	A	95.00%	40		400.9071	3	8.5	70	80	No
				KIEFEQFLPMMQAISNNK	K	D	95.00%	59	M10: Oxidation	728.7051	3	7.4	107	124	No
				KIEFEQFLPMMQAISNNK	K	D	95.00%	79	M10: Oxidation	1100.5480	2	4.2	107	124	No
				KIEFEQFLPMMQAISNNK	K	D	95.00%	63	M10: Oxidation	734.0369	3	7.7	107	124	No
				KIEFEQFLPMMQAISNNK	K	D	95.00%	79	M10: Oxidation, M11: Oxidation	1100.5480	2	4.2	107	124	No
				KIEFEQFLPMMQAISNNK	K	D	95.00%	63	M10: Oxidation, M11: Oxidation	734.0369	3	7.7	107	124	No
				KIEFEQFLPMMQAISNNK	K	D	95.00%	47	M11: Oxidation	1092.5550	2	8.2	107	124	No
				KIEFEQFLPMMQAISNNK	K	D	95.00%	64	M11: Oxidation	728.7050	3	7.3	107	124	No
				KIEFEQFLPMMQAISNNK	K	D	95.00%	81		1084.5550	2	6.8	107	124	No
				KIEFEQFLPMMQAISNNK	K	D	95.00%	60		723.3735	3	7.5	107	124	No
				KIEFEQFLPMMQAISNNKDQATYEDFVEGLR	K	V	95.00%	65	M10: Oxidation, M11: Oxidation	1241.9390	3	8.9	107	137	No
				KIEFEQFLPMMQAISNNKDQATYEDFVEGLR	K	V	95.00%	48	M10: Oxidation, M11: Oxidation	931.7051	4	7.9	107	137	No
				KPVAAAAAAPAPAPAPAPAPAPAK	K	P	95.00%	91		1037.6010	2	6.2	9	32	No
				KPVAAAAAAPAPAPAPAPAPAPAK	K	P	95.00%	54		692.0698	3	5.7	9	32	No
				KPVAAAAAAPAPAPAPAPAPAPAK	K	P	95.00%	45		519.3033	4	3.8	9	32	No
				KPVAAAAAAPAPAPAPAPAPAPAKPK	K	E	95.00%	89		1150.1790	2	8.7	9	34	No
				KPVAAAAAAPAPAPAPAPAPAPAKPK	K	E	95.00%	90		767.1174	3	3.0	9	34	No
				KPVAAAAAAPAPAPAPAPAPAPAKPK	K	E	95.00%	45		575.5897	4	2.4	9	34	No
				KPVAAAAAAPAPAPAPAPAPAPAKPK	K	E	95.00%	37		460.6735	5	3.0	9	34	No
				KVLGNPSNEELNAK	R	K	95.00%	111		756.9080	2	4.0	93	106	No
				KVLGNPSNEELNAK	R	K	95.00%	68		504.9408	3	3.1	93	106	No
				KVLGNPSNEELNAKK	R	I	95.00%	68		820.9603	2	9.4	93	107	No
				KVLGNPSNEELNAKK	R	I	95.00%	27		547.6397	3	3.8	93	107	No
				VFDKEGNGTVMGAELR	R	H	95.00%	90	M11: Oxidation	869.9314	2	6.6	138	153	Yes
				VFDKEGNGTVMGAELR	R	H	95.00%	43	M11: Oxidation	580.2899	3	6.1	138	153	Yes
				VFDKEGNGTVMGAELR	R	H	95.00%	132		861.9331	2	5.7	138	153	Yes
				VFDKEGNGTVMGAELR	R	H	95.00%	51		574.9572	3	4.3	138	153	Yes
				VLGNPSNEELNAK	K	K	95.00%	96		692.8621	2	6.6	94	106	No
				VLGNPSNEELNAKK	K	I	95.00%	71		756.9084	2	4.4	94	107	No
307	IPI00216138	TAGLN	TRANSGELIN.	EFTESQLQEGK	R	H	95.00%	54		648.3149	2	7.6	162	172	No
				KYDEELEER	K	L	95.00%	44		605.7857	2	3.5	21	29	No
				LVNSLYPDGSKPVK	K	V	95.00%	35		506.2883	3	7.7	65	78	No
				TLMALGSLAVTK	R	N	95.00%	35	M3: Oxidation	610.8545	2	7.0	129	140	No
308	IPI00216236; IPI00657955	TNNI2	TROPONIN I, FAST SKELETAL MUSCLE.; 21 KDA PROTEIN.	IDAAEEEK	K	Y	95.00%	38		452.7205	2	7.4	72	79	No
				IDAAEEEKYDMEVR	K	V	95.00%	55	M11: Oxidation	857.3931	2	8.2	72	85	No

				IDAAEEEKYDMEVR	K	V	95.00%	52	M11: Oxidation	571.9301	3	6.1	72	85	No
				LFDLR	K	G	95.00%	31		663.3881	1	7.5	100	104	No
				MSADAMLK	R	A	95.00%	42	M1: Oxidation, M6: Oxidation	449.7077	2	6.7	117	124	No
				SVMLQIAATELEK	K	E	95.00%	98	M3: Oxidation	724.8818	2	-7.8	20	32	No
				SVMLQIAATELEK	K	E	95.00%	105		716.8961	2	8.3	20	32	No
				SVMLQIAATELEKEESR	K	R	95.00%	35	M3: Oxidation	975.4903	2	-6.5	20	36	No
				SVMLQIAATELEKEESR	K	R	95.00%	58	M3: Oxidation	650.6725	3	8.5	20	36	No
				SVMLQIAATELEKEESRR	K	E	95.00%	43		697.3733	3	6.2	20	37	No
				YDMEVR	K	V	95.00%	33	M3: Oxidation	414.6839	2	4.6	80	85	No
309	IPI00216298; IPI00382841; IPI00552768	TXN	THIOREDOXIN.; THIOREDOXIN DELTA 3 (FRAGMENT).; THIOREDOXIN.	EKLEATINELV	K	-	95.00%	31		629.8534	2	7.4	95	105	No
				LEATINELV	K	-	95.00%	34		501.2842	2	8.6	97	105	No
				TAFQEALDAAGDK	K	L	95.00%	92		668.8270	2	5.6	9	21	No
310	IPI00216308	VDAC1	VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1.	GYGFGLIK	K	L	95.00%	44		427.7450	2	5.2	21	28	No
				KLETAVNLAWTAGNSNTR	K	F	95.00%	33		649.3475	3	8.9	201	218	No
				LETAVNLAWTAGNSNTR	K	F	95.00%	111		909.4702	2	9.9	202	218	No
				LGLGLEFQA	K	-	95.00%	47		474.2668	2	5.7	275	283	No
				LTFDSSFSPNTGK	K	K	95.00%	94		700.8437	2	6.9	97	109	No
				LTFDSSFSPNTGKK	K	N	95.00%	57		764.8921	2	7.6	97	110	No
				LTFDSSFSPNTGKK	K	N	95.00%	44		510.2621	3	3.8	97	110	No
				LTLSALLDGK	K	N	95.00%	36		1030.6240	1	8.5	257	266	No
				LTLSALLDGK	K	N	95.00%	88		515.8147	2	6.3	257	266	No
				SENGLEFTSSGSANTETTK	K	V	95.00%	110		980.4501	2	7.1	35	53	No
				TDEFQLHTNVNDGTEFGGSIYQK	K	V	95.00%	60		867.4102	3	9.4	175	197	No
				TKSENGLEFTSSGSANTETTK	K	V	95.00%	49		730.3508	3	7.2	33	53	No
				VNNSSLIGLGYTQTLKPGIK	K	L	95.00%	52		1052.1020	2	6.7	237	256	No
				VNNSSLIGLGYTQTLKPGIK	K	L	95.00%	49		701.7365	3	5.8	237	256	No
				VTGSLETK	K	Y	95.00%	40		417.7357	2	7.5	54	61	No
				VTQSNFAVGYK	R	T	95.00%	44		1213.6140	1	-6.2	164	174	No
				VTQSNFAVGYK	R	T	95.00%	72		607.3187	2	6.5	164	174	No
				WNTDNTLGTEITVEDQLAR	K	G	95.00%	50		726.0294	3	9.2	75	93	No
				WTEYGLTFTEK	R	W	95.00%	65		687.8386	2	8.1	64	74	No
311	IPI00216348; IPI00302712; IPI00744015; IPI00827813; IPI00827859	DYNC1I2	ISOFORM 2C OF CYTOPLASMIC DYNEIN 1 INTERMEDIATE CHAIN 2.; ISOFORM 2B OF CYTOPLASMIC DYNEIN 1 INTERMEDIATE CHAIN 2.; ISOFORM 2A OF CYTOPLASMIC DYNEIN 1 INTERMEDIATE CHAIN 2.; ISOFORM 2F OF CYTOPLASMIC DYNEIN 1 INTERMEDIATE CHAIN 2.; ISOFORM 2E OF CYTOPLASMIC DYNEIN 1 INTERMEDIATE CHAIN 2.	DLEDKEGEIQAGAK	R	L	95.00%	45		751.8776	2	8.9	225	238	No
				SVSTPSEAGSQDSGDGAVGSR	K	R	95.00%	129		975.9449	2	9.3	86	106	No
312	IPI00216461; IPI00784259	ACYP2	ACYLPHOSPHATASE-2.; ACYLPHOSPHATASE, MUSCLE TYPE ISOZYME.	GTVTGQVQGPEDK	K	V	95.00%	78		658.3343	2	8.5	46	58	No
				GTVTGQVQGPEDKVNSMK	K	S	95.00%	37	M17: Oxidation	945.9745	2	9.6	46	63	No
				GTVTGQVQGPEDKVNSMK	K	S	95.00%	48	M17: Oxidation	630.9839	3	6.8	46	63	No
				IGVVGWVK	K	N	95.00%	40		429.2682	2	4.2	34	41	No
				KIGVVGWVK	R	N	95.00%	39		493.3156	2	3.5	33	41	No
				LEYSNFSIR	K	-	95.00%	65		564.7917	2	5.9	90	98	No
				SVDYEVFGR	K	V	95.00%	79		536.2623	2	5.2	9	17	No
313	IPI00216798	MYL2	MYOSIN REGULATORY LIGHT CHAIN 2, VENTRICULAR/CARDIAC MUSCLE ISOFORM.	AGGANSNVFSMFEQTQIQEFK	R	E	95.00%	104	M11: Oxidation	1175.0540	2	7.5	10	30	No
				AGGANSNVFSMFEQTQIQEFK	R	E	95.00%	100		1167.0580	2	9.0	10	30	No
				AGGANSNVFSMFEQTQIQEFK	R	E	95.00%	70		778.3743	3	8.7	10	30	No
				DGFIDKNDLR	R	D	95.00%	61		596.8033	2	1.8	41	50	No
				DTFAALGR	R	V	95.00%	34		850.4471	1	5.5	51	58	No
				DTFAALGR	R	V	95.00%	59		425.7263	2	2.7	51	58	No
				EAFTIMDQNR	K	D	95.00%	72	M6: Oxidation	620.7865	2	1.6	31	40	No
				EAFTIMDQNR	K	D	95.00%	57		1224.5770	1	7.2	31	40	No
				EAFTIMDQNR	K	D	95.00%	83		612.7910	2	4.8	31	40	No
				EAPGPINFTVFLTMFGEK	K	L	95.00%	83	M14: Oxidation	1007.5140	2	9.8	72	89	No
				EAPGPINFTVFLTMFGEK	K	L	95.00%	51	M14: Oxidation	672.0098	3	7.0	72	89	No
				EAPGPINFTVFLTMFGEK	K	L	95.00%	103		999.5148	2	8.5	72	89	No
				EAPGPINFTVFLTMFGEK	K	L	95.00%	65		666.6785	3	7.6	72	89	No
				EEVDQMFAAFPPDVTGNLDYK	K	N	95.00%	81		1193.5520	2	1.7	133	153	No

				EMLTTQAER	R	F	95.00%	35	M2: Oxidation	1094.5220	1	6.2	121	129	No
				EMLTTQAER	R	F	95.00%	66	M2: Oxidation	547.7621	2	1.1	121	129	No
				EMLTTQAER	R	F	95.00%	45		1078.5270	1	6.5	121	129	No
				EMLTTQAER	R	F	95.00%	58		539.7667	2	4.9	121	129	No
				FSKEEVDQMFAAFPPDVTGNLDYK	R	N	95.00%	56	M9: Oxidation	922.1069	3	8.5	130	153	No
				FSKEEVDQMFAAFPPDVTGNLDYK	R	N	95.00%	65		916.7746	3	7.7	130	153	No
				FSKEEVDQMFAAFPPDVTGNLDYK	R	N	95.00%	56		687.8342	4	9.6	130	153	No
				GADPEETILNAFK	K	V	95.00%	89		702.8598	2	7.5	92	104	No
				GADPEETILNAFK	K	V	95.00%	50		468.9075	3	3.9	92	104	No
				LKGADPEETILNAFK	K	V	95.00%	91		823.4513	2	8.8	90	104	No
				LKGADPEETILNAFK	K	V	95.00%	53		549.3019	3	5.9	90	104	No
				NEEIDEMIK	K	E	95.00%	40	M7: Oxidation	1136.5260	1	9.7	63	71	No
				NEEIDEMIK	K	E	95.00%	59	M7: Oxidation	568.7621	2	1.5	63	71	No
				NEEIDEMIK	K	E	95.00%	54		1120.5300	1	9.2	63	71	No
				NEEIDEMIK	K	E	95.00%	57		560.7668	2	5.3	63	71	No
				NLVHIITHGEEK	K	-	95.00%	64		695.3842	2	8.1	154	165	No
				NLVHIITHGEEK	K	-	95.00%	31		463.9243	3	5.7	154	165	No
				NLVHIITHGEEKD	K	-	95.00%	78		752.8939	2	2.5	154	166	No
				NLVHIITHGEEKD	K	-	95.00%	53		502.2667	3	5.4	154	166	No
				RAGGANSNVFSMFEQTQIQEFK	K	E	95.00%	50	M12: Oxidation	835.7394	3	7.7	9	30	No
				VNVKNEEIDEMIK	R	E	95.00%	81	M11: Oxidation	788.9020	2	4.3	59	71	No
				VNVKNEEIDEMIK	R	E	95.00%	53	M11: Oxidation	526.2698	3	2.9	59	71	No
				VNVKNEEIDEMIK	R	E	95.00%	74		780.9063	2	6.6	59	71	No
				VNVKNEEIDEMIK	R	E	95.00%	36		520.9394	3	5.1	59	71	No
314	IPI00216983	CA3	CARBONIC ANHYDRASE 3.	DGIAVIGIFLK	R	I	95.00%	58		1145.7020	1	7.5	138	148	No
				DGIAVIGIFLK	R	I	95.00%	70		573.3542	2	6.1	138	148	No
				DIRHDPSLQPWSVSYDGGSAK	K	T	95.00%	72		772.3803	3	8.3	37	57	No
				EPMTVSSDQMAK	K	L	95.00%	38	M10: Oxidation	670.3014	2	5.7	213	224	No
				EPMTVSSDQMAK	K	L	95.00%	48	M3: Oxidation	670.3012	2	5.4	213	224	No
				EPMTVSSDQMAK	K	L	95.00%	61	M3: Oxidation	678.2995	2	6.6	213	224	No
				EPMTVSSDQMAK	K	L	95.00%	61	M3: Oxidation, M10: Oxidation	678.2995	2	6.6	213	224	No
				EPMTVSSDQMAK	K	L	95.00%	64		662.3040	2	5.7	213	224	No
				EWGYASHNGPDHWHELFPNAK	K	G	95.00%	48		831.3845	3	8.3	4	24	No
				GENQSPVELHTK	K	D	95.00%	75		669.8392	2	3.8	25	36	No
				GENQSPVELHTK	K	D	95.00%	40		446.8968	3	6.8	25	36	No
				GGPLPGPYR	R	L	95.00%	43		457.2508	2	4.4	81	89	No
				HDPSLQPWSVSYDGGSAK	R	T	95.00%	31	S9: Phospho	1005.9440	2	9.7	40	57	No
				HDPSLQPWSVSYDGGSAK	R	T	95.00%	132		965.9564	2	5.9	40	57	No
				HDPSLQPWSVSYDGGSAK	R	T	95.00%	96		644.3076	3	7.0	40	57	No
				IGHENGEFQIFLDALDK	K	I	95.00%	129		973.4946	2	7.8	149	165	No
				IGHENGEFQIFLDALDK	K	I	95.00%	76		649.3319	3	7.2	149	165	No
				IGHENGEFQIFLDALDKIK	K	T	95.00%	42		729.7255	3	7.1	149	167	No
				IGHENGEFQIFLDALDKIK	K	T	95.00%	51		547.5456	4	6.3	149	167	No
				LRQFHLHWGSSDDHGSEHTVDGVK	R	Y	95.00%	62		915.4445	3	9.1	90	113	No
				LRQFHLHWGSSDDHGSEHTVDGVK	R	Y	95.00%	39		686.8351	4	8.8	90	113	No
				QFHLHWGSSDDHGSEHTVDGVK	R	Y	95.00%	61		825.7128	3	6.0	92	113	No
				QRDGIAVIGIFLK	K	I	95.00%	38		477.2930	3	7.0	136	148	No
				SLLSSAENEPPVPLVSNWRPPQPINNR	R	V	95.00%	121		1004.5370	3	8.0	227	253	No
				SLLSSAENEPPVPLVSNWRPPQPINNR	R	V	95.00%	30		753.6547	4	8.4	227	253	No
				VVFDDTYDR	R	S	95.00%	36		1129.5230	1	5.6	68	76	No
				VVFDDTYDR	R	S	95.00%	77		565.2634	2	1.9	68	76	No
				YAAELHLVHWNPK	K	Y	95.00%	93		789.4220	2	8.4	114	126	No
				YAAELHLVHWNPK	K	Y	95.00%	60		526.6141	3	2.3	114	126	No
315	IPI00217030	RPS4X	40S RIBOSOMAL PROTEIN S4, X ISOFORM.	LSNIFVIGK	R	G	95.00%	64		495.8045	2	2.3	222	230	No
				VNDTIQIDLETGK	K	I	95.00%	38		723.3849	2	9.0	156	168	No

316	IPI00217232; IPI00464979	SUCLA2	ISOFORM 2 OF SUCCINYL-COA LIGASE [ADP-FORMING] BETA-CHAIN,MITOCHONDRIAL PRECURSOR.; ISOFORM 1 OF SUCCINYL-COA LIGASE [ADP-FORMING] BETA-CHAIN,MITOCHONDRIAL PRECURSOR.	ALIADSGLK	K	I	95.00%	32		444.2652	2	2.5	396	404	No
				EQALQLAQK	K	M	95.00%	47		1028.5840	1	9.4	217	225	No
				EQALQLAQK	K	M	95.00%	60		514.7937	2	5.2	195	203	No
				FQLPI	K	-	95.00%	31		617.3707	1	7.0	437	441	No
				IFDLQDWTQEDERDKDAAK	K	A	95.00%	63		775.0396	3	8.1	266	284	No
				INFDSNSAYR	K	Q	95.00%	67		593.7825	2	6.8	275	284	No
				LHGGTPANFLDVGGGATVHQVTEAFK	K	L	95.00%	81		875.1182	3	4.7	315	340	No
				LHGGTPANFLDVGGGATVHQVTEAFK	K	L	95.00%	53		656.5908	4	5.0	315	340	No
				LSEIVTLAK	K	Q	95.00%	57		487.3019	2	2.7	421	429	No
				LYSLFLK	K	Y	95.00%	56		442.2713	2	6.1	221	227	No
				MGFPPNIVESAAENMVK	K	L	95.00%	63	M1: Oxidation, M15: Oxidation	933.4477	2	5.2	204	220	No
				MGFPPNIVESAAENMVK	K	L	95.00%	39	M1: Oxidation, M15: Oxidation	622.6336	3	3.9	204	220	No
				REYYFAITMER	R	S	95.00%	45	M9: Oxidation	498.9082	3	2.6	143	153	No
				SFQGPVLIGSSHGGVNIEDVAAESPEAIIK	R	E	95.00%	37		1007.8650	3	9.1	154	183	No
				SFQGPVLIGSSHGGVNIEDVAAESPEAIIKEPIDIEEGIKK	R	E	95.00%	35		1069.0720	4	9.0	154	194	No
				SPDEAYAIAK	K	K	95.00%	70		532.7707	2	6.5	79	88	No
317	IPI00217428; IPI00644184; IPI00651724	UNC45B	ISOFORM 1 OF UNC45 HOMOLOG B.; ISOFORM 2 OF UNC45 HOMOLOG B.; ISOFORM 3 OF UNC45 HOMOLOG B.	AANNLIVLGR	K	E	95.00%	54		520.8184	2	6.9	158	167	No
				ADSAILTDQTK	K	E	95.00%	77		581.8040	2	3.7	640	650	No
				ALIPLALEGTDVGK	K	V	95.00%	70		698.9103	2	5.3	678	691	No
				ALLATLYR	K	N	95.00%	42		460.7856	2	7.1	40	47	No
				DGLQNYEALLGLTNLSGR	R	S	95.00%	110		967.5120	2	9.2	732	749	No
				DGLQNYEALLGLTNLSGR	R	S	95.00%	33		645.3423	3	6.6	732	749	No
				DKALLATLYR	K	N	95.00%	54		582.3457	2	3.9	38	47	No
				DQALNLLNK	R	N	95.00%	40		514.7929	2	3.7	297	305	No
				ETDQLVAVEALIHASTK	R	L	95.00%	92		912.9961	2	7.4	435	451	No
				EVIPELVQLAK	K	F	95.00%	48		619.8763	2	7.0	590	600	No
				GKEEALVLDTK	R	K	95.00%	53		601.8375	2	2.9	262	272	No
				GKEEALVLDTKK	R	D	95.00%	71		665.8862	2	4.5	262	273	No
				GLVIAYNLLAADAELAK	R	K	95.00%	87		873.0031	2	7.6	868	884	No
				IAAVSNPDIAFPGER	K	V	95.00%	73		778.9123	2	6.0	701	715	No
				KPELVLAAVR	K	T	95.00%	53		548.3509	2	4.3	192	201	No
				LGSAGGTDYGLR	K	Q	95.00%	62		583.7955	2	2.1	489	500	No
				LVESELLEILTVVGK	K	Q	95.00%	52		547.9965	3	3.6	886	900	No
				MLASILINK	R	L	95.00%	32	M1: Oxidation	509.8067	2	8.1	353	361	No
				NQNFQEMLR	R	R	95.00%	42	M7: Oxidation	598.2808	2	0.7	110	118	No
				TESYVQAASDASR	K	A	95.00%	72		692.8260	2	7.1	56	68	No
318	IPI00217458	GPT	ALANINE AMINOTRANSFERASE 1.	ALELEQELR	R	Q	95.00%	47		550.8027	2	2.0	45	53	No
				ANIGDAQAMGQRPITFLR	R	Q	95.00%	32	M9: Oxidation	659.0140	3	4.0	66	83	No
				AWALDVAELHR	R	A	95.00%	76		640.8464	2	7.6	213	223	No
				AWALDVAELHR	R	A	95.00%	49		427.5648	3	2.8	213	223	No
				DGGIPADPNNVFLSTGASDAIVTVLK	R	L	95.00%	95		1286.1800	2	8.4	144	169	No
				DGGIPADPNNVFLSTGASDAIVTVLK	R	L	95.00%	68		857.7883	3	7.2	144	169	No
				FTLEYS	K	-	95.00%	30		759.3597	1	4.3	491	496	No
				KPFTEVIR	K	A	95.00%	32		495.2950	2	3.6	58	65	No
				LFLLADEVYQDNVYAAGSQFHSFK	R	K	95.00%	59		921.4620	3	8.8	267	290	No
				LLVAGEGHTR	K	T	95.00%	46		526.8001	2	6.6	170	179	No
				MTILPPLEK	R	L	95.00%	36	M1: Oxidation	529.3032	2	1.5	468	476	No
				QAVLAELAAK	K	A	95.00%	26		507.3084	2	9.4	380	389	No
				VLMEMGPPYAGQQELASFHSTSK	K	G	95.00%	64	M3: Oxidation, M5: Oxidation	847.4023	3	4.5	292	314	No
				VLTLDGMNPR	K	V	95.00%	47	M7: Oxidation	566.2982	2	4.6	20	29	No
319	IPI00217466	HIST1H1D	HISTONE H1.3.	ALAAAGYDVEK	K	N	95.00%	53		554.2931	2	8.8	66	76	No
				ALAAAGYDVEKNNSR	K	I	95.00%	72		789.9022	2	5.7	66	80	No
				ASGPPVSELITK	K	A	95.00%	43		599.8406	2	4.2	36	47	No
				KASGPPVSELITK	R	A	95.00%	80		663.8907	2	7.5	35	47	No

				KASGPPVSELITK	R	A	95.00%	46		442.9287	3	5.2	35	47	No
				SGVSLAALKK	R	A	95.00%	30		487.3087	2	5.1	56	65	No
				VAGAATPKK	K	S	95.00%	28		421.7606	2	3.9	142	150	No
320	IPI00217493	MB	MYOGLOBIN.	ALELFR	K	K	95.00%	28		748.4393	1	4.6	135	140	No
				ALELFRK	K	D	95.00%	46		438.7711	2	4.1	135	141	No
				ASEDLKKHGATVLTALGGILK	K	K	95.00%	26		708.0847	3	6.9	58	78	No
				DMASNYK	K	E	95.00%	33	M2: Oxidation	422.6809	2	3.4	142	148	No
				DMASNYKELGFQG	K	-	95.00%	66	M2: Oxidation	738.3343	2	8.9	142	154	No
				GHHEAEIKPLAQSHATK	K	H	95.00%	96		927.4943	2	9.9	81	97	No
				GHHEAEIKPLAQSHATK	K	H	95.00%	49		618.6634	3	6.7	81	97	No
				GHHEAEIKPLAQSHATK	K	H	95.00%	43		464.2490	4	5.4	81	97	No
				GHPETLEK	K	F	95.00%	44		455.7370	2	3.0	36	43	No
				GHPETLEKFDK	K	F	95.00%	56		650.8351	2	6.5	36	46	No
				GHPETLEKFDK	K	F	95.00%	44		434.2246	3	3.4	36	46	No
				GHPETLEKFDKFK	K	H	95.00%	38		788.4202	2	9.7	36	48	No
				GLSDGEWQLVLNVWGK	M	V	95.00%	113		900.9757	2	8.3	2	17	No
				GLSDGEWQLVLNVWGK	M	V	95.00%	64		600.9848	3	5.6	2	17	No
				GLSDGEWQLVLNVWGKVEADIPGHGQEVLIR	M	L	95.00%	95		1138.9400	3	6.9	2	32	No
				GLSDGEWQLVLNVWGKVEADIPGHGQEVLIR	M	L	95.00%	44		854.4594	4	9.9	2	32	No
				HGATVLTALGGILK	K	K	95.00%	45	T4: Phospho	715.8991	2	9.0	65	78	No
				HGATVLTALGGILK	K	K	95.00%	61	T7: Phospho	715.8988	2	8.6	65	78	No
				HGATVLTALGGILK	K	K	95.00%	39	T7: Phospho	477.6003	3	5.5	65	78	No
				HGATVLTALGGILK	K	K	95.00%	90		1350.8240	1	9.6	65	78	No
				HGATVLTALGGILK	K	K	95.00%	119		675.9068	2	-4.0	65	78	No
				HGATVLTALGGILK	K	K	95.00%	83		450.9459	3	8.1	65	78	No
				HGATVLTALGGILKK	K	K	95.00%	99		739.9622	2	7.0	65	79	No
				HGATVLTALGGILKK	K	K	95.00%	91		493.6431	3	5.0	65	79	No
				HGATVLTALGGILKKK	K	G	95.00%	42		536.3418	3	5.4	65	80	No
				HKIPVKYLEFISECIIQVLQSK	K	H	95.00%	46		872.5009	3	9.0	98	119	No
				HLKSEDEMK	K	A	95.00%	42	M8: Oxidation	566.7716	2	3.9	49	57	No
				HLKSEDEMK	K	A	95.00%	40		558.7758	2	6.9	49	57	No
				HLKSEDEMKASEDLK	K	K	95.00%	33	M8: Oxidation	592.6256	3	7.0	49	63	No
				HPGDFGADAQGAMNK	K	A	95.00%	105	M13: Oxidation	766.3365	2	3.3	120	134	No
				HPGDFGADAQGAMNK	K	A	95.00%	85	M13: Oxidation	511.2267	3	2.9	120	134	No
				HPGDFGADAQGAMNK	K	A	95.00%	107		758.3402	2	4.8	120	134	No
				HPGDFGADAQGAMNK	K	A	95.00%	64		505.8960	3	4.8	120	134	No
				HPGDFGADAQGAMNKALELFR	K	K	95.00%	47	M13: Oxidation	566.0292	4	7.1	120	140	No
				KDMASNYK	R	E	95.00%	45	M3: Oxidation	486.7313	2	8.8	141	148	No
				KDMASNYKELGFQG	R	-	95.00%	70	M3: Oxidation	802.3829	2	9.5	141	154	No
				KGHHEAEIKPLAQSHATK	K	H	95.00%	89		991.5405	2	7.9	80	97	No
				KGHHEAEIKPLAQSHATK	K	H	95.00%	56		661.3615	3	5.7	80	97	No
				KGHHEAEIKPLAQSHATK	K	H	95.00%	50		496.2735	4	6.5	80	97	No
				KHGATVLTALGGILK	K	K	95.00%	90		739.9603	2	4.5	64	78	No
				KHGATVLTALGGILK	K	K	95.00%	58		493.6449	3	8.7	64	78	No
				KHGATVLTALGGILKK	K	K	95.00%	44		536.3434	3	8.4	64	79	No
				KHGATVLTALGGILKK	K	K	95.00%	40		402.5086	4	6.1	64	79	No
				PLAQSHATK	K	H	95.00%	35		952.5292	1	7.9	89	97	No
				PLAQSHATK	K	H	95.00%	70		476.7667	2	4.0	89	97	No
				SEDEMKASEDLKK	K	H	95.00%	37	M5: Oxidation	763.3633	2	8.6	52	64	No
				SEDEMKASEDLKK	K	H	95.00%	32	M5: Oxidation	509.2440	3	7.0	52	64	No
				VEADIPGHGQEVLIR	K	L	95.00%	99		816.9457	2	7.6	18	32	No
				VEADIPGHGQEVLIR	K	L	95.00%	75		544.9625	3	0.3	18	32	No
				YLEFISECIIQVLQSK	K	H	95.00%	39		638.3475	3	9.0	104	119	No
321	IPI00217871	ALDH4A1	DELTA-1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR.	AIEAALAAR	K	K	95.00%	44		443.2638	2	4.6	105	113	No
				ASGTNDKPGGPHYILR	R	W	95.00%	61		841.9376	2	3.4	525	540	No
				ASGTNDKPGGPHYILR	R	W	95.00%	49		561.6277	3	3.4	525	540	No
				ETHKPLGDWSYAYMQ	K	-	95.00%	52	M14: Oxidation	921.4205	2	8.7	549	563	No
				IKVGDPAEDFGTFFSAVIDAK	R	S	95.00%	61		743.0527	3	6.2	375	395	No
				LYVPHSLWPQIK	R	G	95.00%	42		494.2841	3	3.4	354	365	No
				NAAGNFYINDK	R	S	95.00%	59		613.7954	2	1.9	499	509	No
				SADVESVVSGTLR	R	S	95.00%	90		660.3485	2	6.5	326	338	No
				SSPSLTILAGGK	R	C	95.00%	43		565.8287	2	6.5	409	420	No
				STGSIVGQQPFGGAR	K	A	95.00%	64		731.3801	2	5.0	510	524	No
				VANEPVLAFTQGSPER	K	D	95.00%	110		857.9484	2	7.3	32	47	No
				VGDPAEDFGTFFSAVIDAK	K	S	95.00%	117		993.4880	2	9.3	377	395	No

				VGDPAEDFGTFFSAVIDAK	K	S	95.00%	75		662.6597	3	7.0	377	395	No
				YKETLQLVDSTTSYGLTGAVFSQDKDVVQEATK	K	V	95.00%	57		906.2189	4	9.5	463	495	No
322	IPI00217966	LDHA	ISOFORM 1 OF L-LACTATE DEHYDROGENASE A CHAIN.	DLADELALVDVIEDK	K	L	95.00%	121		829.4388	2	9.5	43	57	No
				DLADELALVDVIEDK	K	L	95.00%	88		553.2913	3	2.6	43	57	No
				DLADELALVDVIEDKLK	K	G	95.00%	33		950.0275	2	7.4	43	59	No
				DLADELALVDVIEDKLK	K	G	95.00%	32		633.6872	3	6.7	43	59	No
				DQLIYNLLK	K	E	95.00%	44		1119.6520	1	9.3	6	14	No
				DQLIYNLLK	K	E	95.00%	69		560.3275	2	4.9	6	14	No
				DQLIYNLLKEEQTPQNK	K	I	95.00%	105		1037.5540	2	8.6	6	22	No
				DQLIYNLLKEEQTPQNK	K	I	95.00%	61		692.0383	3	8.1	6	22	No
				EVHKQVVESAYEVIK	K	L	95.00%	73		879.4830	2	8.3	229	243	No
				EVHKQVVESAYEVIK	K	L	95.00%	47		586.6559	3	4.9	229	243	No
				FIIPNVVK	K	Y	95.00%	38		465.2981	2	6.4	119	126	No
				GEMMDLQHGSLFLR	K	T	95.00%	46	M3: Oxidation	825.3982	2	6.4	60	73	No
				GEMMDLQHGSLFLR	K	T	95.00%	37	M3: Oxidation	550.6003	3	4.4	60	73	No
				GEMMDLQHGSLFLR	K	T	95.00%	49	M3: Oxidation	833.3943	2	4.6	60	73	No
				GEMMDLQHGSLFLR	K	T	95.00%	49	M3: Oxidation, M4: Oxidation	833.3943	2	4.6	60	73	No
				GEMMDLQHGSLFLR	K	T	95.00%	43	M3: Oxidation, M4: Oxidation	555.9330	3	6.2	60	73	No
				GEMMDLQHGSLFLR	K	T	95.00%	38	M4: Oxidation	825.3981	2	6.2	60	73	No
				GEMMDLQHGSLFLR	K	T	95.00%	76		817.4020	2	7.8	60	73	No
				GYTSWAIGLSVADLAESIMK	K	N	95.00%	39	M19: Oxidation	1064.5450	2	8.5	246	265	No
				GYTSWAIGLSVADLAESIMK	K	N	95.00%	36		704.7001	3	7.5	246	265	No
				ISGFPK	K	N	95.00%	29		648.3749	1	4.3	150	155	No
				IVSGKDYNVTANSK	K	L	95.00%	97		748.3975	2	7.8	77	90	No
				IVSGKDYNVTANSK	K	L	95.00%	42		499.2664	3	5.2	77	90	No
				KSADTLWGIQK	K	E	95.00%	53		623.8487	2	7.8	318	328	No
				KSADTLWGIQK	K	E	95.00%	55		416.2342	3	5.8	318	328	No
				LKGEMMDLQHGSLFLR	K	T	95.00%	33	M5: Oxidation	630.9947	3	5.9	58	73	No
				LKGEMMDLQHGSLFLR	K	T	95.00%	49	M5: Oxidation	953.9860	2	6.3	58	73	No
				LKGEMMDLQHGSLFLR	K	T	95.00%	55	M5: Oxidation, M6: Oxidation	953.9862	2	6.6	58	73	No
				LKGEMMDLQHGSLFLR	K	T	95.00%	39	M5: Oxidation, M6: Oxidation	636.3266	3	6.3	58	73	No
				LKGEMMDLQHGSLFLR	K	T	95.00%	42	M5: Oxidation, M6: Oxidation	477.4979	4	8.4	58	73	No
				LKGEMMDLQHGSLFLR	K	T	95.00%	37	M6: Oxidation	630.9948	3	6.2	58	73	No
				LKGEMMDLQHGSLFLR	K	T	95.00%	101		937.9928	2	8.3	58	73	No
				LKGEMMDLQHGSLFLR	K	T	95.00%	34		469.4982	4	3.7	58	73	No
				LLIVSNPVDILTYVAWK	K	I	95.00%	151		972.5720	2	7.7	133	149	No
				LLIVSNPVDILTYVAWK	K	I	95.00%	86		648.7171	3	7.5	133	149	No
				LVIITAGAR	K	Q	95.00%	76		457.2954	2	-0.6	91	99	No
				NVNIFK	R	F	95.00%	36		734.4272	1	9.7	113	118	No
				QVVESAYEVIK	K	L	95.00%	88		632.8455	2	3.5	233	243	No
				QVVESAYEVIKLK	K	G	95.00%	28		502.6284	3	7.8	233	245	No
				RVHPVSTMIK	R	G	95.00%	42	M8: Oxidation	592.3368	2	3.1	269	278	No
				SADTLWGIQK	K	E	95.00%	40		1118.5950	1	9.1	319	328	No
				SADTLWGIQK	K	E	95.00%	62		559.7975	2	2.1	319	328	No
				TLHPDLGTDKDKEQWK	K	E	95.00%	49		955.9893	2	4.8	213	228	No
				VTLTSEEEAR	K	L	95.00%	44		1134.5740	1	8.5	306	315	No
				VTLTSEEEAR	K	L	95.00%	71		567.7856	2	-0.9	306	315	No
				VTLTSEEEARLK	K	K	95.00%	35		688.3806	2	7.3	306	317	No
323	IPI00217976; IPI00747283	MAPT	MICROTUBULE-ASSOCIATED PROTEIN TAU.; ISOFORM PNS-TAU OF MICROTUBULE-ASSOCIATED PROTEIN TAU.	EEVDEDRDVDESSPQDSPPSK	K	A	95.00%	45		787.3432	3	5.3	216	236	No
				GPSLGEDTKEADLPEPSEK	R	Q	95.00%	43		666.9924	3	5.1	339	357	No
				HQLLGDLHQEGPPLK	K	G	95.00%	38		561.3080	3	3.2	190	204	No
				IGSLDNITHVPGGGNK	K	K	95.00%	33		789.9219	2	7.5	671	686	No
				LQTAPVPMPDLK	R	N	95.00%	39	M8: Oxidation	663.3650	2	6.0	560	571	No
				VSTEIPASEPDGPSVGR	K	A	95.00%	50		849.4238	2	2.9	275	291	No
324	IPI00218130	PYGM	GLYCOGEN PHOSPHORYLASE, MUSCLE FORM.	APNDFNLK	K	D	95.00%	43		918.4750	1	7.0	249	256	No
				APNDFNLK	K	D	95.00%	51		459.7390	2	1.9	249	256	No
				APNDFNLKDFNVGGYIQAVLDR	K	N	95.00%	137		1233.6360	2	9.2	249	270	No
				APNDFNLKDFNVGGYIQAVLDR	K	N	95.00%	77		822.7585	3	7.4	249	270	No

ARPEFTLPVHFYGHVEHTSQGAK	K	W	95.00%	78		870.1143	3	8.2	193	215	No
ARPEFTLPVHFYGHVEHTSQGAK	K	W	95.00%	54		652.8364	4	6.2	193	215	No
AWDVTVR	K	T	95.00%	34		846.4500	1	3.0	365	371	No
AWDVTVR	K	T	95.00%	50		423.7283	2	1.7	365	371	No
DFNVGGYIQAVLDR	K	N	95.00%	120		783.9009	2	1.5	257	270	No
DFNVGGYIQAVLDR	K	N	95.00%	78		522.9370	3	2.3	257	270	No
DFYELEPHK	K	F	95.00%	44		589.2827	2	3.8	471	479	No
DFYELEPHKFQNK	K	T	95.00%	52		847.9187	2	6.9	471	483	No
DIVNMLMHHDR	K	F	95.00%	42	M5: Oxidation	698.8291	2	2.6	761	771	No
DIVNMLMHHDR	K	F	95.00%	35	M5: Oxidation	706.8248	2	0.1	761	771	No
DIVNMLMHHDR	K	F	95.00%	46	M5: Oxidation, M7: Oxidation	706.8292	2	6.3	761	771	No
DIVNMLMHHDR	K	F	95.00%	33	M5: Oxidation, M7: Oxidation	471.5535	3	2.2	761	771	No
DIVNMLMHHDR	K	F	95.00%	45	M7: Oxidation	698.8303	2	4.4	761	771	No
DYYFALAHTVR	R	D	95.00%	79		678.3436	2	3.4	51	61	No
DYYFALAHTVR	R	D	95.00%	55		452.5653	3	4.0	51	61	No
DYYFALAHTVRDHLVGR	R	W	95.00%	41		678.3528	3	3.5	51	67	No
EIWGVEPSR	R	Q	95.00%	45		1072.5500	1	6.4	824	832	No
EIWGVEPSR	R	Q	95.00%	46		536.7763	2	1.8	824	832	No
EYKVHINPNSLFDIQVK	R	R	95.00%	36		682.0408	3	9.9	553	569	No
EYKVHINPNSLFDIQVK	R	R	95.00%	27		511.7815	4	7.6	553	569	No
FAAYLER	K	E	95.00%	36		869.4558	1	4.2	546	552	No
FAAYLER	K	E	95.00%	47		435.2311	2	2.7	546	552	No
FKVFADYEDYIK	R	C	95.00%	74		769.3890	2	7.9	772	783	No
FKVFADYEDYIK	R	C	95.00%	58		513.2613	3	6.7	772	783	No
GLAGVENVTELK	R	K	95.00%	47		1229.6860	1	9.7	18	29	No
GLAGVENVTELK	R	K	95.00%	84		615.3432	2	3.5	18	29	No
GLAGVENVTELKK	R	N	95.00%	105		679.3906	2	3.1	18	30	No
GLAGVENVTELKK	R	N	95.00%	55		453.2617	3	0.2	18	30	No
GYNAQEYYDR	R	I	95.00%	71		639.7755	2	3.2	726	735	No
GYNAQEYYDRIPELR	R	Q	95.00%	59		943.9611	2	5.6	726	740	No
GYNAQEYYDRIPELR	R	Q	95.00%	66		629.6426	3	4.5	726	740	No
HLHFTLVK	R	D	95.00%	31		994.5856	1	1.7	35	42	No
HLHFTLVK	R	D	95.00%	44		497.7996	2	7.4	35	42	No
HLHFTLVKDR	R	N	95.00%	50		633.3628	2	4.6	35	44	No
HLHFTLVKDR	R	N	95.00%	31		422.5769	3	2.3	35	44	No
HLQIIYEINQR	R	F	95.00%	80		713.8990	2	6.6	400	410	No
HLQIIYEINQR	R	F	95.00%	64		476.2672	3	3.6	400	410	No
IGEDFISDLDQLR	R	K	95.00%	82		760.8860	2	2.8	508	520	No
IGEDFISDLDQLR	R	K	95.00%	63		507.5938	3	3.9	508	520	No
IGEDFISDLDQLRK	R	L	95.00%	107		824.9355	2	5.0	508	521	No
IGEDFISDLDQLRK	R	L	95.00%	75		550.2919	3	3.0	508	521	No
IHSEILKK	R	T	95.00%	28		484.3041	2	6.4	459	466	No
ILVDLER	R	M	95.00%	36		857.5116	1	2.1	353	359	No
ILVDLER	R	M	95.00%	61		429.2592	2	0.9	353	359	No
ILVDLERMDWDK	R	A	95.00%	40	M8: Oxidation	774.8965	2	7.6	353	364	No
ILVDLERMDWDKAWDVTVR	R	T	95.00%	42	M8: Oxidation	792.7458	3	8.2	353	371	No
ISGGWQMEEADDWLR	K	Y	95.00%	95	M7: Oxidation	904.9054	2	6.3	171	185	No
ISGGWQMEEADDWLR	K	Y	95.00%	55	M7: Oxidation	603.6046	3	3.7	171	185	No
ISGGWQMEEADDWLR	K	Y	95.00%	107		896.9098	2	8.5	171	185	No
ISGGWQMEEADDWLR	K	Y	95.00%	48		598.2715	3	1.2	171	185	No
IYYLSLEFYMGR	R	T	95.00%	97	M10: Oxidation	785.8895	2	6.1	83	94	No
KLLSFVDDEAFIR	R	D	95.00%	113		776.9249	2	2.8	521	533	No
KLLSFVDDEAFIR	R	D	95.00%	73		518.2863	3	3.6	521	533	No
KLLSFVDDEAFIRDVAK	R	V	95.00%	93		983.5431	2	6.8	521	537	No
KLLSFVDDEAFIRDVAK	R	V	95.00%	69		656.0327	3	8.8	521	537	No
KLLSFVDDEAFIRDVAK	R	V	95.00%	52		492.2749	4	5.6	521	537	No
LKFAAYLER	K	E	95.00%	55		555.8227	2	5.7	544	552	No
LKQEYFVVAATLQDIIR	R	R	95.00%	139		1004.0780	2	9.8	294	310	No
LKQEYFVVAATLQDIIR	R	R	95.00%	70		669.7180	3	5.0	294	310	No
LKQEYFVVAATLQDIIR	R	R	95.00%	50		502.5422	4	8.5	294	310	No
LLSFVDDEAFIR	K	D	95.00%	94		712.8773	2	2.8	522	533	No
LLSFVDDEAFIR	K	D	95.00%	66		475.5876	3	3.3	522	533	No
LLSFVDDEAFIRDVAK	K	V	95.00%	96		919.4941	2	5.6	522	537	No
LLSFVDDEAFIRDVAK	K	V	95.00%	62		613.3301	3	2.6	522	537	No
LPAPDEAI	R	-	95.00%	33		825.4388	1	3.5	835	842	No
LPAPDEAI	R	-	95.00%	31		413.2227	2	2.0	835	842	No

LRVIFLENYR	R	V	95.00%	26		441.5942	3	6.4	641	650	No
LVTAIGDVVNHDPAVGDR	R	L	95.00%	132		924.4875	2	2.9	623	640	No
LVTAIGDVVNHDPAVGDR	R	L	95.00%	70		616.6608	3	2.8	623	640	No
LVTAIGDVVNHDPAVGDRLR	R	V	95.00%	77		706.3909	3	4.7	623	642	No
MDWDKAWDVTVR	R	T	95.00%	79	M1: Oxidation	769.3644	2	6.4	360	371	No
MDWDKAWDVTVR	R	T	95.00%	51	M1: Oxidation	513.2452	3	5.7	360	371	No
MDWDKAWDVTVR	R	T	95.00%	67		761.3666	2	6.1	360	371	No
MDWDKAWDVTVR	R	T	95.00%	54		507.9123	3	3.4	360	371	No
MSLVEEGAVK	R	R	95.00%	31	M1: Oxidation	1078.5520	1	5.8	429	438	No
MSLVEEGAVK	R	R	95.00%	64	M1: Oxidation	539.7773	2	1.1	429	438	No
MSLVEEGAVK	R	R	95.00%	59		531.7801	2	1.6	429	438	No
MSLVEEGAVKR	R	I	95.00%	63	M1: Oxidation	617.8291	2	3.1	429	439	No
MSLVEEGAVKR	R	I	95.00%	36	M1: Oxidation	412.2218	3	2.7	429	439	No
MSLVEEGAVKR	R	I	95.00%	75		609.8337	2	6.4	429	439	No
NIATSGK	R	F	95.00%	41		690.3815	1	4.2	805	811	No
NLAENISR	R	V	95.00%	38		916.4891	1	4.3	271	278	No
NLAENISR	R	V	95.00%	53		458.7470	2	1.1	271	278	No
NNVVNTMR	R	L	95.00%	53	M7: Oxidation	482.2384	2	1.0	236	243	No
NNVVNTMR	R	L	95.00%	32		474.2423	2	3.7	236	243	No
PEFTLPVHFYGHVEHTSQGAK	R	W	95.00%	35		596.0464	4	-2.5	195	215	No
QEYFVVAATLQDIIR	K	R	95.00%	121		883.4865	2	9.1	296	310	No
QEYFVVAATLQDIIR	K	R	95.00%	56		589.3236	3	3.5	296	310	No
QPDLFK	K	D	95.00%	28		747.4090	1	6.4	755	760	No
QRLPAPDEAI	R	-	95.00%	49		1109.6030	1	6.4	833	842	No
QRLPAPDEAI	R	-	95.00%	79		555.3013	2	-0.8	833	842	No
QVIEQLSSGFFSPK	R	Q	95.00%	130		783.9155	2	4.1	741	754	No
QVIEQLSSGFFSPK	R	Q	95.00%	54		522.9467	3	4.8	741	754	No
REPNKFFVPR	K	T	95.00%	27		645.3630	2	4.7	593	602	No
REPNKFFVPR	K	T	95.00%	48		430.5771	3	2.9	593	602	No
RIYYLSLEFYMGR	K	T	95.00%	48	M11: Oxidation	576.2944	3	2.9	82	94	No
RMSLVEEGAVK	R	R	95.00%	54	M2: Oxidation	412.2219	3	2.9	428	438	No
RMSLVEEGAVKR	R	I	95.00%	66	M2: Oxidation	695.8821	2	6.2	428	439	No
RMSLVEEGAVKR	R	I	95.00%	52	M2: Oxidation	464.2557	3	2.8	428	439	No
RMSLVEEGAVKR	R	I	95.00%	38		687.8815	2	1.7	428	439	No
RMSLVEEGAVKR	R	I	95.00%	56		458.9236	3	1.6	428	439	No
TIAQYAR	R	E	95.00%	37		411.7293	2	4.2	817	823	No
TIFKDFYELEPHK	K	F	95.00%	49	Y7: Phospho	873.9151	2	4.3	467	479	No
TIFKDFYELEPHK	K	F	95.00%	65		833.9360	2	9.4	467	479	No
TIFKDFYELEPHK	K	F	95.00%	49		556.2896	3	2.9	467	479	No
TIFKDFYELEPHK	K	F	95.00%	33		417.4691	4	2.6	467	479	No
TIFKDFYELEPHKFQNK	K	T	95.00%	29		728.7153	3	7.7	467	483	No
TNFDAFPDK	R	V	95.00%	54		1054.4930	1	7.6	325	333	No
TNFDAFPDK	R	V	95.00%	70		527.7473	2	2.0	325	333	No
TNFDAFPDKVAIQLNDTHPSLAIPELMR	R	I	95.00%	48	M27: Oxidation	1057.2130	3	8.0	325	352	No
TNFDAFPDKVAIQLNDTHPSLAIPELMR	R	I	95.00%	62	M27: Oxidation	793.1617	4	7.6	325	352	No
TNFDAFPDKVAIQLNDTHPSLAIPELMR	R	I	95.00%	32		1051.8770	3	3.3	325	352	No
TQQHYYEKDPKR	R	I	95.00%	40		531.6030	3	6.8	71	82	No
VAAAFPGDVDR	R	L	95.00%	61		1117.5700	1	4.7	415	425	No
VAAAFPGDVDR	R	L	95.00%	71		559.2848	2	-2.3	415	425	No
VAAAFPGDVDRLR	R	R	95.00%	53		693.8826	2	5.6	415	427	No
VAAAFPGDVDRLR	R	R	95.00%	36		462.9233	3	3.4	415	427	No
VAIQLNDTHPSLAIPELMR	K	I	95.00%	105	M18: Oxidation	1067.5790	2	8.2	334	352	No
VAIQLNDTHPSLAIPELMR	K	I	95.00%	66	M18: Oxidation	712.0530	3	4.8	334	352	No
VAIQLNDTHPSLAIPELMR	K	I	95.00%	104		1059.5800	2	6.7	334	352	No
VAIQLNDTHPSLAIPELMR	K	I	95.00%	55		706.7212	3	4.5	334	352	No
VEDVDKLDQR	R	G	95.00%	87		608.8141	2	2.4	716	725	No
VEDVDKLDQR	R	G	95.00%	53		406.2118	3	1.9	716	725	No
VFADYEDYIK	K	C	95.00%	56		1262.6010	1	5.4	774	783	No
VFADYEDYIK	K	C	95.00%	80		631.8014	2	0.3	774	783	No
VHINPNSLFDIQVK	K	R	95.00%	111		812.4498	2	3.6	556	569	No
VHINPNSLFDIQVK	K	R	95.00%	49		541.9700	3	5.1	556	569	No
VHINPNSLFDIQVKR	K	I	95.00%	34		890.5015	2	4.5	556	570	No
VHINPNSLFDIQVKR	K	I	95.00%	65		594.0053	3	7.5	556	570	No
VIFLENYR	R	V	95.00%	52		1053.5810	1	7.3	643	650	No
VIFLENYR	R	V	95.00%	63		527.2914	2	1.6	643	650	No
VIPAADLSEQISTAGTEASGTGNMK	K	F	95.00%	118	M24: Oxidation	1232.6090	2	9.3	657	681	No

				VIPAADLSEQISTAGTEASGTGNMK	K	F	95.00%	76	M24: Oxidation	822.0706	3	3.3	657	681	No
				VIPAADLSEQISTAGTEASGTGNMK	K	F	95.00%	38	M24: Oxidation	616.8058	4	4.9	657	681	No
				VIPAADLSEQISTAGTEASGTGNMK	K	F	95.00%	106		1224.6120	2	9.8	657	681	No
				VIPAADLSEQISTAGTEASGTGNMK	K	F	95.00%	68		816.7409	3	5.7	657	681	No
				VLYPNDNFFEGK	R	E	95.00%	83		721.8549	2	4.4	279	290	No
				VSALYKNPR	K	E	95.00%	47		524.3029	2	2.7	788	796	No
				WPVHLLETLLPR	R	H	95.00%	83		737.4387	2	7.5	388	399	No
				WPVHLLETLLPR	R	H	95.00%	50		491.9596	3	3.2	388	399	No
				WVDTQVVLAMPYDTPVPGYR	K	N	95.00%	98	M10: Oxidation	1162.0830	2	6.2	216	235	No
				WVDTQVVLAMPYDTPVPGYR	K	N	95.00%	69	M10: Oxidation	775.0596	3	8.5	216	235	No
				YEFGIFNQK	R	I	95.00%	44		1145.5740	1	9.2	162	170	No
				YEFGIFNQK	R	I	95.00%	64		573.2880	2	4.3	162	170	No
				YGNPWEK	R	A	95.00%	31		893.4239	1	9.2	186	192	No
				YGNPWEK	R	A	95.00%	54		447.2136	2	4.2	186	192	No
325	IPI00218192; IPI00294193; IPI00556036; IPI00760855; IPI00790993	ITIH4; TMEM110	ISOFORM 2 OF INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR.; ISOFORM 1 OF INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR.; INTER-ALPHA (GLOBULIN) INHIBITOR H4 (PLASMA KALLIKREIN-SENSITIVEGLYCOPROTEIN) VARIANT (FRAGMENT).; 101 KDA PROTEIN.; 104 KDA PROTEIN.	AEAQAQYSAAVAK	K	G	95.00%	64		654.3381	2	6.8	99	111	No
				ANTVQEATFQMELPK	R	K	95.00%	37	M11: Oxidation	861.9265	2	4.5	61	75	No
				GPDVLTATVSGK	R	L	95.00%	55		572.8159	2	2.0	501	512	No
				LALDNGGLAR	K	R	95.00%	27		500.2848	2	2.8	429	438	No
				LGVYELLLK	R	V	95.00%	47		524.3295	2	5.2	154	162	No
				NMEQFQVSVSVAPNAK	R	I	95.00%	78	M2: Oxidation	882.9383	2	5.6	124	139	No
				SPEQQETVLDGNLIIR	K	Y	95.00%	63		906.4871	2	8.6	225	240	No
326	IPI00218236	PPP1CB	SERINE/THREONINE-PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT.	AHQVVEDGYEFFAK	R	R	95.00%	85		820.3969	2	6.4	246	259	No
				AHQVVEDGYEFFAK	R	R	95.00%	76		547.2626	3	-1.9	246	259	No
				EIFLSQPILLELEAPLK	R	I	95.00%	99		977.0767	2	7.1	43	59	No
				EIFLSQPILLELEAPLK	R	I	95.00%	27		651.7212	3	8.4	43	59	No
				GVSFTFGADVVSK	R	F	95.00%	56		657.3415	2	0.7	221	233	No
				IKYPENFFLLR	K	G	95.00%	30		720.4111	2	6.4	111	121	No
				IKYPENFFLLR	K	G	95.00%	68		480.6076	3	1.4	111	121	No
				IVQMTEAEVR	K	G	95.00%	48	M4: Oxidation	596.3097	2	5.9	26	35	No
				YPENFFLLR	K	G	95.00%	51		599.8182	2	1.9	113	121	No
327	IPI00218342; IPI00794900	MTHFD1	C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC.; 105 KDA PROTEIN.	AAQAPSSFQLLYDLK	R	L	95.00%	76		826.4469	2	9.8	844	858	No
				AYIQENLELVEK	K	G	95.00%	68		724.8884	2	3.6	761	772	No
				DVDGLTSINAGR	K	L	95.00%	53		609.3077	2	-4.4	123	134	No
				EIGLLSEEVELYGETK	R	A	95.00%	110		904.9675	2	5.5	376	391	No
				EQVPGFTPR	K	L	95.00%	31		515.7726	2	5.0	68	76	No
				GALALAQAVQR	K	A	95.00%	62		549.3275	2	3.6	833	843	No
				GVPTGFILPIR	K	D	95.00%	72		585.3616	2	8.9	918	928	No
				KGEPVSAEDLGVSGALTVLMK	K	D	95.00%	34	M20: Oxidation	706.3803	3	4.2	635	655	No
				KITIGQAPTEK	R	G	95.00%	35		593.3483	2	3.6	543	553	No
				KVVGDVAYDEAK	R	E	95.00%	48		647.3431	2	7.1	290	301	No
				LAILQVGNR	R	D	95.00%	70		492.3074	2	6.8	77	85	No
				LDIDPETITWQR	R	V	95.00%	54		743.8860	2	6.5	560	571	No
				LGIEKTDPTTLTDEEINR	R	F	95.00%	33		682.3564	3	6.3	500	517	No
				MHGGGPTVTAGLPLPK	K	A	95.00%	50	M1: Oxidation	774.9190	2	5.8	706	721	No
				TAHLDEEVNKGDILVVATGQPEMVK	K	G	95.00%	50	M23: Oxidation	903.8055	3	8.7	199	223	No
				TAHLDEEVNKGDILVVATGQPEMVK	K	G	95.00%	31	M23: Oxidation	678.1057	4	8.2	238	262	No
				TDPTTLTDEEINR	K	F	95.00%	34		752.8662	2	7.5	544	556	No
				TDTESELDLISR	K	L	95.00%	78		689.8415	2	3.5	800	811	No
				TPVPSDIDISR	K	S	95.00%	47		600.3195	2	3.3	353	363	No
				VLLSALER	K	L	95.00%	38		450.7818	2	4.3	394	401	No
				VVGDVAYDEAK	K	E	95.00%	51		583.2951	2	7.0	291	301	No
				WMIQYNNLNLK	K	T	95.00%	46	M2: Oxidation	726.8753	2	8.2	342	352	No
				YVVVTGITPTPLGEGK	K	S	95.00%	93		815.9605	2	4.5	410	425	No

328	IPI00218343; IPI00387144; IPI00792677	TUBA1B; TUBA1C	TUBULIN ALPHA-6 CHAIN.; TUBULIN ALPHA-UBIQUITOUS CHAIN.; 46 KDA PROTEIN.	AFVHWYVGEGMEEGEFSEAR	R	E	95.00%	39	M11: Oxidation	782.6829	3	8.3	403	422	Yes
				AVFVDLEPTVIDEVR	R	T	95.00%	55		567.9766	3	4.6	65	79	Yes
				DVNAAIATIK	K	T	95.00%	40		508.2967	2	6.6	327	336	Yes
				EIIDLVLDR	K	I	95.00%	61		543.3165	2	3.8	113	121	Yes
				FDLMYAK	K	R	95.00%	33	M4: Oxidation	452.2205	2	5.0	395	401	Yes
				IHFPLATYAPVISAEK	R	A	95.00%	47		878.9936	2	8.8	265	280	Yes
				IHFPLATYAPVISAEK	R	A	95.00%	65		586.3311	3	7.8	265	280	Yes
				LISQIVSSITASLR	R	F	95.00%	41		744.4507	2	9.3	230	243	Yes
				LISQIVSSITASLR	R	F	95.00%	77		496.6362	3	8.9	230	243	Yes
				NLDIERPTYTNLNR	R	L	95.00%	59		859.9529	2	8.9	216	229	Yes
				QLFHPEQLITGK	R	E	95.00%	39		705.8959	2	6.6	85	96	Yes
				QLFHPEQLITGK	R	E	95.00%	44		470.9336	3	7.3	85	96	Yes
				QLFHPEQLITGKEDAANNYAR	R	G	95.00%	39		805.7460	3	7.0	85	105	Yes
				VGINYQPPTVVPGGDLAK	K	V	95.00%	78		913.0059	2	9.7	353	370	Yes
329	IPI00218414	CA2	CARBONIC ANHYDRASE 2.	AVQQPDGLAVLGIFLK	K	V	95.00%	95		834.9957	2	8.6	133	148	No
				AVQQPDGLAVLGIFLK	K	V	95.00%	58		556.9980	3	5.6	133	148	No
				DFPIAK	K	G	95.00%	26		690.3865	1	5.5	19	24	No
				EPISVSSEQVLK	K	F	95.00%	48		658.3636	2	6.5	213	224	No
				GGPLDGTYR	K	L	95.00%	31		468.2355	2	4.6	81	89	No
				KYAAELHLVHWNTK	K	Y	95.00%	42		570.6459	3	5.4	113	126	No
				KYAAELHLVHWNTK	K	Y	95.00%	31		428.2352	4	2.5	113	126	No
				SADFTNFDPR	K	G	95.00%	65		585.2683	2	5.1	172	181	No
				VVDVLDSIK	K	T	95.00%	37		987.5763	1	3.7	159	167	No
				VVDVLDSIK	K	T	95.00%	52		494.2933	2	6.2	159	167	No
				YAAELHLVHWNTK	K	Y	95.00%	62		527.9484	3	7.5	114	126	No
				YDPSLKPLSVSYDQATSLR	K	I	95.00%	45		714.0409	3	6.7	40	58	No
330	IPI00218474	ENO3	BETA-ENOLASE.	AAVPSGASTGIYEALELR	R	D	95.00%	58	S8: Phospho	942.9679	2	9.0	33	50	Yes
				AAVPSGASTGIYEALELR	R	D	95.00%	42	T9: Phospho	942.9656	2	6.5	33	50	Yes
				AAVPSGASTGIYEALELR	R	D	95.00%	60	Y12: Phospho	942.9658	2	6.8	33	50	Yes
				AAVPSGASTGIYEALELR	R	D	95.00%	162		902.9806	2	4.8	33	50	Yes
				AAVPSGASTGIYEALELR	R	D	95.00%	99		602.3227	3	4.4	33	50	Yes
				AAVPSGASTGIYEALELRDGDK	R	G	95.00%	97		1110.5700	2	7.7	33	54	No
				AAVPSGASTGIYEALELRDGDK	R	G	95.00%	38		740.7137	3	4.7	33	54	No
				DATNVGDEGGFAPNILENNEALELLK	K	T	95.00%	109		1372.1870	2	8.6	203	228	No
				DATNVGDEGGFAPNILENNEALELLK	K	T	95.00%	83		915.1279	3	9.4	203	228	No
				FGANAILGVSLAVCKAGAAEK	K	G	95.00%	43		664.0344	3	4.0	106	126	No
				FMIELDGTENK	K	S	95.00%	56	M2: Oxidation	1312.6170	1	5.6	93	103	No
				FMIELDGTENK	K	S	95.00%	79	M2: Oxidation	656.8116	2	4.4	93	103	No
				GNPTVEVDLHTAK	R	G	95.00%	102		690.8623	2	3.1	16	28	No
				GNPTVEVDLHTAK	R	G	95.00%	57		460.9102	3	1.7	16	28	No
				HIADLAGNPDLILPVPAFNVINGGSHAGNK	R	L	95.00%	77		1007.8780	3	9.1	133	162	No
				IEEALGDK	R	A	95.00%	42		874.4570	1	5.4	413	420	No
				IEEALGDK	R	A	95.00%	67		437.7319	2	4.2	413	420	No
				IEEALGDKAIFAGR	R	K	95.00%	113		745.4082	2	4.7	413	426	No
				IEEALGDKAIFAGR	R	K	95.00%	71		497.2741	3	3.4	413	426	No
				IGAEVYHHLK	R	G	95.00%	32		1166.6380	1	4.5	184	193	No
				IGAEVYHHLK	R	G	95.00%	64		583.8220	2	3.3	184	193	No
				IGAEVYHHLKGVIK	R	A	95.00%	49		521.9736	3	2.4	184	197	No
				KLSVVDQEK	K	V	95.00%	42		523.3012	2	4.9	81	89	No
				KLSVVDQEKVDK	K	F	95.00%	83		694.3983	2	6.5	81	92	No
				KLSVVDQEKVDK	K	F	95.00%	29		463.2670	3	4.0	81	92	No
				LAMQEFMILPVGASSFK	K	E	95.00%	101	M3: Oxidation	942.9921	2	8.4	163	179	No
				LAMQEFMILPVGASSFK	K	E	95.00%	126	M3: Oxidation	950.9893	2	8.2	163	179	No
				LAMQEFMILPVGASSFK	K	E	95.00%	68	M3: Oxidation	634.3282	3	7.1	163	179	No
				LAMQEFMILPVGASSFK	K	E	95.00%	128	M3: Oxidation, M7: Oxidation	950.9893	2	8.1	163	179	No
				LAMQEFMILPVGASSFK	K	E	95.00%	68	M3: Oxidation, M7: Oxidation	634.3282	3	7.1	163	179	No
				LAMQEFMILPVGASSFK	K	E	95.00%	130	M7: Oxidation	942.9920	2	8.4	163	179	No
				LAMQEFMILPVGASSFK	K	E	95.00%	41	M7: Oxidation	628.9936	3	2.5	163	179	No
				LAMQEFMILPVGASSFK	K	E	95.00%	88		934.9957	2	9.7	163	179	No
				LAMQEFMILPVGASSFK	K	E	95.00%	55		623.6662	3	9.3	163	179	No
				LAQSNGWGVMVSHR	K	S	95.00%	73	M10: Oxidation	779.3876	2	5.2	359	372	No
				LAQSNGWGVMVSHR	K	S	95.00%	49	M10: Oxidation	519.9263	3	2.5	359	372	No

				LAQSNGWGVMVSHR	K	S	95.00%	66		771.3892	2	3.9	359	372	No
				LSVVDQEK	K	V	95.00%	43		459.2528	2	3.7	82	89	No
				LSVVDQEKVDK	K	F	95.00%	77		630.3475	2	1.8	82	92	No
				LSVVDQEKVDKFMIELDGTENK	K	S	95.00%	56	M13: Oxidation	851.7718	3	9.3	82	103	No
				NGKYDLDFK	R	S	95.00%	51		550.2766	2	2.6	254	262	No
				NGKYDLDFKSPDDPAR	R	H	95.00%	98		919.4435	2	3.7	254	269	No
				NGKYDLDFKSPDDPAR	R	H	95.00%	46		613.2986	3	4.3	254	269	No
				NGKYDLDFKSPDDPAR	R	H	95.00%	36		460.2248	4	1.8	254	269	No
				RIAQAVEK	K	K	95.00%	31		457.7771	2	4.3	327	334	No
				TAIQAAGYPDK	K	V	95.00%	69		1134.5890	1	8.0	229	239	No
				TAIQAAGYPDK	K	V	95.00%	96		567.7944	2	1.2	229	239	No
				TAIQAAGYPDKVVIGMDVAASEFYR	K	N	95.00%	71	M16: Oxidation	1344.6750	2	3.1	229	253	No
				TAIQAAGYPDKVVIGMDVAASEFYR	K	N	95.00%	78	M16: Oxidation	896.7895	3	6.9	229	253	No
				TAIQAAGYPDKVVIGMDVAASEFYR	K	N	95.00%	62	M16: Oxidation	672.8428	4	5.0	229	253	No
				TAIQAAGYPDKVVIGMDVAASEFYR	K	N	95.00%	71		891.4601	3	9.5	229	253	No
				VDKFMIELDGTENK	K	S	95.00%	106	M5: Oxidation	827.9089	2	6.0	90	103	No
				VDKFMIELDGTENK	K	S	95.00%	54	M5: Oxidation	552.2723	3	0.7	90	103	No
				VNQIGSVTESIQACK	K	L	95.00%	98		788.9106	2	8.1	344	358	No
				VVIGMDVAASEFYR	K	N	95.00%	121	M5: Oxidation	786.8954	2	6.4	240	253	No
				VVIGMDVAASEFYR	K	N	95.00%	72	M5: Oxidation	524.9316	3	3.9	240	253	No
				VVIGMDVAASEFYR	K	N	95.00%	110		778.8991	2	7.8	240	253	No
				YDLDFK	K	S	95.00%	44		400.6961	2	1.4	257	262	Yes
				YDLDFKSPDDPAR	K	H	95.00%	65		769.8630	2	3.3	257	269	No
				YDLDFKSPDDPAR	K	H	95.00%	54		513.5775	3	2.4	257	269	No
				YNQLMR	K	I	95.00%	44	M5: Oxidation	420.7074	2	3.7	407	412	Yes
				YNQLMR	K	I	95.00%	47		412.7092	2	2.0	407	412	No
331	IPI00218568	PCBD1	PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE.	AVGWNELEGR	R	D	95.00%	40		565.7861	2	4.3	22	31	No
				DQLLPNLR	R	A	95.00%	30		484.7828	2	4.8	14	21	No
332	IPI00218570	PGAM2	PHOSPHOGLYCERATE MUTASE 2.	ALPFWNEEIVPQIK	R	A	95.00%	94		842.4643	2	5.7	163	176	No
				ALPFWNEEIVPQIK	R	A	95.00%	54		561.9794	3	6.7	163	176	No
				AMEAVAAQGK	K	A	95.00%	64	M2: Oxidation	496.2521	2	8.2	242	251	No
				ELKPTKPMQFLGDEETVR	K	K	95.00%	29	M8: Oxidation	1067.5560	2	9.0	223	240	No
				ELKPTKPMQFLGDEETVR	K	K	95.00%	54	M8: Oxidation	712.0399	3	8.6	223	240	No
				ELKPTKPMQFLGDEETVR	K	K	95.00%	95		1059.5590	2	9.5	223	240	No
				HGEEQVK	K	I	95.00%	46		413.7093	2	6.0	107	113	No
				HGESTWNQENR	R	F	95.00%	41		453.2041	3	6.2	11	21	No
				HLEGMSDQAIMELNLPTGIPIVYELNK	K	E	95.00%	55	M11: Oxidation	1014.5260	3	9.4	196	222	No
				HLEGMSDQAIMELNLPTGIPIVYELNK	K	E	95.00%	48	M5: Oxidation	1014.5250	3	9.0	196	222	No
				HLEGMSDQAIMELNLPTGIPIVYELNK	K	E	95.00%	63	M5: Oxidation	1019.8570	3	9.6	196	222	No
				HLEGMSDQAIMELNLPTGIPIVYELNK	K	E	95.00%	72	M5: Oxidation, M11: Oxidation	1019.8570	3	9.3	196	222	No
				HPYYNSISK	K	E	95.00%	37		1108.5530	1	9.0	130	138	No
				HYGGLTGLNK	R	A	95.00%	47		1059.5630	1	4.0	91	100	No
				HYGGLTGLNK	R	A	95.00%	56		530.2846	2	2.3	91	100	No
				HYGGLTGLNKAETAAK	R	H	95.00%	104		815.9374	2	7.0	91	106	No
				HYGGLTGLNKAETAAK	R	H	95.00%	48		544.2925	3	3.8	91	106	No
				KAMEAVAAQGK	R	A	95.00%	51	M3: Oxidation	560.3007	2	9.1	241	251	No
				RSFDIPPPPMDEK	R	H	95.00%	48	M10: Oxidation	772.8810	2	7.7	117	129	No
				RSFDIPPPPMDEKHPYYNSISK	R	E	95.00%	31	M10: Oxidation	878.7690	3	9.5	117	138	No
				RVLIAAHGNSLR	K	G	95.00%	60		653.8948	2	8.5	180	191	No
				RVLIAAHGNSLR	K	G	95.00%	58		436.2637	3	3.6	180	191	No
				SFDIPPPPMDEK	R	H	95.00%	70	M9: Oxidation	694.8262	2	2.5	118	129	No
				SFDIPPPPMDEK	R	H	95.00%	59		686.8303	2	4.8	118	129	No
				TLWAILDGTDQMWLPVVR	R	T	95.00%	60	M12: Oxidation	710.7131	3	8.3	66	83	No
				TLWAILDGTDQMWLPVVR	R	T	95.00%	58		1057.5690	2	9.0	66	83	No
				TLWAILDGTDQMWLPVVR	R	T	95.00%	37		705.3801	3	6.5	66	83	No
				VLIAAHGNSLR	R	G	95.00%	76		575.8382	2	-1.1	181	191	No

333	IPI00218571; IPI00514085	PHKB	ISOFORM 1 OF PHOSPHORYLASE B KINASE REGULATORY SUBUNIT BETA.; ISOFORM 2 OF PHOSPHORYLASE B KINASE REGULATORY SUBUNIT BETA.	AYLQLGINEK	K	L	95.00%	54		574.8228	2	5.3	530	539	No
				EAFNEFQK	K	D	95.00%	39		506.7433	2	4.8	1023	1030	No
				FNPILDMLAALK	R	K	95.00%	46	M7: Oxidation	681.3818	2	3.9	624	635	No
				FSSSIAPHITTFLVHGK	K	Q	95.00%	33		921.5034	2	4.2	785	801	No
				FSSSIAPHITTFLVHGK	K	Q	95.00%	31		614.6744	3	8.9	785	801	No
				FSSSIAPHITTFLVHGK	K	Q	95.00%	34		461.2568	4	6.8	785	801	No
				GGDKPALDLYQLSPSEVK	R	Q	95.00%	110		959.0101	2	7.9	891	908	No
				GGDKPALDLYQLSPSEVK	R	Q	95.00%	31		639.6766	3	8.9	884	901	No
				ISDTEELPEFK	R	S	95.00%	74		654.3277	2	7.8	666	676	No
				LLADELISPK	K	D	95.00%	53		549.8269	2	4.2	446	455	No
				QDDMTSFYNTPPLGK	K	R	95.00%	31	M4: Oxidation	865.3974	2	7.1	1041	1055	No
				QVTLGAFGHEEEVISNPLSPR	K	V	95.00%	35		760.7304	3	5.8	809	829	No
				STLLLYQSPTTGLFPTK	K	T	95.00%	93		934.0231	2	8.8	58	74	No
				VIQNIIYYK	R	C	95.00%	38		577.3396	2	7.9	823	831	No
				VPDFGVWER	R	G	95.00%	50		552.7795	2	3.0	208	216	No
				VWQILER	R	T	95.00%	46		472.2742	2	4.3	938	944	No
				YYYVPADFVEYEK	K	N	95.00%	40		843.3969	2	7.1	402	414	No
334	IPI00218733; IPI00783680	SOD1	16 KDA PROTEIN.; SUPEROXIDE DISMUTASE.	GDGPVQGIINFEQK	K	A	95.00%	90		751.3935	2	9.3	11	24	No
				GDGPVQGIINFEQK	K	A	95.00%	69		501.2645	3	8.4	11	24	No
				HVGDLGNVTADK	R	D	95.00%	87		613.3174	2	7.4	83	94	No
335	IPI00218847; IPI00219861; IPI00410615	ACP1	ISOFORM 2 OF LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE.; ISOFORM 1 OF LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE.; ISOFORM 3 OF LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE.	IELLGSYDPQK	K	Q	95.00%	55		631.8409	2	8.4	114	124	No
				LVTDQNISENWR	K	V	95.00%	64		737.8733	2	6.6	30	41	No
				SPIAEAVFR	R	K	95.00%	59		495.2779	2	5.9	20	28	No
				VDSAATSGYEIGNPPDYR	R	G	95.00%	99		956.4471	2	7.3	42	59	No
336	IPI00218848	ATP5I	ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F0 COMPLEX, SUBUNIT E.	ELAEDDSILK	R	-	95.00%	48		566.7939	2	5.3	63	72	No
				MVPPVQVSPLIK	K	L	95.00%	26	M1: Oxidation	662.3954	2	9.0	4	15	No
				YSALFLGVAYGATR	R	Y	95.00%	120		744.9011	2	6.2	19	32	No
				YSALFLGVAYGATR	R	Y	95.00%	44		496.9369	3	6.7	19	32	No
337	IPI00218914	ALDH1A1	RETINAL DEHYDROGENASE 1.	ANNTFYGLSAGVFTK	R	D	95.00%	102		795.4093	2	9.1	421	435	No
				EAGFPPGVVNIVPGYGPTAGAAISSHMDIDK	K	V	95.00%	35	M27: Oxidation	1028.5200	3	9.7	211	241	No
				EEIFGPVQQIMK	K	F	95.00%	56	M11: Oxidation	717.8732	2	5.7	399	410	No
				ELGEYGFHEYTEVK	R	T	95.00%	83		850.8965	2	2.5	477	490	No
				GYFVQPTVFSNVTDEMR	K	I	95.00%	114	M16: Oxidation	1003.4800	2	9.6	379	395	No
				IAKEEIFGPVQQIMK	R	F	95.00%	73	M14: Oxidation	873.9826	2	6.1	396	410	No
				IFINNEWHDSVSGK	K	K	95.00%	90		823.4098	2	8.8	23	36	No
				IFINNEWHDSVSGK	K	K	95.00%	32		549.2731	3	3.8	23	36	No
				IFVEESIYDEFVR	R	R	95.00%	74		823.4152	2	6.8	309	321	No
				ILDLIESGKK	K	E	95.00%	44		558.3403	2	4.5	354	363	No
				LLLATMESMNGGK	R	L	95.00%	69	M6: Oxidation, M9: Oxidation	698.8470	2	3.2	101	113	No
				QAFQIGSPWR	R	T	95.00%	58		595.3126	2	4.6	69	78	No
				TIPIDGNFFTYTR	R	H	95.00%	59		772.8965	2	6.5	144	156	No
				TVTVK	K	I	95.00%	29		547.3508	1	9.6	491	495	No
				VAFTGSTEVGK	K	L	95.00%	44		548.2901	2	3.3	242	252	No
				YILGNPLTPGVTQGPQIDKEQYDK	K	I	95.00%	31		892.1363	3	7.5	330	353	No
338	IPI00219018; IPI00789134; IPI00795257	GAPDH	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE.; GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE.; 32 KDA PROTEIN.	AGAHLQGGAK	K	R	95.00%	59		455.2518	2	5.6	108	117	No
				GALQNIIPASTGAAK	R	A	95.00%	105		706.3998	2	0.5	201	215	No
				GALQNIIPASTGAAK	R	A	95.00%	38		471.2732	3	9.2	126	140	No
				GALQNIIPASTGAAKAVGK	R	V	95.00%	24		589.6806	3	7.5	126	144	No
				GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK	K	L	95.00%	63		1009.9880	4	8.2	272	309	No
				IKWGDAGAEYVVESTGVFTTMEK	K	A	95.00%	114	M21: Oxidation	1267.6170	2	4.9	85	107	No

IKWGDAGAEYVVESTGVFTTMEK	K	A	95.00%	49	M21: Oxidation	845.4177	3	9.7	85	107	No
LEKPAKYDDIK	R	K	95.00%	32		660.3675	2	4.3	249	259	No
LISWYDNEFGYSNR	K	V	95.00%	115		882.4132	2	8.9	310	323	No
LISWYDNEFGYSNR	K	V	95.00%	55		588.6098	3	6.3	310	323	No
LTGMAFR	K	V	95.00%	47	M4: Oxidation	406.2135	2	6.8	228	234	No
LVINGNPITIFQER	K	D	95.00%	97		807.4598	2	6.3	67	80	No
LVINGNPITIFQER	K	D	95.00%	72		538.6418	3	5.0	67	80	No
LVINGNPITIFQERDPSK	K	I	95.00%	97		1021.0670	2	8.7	67	84	No
LVINGNPITIFQERDPSK	K	I	95.00%	50		681.0475	3	9.1	67	84	No
PAKYDDIKK	K	V	95.00%	47		539.3055	2	7.9	252	260	No
RVIISAPSADAPMFVMGVNHEK	K	Y	95.00%	71	M13: Oxidation	795.7446	3	5.2	118	139	No
RVIISAPSADAPMFVMGVNHEK	K	Y	95.00%	69	M13: Oxidation	801.0779	3	7.3	118	139	No
RVIISAPSADAPMFVMGVNHEK	K	Y	95.00%	69	M13: Oxidation, M16: Oxidation	801.0779	3	7.3	118	139	No
RVIISAPSADAPMFVMGVNHEK	K	Y	95.00%	68	M16: Oxidation	795.7451	3	5.8	118	139	No
RVIISAPSADAPMFVMGVNHEK	K	Y	95.00%	90		790.4131	3	5.5	118	139	No
VDIVAINDPFIDLNYMVYMFQYDSTHGK	K	F	95.00%	42	M19: Oxidation	831.9037	4	9.5	28	55	No
VDIVAINDPFIDLNYMVYMFQYDSTHGK	K	F	95.00%	55		1103.5360	3	8.8	28	55	No
VGVNGFGR	K	I	95.00%	45		403.2212	2	3.1	6	13	No
VIHDNFGIVEGLMTTVHAITATQK	K	T	95.00%	85	M13: Oxidation	871.1294	3	6.5	163	186	No
VIHDNFGIVEGLMTTVHAITATQK	K	T	95.00%	65	M13: Oxidation	653.5995	4	7.3	163	186	No
VIHDNFGIVEGLMTTVHAITATQK	K	T	95.00%	35	M13: Oxidation	523.0814	5	7.7	163	186	No
VIHDNFGIVEGLMTTVHAITATQK	K	T	95.00%	37	M13: Oxidation	673.5911	4	7.1	163	186	No
VIHDNFGIVEGLMTTVHAITATQK	K	T	95.00%	37	M13: Oxidation, T20: Phospho	673.5911	4	7.1	163	186	No
VIHDNFGIVEGLMTTVHAITATQK	K	T	95.00%	36	M13: Oxidation, T22: Phospho	673.5913	4	7.3	163	186	No
VIHDNFGIVEGLMTTVHAITATQK	K	T	95.00%	36	T22: Phospho	669.5922	4	6.8	163	186	No
VIHDNFGIVEGLMTTVHAITATQK	K	T	95.00%	95		865.8000	3	9.1	163	186	No
VIHDNFGIVEGLMTTVHAITATQK	K	T	95.00%	80		649.5996	4	5.5	163	186	No
VIISAPSADAPMFVMGVNHEK	R	Y	95.00%	85	M12: Oxidation, M15: Oxidation	1123.0630	2	8.5	119	139	No
VIISAPSADAPMFVMGVNHEK	R	Y	95.00%	52	M12: Oxidation, M15: Oxidation	749.0435	3	6.7	119	139	No
VIISAPSADAPMFVMGVNHEK	R	Y	95.00%	77	M15: Oxidation	1115.0650	2	8.1	119	139	No
VIISAPSADAPMFVMGVNHEK	R	Y	95.00%	35	M15: Oxidation	743.7112	3	5.9	119	139	No
VIISAPSADAPMFVMGVNHEK	R	Y	95.00%	121		1107.0680	2	8.4	119	139	No
VIISAPSADAPMFVMGVNHEK	R	Y	95.00%	45		738.3791	3	5.3	119	139	No
VIPELNGK	K	L	95.00%	27		869.5164	1	7.7	220	227	No
VPTANVSVVDLTCR	R	L	95.00%	128		737.3963	2	7.6	235	248	No
VVDLMAHMASK	R	-	95.00%	54	M5: Oxidation	609.3091	2	6.7	324	334	No
VVDLMAHMASK	R	-	95.00%	57	M5: Oxidation	617.3064	2	6.3	324	334	No
VVDLMAHMASK	R	-	95.00%	36	M5: Oxidation	411.8731	3	5.2	324	334	No
VVDLMAHMASK	R	-	95.00%	57	M5: Oxidation, M8: Oxidation	617.3064	2	6.3	324	334	No
VVDLMAHMASK	R	-	95.00%	36	M5: Oxidation, M8: Oxidation	411.8731	3	5.2	324	334	No
VVDLMAHMASK	R	-	95.00%	61	M8: Oxidation	609.3074	2	3.9	324	334	No
VVDLMAHMASK	R	-	95.00%	61		601.3104	2	4.7	324	334	No
VVDLMAHMASKE	R	-	95.00%	63	M5: Oxidation	673.8296	2	4.9	324	335	No
VVDLMAHMASKE	R	-	95.00%	37	M5: Oxidation	449.5552	3	3.7	324	335	No
VVDLMAHMASKE	R	-	95.00%	70	M5: Oxidation	681.8275	2	5.5	324	335	No
VVDLMAHMASKE	R	-	95.00%	52	M5: Oxidation	454.8871	3	4.4	249	260	No
VVDLMAHMASKE	R	-	95.00%	70	M5: Oxidation, M8: Oxidation	681.8275	2	5.5	324	335	No

				VVDLMAHMASKE	R	-	95.00%	52	M5: Oxidation, M8: Oxidation	454.8871	3	4.4	249	260	No
				VVDLMAHMASKE	R	-	95.00%	70	M8: Oxidation	673.8275	2	1.7	324	335	No
				VVDLMAHMASKE	R	-	95.00%	36	M8: Oxidation	449.5545	3	2.2	324	335	No
				VVDLMAHMASKE	R	-	95.00%	81		665.8329	2	6.1	324	335	No
				VVDLMAHMASKE	R	-	95.00%	35		444.2246	3	6.1	324	335	No
				WGDAGAEYVVESTGVFTTMEK	K	A	95.00%	153	M19: Oxidation	1147.0320	2	9.9	87	107	No
				WGDAGAEYVVESTGVFTTMEK	K	A	95.00%	107	M19: Oxidation	765.0239	3	9.8	87	107	No
				WGDAGAEYVVESTGVFTTMEK	K	A	95.00%	152		1139.0330	2	8.6	87	107	No
				WGDAGAEYVVESTGVFTTMEK	K	A	95.00%	72		759.6900	3	7.0	87	107	No
339	IPI00219025	GLRX	GLUTAREDOXIN-1.	AQEILSQLPIK	R	Q	95.00%	72		620.3755	2	9.5	29	39	No
				RAQEILSQLPIK	R	Q	95.00%	91		465.9517	3	4.8	28	39	No
340	IPI00219029	GOT1	ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC.	APPSVFAEVPQAQPVLVFK	M	L	95.00%	111		1012.5740	2	8.9	2	20	No
				APPSVFAEVPQAQPVLVFK	M	L	95.00%	69		675.3845	3	7.8	2	20	No
				EPESILQVLSQMEK	K	I	95.00%	51	M12: Oxidation	823.9260	2	7.8	277	290	No
				EPESILQVLSQMEK	K	I	95.00%	95		815.9230	2	1.0	277	290	No
				FLFPFFDSAYQGFASGNLER	R	D	95.00%	105		1157.0600	2	5.7	217	236	No
				FLFPFFDSAYQGFASGNLER	R	D	95.00%	71		771.7112	3	8.7	217	236	No
				HIYLLPSGR	K	I	95.00%	45		1055.6080	1	7.4	379	387	No
				HIYLLPSGR	K	I	95.00%	35		528.3082	2	7.9	379	387	No
				IANDNSLNHEYLPILGLAEFR	K	S	95.00%	122		1200.1310	2	7.6	61	81	No
				IANDNSLNHEYLPILGLAEFR	K	S	95.00%	57		800.4241	3	8.6	61	81	No
				IANDNSLNHEYLPILGLAEFR	K	S	95.00%	40		600.5701	4	8.8	61	81	No
				IGADFLAR	R	W	95.00%	33		862.4842	1	6.2	115	122	No
				IGADFLAR	R	W	95.00%	86		431.7443	2	2.2	115	122	No
				INVSGLTTK	R	N	95.00%	48		932.5414	1	-0.4	388	396	No
				INVSGLTTK	R	N	95.00%	53		466.7754	2	1.3	388	396	No
				ITWSNPPAQGAR	R	I	95.00%	82		649.3370	2	0.6	294	305	No
				IVASTLSNPELFEEWTGNVK	R	T	95.00%	83		1117.5810	2	9.0	306	325	No
				IVASTLSNPELFEEWTGNVK	R	T	95.00%	67		745.3892	3	7.9	306	325	No
				KVNLGVGAYR	R	T	95.00%	69		538.8179	2	5.9	33	42	No
				LALGDDSPALK	R	E	95.00%	51		1099.6060	1	4.9	87	97	No
				LALGDDSPALK	R	E	95.00%	72		550.3052	2	2.1	87	97	No
				LALGDDSPALKEK	R	R	95.00%	68		678.8738	2	1.5	87	99	No
				NFGLYNER	K	V	95.00%	31		1012.4890	1	4.0	260	267	No
				NFGLYNER	K	V	95.00%	49		506.7469	2	0.7	260	267	No
				NLDYVATSIHEAVTK	K	I	95.00%	134		830.9374	2	7.4	397	411	No
				NLDYVATSIHEAVTK	K	I	95.00%	56		554.2923	3	4.0	397	411	No
				NTPVYVSSPTWENHNAVFSAAGFK	K	D	95.00%	43		875.0981	3	8.0	131	154	No
				QVEYLVNEK	K	H	95.00%	52		1121.5930	1	7.6	370	378	No
				QVEYLVNEK	K	H	95.00%	60		561.2977	2	2.8	370	378	No
				RVGGVQSLGGTGALR	K	I	95.00%	94		714.4111	2	4.2	100	114	No
				RVGGVQSLGGTGALR	K	I	95.00%	55		476.6093	3	2.7	100	114	No
				TPGTWNHITDQIGMFSFTGLNPK	K	Q	95.00%	47	M14: Oxidation	1289.6200	2	-2.7	347	369	No
				TPGTWNHITDQIGMFSFTGLNPK	K	Q	95.00%	100	M14: Oxidation	860.0925	3	8.5	347	369	No
				VGGVQSLGGTGALR	R	I	95.00%	110		636.3604	2	4.4	101	114	No
				VGNLTVVGK	R	E	95.00%	72		443.7729	2	1.8	268	276	No
				VGNLTVVGKEPESILQVLSQMEK	R	I	95.00%	66	M21: Oxidation	838.7947	3	7.9	268	290	No
				VGNLTVVGKEPESILQVLSQMEK	R	I	95.00%	29		833.4634	3	8.2	268	290	No
				VNLGVGAYR	K	T	95.00%	62		474.7682	2	2.0	34	42	No
341	IPI00219034	NDUFA8	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 8.	PGIVELPTLEELKVDEVK	M	I	95.00%	69		670.0516	3	8.5	2	19	No
				PRPDPSPEIEGDLQPATHGSR	R	F	95.00%	41		564.7841	4	5.3	146	166	No
				TDRPLPENPYHSR	K	P	95.00%	37		527.9338	3	5.2	133	145	No
				VKTDRPLPENPYHSR	K	P	95.00%	44		603.6544	3	3.7	131	145	No
342	IPI00219067; IPI00639805; IPI00645360; IPI00645711	GSTM2	GLUTATHIONE S-TRANSFERASE MU 2.; 26 KDA PROTEIN.; GLUTATHIONE TRANSFERASE.; 28 KDA PROTEIN.	EDILENQFMDSR	R	M	95.00%	44	M9: Oxidation	756.8418	2	7.7	97	108	No
				EQIREDILENQFMDSR	K	M	95.00%	39	M13: Oxidation	680.3285	3	9.5	93	108	No
				ITFVDFIAYDVLER	K	N	95.00%	44		567.6402	3	8.8	153	166	No

				ITQSNAILR	K	Y	95.00%	79		508.3018	2	5.6	70	78	Yes
				KYTMGDAPDYDR	K	S	95.00%	69	M4: Oxidation	724.3179	2	8.0	32	43	No
				KYTMGDAPDYDR	K	S	95.00%	44	M4: Oxidation	483.2135	3	5.9	32	43	No
				LGLDFPNLPYLIDGTHK	K	I	95.00%	73		957.0208	2	8.4	53	69	No
				LGLDFPNLPYLIDGTHK	K	I	95.00%	35		638.3497	3	8.3	53	69	No
				LKPEYLQALPEMLK	K	L	95.00%	30	M12: Oxidation	844.9758	2	8.1	123	136	No
				LLLEYTDSSYEEK	R	K	95.00%	80		795.3910	2	9.8	19	31	No
				LLLEYTDSSYEEKK	R	Y	95.00%	55		859.4392	2	9.9	19	32	No
				LYSQFLGK	K	Q	95.00%	35		478.2687	2	4.3	137	144	No
				PMTLGYWNIR	M	G	95.00%	35	M2: Oxidation	633.8246	2	8.6	2	11	No
				PMTLGYWNIR	M	G	95.00%	61		625.8245	2	4.5	2	11	No
				YTMGDAPDYDR	K	S	95.00%	43	M3: Oxidation	660.2703	2	8.6	33	43	No
343	IPI00219077	LTA4H	ISOFORM 1 OF LEUKOTRIENE A-4 HYDROLASE.	ASMHPVTAMLVGK	K	D	95.00%	59	M3: Oxidation, M9: Oxidation	458.5713	3	4.5	594	606	No
				DGETPDPEDPSR	R	K	95.00%	31		657.7813	2	7.2	176	187	No
				EDDLNSFNATDLK	K	D	95.00%	94		741.3466	2	6.1	481	493	No
				ELVALMSAIR	K	D	95.00%	50	M6: Oxidation	559.8203	2	7.4	166	175	No
				GSPMEISLPIALSK	K	N	95.00%	70	M4: Oxidation	729.9012	2	4.6	84	97	No
				HFNALGGWGELQNSVK	R	T	95.00%	79		586.3020	3	7.6	340	355	No
				LTYTAEVSVPK	K	E	95.00%	78		604.3355	2	4.7	155	165	No
				LVVDLTDIDPDVAYSSVPYEK	K	G	95.00%	106		1169.5960	2	5.4	366	386	No
				LVVDLTDIDPDVAYSSVPYEK	K	G	95.00%	45		780.0694	3	9.3	366	386	No
				MQEVYNFNAINNSEIR	R	F	95.00%	131	M1: Oxidation	979.4633	2	5.7	521	536	No
				SAYEFSETESMLK	K	I	95.00%	67	M11: Oxidation	769.3457	2	6.7	231	243	No
				SLSNVIAHEISHSWTGNLVTNK	K	T	95.00%	48		803.0884	3	5.4	289	310	No
				TLTGTAALTVQSQEDNLR	R	S	95.00%	116		959.5057	2	7.9	34	51	No
				TLTGTAALTVQSQEDNLR	R	S	95.00%	40		640.0049	3	5.7	34	51	No
				WEDAIPLALK	K	M	95.00%	41		578.3275	2	4.8	548	557	No
344	IPI00031801; IPI00219147; IPI00219148; IPI00555698	CSDA	ISOFORM 1 OF DNA-BINDING PROTEIN A.; ISOFORM 2 OF DNA-BINDING PROTEIN A.; ISOFORM 3 OF DNA-BINDING PROTEIN A.; CSDA PROTEIN VARIANT (FRAGMENT).	AGEAPTENPAPPTQQSSAE	K	-	95.00%	53		941.4332	2	6.2	285	303	No
				GAEAANVTGPDGVPVEGSR	K	Y	95.00%	105		891.9388	2	4.1	151	169	No
				NAGEIGEMKDGVPEGAQLQGPVHR	R	N	95.00%	54	M8: Oxidation	835.7471	3	4.1	191	214	No
				PAPAVGEAEDKENQQATSGPNQPSVR	R	R	95.00%	72		893.0991	3	0.0	232	257	No
				SVGDGETVEFDVVEGEK	R	G	95.00%	118		898.4222	2	7.0	134	150	Yes
345	IPI00219207	RTN4	ISOFORM 3 OF RETICULON-4.	AYLESEVAISEELVQK	R	Y	95.00%	60		603.3212	3	8.4	82	97	No
				GVIQAIQK	K	S	95.00%	50		428.7689	2	4.8	66	73	No
				HQAQIDHYLGLANK	R	N	95.00%	116		804.4237	2	6.3	165	178	No
				HQAQIDHYLGLANK	R	N	95.00%	72		536.6174	3	4.3	165	178	No
				HQAQIDHYLGLANK	R	N	95.00%	38		402.7154	4	5.5	165	178	No
				LFLVDDLVDSLK	R	F	95.00%	64		688.8945	2	9.6	116	127	No
				VVDLLYWR	K	D	95.00%	58		532.3046	2	6.9	12	19	No
346	IPI00219217	LDHB	L-LACTATE DEHYDROGENASE B CHAIN.	EKLIAPVAEEEATVPNNK	K	I	95.00%	100		976.5281	2	7.3	6	23	No
				FIIPQIVK	K	Y	95.00%	32		479.3126	2	3.6	120	127	No
				GLTSVINQK	R	L	95.00%	37		959.5605	1	8.1	300	308	No
				GLTSVINQK	R	L	95.00%	52		480.2823	2	4.3	300	308	No
				IVADKDYSVTANSK	K	I	95.00%	105		755.8990	2	9.8	78	91	No
				IVADKDYSVTANSK	K	I	95.00%	41		504.2657	3	4.0	78	91	No
				IVVVTAGVR	K	Q	95.00%	71		457.2970	2	3.1	92	100	No
				LIAPVAEEEATVPNNK	K	I	95.00%	101		847.9578	2	6.7	8	23	No
				LKDDEVAQLK	K	K	95.00%	44		579.8262	2	6.1	309	318	No
				LKDDEVAQLKK	K	S	95.00%	28		643.8713	2	1.8	309	319	No
				LKDDEVAQLKK	K	S	95.00%	58		429.5841	3	3.2	309	319	No
				MVVESAYEVIK	K	L	95.00%	65	M1: Oxidation	642.3356	2	6.0	234	244	No
				MVVESAYEVIK	K	L	95.00%	50		634.3378	2	5.5	234	244	No
				SADTLWDIQK	K	D	95.00%	57		588.8020	2	5.1	320	329	No
				SADTLWDIQKDLK	K	D	95.00%	31		766.9094	2	9.6	320	332	No
				SADTLWDIQKDLKDL	K	-	95.00%	53		587.6467	3	9.6	320	334	No
				SLADELALVDVLEDK	K	L	95.00%	92		815.4404	2	8.6	44	58	No
				SLADELALVDVLEDK	K	L	95.00%	55		543.9612	3	5.5	44	58	No
				SLADELALVDVLEDKLK	K	G	95.00%	53		936.0292	2	6.7	44	60	No
				SLADELALVDVLEDKLK	K	G	95.00%	41		624.3565	3	8.4	44	60	No
347	IPI00219219	LGALS1	GALECTIN-1.	DGGAWGTEQR	K	E	95.00%	43		538.7466	2	8.4	65	74	No
				LNLEAINYMAADGDFK	R	I	95.00%	82	M9: Oxidation	900.9319	2	4.5	113	128	No
				LNLEAINYMAADGDFK	R	I	95.00%	109		892.9372	2	7.6	113	128	No
				LPDGYEFK	K	F	95.00%	33		968.4822	1	9.5	101	108	No
				SFVLNLGK	K	D	95.00%	27		877.5209	1	7.0	30	37	No

				SFVLNLGK	K	D	95.00%	55		439.2629	2	3.7	30	37	No
348	IPI00219226; IPI00796706	HRC	SARCOPLASMIC RETICULUM HISTIDINE-RICH CALCIUM-BINDING PROTEINPRECURSOR.; 81 KDA PROTEIN.	FTIIPNPLDR	R	R	95.00%	48		593.3394	2	6.4	584	593	No
				HQGHGIEEDEDVSDGHHHR	R	D	95.00%	58		730.9870	3	7.0	273	291	No
				HQGHGIEEDEDVSDGHHHR	R	D	95.00%	86		548.4910	4	4.9	273	291	No
				SHEEDDNDDDDVSTEYGHQAHR	R	H	95.00%	43		643.5078	4	7.3	299	320	No
				SHSHQDEDEDEVVSSEHHHHILR	R	H	95.00%	35	S14: Phospho	710.5558	4	6.5	157	179	No
				VGDEGVSGEEVFAEHGGQAR	K	G	95.00%	33	S7: Phospho	703.9739	3	8.6	113	132	No
				VGDEGVSGEEVFAEHGGQAR	K	G	95.00%	50		1015.4710	2	6.0	113	132	No
				VGDEGVSGEEVFAEHGGQAR	K	G	95.00%	73		677.3148	3	3.4	113	132	No
				VPREEDEEVSAELGHQAPSHR	R	Q	95.00%	44		593.7908	4	7.0	422	442	No
349	IPI00219381	NDUFA2	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 2.	ALENVLSGK	R	-	95.00%	33		465.7690	2	4.4	90	98	No
				ANPDLPILIR	K	E	95.00%	46		561.3424	2	7.5	47	56	No
				KANPDLPILIR	K	E	95.00%	36		417.2615	3	4.3	46	56	No
350	IPI00219383	NDUFB3	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 3.	IEGTPLETIQK	K	K	95.00%	49		614.8464	2	4.8	24	34	No
				SVSFSDVFFK	K	G	95.00%	56		581.7976	2	7.6	60	69	No
351	IPI00219446; IPI00795288	PEBP1	PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN 1.; 22 KDA PROTEIN.	EWHHFLVVNMK	R	G	95.00%	52	M10: Oxidation	728.3712	2	9.6	83	93	No
				GNDISSGTVLSDYVGSGPPK	K	G	95.00%	121		975.4831	2	6.4	94	113	No
				GNDISSGTVLSDYVGSGPPK	K	G	95.00%	50		650.6580	3	6.4	94	113	No
				LYEQLSGK	K	-	95.00%	46		937.5069	1	7.8	180	187	No
				LYEQLSGK	K	-	95.00%	55		469.2559	2	4.8	180	187	No
				LYTLVLTDPDAPSR	K	K	95.00%	100		780.9206	2	3.8	63	76	No
				LYTLVLTDPDAPSR	K	K	95.00%	42		520.9518	3	7.7	63	76	No
				LYTLVLTDPDAPSRK	K	D	95.00%	66		844.9724	2	8.5	63	77	No
				LYTLVLTDPDAPSRK	K	D	95.00%	69		563.6491	3	5.3	63	77	No
				NRPTSISWDGLDSGK	K	L	95.00%	87		816.9096	2	8.0	48	62	No
				NRPTSISWDGLDSGK	K	L	95.00%	47		544.9421	3	7.5	48	62	No
				VLTPTQVK	K	N	95.00%	27		443.2765	2	4.7	40	47	No
				WSGPLSLQEVDEQPQHPLHVTYAGAAVDELGK	K	V	95.00%	43		1157.9190	3	6.9	8	39	No
				WSGPLSLQEVDEQPQHPLHVTYAGAAVDELGK	K	V	95.00%	33		868.6923	4	7.7	8	39	No
				YREWHHFLVVNMK	K	G	95.00%	36	M12: Oxidation	592.3035	3	5.5	81	93	No
				YREWHHFLVVNMK	K	G	95.00%	31	M12: Oxidation	444.4792	4	4.7	81	93	No
				YVWLVYEQDRPLK	R	C	95.00%	66		854.9640	2	8.0	120	132	No
				YVWLVYEQDRPLK	R	C	95.00%	33		570.3123	3	8.7	120	132	No
352	IPI00219525; IPI00747533	PGD	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING.; 53 KDA PROTEIN.	AGQAVDDFIEK	K	L	95.00%	45		596.7998	2	5.5	77	87	No
				DYFGAHTYELLAK	R	P	95.00%	42		764.3830	2	6.4	448	460	No
				GILFVGSGVSGGEEGAR	K	Y	95.00%	86		796.4124	2	5.5	120	136	No
				IISYAQGFMLLR	K	Q	95.00%	88	M9: Oxidation	714.3957	2	8.0	332	343	No
				IKDAFDRNPELQNLLLDDFFK	K	S	95.00%	47		851.1201	3	9.7	376	396	No
				LVPLLDTGDIIIDGGNSEYR	K	D	95.00%	127		1080.5710	2	7.2	88	107	No
				VDDFLANEAK	K	G	95.00%	43		561.2810	2	5.4	39	48	No
353	IPI00219526	PGM1	ISOFORM 1 OF PHOSPHOGLUCOMUTASE-1.	ADNFEYSDPVDGSISR	K	N	95.00%	117		886.3980	2	6.1	471	486	No
				ADNFEYSDPVDGSISR	K	N	95.00%	40		591.2697	3	9.0	471	486	No
				AIGGIILTASHNPGGPNGDFGIK	K	F	95.00%	97		1103.5920	2	6.4	108	130	No
				AIGGIILTASHNPGGPNGDFGIK	K	F	95.00%	78		736.0624	3	4.2	108	130	No
				AIGGIILTASHNPGGPNGDFGIK	K	F	95.00%	40		552.2988	4	4.2	108	130	No
				DLEALMFDR	K	S	95.00%	43	M6: Oxidation	1125.5360	1	9.2	444	452	No
				DLEALMFDR	K	S	95.00%	59	M6: Oxidation	563.2689	2	4.2	444	452	No
				DLEALMFDR	K	S	95.00%	54		555.2721	2	5.4	444	452	No
				EAIQLIAR	K	I	95.00%	41		913.5500	1	3.1	69	76	No
				EAIQLIAR	K	I	95.00%	74		457.2798	2	4.9	69	76	No
				ELLSGPNR	K	L	95.00%	35		885.4814	1	2.2	210	217	No
				ELLSGPNR	K	L	95.00%	30		443.2447	2	2.4	210	217	No
				FFGNLMDASK	K	L	95.00%	34	M6: Oxidation	1145.5390	1	7.6	361	370	No
				FFGNLMDASK	K	L	95.00%	68	M6: Oxidation	573.2709	2	3.4	361	370	No
				FFGNLMDASK	K	L	95.00%	44		565.2741	2	4.4	361	370	No
				FKPFTVEIVDSVEAYATMLR	K	S	95.00%	96	M18: Oxidation	1166.6050	2	5.7	181	200	No
				FKPFTVEIVDSVEAYATMLR	K	S	95.00%	52	M18: Oxidation	778.0734	3	6.3	181	200	No
				FKPFTVEIVDSVEAYATMLR	K	S	95.00%	48	M18: Oxidation	583.8077	4	7.4	181	200	No
				FKPFTVEIVDSVEAYATMLR	K	S	95.00%	54		772.7440	3	9.2	181	200	No

FNISNGGPAPEAITDK	K	I	95.00%	131		815.9134	2	6.9	131	146	No
FNISNGGPAPEAITDKIFQISK	K	T	95.00%	99		1174.1300	2	9.9	131	152	No
FNISNGGPAPEAITDKIFQISK	K	T	95.00%	50		783.0894	3	9.7	131	152	No
HGFFVNPSDSVAVIAANIFSIPYFQQTGVR	K	G	95.00%	43		1094.5740	3	9.8	300	329	No
IALYETPTGWK	K	F	95.00%	67		639.8436	2	4.5	350	360	No
IDAMHGVVGPYVK	R	K	95.00%	63	M4: Oxidation	701.3654	2	2.0	222	234	No
IDAMHGVVGPYVK	R	K	95.00%	54	M4: Oxidation	467.9129	3	2.1	222	234	No
IDAMHGVVGPYVK	R	K	95.00%	51		693.3685	2	2.8	222	234	No
IFQISK	K	T	95.00%	35		735.4427	1	2.9	147	152	No
INQDPQVMLAPLISIALK	K	V	95.00%	121	M8: Oxidation	990.5721	2	7.9	528	545	No
INQDPQVMLAPLISIALK	K	V	95.00%	73	M8: Oxidation	660.7169	3	7.2	528	545	No
INQDPQVMLAPLISIALK	K	V	95.00%	87		982.5747	2	8.0	528	545	No
INQDPQVMLAPLISIALK	K	V	95.00%	35		655.3855	3	7.6	528	545	No
IRIDAMHGVVGPYVK	K	K	95.00%	56	M6: Oxidation	835.9620	2	6.5	220	234	No
IRIDAMHGVVGPYVK	K	K	95.00%	41	M6: Oxidation	557.6418	3	2.7	220	234	No
IRIDAMHGVVGPYVK	K	K	95.00%	40	M6: Oxidation	418.4824	4	0.4	220	234	No
KQSVEDILK	R	D	95.00%	56		530.3091	2	4.8	406	414	No
KQSVEDILKDHWQK	R	Y	95.00%	55		877.4737	2	9.0	406	419	No
KQSVEDILKDHWQK	R	Y	95.00%	50		585.3159	3	4.5	406	419	No
KQSVEDILKDHWQK	R	Y	95.00%	31		439.2382	4	3.1	406	419	No
LIFTDGSR	R	I	95.00%	29		908.4852	1	1.1	492	499	No
LIFTDGSR	R	I	95.00%	58		454.7479	2	4.2	492	499	No
LSGTGSAGATIR	R	L	95.00%	105		545.7987	2	3.5	504	515	No
LYIDSYEK	R	D	95.00%	41		1030.5190	1	9.2	516	523	No
LYIDSYEK	R	D	95.00%	35		515.7607	2	3.7	516	523	No
LYIDSYEKDVAK	R	I	95.00%	95		722.3742	2	2.3	516	527	No
MMKDLEALMFDR	K	S	95.00%	45	M1: Oxidation, M2: Oxidation, M9: Oxidation	774.3525	2	4.0	441	452	No
MMKDLEALMFDR	K	S	95.00%	35	M1: Oxidation, M2: Oxidation, M9: Oxidation	516.5728	3	7.7	441	452	No
QEATLVVGGDGR	R	F	95.00%	49		1201.6260	1	6.9	53	64	No
QEATLVVGGDGR	R	F	95.00%	114		601.3146	2	2.9	53	64	No
QFSANDKVYTVEK	K	A	95.00%	70		764.8893	2	3.9	458	470	No
QSVEDILK	K	D	95.00%	43		466.2601	2	2.4	407	414	No
SGEHDFGAAFDGDGDR	K	N	95.00%	100		826.8357	2	3.5	278	293	No
SGEHDFGAAFDGDGDR	K	N	95.00%	36		551.5610	3	5.8	278	293	No
SGEHDFGAAFDGDGDRNMILGK	K	H	95.00%	107	M18: Oxidation	1163.0230	2	7.6	278	299	No
SGEHDFGAAFDGDGDRNMILGK	K	H	95.00%	46	M18: Oxidation	775.6808	3	2.6	278	299	No
SGEHDFGAAFDGDGDRNMILGK	K	H	95.00%	43	M18: Oxidation	582.0130	4	3.4	278	299	No
SIFDFSALK	R	E	95.00%	34		1027.5530	1	6.5	201	209	No
SIFDFSALK	R	E	95.00%	76		514.2786	2	2.7	201	209	No
SMPTSGALDR	R	V	95.00%	54	M2: Oxidation	525.7508	2	4.5	334	343	No
TIEEYAVCPDLK	K	V	95.00%	45		690.8436	2	5.1	153	164	No
TQAYQDQKPGTSGLR	K	K	95.00%	107		825.4191	2	3.3	9	23	No
TQAYQDQKPGTSGLR	K	K	95.00%	67		550.6149	3	2.4	9	23	No
VDLGVLGK	K	Q	95.00%	43		800.4899	1	1.9	165	172	No
VDLGVLGK	K	Q	95.00%	62		400.7490	2	2.2	165	172	No
VFQSSANYAENFIQSIISTVEPAQR	K	Q	95.00%	105		1400.2150	2	9.9	28	52	No
VFQSSANYAENFIQSIISTVEPAQR	K	Q	95.00%	84		933.8113	3	8.5	28	52	No
VFQSSANYAENFIQSIISTVEPAQR	K	Q	95.00%	81		700.6094	4	6.9	28	52	No
YDYEEVEAEGANK	R	M	95.00%	122		758.8278	2	2.3	428	440	No
YDYEEVEAEGANK	R	M	95.00%	40		506.2211	3	2.2	428	440	No
YDYEEVEAEGANKMMK	R	D	95.00%	52	M14: Oxidation, M15: Oxidation	969.9148	2	6.0	428	443	No
YDYEEVEAEGANKMMK	R	D	95.00%	40	M14: Oxidation, M15: Oxidation	646.9437	3	2.8	428	443	No

354	IPI00218371; IPI00219616; IPI00643000; IPI00816572	PRPS1; PRPS1L1	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE III.; RIBOSE-PHOSPHATE PYROPHOSPHOKINASE I.; PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1.; PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1 VARIANT (FRAGMENT).	IADRLGLELGK	K	V	95.00%	25		592.8585	2	7.3	19	29	No
				IFSGSSHQDLSQK	K	I	95.00%	78		717.3597	2	6.4	6	18	No
				VYAILTHGIFSGPAISR	R	I	95.00%	61		901.4941	2	-9.0	244	260	No
355	IPI00219684	FABP3	FATTY ACID-BINDING PROTEIN, HEART.	LGVEFDETTADDR	K	K	95.00%	108		734.3379	2	5.1	67	79	No
				LGVEFDETTADDRK	K	V	95.00%	79		798.3868	2	6.4	67	80	No
				LGVEFDETTADDRK	K	V	95.00%	53		532.5939	3	6.7	67	80	No
				NFDDYMK	K	S	95.00%	36	M6: Oxidation	474.6956	2	6.2	16	22	No
				NGDILTLK	K	T	95.00%	31		873.5120	1	8.3	46	53	No
				NGDILTLK	K	T	95.00%	65		437.2604	2	9.6	46	53	No
				NTEISFK	K	L	95.00%	39		838.4368	1	6.8	60	66	No
				NTEISFK	K	L	95.00%	34		419.7214	2	4.6	60	66	No
				QVASMTKPTTIIEK	R	N	95.00%	61	M5: Oxidation	781.9337	2	8.4	32	45	No
				SIVTLDGGK	K	L	95.00%	46		889.5073	1	8.6	83	91	No
				SIVTLDGGK	K	L	95.00%	42		445.2549	2	2.8	83	91	No
				SLGVGFATR	K	Q	95.00%	65		454.2564	2	5.4	23	31	No
				WDGQETTLVR	K	E	95.00%	98		602.8043	2	3.5	98	107	No
356	IPI00219685	NDUFA13	CELL DEATH-REGULATORY PROTEIN GRIM19.	ENLEEEAIIMK	R	D	95.00%	68	M10: Oxidation	667.8353	2	8.5	172	182	No
				IALLPLLQAETDRR	R	T	95.00%	23		536.9885	3	3.6	152	165	No
				LQIEDFEAR	R	I	95.00%	58		560.7897	2	6.6	143	151	No
				VGESVFHTTR	K	W	95.00%	62		566.7956	2	7.4	189	198	No
				VKQDMPPPGGYGPIDYK	K	R	95.00%	38	M5: Oxidation	626.6461	3	6.1	89	105	No
				WVPPLIGELYGLR	R	T	95.00%	47		504.9611	3	6.2	199	211	No
357	IPI00219729	SLC25A11	MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN.	AVVVNAAQLASYSQSK	R	Q	95.00%	94		818.4473	2	10.0	191	206	No
				AVVVNAAQLASYSQSK	R	Q	95.00%	60		545.9653	3	6.0	191	206	No
				EEGVLTLWR	R	G	95.00%	51		551.8040	2	9.4	174	182	No
				GIYTGLSAGLLR	R	Q	95.00%	85		610.8601	2	9.7	79	90	No
				LGIYTVLFER	R	L	95.00%	85		605.8498	2	6.7	99	108	No
				LTGADGTPPGFLLK	R	A	95.00%	75		693.8917	2	8.5	109	122	No
				NVFNALIR	K	I	95.00%	41		473.7819	2	9.0	163	170	No
				TSFHALTSILK	K	A	95.00%	54		609.3488	2	0.3	63	73	No
				TSFHALTSILK	K	A	95.00%	32		406.5702	3	4.5	63	73	No
				YEGFFSLWK	R	G	95.00%	53		588.7941	2	6.3	272	280	No
358	IPI00219757; IPI00796076; IPI00797321	GSTP1	GLUTATHIONE S-TRANSFERASE P.; 23 KDA PROTEIN.; 21 KDA PROTEIN.	AFLASPEYVNLPINGNGK	K	-	95.00%	33		952.4968	2	-3.2	192	209	No
				ALPGQLKPFETLLSQNQGGK	K	T	95.00%	63		1063.5900	2	5.2	122	141	No
				ALPGQLKPFETLLSQNQGGK	K	T	95.00%	37		709.3987	3	9.0	122	141	No
				DQQEAALVDMVNDGVEDLR	K	C	95.00%	77	M10: Oxidation	711.6704	3	8.7	83	101	No
				DQQEAALVDMVNDGVEDLR	K	C	95.00%	112		1058.9950	2	0.3	83	101	No
				FQDGDLTLYQSNTILR	K	H	95.00%	143		942.4877	2	9.1	56	71	No
				MLLADQGQSWK	R	E	95.00%	49	M1: Oxidation	646.8235	2	6.2	20	30	No
				PPYTVVYFPVR	M	G	95.00%	64		669.3721	2	7.8	2	12	No
359	IPI00219796	TNNC2	TROPONIN C, SKELETAL MUSCLE.	AAFDMFDADGGGDISVK	K	E	95.00%	128	M5: Oxidation	866.3891	2	9.6	22	38	No
				AAFDMFDADGGGDISVK	K	E	95.00%	100		858.3898	2	7.5	22	38	No
				ASGEHVTDEEIESLMK	R	D	95.00%	90	M15: Oxidation	895.9167	2	7.6	122	137	No
				ASGEHVTDEEIESLMK	R	D	95.00%	84		887.9206	2	9.1	122	137	No
				ASGEHVTDEEIESLMKDGDK	R	N	95.00%	51	M15: Oxidation	736.0053	3	8.1	122	141	No
				ASGEHVTDEEIESLMKDGDKNNDGR	R	I	95.00%	47	M15: Oxidation	921.4199	3	9.5	122	146	No
				DGDKNNDGRIDFDEFLK	K	M	95.00%	33		666.6482	3	4.2	138	154	No
				ELGTVMR	K	M	95.00%	39	M6: Oxidation	411.2155	2	4.9	39	45	No
				IDFDEFLK	R	M	95.00%	32		1026.5250	1	9.4	147	154	No
				IDFDEFLK	R	M	95.00%	54		513.7633	2	3.6	147	154	No
				NADGYIDPEELAEIFR	R	A	95.00%	56		617.9684	3	7.1	106	121	No
				NNDGRIDFDEFLK	K	M	95.00%	34		791.8866	2	9.5	142	154	No
				SYLSEEMIAEFK	R	A	95.00%	86	M7: Oxidation	731.8497	2	9.7	10	21	No
				SYLSEEMIAEFK	R	A	95.00%	30	M7: Oxidation	488.2329	3	3.8	10	21	No
				SYLSEEMIAEFK	R	A	95.00%	93		723.8522	2	9.6	10	21	No
360	IPI00219910; IPI00783862	BLVRB	23 KDA PROTEIN.; FLAVIN REDUCTASE.	DSSRLPSEGPRPAHVVVGDVLQAADVDK	R	T	95.00%	27		729.3884	4	9.5	41	68	No
				LPSEGPRPAHVVVGDVLQAADVDK	R	T	95.00%	97		823.7807	3	6.5	45	68	No
				LPSEGPRPAHVVVGDVLQAADVDK	R	T	95.00%	40		618.0884	4	8.1	45	68	No
				LQAVTDDHIR	R	M	95.00%	60		584.3146	2	7.7	130	139	No

				NDLSPTTVMSEGAR	R	N	95.00%	77	M9: Oxidation	747.3550	2	7.7	84	97	No
				PAHVVVGDVLQAADVDK	R	T	95.00%	110		866.9727	2	8.1	52	68	No
				PAHVVVGDVLQAADVDK	R	T	95.00%	68		578.3168	3	6.6	52	68	No
				TVAGQDAVIVLLGTR	K	N	95.00%	116		756.9487	2	9.5	69	83	No
				TVAGQDAVIVLLGTR	K	N	95.00%	48		504.9677	3	8.1	69	83	No
				YVAVMPPHIGDQPLTGAYTVTLDGR	K	G	95.00%	62	M5: Oxidation	896.4605	3	5.7	151	175	No
361	IPI00219913; IPI00640357	USP14	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 14.; UBIQUITIN SPECIFIC PROTEASE 14 ISOFORM B.	AQLFALTGVQPAR	K	Q	95.00%	94		686.3954	2	5.8	31	43	No
				ASGEMASAQYITAALR	R	D	95.00%	94	M5: Oxidation	828.4120	2	6.0	142	157	No
				EKFEGVELNTDEPPMVFK	K	A	95.00%	42	M15: Oxidation	709.0154	3	6.5	13	30	No
				FDDDKVSIVTPEDILR	K	L	95.00%	69		931.4885	2	7.5	450	465	No
				FEGVELNTDEPPMVFK	K	A	95.00%	75	M13: Oxidation	934.4502	2	7.3	15	30	No
				LEAIEDDSVKETDSSSASAATPSK	K	K	95.00%	47		813.3901	3	5.2	215	238	No
				LPAYLTIQMVR	R	F	95.00%	66	M9: Oxidation	660.8766	2	7.8	320	330	No
				RVEIMEEESEQ	R	-	95.00%	71	M5: Oxidation	697.8154	2	8.6	484	494	No
				SLIDQFFGVEFETTMK	K	C	95.00%	87	M15: Oxidation	954.4675	2	8.8	241	256	No
362	IPI00219953; IPI00514049; IPI00514929	CMPK	CYTIDYLATE KINASE.; CYTIDYLATE KINASE.; CYTIDYLATE KINASE.	FLIDGFPR	K	N	95.00%	48		482.7678	2	2.2	121	128	No
				IQTYLQSTKPIIDLYEEMGK	R	V	95.00%	47	M18: Oxidation	796.0847	3	7.0	184	203	No
				YGYTHLSAGELLR	K	D	95.00%	49		493.9293	3	8.5	59	71	No
363	IPI00219983; IPI00796892	CACNB1	ISOFORM 2 OF VOLTAGE-DEPENDENT L-TYPE CALCIUM CHANNEL SUBUNIT BETA-1.; 71 KDA PROTEIN.	ALFDFLK	K	H	95.00%	45		427.2473	2	5.0	296	302	No
				ATHPPSSTPPNPLLNR	K	T	95.00%	54		849.9549	2	5.4	456	471	No
				GSVVPQEQEHAM	R	-	95.00%	40	M12: Oxidation	664.3042	2	4.0	512	523	No
				HLNVQIAASEK	K	L	95.00%	34		605.3393	2	9.6	411	421	No
				NLGFWGGLESSQR	R	G	95.00%	32		725.8615	2	5.0	499	511	No
				SGDNSSSSLGDVVTGTR	K	R	95.00%	105		819.8869	2	5.4	186	202	No
				SSLAEVQSEIER	R	I	95.00%	85		674.3445	2	4.3	342	353	No
				TLQLVALDADTINHPAQLSK	R	T	95.00%	62		716.7330	3	7.7	360	379	No
				TSLAPIIVYIK	K	I	95.00%	55		609.3838	2	7.2	380	390	No
				TSVSSVTTPPPHGK	K	R	95.00%	51		697.8724	2	6.3	241	254	No
				TSVSSVTTPPPHGK	K	R	95.00%	35		465.5843	3	6.6	241	254	No
364	IPI00220063	NDUFS5	NADH DEHYDROGENASE [UBIQUINONE] IRON-SULFUR PROTEIN 5.	FGLNIDR	R	W	95.00%	57		417.7287	2	2.6	10	16	No
				PFLDIQK	M	R	95.00%	46		430.7513	2	7.5	2	8	No
				WLTIQSGEQPYK	R	M	95.00%	47		725.3766	2	5.2	17	28	No
365	IPI00220301	PRDX6	PEROXIREDOXIN-6.	DGDSVMVLPTIPEEEAK	K	K	95.00%	55	M6: Oxidation	923.4521	2	9.1	183	199	No
				DGDSVMVLPTIPEEEAK	K	K	95.00%	49		915.4534	2	7.8	183	199	No
				DGDSVMVLPTIPEEEAKK	K	L	95.00%	39	M6: Oxidation	987.5001	2	9.1	183	200	No
				DGDSVMVLPTIPEEEAKK	K	L	95.00%	47	M6: Oxidation	658.6681	3	7.3	183	200	No
				ELAILLGMLDPAEKDEK	R	G	95.00%	32	M8: Oxidation	950.9999	2	-1.3	109	125	No
				ELAILLGMLDPAEKDEK	R	G	95.00%	41	M8: Oxidation	634.3420	3	8.3	109	125	No
				ELAILLGMLDPAEKDEK	R	G	95.00%	74		943.0109	2	7.5	109	125	No
				ELAILLGMLDPAEKDEK	R	G	95.00%	40		629.0078	3	4.3	109	125	No
				FHDFLGDSWGILFSHPR	R	D	95.00%	62		677.6729	3	7.6	25	41	No
				FHDFLGDSWGILFSHPR	R	D	95.00%	36		508.5059	4	6.0	25	41	No
				LIALSIDSVEDHLAWSK	K	D	95.00%	101		949.0168	2	9.7	68	84	No
				LIALSIDSVEDHLAWSK	K	D	95.00%	31		633.0117	3	6.4	68	84	No
				LPFPIIDDR	K	N	95.00%	67		543.3088	2	9.2	98	106	No
				LSILYPATTGR	K	N	95.00%	64		596.3445	2	6.0	145	155	No
				NFDEILR	R	V	95.00%	34		906.4758	1	8.0	156	162	No
				NFDEILR	R	V	95.00%	45		453.7406	2	5.3	156	162	No
				PGGLLLGDVAPNFEANTTVGR	M	I	95.00%	113		1049.5590	2	7.4	2	22	No
				PGGLLLGDVAPNFEANTTVGR	M	I	95.00%	92		700.0413	3	7.1	2	22	No
				VVFVFGPDK	R	K	95.00%	35		504.2858	2	7.1	133	141	No
				VVFVFGPDKK	R	L	95.00%	68		568.3344	2	8.3	133	142	No
				VVISLQLTAEK	R	R	95.00%	88		600.8694	2	8.7	163	173	No
				VVISLQLTAEKR	R	V	95.00%	57		678.9205	2	8.5	163	174	No
				VVISLQLTAEKR	R	V	95.00%	33		452.9492	3	7.7	163	174	No
366	IPI00220342	DDAH1	NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1.	GAEILADTFK	R	D	95.00%	57		1064.5700	1	6.0	150	159	No
				GAEILADTFK	R	D	95.00%	69		532.7877	2	4.2	150	159	No
				GAEILADTFKDYAVSTVPVADGLHLK	R	S	95.00%	33		910.8245	3	8.1	150	175	No
				LKDHMLIPVSMSELEK	K	V	95.00%	38	M5: Oxidation, M11: Oxidation	634.6659	3	5.5	252	267	No

				LQLNIVEMKDENATLDGGDVLFTGR	K	E	95.00%	49	M8: Oxidation	922.1406	3	8.5	112	136	No
				TPEEYPESAK	R	V	95.00%	41		575.7707	2	5.7	238	247	No
367	IPI00220362	HSPE1	10 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL.	FLPLFDR	K	V	95.00%	28		454.2590	2	6.7	9	15	No
				GGEIQPVSVK	K	V	95.00%	53		507.2880	2	4.9	57	66	No
				GGIMLPEK	K	S	95.00%	38	M4: Oxidation	430.7328	2	2.7	29	36	No
				KFLPLFDR	R	V	95.00%	39		518.3067	2	6.0	8	15	No
				VLQATVVAVGSGSK	K	G	95.00%	62		658.3895	2	9.6	41	54	No
				VVLDDKDYFLFR	K	D	95.00%	38		765.4092	2	6.6	81	92	No
				VVLDDKDYFLFR	K	D	95.00%	58		510.6102	3	9.5	81	92	No
368	IPI00220373	IDE	INSULIN-DEGRADING ENZYME.	AFIPQLLSR	K	L	95.00%	28		522.8176	2	6.4	714	722	No
				EMLAVDAPR	K	R	95.00%	29	M2: Oxidation	509.2597	2	7.4	942	950	No
				NLYVTFPIPDLQK	R	Y	95.00%	45		774.4344	2	8.7	312	324	No
				VEAFLITMEK	R	S	95.00%	35	M8: Oxidation	598.8185	2	4.6	863	872	No
369	IPI00220391; IPI00220558; IPI00783826	RYR1	565 KDA PROTEIN.; ISOFORM 2 OF RYANODINE RECEPTOR 1.; ISOFORM 1 OF RYANODINE RECEPTOR 1.	AEGLGMVNEDGTVINR	K	Q	95.00%	84	M6: Oxidation	845.9133	2	6.9	3849	3864	No
				ARPELLQSHFIPTIGR	R	L	95.00%	30		612.3536	3	8.5	3351	3366	No
				ATVDAEGNFDPRPVETLNVIIPEK	K	L	95.00%	39		875.4648	3	8.3	2727	2750	No
				EGAPGGTPQAGGEAQPAR	K	A	95.00%	40		825.9006	2	5.8	1354	1371	No
				IQNNWSYGENIDEELK	K	T	95.00%	59		976.4620	2	6.4	2771	2786	No
				LAQDSSQIELLK	K	E	95.00%	37		672.8779	2	7.6	3999	4010	No
				LTPAQTTLVDR	R	L	95.00%	28		607.8452	2	6.3	976	986	No
				NYNLQMSGETLK	R	T	95.00%	42	M6: Oxidation	707.3438	2	8.0	918	929	No
				SFFESASEDIEK	R	M	95.00%	58		694.8199	2	7.0	3096	3107	No
				VESLAAFAER	R	Y	95.00%	46		546.7914	2	5.6	1955	1964	No
				VVTVTMGDEQGNVHSSLK	R	C	95.00%	74	M6: Oxidation	958.9800	2	7.1	1470	1487	No
				VVTVTMGDEQGNVHSSLK	R	C	95.00%	32	M6: Oxidation	639.6538	3	3.7	1470	1487	No
370	IPI00220416; IPI00643836; IPI00790644; IPI00798386	UQCRB	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KDA PROTEIN.; UQCRB PROTEIN.; 16 KDA PROTEIN.; 12 KDA PROTEIN.	DDTIYEDEDVKEAIR	R	R	95.00%	82		905.9257	2	4.7	35	49	No
				DDTIYEDEDVKEAIR	R	R	95.00%	41		604.2870	3	5.7	35	49	No
				LPENLYNDR	R	M	95.00%	60		567.2874	2	6.9	51	59	No
				RLPENLYNDR	R	M	95.00%	51		645.3364	2	3.6	50	59	No
				WYYNAAGFNK	K	L	95.00%	39		617.2911	2	4.3	20	29	No
371	IPI00220467; IPI00395442; IPI00643758	TNNT1	ISOFORM 2 OF TROPONIN T, SLOW SKELETAL MUSCLE.; ISOFORM 1 OF TROPONIN T, SLOW SKELETAL MUSCLE.; ISOFORM 3 OF TROPONIN T, SLOW SKELETAL MUSCLE.	AQELSDWIHQLESEK	K	F	95.00%	106		906.9481	2	6.3	196	210	No
				AQELSDWIHQLESEK	K	F	95.00%	39		604.9668	3	4.3	196	210	No
				AQELSDWIHQLESEKFDLMAK	K	L	95.00%	56	M19: Oxidation	845.4214	3	9.9	196	216	No
				AQELSDWIHQLESEKFDLMAK	K	L	95.00%	40		840.0853	3	4.6	196	216	No
				IPEGERVDFDDIHR	K	K	95.00%	57		849.4216	2	6.1	44	57	No
				IPEGERVDFDDIHR	K	K	95.00%	43		566.6187	3	9.0	44	57	No
				IPEGERVDFDDIHR	K	K	95.00%	34		425.2154	4	7.6	44	57	No
				KEEEELVALK	K	E	95.00%	56		594.3326	2	4.1	80	89	Yes
				KKEEEELVALK	R	E	95.00%	79		658.3810	2	5.0	79	89	Yes
				KKEEEELVALK	R	E	95.00%	51		439.2556	3	2.7	79	89	Yes
				KKPLDIDYMGEEQLR	R	E	95.00%	68	M9: Oxidation	925.9748	2	5.1	179	193	No
				KKPLDIDYMGEEQLR	R	E	95.00%	66	M9: Oxidation	617.6523	3	4.7	179	193	No
				KKPLDIDYMGEEQLR	R	E	95.00%	35		612.3204	3	4.4	179	193	No
				KPLDIDYMGEEQLR	K	E	95.00%	60	M8: Oxidation	861.9279	2	6.0	180	193	No
				KVLSNMGAHFGGYLVK	K	A	95.00%	43	M6: Oxidation	868.9582	2	-4.1	152	167	No
				PSRPVVPPLIPPK	K	I	95.00%	23		698.9415	2	4.9	31	43	No
				PSRPVVPPLIPPK	K	I	95.00%	59		466.2959	3	2.7	31	43	No
				PVVPPLIPPK	R	I	95.00%	42		528.8480	2	5.5	34	43	No
				VDFDDIHR	R	K	95.00%	46		508.7466	2	5.0	50	57	No
				VLSNMGAHFGGYLVK	K	A	95.00%	88	M5: Oxidation	804.9194	2	6.3	142	156	No
				VLSNMGAHFGGYLVK	K	A	95.00%	37	M5: Oxidation	536.9490	3	6.5	153	167	No
				VLSNMGAHFGGYLVK	K	A	95.00%	99		796.9215	2	5.8	142	156	No
				VLSNMGAHFGGYLVK	K	A	95.00%	36		531.6166	3	5.1	142	156	No
				YEINVLYNR	K	I	95.00%	67		592.3130	2	5.9	222	230	No
372	IPI00220487	ATP5H	ISOFORM 1 OF ATP SYNTHASE D CHAIN, MITOCHONDRIAL.	AGLVDDFEK	K	K	95.00%	32		497.2506	2	3.9	64	72	No
				AGLVDDFEKK	K	F	95.00%	58		561.3013	2	9.1	64	73	No
				IVEYEKEMEK	R	M	95.00%	53	M8: Oxidation	657.3216	2	4.1	112	121	No
				LAALPENPPAIDWAYYK	R	A	95.00%	51		644.6743	3	8.4	42	58	No

				SWNETLTSR	K	L	95.00%	63		547.2713	2	6.4	33	41	No
				TIDWVAFAEIIPQNQK	K	A	95.00%	38		625.0043	3	5.9	10	25	No
				VPVPEDKYTAQVDAEEK	K	E	95.00%	51		639.9893	3	3.9	79	95	No
				VPVPEDKYTAQVDAEEKEDVK	K	S	95.00%	38		797.0718	3	9.3	79	99	No
				YTAQVDAEEKEDVK	K	S	95.00%	54		812.8966	2	9.0	86	99	No
				YTAQVDAEEKEDVK	K	S	95.00%	30		542.2657	3	6.5	86	99	No
373	IPI00220642	YWHAG	14-3-3 PROTEIN GAMMA.	DSTLIMQLLR	K	D	95.00%	65	M6: Oxidation	603.3372	2	8.2	218	227	Yes
				LAEQAERYDDMAAAMK	R	N	95.00%	37	M11: Oxidation, M15: Oxidation	615.6140	3	5.6	13	28	No
				NLLSVAYK	R	N	95.00%	33		907.5325	1	7.9	43	50	Yes
				NLLSVAYK	R	N	95.00%	39		454.2683	2	3.9	43	50	Yes
				NVTELNEPLSNEER	K	N	95.00%	102		822.4043	2	7.9	29	42	No
				NVTELNEPLSNEER	K	N	95.00%	35		548.6033	3	3.9	29	42	No
				TAFDDAIAELDTLNEDSYK	K	D	95.00%	75		711.0029	3	9.9	199	217	No
				YDDMAAAMK	R	N	95.00%	49	M4: Oxidation, M8: Oxidation	524.2131	2	5.2	20	28	No
				YLAEVATGEK	R	R	95.00%	52		1080.5660	1	7.3	133	142	No
				YLAEVATGEK	R	R	95.00%	53		540.7853	2	4.6	133	142	No
				YLAEVATGEKR	R	A	95.00%	37		618.8387	2	8.6	133	143	No
374	IPI00220644	PKM2	ISOFORM M1 OF PYRUVATE KINASE ISOZYMES M1/M2.	APIIAVTR	R	N	95.00%	35		840.5320	1	1.4	448	455	Yes
				APIIAVTR	R	N	95.00%	62		420.7706	2	3.1	448	455	Yes
				ASSHSTDLMEAMAMGSVEASYK	R	C	95.00%	59	M12: Oxidation, M14: Oxidation	779.0074	3	7.5	401	422	No
				ASSHSTDLMEAMAMGSVEASYK	R	C	95.00%	42	M14: Oxidation	773.6760	3	7.9	401	422	No
				ASSHSTDLMEAMAMGSVEASYK	R	C	95.00%	62	M9: Oxidation, M12: Oxidation	779.0058	3	5.4	401	422	No
				ASSHSTDLMEAMAMGSVEASYK	R	C	95.00%	103	M9: Oxidation, M12: Oxidation	1176.0080	2	10.0	401	422	No
				ASSHSTDLMEAMAMGSVEASYK	R	C	95.00%	80	M9: Oxidation, M12: Oxidation	784.3365	3	4.3	401	422	No
				ASSHSTDLMEAMAMGSVEASYK	R	C	95.00%	103	M9: Oxidation, M12: Oxidation, M14: Oxidation	1176.0080	2	10.0	401	422	No
				ASSHSTDLMEAMAMGSVEASYK	R	C	95.00%	80	M9: Oxidation, M12: Oxidation, M14: Oxidation	784.3365	3	4.3	401	422	No
				ASSHSTDLMEAMAMGSVEASYK	R	C	95.00%	55	M9: Oxidation, M14: Oxidation	779.0058	3	5.4	401	422	No
				DPVQEAWAEDVDLR	K	V	95.00%	105		821.8973	2	9.4	476	489	Yes
				DPVQEAWAEDVDLR	K	V	95.00%	65		548.2656	3	5.9	476	489	Yes
				EAEAAMFHR	R	K	95.00%	51	M6: Oxidation	539.2463	2	5.7	384	392	No
				EAEAAMFHR	R	K	95.00%	58		531.2472	2	2.5	384	392	No
				FDEILEASDGIMVAR	R	G	95.00%	120	M12: Oxidation	841.4142	2	5.8	280	294	Yes
				FGVEQDVDMVFASFIR	K	K	95.00%	121	M9: Oxidation	938.4593	2	8.4	231	246	Yes
				FGVEQDVDMVFASFIR	K	K	95.00%	67	M9: Oxidation	625.9751	3	7.8	231	246	Yes
				FGVEQDVDMVFASFIR	K	K	95.00%	135		930.4608	2	7.4	231	246	Yes
				FGVEQDVDMVFASFIR	K	K	95.00%	63		620.6429	3	7.0	231	246	Yes
				FGVEQDVDMVFASFIRK	K	A	95.00%	39	M9: Oxidation	668.6734	3	7.2	231	247	Yes
				GADFLVTEVENGGSLGSK	K	K	95.00%	125		890.4471	2	5.5	189	206	Yes
				GADFLVTEVENGGSLGSK	K	K	95.00%	62		593.9673	3	5.4	189	206	Yes
				GADFLVTEVENGGSLGSKK	K	G	95.00%	101		954.4987	2	9.5	189	207	Yes
				GADFLVTEVENGGSLGSKK	K	G	95.00%	57		636.6658	3	5.3	189	207	Yes
				GDLGIEIPAEK	R	V	95.00%	48		1141.6160	1	4.6	295	305	Yes
				GDLGIEIPAEK	R	V	95.00%	69		571.3098	2	0.9	295	305	Yes
				GDVVIVLTGWRPGSGFTNTMR	K	V	95.00%	59	M20: Oxidation	760.3990	3	9.1	506	526	Yes
				GDYPLEAVR	K	M	95.00%	48		1019.5200	1	3.7	368	376	Yes
				GDYPLEAVR	K	M	95.00%	55		510.2637	2	3.2	368	376	Yes
				GPEIR	K	T	95.00%	30		571.3227	1	4.0	116	120	Yes
				GSGTAEVELK	K	K	95.00%	54		495.7619	2	5.2	126	135	Yes
				GSGTAEVELKK	K	G	95.00%	53		559.8099	2	5.5	126	136	Yes
				GVNLPGAAVDLPAVSEK	K	D	95.00%	137		818.9545	2	6.1	208	224	Yes
				GVNLPGAAVDLPAVSEK	K	D	95.00%	59		546.3052	3	5.4	208	224	Yes
				GVNLPGAAVDLPAVSEKDIQDLK	K	F	95.00%	92		1175.1470	2	7.8	208	230	Yes
				GVNLPGAAVDLPAVSEKDIQDLK	K	F	95.00%	64		783.7662	3	6.9	208	230	Yes
				IENHEGVR	K	R	95.00%	48		477.2477	2	7.5	271	278	Yes

				IISKIENHEGVR	K	R	95.00%	27		465.5977	3	1.3	267	278	No
				ITLDNAYMEK	K	C	95.00%	50	M8: Oxidation	1213.5850	1	6.1	142	151	Yes
				ITLDNAYMEK	K	C	95.00%	75	M8: Oxidation	607.2951	2	3.9	142	151	Yes
				ITLDNAYMEK	K	C	95.00%	61		599.2980	2	4.5	142	151	Yes
				IYVDDGLISLQVK	K	Q	95.00%	111		731.9161	2	5.8	174	186	Yes
				IYVDDGLISLQVK	K	Q	95.00%	49		488.2799	3	5.6	174	186	Yes
				KGDVVIVLTGWR	K	P	95.00%	84		671.9004	2	6.1	505	516	Yes
				KGDVVIVLTGWR	K	P	95.00%	57		448.2683	3	3.2	505	516	Yes
				KGDVVIVLTGWRPGSGFTNTMR	K	V	95.00%	41	M21: Oxidation	803.0960	3	7.0	505	526	Yes
				KGDVVIVLTGWRPGSGFTNTMR	K	V	95.00%	42	M21: Oxidation	602.5722	4	4.1	505	526	Yes
				KGVNLPGAAVDLPAVSEK	K	D	95.00%	145		883.0006	2	4.1	207	224	Yes
				KGVNLPGAAVDLPAVSEK	K	D	95.00%	51		589.0039	3	5.6	207	224	Yes
				KGVNLPGAAVDLPAVSEKDIQDLK	K	F	95.00%	90		1239.1940	2	7.4	207	230	Yes
				KGVNLPGAAVDLPAVSEKDIQDLK	K	F	95.00%	96		826.4634	3	5.1	207	230	Yes
				KGVNLPGAAVDLPAVSEKDIQDLK	K	F	95.00%	49		620.0998	4	5.6	207	230	Yes
				KLFEELVR	R	A	95.00%	34		1033.6110	1	6.4	393	400	No
				KLFEELVR	R	A	95.00%	60		517.3075	2	2.4	393	400	No
				LDIDSPPITAR	R	N	95.00%	50		1197.6590	1	9.0	33	43	Yes
				LDIDSPPITAR	R	N	95.00%	77		599.3289	2	1.5	33	43	Yes
				LFEELVR	K	A	95.00%	33		905.5154	1	6.3	394	400	No
				LFEELVR	K	A	95.00%	63		453.2602	2	3.2	394	400	No
				LNFSHGTHEYHAETIK	R	N	95.00%	112		942.4594	2	3.6	74	89	Yes
				LNFSHGTHEYHAETIK	R	N	95.00%	68		628.6415	3	2.5	74	89	Yes
				MQHLIAR	R	E	95.00%	43	M1: Oxidation	442.7448	2	4.7	377	383	Yes
				MQHLIAR	R	E	95.00%	35		434.7470	2	4.0	377	383	No
				NTGIICTIGPASR	R	S	95.00%	57		651.8483	2	3.6	44	56	Yes
				PGSGFTNTMR	R	V	95.00%	67	M9: Oxidation	542.2517	2	5.7	517	526	Yes
				PVAVALDTK	R	G	95.00%	46		913.5423	1	6.9	107	115	No
				PVAVALDTK	R	G	95.00%	50		457.2738	2	4.1	107	115	Yes
				PVAVALDTKGPEIR	R	T	95.00%	40		733.4247	2	2.4	107	120	Yes
				PVAVALDTKGPEIR	R	T	95.00%	58		489.2866	3	4.2	107	120	Yes
				QKGADFLVTEVENGGSLGSK	K	K	95.00%	112		1018.5240	2	5.3	187	206	Yes
				QKGADFLVTEVENGGSLGSK	K	K	95.00%	69		679.3526	3	5.9	187	206	Yes
				QKGADFLVTEVENGGSLGSKK	K	G	95.00%	41		722.0516	3	6.5	187	207	Yes
				RFDEILEASDGIMVAR	R	G	95.00%	91	M13: Oxidation	919.4687	2	9.6	279	294	Yes
				RFDEILEASDGIMVAR	R	G	95.00%	75	M13: Oxidation	613.3121	3	4.7	279	294	Yes
				RFDEILEASDGIMVAR	R	G	95.00%	84		911.4675	2	5.6	279	294	Yes
				RFDEILEASDGIMVAR	R	G	95.00%	55		607.9806	3	5.1	279	294	Yes
				SVETLKEMIK	R	S	95.00%	50	M8: Oxidation	597.3297	2	5.3	57	66	Yes
				TATESFASDPILYR	R	P	95.00%	89		785.8962	2	5.9	93	106	Yes
				TATESFASDPILYR	R	P	95.00%	66		524.2676	3	7.6	93	106	No
				TATESFASDPILYRPVAVALDTK	R	G	95.00%	59		1233.1580	2	6.2	93	115	Yes
				TATESFASDPILYRPVAVALDTK	R	G	95.00%	67		822.4424	3	7.7	93	115	Yes
				TATESFASDPILYRPVAVALDTKGPEIR	R	T	95.00%	61		1006.5450	3	7.8	93	120	Yes
				VFLAQK	K	M	95.00%	45		705.4304	1	0.5	306	311	Yes
				VLGEK	K	G	95.00%	34		545.3339	1	7.2	257	261	Yes
				VNFAMNVGK	R	A	95.00%	45	M5: Oxidation	995.5024	1	4.0	490	498	Yes
				VNFAMNVGK	R	A	95.00%	70	M5: Oxidation	498.2536	2	1.0	490	498	Yes
				VNFAMNVGK	R	A	95.00%	39		979.5096	1	6.2	490	498	Yes
				VNFAMNVGK	R	A	95.00%	69		490.2569	2	2.6	490	498	Yes
				VVEVGSK	K	I	95.00%	34		717.4197	1	7.1	167	173	Yes
				VVPVP	R	-	95.00%	21		510.3314	1	4.4	527	531	Yes
375	IPI00220706; IPI00554676; IPI00749035; IPI00816084; IPI00816618	HBE1; HBG1; HBG2	HEMOGLOBIN SUBUNIT GAMMA-1.; HEMOGLOBIN SUBUNIT GAMMA-2.; 17 KDA PROTEIN.; GAMMA-G GLOBIN (FRAGMENT).; HEMOGLOBIN GAMMA-G (FRAGMENT).	EFTPEVQASWQK	K	M	95.00%	53		725.3615	2	9.3	122	133	No
				LHVDPENFK	K	L	95.00%	42		549.7849	2	3.1	97	105	No
				LLVVYPWTQR	R	F	95.00%	71		637.8707	2	5.7	25	34	Yes
				LLVVYPWTQR	R	F	95.00%	40		425.5841	3	8.3	25	34	Yes
				VLTSLGDAIK	K	H	95.00%	47		508.8069	2	6.5	61	70	No
				VNVEDAGGETLGR	K	L	95.00%	111		658.8315	2	7.9	19	31	No

376	IPI00220741; IPI00641363	SPTA1	SPECTRIN ALPHA CHAIN, ERYTHROCYTE.; SPECTRIN, ALPHA, ERYTHROCYTIC 1.	AAVGQEEIQLR	K	L	95.00%	63		607.3357	2	7.8	1785	1795	No
				DHEDFLASLAR	K	A	95.00%	51		637.3179	2	8.0	2086	2096	No
				DVTEAIQWIK	R	E	95.00%	30		601.8306	2	9.3	272	281	No
				ETGTLESQLEANK	K	R	95.00%	51		710.3570	2	6.5	2190	2202	No
				GTQLHEANQQLQFENNAEDLQR	K	W	95.00%	48		861.7512	3	7.5	680	701	No
				HQSLEAEVQTK	K	S	95.00%	41		635.3289	2	4.7	94	104	No
				KAENTGVELDDVWELQK	K	K	95.00%	50		658.6633	3	-4.1	1102	1118	No
				LADDEDYKDIQNLK	K	S	95.00%	68		840.4150	2	5.4	604	617	No
				LPEITDLKDK	R	L	95.00%	41		586.3369	2	7.1	1987	1996	No
				LSEVASLWEELLEATK	R	Q	95.00%	85		909.4875	2	7.3	662	677	No
				VLETAEEIQER	K	R	95.00%	79		658.8442	2	8.2	17	27	No
377	IPI00220766	GLO1	LACTOYLGLUTATHIONE LYASE.	DFLLQQTMLR	K	V	95.00%	69	M8: Oxidation	640.8426	2	7.7	29	38	No
				IAWALSR	K	K	95.00%	43		408.7425	2	5.0	89	95	No
				KSLDFYTR	K	V	95.00%	37		515.2756	2	6.3	44	51	No
				RFEELGVK	K	F	95.00%	45		489.2792	2	8.7	141	148	No
				SLDFYTR	K	V	95.00%	40		451.2274	2	5.6	45	51	No
				VLGMTLIQK	R	C	95.00%	53	M4: Oxidation	509.8067	2	8.1	52	60	No
378	IPI00220916; IPI00375714	HSPB7	ISOFORM 2 OF HEAT-SHOCK PROTEIN BETA-7.; HEAT SHOCK 27KDA PROTEIN FAMILY, MEMBER 7.	ALPAQDPPMEK	R	A	95.00%	50	M9: Oxidation	606.8036	2	4.8	33	43	No
				ALSMFSDDFGSFMR	K	P	95.00%	58	M4: Oxidation, M13: Oxidation	821.8555	2	9.1	44	57	No
				DFSPEDIIVTTSNNHIEVR	R	A	95.00%	48		729.3684	3	7.7	95	113	No
				LAADGTVMNTFAHK	K	C	95.00%	62	M8: Oxidation	746.3721	2	6.5	117	130	No
				RHPHTEHVQQTFR	R	T	95.00%	36		836.9317	2	8.0	158	170	No
				RHPHTEHVQQTFR	R	T	95.00%	33		558.2895	3	6.5	158	170	No
				TLGDAYEFAVDVR	K	D	95.00%	53		728.3658	2	8.0	82	94	No
379	IPI00221092	RPS16	40S RIBOSOMAL PROTEIN S16.	GGGHVAQIYAIR	K	Q	95.00%	31		621.3467	2	8.1	74	85	No
				GPLQSVQVFGR	K	K	95.00%	73		594.3354	2	7.7	5	15	No
				LLEPVLLLGK	K	E	95.00%	32		547.8680	2	8.3	51	60	No
380	IPI00221127	MYLK2	MYOSIN LIGHT CHAIN KINASE 2, SKELETAL/CARDIAC MUSCLE.	AEEGKNILAESQK	K	E	95.00%	53		708.8744	2	5.3	193	205	No
				APASEKGDGTLAQPSTSSQGPK	K	G	95.00%	47		705.3541	3	4.6	56	77	No
				DFVSNLIVK	K	D	95.00%	32		517.7989	2	1.2	515	523	No
				GDGTLAQPSTSSQGPK	K	G	95.00%	37		765.8779	2	5.1	62	77	No
				GEGDRGGGPAEGSAGPPAALPQQTATPETSVK	K	K	95.00%	63		997.4952	3	8.1	78	109	No
				GGGPAEGSAGPPAALPQQTATPETSVK	R	K	95.00%	44		826.0887	3	7.3	83	109	No
				GIEFQAVPSEK	R	S	95.00%	57		602.8162	2	2.6	227	237	No
				GPTGERPLAAGKDPGPPDPK	K	K	95.00%	35		653.0120	3	2.6	23	42	No
				IIDFGLAR	K	R	95.00%	56		452.7684	2	3.5	424	431	No
				ISSSGALMALGV	K	-	95.00%	74	M8: Oxidation	561.3006	2	5.1	585	596	No
				KNFIAVSAANR	K	F	95.00%	43		595.8397	2	5.9	571	581	No
				NFIAVSAANR	K	F	95.00%	59		531.7898	2	2.1	572	581	No
				TGNVSSEFSMNSK	R	E	95.00%	66	M10: Oxidation	702.3133	2	5.6	276	288	No
381	IPI00221222	SUB1	ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15.	DDNMFQIGK	R	M	95.00%	33	M4: Oxidation	542.2479	2	9.0	60	68	No
				EQISDIDDAVR	K	K	95.00%	45		630.8119	2	6.9	115	125	No
382	IPI00221305	CAMK2B	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE IIB ISOFORM 1.	AGAYDFPSPEWDTVTPEAK	K	N	95.00%	73		1040.9880	2	8.3	228	246	Yes
				DLKPENLLLASK	R	C	95.00%	48		670.8962	2	4.1	136	147	Yes
				DLKPENLLLASK	R	C	95.00%	41		447.5987	3	0.9	136	147	Yes
				FTDEYQLYEDIGK	R	G	95.00%	88		810.8827	2	8.7	10	22	No
				FYFENLLAK	R	N	95.00%	43		572.8088	2	4.8	585	593	No
				ISDILNSVR	R	R	95.00%	66		508.7918	2	1.8	450	458	No
				NLINQMLTINPAK	K	R	95.00%	42	M6: Oxidation	743.4136	2	6.2	247	259	Yes
				TTEQLIEAVNNGDFEAYAK	K	I	95.00%	61		1057.0170	2	8.1	541	559	No
				VPDILSSVR	R	R	95.00%	60		493.2899	2	3.7	412	420	No
383	IPI00239077	HINT1	HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN 1.	AQVARPGGDTIFGK	K	I	95.00%	59		708.8899	2	8.4	8	21	No
				KHISQISVAEDDDESLLGHLMIVGK	K	K	95.00%	48	M21: Oxidation	688.3634	4	9.8	58	82	No
				MVVNEGSDGGQSVYHVHLHVLGGR	R	Q	95.00%	66	M1: Oxidation	855.0922	3	5.4	96	119	No
				MVVNEGSDGGQSVYHVHLHVLGGR	R	Q	95.00%	59	M1: Oxidation	641.5735	4	9.2	96	119	No

384	IPI00243742	MYL3	MYOSIN LIGHT POLYPEPTIDE 3.	AAPAPAPPPEPERPK	K	E	95.00%	78		762.9166	2	5.0	19	33	No
				AAPAPAPPPEPERPK	K	E	95.00%	44		508.9456	3	2.3	19	33	No
				AAPAPAPPPEPERPKEVEFDASK	K	I	95.00%	32		810.7540	3	6.4	19	41	No
				ALGQNPTQAEVLR	R	V	95.00%	110		698.8840	2	3.8	82	94	No
				ALGQNPTQAEVLR	R	V	95.00%	56		466.2599	3	6.6	82	94	No
				DTGTYEDFVEGLR	K	V	95.00%	86		751.3503	2	7.7	126	138	No
				DTGTYEDFVEGLR	K	V	95.00%	49		501.2364	3	8.1	126	138	No
				EAFMLFDR	K	T	95.00%	74	M4: Oxidation	522.7468	2	3.2	56	63	No
				EAFMLFDR	K	T	95.00%	38		1028.4970	1	8.7	56	63	No
				EAFMLFDR	K	T	95.00%	48		514.7499	2	4.2	56	63	No
				EGNGTVMGAELR	K	H	95.00%	46	M7: Oxidation	625.2998	2	5.7	143	154	Yes
				EGNGTVMGAELR	K	H	95.00%	67		617.3024	2	5.8	143	154	Yes
				EVEFDASK	K	I	95.00%	33		924.4379	1	6.9	34	41	No
				EVEFDASK	K	I	95.00%	30		462.7225	2	6.3	34	41	No
				HIMSS	K	-	95.00%	21		574.2687	1	5.0	191	195	No
				HVLATLGER	R	L	95.00%	57		995.5731	1	9.3	155	163	No
				HVLATLGER	R	L	95.00%	66		498.2840	2	-3.7	155	163	No
				IEFTPEQIEEFK	K	E	95.00%	86		755.3837	2	7.7	44	55	No
				IEFTPEQIEEFK	K	E	95.00%	48		503.9256	3	8.8	44	55	No
				IEFTPEQIEEFKEAFMLFDR	K	T	95.00%	34	M16: Oxidation	845.7506	3	9.5	44	63	No
				IKIEFTPEQIEEFK	K	E	95.00%	87		875.9752	2	8.9	42	55	No
				IKIEFTPEQIEEFK	K	E	95.00%	71		584.3176	3	5.9	42	55	No
				IKIEFTPEQIEEFKEAFMLFDR	K	T	95.00%	64	M18: Oxidation	694.8585	4	7.0	42	63	No
				IKIEFTPEQIEEFKEAFMLFDR	K	T	95.00%	36		690.8611	4	9.1	42	63	No
				ITYGQCGDVLR	K	A	95.00%	52		612.8101	2	6.2	71	81	No
				LTEDEVEK	R	L	95.00%	46		481.7409	2	5.8	164	171	No
				MMDFETFLPMLQHISK	K	N	95.00%	70	M1: Oxidation	992.4822	2	9.1	108	123	No
				MMDFETFLPMLQHISK	K	N	95.00%	66	M1: Oxidation	661.9880	3	5.0	108	123	No
				MMDFETFLPMLQHISK	K	N	95.00%	42	M1: Oxidation	667.3206	3	6.5	108	123	No
				MMDFETFLPMLQHISK	K	N	95.00%	48	M1: Oxidation	1008.4770	2	9.3	108	123	No
				MMDFETFLPMLQHISK	K	N	95.00%	42	M1: Oxidation, M2: Oxidation	667.3206	3	6.5	108	123	No
				MMDFETFLPMLQHISK	K	N	95.00%	48	M1: Oxidation, M2: Oxidation, M10: Oxidation	1008.4770	2	9.3	108	123	No
				MMDFETFLPMLQHISK	K	N	95.00%	39	M1: Oxidation, M2: Oxidation, M10: Oxidation	672.6491	3	1.7	108	123	No
				MMDFETFLPMLQHISK	K	N	95.00%	56	M10: Oxidation	992.4820	2	8.9	108	123	No
				MMDFETFLPMLQHISK	K	N	95.00%	83	M2: Oxidation	992.4825	2	9.5	108	123	No
				MMDFETFLPMLQHISK	K	N	95.00%	67	M2: Oxidation	661.9891	3	6.6	108	123	No
				MMDFETFLPMLQHISK	K	N	95.00%	49	M2: Oxidation	1000.4780	2	7.8	108	123	No
				MMDFETFLPMLQHISK	K	N	95.00%	49	M2: Oxidation, M10: Oxidation	1000.4780	2	7.8	108	123	No
				MMDFETFLPMLQHISK	K	N	95.00%	56		984.4814	2	5.8	108	123	No
				MMDFETFLPMLQHISK	K	N	95.00%	52		656.6579	3	7.3	108	123	No
				NKDTGTYEDFVEGLR	K	V	95.00%	116		872.4194	2	6.7	124	138	No
				NKDTGTYEDFVEGLR	K	V	95.00%	72		581.9503	3	9.2	124	138	No
				VFDKEGNGTVMGAELR	R	H	95.00%	90	M11: Oxidation	869.9314	2	6.6	139	154	Yes
				VFDKEGNGTVMGAELR	R	H	95.00%	43	M11: Oxidation	580.2899	3	6.1	139	154	Yes
				VFDKEGNGTVMGAELR	R	H	95.00%	132		861.9331	2	5.7	139	154	Yes
				VFDKEGNGTVMGAELR	R	H	95.00%	51		574.9572	3	4.3	139	154	Yes
385	IPI00246058	PDCD6IP	PDCD6IP PROTEIN.	ELPELLQR	K	N	95.00%	31		499.2904	2	4.5	444	451	No
				ETVLSALSR	K	E	95.00%	32		488.2789	2	2.6	165	173	No
				FYNELTEILVR	K	F	95.00%	55		698.8813	2	5.2	681	691	No
				LALASLGYEK	K	S	95.00%	58		532.8052	2	3.1	111	120	No
				LANQAADYFGDAFK	K	Q	95.00%	75		765.8710	2	7.4	216	229	No
				LLDEEEATDNDLR	R	A	95.00%	95		766.8655	2	9.7	462	474	No
				MVPVSVQQSLAAYNQR	K	K	95.00%	112	M1: Oxidation	903.9669	2	4.9	363	378	No
				NIQVSHQEFSK	K	M	95.00%	38		658.8376	2	5.7	633	643	No
				SLLSNLDEVKK	K	E	95.00%	59		623.3602	2	5.6	559	569	No
				SLLSNLDEVKK	K	E	95.00%	28		415.9087	3	4.0	559	569	No
				SVIEQGGIQTVDQLIK	R	E	95.00%	103		864.4865	2	6.1	428	443	No
				TMQGSEVVNVLK	K	S	95.00%	40	M2: Oxidation	660.8497	2	6.3	547	558	No
				TPSNELYKPLR	R	A	95.00%	33		659.3665	2	6.3	484	494	No
386	IPI00246975	GSTM3	GLUTATHIONE S-TRANSFERASE MU 3.	FSWFAGEK	K	L	95.00%	40		486.2384	2	6.4	149	156	No
				IRVDIIENQVMDFR	K	T	95.00%	31	M11: Oxidation	588.6464	3	6.9	99	112	No
				ITQSNAILR	K	Y	95.00%	79		508.3018	2	5.6	74	82	Yes

387	IPI00255554; IPI00410073	GPR123	ISOFORM 1 OF PROBABLE G-PROTEIN COUPLED RECEPTOR 123.; ISOFORM 2 OF PROBABLE G-PROTEIN COUPLED RECEPTOR 123.	AAAQKTGR	K	L	95.00%	30		401.7302	2	-1.2	144	151	No
				VLIINTPSGR	R	T	95.00%	24		535.3234	2	1.7	320	329	No
388	IPI00289499	ATIC	BIFUNCTIONAL PURINE BIOSYNTHESIS PROTEIN PURH.	ALFEEVPELLTEAEK	K	K	95.00%	31		859.4451	2	-4.5	510	524	No
				ALFEEVPELLTEAEKK	K	E	95.00%	30		616.0053	3	8.1	510	525	No
				APGQLALFSVSDK	M	T	95.00%	85		666.8655	2	5.0	2	14	No
				DLIVATIAVK	R	Y	95.00%	57		521.8321	2	4.7	417	426	No
				EVSDGIIAPGYEEEALTILSK	R	K	95.00%	62		1117.5840	2	7.3	336	356	No
				EVSDGIIAPGYEEEALTILSK	R	K	95.00%	50		745.3913	3	6.0	336	356	No
				HVSPAGAAVGIPLSEDEAK	K	V	95.00%	85		924.4817	2	2.7	267	285	No
				HVSPAGAAVGIPLSEDEAK	K	V	95.00%	37		616.6568	3	2.2	267	285	No
				LDFNLIR	R	V	95.00%	52		445.7604	2	3.4	91	97	No
				NLTALGLNLVASGGTAK	R	A	95.00%	97		800.4613	2	4.7	23	39	No
				RAEISNAIDQYVTGTIGEDEDLIK	K	W	95.00%	62		884.1174	3	5.8	484	507	No
				SLFSNVVTK	K	N	95.00%	32		497.7841	2	3.0	398	406	No
				YGMNPHQTPAQLYTLQPK	R	L	95.00%	56	M3: Oxidation	701.6865	3	4.8	208	225	No
389	IPI00289758	CAPN2	CALPAIN-2 CATALYTIC SUBUNIT PRECURSOR.	IMVDMLDSDGSGK	K	L	95.00%	44	M2: Oxidation, M5: Oxidation	700.3138	2	7.9	579	591	No
				NPWGEVEWTGR	R	W	95.00%	67		665.8187	2	8.6	286	296	No
				SDTFINLR	R	E	95.00%	45		483.2601	2	7.0	462	469	No
390	IPI00290416	GTPBP9	ISOFORM 1 OF PUTATIVE GTP-BINDING PROTEIN 9.	FYHDWNDKEIEVLNK	R	H	95.00%	72		975.4804	2	6.8	202	216	No
				FYHDWNDKEIEVLNK	R	H	95.00%	47		650.6544	3	4.0	202	216	No
				IGIVGLPNVGK	K	S	95.00%	58		533.8376	2	4.3	25	35	No
				IPAFLNVVDIAGLVK	K	G	95.00%	118		784.9807	2	7.5	84	98	No
				IPAFLNVVDIAGLVK	K	G	95.00%	76		523.6553	3	5.4	84	98	No
				LQELSAEER	K	Q	95.00%	36		537.7785	2	5.6	271	279	No
				NYIVEDGDIIFFK	R	F	95.00%	61		786.9073	2	7.5	374	386	No
				PMVYLVNLSEKDYIR	K	K	95.00%	43	M2: Oxidation	619.3315	3	8.6	224	238	No
				WLIKIK	K	E	95.00%	25		400.7729	2	-2.5	243	248	No
				YEDFKEEGSENAVK	K	A	95.00%	42		822.8796	2	7.3	350	363	No
				YLEANMTQSALPK	K	I	95.00%	75	M6: Oxidation	741.3756	2	8.2	282	294	No
391	IPI00290553; IPI00793673	ALDH1L1	10-FORMYLTETRAHYDROFOLATE DEHYDROGENASE.; FORMYLTETRAHYDROFOLATE DEHYDROGENASE ISOFORM A VARIANT.	ADPLGLEAEKDGVPVFK	K	Y	95.00%	38		892.9837	2	8.9	39	55	No
				AGLILFGNDDK	K	M	95.00%	31		581.8138	2	7.6	275	285	No
				ANATEFGLASGVFTR	R	D	95.00%	49		770.8981	2	8.1	827	841	No
				DLGEAALNEYLR	K	V	95.00%	71		682.3513	2	6.4	893	904	No
				FADGDLDAVLSR	R	A	95.00%	76		639.8256	2	7.9	815	826	No
				GAASSVLELTEAELVTAEAVR	K	S	95.00%	51		706.0500	3	9.7	308	328	No
				HGSIIYHPSLLPR	R	H	95.00%	34		497.2829	3	3.3	110	122	No
				IGFTGSTEVGK	K	H	95.00%	39		548.2917	2	6.1	646	656	No
				IQGSTIPINQAR	K	P	95.00%	49		649.3702	2	7.4	540	551	No
				LFVEDSIHDEFVR	R	R	95.00%	32		803.4028	2	4.0	723	735	No
				LFVEDSIHDEFVR	R	R	95.00%	32		535.9391	3	6.5	713	725	No
				LPQPEEGATYEGIQK	R	K	95.00%	62		830.4174	2	2.1	191	205	No
				LPQPEEGATYEGIQKK	R	E	95.00%	36		596.6472	3	4.2	191	206	No
				LQAGTVFVNTYNK	K	T	95.00%	65		727.8929	2	9.3	853	865	No
				TDVAAPFGGFK	K	Q	95.00%	37		555.2873	2	3.2	876	886	No
				VLEVEDSTDFFK	K	S	95.00%	77		714.8544	2	7.8	348	359	No
392	IPI00290566	TCP1	T-COMPLEX PROTEIN 1 SUBUNIT ALPHA.	AFHNEAQVNPER	R	K	95.00%	30		706.3461	2	8.8	469	480	No
				DDKHGSYEDAVHSGALND	K	-	95.00%	32		643.9512	3	8.5	539	556	No
				EQLAIAEFAR	R	S	95.00%	53		574.3117	2	3.7	434	443	No
				LGVQVVITDPEKLDQIR	K	Q	95.00%	40		641.7068	3	6.9	248	264	No
				MLVDDIGDVTITNDGATILK	K	L	95.00%	129	M1: Oxidation	1060.5530	2	8.5	44	63	No
				MLVDDIGDVTITNDGATILK	K	L	95.00%	40	M1: Oxidation	707.3706	3	7.6	44	63	No
				SLLVIPNTLAVNAAQDSTDLVAK	R	L	95.00%	101		1177.1640	2	9.5	444	466	No
				SQNVMAAASIANIVK	R	S	95.00%	111	M5: Oxidation	766.9138	2	6.1	19	33	No
				YINENLIVNTDELGR	R	D	95.00%	98		881.9582	2	6.2	131	145	No
				YPVNSVNILK	R	A	95.00%	36		573.8326	2	4.5	190	199	No

393	IPI00290770; IPI00552715; IPI00553185; IPI00744315	CCT3	CHAPERONIN CONTAINING TCP1, SUBUNIT 3 ISOFORM B.; CHAPERONIN CONTAINING TCP1, SUBUNIT 3 ISOFORM C.; T-COMPLEX PROTEIN 1 SUBUNIT GAMMA.; 60 KDA PROTEIN.	AVAQALEVIPR	R	T	95.00%	73		583.8515	2	4.6	438	448	No
				ELGIWEPLAVK	K	L	95.00%	46		627.8625	2	5.8	491	501	No
				GISDLAQHYLMR	K	A	95.00%	60	M11: Oxidation	710.3596	2	4.0	294	305	No
				GISDLAQHYLMR	K	A	95.00%	41	M11: Oxidation	473.9101	3	6.4	294	305	No
				IVLLDSSLEYK	R	K	95.00%	55		640.3661	2	7.3	237	247	No
				IVSRPEELREDDVGTGAGLLEIK	R	K	95.00%	36		832.7871	3	5.9	330	352	No
				IVSRPEELREDDVGTGAGLLEIK	R	K	95.00%	31		624.8413	4	4.3	330	352	No
				KGESQTDIEITREEDFTR	K	I	95.00%	34		718.6866	3	5.8	248	265	No
				KGESQTDIEITREEDFTR	K	I	95.00%	37		539.2659	4	3.9	248	265	No
				TAVETAVLLLR	K	I	95.00%	108		593.3676	2	5.6	507	517	No
394	IPI00291005	MDH1	MALATE DEHYDROGENASE, CYTOPLASMIC.	DLDVAILVGSMPR	K	R	95.00%	94	M11: Oxidation	701.3810	2	9.1	80	92	No
				DLDVAILVGSMPR	K	R	95.00%	48	M11: Oxidation	467.9224	3	7.1	80	92	No
				DLDVAILVGSMPR	K	R	95.00%	44		693.3828	2	8.0	80	92	No
				DVIATDKEDVAFK	K	D	95.00%	99		725.8823	2	9.4	67	79	No
				DVIATDKEDVAFK	K	D	95.00%	45		484.2550	3	4.3	67	79	No
				ELTEEKESAFEFLSSA	K	-	95.00%	59		908.9340	2	6.0	319	334	No
				ESAFEFLSSA	K	-	95.00%	66		544.2562	2	9.1	325	334	No
				EVGVYEALK	K	D	95.00%	30		1007.5430	1	1.8	206	214	No
				EVGVYEALK	K	D	95.00%	40		504.2779	2	6.7	206	214	No
				EVGVYEALKDDSWLK	K	G	95.00%	89		876.4524	2	6.4	206	220	No
				EVGVYEALKDDSWLK	K	G	95.00%	32		584.6364	3	4.5	206	220	No
				FVEGLPINDFSR	K	E	95.00%	67		697.3640	2	6.1	299	310	No
				GEFVTTVQQR	K	G	95.00%	74		582.8060	2	2.3	221	230	No
				LGVTANDVK	K	N	95.00%	34		916.5185	1	8.8	171	179	No
				LGVTANDVK	K	N	95.00%	60		458.7596	2	1.1	171	179	No
				NVIIWGNHSSTQYPDVNHAK	K	V	95.00%	54		760.7143	3	4.8	180	199	No
				SQGAALDKYAK	K	K	95.00%	63		576.3095	2	4.3	111	121	No
				VLVTGAAGQIAYSLLYSIGNGSVFGK	R	D	95.00%	87		862.4785	3	8.5	7	32	No
395	IPI00291006	MDH2	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.	AGAGSATLSMAYAGAR	K	F	95.00%	124	M10: Oxidation	735.8558	2	1.8	242	257	No
				AGAGSATLSMAYAGAR	K	F	95.00%	48	M10: Oxidation	490.9088	3	6.6	242	257	No
				AGAGSATLSMAYAGAR	K	F	95.00%	72		727.8621	2	7.0	242	257	No
				AKAGAGSATLSMAYAGAR	K	F	95.00%	53	M12: Oxidation	835.4255	2	6.0	240	257	No
				AKAGAGSATLSMAYAGAR	K	F	95.00%	45	M12: Oxidation	557.2873	3	7.8	240	257	No
				ANTFVAELK	R	G	95.00%	34		992.5497	1	8.1	177	185	No
				ANTFVAELK	R	G	95.00%	74		496.7764	2	3.4	177	185	No
				ANTFVAELKGLDPAR	R	V	95.00%	55		801.4431	2	8.2	177	191	No
				ANTFVAELKGLDPAR	R	V	95.00%	45		534.6315	3	8.5	177	191	No
				FVFSLVDAMNGK	R	E	95.00%	66	M9: Oxidation	672.3434	2	9.0	258	269	No
				FVFSLVDAMNGK	R	E	95.00%	82		664.3442	2	6.5	258	269	No
				GLDPARVNVPVIGGHAGK	K	T	95.00%	44		586.3383	3	9.6	186	203	No
				HGVYNPNKIFGVTTLDIVR	K	A	95.00%	40		715.0674	3	9.5	158	176	No
				IFGVTTLDIVR	K	A	95.00%	68		617.3683	2	6.5	166	176	No
				IQEAGTEVVK	R	A	95.00%	66		537.2971	2	1.7	230	239	No
				KGEDFVK	K	T	95.00%	30		411.7255	2	8.2	329	335	No
				LTLYDIAHTPGVAADLSHIETK	R	A	95.00%	89		789.0914	3	7.6	53	74	No
				MISDAIPELK	K	A	95.00%	62	M1: Oxidation	566.8037	2	6.1	315	324	No
				MISDAIPELK	K	A	95.00%	58		558.8061	2	5.9	315	324	No
				VAVLGASGGIGQPLSLLLK	K	N	95.00%	142		897.0569	2	8.7	27	45	No
				VAVLGASGGIGQPLSLLLK	K	N	95.00%	60		598.3719	3	5.4	27	45	No
				VDFPQDQLTALTGR	K	I	95.00%	111		780.9121	2	8.9	216	229	No
				VDFPQDQLTALTGR	K	I	95.00%	47		520.9444	3	9.7	216	229	No
				VNVPVIGGHAGK	R	T	95.00%	81		574.3345	2	2.0	192	203	No
				VSSFEEKMISDAIPELK	K	A	95.00%	30	M8: Oxidation	647.0016	3	8.1	308	324	No
396	IPI00291175; IPI00307162	VCL	ISOFORM 1 OF VINCULIN.; ISOFORM 2 OF VINCULIN.	AGEVINQPMMMAAR	K	Q	95.00%	68	M9: Oxidation, M10: Oxidation, M11: Oxidation	783.8621	2	5.5	890	903	No
				AIPDLTAPVAAVQAAVSNLVR	K	V	95.00%	127		1038.6030	2	7.5	36	56	No
				AIPDLTAPVAAVQAAVSNLVR	K	V	95.00%	62		692.7371	3	6.7	36	56	No
				ALASQLQDSLK	R	D	95.00%	71		587.3306	2	4.5	571	581	No
				AQQVSQGLDVLTAK	K	V	95.00%	90		729.4048	2	3.5	353	366	No
				AQQVSQGLDVLTAK	K	V	95.00%	59		486.6054	3	2.8	353	366	No
				AVAGNISDPGLQK	K	S	95.00%	64		635.3481	2	6.2	803	815	No

				DPSASPGDAGEQAIR	R	Q	95.00%	80		735.8521	2	9.4	286	300	No
				EAFQPQEPDFPPPPPDLEQLR	R	L	95.00%	51		816.4087	3	9.0	833	853	No
				ELLPVLISAMK	K	I	95.00%	37	M10: Oxidation	615.3675	2	7.3	200	210	No
				ELLPVLISAMK	K	I	95.00%	29		607.3670	2	2.4	200	210	No
				ELTPQVVSAAR	R	I	95.00%	66		585.8319	2	6.6	670	680	No
				ETVQTTEDQILK	K	R	95.00%	49		702.8705	2	7.6	60	71	No
				ETVQTTEDQILKR	K	D	95.00%	85		780.9178	2	2.7	60	72	No
				GILSGTSDLLLTFDEAEVR	R	K	95.00%	80		1018.5370	2	5.3	114	132	No
				GILSGTSDLLLTFDEAEVRK	R	I	95.00%	31		722.0608	3	7.7	114	133	No
				GWLRDPSASPGDAGEQAIR	K	Q	95.00%	56		661.6642	3	4.2	282	300	No
				KIDAAQNWLADPNGGPEGEEQIR	K	G	95.00%	52		836.7485	3	7.0	387	409	No
				LANVMMGPYR	R	Q	95.00%	40	M5: Oxidation, M6: Oxidation	592.2875	2	5.8	529	538	No
				LLAVAATAPPDAPNREEVFDER	K	A	95.00%	47		794.4128	3	5.3	608	629	No
				LVQAAQMLQSDPYSVPAR	K	D	95.00%	89	M7: Oxidation	995.5135	2	6.2	88	105	No
				LVQAAQMLQSDPYSVPAR	K	D	95.00%	47	M7: Oxidation	664.0120	3	6.7	88	105	No
				MALLMAEMSR	R	L	95.00%	46	M1: Oxidation, M5: Oxidation, M8: Oxidation	600.7789	2	6.2	926	935	No
				MLGQMTDQVADLR	K	A	95.00%	89	M1: Oxidation, M5: Oxidation	755.3590	2	3.9	327	339	No
				MQEAMTQEVSDVFSDTTTPIK	R	L	95.00%	150	M1: Oxidation, M5: Oxidation	1195.5520	2	8.8	587	607	No
				MQEAMTQEVSDVFSDTTTPIK	R	L	95.00%	40	M1: Oxidation, M5: Oxidation	797.3683	3	6.3	587	607	No
				MSAEINEIIR	K	V	95.00%	79	M1: Oxidation	596.3086	2	4.3	237	246	No
				MSAEINEIIR	K	V	95.00%	75		588.3099	2	2.1	237	246	No
				MTGLVDEAIDTK	K	S	95.00%	80	M1: Oxidation	654.8266	2	7.2	709	720	No
				NPGNQAAYEHFETMK	R	N	95.00%	59	M14: Oxidation	876.8909	2	4.9	685	699	No
				NQGIEEALK	K	N	95.00%	33		501.2688	2	2.8	220	228	No
				QVATALQNLQTK	K	T	95.00%	76		657.8772	2	6.3	465	476	No
				SLGEISALTSK	R	L	95.00%	68		553.3109	2	3.1	434	444	No
				SLLDASEEAIKK	K	D	95.00%	89		652.3611	2	2.6	721	732	No
				STVEGIQASVK	K	T	95.00%	74		559.8090	2	3.9	656	666	No
				TDAGFTLR	R	W	95.00%	30		440.7316	2	2.8	1050	1057	No
				TIESILEPVAQQISHLVIMHEEGEVDGK	R	A	95.00%	50	M19: Oxidation	1039.8740	3	9.2	8	35	No
				TISPMVMDAK	K	A	95.00%	34	M5: Oxidation, M7: Oxidation	562.7731	2	4.6	793	802	No
				TNISDEESEQATEMLVHNAQNLMQSVK	R	E	95.00%	109	M14: Oxidation, M23: Oxidation	1026.8150	3	9.9	1009	1035	No
				VAMANIQPQMLVAGATSIAR	K	R	95.00%	121	M3: Oxidation, M10: Oxidation	1037.5510	2	7.2	739	758	No
				VAMANIQPQMLVAGATSIAR	K	R	95.00%	46	M3: Oxidation, M10: Oxidation	692.0361	3	6.6	739	758	No
				VDQLTAQLADLAAR	R	G	95.00%	94		742.9134	2	7.7	548	561	No
				VGKETVQTTEDQILKR	R	D	95.00%	42		615.6770	3	3.7	57	72	No
				VLQLTSWDEDAWASK	R	D	95.00%	60		874.9359	2	8.2	247	261	No
				VMLVNSMNTVK	R	E	95.00%	35	M2: Oxidation, M7: Oxidation	634.3278	2	7.0	189	199	No
				WIDNPTVDDR	R	G	95.00%	58		615.7951	2	5.5	503	512	No
397	IPI00291922	PSMA5	PROTEASOME SUBUNIT ALPHA TYPE 5.	AIGSASEGAQSSLQEVYHK	R	S	95.00%	39		654.6615	3	6.2	169	187	No
				ITSPLMEPSSIEK	R	I	95.00%	64	M6: Oxidation	724.3780	2	8.8	54	66	No
				LFQVEYAIEAIK	R	L	95.00%	75		712.4024	2	9.3	21	32	No
398	IPI00291928; IPI00646415	RAB14	RAS-RELATED PROTEIN RAB-14.; 20 KDA PROTEIN.	GAAGALMVYDITR	R	R	95.00%	56	M7: Oxidation	677.3511	2	7.8	83	95	No
				LQIWDTAGQER	K	F	95.00%	51		658.8402	2	9.5	62	72	Yes
				YIIIGDMGVGK	K	S	95.00%	30	M7: Oxidation	591.3193	2	5.6	14	24	No

399	IPI00293464; IPI00784120; IPI00786914; IPI00787250	DDB1	DNA DAMAGE-BINDING PROTEIN 1.; 127 KDA PROTEIN.; DAMAGE-SPECIFIC DNA BINDING PROTEIN 1.; SIMILAR TO DNA DAMAGE-BINDING PROTEIN 1 (DAMAGE-SPECIFIC DNA-BINDINGPROTEIN 1) (UV-DAMAGED DNA-BINDING FACTOR) (DDB P127 SUBUNIT) (DDBA)(UV-DAMAGED DNA-BINDING PROTEIN 1) (UV-DDB 1) (XERODERMA PIGMENTOSUMGROUP E-COMPLEMENTING PROTEIN) (XPCE) (XP...	ALYYLQIHPQELR	R	Q	95.00%	30		548.6405	3	9.0	515	527	No
				IAVMELFRPK	K	G	95.00%	28	M4: Oxidation	407.2355	3	2.7	61	70	No
				IEVQDTSGGTTALRPSASTQALSSSVSSSK	R	L	95.00%	76		984.8394	3	9.0	740	769	No
				IVVFQYSDGK	R	L	95.00%	33		578.3091	2	4.5	848	857	No
				LLASINSTVR	K	L	95.00%	34		537.3236	2	6.9	880	889	No
				SVLLLAYKPMEGNFEEIAR	R	D	95.00%	27	M10: Oxidation	732.7237	3	8.2	929	947	No
				VTLGTQPTVLR	K	T	95.00%	49		592.8573	2	5.3	629	639	No
				YLAIAPPIIK	K	Q	95.00%	26		549.8545	2	7.4	245	254	No
400	IPI00293867; IPI00472043	DDT	D-DOPACHROME DECARBOXYLASE.; SIMILAR TO D-DOPACHROME TAUTOMERASE.	PFLELDTNLPANR	M	V	95.00%	80		750.4041	2	9.6	2	14	No
				SHSAHFFEFLTK	R	E	95.00%	44		484.2471	3	9.5	76	87	No
401	IPI00293975	GPX1	GLUTATHIONE PEROXIDASE 1 ISOFORM 1.	FLVGPDGVPLRR	K	Y	95.00%	28		442.5977	3	5.9	167	178	No
				NDVAWNFEK	R	F	95.00%	49		561.7664	2	2.6	158	166	No
				PLAGGEPVSLGSLR	R	G	95.00%	25		676.8874	2	9.6	23	36	No
				YVRPGGGFEPNFMLFEK	K	C	95.00%	34	M13: Oxidation	668.6640	3	3.7	98	114	No
402	IPI00294073	COQ7	UBIQUINONE BIOSYNTHESIS PROTEIN COQ7 HOMOLOG.	FNELMVMFR	K	V	95.00%	34	M5: Oxidation, M7: Oxidation	609.7920	2	9.0	97	105	No
				SSGMTLDNISR	R	A	95.00%	60	M4: Oxidation	598.7872	2	7.0	36	46	No
				TLMEEDPEKYEELLQLIK	R	K	95.00%	31	M3: Oxidation	746.3867	3	8.0	155	172	Yes
403	IPI00294186; IPI00749059	LACTB	ISOFORM 1 OF SERINE BETA-LACTAMASE-LIKE PROTEIN LACTB, MITOCHONDRIALPRECURSOR.; LACTB PROTEIN.	EKFENSIESLR	R	L	95.00%	43		676.3496	2	4.2	296	306	No
				FGNAMLYGYQVGLFK	K	N	95.00%	62	M5: Oxidation	862.4382	2	9.8	410	424	No
				IFHDLDMLTTVQEENEPVIYNR	K	A	95.00%	38	M7: Oxidation	898.1103	3	8.3	350	371	No
				IKDEVGAPGIVVGVSVDGK	R	E	95.00%	79		920.0195	2	4.4	118	136	No
				LLISHLSGIR	R	H	95.00%	62		554.8481	2	3.6	212	221	No
				LVNTPYVDNSYK	R	W	95.00%	44		706.8629	2	8.4	383	394	No
				WAGGGFLSTVGDLLK	K	F	95.00%	112		760.9163	2	8.7	395	409	No
404	IPI00294187	PADI2	PROTEIN-ARGININE DEIMINASE TYPE-2.	AFFPNMVNMIVLDK	R	D	95.00%	64	M6: Oxidation, M9: Oxidation	835.9212	2	3.6	583	596	No
				DGNLKDFPVK	R	E	95.00%	43		566.8063	2	3.7	374	383	No
				DNYLFLK	K	E	95.00%	36		456.7467	2	2.5	316	322	No
				ELGLTEQDIIDLPALFK	K	M	95.00%	116		958.0335	2	8.3	558	574	No
				ELGLTEQDIIDLPALFK	K	M	95.00%	51		639.0253	3	8.8	558	574	No
				ELLGPDFGYVTR	K	E	95.00%	74		683.8592	2	7.1	384	395	No
				GFPVVLDSPR	K	D	95.00%	58		543.8047	2	6.3	364	373	No
				HSEHVWVEVVR	K	D	95.00%	40		459.5735	3	-1.9	44	54	No
				ILIGSSFPLSGGR	R	R	95.00%	87		652.3760	2	5.1	429	441	No
				ILSNESLVQENLYFQR	K	C	95.00%	102		977.0126	2	4.7	531	546	No
				ILSNESLVQENLYFQR	K	C	95.00%	52		651.6785	3	5.9	531	546	No
				VGVFYVENPFFGQR	K	Y	95.00%	84		829.9265	2	7.4	212	225	No
				VTMSQASTEASSDK	R	V	95.00%	47	M3: Oxidation	729.3314	2	8.3	79	92	No
				VTMSQASTEASSDK	R	V	95.00%	64		721.3337	2	8.0	79	92	No
				WIQDEIEFGYIEAPHK	R	G	95.00%	104		987.9912	2	7.1	348	363	No
				WIQDEIEFGYIEAPHK	R	G	95.00%	63		658.9966	3	6.9	348	363	No
				WLLSPSTTLR	R	V	95.00%	31		587.3392	2	6.1	69	78	No
405	IPI00294398; IPI00298406	HADH	ISOFORM 1 OF HYDROXYACYL-COENZYME A DEHYDROGENASE, MITOCHONDRIALPRECURSOR.; ISOFORM 2 OF HYDROXYACYL-COENZYME A DEHYDROGENASE, MITOCHONDRIALPRECURSOR.	AGDEFVEK	K	T	95.00%	39		447.7163	2	4.2	88	95	No
				DTPGFIVNR	K	L	95.00%	29		1018.5410	1	8.9	213	221	No
				DTPGFIVNR	K	L	95.00%	42		509.7734	2	6.5	213	221	No
				FAGLHFFNPVPVMK	R	L	95.00%	57	M13: Oxidation	810.4314	2	8.7	166	179	No
				FAGLHFFNPVPVMK	R	L	95.00%	47	M13: Oxidation	540.6220	3	5.9	166	179	No
				FAGLHFFNPVPVMK	R	L	95.00%	38		802.4332	2	7.8	166	179	No
				FAGLHFFNPVPVMK	R	L	95.00%	41		535.2899	3	4.9	166	179	No

				FIVDGWHEMDAENPLHQPSPSLNK	K	L	95.00%	41		921.1127	3	6.5	272	295	No
				GDASKEDIDTAMK	R	L	95.00%	59	M12: Oxidation	698.8226	2	7.5	237	249	No
				GDASKEDIDTAMK	R	L	95.00%	42	M12: Oxidation	466.2159	3	3.8	237	249	No
				HVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAK	K	S	95.00%	41	M10: Oxidation	726.5963	5	3.7	29	65	No
				HVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAK	K	S	95.00%	31		903.9998	4	9.3	29	65	No
				LLVPYLMEAIR	R	L	95.00%	66	M7: Oxidation	667.3874	2	8.7	222	232	No
				LLVPYLMEAIR	R	L	95.00%	58		659.3886	2	6.7	222	232	No
				LVEVIK	K	T	95.00%	26		700.4675	1	9.2	180	185	No
				TFESLVDFSK	K	A	95.00%	71		586.8013	2	9.3	193	202	No
406	IPI00294911		SDHB	SUCCINATE DEHYDROGENASE [UBIQUINONE] IRON-SULFUR SUBUNIT,MITOCHONDRIAL PRECURSOR.	AGDKPHMQTYEVDLNK	K	C	95.00%	51	M7: Oxidation	931.4472	2	5.9	52	67	No
					AGDKPHMQTYEVDLNK	K	C	95.00%	48	M7: Oxidation	621.3000	3	4.8	52	67	No
					DLVPDLSNFYAQYK	K	S	95.00%	34		836.9206	2	6.6	138	151	No
					IKNEVDSTLTFR	K	R	95.00%	57		711.8874	2	5.4	79	90	No
					IKNEVDSTLTFR	K	R	95.00%	37		474.9269	3	4.0	79	90	No
					LQDPFSLYR	K	C	95.00%	47		569.8031	2	7.5	234	242	No
					NEVDSTLTFR	K	R	95.00%	35		591.2964	2	3.9	81	90	No
					QQYLQSIEER	K	E	95.00%	44		647.3279	2	3.1	168	177	No
					SIEPYLK	K	K	95.00%	27		425.2418	2	4.1	152	158	No
					YLGPAVLMQAYR	K	W	95.00%	62	M8: Oxidation	699.3728	2	9.0	206	217	No
407	IPI00294959		LDB3	ISOFORM 2 OF LIM DOMAIN-BINDING PROTEIN 3.	AAQSQLSQGDLVVAIDGVNTDTMTHLEAQNK	K	I	95.00%	135	M23: Oxidation	1090.8760	3	6.4	38	68	No
					AAQSQLSQGDLVVAIDGVNTDTMTHLEAQNK	K	I	95.00%	63	M23: Oxidation	818.4085	4	6.0	38	68	No
					DFNMPLTISR	K	I	95.00%	53	M4: Oxidation	605.3036	2	4.5	22	31	No
					DFNMPLTISR	K	I	95.00%	31		597.3060	2	4.4	22	31	No
					DLAVDSASPVYQAVIK	K	S	95.00%	54	Y11: Phospho	878.4399	2	8.5	189	204	No
					DLAVDSASPVYQAVIK	K	S	95.00%	114		838.4539	2	5.5	189	204	No
					DLAVDSASPVYQAVIK	K	S	95.00%	66		559.3046	3	4.4	189	204	No
					DSALSTHKPIEVK	K	G	95.00%	55		712.8923	2	1.3	129	141	No
					DSALSTHKPIEVK	K	G	95.00%	42		475.5997	3	5.9	129	141	No
					DYINLFSTK	K	C	95.00%	48		1100.5710	1	7.3	550	558	No
					DYINLFSTK	K	C	95.00%	52		550.7886	2	6.0	550	558	No
					FNPSALKDSALSTHKPIEVK	R	G	95.00%	35		728.0710	3	4.5	122	141	No
					GGPAYTPAGPQVPPLAR	R	G	95.00%	93		824.9488	2	5.1	407	423	No
					GPFLVAMGR	R	S	95.00%	60	M7: Oxidation	482.2604	2	4.6	450	458	No
					GPFLVAMGR	R	S	95.00%	51		474.2622	2	3.0	450	458	No
					ILAQMTGTEFMQDPDEEALR	R	R	95.00%	72	M5: Oxidation, M11: Oxidation	1164.0410	2	9.0	230	249	No
					ILAQMTGTEFMQDPDEEALR	R	R	95.00%	50	M5: Oxidation, M11: Oxidation	776.3610	3	5.9	230	249	No
					ILAQMTGTEFMQDPDEEALRR	R	S	95.00%	42	M11: Oxidation	823.0633	3	5.8	230	250	No
					ILAQMTGTEFMQDPDEEALRR	R	S	95.00%	57	M5: Oxidation, M11: Oxidation	828.3950	3	5.9	230	250	No
					IMGEVMHALR	K	Q	95.00%	54	M2: Oxidation, M6: Oxidation	594.7989	2	2.5	507	516	No
					IMGEVMHALR	K	Q	95.00%	48		578.8055	2	5.2	507	516	No
					LQGGKDFNMPLTISR	R	I	95.00%	68	M9: Oxidation	846.9435	2	2.7	17	31	No
					LQGGKDFNMPLTISR	R	I	95.00%	46	M9: Oxidation	564.9650	3	2.7	17	31	No
					RPIPISTTAPPVQTPLPVIPHQK	K	V	95.00%	73		829.8263	3	7.2	85	107	No
					RPIPISTTAPPVQTPLPVIPHQK	K	V	95.00%	27		622.6229	4	9.1	85	107	No
					SASYNLSLTLQK	K	S	95.00%	86		662.8620	2	3.7	71	82	No
					SKRPIPISTTAPPVQTPLPVIPHQK	K	V	95.00%	53		901.5352	3	6.5	83	107	No
					SKRPIPISTTAPPVQTPLPVIPHQK	K	V	95.00%	64		676.4044	4	8.0	83	107	No
					SKRPIPISTTAPPVQTPLPVIPHQK	K	V	95.00%	30		541.3224	5	3.0	83	107	No
					SQNKPEDEADEWAR	K	R	95.00%	77		837.8750	2	3.6	205	218	No
					SQNKPEDEADEWAR	K	R	95.00%	47		558.9188	3	2.7	205	218	No
					SRPQASSYSPAVAASSAPATHTSYSEGPAAPAPK	R	P	95.00%	94		1100.5450	3	8.6	251	284	No
					SRPQASSYSPAVAASSAPATHTSYSEGPAAPAPK	R	P	95.00%	86		825.6575	4	4.1	251	284	No
					SRPQASSYSPAVAASSAPATHTSYSEGPAAPAPKPR	R	V	95.00%	94		888.9462	4	4.2	251	286	No

				SRPQASSYSPAVAASSAPATHTSYSEGPAAPAPKPR	R	V	95.00%	70		711.3574	5	2.5	251	286	No
				VVVNSPANADYQER	K	F	95.00%	89		781.3884	2	5.1	108	121	No
				VVVNSPANADYQER	K	F	95.00%	67		521.2606	3	3.4	108	121	No
408	IPI00295386	CBR1	CARBONYL REDUCTASE [NADPH] 1.	FHQLDIDDLQSIR	R	A	95.00%	44		533.9455	3	4.7	59	71	No
				GQAAVQQLQAEGLSPR	R	F	95.00%	84		826.9468	2	8.3	43	58	No
				GQAAVQQLQAEGLSPR	R	F	95.00%	32		551.6335	3	7.7	43	58	No
				LFSGDVVLTAR	R	D	95.00%	52		589.3373	2	7.4	28	38	No
				VVNVSSIMSVR	R	A	95.00%	57	M8: Oxidation	603.8333	2	6.1	135	145	No
409	IPI00295400; IPI00412737	WARS	TRYPTOPHANYL-TRNA SYNTHETASE, CYTOPLASMIC.; TRYPTOPHANYL-TRNA SYNTHETASE ISOFORM B.	ALIEVLQPLIAEHQAR	K	R	95.00%	50		601.0195	3	4.9	433	448	No
				DLTLDQAYSYAVENAK	K	D	95.00%	95		900.9443	2	8.4	205	220	No
				DMNQVLDAYENK	R	K	95.00%	47	M2: Oxidation	728.3307	2	7.5	101	112	No
				GIDYDKLIVR	K	F	95.00%	75		596.3441	2	5.3	97	106	No
				ISFPAIQAAPSFSNSFPQIFR	K	D	95.00%	41		1163.0960	2	-8.1	278	298	No
				MSASDPNSSIFLTDTAK	K	Q	95.00%	106	M1: Oxidation	900.9264	2	6.8	350	366	No
				PALLHSTFFPALQGAQTK	K	M	95.00%	48		643.0247	3	7.3	332	349	No
				TFIFSDLDYMGMSSGFYK	K	N	95.00%	37	M10: Oxidation, M12: Oxidation	1070.9730	2	6.2	232	249	No
410	IPI00295777; IPI00797300	GPD1	GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+], CYTOPLASMIC.; 35 KDA PROTEIN.	ANATGISLIK	K	G	95.00%	28		987.5910	1	7.2	111	120	No
				ANATGISLIK	K	G	95.00%	85		494.2974	2	3.2	88	97	No
				DPAQGQLLK	K	E	95.00%	50		485.2757	2	6.5	170	178	No
				ELMQTPNFR	K	I	95.00%	57	M3: Oxidation	576.2823	2	4.2	179	187	No
				ELYSILQHK	R	G	95.00%	43		565.8176	2	5.5	305	313	No
				FPLFMAVYK	K	V	95.00%	30	M5: Oxidation	566.3020	2	4.3	319	327	No
				GLVDKFPLFMAVYK	K	V	95.00%	44	M10: Oxidation	548.6370	3	4.8	291	304	No
				GLVDKFPLFMAVYK	K	V	95.00%	75		814.4573	2	8.8	291	304	No
				GLVDKFPLFMAVYK	K	V	95.00%	31		543.3067	3	7.3	314	327	No
				IVGGNAAQLAQFDPR	K	V	95.00%	88		778.9192	2	7.7	21	35	No
				IVGGNAAQLAQFDPR	K	V	95.00%	59		519.6137	3	4.4	21	35	No
				KLTEIINTQHENVK	K	Y	95.00%	105		833.9653	2	5.9	49	62	No
				KLTEIINTQHENVK	K	Y	95.00%	46		556.3141	3	8.3	49	62	No
				KVAEAFAR	R	T	95.00%	31		446.2588	2	5.2	272	279	No
				LGIPMSVLMGANIASEVADEK	R	F	95.00%	107	M5: Oxidation, M9: Oxidation	1089.0530	2	6.5	117	137	No
				LGIPMSVLMGANIASEVADEK	R	F	95.00%	82	M5: Oxidation, M9: Oxidation	726.3708	3	6.1	117	137	No
				LGLMEMIAFAK	R	L	95.00%	56	M4: Oxidation, M6: Oxidation	628.3281	2	4.1	230	240	No
				LGLMEMIAFAK	R	L	95.00%	73		612.3343	2	6.1	207	217	No
				LISEVIGER	K	L	95.00%	71		508.2945	2	2.2	131	139	No
				LTEIINTQHENVK	K	Y	95.00%	102		769.9187	2	7.5	50	62	No
				LTEIINTQHENVK	K	Y	95.00%	29		513.6132	3	3.9	50	62	No
				SIEQLEKELLNGQK	K	L	95.00%	33		543.6379	3	7.3	283	296	No
				VTMWVFEEDIGGK	R	K	95.00%	60	M3: Oxidation	763.8677	2	4.7	36	48	No
				VTMWVFEEDIGGKK	R	L	95.00%	71	M3: Oxidation	827.9175	2	7.2	36	49	No
				VTMWVFEEDIGGKK	R	L	95.00%	51	M3: Oxidation	552.2812	3	7.6	36	49	No
411	IPI00296053; IPI00759715	FH	ISOFORM MITOCHONDRIAL OF FUMARATE HYDRATASE, MITOCHONDRIAL PRECURSOR.; ISOFORM CYTOPLASMIC OF FUMARATE HYDRATASE, MITOCHONDRIAL PRECURSOR.	AAAEVNQDYGLDPK	R	I	95.00%	93		745.8626	2	3.0	102	115	No
				AIEMLGGELGSK	R	I	95.00%	75	M4: Oxidation	610.8151	2	2.1	161	172	No
				AIEMLGGELGSK	R	I	95.00%	71		602.8193	2	4.8	161	172	No
				ETAIELGYLTAEQFDEWVKPK	K	D	95.00%	117		1234.1350	2	9.2	484	504	No
				ETAIELGYLTAEQFDEWVKPK	K	D	95.00%	38		823.0906	3	6.7	484	504	No
				IEYDTFGELK	R	V	95.00%	68		607.8038	2	4.3	52	61	No
				IEYDTFGELKVPNDK	R	Y	95.00%	59		884.4515	2	8.2	52	66	No
				IEYDTFGELKVPNDKYYGAQTVR	R	S	95.00%	47		902.7932	3	8.3	52	74	No
				IYELAAGGTAVGTGLNTR	R	I	95.00%	124		882.4745	2	6.7	269	286	No
				IYELAAGGTAVGTGLNTR	R	I	95.00%	75		588.6513	3	5.1	269	286	No
				LMNESLMLVTALNPHIGYDK	K	A	95.00%	82	M2: Oxidation, M7: Oxidation	1146.0840	2	8.2	448	467	No
				LMNESLMLVTALNPHIGYDK	K	A	95.00%	70	M2: Oxidation, M7: Oxidation	764.3906	3	6.3	448	467	No
				LNDHFPLVVWQTGSGTQTNMNVNEVISNR	K	A	95.00%	72	M20: Oxidation	1096.2090	3	5.7	132	160	No
				MPTPVIK	R	A	95.00%	30	M1: Oxidation	401.2324	2	3.0	88	94	No

				SGLGELILPENEPGSSIMPGK	R	V	95.00%	79	M18: Oxidation	1071.0520	2	7.5	351	371	No
				SGLGELILPENEPGSSIMPGK	R	V	95.00%	43	M18: Oxidation	714.3710	3	8.0	351	371	No
				SKEFAQIIK	K	I	95.00%	38		532.3138	2	4.2	222	230	No
				THTQDAVPLTLGQEFSGYVQQVK	R	Y	95.00%	79		1273.6610	2	9.8	234	256	No
				THTQDAVPLTLGQEFSGYVQQVK	R	Y	95.00%	62		849.4390	3	4.9	234	256	No
				VAALTGLPFVTAPNK	K	F	95.00%	110		749.9402	2	6.1	297	311	No
				VPNDKYYGAQTVR	K	S	95.00%	37		755.8888	2	2.8	62	74	No
				VPNDKYYGAQTVR	K	S	95.00%	32		504.2620	3	3.3	62	74	No
				YYGAQTVR	K	S	95.00%	42		479.2469	2	6.9	67	74	No
412	IPI00296190; IPI00646289; IPI00646889	C10orf58	UNCHARACTERIZED PROTEIN C10ORF58 PRECURSOR.; 25 KDA PROTEIN.; 24 KDA PROTEIN.	AALEYLEDIDLK	K	T	95.00%	62		696.8729	2	8.3	44	55	No
				VNLLSVLEAAK	K	M	95.00%	82		578.8550	2	6.9	207	217	No
413	IPI00296635	GBE1	1,4-ALPHA-GLUCAN BRANCHING ENZYME.	FLLSNIR	R	W	95.00%	37		431.7624	2	2.3	337	343	No
				IVLDSDAAEYGGHQR	K	L	95.00%	117		815.8980	2	3.4	648	662	No
				IYESHVGISSHEGK	R	V	95.00%	43		514.9260	3	4.4	199	212	No
				LLEIDPYLKPYAVDFQR	R	R	95.00%	51		1040.5660	2	5.5	31	47	No
				LLEIDPYLKPYAVDFQR	R	R	95.00%	45		694.0467	3	6.0	31	47	No
				RQFHLTDDDLLR	R	Y	95.00%	32		510.2706	3	5.7	565	576	No
				VALILQNVDLPN	R	-	95.00%	53		654.8829	2	3.8	691	702	No
				YGWLAAPQAYVSEK	R	H	95.00%	44		791.9059	2	8.6	594	607	No
414	IPI00297779	CCT2	T-COMPLEX PROTEIN 1 SUBUNIT BETA.	AAHSEGNTTAGLDMR	R	E	95.00%	42	M14: Oxidation	516.2401	3	8.1	467	481	No
				DASLMVTNDGATILK	R	N	95.00%	49	M5: Oxidation	782.8999	2	1.6	58	72	No
				EALLSSAVDHGSDEVK	R	F	95.00%	61		828.9111	2	3.8	139	154	No
				GATQQILDEAER	R	S	95.00%	93		665.8374	2	5.0	377	388	No
				ILIANTGMDTDKIK	K	I	95.00%	36	M8: Oxidation	774.9236	2	5.4	237	250	No
				LALVTGGEIASTFDHPELVK	R	L	95.00%	39		699.7162	3	4.5	323	342	No
				LAVEAVLR	K	L	95.00%	58		435.7756	2	2.4	182	189	No
				LGGSLADSYLDEGFLLDKK	K	I	95.00%	56		681.0264	3	6.8	205	223	No
				LIEEVMIGEDK	K	L	95.00%	51	M6: Oxidation	646.3289	2	3.3	348	358	No
				LTSFIGAIAIGDLVK	R	S	95.00%	89		759.4557	2	5.9	26	40	No
				MLPTIIADNAGYDSADLVAQLR	R	A	95.00%	53	M1: Oxidation	788.4066	3	5.4	445	466	No
				VQDDEVGDGTTSVTVLAAELLR	R	E	95.00%	74		763.3974	3	6.2	90	111	No
415	IPI00298423	PDHX	PYRUVATE DEHYDROGENASE PROTEIN X COMPONENT, MITOCHONDRIAL PRECURSOR.	ANLENPIR	K	L	95.00%	61		463.7578	2	2.0	492	499	No
				GIQEIADSVK	K	A	95.00%	42		1059.5760	1	6.3	385	394	No
				GIQEIADSVK	K	A	95.00%	69		530.2906	2	4.3	385	394	No
				GLLTPIIK	K	D	95.00%	28		854.5787	1	8.2	372	379	No
				GLLTPIIK	K	D	95.00%	34		427.7912	2	3.4	372	379	No
				HSLDASQGTATGPR	K	G	95.00%	74		699.3492	2	9.4	195	208	No
				HSLDASQGTATGPR	K	G	95.00%	49		466.5651	3	1.6	195	208	No
				ILMPSLSPTMEEGNIVK	K	W	95.00%	55	M3: Oxidation, M10: Oxidation	945.9890	2	7.7	59	75	No
				ITESRPTPAPTATPTAPSPLQATAGPSYPR	K	P	95.00%	61		1011.8660	3	5.6	228	257	No
				LGSLIGLIVEEGEDWK	R	H	95.00%	103		879.4787	2	9.4	124	139	No
				LGSLIGLIVEEGEDWK	R	H	95.00%	53		586.6528	3	5.5	124	139	No
				PSEPRPSPEPQISIPVKK	K	E	95.00%	35		662.7089	3	4.3	156	173	No
				PSPEPQISIPVKK	R	E	95.00%	40		473.9490	3	7.1	161	173	No
				QLITVTMSSDSR	R	V	95.00%	55	M7: Oxidation	677.3430	2	7.2	465	476	No
				QMPDVNVSWDGEGPK	K	Q	95.00%	68	M2: Oxidation	837.8794	2	4.4	342	356	No
				VSVNDFIIK	K	A	95.00%	42		517.8004	2	4.0	326	334	No
				VVDDELATR	R	F	95.00%	61		509.2661	2	2.6	477	485	No
416	IPI00298547	PARK7	PROTEIN DJ-1.	ALVILAK	R	G	95.00%	25		727.5149	1	9.1	6	12	No
				DGLILTSR	K	G	95.00%	58		437.7576	2	8.5	149	156	No
				EGPYDVVVLPGGNLGAQNLSESAAVK	K	E	95.00%	72		862.1218	3	9.3	64	89	No
				GAEEMETVIPVDVMR	K	R	95.00%	66	M5: Oxidation, M14: Oxidation	854.4066	2	6.9	13	27	No
				GAEEMETVIPVDVMR	K	R	95.00%	55		838.4136	2	9.3	13	27	No
				GPGTSFEFALAIVEALNGK	R	E	95.00%	134		961.0168	2	9.7	157	175	No
				GPGTSFEFALAIVEALNGK	R	E	95.00%	50		641.0134	3	9.0	157	175	No
				VTTHPLAK	K	D	95.00%	32		433.7614	2	5.7	123	130	No
				VTVAGLAGK	K	D	95.00%	32		408.2570	2	8.5	33	41	No
417	IPI00298933	CASQ2	CALSEQUESTRIN-2 PRECURSOR.	AFEEAAEHFQPYIK	K	F	95.00%	62		840.4156	2	9.7	181	194	No
				AIGFVMVDAK	K	K	95.00%	48	M6: Oxidation	1066.5640	1	2.6	88	97	No
				AIGFVMVDAK	K	K	95.00%	71	M6: Oxidation	533.7858	2	2.9	88	97	No

				EIVLELVAQVLEHK	K	A	95.00%	104		810.4772	2	5.7	74	87	No
				EIVLELVAQVLEHK	K	A	95.00%	43		540.6534	3	4.5	74	87	No
				FFATFDK	K	G	95.00%	30		875.4331	1	3.1	195	201	No
				FFATFDK	K	G	95.00%	35		438.2207	2	3.7	195	201	No
				KLGFDEEGSLYILK	K	G	95.00%	84		806.4407	2	6.2	105	118	No
				KLGFDEEGSLYILK	K	G	95.00%	58		537.9611	3	2.4	105	118	No
				KLGFDEEGSLYILKGDR	K	T	95.00%	57		647.3483	3	8.2	105	121	No
				LEVQAFER	K	I	95.00%	69		496.2674	2	5.8	153	160	No
				LGFDEEGSLYILK	K	G	95.00%	82		742.3929	2	6.3	106	118	No
				MNEVDFYEPFMDEPIAIPNKPYTEEELVEFVK	K	E	95.00%	56	M1: Oxidation, M11: Oxidation	1298.9490	3	7.3	211	242	No
				QVLKK	K	Y	95.00%	30		615.4246	1	8.2	44	48	No
				SDPDGYEFLEILK	K	Q	95.00%	81		763.3804	2	6.6	277	289	No
418	IPI00298961; IPI00784388	XPO1	EXPORTIN-1.; 123 KDA PROTEIN.	AIIASNIMYIVGQYPR	K	F	95.00%	43	M8: Oxidation	608.9981	3	5.8	538	553	No
				EFAGEDTSDLFLEER	K	E	95.00%	110		879.4038	2	7.2	1024	1038	No
				EPEVLSTMAIIVNK	R	L	95.00%	57	M8: Oxidation	780.4288	2	9.2	797	810	No
				ETLVYLTHLDYVDTER	R	I	95.00%	43		983.9978	2	5.8	459	474	No
				ETLVYLTHLDYVDTER	R	I	95.00%	34		656.3360	3	8.1	459	474	No
				MAKPEEVLVVENDQGEVVR	R	E	95.00%	48	M1: Oxidation	719.7064	3	8.0	424	442	No
				MAQEVLTHLK	R	E	95.00%	29	M1: Oxidation	593.3226	2	5.9	45	54	No
				SAFPHLQDAQVK	K	L	95.00%	49		670.8581	2	9.0	984	995	No
				YYGLQILENVIK	K	T	95.00%	78		726.9108	2	2.4	77	88	No
419	IPI00299000; IPI00794875; IPI00807557	PA2G4	PROLIFERATION-ASSOCIATED PROTEIN 2G4.; 41 KDA PROTEIN.; HYPOTHETICAL PROTEIN (FRAGMENT).	EGEFVAQFK	K	F	95.00%	39		527.7659	2	2.8	342	350	No
				FDAMPFTLR	R	A	95.00%	34	M4: Oxidation	557.2762	2	3.7	303	311	No
				FTVLLMPNGPMR	K	I	95.00%	42	M6: Oxidation, M11: Oxidation	704.3635	2	4.3	351	362	No
				HELLQPFNVLYEK	K	E	95.00%	50		543.9620	3	3.7	329	341	No
				ITSGPFEPDLYK	R	S	95.00%	70		683.8518	2	4.6	363	374	No
				SEMEVQDAELK	K	A	95.00%	58	M3: Oxidation	647.8002	2	6.8	345	355	No
				TAENATSGETLEENEAGD	K	-	95.00%	104		919.3884	2	6.1	377	394	No
				TIIQNPTDQQK	K	K	95.00%	55		643.3442	2	4.0	200	210	No
420	IPI00299033	KPNA3	IMPORTIN ALPHA-3 SUBUNIT.	DSQVVQVVLDGLK	K	N	95.00%	71		700.3982	2	6.3	424	436	No
				EAAWAISNLTISGR	K	K	95.00%	92		744.9005	2	8.1	387	400	Yes
				IEVLQQHENEDIYK	K	L	95.00%	69		879.4453	2	6.6	462	475	No
				KLLSSDRNPPIDDLIK	R	S	95.00%	27		608.6829	3	5.2	97	112	Yes
				LLSSDRNPPIDDLIK	K	S	95.00%	55		848.4745	2	7.6	98	112	Yes
				NPPIDDLIK	R	S	95.00%	39		512.7897	2	3.3	104	112	Yes
				NVPQEESLEDSDVDADFK	R	A	95.00%	100		1018.9570	2	6.1	50	67	No
				SGILPILVK	K	C	95.00%	49		470.3182	2	4.4	113	121	No
421	IPI00299155; IPI00789638; IPI00790038; IPI00790207; IPI00795606	PSMA4	PROTEASOME SUBUNIT ALPHA TYPE 4.; PSMA4 PROTEIN.; 25 KDA PROTEIN.; 27 KDA PROTEIN.; 26 KDA PROTEIN.	LLDEVFFSEK	K	I	95.00%	69		613.8234	2	6.6	31	40	No
				LSAEKVEIATLTR	K	E	95.00%	34		477.6139	3	2.7	182	194	No
				VEIATLTR	K	E	95.00%	46		451.7710	2	3.2	211	218	No
422	IPI00299456	FBP2	FRUCTOSE-1,6-BISPHOSPHATASE ISOZYME 2.	AGLAHLYGIAGSVNVTGDEVK	K	K	95.00%	73		691.0383	3	8.3	52	72	No
				FPEDGSAPYGAR	K	Y	95.00%	33		633.7954	2	5.8	233	244	No
				GTGELTQLLNSMLTAIK	K	A	95.00%	68	M12: Oxidation	903.4950	2	7.5	27	43	No
				GTGELTQLLNSMLTAIK	K	A	95.00%	41	M12: Oxidation	602.6655	3	6.8	27	43	No
				GTGELTQLLNSMLTAIK	K	A	95.00%	102		895.4980	2	8.0	27	43	No
				GTGELTQLLNSMLTAIK	K	A	95.00%	44		597.3341	3	7.2	27	43	No
				IYSLNEGYAK	K	Y	95.00%	41		1157.5940	1	8.2	209	218	No
				IYSLNEGYAK	K	Y	95.00%	64		579.2982	2	3.6	209	218	No
				KAGLAHLYGIAGSVNVTGDEVK	R	K	95.00%	71		733.7369	3	8.1	51	72	No
				KFPEDGSAPYGAR	K	Y	95.00%	76		697.8433	2	6.0	232	244	No
				KFPEDGSAPYGAR	K	Y	95.00%	35		465.5639	3	3.9	232	244	No
				KKFPEDGSAPYGAR	K	Y	95.00%	59		761.8931	2	8.4	231	244	No
				KKFPEDGSAPYGAR	K	Y	95.00%	36		508.2631	3	5.5	231	244	No
				SPFETDMLTLTR	R	Y	95.00%	90	M7: Oxidation	713.8551	2	9.3	5	16	No
				SPFETDMLTLTR	R	Y	95.00%	74		705.8574	2	9.0	5	16	No
				TLVYGGIFLYPANQK	R	S	95.00%	99		842.4657	2	7.3	256	270	No
				YFDAATTEYVQK	K	K	95.00%	68		718.3448	2	4.9	219	230	No
				YFDAATTEYVQKK	K	K	95.00%	94		782.3928	2	5.2	219	231	No
				YVGSMVADVHR	R	T	95.00%	66	M5: Oxidation	625.3064	2	4.0	245	255	No
				YVGSMVADVHR	R	T	95.00%	33	M5: Oxidation	417.2066	3	3.4	245	255	No

423	IPI00299608; IPI00456695	PSMD1	ISOFORM 1 OF 26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 1.; ISOFORM 2 OF 26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 1.	AAVESLGFILFR	R	T	95.00%	80		661.8824	2	7.3	617	628	No
				DTSEDIEELVEPVAAHGPK	K	I	95.00%	47		679.3360	3	4.7	916	934	No
				EALQLMATYLPK	K	D	95.00%	29	M6: Oxidation	697.3792	2	7.4	418	429	No
				FTATASLGVIHK	K	G	95.00%	50		622.8549	2	1.3	402	413	No
				FTATASLGVIHK	K	G	95.00%	40		415.5739	3	4.5	402	413	No
				GLAVGIALVMYGR	R	M	95.00%	39	M10: Oxidation	668.3822	2	8.0	547	559	No
				HGGSLGLGLAAMGTAR	R	Q	95.00%	44	M12: Oxidation	495.5957	3	4.7	475	490	No
				KKEPEPNFQLLDNPAR	K	V	95.00%	61		632.6743	3	4.8	868	883	No
				LLHVAVSDVNDDVRR	R	A	95.00%	42		569.9790	3	4.2	602	616	No
				LLHVAVSDVNDDVRR	R	A	95.00%	33		427.7361	4	3.9	602	616	No
				QDVYDLLK	R	T	95.00%	28		497.2690	2	4.4	491	498	No
				TILESNDVPGMLAYSLK	K	L	95.00%	70	M11: Oxidation	933.9862	2	6.3	166	182	No
				TVGTPIASVPGSTNTGTVPGSEKDSDSMETEEK	R	T	95.00%	38	M28: Oxidation	1108.8550	3	6.2	270	302	No
424	IPI00299977	PHPT1	14 KDA PHOSPHOHISTIDINE PHOSPHATASE.	IHVYGYSMAYGPAQHAISTEK	K	I	95.00%	37	M8: Oxidation	585.5382	4	7.0	88	108	No
				KIHVYGYSMAYGPAQHAISTEK	K	I	95.00%	44	M9: Oxidation	823.0818	3	8.7	87	108	No
				KIHVYGYSMAYGPAQHAISTEK	K	I	95.00%	30	M9: Oxidation	617.5622	4	6.9	87	108	No
				WAEYHADIYDK	K	V	95.00%	67		705.8271	2	9.4	49	59	No
425	IPI00300074	FARSB	PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN.	AAGASDVVLYK	K	I	95.00%	34		547.3008	2	3.9	54	64	No
				DLLFQALGR	R	T	95.00%	54		516.7983	2	4.1	9	17	No
				DRYDSFIELQEK	K	L	95.00%	43		771.8793	2	4.2	134	145	No
				LFEISDIVIK	K	D	95.00%	41		588.8518	2	6.4	474	483	No
				LGVLHPDVITK	K	F	95.00%	29		596.3601	2	1.6	561	571	No
				NPGFEIIHGLLDR	K	I	95.00%	48		740.9041	2	6.0	505	517	No
				TYTIANQFPLNK	K	L	95.00%	73		705.3787	2	4.6	384	395	No
426	IPI00300285; IPI00783874	HDHD2	29 KDA PROTEIN.; HALOACID DEHALOGENASE-LIKE HYDROLASE DOMAIN CONTAINING 2.	LLLDGAPLIAIHK	R	A	95.00%	41		458.6260	3	7.2	140	152	No
				TFFLEALR	K	G	95.00%	60		498.7814	2	3.1	183	190	No
427	IPI00300567; IPI00398758	DCI	ISOFORM 1 OF 3,2-TRANS-ENOYL-COA ISOMERASE, MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF 3,2-TRANS-ENOYL-COA ISOMERASE, MITOCHONDRIAL PRECURSOR.	AVQELWLR	K	L	95.00%	45		507.7939	2	6.3	127	134	No
				DADVQNFVSFISK	R	D	95.00%	91		735.3746	2	9.4	271	283	No
				DTLENTIGHR	K	A	95.00%	32		578.2956	2	6.3	174	183	No
				SLQMYLER	K	L	95.00%	45	M4: Oxidation	528.2662	2	4.7	272	279	No
				VLVEPDAGAGVAVMK	R	F	95.00%	72	M14: Oxidation	736.4020	2	9.0	47	61	No
				VLVEPDAGAGVAVMK	R	F	95.00%	64	M14: Oxidation	491.2692	3	6.1	47	61	No
				VLVEPDAGAGVAVMK	R	F	95.00%	69		728.4028	2	6.6	47	61	No
428	IPI00301028	TRIM72	ISOFORM 1 OF TRIPARTITE MOTIF-CONTAINING PROTEIN 72.	ALMPALEELTFDPSSAHPSLVVSSSGR	R	R	95.00%	68	M3: Oxidation	938.8137	3	9.6	283	309	No
				AVAVVAHQQLSEGEHYWEVDVGDKPR	K	W	95.00%	53		973.8220	3	3.9	331	356	No
				AVAVVAHQQLSEGEHYWEVDVGDKPR	K	W	95.00%	44		730.6215	4	8.0	331	356	No
				EKSVAVLEHQLVEVEETVR	K	Q	95.00%	54		732.0659	3	4.7	148	166	No
				ELGSLNSYLEQLR	R	Q	95.00%	89		761.4055	2	7.7	208	220	No
				ILAESPPPAR	K	L	95.00%	34		1050.6020	1	6.6	251	260	No
				ILAESPPPAR	K	L	95.00%	58		525.8033	2	3.7	251	260	No
				ILEAHVEAK	K	E	95.00%	44		505.2907	2	5.2	390	398	No
				LDIQLPIISDDFK	R	F	95.00%	95		758.9217	2	5.9	261	273	No
				LDIQLPIISDDFK	R	F	95.00%	49		506.2824	3	3.2	261	273	No
				LHAVPSQGLWLLGLR	R	E	95.00%	72		830.4965	2	9.1	372	386	No
				LHAVPSQGLWLLGLR	R	E	95.00%	50		553.9985	3	5.8	372	386	No
				LLPAAEAHAR	R	L	95.00%	46		524.8027	2	6.8	119	128	No
				RELGSLNSYLEQLR	R	Q	95.00%	53		559.9720	3	4.7	207	220	No
				SVAVLEHQLVEVEETVR	K	Q	95.00%	128		969.0275	2	6.6	150	166	No
				SVAVLEHQLVEVEETVR	K	Q	95.00%	46		646.3526	3	4.0	150	166	No
				VFLAALEGSLDR	R	E	95.00%	108		645.8606	2	5.8	181	192	No
				VFLAALEGSLDREAER	R	V	95.00%	46		888.4766	2	9.1	181	196	No
				VFLAALEGSLDREAER	R	V	95.00%	71		592.6530	3	8.0	181	196	No
				VLEEVADKPQTEFLMK	K	Y	95.00%	65	M15: Oxidation	946.9936	2	5.9	225	240	No
				VLEEVADKPQTEFLMK	K	Y	95.00%	52	M15: Oxidation	631.6653	3	6.4	225	240	No
				VRGEAGVALR	R	R	95.00%	32		514.3079	2	6.4	197	206	No

				WALGVIAAEAPR	R	R	95.00%	104		627.3567	2	3.9	357	368	No
				WALGVIAAEAPR	R	R	95.00%	66		418.5739	3	4.2	357	368	No
429	IPI00301419; IPI00798179	COPS7A	COP9 SIGNALOSOME COMPLEX SUBUNIT 7A.; 18 KDA PROTEIN.	ELAESDFASTFR	R	L	95.00%	62		686.8297	2	9.6	54	65	No
				LEVDYSIGR	R	D	95.00%	42		526.2791	2	7.4	152	160	No
430	IPI00301464; IPI00412663; IPI00783326	SGCA	ISOFORM SGCA-1 OF ALPHA-SARCOGLYCAN PRECURSOR.; ISOFORM SGCA-2 OF ALPHA-SARCOGLYCAN PRECURSOR.; 43 KDA PROTEIN.	GLQVIEVTAYNR	R	D	95.00%	83		681.8768	2	5.6	99	110	No
				SHDAEEVLPSTPASR	R	F	95.00%	86		798.3909	2	4.5	142	156	No
				VDSAQVPLILDQH	R	-	95.00%	79		717.8874	2	5.3	375	387	No
431	IPI00302592; IPI00333541; IPI00644576	FLNA	FILAMIN A, ALPHA.; FILAMIN-A.; FILAMIN A, ALPHA.	AFGPGLQGGSAGSPAR	K	F	95.00%	61		715.3703	2	9.6	1072	1087	No
				ANLPQSFQVDTSK	R	A	95.00%	68		717.8717	2	8.8	1465	1477	No
				AYGPGIEPTGNMVK	R	K	95.00%	40	M12: Oxidation	725.3611	2	6.7	286	299	No
				DAGEGLLAVQITDPEGKPK	K	K	95.00%	73		969.5171	2	3.8	1574	1592	No
				DLAEDAPWK	K	K	95.00%	35		522.7562	2	4.0	34	42	Yes
				EATTEFSVDAR	R	A	95.00%	30		613.2936	2	7.7	1273	1283	No
				GQHVPGSPFQFTVGPLGEGGAHK	K	V	95.00%	48		768.7294	3	8.7	2210	2232	No
				GQHVPGSPFQFTVGPLGEGGAHK	K	V	95.00%	53		576.7983	4	7.5	2210	2232	No
				IQQNTFTR	K	W	95.00%	44		504.2695	2	3.8	44	51	Yes
				LIALLEVLSQK	R	K	95.00%	103		613.8940	2	6.3	77	87	No
				LIALLEVLSQK	R	K	95.00%	43		409.5984	3	5.8	77	87	No
				LLGWIQNK	R	L	95.00%	61		486.2915	2	7.5	172	179	No
				SAGQGEVLVYVEDPAGHQEEAK	R	V	95.00%	40		771.7102	3	6.4	310	331	No
				SPFSVAVSPSLDLSK	K	I	95.00%	42		767.4178	2	7.5	959	973	No
				TGVAVNKPAEFTVDAK	K	H	95.00%	49		823.9491	2	9.0	685	700	No
				VANPSGNLTETYVQDR	R	G	95.00%	94		882.4380	2	6.6	1297	1312	No
				VTAQGPGLEPSGNIANK	K	T	95.00%	77		826.9383	2	4.9	384	400	No
				YGGQPVPNFPSK	K	L	95.00%	32		645.8309	2	4.4	1235	1246	No
432	IPI00302925; IPI00784090	CCT8	CHAPERONIN CONTAINING TCP1, SUBUNIT 8 (THETA) VARIANT.; T-COMPLEX PROTEIN 1 SUBUNIT THETA.	AIADTGANVVVTGGK	K	V	95.00%	101		686.8777	2	2.7	282	296	No
				DIDEVSSLLR	R	T	95.00%	59		573.8067	2	4.2	158	167	No
				DMLEAGILDTYLGK	K	Y	95.00%	90	M2: Oxidation	777.8941	2	4.8	493	506	No
				EDGAISTIVLR	K	G	95.00%	37		587.3307	2	4.7	370	380	No
				FAEAFEAIPR	K	A	95.00%	68		575.8021	2	5.8	441	450	No
				HFSGLEEAVYR	K	N	95.00%	40		654.3253	2	3.4	21	31	No
				LATNAAVTVLR	K	V	95.00%	74		564.8428	2	3.1	512	522	No
				LFVTNDAATILR	K	E	95.00%	105		667.3828	2	7.3	63	74	No
				NVGLDIEAEVPAVK	K	D	95.00%	69		727.4040	2	6.7	477	490	No
				YNIMLVR	K	L	95.00%	39	M4: Oxidation	462.7548	2	4.4	308	314	No
433	IPI00303258	LMCD1	LIM AND CYSTEINE-RICH DOMAINS PROTEIN 1.	DPTFDTITYEWAPPGVTQK	K	L	95.00%	64		1083.5330	2	8.8	110	128	No
				EKQPVTGTEGAFYR	K	R	95.00%	69		791.8990	2	2.2	140	153	No
				EKQPVTGTEGAFYR	K	R	95.00%	47		528.2689	3	2.7	140	153	No
				GAAPPDSPVVYSDR	K	A	95.00%	62		715.8524	2	3.7	248	261	No
				GLLENELK	R	L	95.00%	37		458.2633	2	3.7	173	180	No
				KMSLGQLQSAR	K	G	95.00%	59	M2: Oxidation	617.8372	2	7.1	14	24	No
				LGLQYMELIPK	K	E	95.00%	55	M6: Oxidation	660.8713	2	8.1	129	139	No
				MIMTNPIATGK	R	D	95.00%	52	M1: Oxidation, M3: Oxidation	604.8082	2	5.5	99	109	No
				MSLGQLQSAR	K	G	95.00%	58	M1: Oxidation	553.7858	2	0.8	15	24	No
				QLMHQLPIYDQDPSR	R	C	95.00%	61	M3: Oxidation	928.9609	2	9.3	156	170	No
				QLMHQLPIYDQDPSR	R	C	95.00%	52	M3: Oxidation	619.6406	3	5.0	156	170	No
				QPVTGTEGAFYR	K	R	95.00%	45		663.3303	2	2.9	142	153	No
				SEALGVGEVALPGQGGLPK	K	E	95.00%	108		889.9945	2	8.7	191	209	No
				SEALGVGEVALPGQGGLPK	K	E	95.00%	29		593.6618	3	2.3	191	209	No
				SEALGVGEVALPGQGGLPKEEGK	K	Q	95.00%	79		741.4011	3	9.2	191	213	No
434	IPI00303476	ATP5B	ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL PRECURSOR.	ADKLAEEHSS	K	-	95.00%	32		543.7590	2	3.1	520	529	No
				AHGGYSVFAGVGER	K	T	95.00%	114		703.8459	2	1.7	226	239	No
				AHGGYSVFAGVGER	K	T	95.00%	55		469.5676	3	4.0	226	239	No
				AIAELGIYPAVDPLDSTSR	R	I	95.00%	114		994.5288	2	7.8	388	406	No
				AIAELGIYPAVDPLDSTSR	R	I	95.00%	71		663.3547	3	7.1	388	406	No
				DQEGQDVLLFIDNIFR	R	F	95.00%	133		961.4921	2	5.3	295	310	No

DQEGQDVLLFIDNIFR	R	F	95.00%	87		641.3314	3	6.5	295	310	No
EGNDLYHEMIESGVINLK	R	D	95.00%	84	M9: Oxidation	1039.0070	2	7.5	242	259	No
EGNDLYHEMIESGVINLK	R	D	95.00%	73	M9: Oxidation	693.0071	3	6.9	242	259	No
EGNDLYHEMIESGVINLK	R	D	95.00%	56		1031.0080	2	5.3	242	259	No
EGNDLYHEMIESGVINLK	R	D	95.00%	44		687.6755	3	7.1	242	259	No
FLSQPFQVAEVFTGHMGK	R	L	95.00%	93	M16: Oxidation	1020.0150	2	7.8	463	480	No
FLSQPFQVAEVFTGHMGK	R	L	95.00%	63	M16: Oxidation	680.3444	3	5.6	463	480	No
FLSQPFQVAEVFTGHMGK	R	L	95.00%	57		675.0131	3	6.1	463	480	No
FTQAGSEVSALLGR	R	I	95.00%	105		718.3864	2	7.3	311	324	No
FTQAGSEVSALLGR	R	I	95.00%	65		479.2591	3	5.0	311	324	No
GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	K	A	95.00%	46	M20: Oxidation	1122.8950	3	9.9	490	519	No
GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	K	A	95.00%	59	M20: Oxidation	842.4225	4	9.2	490	519	No
GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	K	A	95.00%	34		838.4243	4	9.9	490	519	No
GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	K	A	95.00%	90		1238.9800	3	10.0	352	387	No
GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	K	A	95.00%	35		929.4862	4	9.4	352	387	No
IGLFGGAGVGK	K	T	95.00%	39		975.5690	1	6.3	202	212	No
IGLFGGAGVGK	K	T	95.00%	61		488.2884	2	6.2	202	212	No
IMDPNIVGSEHYDVAR	R	G	95.00%	116	M2: Oxidation	916.4394	2	3.4	407	422	No
IMDPNIVGSEHYDVAR	R	G	95.00%	72	M2: Oxidation	611.2952	3	2.9	407	422	No
IMNVIGEPIDER	R	G	95.00%	91	M2: Oxidation	701.3586	2	3.2	144	155	No
IMNVIGEPIDER	R	G	95.00%	67		693.3625	2	5.1	144	155	No
IMNVIGEPIDERGPIK	R	T	95.00%	72	M2: Oxidation	898.9905	2	8.3	144	159	No
IMNVIGEPIDERGPIK	R	T	95.00%	40	M2: Oxidation	599.6602	3	3.7	144	159	No
IPSAVGYQPTLATDMGTMQER	R	I	95.00%	87	M15: Oxidation	1141.5530	2	7.6	325	345	No
IPSAVGYQPTLATDMGTMQER	R	I	95.00%	89	M15: Oxidation	1149.5520	2	9.6	325	345	No
IPSAVGYQPTLATDMGTMQER	R	I	95.00%	87	M15: Oxidation	766.7002	3	4.4	325	345	No
IPSAVGYQPTLATDMGTMQER	R	I	95.00%	89	M15: Oxidation, M18: Oxidation	1149.5520	2	9.6	325	345	No
IPSAVGYQPTLATDMGTMQER	R	I	95.00%	91	M15: Oxidation, M18: Oxidation	766.7007	3	5.0	325	345	No
IPSAVGYQPTLATDMGTMQER	R	I	95.00%	91	M18: Oxidation	1141.5530	2	7.8	325	345	No
IPSAVGYQPTLATDMGTMQER	R	I	95.00%	65	M18: Oxidation	761.3701	3	6.4	325	345	No
IPVGPETLGR	K	I	95.00%	55		1038.6010	1	6.1	134	143	No
IPVGPETLGR	K	I	95.00%	70		519.8018	2	0.8	134	143	No
KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	K	A	95.00%	137		1281.6580	3	-5.8	351	387	No
KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	K	A	95.00%	58		961.5087	4	7.9	351	387	No
LVLEVAQHLGESTVR	R	T	95.00%	130		825.9633	2	0.4	95	109	No
LVLEVAQHLGESTVR	R	T	95.00%	71		550.9806	3	5.0	95	109	No
LVPLKETIK	K	G	95.00%	26		1040.6760	1	3.5	481	489	No
LVPLKETIK	K	G	95.00%	50		520.8408	2	1.5	481	489	No
QFAPIHAEAPEFMEMSVEQEILVTGIK	K	V	95.00%	37	M13: Oxidation	1020.8370	3	-3.6	162	188	No
QFAPIHAEAPEFMEMSVEQEILVTGIK	K	V	95.00%	74	M13: Oxidation	1026.1810	3	8.4	162	188	No
QFAPIHAEAPEFMEMSVEQEILVTGIK	K	V	95.00%	56	M13: Oxidation	769.8849	4	5.0	162	188	No
QFAPIHAEAPEFMEMSVEQEILVTGIK	K	V	95.00%	74	M13: Oxidation, M15: Oxidation	1026.1810	3	8.4	162	188	No
QFAPIHAEAPEFMEMSVEQEILVTGIK	K	V	95.00%	56	M13: Oxidation, M15: Oxidation	769.8849	4	5.0	162	188	No
QFAPIHAEAPEFMEMSVEQEILVTGIK	K	V	95.00%	45	M15: Oxidation	1020.8370	3	-3.3	162	188	No
SLQDIIAILGMDELSEEDK	K	L	95.00%	131	M11: Oxidation	1068.0350	2	8.7	433	451	No
SLQDIIAILGMDELSEEDK	K	L	95.00%	42	M11: Oxidation	712.3574	3	6.2	433	451	No
SLQDIIAILGMDELSEEDKLTVSR	K	A	95.00%	101	M11: Oxidation	897.8032	3	6.6	433	456	No
SLQDIIAILGMDELSEEDKLTVSR	K	A	95.00%	85	M11: Oxidation	673.6050	4	7.5	433	456	No
SLQDIIAILGMDELSEEDKLTVSR	K	A	95.00%	85		892.4738	3	9.1	433	456	No
SLQDIIAILGMDELSEEDKLTVSR	K	A	95.00%	58		669.6068	4	8.4	433	456	No
TIAMDGTEGLVR	R	G	95.00%	85	M4: Oxidation	639.8239	2	2.8	110	121	No

				TIAMDGTEGLVR	R	G	95.00%	76		631.8275	2	4.4	110	121	No
				TREGNDLYHEMIESGVINLK	R	D	95.00%	59	M11: Oxidation	1167.5810	2	6.5	240	259	No
				TREGNDLYHEMIESGVINLK	R	D	95.00%	53	M11: Oxidation	778.7233	3	6.2	240	259	No
				TREGNDLYHEMIESGVINLK	R	D	95.00%	47	M11: Oxidation	584.2928	4	3.5	240	259	No
				TREGNDLYHEMIESGVINLK	R	D	95.00%	79		773.3917	3	6.2	240	259	No
				TREGNDLYHEMIESGVINLK	R	D	95.00%	46		580.2962	4	7.1	240	259	No
				TVLIMELINNVAK	K	A	95.00%	99	M5: Oxidation	737.4262	2	6.5	213	225	No
				TVLIMELINNVAK	K	A	95.00%	71	M5: Oxidation	491.9544	3	8.4	213	225	No
				TVLIMELINNVAK	K	A	95.00%	95		729.4305	2	9.0	213	225	No
				VALTGLTVAEYFR	R	D	95.00%	122		720.4020	2	4.4	282	294	No
				VALTGLTVAEYFR	R	D	95.00%	83		480.6042	3	4.8	282	294	No
				VALVYGQMNEPPGAR	K	A	95.00%	127	M8: Oxidation	809.4089	2	2.4	265	279	No
				VALVYGQMNEPPGAR	K	A	95.00%	50	M8: Oxidation	539.9427	3	4.1	265	279	No
				VALVYGQMNEPPGAR	K	A	95.00%	110		801.4127	2	4.0	265	279	No
				VLDSGAPIK	K	I	95.00%	45		899.5261	1	6.4	125	133	No
				VLDSGAPIK	K	I	95.00%	79		450.2650	2	2.2	125	133	No
				VLDSGAPIKIPVGPETLGR	K	I	95.00%	109		960.0607	2	8.6	125	143	No
				VLDSGAPIKIPVGPETLGR	K	I	95.00%	88		640.3743	3	5.3	125	143	No
				VVDLLAPYAK	K	G	95.00%	51		1088.6440	1	7.2	189	198	No
				VVDLLAPYAK	K	G	95.00%	55		544.8221	2	0.6	189	198	No
435	IPI00303568; IPI00395565; IPI00514138	PTGES2	PROSTAGLANDIN E SYNTHASE 2.; PROSTAGLANDIN E SYNTHASE 2 ISOFORM 2.; 29 KDA PROTEIN.	SAAQLSLSSR	R	L	95.00%	32		510.2808	2	5.4	90	99	No
				TPTEALASFDYIVR	R	E	95.00%	77		791.9162	2	8.1	62	75	No
				YMGAAAMYLISK	K	R	95.00%	36	M2: Oxidation, M7: Oxidation	675.8322	2	9.6	89	100	No
436	IPI00303882	M6PRBP1	ISOFORM B OF MANNOSE-6-PHOSPHATE RECEPTOR-BINDING PROTEIN 1.	DTVATQLSEAVDATR	K	G	95.00%	87		788.8993	2	5.6	141	155	No
				GLDKLEENLPILQQPTEK	R	V	95.00%	46		689.0483	3	5.1	99	116	No
				IATSLDGFDVASVQQQR	R	Q	95.00%	102		917.9764	2	8.2	214	230	No
				LEPQIASASEYAHR	K	G	95.00%	85		786.3978	2	3.9	85	98	No
				LGQMVLSGVDTVLGK	R	S	95.00%	84	M4: Oxidation	766.9262	2	5.7	181	195	No
				LGQMVLSGVDTVLGK	R	S	95.00%	35	M4: Oxidation	511.6189	3	3.3	181	195	No
				SEEWADNHLPLTDAELAR	K	I	95.00%	62		689.6696	3	7.1	196	213	No
				SVVTGGVQSVMGSR	K	L	95.00%	84	M11: Oxidation	690.3530	2	2.1	167	180	No
				TLTAAAVSGAQPILSK	R	L	95.00%	43		764.4485	2	9.4	69	84	No
				VSGAQEMVSSAK	K	D	95.00%	61	M7: Oxidation	605.2957	2	4.3	129	140	No
437	IPI00304925; IPI00807640	HSPA1A; HSPA1B	HEAT SHOCK 70 KDA PROTEIN 1.; HEAT SHOCK 70KDA PROTEIN 1B.	AFYPEEISSMVLTK	K	M	95.00%	100	M10: Oxidation	815.9094	2	4.4	113	126	No
				AFYPEEISSMVLTK	K	M	95.00%	40	M10: Oxidation	544.2754	3	4.3	113	126	No
				AQIHDLVLVGGSTR	K	I	95.00%	92		733.4114	2	1.4	329	342	No
				AQIHDLVLVGGSTR	K	I	95.00%	40		489.2786	3	4.8	329	342	No
				ATAGDTHLGGEDFDNR	K	L	95.00%	93		838.3727	2	3.7	221	236	No
				ATAGDTHLGGEDFDNR	K	L	95.00%	64		559.2514	3	4.3	221	236	No
				DAGVIAGLNVLR	K	I	95.00%	102		599.3562	2	7.3	160	171	No
				FGDPVVQSDMK	K	H	95.00%	58	M10: Oxidation	619.7940	2	5.9	78	88	No
				HWPFQVINDGDKPK	K	V	95.00%	63		560.9581	3	5.0	89	102	No
				IINEPTAAAIAYGLDR	R	T	95.00%	140		844.4603	2	6.3	172	187	No
				IINEPTAAAIAYGLDR	R	T	95.00%	59		563.3094	3	6.1	172	187	No
				LDKAQIHDLVLVGGSTR	K	I	95.00%	108		911.5180	2	5.1	326	342	No
				LDKAQIHDLVLVGGSTR	K	I	95.00%	61		608.0134	3	3.0	326	342	No
				LLQDFFNGR	K	D	95.00%	42		1109.5820	1	6.4	349	357	No
				LLQDFFNGR	K	D	95.00%	55		555.2931	2	3.5	349	357	No
				LVNHFVEEFK	R	R	95.00%	50		631.3351	2	3.4	237	246	No
				LVNHFVEEFK	R	R	95.00%	43		421.2257	3	2.7	237	246	No
				LVNHFVEEFKR	R	K	95.00%	38		709.3867	2	4.6	237	247	No
				LVNHFVEEFKR	R	K	95.00%	48		473.2583	3	0.2	237	247	No
				MKEIAEAYLGYPVTNAVITVPAYFNDSQR	K	Q	95.00%	49	M1: Oxidation	1092.8900	3	8.6	127	155	No
				NALESYAFNMK	K	S	95.00%	76	M10: Oxidation	652.3064	2	4.4	540	550	No
				NQVALNPQNTVFDAK	K	R	95.00%	121		829.9344	2	6.5	57	71	No
				NQVALNPQNTVFDAKR	K	L	95.00%	52		907.9852	2	6.3	57	72	No
				QTQIFTTYSDNQPGVLIQVYEGER	K	A	95.00%	66		929.4631	3	3.7	424	447	No
				SINPDEAVAYGAAVQAAILMGDK	K	S	95.00%	131	M20: Oxidation	1160.5870	2	7.4	362	384	No
				SINPDEAVAYGAAVQAAILMGDK	K	S	95.00%	64	M20: Oxidation	774.0588	3	4.8	362	384	No
				TTPSYVAFTDTER	R	L	95.00%	100		744.3601	2	7.1	37	49	Yes
				VEIIANDQGNR	K	T	95.00%	52		1228.6370	1	7.0	26	36	Yes

				VEIIANDQGNR	K	T	95.00%	81		614.8218	2	5.9	26	36	Yes
438	IPI00305166	SDHA	SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT,MITOCHONDRIAL PRECURSOR.	GEGGILINSQGER	R	F	95.00%	84		665.3450	2	4.3	313	325	No
				HTLSYVDVGTGK	K	V	95.00%	41		638.8351	2	6.7	625	636	No
				IDEYDYSKPIQGQQK	R	K	95.00%	81		906.4459	2	1.1	601	615	No
				IDEYDYSKPIQGQQK	R	K	95.00%	59		604.6346	3	3.5	601	615	No
				KHTLSYVDVGTGK	R	V	95.00%	71		702.8809	2	3.6	624	636	No
				KHTLSYVDVGTGK	R	V	95.00%	48		468.9224	3	1.9	624	636	No
				KPFEEHWR	K	K	95.00%	37		564.7869	2	6.2	616	623	No
				LGANSLLDLVVFGR	R	A	95.00%	117		737.4294	2	5.5	452	465	No
				LGANSLLDLVVFGR	R	A	95.00%	56		491.9565	3	7.4	452	465	No
				NTVVATGGYGR	K	T	95.00%	74		547.7869	2	6.0	251	261	No
				SHTVAAQGGINAALGNMEEDNWR	R	W	95.00%	59	M17: Oxidation	819.7198	3	9.0	98	120	No
				SMQNHAAVFR	K	V	95.00%	56	M2: Oxidation	588.7852	2	3.5	518	527	No
				SMTLEIR	R	E	95.00%	32	M2: Oxidation	433.2276	2	2.2	346	352	No
				TGHSLLHTLYGR	R	S	95.00%	80		677.8676	2	3.1	196	207	No
				VPPIKPNAGEESVMNLDK	K	L	95.00%	74	M14: Oxidation	977.5049	2	3.2	481	498	No
				VPPIKPNAGEESVMNLDK	K	L	95.00%	47	M14: Oxidation	652.0066	3	4.4	481	498	No
				VRIDEYDYSKPIQGQQK	K	K	95.00%	78		1034.0370	2	7.3	599	615	No
				VRIDEYDYSKPIQGQQK	K	K	95.00%	48		689.6914	3	3.5	599	615	No
				VSDSISAQYPVVDHEFDAVVVGAGGAGLR	K	A	95.00%	38		972.4968	3	7.2	47	75	No
				VTLEYRPVIDK	K	T	95.00%	72		666.8820	2	2.5	637	647	No
439	IPI00305383	UQCRC2	UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN 2, MITOCHONDRIALPRECURSOR.	ATAAPAGAPPQPQDLEFTK	K	L	95.00%	98		955.4943	2	7.6	24	42	No
				ATAAPAGAPPQPQDLEFTK	K	L	95.00%	44		637.3300	3	4.3	24	42	No
				AVAFQNPQTHVIENLHAAAYR	K	N	95.00%	87		784.0795	3	7.5	163	183	No
				GDVDILMEFLLNVTTAPEFR	R	R	95.00%	69	M7: Oxidation	766.0632	3	8.9	128	147	No
				LPNGLVIASLENYSPVSR	K	I	95.00%	125		965.0312	2	5.2	43	60	No
				LPNGLVIASLENYSPVSR	K	I	95.00%	64		643.6911	3	6.8	43	60	No
				MALIGLGVSHPVLK	R	Q	95.00%	99	M1: Oxidation	725.9299	2	4.2	218	231	No
				MALIGLGVSHPVLK	R	Q	95.00%	60	M1: Oxidation	484.2892	3	4.3	218	231	No
				MALIGLGVSHPVLK	R	Q	95.00%	86		717.9340	2	6.5	218	231	No
				MALIGLGVSHPVLK	R	Q	95.00%	54		478.9575	3	4.3	218	231	No
				QVAEQFLNMR	K	G	95.00%	82	M9: Oxidation	626.3145	2	4.5	232	241	No
				RWEVADLQPQLK	R	I	95.00%	86		741.9111	2	4.9	148	159	No
				RWEVADLQPQLK	R	I	95.00%	66		494.9431	3	4.5	148	159	No
				SMAASGNLGHTPFVDEL	K	-	95.00%	82	M2: Oxidation	881.4176	2	8.8	437	453	No
				SMAASGNLGHTPFVDEL	K	-	95.00%	65		873.4186	2	7.1	437	453	No
				TIAQGNLSNTDVQAAK	K	N	95.00%	116		815.9266	2	3.1	360	375	No
				TIAQGNLSNTDVQAAK	K	N	95.00%	51		544.2890	3	6.8	360	375	No
				VTSEELHYFVQNHFTSAR	K	M	95.00%	86		1083.0320	2	6.5	200	217	No
				VTSEELHYFVQNHFTSAR	K	M	95.00%	58		722.3581	3	8.1	200	217	No
				WEVADLQPQLK	R	I	95.00%	48		663.8607	2	5.6	149	159	No
				YEDFSNLGTTHLLR	R	L	95.00%	93		833.4233	2	9.0	71	84	No
				YEDFSNLGTTHLLR	R	L	95.00%	63		555.9489	3	4.3	71	84	No
440	IPI00305978	AKR7A2	AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2.	ALQAAYGASAPSVTSAALR	K	W	95.00%	89		902.9885	2	7.4	279	297	No
				EHHFEAIALVEK	K	A	95.00%	44		474.9186	3	1.4	267	278	No
				FYAYNPLAGGLLTGK	R	Y	95.00%	84		792.9309	2	7.0	222	236	No
				VASVLGTMEMGR	R	R	95.00%	44	M8: Oxidation, M10: Oxidation	641.8155	2	7.4	38	49	No
441	IPI00306301	PDHA1	PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT, SOMATIC FORM,MITOCHONDRIAL PRECURSOR.	EIEDAAQFATADPEPPLEELGYHIYSSDPPFEVR	K	G	95.00%	53		1278.2790	3	9.4	345	378	No
				EILAELTGR	R	K	95.00%	44		1001.5730	1	9.4	133	141	No
				EILAELTGR	R	K	95.00%	60		501.2876	2	4.1	133	141	No
				GPILMELQTYR	K	Y	95.00%	60	M5: Oxidation	668.8545	2	5.6	278	288	No
				LEEGPPVTTVLTR	R	E	95.00%	93		706.3987	2	6.9	46	58	No
				MVNSNLASVEELK	R	E	95.00%	69	M1: Oxidation	725.3733	2	8.9	324	336	No
				MVNSNLASVEELKEIDVEVR	R	K	95.00%	124	M1: Oxidation	1145.5940	2	9.3	324	343	No
				MVNSNLASVEELKEIDVEVR	R	K	95.00%	73	M1: Oxidation	764.0647	3	8.1	324	343	No
				MVNSNLASVEELKEIDVEVRK	R	E	95.00%	50	M1: Oxidation	806.7636	3	8.4	324	344	No
				MVNSNLASVEELKEIDVEVRK	R	E	95.00%	45	M1: Oxidation	605.3215	4	3.2	324	344	No
				NFANDATFEIK	R	K	95.00%	38		635.3127	2	4.8	29	39	No
				RGDFIPGLR	K	V	95.00%	45		515.7947	2	1.4	245	253	No
				SDPIMLLK	K	D	95.00%	43	M5: Oxidation	466.7617	2	2.7	314	321	No

				SGKGPILMELQTYR	R	Y	95.00%	55	M8: Oxidation	536.9530	3	0.8	275	288	No
				SKSDPIMLLK	R	D	95.00%	45	M7: Oxidation	574.3256	2	3.0	312	321	No
				YGMGTSVER	R	A	95.00%	46	M3: Oxidation	508.2297	2	-0.3	227	235	No
				YHGHSMSDPGVSYR	R	T	95.00%	50	M6: Oxidation	536.9052	3	8.4	289	302	No
				YHGHSMSDPGVSYR	R	T	95.00%	46	S5: Phospho, M6: Oxidation	563.5586	3	4.4	289	302	No
				YHGHSMSDPGVSYR	R	T	95.00%	32	Y1: Phospho, M6: Oxidation	563.5594	3	5.9	289	302	No
				YHGHSMSDPGVSYR	R	T	95.00%	37		531.5708	3	3.3	289	302	No
442	IPI00306720; IPI00796142	COX7A1	CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-HEART, MITOCHONDRIAL PRECURSOR.; PROTEIN.	GGIVDNILYR	K	V	95.00%	60		560.3142	2	3.7	45	54	No
				LFQEDNDIPLYLK	K	G	95.00%	90		804.4280	2	9.9	32	44	No
443	IPI00307749; IPI00419604	NDUFS7	NADH DEHYDROGENASE [UBIQUINONE] IRON-SULFUR PROTEIN 7, MITOCHONDRIALPRECURSOR.; CDNA FLJ34850 FIS, CLONE NT2NE2011758, HIGHLY SIMILAR TO NADH-UBIQUINONE OXIDOREDUCTASE 20 KDA SUBUNIT.	LDDLVNWAR	K	R	95.00%	71		551.2930	2	8.0	74	82	No
				QSDVMIVAGTLTNK	R	M	95.00%	97	M5: Oxidation	746.8953	2	9.7	123	136	No
				VYDQMPEPR	K	Y	95.00%	42	M5: Oxidation	575.7694	2	9.2	144	152	No
444	IPI00307755	PRKAA2	5'-AMP-ACTIVATED PROTEIN KINASE CATALYTIC SUBUNIT ALPHA-2.	DLKPENVLLDAHMNAK	R	I	95.00%	40	M13: Oxidation	608.6518	3	3.7	139	154	No
				GGVFYIPEYLNR	R	S	95.00%	48		714.3757	2	8.0	228	239	No
				IADFGLSNMMSDGEFLR	K	T	95.00%	62	M9: Oxidation, M10: Oxidation	967.9431	2	7.9	155	171	No
				IGHYVLGDTLGVGTFGK	K	V	95.00%	118		867.4697	2	5.1	13	29	No
				IGHYVLGDTLGVGTFGK	K	V	95.00%	43		578.6494	3	5.6	13	29	No
				MSLQLYLVDNR	K	S	95.00%	80	M1: Oxidation	684.3603	2	9.8	453	463	No
				SIDDEVVEQR	K	S	95.00%	37		595.2856	2	-5.8	471	480	No
				SYLLDFK	R	S	95.00%	29		443.2410	2	2.1	464	470	No
445	IPI00328156; IPI00639878	MAOB	AMINE OXIDASE [FLAVIN-CONTAINING] B.; MONOAMINE OXIDASE B.	ENVLVETLNHEMYEAK	R	Y	95.00%	75	M12: Oxidation	967.9665	2	4.2	243	258	No
				FVGGSGQVSER	K	I	95.00%	68		561.7823	2	2.2	210	220	No
				IHFNPPLPMMR	K	N	95.00%	35	M9: Oxidation, M10: Oxidation	692.8504	2	4.2	272	282	No
				IMDLLGDR	R	V	95.00%	36	M2: Oxidation	474.7480	2	5.9	221	228	No
				KFVGGSGQVSER	R	I	95.00%	32		417.5558	3	2.0	209	220	No
				LERPVIYIDQTR	K	E	95.00%	51		751.9276	2	9.3	231	242	No
				LERPVIYIDQTR	K	E	95.00%	51		501.6180	3	3.3	231	242	No
				LIGLTTIFSATALGFLAHK	R	R	95.00%	118		987.5809	2	5.5	495	513	No
				LIGLTTIFSATALGFLAHK	R	R	95.00%	36		658.7243	3	7.1	495	513	No
				LIGLTTIFSATALGFLAHKR	R	G	95.00%	34		1065.6340	2	7.2	495	514	No
				LLHDSGLNVVVLEAR	K	D	95.00%	92		817.9705	2	6.2	22	36	No
				LLHDSGLNVVVLEAR	K	D	95.00%	49		545.6489	3	4.8	22	36	No
				PVIYIDQTR	R	E	95.00%	40		552.8073	2	1.2	234	242	No
				VKLERPVIYIDQTR	R	E	95.00%	35		865.5080	2	6.6	229	242	No
				VKLERPVIYIDQTR	R	E	95.00%	37		577.3392	3	3.0	229	242	No
				VLGSLEALEPVHYEEK	K	N	95.00%	72		906.9779	2	5.3	371	386	No
				VPLGSVIK	R	C	95.00%	23		812.5326	1	9.7	289	296	No
				VPLGSVIK	R	C	95.00%	35		406.7673	2	2.5	289	296	No
				YVDLGGSYVGPTQNR	K	I	95.00%	101		813.4055	2	6.6	53	67	No
				YVISAIPPTLGMK	K	I	95.00%	58	M12: Oxidation	703.3962	2	5.6	259	271	No
446	IPI00328318; IPI00514126	AGL	AMYLO-1,6-GLUCOSIDASE, 4-ALPHA-GLUCANOTRANSFERASE ISOFORM 1 VARIANT.; ISOFORM 1 OF GLYCOGEN DEBRANCHING ENZYME.	AVTVYTNYPFPGETFNR	K	E	95.00%	116		988.4905	2	9.0	44	60	No
				AVTVYTNYPFPGETFNR	K	E	95.00%	45		659.3285	3	7.4	44	60	No
				DENSINGTPDITVEIR	K	E	95.00%	109		886.9415	2	4.6	792	807	No
				DGSAVEIVGLSK	R	S	95.00%	62		1174.6400	1	7.0	1280	1291	No
				DGSAVEIVGLSK	R	S	95.00%	94		587.8210	2	1.8	1282	1293	No
				DTFIALR	R	G	95.00%	30		835.4741	1	7.3	1102	1108	No
				DTFIALR	R	G	95.00%	47		418.2388	2	2.2	1102	1108	No
				EAMSAYNSHEEGR	R	L	95.00%	31	M3: Oxidation	748.8109	2	4.4	580	592	No
				ESGYNMIHFTPLQTLGLSR	K	S	95.00%	54	M6: Oxidation	1090.5550	2	9.9	152	170	No
				ESGYNMIHFTPLQTLGLSR	K	S	95.00%	36	M6: Oxidation	727.3711	3	7.6	152	170	No
				ESGYNMIHFTPLQTLGLSR	K	S	95.00%	94		1082.5540	2	6.1	152	170	No
				FPSLPILSPALMDVPYR	K	L	95.00%	81	M12: Oxidation	966.5261	2	7.1	1053	1069	No
				FPSLPILSPALMDVPYR	K	L	95.00%	42	M12: Oxidation	644.6863	3	6.6	1053	1069	No
				FPSLPILSPALMDVPYR	K	L	95.00%	85		958.5308	2	9.4	1055	1071	No

GFIQVYVDQVDEDIVAVTR	K	H	95.00%	161		1083.5660	2	7.4	716	734	No
GFIQVYVDQVDEDIVAVTR	K	H	95.00%	80		722.7124	3	6.1	716	734	No
GILLITGR	R	Y	95.00%	32		842.5494	1	3.3	1109	1116	No
GILLITGR	R	Y	95.00%	57		421.7780	2	1.9	1109	1116	No
GIPALIENDHHMNSIR	K	K	95.00%	62	M12: Oxidation	916.9628	2	5.5	270	285	No
GPNEYIQEIEFENLSPGSVIIFR	K	V	95.00%	62		884.4590	3	9.9	827	849	No
GYDELVPHQISVVSEER	R	F	95.00%	92		978.9932	2	6.1	659	675	No
GYDELVPHQISVVSEER	R	F	95.00%	91		652.9982	3	6.2	660	676	No
HGLIPNLLGEGIYAR	R	Y	95.00%	75		811.9597	2	5.7	1133	1147	No
HGLIPNLLGEGIYAR	R	Y	95.00%	66		541.6407	3	2.6	1135	1149	No
HSPSIHQSVVAVSR	R	T	95.00%	100		752.4082	2	3.7	735	748	No
HSPSIHQSVVAVSR	R	T	95.00%	61		501.9410	3	2.8	737	750	No
IEEVVLEAR	K	T	95.00%	69		529.3026	2	7.4	774	782	No
IIWEDIFPK	K	L	95.00%	50		580.8257	2	6.7	287	295	No
ILLLNEMEK	R	L	95.00%	32	M7: Oxidation	559.8143	2	6.8	10	18	No
ILLLNEMEKLEK	R	T	95.00%	33	M7: Oxidation	744.9228	2	1.9	9	20	No
ILLLNEMEKLEK	R	T	95.00%	57		736.9261	2	3.0	9	20	No
IPFASLASR	K	L	95.00%	41		961.5505	1	3.6	890	898	No
IPFASLASR	K	L	95.00%	70		481.2791	2	3.4	890	898	No
KDENSINGTPDITVEIR	R	E	95.00%	132		950.9925	2	8.1	791	807	No
KDENSINGTPDITVEIR	R	E	95.00%	51		634.3284	3	4.0	791	807	No
KIIWEDIFPK	R	L	95.00%	68		644.8738	2	6.9	286	295	No
KIIWEDIFPK	R	L	95.00%	50		430.2508	3	4.5	286	295	No
KNIFPYHEVTVK	K	R	95.00%	30		492.2761	3	4.6	1305	1316	No
KYTEITATYFQGVR	K	L	95.00%	79		838.9401	2	4.5	511	524	No
KYTEITATYFQGVR	K	L	95.00%	45		559.6305	3	6.6	511	524	No
KYTWNDVGQLVEK	R	L	95.00%	105		790.4136	2	4.6	191	203	No
KYTWNDVGQLVEK	R	L	95.00%	45		527.2787	3	5.4	191	203	No
LEQGYELQFR	R	L	95.00%	68		641.8278	2	3.4	25	34	No
LFHVSEDPSDLNEK	K	H	95.00%	65		815.3980	2	7.4	1338	1351	No
LFHVSEDPSDLNEK	K	H	95.00%	31		543.9335	3	5.5	1340	1353	No
LFHVSEDPSDLNEKHPNLVHK	K	R	95.00%	32		819.0911	3	8.6	1340	1360	No
LGISSLIR	R	E	95.00%	68		429.7762	2	3.9	572	579	No
LGPTLQGK	R	A	95.00%	34		407.2470	2	3.2	36	43	No
LMGPETTAK	R	T	95.00%	44	M2: Oxidation	482.2478	2	5.7	1468	1476	No
LTLAELNQILYR	R	C	95.00%	80		723.9253	2	7.4	899	910	No
LTLAELNQILYR	R	C	95.00%	61		482.9526	3	6.9	901	912	No
LWEFFQVDVNK	K	A	95.00%	86		712.8708	2	8.7	298	308	No
MYPTDDSAPLPAGTLDQPLFEVIQEAMQK	R	H	95.00%	63	M1: Oxidation, M27: Oxidation	1079.8610	3	10.0	1182	1210	No
NFAEPGSEVYLR	R	R	95.00%	81		691.3443	2	4.0	471	482	No
NHLTQFSPHFK	R	S	95.00%	70		678.3500	2	4.5	865	875	No
NHLTQFSPHFK	R	S	95.00%	52		452.5691	3	4.1	865	875	No
NIFPYHEVTVK	K	R	95.00%	42		673.8632	2	5.6	1304	1314	No
NIILAFAGTLR	R	H	95.00%	103		594.8631	2	6.6	1122	1132	No
NMKDEGFNITAGVDEETGFVYGGNR	R	F	95.00%	78	M2: Oxidation	912.7546	3	9.9	1231	1255	No
QMSSFVQNGSTFVK	K	H	95.00%	45	M2: Oxidation	788.3793	2	1.9	1027	1040	No
QMSSFVQNGSTFVK	K	H	95.00%	65		780.3842	2	4.9	1025	1038	No
SDPNQHLTIIQDPEYR	K	R	95.00%	80		963.4762	2	4.5	327	342	No
SDPNQHLTIIQDPEYR	K	R	95.00%	52		642.6531	3	4.1	327	342	No
SGDWMIDYVSNR	R	L	95.00%	76	M5: Oxidation	729.8240	2	5.4	962	973	No
SGDWMIDYVSNR	R	L	95.00%	67		721.8262	2	4.9	962	973	No
SGGGYIVVDPILR	K	V	95.00%	87		673.3792	2	1.8	103	115	No
SGSLAVDNADPILK	K	I	95.00%	86		700.3780	2	3.3	876	889	No
SGSLAVDNADPILKIPFASLASR	K	L	95.00%	36		781.4365	3	9.4	878	900	No
SLDWENPTER	R	E	95.00%	45		623.7907	2	2.4	64	73	No
TIVLVK	K	N	95.00%	25		672.4686	1	3.7	1479	1484	No
VSLDPHAQVAVGILR	R	N	95.00%	85		787.9604	2	7.0	850	864	No
VSLDPHAQVAVGILR	R	N	95.00%	69		525.6409	3	3.1	850	864	No
VSYDEWNR	K	K	95.00%	57		534.7439	2	4.7	1324	1331	No
WLLELSK	R	K	95.00%	32		444.7652	2	3.4	1296	1302	No
WNPEALPSNTGEVNFQSGIIAAR	K	C	95.00%	64		1236.1270	2	5.5	680	702	No
WNPEALPSNTGEVNFQSGIIAAR	K	C	95.00%	55		824.4214	3	6.8	680	702	No
YAGLQGLMSVLAEIRPK	K	N	95.00%	67	M8: Oxidation	931.5231	2	9.3	933	949	No
YAGLQGLMSVLAEIRPK	K	N	95.00%	55	M8: Oxidation	621.3492	3	5.8	933	949	No
YAGLQGLMSVLAEIRPK	K	N	95.00%	89		923.5254	2	9.1	933	949	No

				YAGLQGLMSVLAEIRPK	K	N	95.00%	61		616.0158	3	3.0	933	949	No
				YTEITATYFQGVR	K	L	95.00%	56		774.8965	2	9.9	513	525	No
				YTWNDVGQLVEK	K	L	95.00%	81		726.3665	2	5.6	193	204	No
447	IPI00328328; IPI00409717	EIF4A2	ISOFORM 1 OF EUKARYOTIC INITIATION FACTOR 4A-II.; ISOFORM 2 OF EUKARYOTIC INITIATION FACTOR 4A-II.	DFTVSALHGDMDQK	R	E	95.00%	38	M11: Oxidation	790.3640	2	8.7	297	310	No
				ETQALVLAPTR	K	E	95.00%	39		599.8453	2	2.6	101	111	No
				GFKDQIYEIFQK	R	L	95.00%	67		758.4024	2	8.0	192	203	No
				GFKDQIYEIFQK	R	L	95.00%	40		505.9362	3	5.3	192	203	No
				GIYAYGFEKPSAIQQR	R	A	95.00%	86		914.4799	2	6.8	47	62	No
				GIYAYGFEKPSAIQQR	R	A	95.00%	60		609.9871	3	3.4	47	62	No
				GYDVIAQAQSGTGK	K	T	95.00%	104		697.8531	2	4.8	70	83	No
				KEELTLEGIK	K	Q	95.00%	40		580.3350	2	3.8	239	248	No
				KGVAINFVTEEDKR	R	I	95.00%	36		803.4403	2	7.8	370	383	No
				KGVAINFVTEEDKR	R	I	95.00%	59		535.9606	3	3.8	370	383	No
				LQAEAPHIVVGTPGR	K	V	95.00%	79		772.9384	2	8.9	148	162	No
				LQAEAPHIVVGTPGR	K	V	95.00%	43		515.6255	3	3.6	148	162	No
				MFVLDEADEMLSR	K	G	95.00%	89	M1: Oxidation, M10: Oxidation	794.3610	2	6.7	179	191	No
				VLITTDLLAR	R	G	95.00%	50		557.8507	2	8.8	326	335	No
448	IPI00328534; IPI00658052	SRL	ISOFORM 2 OF SARCALUMENIN PRECURSOR.; ISOFORM 1 OF SARCALUMENIN PRECURSOR.	ADLIFVVFDPTK	R	L	95.00%	78		682.8831	2	8.4	677	688	No
				ADNLATQMLMR	K	V	95.00%	57	M8: Oxidation, M10: Oxidation	648.3099	2	2.5	641	651	No
				AITQELPGLLGSLGLGK	R	N	95.00%	119		833.9955	2	5.1	818	834	No
				AITQELPGLLGSLGLGK	R	N	95.00%	77		556.3329	3	5.0	818	834	No
				DFFGINPISSFK	K	L	95.00%	48		686.3553	2	5.8	787	798	No
				DIVEDPDKFYIFK	K	T	95.00%	65		814.9201	2	6.8	829	841	No
				DKMTFFSDGELVFK	K	D	95.00%	43	M3: Oxidation	840.4080	2	5.3	815	828	No
				DKMTFFSDGELVFK	K	D	95.00%	45	M3: Oxidation	560.6079	3	5.3	815	828	No
				EAYKDFFGINPISSFK	R	L	95.00%	96		931.9778	2	7.9	783	798	No
				EAYKDFFGINPISSFK	R	L	95.00%	55		621.6522	3	4.3	783	798	No
				EPQEAREPQEGAELPEATGTTSHR	R	D	95.00%	69		874.0862	3	7.3	413	436	No
				EPQEGAELPEATGTTSHR	R	D	95.00%	32		637.3034	3	2.7	419	436	No
				ESPIIVAQEETEDANEEAPLRDR	R	S	95.00%	52		871.0947	3	7.5	472	494	No
				FGQNFLEK	K	L	95.00%	72		491.7558	2	4.0	624	631	No
				IHALLVDR	R	Y	95.00%	46		936.5722	1	9.6	801	808	No
				IHALLVDR	R	Y	95.00%	45		468.7859	2	0.8	726	733	No
				IYHSSIKPLEQSYK	K	Y	95.00%	62		846.9589	2	8.2	447	460	No
				IYHSSIKPLEQSYK	K	Y	95.00%	43		564.9733	3	4.8	522	535	No
				KIYHSSIKPLEQSYK	R	Y	95.00%	99		911.0022	2	3.0	446	460	No
				KIYHSSIKPLEQSYK	R	Y	95.00%	44		607.6709	3	3.3	521	535	No
				LDVGLELEMLFR	K	Q	95.00%	76	M9: Oxidation	725.8888	2	5.6	689	700	No
				LIGIEVPHK	K	L	95.00%	68		503.3106	2	3.5	557	565	No
				LLLHYPDGR	K	E	95.00%	28		542.3060	2	8.2	66	74	No
				MTFFSDGELVFK	K	D	95.00%	75	M1: Oxidation	718.8466	2	5.8	742	753	No
				STMINYLLGLENTR	K	Y	95.00%	87	M3: Oxidation	820.9267	2	8.4	566	579	No
				STMINYLLGLENTR	K	Y	95.00%	49	M3: Oxidation	547.6190	3	5.9	491	504	No
				STMINYLLGLENTR	K	Y	95.00%	55		812.9294	2	8.6	491	504	No
				TIEGIVMAADSAR	K	S	95.00%	98	M7: Oxidation	675.3431	2	3.6	604	616	No
				TIEGIVMAADSAR	K	S	95.00%	53	M7: Oxidation	450.5657	3	5.8	529	541	No
				TLMLNEDKPSDDYSAVLQR	K	L	95.00%	121	M3: Oxidation	1106.0420	2	7.2	425	443	No
				TLMLNEDKPSDDYSAVLQR	K	L	95.00%	69	M3: Oxidation	737.6957	3	5.0	425	443	No
				VTFVDTPGIIENR	R	K	95.00%	80		730.8961	2	6.4	570	582	No
				YQLYTGAEPTTSEFTVLMHGPK	R	L	95.00%	47	M18: Oxidation	829.4097	3	8.8	580	601	No
449	IPI00329200; IPI00783829; IPI00793443	RANBP5	127 KDA PROTEIN.; IMPORTIN BETA-3.; RAN BINDING PROTEIN 5.	ATAAFILANEHNVALFK	R	H	95.00%	39		610.6727	3	6.1	214	230	No
				EFQQYLPVVMGPLMK	K	T	95.00%	33	M10: Oxidation, M14: Oxidation	906.4655	2	8.5	636	650	No
				EGFVEYTEQVVK	K	L	95.00%	50		714.3618	2	6.9	712	723	No
				FLFDSVSSQNVGLR	K	E	95.00%	89		784.9125	2	6.5	153	166	No
				FMQDASDVMQLLLK	K	T	95.00%	85	M2: Oxidation, M9: Oxidation	835.9184	2	9.3	591	604	No
				FVPYYDLFMPSLK	K	H	95.00%	33	M9: Oxidation	818.4186	2	9.9	545	557	No
				ITFLLQAIR	K	N	95.00%	80		537.8409	2	5.8	60	68	No
				LVLEQVVTSIASVADTAEEK	K	F	95.00%	89		701.3831	3	5.0	525	544	No

				NLIDEDGNNQWPEGLK	R	F	95.00%	56		921.4415	2	4.2	137	152	No
				QAEETYENIPGQSK	K	I	95.00%	61		797.3793	2	6.8	46	59	No
				SELLMIIQMETQSSMR	K	K	95.00%	42	M5: Oxidation, M9: Oxidation, M15: Oxidation	648.9799	3	8.1	109	124	No
				SLLIPYLDNLVK	K	H	95.00%	41		694.4163	2	3.3	494	505	No
				SLVEIADTVPK	K	Y	95.00%	53		586.3342	2	2.6	257	267	No
				VSDILHSIFSSYK	K	E	95.00%	43		499.2669	3	3.7	868	880	No
450	IPI00329331	UGP2	ISOFORM 1 OF UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE 2.	AMSQDGASQFQEVIR	K	Q	95.00%	114	M2: Oxidation	841.8988	2	5.3	11	25	No
				EFPTVPLVK	R	L	95.00%	28		1029.6060	1	7.4	423	431	No
				ESLLPVAK	K	D	95.00%	32		428.7620	2	2.0	199	206	No
				GLPDNISSVLNK	R	L	95.00%	83		628.8452	2	-2.0	96	107	No
				GPSVDWGK	K	I	95.00%	43		423.2140	2	5.1	70	77	No
				GTVIIIANHGDR	K	I	95.00%	57		633.3575	2	8.3	474	485	No
				GTVIIIANHGDR	K	I	95.00%	47		422.5719	3	2.6	474	485	No
				GTVIIIANHGDRIDIPPGAVLENK	K	I	95.00%	64		838.1394	3	5.3	474	497	No
				IDIPPGAVLENK	R	I	95.00%	61		633.3625	2	5.1	486	497	No
				IFNTNNLWISLAAVK	K	R	95.00%	107		852.4859	2	9.1	326	340	No
				IFNTNNLWISLAAVK	K	R	95.00%	41		568.6567	3	3.4	326	340	No
				ILTTASSHEFEHTK	K	K	95.00%	78		800.9034	2	1.2	39	52	No
				ILTTASSHEFEHTKK	K	D	95.00%	67		864.9529	2	3.5	39	53	No
				ILTTASSHEFEHTKK	K	D	95.00%	42		576.9708	3	2.8	39	53	No
				INKESLLPVAK	R	D	95.00%	67		606.3744	2	3.8	196	206	No
				INKESLLPVAK	R	D	95.00%	31		404.5852	3	2.9	196	206	No
				IQRPPEDSIQPYEK	K	I	95.00%	73		850.4388	2	2.4	78	91	No
				IQRPPEDSIQPYEK	K	I	95.00%	63		567.2954	3	2.9	78	91	No
				IYTFNQSR	K	Y	95.00%	38		514.7635	2	2.6	185	192	No
				LQEQNAIDMEIIVNAK	R	T	95.00%	80	M9: Oxidation	922.9810	2	6.2	342	357	No
				LQEQNAIDMEIIVNAK	R	T	95.00%	53	M9: Oxidation	615.6563	3	5.6	342	357	No
				LVEIAQVPK	R	A	95.00%	39		996.6146	1	5.2	304	312	No
				LVEIAQVPK	R	A	95.00%	56		498.8101	2	2.9	304	312	No
				NENTFLDLTVQQIEHLNK	R	T	95.00%	123		1078.5630	2	8.5	134	151	No
				NENTFLDLTVQQIEHLNK	R	T	95.00%	48		719.3762	3	6.5	134	151	No
				RFESIPDMLELDHLTVSGDVTFGK	R	N	95.00%	92	M8: Oxidation	908.1250	3	7.2	445	468	No
				RLQEQNAIDMEIIVNAK	K	T	95.00%	41	M10: Oxidation	667.6891	3	3.8	341	357	No
				SFENSLGINVPR	K	S	95.00%	79		666.8523	2	4.1	378	389	No
				SFENSLGINVPR	K	S	95.00%	47		444.9037	3	3.1	378	389	No
				TLDGGLNVIQLETAVGAAIK	K	S	95.00%	133		992.0695	2	9.2	358	377	No
				TLDGGLNVIQLETAVGAAIK	K	S	95.00%	72		661.7142	3	7.1	358	377	No
				TTSDLLLVMSNLYSLNAGSLTMSEK	K	R	95.00%	63	M9: Oxidation, M22: Oxidation	907.4588	3	8.8	397	421	No
				TYNTDVPLVLMNSFNTDEDTKK	K	I	95.00%	48	M11: Oxidation	854.4149	3	8.2	152	173	No
451	IPI00329572; IPI00783170	PACSIN3	49 KDA PROTEIN.; PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE IN NEURONS PROTEIN 3.	ADSAVSQEQLR	K	K	95.00%	44		602.3041	2	2.9	176	186	No
				ALYDYAGQEADELSFR	R	A	95.00%	121		924.4346	2	8.7	371	386	No
				ALYDYAGQEADELSFR	R	A	95.00%	71		616.6241	3	6.2	371	386	No
				AQYEQTLAELHR	K	Y	95.00%	69		729.8729	2	2.5	204	215	No
				AQYEQTLAELHR	K	Y	95.00%	45		486.9181	3	3.1	204	215	No
				AYAQQLADWAR	K	K	95.00%	72		646.8269	2	5.6	52	62	No
				DLHQGIEAASDEEDLR	R	W	95.00%	100		899.4211	2	4.8	267	282	No
				DLHQGIEAASDEEDLR	R	W	95.00%	52		599.9496	3	4.2	267	282	No
				DMLLTLHQHLDLSSSEK	K	F	95.00%	38	M2: Oxidation	661.6708	3	5.5	244	260	No
				GAFHRPVLGGFR	R	E	95.00%	36		657.3679	2	3.6	116	127	No
				LSALHLEVR	R	E	95.00%	39		519.3112	2	3.5	91	99	No
				SPDEVTLTSIVPTR	R	D	95.00%	114		757.9119	2	6.0	319	332	No
452	IPI00329745; IPI00477140; IPI00783271	LRPPRC	CDNA FLJ43793 FIS, CLONE TESTI4000014, HIGHLY SIMILAR TO 130 KDALEUCINE-RICH PROTEIN.; HYPOTHETICAL PROTEIN LRPPRC.; LEUCINE-RICH PPR MOTIF-CONTAINING PROTEIN.	AGYPQYVSEILEK	K	V	95.00%	51		748.8910	2	6.9	315	327	No
				DAGIEPGPDTYLALLNAYAEK	R	G	95.00%	92		1111.0660	2	9.6	260	280	No
				DLPVTEAVFSALVTGHAR	K	A	95.00%	113		942.0124	2	7.5	227	244	No
				DLPVTEAVFSALVTGHAR	K	A	95.00%	30		628.3423	3	4.5	227	244	No
				EQNIVFNAETYSNLIK	K	L	95.00%	93		941.9888	2	7.8	1060	1075	No
				GAYDIFLNAK	K	E	95.00%	68		556.2955	2	3.7	1050	1059	No
				GDVENIEVVQK	K	M	95.00%	48		615.3249	2	3.3	1153	1163	No

				GFTLNDAANSR	K	L	95.00%	56		583.2853	2	2.2	1099	1109	No
				IQEENVIPR	K	E	95.00%	47		549.3032	2	2.6	981	989	No
				KGAYDIFLNAK	K	E	95.00%	63		620.3458	2	7.9	1049	1059	No
				LGAVYDVSHYNALLK	K	V	95.00%	45		831.9483	2	2.0	156	170	No
				LLAEILR	R	E	95.00%	54		414.2733	2	3.9	995	1001	No
				LQDAINILK	K	E	95.00%	43		514.3143	2	5.1	764	772	No
				MEEANIQPNR	K	V	95.00%	42	M1: Oxidation	609.2871	2	6.5	188	197	No
				MVFINNIALAQIK	K	N	95.00%	48	M1: Oxidation	745.9299	2	7.7	1177	1189	No
				NLLESYHVPELIK	R	D	95.00%	71		777.9365	2	7.6	628	640	No
				NNNIDAAIENIENMLTSENK	K	V	95.00%	143	M14: Oxidation	1132.0360	2	5.3	1190	1209	No
				NNNIDAAIENIENMLTSENK	K	V	95.00%	54	M14: Oxidation	755.0256	3	4.3	1190	1209	No
				NVQGIIEILK	K	G	95.00%	52		563.8483	2	4.4	454	463	No
				SEAANGNLDFVLSFLK	R	S	95.00%	132		862.9513	2	5.1	514	529	No
				SGGLGGSHALLLLR	R	S	95.00%	44		675.8988	2	2.8	115	128	No
				SGGLGGSHALLLLR	R	S	95.00%	49		450.9357	3	4.0	115	128	No
				SNTLPISLQSIR	K	S	95.00%	72		664.8832	2	3.5	530	541	No
				SSLLLGFR	R	R	95.00%	54		446.7683	2	3.5	542	549	No
				SVLELIPELNEKEEAYNSLMK	K	S	95.00%	32	M20: Oxidation	822.4283	3	8.4	1306	1326	No
				TKDLPVTEAVFSALVTGHAR	K	A	95.00%	84		704.7255	3	7.4	225	244	No
				TKDLPVTEAVFSALVTGHAR	K	A	95.00%	68		528.7956	4	6.5	225	244	No
				TVLDQQQTPSR	K	L	95.00%	50		636.8351	2	5.8	1137	1147	No
				TVQLTSSELESTLETLK	K	A	95.00%	51		940.0078	2	8.7	656	672	No
				TVQLTSSELESTLETLK	K	A	95.00%	53		627.0045	3	3.3	656	672	No
				VIEEQLEPAVEK	K	I	95.00%	66		692.3757	2	4.5	1225	1236	No
				VIEPQYFGLAYLFR	K	K	95.00%	76		858.4699	2	9.1	1210	1223	No
				VIEPQYFGLAYLFR	K	K	95.00%	45		572.6487	3	8.3	1210	1223	No
				YAGEPVPFIEPPESFEFYAQQLR	K	K	95.00%	42		905.4514	3	9.0	1365	1387	No
453	IPI00329801	ANXA5	ANNEXIN A5.	DLLDDLKSELTGK	R	F	95.00%	36		482.9314	3	6.2	64	76	No
				DLLDDLKSELTGKFEK	R	L	95.00%	52		617.6690	3	8.4	64	79	No
				ETSGNLEQLLLAVVK	R	S	95.00%	52		538.6475	3	9.6	228	242	No
				FITIFGTR	K	S	95.00%	36		477.7776	2	6.5	194	201	No
				GAGTDDHTLIR	K	V	95.00%	66		578.2963	2	7.4	261	271	No
				GLGTDEESILTLLTSR	K	S	95.00%	61		568.9758	3	5.4	30	45	No
				GTVTDFPGFDER	R	A	95.00%	35		670.8135	2	5.0	7	18	No
				LIVALMKPSR	K	L	95.00%	35	M6: Oxidation	572.3513	2	2.0	80	89	No
				LYDAYELK	R	H	95.00%	49		507.7632	2	3.8	90	97	No
				MLVVLLQANR	R	D	95.00%	65	M1: Oxidation	586.8461	2	1.6	152	161	No
				NFATSLYSMIK	K	G	95.00%	60	M9: Oxidation	645.8293	2	8.0	291	301	No
				SEIDLFNIR	R	K	95.00%	49		553.8016	2	9.7	277	285	No
				SEIDLFNIRK	R	E	95.00%	36		617.8477	2	6.4	277	286	No
				SIPAYLAETLYYAMK	R	G	95.00%	65	M14: Oxidation	875.4414	2	-1.3	246	260	No
				VLTEIIASR	K	T	95.00%	68		501.3066	2	5.9	109	117	No
				WGTDEEKFITIFGTR	K	S	95.00%	44		600.6414	3	6.4	187	201	No
454	IPI00332106; IPI00645060	PBXIP1	PRE-B-CELL LEUKEMIA HOMEOBOX INTERACTING PROTEIN 1.; PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR INTERACTING PROTEIN 1.	ALESELQQLR	R	A	95.00%	72		593.8281	2	4.2	326	335	No
				ELPLSPAFFGEDGIFR	K	H	95.00%	110		897.9645	2	8.0	635	650	No
				EQLEAEAQALR	K	Q	95.00%	47		629.3311	2	8.3	385	395	No
				GALQQGEAFQR	R	A	95.00%	79		602.8095	2	3.0	315	325	No
				GLEEENAQLR	K	G	95.00%	51		579.7939	2	3.7	305	314	No
				LLGSVQQDLER	R	S	95.00%	79		629.3457	2	2.5	404	414	No
				LLQAQLQAQKEELQSLMHQPK	R	G	95.00%	31	M17: Oxidation	826.4512	3	7.8	284	304	No
				LPWAGQLTK	R	E	95.00%	26		507.2949	2	3.5	626	634	No
				QEGLTFFGTELAPVR	R	Q	95.00%	80		832.9428	2	7.6	597	611	No
				QKEQLEAEAQALR	K	Q	95.00%	66		757.4080	2	6.9	383	395	No
				QVLPDPEVLEAVGDR	R	Q	95.00%	72		818.9389	2	9.2	231	245	No
455	IPI00220906; IPI00333838	ACOT1; ACOT2	ISOFORM 1 OF ACYL-COENZYME A THIOESTERASE 2.; ACYL-COENZYME A THIOESTERASE 1.	AATLILEPAGR	M	C	95.00%	45		556.3290	2	2.3	2	12	No
				ADTLGELDLER	R	A	95.00%	67		616.3147	2	3.5	54	64	No
				AESTFLFLVGQDDHNWK	R	S	95.00%	49		669.6641	3	7.5	314	330	No
				APALGGSFAGLEPMGLLWALEPEKPLVR	R	L	95.00%	66		973.8738	3	8.7	65	92	No
				ASLHALVGSPIIWGGEPR	R	A	95.00%	65		930.5184	2	8.4	372	389	No
				ASLHALVGSPIIWGGEPR	R	A	95.00%	59		620.6802	3	6.2	372	389	No
				DGYADIVDVLNSPLEGPDQK	K	S	95.00%	61		715.6898	3	8.4	287	306	No
				GFAVMALAYYNYEDLPK	K	T	95.00%	35	M5: Oxidation	990.9840	2	9.3	182	198	No

				GLAPEQPVTLR	R	A	95.00%	44		590.8404	2	3.2	25	35	No
				GPGVGLLGISK	K	G	95.00%	71		499.3077	2	2.8	223	233	No
				TPLAVELEVLDGHDPDPGR	R	L	95.00%	115		1015.5210	2	7.2	100	118	No
				TPLAVELEVLDGHDPDPGR	R	L	95.00%	61		677.3484	3	4.8	100	118	No
				YFLPPGVR	R	R	95.00%	29		474.7708	2	3.1	128	135	No
				YKGETLPPVGVNR	R	N	95.00%	46		715.3968	2	3.7	267	279	No
				YRADTLGELDLER	R	A	95.00%	82		775.8987	2	5.1	52	64	No
				YRADTLGELDLER	R	A	95.00%	51		517.6009	3	3.5	52	64	No
456	IPI00334775; IPI00414676	HSP90AB1	85 KDA PROTEIN.; HEAT SHOCK PROTEIN HSP 90-BETA.	ADLINNLGTIAK	K	S	95.00%	30		1242.7100	1	2.8	96	107	Yes
				ADLINNLGTIAK	K	S	95.00%	64		621.8598	2	4.6	96	107	Yes
				ALLFIPR	R	R	95.00%	48		415.2706	2	3.9	331	337	No
				DNSTMGYMMAK	R	K	95.00%	55	M5: Oxidation, M8: Oxidation, M9: Oxidation	648.7559	2	10.0	613	623	No
				EDQTEYLEER	K	R	95.00%	52		656.2938	2	7.0	187	196	Yes
				EGLELPEDEEEK	K	K	95.00%	48		708.8251	2	2.8	539	550	Yes
				EGLELPEDEEEKKK	K	M	95.00%	58		836.9250	2	8.2	539	552	No
				EKYIDQEELNK	K	T	95.00%	42		704.8553	2	4.7	274	284	Yes
				ELISNASDALDK	R	I	95.00%	57		638.3295	2	6.1	42	53	Yes
				ELISNASDALDKIR	R	Y	95.00%	83		772.9214	2	4.1	42	55	No
				EQVANSAFVER	K	V	95.00%	63		625.3141	2	2.3	492	502	No
				GVVDSEDLPLNISR	R	E	95.00%	96		757.4001	2	4.0	379	392	Yes
				GVVDSEDLPLNISR	R	E	95.00%	51		505.2707	3	6.7	379	392	Yes
				HFSVEGQLEFR	K	A	95.00%	73		674.8394	2	4.4	320	330	Yes
				HFSVEGQLEFR	K	A	95.00%	50		450.2282	3	3.0	320	330	Yes
				HLEINPDHPIVETLR	K	Q	95.00%	85		891.9824	2	3.6	625	639	No
				HLEINPDHPIVETLR	K	Q	95.00%	57		594.9901	3	2.3	625	639	No
				HNDDEQYAWESSAGGSFTVR	K	A	95.00%	61		752.6616	3	4.3	149	168	No
				HSQFIGYPITLYLEK	K	E	95.00%	91		904.9895	2	6.8	205	219	No
				HSQFIGYPITLYLEK	K	E	95.00%	52		603.6628	3	7.6	205	219	No
				IDIIPNPQER	K	T	95.00%	55		597.8301	2	3.2	73	82	No
				IRYESLTDPSKLDSGK	K	E	95.00%	52		603.6533	3	2.4	54	69	Yes
				KHLEINPDHPIVETLR	K	Q	95.00%	32		637.6894	3	3.7	624	639	No
				KHLEINPDHPIVETLR	K	Q	95.00%	48		478.5202	4	6.2	624	639	No
				LGLGIDEDEVAAEEPNAAVPDEIPPLEGDEDASR	K	M	95.00%	79		1178.2310	3	8.6	686	719	No
				NPDDITQEEYGEFYK	R	S	95.00%	93		924.4045	2	1.9	292	306	No
				RAPFDLFENK	R	K	95.00%	46		618.8262	2	5.4	338	347	No
				RAPFDLFENK	R	K	95.00%	34		412.8866	3	5.0	338	347	No
				RAPFDLFENKK	R	K	95.00%	53		455.5837	3	2.1	338	348	No
				SIYYITGESK	K	E	95.00%	36		1160.5950	1	9.6	482	491	No
				SIYYITGESK	K	E	95.00%	45		580.7983	2	4.2	482	491	No
				SLTNDWEDHLAVK	K	H	95.00%	88		764.3835	2	9.7	307	319	Yes
				TLTLVDTGIGMTK	R	A	95.00%	102	M11: Oxidation	683.3706	2	2.2	83	95	No
				TLTLVDTGIGMTK	R	A	95.00%	69		675.3736	2	2.9	83	95	No
				VILHLKEDQTEYLEER	K	R	95.00%	92		1008.0330	2	6.8	181	196	Yes
				VILHLKEDQTEYLEER	K	R	95.00%	79		672.3587	3	7.6	181	196	Yes
				YESLTDPSK	R	L	95.00%	32		1039.4990	1	4.2	56	64	Yes
				YESLTDPSK	R	L	95.00%	35		520.2534	2	4.0	56	64	Yes
				YESLTDPSKLDSGK	R	E	95.00%	86		770.3819	2	1.0	56	69	Yes
				YHTSQSGDEMTSLSEYVSR	R	M	95.00%	116	M10: Oxidation	1096.9800	2	5.5	457	475	No
				YHTSQSGDEMTSLSEYVSR	R	M	95.00%	62	M10: Oxidation	731.6540	3	2.8	457	475	No
				YIDQEELNK	K	T	95.00%	72		576.2863	2	5.2	276	284	Yes
457	IPI00337541	NNT	NAD(P) TRANSHYDROGENASE, MITOCHONDRIAL PRECURSOR.	APMVNPTLGVHEADLLK	R	T	95.00%	55	M3: Oxidation	910.9915	2	9.3	130	146	No
				APMVNPTLGVHEADLLK	R	T	95.00%	47	M3: Oxidation	607.6618	3	6.4	130	146	No
				AQYPIADLVK	K	M	95.00%	30		559.3190	2	3.7	940	949	No
				EVLASDLVVK	K	V	95.00%	29		536.8206	2	7.2	118	127	No
				GITHIGYTDLPSR	K	M	95.00%	58		715.3829	2	9.6	367	379	No
				GITHIGYTDLPSR	K	M	95.00%	48		477.2559	3	5.5	367	379	No
				ILIVGGGVAGLASAGAAK	K	S	95.00%	141		762.9662	2	8.6	230	247	No
				MATQASTLYSNNITK	R	L	95.00%	120	M1: Oxidation	829.9106	2	4.6	380	394	No
				QGFNVVVESGAGEASK	K	F	95.00%	77		789.8966	2	5.7	85	100	No
				SLGAEPLEVDLK	K	E	95.00%	57		635.8511	2	3.7	268	279	No
				TTVLAMDQVPR	K	V	95.00%	53	M6: Oxidation	623.8310	2	6.1	172	182	No
				VALSPAGVQNLVK	R	Q	95.00%	81		648.3913	2	4.6	72	84	No
				VRAPMVNPTLGVHEADLLK	K	T	95.00%	39	M5: Oxidation	692.7203	3	8.5	128	146	No
				VRAPMVNPTLGVHEADLLK	K	T	95.00%	30	M5: Oxidation	519.7905	4	5.2	128	146	No
				VTIAQGYDALSSMANIAGYK	R	A	95.00%	30	M13: Oxidation	697.0211	3	9.7	183	202	No

458	IPI00337741	APEH	ACYLAMINO-ACID-RELEASING ENZYME.	ALDVSASDDEIAR	K	L	95.00%	81		681.3326	2	1.9	181	193	No
				GSTGFGQDSILSLPGNVGHQDVK	R	D	95.00%	39		771.7258	3	6.0	539	561	No
				QFLEVWEK	K	N	95.00%	30		539.7866	2	7.2	119	126	No
				QVLLSEPEEAAALYR	R	G	95.00%	83		844.9520	2	6.0	4	18	No
				QYLVFHDGDSVVFAGPAGNSVETR	R	G	95.00%	67		855.7540	3	3.5	66	89	No
				SALYYVDLIGGK	R	C	95.00%	57		649.8558	2	3.2	280	291	No
				SFNLSALEK	K	H	95.00%	33		504.7745	2	4.7	132	140	No
				TPLLLMLGQEDR	K	R	95.00%	73	M6: Oxidation	701.3783	2	5.2	665	676	No
				VTSVVVDVVPR	K	Q	95.00%	77		585.3512	2	4.4	340	350	No
459	IPI00374208	CAND2	CULLIN-ASSOCIATED NEDD8-DISSOCIATED PROTEIN 2.	AVAALLTIPEVGK	R	S	95.00%	66		641.3982	2	7.9	1067	1079	No
				AVLLEALGSPSEDVR	K	A	95.00%	91		778.4274	2	8.8	771	785	No
				AVLLEALGSPSEDVR	K	A	95.00%	33		519.2858	3	5.6	771	785	No
				DLLDDILPLLYQETK	R	I	95.00%	91		894.9933	2	8.3	931	945	No
				DLLDDILPLLYQETK	R	I	95.00%	57		596.9980	3	8.1	931	945	No
				DSIQLDEDSER	K	K	95.00%	44		653.7954	2	5.0	37	47	No
				FMATSDLMSELQK	R	D	95.00%	72	M2: Oxidation, M8: Oxidation	766.8569	2	5.4	24	36	No
				LGDDLEPTLLLLLDR	R	L	95.00%	81		848.4857	2	5.8	513	527	No
				LGDDLEPTLLLLLDR	R	L	95.00%	40		565.9929	3	5.3	513	527	No
				LISLLTAPVYEQAVDGGPGLHK	K	Q	95.00%	46		760.0942	3	9.6	684	705	No
				LVLVNPSFLLPR	K	L	95.00%	61		684.4312	2	9.5	870	881	No
				MLDPEPYVGEMSAVTLAR	R	L	95.00%	108	M1: Oxidation, M11: Oxidation	1005.9890	2	9.2	467	484	No
				RQYLLLHSLR	R	E	95.00%	61		433.5992	3	9.5	817	826	No
				SNPELAALFESIQK	R	D	95.00%	84		773.9142	2	5.8	1092	1105	No
				SNPELAALFESIQK	R	D	95.00%	65		516.2777	3	3.7	1092	1105	No
				SPIMADFSSQIR	K	S	95.00%	62	M4: Oxidation	684.3406	2	7.7	1080	1091	No
				VGAGSLPDFLPFLLEQIEAEPR	R	R	95.00%	68		800.1004	3	8.2	795	816	No
460	IPI00374657	VAPA	VESICLE-ASSOCIATED MEMBRANE PROTEIN-ASSOCIATED PROTEIN A ISOFORM 1.	FKGPFTDVVTTNLK	K	L	95.00%	35		522.9612	3	9.4	25	38	No
				GPFTDVVTTNLK	K	L	95.00%	83		646.3526	2	5.7	27	38	No
				HEQILVLDPPTDLK	K	F	95.00%	34		539.9692	3	3.8	11	24	No
				KVAHSDKPGSTSTASFR	R	D	95.00%	63		592.6436	3	6.4	250	266	No
				KVAHSDKPGSTSTASFR	R	D	95.00%	32		444.7342	4	5.4	250	266	No
				VAHSDKPGSTSTASFR	K	D	95.00%	51		824.4147	2	7.6	251	266	No
				VAHSDKPGSTSTASFR	K	D	95.00%	39		549.9449	3	6.1	251	266	No
461	IPI00376005; IPI00411704	EIF5A	ISOFORM 2 OF EUKARYOTIC TRANSLATION INITIATION FACTOR 5A-1.; ISOFORM 1 OF EUKARYOTIC TRANSLATION INITIATION FACTOR 5A-1.	EDLRLPEGDLGK	R	E	95.00%	34		671.3586	2	5.6	140	151	No
				NDFQLIGIQDGYLSLLQDSGEVR	R	E	95.00%	124		1290.6620	2	8.0	117	139	No
				RNDFQLIGIQDGYLSLLQDSGEVR	K	E	95.00%	80		912.8117	3	8.7	86	109	No
				VHLVGIDIFTGK	K	K	95.00%	71		649.8835	2	9.1	86	97	No
				VHLVGIDIFTGK	K	K	95.00%	48		433.5919	3	9.7	86	97	No
462	IPI00377167	SMTNL1	SIMILAR TO SMOOTHELIN-LIKE 1.	AINEGPPTESGKQEK	K	A	95.00%	68		792.9048	2	9.3	59	73	No
				ATVEEEDAKTASQEETGQR	K	K	95.00%	46		693.6567	3	3.2	182	200	No
				AVVEDEAKAEPK	K	E	95.00%	42		643.3409	2	7.7	223	234	No
				FFPDAFDYAELDPAK	K	R	95.00%	90		873.4147	2	8.7	438	452	No
				FGGAASGPTALFR	K	N	95.00%	85		626.3317	2	5.5	374	386	No
				HNFTLAFSTAEK	R	L	95.00%	68		683.3479	2	5.6	455	466	No
				KEDGEKEETTVGSQEMTGR	K	K	95.00%	33	M16: Oxidation	532.4976	4	7.2	114	132	No
				LSEDGTTVSPAADNPEMSGGGAPAEETK	K	G	95.00%	58	M17: Oxidation	912.0737	3	2.0	26	53	No
				LSEDGTTVSPAADNPEMSGGGAPAEETKGTAGK	K	A	95.00%	71	M17: Oxidation	1050.1510	3	5.1	26	58	No
463	IPI00377214; IPI00465264	NLRX1	NLR FAMILY MEMBER X1 ISOFORM 2.; NLR FAMILY MEMBER X1 ISOFORM 1.	ALPLLFNLIK	R	V	95.00%	26		571.3732	2	3.0	548	557	No
				FSAEVLSSLR	R	Q	95.00%	80		554.8062	2	4.0	690	699	No
				LFPSASATEAIQR	R	H	95.00%	69		695.8765	2	8.7	69	81	No
				QFGPTFALDTVHVDPVIR	R	E	95.00%	44		671.3652	3	9.5	99	116	No
				TLLPVFLR	R	A	95.00%	27		479.8122	2	7.8	744	751	No
464	IPI00382470; IPI00784295; IPI00789847	HSP90AA1	HEAT SHOCK PROTEIN HSP 90-ALPHA 2.; HEAT SHOCK PROTEIN HSP 90-ALPHA.; PROTEIN.	ADLINNLGTIAK	K	S	95.00%	30		1242.7100	1	2.8	153	164	Yes

				ADLINNLGTIAK	K	S	95.00%	64		621.8598	2	4.6	223	234	Yes
				ALLFVPR	R	R	95.00%	43		408.2624	2	3.2	391	397	No
				APFDLFENR	R	K	95.00%	46		554.7783	2	5.3	469	477	No
				DQVANSAFVER	K	L	95.00%	67		618.3090	2	6.5	622	632	No
				EDQTEYLEER	K	R	95.00%	52		656.2938	2	7.0	314	323	Yes
				EGLELPEDEEEK	K	K	95.00%	48		708.8251	2	2.8	669	680	Yes
				EGLELPEDEEEKKK	K	Q	95.00%	58		836.9250	2	8.2	669	682	No
				EKYIDQEELNK	K	T	95.00%	42		704.8553	2	4.7	404	414	Yes
				ELHINLIPNKQDR	K	T	95.00%	44		795.4459	2	4.6	197	209	No
				ELHINLIPNKQDR	K	T	95.00%	31		530.6335	3	5.2	197	209	No
				ELISNSSDALDK	R	I	95.00%	60		646.3274	2	6.8	169	180	No
				ELISNSSDALDKIR	R	Y	95.00%	104		780.9207	2	6.6	169	182	No
				GVVDSEDLPLNISR	R	E	95.00%	96		757.4001	2	4.0	509	522	Yes
				GVVDSEDLPLNISR	R	E	95.00%	51		505.2707	3	6.7	509	522	Yes
				HFSVEGQLEFR	K	A	95.00%	73		674.8394	2	4.4	450	460	Yes
				HFSVEGQLEFR	K	A	95.00%	50		450.2282	3	3.0	380	390	Yes
				HIYYITGETK	K	D	95.00%	45		612.8213	2	6.8	612	621	No
				HLEINPDHSIIETLR	K	Q	95.00%	101		893.9809	2	4.8	685	699	No
				HLEINPDHSIIETLR	K	Q	95.00%	49		596.3235	3	5.3	755	769	No
				HNDDEQYAWESSAGGSFTVR	K	T	95.00%	61		752.6616	3	4.3	206	225	No
				HSQFIGYPITLFVEK	K	E	95.00%	85		889.9849	2	7.8	332	346	No
				HSQFIGYPITLFVEK	K	E	95.00%	55		593.6586	3	6.7	332	346	No
				IRYESLTDPSKLDSGK	K	E	95.00%	52		603.6533	3	2.4	111	126	Yes
				KHLEINPDHSIIETLR	K	Q	95.00%	44		639.0215	3	4.5	684	699	No
				KHLEINPDHSIIETLR	K	Q	95.00%	41		479.5178	4	3.9	754	769	No
				NPDDITNEEYGEFYK	R	S	95.00%	106		917.4004	2	5.9	422	436	No
				RAPFDLFENR	R	K	95.00%	45		632.8298	2	6.3	468	477	No
				SLTNDWEDHLAVK	K	H	95.00%	88		764.3835	2	9.7	437	449	Yes
				TLTIVDTGIGMTK	R	A	95.00%	102	M11: Oxidation	683.3706	2	2.2	140	152	No
				TLTIVDTGIGMTK	R	A	95.00%	69		675.3736	2	2.9	140	152	No
				VILHLKEDQTEYLEER	K	R	95.00%	92		1008.0330	2	6.8	238	253	Yes
				VILHLKEDQTEYLEER	K	R	95.00%	79		672.3587	3	7.6	308	323	Yes
				YESLTDPSK	R	L	95.00%	32		1039.4990	1	4.2	183	191	Yes
				YESLTDPSK	R	L	95.00%	35		520.2534	2	4.0	183	191	Yes
				YESLTDPSKLDSGK	R	E	95.00%	86		770.3819	2	1.0	113	126	Yes
				YIDQEELNK	K	T	95.00%	72		576.2863	2	5.2	406	414	Yes
				YYTSASGDEMVSLK	R	D	95.00%	87	M10: Oxidation	783.8558	2	2.6	517	530	No
465	IPI00382894	TPM3	TROPOMYOSIN 3.	AADESER	K	G	95.00%	29		777.3453	1	9.6	83	89	Yes
				AISEELDHALNDMTSI	K	-	95.00%	65	M13: Oxidation	887.9175	2	5.8	233	248	Yes
				AISEELDHALNDMTSI	K	-	95.00%	35	M13: Oxidation	592.2813	3	6.4	233	248	Yes
				ALKDEEKMELQEIQLK	R	E	95.00%	95	M8: Oxidation	981.0244	2	7.2	98	113	Yes
				ALKDEEKMELQEIQLK	R	E	95.00%	46	M8: Oxidation	654.3511	3	5.5	98	113	Yes
				ALKDEEKMELQEIQLK	R	E	95.00%	38	M8: Oxidation	491.0146	4	4.2	98	113	Yes
				DEEKMELQEIQLK	K	E	95.00%	47	M5: Oxidation	824.9163	2	8.6	101	113	Yes
				EDKYEEEIK	K	I	95.00%	30		591.7847	2	7.0	182	190	Yes
				EQAEAEVASLNR	R	R	95.00%	61		658.8309	2	7.2	43	54	No
				HIAEEADRKYEEVAR	K	K	95.00%	53		908.4615	2	8.9	117	131	Yes
				ILTDKLKEAETR	K	A	95.00%	56		708.9106	2	4.8	191	202	Yes
				IQLVEEELDR	R	A	95.00%	83		622.3349	2	6.8	56	65	Yes
				IQLVEEELDRAQER	R	L	95.00%	66		864.4579	2	8.8	56	69	Yes
				IQLVEEELDRAQER	R	L	95.00%	52		576.6364	3	0.4	56	69	Yes
				IQVLQQQADDAEER	K	A	95.00%	103		821.9120	2	7.5	14	27	No
				KIQVLQQQADDAEER	R	A	95.00%	100		885.9620	2	9.8	13	27	No
				KLVIIEGDLER	R	T	95.00%	63		642.8848	2	6.7	132	142	Yes
				KLVIIEGDLER	R	T	95.00%	54		428.9252	3	5.3	132	142	Yes
				KLVIIEGDLERTEER	R	A	95.00%	31		900.5034	2	6.6	132	146	Yes
				KLVIIEGDLERTEER	R	A	95.00%	40		600.6729	3	8.9	132	146	Yes
				LATALQKLEEAEK	R	A	95.00%	87		722.4111	2	5.7	70	82	Yes
				LATALQKLEEAEK	R	A	95.00%	38		481.9438	3	6.8	70	82	Yes
				LATALQKLEEAEKAADESER	R	G	95.00%	71		734.7194	3	7.8	70	89	Yes
				LATALQKLEEAEKAADESER	R	G	95.00%	30		551.2904	4	5.8	70	89	Yes
				LEEAEKAADESER	K	G	95.00%	94		738.8469	2	2.8	77	89	Yes
				LEEAEKAADESER	K	G	95.00%	63		492.8999	3	1.4	77	89	Yes
				LEEAEKAADESERGMK	K	V	95.00%	62	M15: Oxidation	904.9289	2	9.0	77	92	Yes
				LEEAEKAADESERGMK	K	V	95.00%	37	M15: Oxidation	603.6193	3	4.7	77	92	Yes
				LVIIEGDLER	K	T	95.00%	69		578.8371	2	7.3	133	142	Yes
				MELQEIQLK	K	E	95.00%	51	M1: Oxidation	574.3087	2	5.3	105	113	Yes
				RIQLVEEELDR	R	A	95.00%	73		700.3859	2	6.7	55	65	Yes
				RIQLVEEELDR	R	A	95.00%	60		467.2593	3	5.4	55	65	Yes
				RIQLVEEELDRAQER	R	L	95.00%	41		628.6716	3	2.7	55	69	Yes

				RIQLVEEELDRAQER	R	L	95.00%	48		471.7569	4	5.3	55	69	Yes
				TIDDLEDELYAQK	K	L	95.00%	91		776.8795	2	8.1	216	228	Yes
				TIDDLEDELYAQK	K	L	95.00%	45		518.2560	3	8.8	216	228	Yes
				YSQKEDKYEEEIK	K	I	95.00%	78		844.9086	2	4.3	178	190	Yes
				YSQKEDKYEEEIK	K	I	95.00%	31		563.6105	3	8.1	178	190	Yes
466	IPI00383046	CMBL	CARBOXYMETHYLENEBUTENOLIDASE-LIKE.	AGVSVYGIVK	R	D	95.00%	43		496.7957	2	5.7	150	159	No
				AGVSVYGIVKDSEDIYNLK	R	N	95.00%	59		690.7040	3	9.9	150	168	No
				DSEDIYNLK	K	N	95.00%	70		548.7646	2	4.5	160	168	No
				DVSLLTQK	K	L	95.00%	59		903.5233	1	8.9	186	193	No
				DVSLLTQK	K	L	95.00%	37		452.2645	2	6.6	186	193	No
				LEYGGLGR	R	E	95.00%	32		432.7352	2	5.2	16	23	No
				NLIEWLNK	R	Y	95.00%	40		515.2954	2	9.1	236	243	No
				TFSGQTHGFVHR	K	K	95.00%	68		687.3440	2	6.3	206	217	No
467	IPI00011454; IPI00383581; IPI00441414; IPI00472068	GANAB	ISOFORM 2 OF NEUTRAL ALPHA-GLUCOSIDASE AB PRECURSOR.; ISOFORM 1 OF NEUTRAL ALPHA-GLUCOSIDASE AB PRECURSOR.; ISOFORM 3 OF NEUTRAL ALPHA-GLUCOSIDASE AB PRECURSOR.; 107 KDA PROTEIN.	DVHNIYGLYVHMATADGLR	R	Q	95.00%	34	M12: Oxidation	721.0276	3	8.0	570	588	No
				LSFQHDPETSVLVLR	R	K	95.00%	52		580.9842	3	5.0	915	929	No
				MMDYLQGSGETPQTDVR	K	W	95.00%	87	M1: Oxidation, M2: Oxidation	980.4322	2	6.9	338	354	No
				QYASLTGTQALPPLFSLGYHQSR	R	W	95.00%	91		845.7800	3	9.8	400	422	No
				SLLLSVNAR	R	G	95.00%	38		486.7988	2	5.8	165	173	No
				VSQGSKDPAEGDGAQPEETPR	R	D	95.00%	36		719.0081	3	8.3	186	206	No
				VVIIGAGKPAAVVLQTK	R	G	95.00%	51		555.3565	3	3.7	892	908	No
				YRVPDVLVADPPIAR	R	L	95.00%	30		560.9897	3	5.5	113	127	No
468	IPI00384280	PCYOX1	PRENYLCYSTEINE OXIDASE PRECURSOR.	EKEDPEPSTDGTYVWK	R	I	95.00%	86		940.9373	2	6.0	391	406	No
				FLNEMIAPVMR	K	V	95.00%	49	M5: Oxidation, M10: Oxidation	676.8424	2	4.7	212	222	No
				IAIIGAGIGGTSAAYYLR	K	Q	95.00%	99		884.0024	2	9.3	37	54	No
				IFSQETLTK	K	A	95.00%	38		533.7951	2	3.5	407	415	No
				LATMMVQGQEYEAGGSVIHPLNLHMK	R	R	95.00%	53	M4: Oxidation, M5: Oxidation, M25: Oxidation	968.1421	3	7.2	75	100	No
				LATMMVQGQEYEAGGSVIHPLNLHMK	R	R	95.00%	41	M4: Oxidation, M5: Oxidation, M25: Oxidation	726.3574	4	5.7	75	100	No
				LFLSYDYAVK	K	K	95.00%	41		609.8279	2	5.6	421	430	No
				MHMWVEDVLDK	R	F	95.00%	42	M1: Oxidation, M3: Oxidation	717.8300	2	8.7	152	162	No
				MYEVVYQIGTETR	K	S	95.00%	86	M1: Oxidation	802.8893	2	4.8	292	304	No
				SDFYDIVLVATPLNR	R	K	95.00%	52		861.9645	2	8.3	305	319	No
				SDFYDIVLVATPLNR	R	K	95.00%	57		574.9751	3	1.6	305	319	No
				SNLISGSVMYIEEK	K	T	95.00%	90	M9: Oxidation	793.3979	2	6.2	267	280	No
				TLLETLQK	R	A	95.00%	29		473.2865	2	3.1	198	205	No
				YGFQSLR	R	M	95.00%	40		435.7293	2	3.9	145	151	No
				YQSHDYAFSSVEK	R	L	95.00%	87		780.8585	2	7.9	169	181	No
469	IPI00384938; IPI00423463; IPI00423464; IPI00423466; IPI00448925; IPI00448938; IPI00472610; IPI00645363; IPI00761159; IPI00784810; IPI00784817; IPI00784822; IPI00784828; IPI00784842; IPI00785084; IPI00807531; IPI00815926; IPI00816314; IPI00816681; IPI00829944	IGHG1; IGHM	HYPOTHETICAL PROTEIN DKFZP686N02209.; HYPOTHETICAL PROTEIN DKFZP686O01196.; HYPOTHETICAL PROTEIN DKFZP686K03196.; HYPOTHETICAL PROTEIN DKFZP686H20196.; IGHG1 PROTEIN.; IGHG1 PROTEIN.; IGHM PROTEIN.; HYPOTHETICAL PROTEIN DKFZP686P15220.; IGHM PROTEIN.; IGHG1 PROTEIN.; ANTI-RHD MONOCLONAL T125 GAMMA1 HEAVY CHAIN PRECURSOR.; IGHV4-31 PROTEIN.; HYPOTHETICAL PROTEIN DKFZP686C11235.; HYPOTHETICAL PROTEIN DKFZP686G11190.; HYPOTHETICAL PROTEIN IGHG1.; IGHG1 PROTEIN.; IGHG1 PROTEIN.; HYPOTHETICAL PROTEIN DKFZP686I15196.; HEPATITIS B VIRUS RECEPTOR BINDING PROTEIN (FRAGMENT).; IGHG1 PROTEIN.	ALPAPIEK	K	T	95.00%	34		838.5054	1	1.7	355	362	No
				DTLMISR	K	T	95.00%	53	M4: Oxidation	426.2194	2	1.4	277	283	Yes
				EPQVYTLPPSR	R	D	95.00%	48		643.8439	2	4.3	373	383	No
				EPQVYTLPPSRDELTK	R	N	95.00%	69		936.9926	2	3.5	373	388	No
				EPQVYTLPPSRDELTK	R	N	95.00%	36		624.9998	3	6.8	373	388	No

				FNWYVDGVEVHNAK	K	T	95.00%	78		839.4092	2	4.9	303	316	No
				FNWYVDGVEVHNAK	K	T	95.00%	64		559.9426	3	5.7	303	316	No
				GFYPSDIAVEWESNGQPENNYK	K	T	95.00%	81		1272.5700	2	0.0	399	420	Yes
				GFYPSDIAVEWESNGQPENNYK	K	T	95.00%	36		848.7162	3	0.5	399	420	Yes
				GPSVFPLAPSSK	K	S	95.00%	50		1186.6530	1	4.6	150	161	No
				GPSVFPLAPSSK	K	S	95.00%	64		593.8312	2	6.2	150	161	No
				GTLVTVSSASTK	R	G	95.00%	48		575.8223	2	4.1	138	149	No
				TTPPVLDSDGSFFLYSK	K	L	95.00%	95		937.4691	2	4.2	421	437	No
				TTPPVLDSDGSFFLYSK	K	L	95.00%	66		625.3144	3	2.8	421	437	No
				VVSVLTVLHQDWLNGK	R	E	95.00%	89		904.5143	2	7.6	330	345	No
				VVSVLTVLHQDWLNGK	R	E	95.00%	56		603.3447	3	6.1	330	345	No
470	IPI00386271	SLC25A12	CALCIUM-BINDING MITOCHONDRIAL CARRIER PROTEIN ARALAR1.	DLGIFGLYK	R	G	95.00%	40		1025.5750	1	7.5	474	482	No
				DLGIFGLYK	R	G	95.00%	58		513.2899	2	4.5	474	482	No
				DVEVTKEEFAQSAIR	K	Y	95.00%	108		861.4429	2	4.0	245	259	No
				DVEVTKEEFAQSAIR	K	Y	95.00%	42		574.6340	3	8.9	245	259	No
				FGLYLPK	K	F	95.00%	39		419.2487	2	2.5	653	659	No
				FKSPSVAVVQPK	K	A	95.00%	46		643.8793	2	2.8	660	671	No
				FKSPSVAVVQPK	K	A	95.00%	34		429.5891	3	3.4	660	671	No
				FTLGSVAGAVGATAVYPIDLVK	R	T	95.00%	122		1075.1080	2	7.7	330	351	No
				FTLGSVAGAVGATAVYPIDLVK	R	T	95.00%	102		717.0723	3	4.8	330	351	No
				GLIPQLIGVAPEK	R	A	95.00%	94		667.9095	2	4.5	391	403	No
				GSGSVVGELMYK	R	N	95.00%	58	M10: Oxidation	621.8090	2	4.9	359	370	No
				HLNYTEFTQFLQELQLEHAR	K	Q	95.00%	76		839.7602	3	4.9	144	163	No
				HLNYTEFTQFLQELQLEHAR	K	Q	95.00%	59		630.0727	4	6.0	144	163	No
				IADLPPANPDHIGGYR	R	L	95.00%	75		853.4437	2	7.7	625	640	No
				IADLPPANPDHIGGYR	R	L	95.00%	35		569.2956	3	2.7	625	640	No
				IAPLAEGALPYNLAELQR	R	Q	95.00%	116		970.0456	2	9.3	292	309	No
				IAPLAEGALPYNLAELQR	R	Q	95.00%	88		647.0302	3	4.9	292	309	No
				ILREEGPSAFWK	K	G	95.00%	57		716.8871	2	5.2	567	578	No
				ILREEGPSAFWK	K	G	95.00%	33		478.2606	3	5.1	567	578	No
				IVQLLAGVADQTK	K	D	95.00%	99		678.4000	2	1.6	56	68	No
				IVQLLAGVADQTK	K	D	95.00%	53		452.6038	3	4.2	56	68	No
				IYSTLAGTR	K	K	95.00%	28		491.2737	2	2.7	235	243	No
				KDVEVTKEEFAQSAIR	R	Y	95.00%	97		925.4885	2	1.7	244	259	No
				KDVEVTKEEFAQSAIR	R	Y	95.00%	82		617.3301	3	4.7	244	259	No
				KIYSTLAGTR	R	K	95.00%	37		555.3239	2	7.0	234	243	No
				LATATFAGIENK	R	F	95.00%	49		1235.6720	1	6.5	641	652	No
				LATATFAGIENK	R	F	95.00%	100		618.3379	2	3.6	641	652	No
				LLLADENGHVGGLNLLAAGAMAGVPAASLVTPADVIK	K	T	95.00%	48	M21: Oxidation	889.4955	4	9.3	507	543	No
				LQVAGEITTGPR	R	V	95.00%	85		621.3491	2	3.8	454	465	No
				LTLADIER	R	I	95.00%	41		930.5309	1	5.1	284	291	No
				LTLADIER	R	I	95.00%	50		465.7684	2	3.0	284	291	No
				LTVNDFVR	K	D	95.00%	69		482.2680	2	1.8	407	414	No
				NIFLQYASTEVDGER	R	Y	95.00%	107		871.4308	2	8.1	18	32	No
				NIFLQYASTEVDGER	R	Y	95.00%	52		581.2888	3	6.4	18	32	No
				NIFLQYASTEVDGERYMTPEDFVQR	R	Y	95.00%	69	M17: Oxidation	1008.8160	3	8.9	18	42	No
				PIWLQIAESAYR	R	F	95.00%	93		723.8970	2	8.0	318	329	No
				QQSPGLGRPIWLQIAESAYR	R	F	95.00%	33		757.4114	3	6.1	310	329	No
				SGMISGLDFSDIMVTIR	K	S	95.00%	120	M3: Oxidation, M13: Oxidation	937.4627	2	7.2	174	190	No
				SGNGEVTFENVK	K	E	95.00%	55		640.8121	2	3.2	101	112	No
				SPSVAVVQPK	K	A	95.00%	76		506.2976	2	3.5	662	671	No
				VSALNVLR	R	D	95.00%	65		436.2729	2	1.5	466	473	No
				WFYIDFGGLKPAGSEPTPK	R	S	95.00%	39		704.0302	3	4.5	604	622	No
				YEGFFGLYR	R	G	95.00%	53		576.2835	2	5.7	382	390	No
				YLGLYNDPNSNPK	R	I	95.00%	76		747.8697	2	5.9	43	55	No
				YMTPEDFVQR	R	Y	95.00%	34	M2: Oxidation	651.2985	2	4.2	33	42	No
471	IPI00394740	TNNT3	ISOFORM 4 OF TROPONIN T, FAST SKELETAL MUSCLE.	ALSSMGANYSSYLAK	K	A	95.00%	94	M5: Oxidation	789.8830	2	6.9	140	154	Yes
				DLMELQALIDSHFEAR	K	K	95.00%	43	M3: Oxidation	635.3187	3	9.4	61	76	Yes
				IPEGEKVDFDDIQK	K	K	95.00%	83		816.9171	2	8.5	42	55	Yes
				IPEGEKVDFDDIQK	K	K	95.00%	30		544.9458	3	5.7	42	55	Yes
				KKEEEELVALK	R	E	95.00%	35		658.3816	2	6.0	77	87	Yes

				KKEEEELVALK	R	E	95.00%	44		439.2566	3	4.9	77	87	Yes
				KPLNIDHLGEDK	R	L	95.00%	35		689.8743	2	5.3	178	189	Yes
				KPLNIDHLGEDKLR	R	D	95.00%	51		549.9822	3	7.6	178	191	Yes
				KPLNIDHLGEDKLR	R	D	95.00%	40		412.7382	4	6.7	178	191	Yes
				RKPLNIDHLGEDK	R	L	95.00%	43		767.9283	2	9.4	177	189	Yes
				RKPLNIDHLGEDK	R	L	95.00%	41		512.2858	3	4.8	177	189	Yes
				VDFDDIQK	K	K	95.00%	32		490.2428	2	4.0	48	55	No
				YDIMNVR	K	A	95.00%	35	M4: Oxidation	463.7263	2	4.4	220	226	No
472	IPI00394847; IPI00784051	SMTNL2	SMOOTHELIN-LIKE 2.; CDNA FLJ42461 FIS, CLONE BRACE2026836, MODERATELY SIMILAR TO MUSMUSCULUS SMOOTHELIN L1, LARGE ISOFORM.	LPHQPVTAITR	R	V	95.00%	27		411.5769	3	2.8	192	202	No
				NSSFTWSVPSSGYGAVTASK	K	H	95.00%	64		1016.9940	2	9.0	246	265	No
				SQSFGVASASSIK	R	Q	95.00%	47	S3: Phospho	674.8154	2	6.1	342	354	No
				SQSFGVASASSIK	R	Q	95.00%	40		634.8326	2	7.0	342	354	No
				YEAALEGAVR	R	A	95.00%	34		539.7838	2	6.0	20	29	No
473	IPI00395769; IPI00478410	ATP5C1	ISOFORM HEART OF ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR.; ISOFORM LIVER OF ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR.	EVMLVGIGDK	K	I	95.00%	58	M3: Oxidation	538.7900	2	5.4	127	136	No
				HLLIGVSSDR	K	G	95.00%	70		548.8119	2	4.1	91	100	No
				IYGLGSLALYEK	R	A	95.00%	88		663.8752	2	8.7	68	79	No
				SEVATLTAAGK	K	E	95.00%	66		524.2917	2	6.5	116	126	No
				THSDQFLVAFK	R	E	95.00%	80		646.8412	2	8.1	144	154	No
				THSDQFLVAFK	R	E	95.00%	48		431.5630	3	7.1	144	154	No
474	IPI00396171; IPI00745518	MAP4	ISOFORM 1 OF MICROTUBULE-ASSOCIATED PROTEIN 4.; MICROTUBULE-ASSOCIATED PROTEIN 4 ISOFORM 1 VARIANT (FRAGMENT).	DMAQLPETEIAPAK	K	D	95.00%	31	M2: Oxidation	765.3783	2	-2.4	505	518	No
				DMQPSMESDMALVK	K	D	95.00%	73	M2: Oxidation, M6: Oxidation, M10: Oxidation	815.3484	2	4.9	319	332	No
				DMSPLSETEMALGK	K	D	95.00%	34	M2: Oxidation, M10: Oxidation	770.8549	2	9.3	533	546	No
				EIEMASEERPPAQALEIMMGLK	K	T	95.00%	38	M4: Oxidation, M18: Oxidation, M19: Oxidation	841.0787	3	8.5	253	274	No
				LATNTSAPDLK	R	N	95.00%	43		565.8112	2	7.7	951	961	Yes
				NVVLPTETEVAPAK	K	D	95.00%	33		734.4115	2	6.2	361	374	No
				TDYIPLLDVDEK	K	T	95.00%	31		710.8601	2	-6.4	73	84	No
				VALSSETEVALAR	K	D	95.00%	86		673.3754	2	7.6	464	476	No
				VGSLDNVGHLPAGGAVK	K	I	95.00%	68		795.9405	2	7.9	1099	1115	No
475	IPI00396378; IPI00414696	HNRPA2B1	ISOFORM B1 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1.; ISOFORM A2 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1.	GGGGNFGPGPGSNFR	R	G	95.00%	45		689.3212	2	3.3	214	228	No
				GGNFGFGDSR	R	G	95.00%	36		507.2288	2	5.7	204	213	No
				IDTIEIITDR	K	Q	95.00%	78		594.8332	2	9.0	126	135	No
476	IPI00100197; IPI00397571	NSFL1C	ISOFORM 1 OF NSFL1 COFACTOR P47.; ISOFORM 3 OF NSFL1 COFACTOR P47.	ASSSILIDESEPTTNIQIR	K	L	95.00%	112		1037.5450	2	7.9	283	301	No
				ASSSILIDESEPTTNIQIR	K	L	95.00%	40		692.0315	3	5.8	285	303	No
				DLIHDQDEDEEEEEGQR	R	F	95.00%	41		1043.4380	2	9.1	77	93	No
				DLIHDQDEDEEEEEGQR	R	F	95.00%	46		695.9582	3	4.9	77	93	No
				DLIHDQDEDEEEEEGQR	R	S	95.00%	33		695.9609	3	8.7	77	93	No
				EFVAVTGAEEDR	R	A	95.00%	51		661.8194	2	6.1	11	22	No
				LGAAPEEESAYVAGEK	R	R	95.00%	45		810.8952	2	4.2	157	172	No
				LGSTAPQVLSTSSPAQQAENEAK	K	A	95.00%	60		772.0582	3	2.6	262	284	No
				SGFSLDNGELR	K	S	95.00%	49		597.7938	2	3.6	189	199	No
				SPNELVDDLFK	K	G	95.00%	63		638.8312	2	9.4	114	124	No
				SYQDPSNAQFLESIR	R	R	95.00%	106		877.9269	2	6.3	202	216	No
477	IPI00398121; IPI00470891	CSDE1	HYPOTHETICAL PROTEIN DKFZP779B0247.; ISOFORM LONG OF COLD SHOCK DOMAIN-CONTAINING PROTEIN E1.	IKQEILPEER	K	M	95.00%	37		627.8621	2	8.3	136	145	No
				NITLDDASAPR	K	L	95.00%	44		586.8018	2	3.9	774	784	No
478	IPI00398958	LOC387867	SIMILAR TO 40S RIBOSOMAL PROTEIN SA.	FAAATGATPIAGR	K	F	95.00%	28		602.3312	2	4.9	90	102	Yes
				LLVVTDPR	R	A	95.00%	34		456.7806	2	1.7	121	128	No
479	IPI00220402; IPI00410126	PPP1R2; PPP1R2P3	PROTEIN PHOSPHATASE INHIBITOR 2.; PPP1R2P3 PROTEIN.	IQEQESSGEEDSDLSPEER	R	E	95.00%	44		1082.4630	2	0.5	116	134	No
				KLAAAEGLEPK	K	Y	95.00%	53		563.8312	2	6.4	103	113	No
				TSTTSSMVASAEQPR	K	R	95.00%	90	M7: Oxidation	784.8716	2	8.2	19	33	No

480	IPI00410261	MYBPC1	MYOSIN BINDING PROTEIN C, SLOW TYPE ISOFORM 1.	ADAAEYSVMTTGGQSSAK	K	L	95.00%	139	M9: Oxidation	895.4062	2	7.3	433	450	Yes
				ADAAEYSVMTTGGQSSAK	K	L	95.00%	71	M9: Oxidation	597.2717	3	4.5	433	450	Yes
				ADAAEYSVMTTGGQSSAK	K	L	95.00%	123		887.4032	2	1.1	433	450	Yes
				ADAAEYSVMTTGGQSSAK	K	L	95.00%	76		591.9394	3	3.4	433	450	Yes
				AIMEGSGR	K	I	95.00%	50	M3: Oxidation	418.7039	2	7.5	590	597	Yes
				AKDNFAGNYR	K	C	95.00%	58		578.2838	2	4.3	157	166	Yes
				AVNAAGASEPK	K	Y	95.00%	63		507.7670	2	4.1	819	829	Yes
				AVNDLGTVEIECK	K	L	95.00%	96		695.8511	2	4.0	1128	1140	Yes
				DDGNAAITGYTIQK	K	A	95.00%	85		733.8652	2	6.5	964	977	Yes
				DDSGVYHINLK	R	N	95.00%	70		630.8180	2	4.6	617	627	Yes
				DGAEIDKNQINIR	K	N	95.00%	97		743.3899	2	3.8	883	895	Yes
				DGAEIDKNQINIR	K	N	95.00%	69		495.9286	3	2.5	883	895	Yes
				DNFAGNYR	K	C	95.00%	39		956.4313	1	9.2	159	166	Yes
				DNFAGNYR	K	C	95.00%	41		478.7162	2	2.2	159	166	Yes
				DSDWTLVETPPGEEQAK	K	Q	95.00%	86		951.4490	2	6.7	58	74	No
				EAGTTPAKDEEEVSPPSALPPGLGSR	K	A	95.00%	55		864.7709	3	6.8	27	52	No
				EENEVPAPAPPPEEPSKEK	K	E	95.00%	56		1037.5070	2	3.4	8	26	Yes
				EIIEPPK	K	I	95.00%	43		825.4747	1	2.8	839	845	Yes
				EIIEPPKIR	K	I	95.00%	26		547.8343	2	3.0	839	847	Yes
				EPPIMVTK	R	Q	95.00%	47	M5: Oxidation	465.7539	2	3.1	364	371	Yes
				EPPIMVTK	R	Q	95.00%	34		457.7560	2	2.0	364	371	Yes
				EVKQQEEEPQVDVWELLK	R	N	95.00%	33		742.7187	3	4.9	223	240	Yes
				FTITGLPTDAK	K	I	95.00%	27		1163.6410	1	8.1	802	812	Yes
				FTITGLPTDAK	K	I	95.00%	67		582.3214	2	3.0	802	812	Yes
				FVETASIDIQIIDRPGPPQIVK	K	I	95.00%	65		812.7964	3	9.4	925	946	Yes
				FVVELADPK	R	L	95.00%	68		509.2860	2	1.9	297	305	Yes
				FVVELADPKLEVK	R	W	95.00%	71		743.9330	2	3.9	297	309	Yes
				FVVELADPKLEVK	R	W	95.00%	66		496.2915	3	4.4	297	309	Yes
				GKWMDLASK	K	A	95.00%	34	M4: Oxidation	526.2684	2	3.9	122	130	Yes
				HILIIEGATK	K	A	95.00%	54		1094.6640	1	5.8	423	432	Yes
				HILIIEGATK	K	A	95.00%	66		547.8336	2	1.6	423	432	Yes
				IAFQYGITDLR	K	G	95.00%	78		648.8547	2	4.7	250	260	Yes
				IEDVWGENVALTWTPPK	K	D	95.00%	112		978.0048	2	5.1	947	963	Yes
				IEDVWGENVALTWTPPKDDGNAAITGYTIQK	K	A	95.00%	56		1134.9090	3	7.6	947	977	Yes
				IFAVNAIGISK	R	P	95.00%	48		1132.6820	1	8.1	719	729	Yes
				IFAVNAIGISK	R	P	95.00%	112		566.8414	2	1.6	719	729	Yes
				IFAVNAIGISKPSMPSR	R	P	95.00%	56	M14: Oxidation	902.5020	2	9.4	719	735	Yes
				IFAVNAIGISKPSMPSR	R	P	95.00%	75	M14: Oxidation	602.0012	3	4.9	719	735	Yes
				IFAVNAIGISKPSMPSR	R	P	95.00%	41		596.6678	3	2.0	719	735	Yes
				IILDGLDADNTVTVIAGNK	K	L	95.00%	162		971.5355	2	6.8	549	567	Yes
				IILDGLDADNTVTVIAGNK	K	L	95.00%	73		648.0248	3	4.7	549	567	Yes
				ILDPAYQVDK	K	G	95.00%	37		1161.6200	1	3.4	282	291	Yes
				ILDPAYQVDK	K	G	95.00%	87		581.3116	2	-0.4	282	291	Yes
				ILDPAYQVDKGGR	K	V	95.00%	47		716.3871	2	4.6	282	294	Yes
				ILTPLTDQTVNLGK	K	E	95.00%	96		756.9391	2	4.3	460	473	Yes
				ILTPLTDQTVNLGK	K	E	95.00%	47		504.9620	3	4.2	460	473	Yes
				IRTESYPDSSTLVIDIAER	R	D	95.00%	57		722.3801	3	7.1	598	616	Yes
				IRTESYPDSSTLVIDIAERDDSGVYHINLK	R	N	95.00%	78		852.4421	4	9.4	598	627	Yes
				KDGAEIDKNQINIR	K	N	95.00%	107		807.4402	2	7.0	882	895	Yes
				KDGAEIDKNQINIR	K	N	95.00%	57		538.6268	3	2.1	882	895	Yes
				KDGAEIDKNQINIR	K	N	95.00%	33		404.2223	4	2.9	882	895	Yes
				KDSDWTLVETPPGEEQAK	R	Q	95.00%	61	S3: Phospho	1055.4810	2	7.3	57	74	No
				KDSDWTLVETPPGEEQAK	R	Q	95.00%	137		1015.4990	2	8.8	57	74	No
				KDSDWTLVETPPGEEQAK	R	Q	95.00%	47		677.3334	3	6.0	57	74	No
				KEENEVPAPAPPPEEPSK	K	E	95.00%	89		972.9900	2	8.3	7	24	Yes
				KEENEVPAPAPPPEEPSKEK	K	E	95.00%	47		1101.5590	2	7.8	7	26	Yes
				KEENEVPAPAPPPEEPSKEK	K	E	95.00%	57		734.7073	3	5.9	7	26	Yes
				KHILIIEGATK	K	A	95.00%	53		611.8817	2	2.5	422	432	Yes
				KHILIIEGATK	K	A	95.00%	59		408.2568	3	1.8	422	432	Yes
				KMIEGVAYEVR	K	I	95.00%	74	M2: Oxidation	655.8452	2	3.6	708	718	Yes
				KMIEGVAYEVR	K	I	95.00%	42	M2: Oxidation	437.5661	3	3.6	708	718	Yes
				KMIEGVAYEVR	K	I	95.00%	90		647.8469	2	2.3	708	718	Yes
				KMIEGVAYEVR	K	I	95.00%	50		432.2339	3	2.5	708	718	Yes
				LEIPISGEPPPK	R	A	95.00%	64		638.8652	2	5.5	570	581	Yes
				LEIPISGEPPPK	R	A	95.00%	42		426.2447	3	2.3	570	581	Yes
				LRLEIPISGEPPPK	K	A	95.00%	66		773.4575	2	4.1	568	581	Yes

LRLEIPISGEPPPK	K	A	95.00%	64		515.9741	3	3.7	568	581	Yes
LSVDLKPLK	K	I	95.00%	41		1012.6450	1	3.6	451	459	Yes
LSVDLKPLK	K	I	95.00%	64		506.8260	2	3.1	451	459	Yes
LVIANALTEDEGDYVFAPDAYNVTLPAK	K	V	95.00%	49		1003.8520	3	10.0	513	540	Yes
LVIANALTEDEGDYVFAPDAYNVTLPAK	K	V	95.00%	55		753.1393	4	8.0	513	540	Yes
MFSNQGVCTLEIR	R	K	95.00%	43	M1: Oxidation	757.3683	2	9.5	1102	1114	Yes
MIEGVAYEVR	K	I	95.00%	39	M1: Oxidation	1182.5940	1	9.2	709	718	Yes
MIEGVAYEVR	K	I	95.00%	78	M1: Oxidation	591.7964	2	1.7	709	718	Yes
MIEGVAYEVR	K	I	95.00%	71		583.7996	2	2.7	709	718	Yes
NEAGEAHASIK	K	V	95.00%	61		563.7816	2	5.4	628	638	Yes
NGEEIIPGPK	K	S	95.00%	57		1053.5640	1	5.0	402	411	Yes
NGEEIIPGPK	K	S	95.00%	58		527.2845	2	2.8	402	411	Yes
NGLPVQESDR	K	L	95.00%	53		557.7797	2	2.1	492	501	Yes
NGLPVQESDRLK	K	V	95.00%	42		678.3714	2	4.9	492	503	Yes
NSETDTIIFIR	R	K	95.00%	79		654.8476	2	5.6	896	906	Yes
NSETDTIIFIR	R	K	95.00%	35		436.9025	3	9.0	896	906	Yes
PFVPLAVTSPPTLLTVDSVTDTTVTMR	R	W	95.00%	61	M26: Oxidation	958.8519	3	7.9	736	762	Yes
PRPELTWK	K	K	95.00%	32		513.7922	2	2.6	874	881	Yes
PSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMR	K	W	95.00%	97	M3: Oxidation, M32: Oxidation	1182.6250	3	9.8	730	762	Yes
PSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMR	K	W	95.00%	58	M3: Oxidation, M32: Oxidation	887.2193	4	8.5	730	762	Yes
QNANSQLSILFIEKPQGGTVK	K	V	95.00%	92		1136.6270	2	7.4	75	95	Yes
QNANSQLSILFIEKPQGGTVK	K	V	95.00%	77		758.0852	3	4.3	75	95	Yes
QQEEEPQVDVWELLK	K	N	95.00%	90		935.4717	2	6.4	226	240	Yes
QQEEEPQVDVWELLK	K	N	95.00%	57		623.9840	3	6.8	226	240	Yes
RSGEGQEDAGELDFSGLLK	K	R	95.00%	115		1004.4930	2	7.6	202	220	Yes
RSGEGQEDAGELDFSGLLK	K	R	95.00%	80		669.9971	3	6.6	202	220	Yes
RVGEAVNLVIPFQGK	R	P	95.00%	63		813.9752	2	5.6	859	873	Yes
RVGEAVNLVIPFQGK	R	P	95.00%	42		542.9863	3	6.0	859	873	Yes
RVGEAVNLVIPFQGKPR	R	P	95.00%	50		627.3699	3	3.6	859	875	Yes
RVGEAVNLVIPFQGKPR	R	P	95.00%	33		470.7787	4	2.3	859	875	Yes
SGEGQEDAGELDFSGLLK	R	R	95.00%	133		926.4421	2	8.0	203	220	Yes
SGEGQEDAGELDFSGLLK	R	R	95.00%	95		617.9633	3	6.9	203	220	Yes
SGEGQEDAGELDFSGLLKR	R	R	95.00%	81		1004.4940	2	8.9	203	221	Yes
SGEGQEDAGELDFSGLLKR	R	R	95.00%	73		669.9985	3	8.7	203	221	Yes
SHSGKYDLQVK	R	V	95.00%	37		631.3340	2	4.8	911	921	Yes
SMEWFTVIEHYHR	K	T	95.00%	78	M2: Oxidation	875.9104	2	6.9	982	994	Yes
SMEWFTVIEHYHR	K	T	95.00%	50	M2: Oxidation	584.2774	3	9.0	982	994	Yes
SMEWFTVIEHYHR	K	T	95.00%	68		867.9137	2	7.8	982	994	Yes
SMEWFTVIEHYHR	K	T	95.00%	45		578.9436	3	5.3	982	994	Yes
TESYPDSSTLVIDIAER	R	D	95.00%	120		948.4720	2	6.4	600	616	Yes
TESYPDSSTLVIDIAERDDSGVYHINLK	R	N	95.00%	72		1046.5220	3	7.5	600	627	Yes
TESYPDSSTLVIDIAERDDSGVYHINLK	R	N	95.00%	54		785.1423	4	5.8	600	627	Yes
TKFTITGLPTDAK	K	I	95.00%	81		696.8935	2	3.6	800	812	Yes
TKFTITGLPTDAK	K	I	95.00%	41		464.9308	3	1.8	800	812	Yes
TSATITELVIGNEYYFR	R	V	95.00%	111		989.0104	2	8.2	995	1011	Yes
TSATITELVIGNEYYFR	R	V	95.00%	94		659.6745	3	5.6	995	1011	Yes
VAIVDDPR	K	Y	95.00%	55		442.7470	2	2.1	1092	1099	Yes
VDKFVETASIDIQIIDRPGPPQIVK	K	I	95.00%	51		926.8603	3	8.8	922	946	Yes
VDKFVETASIDIQIIDRPGPPQIVK	K	I	95.00%	89		695.3967	4	8.1	922	946	Yes
VGEAVNLVIPFQGK	R	P	95.00%	91		735.9244	2	6.0	860	873	Yes
VGEAVNLVIPFQGK	R	P	95.00%	29		490.9518	3	5.1	860	873	Yes
VGEAVNLVIPFQGKPR	R	P	95.00%	39		862.5040	2	8.2	860	875	Yes
VGEAVNLVIPFQGKPR	R	P	95.00%	50		575.3367	3	5.0	860	875	Yes
VGEAVNLVIPFQGKPRPELTWK	R	K	95.00%	43		826.8074	3	7.7	860	881	Yes
VGEDITFIAK	K	V	95.00%	44		1092.6030	1	7.6	96	105	Yes
VGEDITFIAK	K	V	95.00%	89		546.8023	2	2.2	96	105	Yes
VHVIDPPK	K	I	95.00%	34		452.7675	2	1.6	541	548	Yes
VHVIDPPKIILDGLDADNTVTVIAGNK	K	L	95.00%	67		943.1994	3	9.0	541	567	Yes

				VHVIDPPKIILDGLDADNTVTVIAGNK	K	L	95.00%	44		707.6511	4	8.4	541	567	Yes
				VIYQGVNTPGQPVFLEGQQQSLHNK	K	D	95.00%	60		927.8216	3	6.0	1145	1169	No
				VIYQGVNTPGQPVFLEGQQQSLHNKDF	K	-	95.00%	45		1015.1900	3	8.7	1145	1171	No
				VKAEDLLR	K	K	95.00%	32		943.5627	1	5.2	106	113	Yes
				VKAEDLLR	K	K	95.00%	47		472.2841	2	2.7	106	113	Yes
				VKAVNAAGASEPK	R	Y	95.00%	42		621.3520	2	8.8	817	829	Yes
				VKAVNAAGASEPK	R	Y	95.00%	30		414.5682	3	2.9	817	829	Yes
				VYTFEMQIIK	R	A	95.00%	59	M6: Oxidation	644.3419	2	7.8	147	156	Yes
				VYTFEMQIIK	R	A	95.00%	52		636.3411	2	2.6	147	156	Yes
				WMDLASK	K	A	95.00%	31	M2: Oxidation	866.4106	1	2.6	124	130	Yes
				WMDLASK	K	A	95.00%	35	M2: Oxidation	433.7089	2	2.0	124	130	Yes
				YYSQPILVK	K	E	95.00%	64		555.8160	2	3.7	830	838	Yes
481	IPI00410714	HBA1; HBA2	HEMOGLOBIN SUBUNIT ALPHA.	AAWGK	K	V	95.00%	27		532.2899	1	2.9	13	17	No
				AAWGKVGAHAGEYGAEALER	K	M	95.00%	62		681.6757	3	3.2	13	32	No
				FLASVSTVLTSK	K	Y	95.00%	37		1252.7240	1	6.8	129	140	No
				FLASVSTVLTSK	K	Y	95.00%	98		626.8607	2	-1.5	129	140	No
				FLASVSTVLTSKYR	K	-	95.00%	36		524.6351	3	6.3	129	142	No
				KVADALTNAVAHVDDMPNALSALSDLHAHK	K	L	95.00%	87	M16: Oxidation	1047.5420	3	9.3	62	91	No
				KVADALTNAVAHVDDMPNALSALSDLHAHK	K	L	95.00%	62	M16: Oxidation	785.9086	4	9.9	62	91	No
				KVADALTNAVAHVDDMPNALSALSDLHAHK	K	L	95.00%	38	M16: Oxidation	628.9261	5	6.3	62	91	No
				KVADALTNAVAHVDDMPNALSALSDLHAHK	K	L	95.00%	35	M16: Oxidation	524.2720	6	4.1	62	91	No
				KVADALTNAVAHVDDMPNALSALSDLHAHK	K	L	95.00%	113		1042.2080	3	7.2	62	91	No
				KVADALTNAVAHVDDMPNALSALSDLHAHK	K	L	95.00%	59		781.9079	4	7.4	62	91	No
				KVADALTNAVAHVDDMPNALSALSDLHAHK	K	L	95.00%	47		625.7263	5	4.8	62	91	No
				LRVDPVNFK	K	L	95.00%	48		544.3177	2	1.0	92	100	No
				MFLSFPTTK	R	T	95.00%	42	M1: Oxidation	1087.5540	1	3.9	33	41	No
				MFLSFPTTK	R	T	95.00%	60	M1: Oxidation	544.2760	2	-5.3	33	41	No
				MFLSFPTTK	R	T	95.00%	33		1071.5620	1	6.3	33	41	No
				MFLSFPTTK	R	T	95.00%	68		536.2849	2	6.5	33	41	No
				TYFPHFDLSHGSAQVK	K	G	95.00%	100		917.4568	2	7.3	42	57	No
				TYFPHFDLSHGSAQVK	K	G	95.00%	48		611.9703	3	1.5	42	57	No
				VADALTNAVAHVDDMPNALSALSDLHAHK	K	L	95.00%	88	M15: Oxidation	1004.8420	3	8.8	63	91	No
				VADALTNAVAHVDDMPNALSALSDLHAHK	K	L	95.00%	70	M15: Oxidation	603.3080	5	8.0	63	91	No
				VADALTNAVAHVDDMPNALSALSDLHAHK	K	L	95.00%	84		999.5090	3	7.3	63	91	No
				VADALTNAVAHVDDMPNALSALSDLHAHK	K	L	95.00%	49		600.1067	5	4.2	63	91	No
				VDPVNFK	R	L	95.00%	49		409.7279	2	8.4	94	100	No
				VGAHAGEYGAEALER	K	M	95.00%	109		765.3748	2	4.4	18	32	No
				VGAHAGEYGAEALER	K	M	95.00%	67		510.5855	3	3.8	18	32	No
				VLSPADK	M	T	95.00%	40		729.4198	1	6.9	2	8	No
				VLSPADKTNVK	M	A	95.00%	71		586.3411	2	4.8	2	12	No
482	IPI00411375; IPI00743873	MAP4	MICROTUBULE-ASSOCIATED PROTEIN 4 ISOFORM 2.; 76 KDA PROTEIN.	ITELESVSLPTPEIQSDFLHSK	K	V	95.00%	66		824.1011	3	6.4	286	307	No
				KVDLTLLSPK	K	S	95.00%	48		557.3520	2	6.9	262	271	No
				LATNTSAPDLK	R	N	95.00%	43		565.8112	2	7.7	658	668	Yes
				NEAGIDEGHVIGESESVHSGASK	K	H	95.00%	37		770.3661	3	7.9	146	168	No
				TTTLSGTAPAAGVVPSR	K	V	95.00%	55		793.4338	2	3.0	607	623	No
				VGSLDNVGHLPAGGAVK	K	T	95.00%	68		795.9405	2	7.9	806	822	No
483	IPI00024989; IPI00411680; IPI00828189	PCMT1	PROTEIN-L-ISOASPARTATE (D-ASPARTATE) O-METHYLTRANSFERASE.; ISOFORM 1 OF PROTEIN-L-ISOASPARTATE(D-ASPARTATE) O-METHYLTRANSFERASE.; ISOFORM 2 OF PROTEIN-L-ISOASPARTATE(D-ASPARTATE) O-METHYLTRANSFERASE.	ELVDDSINNVR	K	K	95.00%	63		637.3289	2	8.6	114	124	No
				KDDPTLLSSGR	R	V	95.00%	59		594.8190	2	6.4	125	135	No

				MGYAEEAPYDAIHVGAAAPVVPQALIDQLKPGGR	R	L	95.00%	31		876.9614	4	7.7	145	178	No
				MKPLMGVIYVPLTDKEK	K	Q	95.00%	33	M1: Oxidation, M5: Oxidation	665.3685	3	9.4	205	221	No
				SGGASHSELIHNLR	K	K	95.00%	66		739.3831	2	5.0	5	18	No
				SGGASHSELIHNLR	K	K	95.00%	61		493.2582	3	5.3	5	18	No
				SGGASHSELIHNLRK	K	N	95.00%	56		803.4333	2	7.9	5	19	No
				SGGASHSELIHNLRK	K	N	95.00%	42		535.9579	3	7.5	5	19	No
				TDKVFEVMLATDR	K	S	95.00%	63	M8: Oxidation	770.8946	2	8.5	25	37	No
				TDKVFEVMLATDR	K	S	95.00%	49	M8: Oxidation	514.2653	3	7.7	25	37	No
				VFEVMLATDR	K	S	95.00%	55	M5: Oxidation	598.8068	2	6.0	28	37	No
				VQLVVGDGR	R	M	95.00%	31		471.7743	2	3.7	136	144	No
484	IPI00412713	SAMM50	SORTING AND ASSEMBLY MACHINERY COMPONENT 50 HOMOLOG.	DVVVQHVHFDGLGR	K	T	95.00%	44		526.6139	3	4.6	44	57	No
				ETSYGLSFFKPR	K	P	95.00%	67		716.3710	2	4.9	169	180	No
				ETSYGLSFFKPR	K	P	95.00%	37		477.9171	3	5.9	169	180	No
				GMSAEYSFPIWK	R	T	95.00%	61	M2: Oxidation	716.3383	2	4.8	210	221	No
				LTGSYNTMVGNNEGSMVLGLK	R	L	95.00%	39	M8: Oxidation, M16: Oxidation	1109.0410	2	9.3	128	148	No
				QEILENKDVVVQHVHFDGLGR	K	T	95.00%	33		811.4330	3	6.1	37	57	No
				QEILENKDVVVQHVHFDGLGR	K	T	95.00%	34		608.8264	4	5.6	37	57	No
				SSLSHAMVIDSR	K	N	95.00%	58	M7: Oxidation	659.8290	2	5.7	256	267	No
				SSLSHAMVIDSR	K	N	95.00%	51	M7: Oxidation	440.2205	3	2.6	256	267	No
				VNQELAGYTGGDVSFIK	K	E	95.00%	43		899.4593	2	4.7	281	297	No
				VNQELAGYTGGDVSFIKEDFELQLNK	K	Q	95.00%	52		972.1639	3	9.9	281	306	No
				VTFQFSYGTK	K	E	95.00%	64		589.3010	2	4.1	159	168	No
				VTGQFPWSSLR	K	E	95.00%	65		639.3387	2	4.3	195	205	No
485	IPI00413318; IPI00473047	PRKAG1	5'-AMP-ACTIVATED PROTEIN KINASE SUBUNIT GAMMA-1.; CDNA FLJ40287 FIS, CLONE TESTI2027909, HIGHLY SIMILAR TO 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT.	FDVINLAAEK	K	T	95.00%	34		560.3093	2	5.1	253	262	No
				GIVSLSDILQALVLTGGEK	K	K	95.00%	61		638.3758	3	8.2	320	338	No
				LPVIDPESGNTLYILTHK	R	R	95.00%	61		670.7078	3	8.0	162	179	No
				LVVFDTSLQVK	K	K	95.00%	61		624.8703	2	9.9	48	58	No
				LVVVDENDVVK	R	G	95.00%	55		614.8461	2	4.5	309	319	No
				TYNNLDVSVTK	K	A	95.00%	53		627.3268	2	6.4	254	264	No
486	IPI00413344; IPI00796024	CFL2	COFILIN-2.; PROTEIN.	FTGIKHEWQVNGLDDIKDR	K	S	95.00%	30		568.5488	4	8.6	128	146	No
				HEWQVNGLDDIK	K	D	95.00%	32		727.3644	2	9.2	133	144	No
				HEWQVNGLDDIKDR	K	S	95.00%	89		862.9274	2	6.5	133	146	No
				HEWQVNGLDDIKDR	K	S	95.00%	82		575.6193	3	3.8	133	146	No
				KEDLVFIFWAPESAPLK	K	S	95.00%	74		995.5481	2	9.5	96	112	No
				KEDLVFIFWAPESAPLK	K	S	95.00%	40		664.0337	3	8.0	96	112	No
				LGGNVVVSLEGKPL	K	-	95.00%	103		691.4113	2	6.5	153	166	No
				LGGNVVVSLEGKPL	K	-	95.00%	46		461.2773	3	7.6	153	166	No
				QIIVEEAK	R	Q	95.00%	33		929.5379	1	7.6	46	53	No
				QIIVEEAK	R	Q	95.00%	40		465.2716	2	4.9	46	53	No
				QILVGDIGDTVEDPYTSFVK	K	L	95.00%	47		732.7123	3	6.1	70	89	No
				YALYDATYETK	R	E	95.00%	75		669.3209	2	5.4	82	92	No
487	IPI00413641	AKR1B1	ALDOSE REDUCTASE.	AIGISNFNHLQVEMILNKPGLK	K	Y	95.00%	30	M14: Oxidation	818.1245	3	7.9	156	177	No
				EELFIVSK	R	L	95.00%	36		482.7726	2	1.8	71	78	No
				EQVVKREELFIVSK	R	L	95.00%	36		852.4936	2	5.7	65	78	No
				GIVVTAYSPLGSPDRPWAKPEDPSLLEDPR	K	I	95.00%	31		1088.2410	3	9.7	204	233	No
				HNKTTAQVLIR	K	F	95.00%	47		427.5877	3	2.7	241	251	No
				LDYLDLYLIHWPTGFKPGK	K	E	95.00%	58		759.4139	3	6.1	102	120	No
				MPILGLGTWK	K	S	95.00%	47	M1: Oxidation	566.3204	2	8.1	13	22	No
				NLVVIPK	R	S	95.00%	37		782.5187	1	5.9	257	263	No
				REELFIVSK	K	L	95.00%	60		560.8240	2	3.1	70	78	No
				SPPGQVTEAVK	K	V	95.00%	74		556.8044	2	4.9	23	33	No
				TLSDLKLDYLDLYLIHWPTGFKPGK	K	E	95.00%	52		734.1580	4	9.2	96	120	No
				TLSDLKLDYLDLYLIHWPTGFKPGK	K	E	95.00%	27		587.5271	5	7.7	96	120	No
				TTAQVLIR	K	F	95.00%	53		451.2803	2	6.3	244	251	No
				VAIDVGYR	K	H	95.00%	34		892.4980	1	9.8	34	41	No
				VAIDVGYR	K	H	95.00%	50		446.7506	2	4.6	34	41	No
488	IPI00414320	ANXA11	ANNEXIN A11.	AHLVAVFNEYQR	R	M	95.00%	79		723.8826	2	5.5	389	400	No
				AHLVAVFNEYQR	R	M	95.00%	41		482.9228	3	2.4	389	400	No

				DAQELYAAGENR	R	L	95.00%	58		668.8128	2	3.4	360	371	No
				DESTNVDMSLAQR	R	D	95.00%	52	M8: Oxidation	741.3364	2	7.2	347	359	No
				EMSGDLEEGMLAVVK	R	C	95.00%	98	M2: Oxidation, M10: Oxidation	820.3881	2	7.5	413	427	No
				GTITDAPGFDPLR	R	D	95.00%	43		680.3517	2	3.3	192	204	No
				GTITDAPGFDPLRDAEVLR	R	K	95.00%	31		1022.0350	2	5.1	192	210	No
				GTITDAPGFDPLRDAEVLR	R	K	95.00%	32		681.6938	3	7.1	192	210	No
				LLISLSQGNRDESTNVDMSLAQR	R	D	95.00%	59	M18: Oxidation	855.1047	3	7.7	337	359	No
				SETDLLDIR	R	S	95.00%	56		531.2792	2	2.3	462	470	No
				SLYHDISGDTSGDYRK	K	I	95.00%	42		605.2848	3	1.7	480	495	No
				TPVLFDIYEIK	K	E	95.00%	62		669.3765	2	7.0	272	282	No
489	IPI00418169; IPI00455315	ANXA2	ANNEXIN A2 ISOFORM 1.; ANNEXIN A2.	AEDGSVIDYELIDQDAR	R	D	95.00%	90		954.9540	2	9.0	198	214	No
				AYTNFDAER	K	D	95.00%	40		543.7498	2	5.7	47	55	No
				AYTNFDAERDALNIETAIK	K	T	95.00%	48		719.0334	3	8.2	47	65	No
				DALNIETAIK	R	T	95.00%	62		544.3067	2	5.1	56	65	No
				DLYDAGVK	R	R	95.00%	43		880.4463	1	5.3	215	222	No
				GVDEVTIVNILTNR	K	S	95.00%	93		771.9352	2	8.6	68	81	No
				GVDEVTIVNILTNR	K	S	95.00%	72		514.9583	3	6.4	68	81	No
				LSLEGDHSTPPSAYGSVK	K	A	95.00%	89		922.9631	2	8.2	29	46	No
				QDIAFAYQR	R	R	95.00%	59		556.2846	2	6.9	87	95	No
				RAEDGSVIDYELIDQDAR	R	D	95.00%	34		689.0052	3	7.7	197	214	No
				SALSGHLETVILGLLK	K	T	95.00%	116		826.0004	2	8.1	107	122	No
				SALSGHLETVILGLLK	K	T	95.00%	72		551.0028	3	7.8	107	122	No
				SLYYYIQQDTK	K	G	95.00%	62		711.3544	2	4.0	332	342	No
				SLYYYIQQDTKGDYQK	K	A	95.00%	49		671.6643	3	8.2	332	347	No
				SYSPYDMLESIR	K	K	95.00%	41	M7: Oxidation	738.8450	2	9.6	252	263	No
				SYSPYDMLESIRK	K	E	95.00%	58	M7: Oxidation	802.8917	2	7.8	252	264	No
				TDLEKDIISDTSGDFRK	K	L	95.00%	87		647.3305	3	7.4	171	187	No
				TKGVDEVTIVNILTNR	K	S	95.00%	79		886.5068	2	7.8	66	81	No
				TKGVDEVTIVNILTNR	K	S	95.00%	34		591.3415	3	9.5	66	81	No
				TNQELQEINR	R	V	95.00%	69		622.8201	2	7.1	154	163	No
				TPAQYDASELK	K	A	95.00%	50		611.8047	2	4.8	123	133	No
490	IPI00418217; IPI00797844	ANKRD2	ISOFORM 1 OF ANKYRIN REPEAT DOMAIN-CONTAINING PROTEIN 2.; ANKYRIN REPEAT DOMAIN 2.	ASLEGHMEILEK	R	L	95.00%	72	M7: Oxidation	686.8435	2	0.6	161	172	No
				DALAASHEPPPEPEEITGPVDEETFLK	R	A	95.00%	91		973.4774	3	7.4	101	127	No
				DKLLSTPLHVAVR	R	T	95.00%	59		483.6262	3	2.9	217	229	No
				DREGDTALHDAVR	R	L	95.00%	37		727.8603	2	9.5	250	262	No
				DREGDTALHDAVR	R	L	95.00%	46		485.5743	3	5.8	250	262	No
				EIIDVGGIQNLIELR	R	K	95.00%	132		841.4846	2	7.3	78	92	No
				LLDNGATVDFQDR	K	L	95.00%	102		732.3643	2	5.1	173	185	No
				LLLLHGADMMTK	K	N	95.00%	52	M9: Oxidation, M10: Oxidation	687.8617	2	2.0	271	282	No
				LLQSHGADTNVR	K	D	95.00%	63		655.8513	2	10.0	232	243	No
				LLQSHGADTNVR	K	D	95.00%	44		437.5674	3	3.8	232	243	No
				LLSTPLHVAVR	K	T	95.00%	86		603.3743	2	3.1	219	229	No
				LLSTPLHVAVR	K	T	95.00%	35		402.5850	3	1.8	219	229	No
				QKLPMDLLVLEDEKHHGAQSAALQK	R	V	95.00%	37	M5: Oxidation	939.1713	3	7.3	37	61	No
				QKLPMDLLVLEDEKHHGAQSAALQK	R	V	95.00%	28	M5: Oxidation	704.6288	4	5.0	37	61	No
				TGQVEIVEHFLSLGLEINAR	R	D	95.00%	60		742.4081	3	7.1	230	249	No
				TPTDLVQLWQADTR	K	H	95.00%	108		822.4286	2	5.9	288	301	No
491	IPI00418471; IPI00827679	VIM	VIMENTIN.; 50 KDA PROTEIN.	DGQVINETSQHHDDLE	R	-	95.00%	42		918.9066	2	2.9	451	466	No
				EEAENTLQSFR	R	Q	95.00%	69		662.3158	2	4.3	197	207	No
				EMEENFAVEAANYQDTIGR	R	L	95.00%	132	M2: Oxidation	1101.9940	2	8.6	346	364	No
				EMEENFAVEAANYQDTIGR	R	L	95.00%	44	M2: Oxidation	734.9961	3	5.1	346	364	No
				ETNLDSLPLVDTHSK	R	R	95.00%	67		834.9296	2	4.1	425	439	No
				EYQDLLNVK	R	M	95.00%	49		1121.5950	1	9.6	382	390	Yes
				EYQDLLNVK	R	M	95.00%	65		561.2985	2	4.1	382	390	Yes
				ILLAELEQLK	K	G	95.00%	79		585.3639	2	4.5	130	139	No
				ILLAELEQLKGQGK	K	S	95.00%	88		770.4626	2	4.0	130	143	No
				ILLAELEQLKGQGK	K	S	95.00%	24		513.9778	3	4.3	130	143	No
				ISLPLPNFSSLNLR	R	E	95.00%	51		785.9565	2	6.0	411	424	No
				KVESLQEEIAFLK	R	K	95.00%	75		767.4371	2	8.8	223	235	No
				KVESLQEEIAFLK	R	K	95.00%	63		511.9593	3	6.1	223	235	No
				KVESLQEEIAFLKK	R	L	95.00%	46		554.6570	3	4.6	223	236	No
				LGDLYEEEMR	R	E	95.00%	37	M9: Oxidation	635.7874	2	3.4	146	155	No

				LQDEIQNMKEEMAR	R	H	95.00%	43	M8: Oxidation, M12: Oxidation	883.9133	2	7.5	365	378	No
				LQEEMLQREEAENTLQSFR	K	Q	95.00%	43	M5: Oxidation	789.7176	3	5.2	189	207	No
				MALDIEIATYR	K	K	95.00%	58	M1: Oxidation	656.3386	2	5.7	391	401	No
				MFGGPGTASRPSSSR	R	S	95.00%	38	M1: Oxidation	504.2428	3	3.6	14	28	No
				NLQEAEEWYK	K	S	95.00%	46		655.3090	2	2.8	283	292	No
				SLYASSPGGVYATR	R	S	95.00%	93		714.8626	2	3.6	51	64	No
				TNEKVELQELNDR	R	F	95.00%	84		794.4053	2	3.0	101	113	Yes
				TNEKVELQELNDR	R	F	95.00%	50		529.9399	3	3.9	101	113	Yes
				TYSLGSALRPSTSR	R	S	95.00%	36		748.3995	2	2.8	37	50	No
				VELQELNDR	K	F	95.00%	43		558.2911	2	4.2	105	113	Yes
				VEVERDNLAEDIMR	R	L	95.00%	34	M13: Oxidation	852.9219	2	7.8	171	184	No
				VEVERDNLAEDIMR	R	L	95.00%	54	M13: Oxidation	568.9468	3	1.1	171	184	No
492	IPI00419273; IPI00549919	CUL4A	ISOFORM 1 OF CULLIN-4A.; ISOFORM 2 OF CULLIN-4A.	ETVEEQVSTTER	K	V	95.00%	30		704.3410	2	9.8	576	587	No
				RPNKPAELIAK	K	H	95.00%	28		412.9213	3	4.1	301	311	No
493	IPI00419307; IPI00554737	PPP2R1A	ALPHA ISOFORM OF REGULATORY SUBUNIT A, PROTEIN PHOSPHATASE 2.; SERINE/THREONINE-PROTEIN PHOSPHATASE 2A 65 KDA REGULATORY SUBUNIT AALPHA ISOFORM.	AISHEHSPSDLEAHFVPLVK	R	R	95.00%	51		738.3858	3	2.9	114	133	No
				AISHEHSPSDLEAHFVPLVK	R	R	95.00%	46		554.0421	4	4.3	114	133	No
				DNTIEHLLPLFLAQLK	K	D	95.00%	44		622.3594	3	4.6	359	374	No
				IGPILDNSTLQSEVKPILEK	K	L	95.00%	105		1097.6290	2	7.3	547	566	No
				IGPILDNSTLQSEVKPILEK	K	L	95.00%	46		732.0881	3	6.7	547	566	No
				KLSTIALALGVER	K	T	95.00%	77		685.9261	2	5.2	34	46	No
				LAGGDWFTSR	R	T	95.00%	32		555.2761	2	5.7	135	144	No
				LSTIALALGVER	K	T	95.00%	79		621.8789	2	6.2	35	46	No
				MAGDPVANVR	R	F	95.00%	63	M1: Oxidation	523.2618	2	5.5	528	537	No
				QLSQSLLPAIVELAEDAK	R	W	95.00%	83		963.0417	2	8.3	399	416	No
				QLSQSLLPAIVELAEDAK	R	W	95.00%	79		642.3641	3	8.8	399	416	No
				SALASVIMGLSPILGK	K	D	95.00%	73	M8: Oxidation	786.9602	2	5.7	343	358	No
				SALASVIMGLSPILGK	K	D	95.00%	69	M8: Oxidation	524.9755	3	4.5	343	358	No
				SEIIPMFSNLASDEQDSVR	K	L	95.00%	104	M6: Oxidation	1077.5150	2	9.0	203	221	No
				SEIIPMFSNLASDEQDSVR	K	L	95.00%	34	M6: Oxidation	718.6797	3	9.9	203	221	No
				VLAMSGDPNYLHR	K	M	95.00%	58	M4: Oxidation	744.8686	2	1.7	486	498	No
				YMVADKFTELQK	R	A	95.00%	61	M2: Oxidation	744.8783	2	5.2	261	272	No
				YMVADKFTELQK	R	A	95.00%	38	M2: Oxidation	496.9206	3	3.5	261	272	No
494	IPI00419424; IPI00430808; IPI00430820; IPI00430847; IPI00440577; IPI00472961; IPI00478600; IPI00550731; IPI00554675; IPI00746963; IPI00761125; IPI00784070; IPI00784661; IPI00784773; IPI00784865; IPI00784985; IPI00807459; IPI00816118; IPI00827488	IGKC; IGKV1-5	IGKV1-5 PROTEIN.; IGKC PROTEIN.; IGKV1-5 PROTEIN.; IGKC PROTEIN.; IGKV2-24 PROTEIN.; IGKC PROTEIN.; IGKV1-5 PROTEIN.; HYPOTHETICAL PROTEIN.; ANTI-RHD MONOCLONAL T125 KAPPA LIGHT CHAIN PRECURSOR.; IGKC PROTEIN.; IGKC PROTEIN.; IGKC PROTEIN.; HYPOTHETICAL PROTEIN.; HYPOTHETICAL PROTEIN.; HYPOTHETICAL PROTEIN.; HYPOTHETICAL PROTEIN.; HYPOTHETICAL PROTEIN.; IGKC PROTEIN.; IGKC PROTEIN.	DSTYSLSSTLTLSK	K	A	95.00%	66		751.8904	2	9.3	196	209	No
				FSGSGSGTDFTLK	R	I	95.00%	40		652.3171	2	7.1	87	99	No
				TVAAPSVFIFPPSDEQLK	R	S	95.00%	68		973.5273	2	9.8	135	152	No
				TVAAPSVFIFPPSDEQLK	R	S	95.00%	47		649.3537	3	9.0	135	152	No
				VDNALQSGNSQESVTEQDSK	K	D	95.00%	139		1068.4920	2	3.3	176	195	No
				VDNALQSGNSQESVTEQDSK	K	D	95.00%	66		712.6664	3	6.7	176	195	No
495	IPI00419585	LOC653214; LOC654188; PPIA	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A.	EGMNIVEAMER	K	F	95.00%	33	M3: Oxidation, M9: Oxidation	655.7945	2	6.9	134	144	No
				FEDENFILK	K	H	95.00%	56		577.7955	2	8.2	83	91	No
				SIYGEKFEDENFILK	K	H	95.00%	99		916.4647	2	5.3	77	91	No
				TEWLDGK	K	H	95.00%	36		424.7141	2	5.5	119	125	No
				VKEGMNIVEAMER	K	F	95.00%	53	M5: Oxidation, M11: Oxidation	769.3780	2	8.3	132	144	No
				VNPTVFFDIAVDGEPLGR	M	V	95.00%	110		973.5143	2	9.3	2	19	No
				VSFELFADK	R	V	95.00%	54		528.2795	2	9.1	20	28	No
				VSFELFADKVPK	R	T	95.00%	70		690.3884	2	8.1	20	31	No
				VSFELFADKVPK	R	T	95.00%	45		460.5943	3	7.0	20	31	No
496	IPI00420049; IPI00739670	C1orf170	SIMILAR TO ZK84.1.; SIMILAR TO ZK84.1.	AGQEELGPGPAGAPEPGPR	K	S	95.00%	46		893.9478	2	8.3	129	147	No
				GGGHTGASASAQTGSPLLPAASPETAK	K	L	95.00%	50		807.7407	3	2.0	98	124	No
				MTESSGLVSTPVPR	R	A	95.00%	60	M1: Oxidation	738.8742	2	2.5	344	357	No

				SASEGAGPGTPLKPAVVER	R	L	95.00%	40		608.3296	3	3.9	596	614	No
				SASQGAGPGTPLKPAVVER	R	L	95.00%	33		608.0011	3	2.9	596	614	No
				SPVQEDRPGPGLGLSTPVPVTEQGTDQIR	R	T	95.00%	82		1010.8640	3	8.2	148	176	No
				TALLANVGTISAIR	K	Y	95.00%	90		700.4221	2	6.4	664	677	No
497	IPI00420108	DLST	DIHYDROLIPOYLLYSINE-RESIDUE SUCCINYLTRANSFERASE COMPONENT OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX, MITOCHONDRIAL PRECURSOR.	AKPAEAPAAAAPK	K	A	95.00%	32		596.8439	2	9.1	153	165	No
				ASAFALQEQPVVNAVIDDTTK	K	E	95.00%	163		1109.0820	2	6.8	287	307	No
				ASAFALQEQPVVNAVIDDTTK	K	E	95.00%	81		739.7230	3	5.9	287	307	No
				ASAFALQEQPVVNAVIDDTTKEVVYR	K	D	95.00%	72		955.1753	3	9.2	287	312	No
				EAVTFLR	R	K	95.00%	36		418.2390	2	2.8	431	437	No
				GLVVPVIR	R	N	95.00%	55		426.7892	2	3.9	326	333	No
				LGFMSAFVK	K	A	95.00%	55	M4: Oxidation	508.2704	2	4.0	278	286	No
				NVEAMNFADIER	R	T	95.00%	105	M5: Oxidation	712.8309	2	4.3	334	345	No
				TPAFAESVTEGDVR	K	W	95.00%	124		739.8636	2	4.5	75	88	No
				TPAFAESVTEGDVRWEK	K	A	95.00%	72		961.4774	2	9.0	75	91	No
				VEGGTPLFTLR	K	K	95.00%	80		595.3353	2	3.8	134	144	No
				VEVRPMMYVALTYDHR	K	L	95.00%	51	M6: Oxidation, M7: Oxidation	671.3323	3	3.9	410	425	No
				VLLLDL	R	-	95.00%	30		685.4566	1	9.4	448	453	No
498	IPI00427330	SBDS	SHWACHMAN-BODIAN-DIAMOND SYNDROME PROTEIN.	DVEEGDEKFE	K	-	95.00%	29		598.7536	2	2.8	241	250	No
				GSLEVLNLK	K	D	95.00%	37		486.7938	2	7.0	232	240	No
				RPYTVILIER	K	A	95.00%	35		420.5898	3	4.8	126	135	No
499	IPI00434580; IPI00479390	MYOM1	MYOMESIN 1.; MYOM1 PROTEIN.	AASAYDYGSSHGLTDSSLLLDDYSSK	K	L	95.00%	56		908.4221	3	6.6	86	111	No
				AINQAGVGKPSDLAGPVVAETR	R	P	95.00%	40		717.3955	3	6.4	1117	1138	No
				AINQAGVGKPSDLAGPVVAETRPGTK	R	E	95.00%	78		845.1361	3	7.3	1117	1142	No
				AINQAGVGKPSDLAGPVVAETRPGTK	R	E	95.00%	39		634.1028	4	5.4	1021	1046	No
				ASASSSQQQASQHALSSEVSR	R	K	95.00%	88		716.0110	3	2.5	64	84	No
				ATLTFSHLNKEDEGLYTIR	R	V	95.00%	50		736.7211	3	8.0	465	483	No
				ATLTFSHLNKEDEGLYTIR	R	V	95.00%	31		552.7913	4	5.3	465	483	No
				ATNHSTVVLVGDVFK	K	K	95.00%	78		793.9356	2	5.7	1325	1339	No
				ATNHSTVVLVGDVFKK	K	L	95.00%	50		572.3251	3	6.1	1325	1340	No
				ATNHSTVVLVGDVFKK	K	L	95.00%	35		429.4947	4	3.5	1325	1340	No
				AVNAAGLSEYSQDSEAIEVK	R	A	95.00%	127		1041.0110	2	4.5	813	832	No
				DADAEIEGAPAAPLDVK	R	C	95.00%	110		841.4256	2	8.7	501	517	No
				DAGIYEVILK	K	D	95.00%	29		560.8220	2	9.4	1422	1431	No
				DAGIYEVILKDDR	K	G	95.00%	64		753.9015	2	9.6	1422	1434	No
				DSLVLQWKPPVHSGR	K	T	95.00%	46		573.6482	3	-3.2	1053	1067	No
				DSMVLGWK	R	Q	95.00%	46	M3: Oxidation	476.2374	2	6.2	948	955	No
				DYVSTEDSPR	K	L	95.00%	57		584.7632	2	5.3	1174	1183	No
				EGVSYVFR	K	V	95.00%	36		478.7477	2	3.7	1107	1114	No
				ENLPSDYMVPIFSGR	K	Q	95.00%	58	M8: Oxidation	870.9245	2	8.3	130	144	No
				FALFDLAEGK	R	S	95.00%	55		555.8002	2	8.0	697	706	No
				FHAGASTMPLSFGVTPYGYASR	R	F	95.00%	67	M8: Oxidation	778.3798	3	9.2	381	402	No
				FPVTGLIEGR	R	S	95.00%	61		544.8122	2	5.5	569	578	No
				HFQPEIQWYR	K	N	95.00%	43		702.3506	2	5.2	436	445	No
				HFQPEIQWYR	K	N	95.00%	39		468.5696	3	5.0	436	445	No
				HVSGITDTEEER	K	I	95.00%	45		686.8254	2	6.1	147	158	No
				IALSATDLK	K	I	95.00%	47		466.2786	2	3.1	1363	1371	No
				IGGAEITGYYVNYR	K	E	95.00%	97		788.3986	2	5.5	864	877	No
				IKEAAAYIAQR	R	N	95.00%	60		617.3537	2	3.2	159	169	No
				IQSTAEGIQLYSFVTYYVEDLK	K	V	95.00%	95		856.4424	3	7.5	1468	1489	No
				KAASAYDYGSSHGLTDSSLLLDDYSSK	R	L	95.00%	79		951.1208	3	6.7	85	111	No
				KDSLVLQWKPPVHSGR	R	T	95.00%	35		462.5128	4	-0.9	1052	1067	No
				LLALSHEHKFPTVPVK	R	S	95.00%	35		908.5330	2	5.2	1232	1247	No
				LLALSHEHKFPTVPVK	R	S	95.00%	41		606.0255	3	6.7	1232	1247	No
				LNEDHLLHAPEFIIKPR	K	S	95.00%	64		681.3805	3	3.3	268	284	No
				LNEDHLLHAPEFIIKPR	K	S	95.00%	36		511.2895	4	7.7	268	284	No
				LQDEDEGTYTFQLQDGK	K	A	95.00%	135		993.9574	2	6.8	1308	1324	No

				MAALESLK	R	G	95.00%	31	M1: Oxidation	439.7385	2	3.8	1672	1679	No
				NLLASEEGITTPK	R	Q	95.00%	82		686.8741	2	5.7	170	182	No
				NLLASEEGITTSK	R	Q	95.00%	96		681.8627	2	4.2	170	182	No
				NQVPINVHANPGK	K	Y	95.00%	50		694.3802	2	5.7	313	325	No
				NTDTSVVVSWEESK	R	D	95.00%	66		790.8797	2	4.5	750	763	No
				NTGIIEMFMEK	R	L	95.00%	44	M7: Oxidation, M9: Oxidation	672.8164	2	5.2	1297	1307	No
				QATSALQQEETSEK	K	K	95.00%	106		775.3740	2	3.5	225	238	No
				QATSALQQEETSEKK	K	S	95.00%	76		839.4243	2	6.5	225	239	No
				QPAVDGGSPILGYFIDK	K	C	95.00%	61		888.9672	2	5.2	532	548	No
				RASASSSQQQASQHALSSEVSR	R	K	95.00%	36	S3: Phospho	794.7039	3	7.1	63	84	No
				SAVYTQGSTAYSSR	R	S	95.00%	88		739.3531	2	4.4	36	49	No
				SELAVEILEK	K	G	95.00%	78		565.8217	2	4.1	1152	1161	No
				SYVVLSWKPPGQR	R	G	95.00%	43		506.2845	3	6.7	652	664	No
				TAYFTINGVSTADSGK	R	Y	95.00%	94		816.4071	2	9.0	1628	1643	No
				TGVTGEQIWLQINEPTPNDKGK	K	Y	95.00%	32		809.0884	3	5.4	1507	1528	No
				TLEETETYHAK	K	L	95.00%	36		661.3206	2	4.2	257	267	No
				TPVTGYFVDLK	R	E	95.00%	80		620.3409	2	9.2	1068	1078	No
				VLGGLPDVVTIQEGK	R	A	95.00%	84		762.9396	2	4.8	1574	1588	No
				VNTELPVK	R	S	95.00%	30		450.2653	2	2.9	686	693	No
				VNYIFNEK	K	E	95.00%	34		513.7688	2	3.7	1179	1186	No
				VSEPVAALDPAEK	R	A	95.00%	81		663.3557	2	6.3	598	610	No
				VVITPEIK	R	H	95.00%	27		898.5642	1	3.1	428	435	No
				VVITPEIK	R	H	95.00%	32		449.7855	2	1.8	428	435	No
				WVQTLWSGER	K	A	95.00%	32		631.3206	2	0.3	455	464	No
				YVMELFDGK	K	T	95.00%	55	M3: Oxidation	559.2689	2	5.4	1529	1537	No
500	IPI00440493	ATP5A1	ATP SYNTHASE SUBUNIT ALPHA, MITOCHONDRIAL PRECURSOR.	APGIIPR	K	I	95.00%	27		723.4533	1	2.0	176	182	No
				AVDSLVPIGR	K	G	95.00%	54		1026.6020	1	6.5	195	204	No
				AVDSLVPIGR	K	G	95.00%	82		513.8012	2	-0.4	195	204	No
				EAYPGDVFYLHSR	R	L	95.00%	90		777.3746	2	1.7	335	347	No
				EAYPGDVFYLHSR	R	L	95.00%	49		518.5857	3	1.8	335	347	No
				EIVTNFLAGFEA	K	-	95.00%	97		655.8392	2	5.6	542	553	No
				ELIIGDR	R	Q	95.00%	35		815.4664	1	4.4	208	214	No
				ELIIGDR	R	Q	95.00%	37		408.2357	2	1.0	208	214	No
				EPMQTGIK	R	A	95.00%	44	M3: Oxidation	460.2358	2	8.4	187	194	No
				EVAAFAQFGSDLDAATQQLLSR	R	G	95.00%	160		1169.5990	2	9.7	442	463	No
				EVAAFAQFGSDLDAATQQLLSR	R	G	95.00%	100		780.0657	3	5.8	442	463	No
				FENAFLSHVVSQHQALLGTIR	K	A	95.00%	127		1184.1430	2	8.7	507	527	No
				FENAFLSHVVSQHQALLGTIR	K	A	95.00%	81		789.7629	3	6.8	507	527	No
				FENAFLSHVVSQHQALLGTIR	K	A	95.00%	53		592.5723	4	3.7	507	527	No
				FNDGSDEK	R	K	95.00%	31		456.1934	2	4.8	232	239	No
				GIRPAINVGLSVSR	K	V	95.00%	74		719.9337	2	7.0	403	416	No
				GIRPAINVGLSVSR	K	V	95.00%	65		480.2902	3	3.9	403	416	No
				GMSLNLEPDNVGVVVFGNDK	K	L	95.00%	135	M2: Oxidation	1060.5300	2	8.8	104	123	No
				GMSLNLEPDNVGVVVFGNDK	K	L	95.00%	74	M2: Oxidation	707.3543	3	6.7	104	123	No
				GYLDKLEPSK	R	I	95.00%	47		1149.6210	1	4.8	494	503	No
				GYLDKLEPSK	R	I	95.00%	60		575.3137	2	3.3	494	503	No
				HALIIYDDLSK	K	Q	95.00%	103		644.3523	2	1.3	306	316	No
				ILGADTSVDLEETGR	R	V	95.00%	156		788.3987	2	1.6	59	73	No
				ISEQSDAK	K	L	95.00%	46		439.2195	2	5.1	532	539	No
				ISVREPMQTGIK	R	A	95.00%	34	M7: Oxidation	687.8760	2	1.9	183	194	No
				ISVREPMQTGIK	R	A	95.00%	45		679.8796	2	3.3	183	194	No
				ITKFENAFLSHVVSQHQALLGTIR	K	A	95.00%	91		903.8414	3	9.3	504	527	No
				ITKFENAFLSHVVSQHQALLGTIR	K	A	95.00%	52		678.1311	4	6.5	504	527	No
				ITKFENAFLSHVVSQHQALLGTIR	K	A	95.00%	32		542.7051	5	4.0	504	527	No
				LELAQYR	K	E	95.00%	50		446.7505	2	4.3	435	441	No
				LKEIVTNFLAGFEA	K	-	95.00%	94		776.4277	2	3.3	540	553	No
				LKEIVTNFLAGFEA	K	-	95.00%	41		517.9572	3	8.8	540	553	No
				LTDADAMK	R	Y	95.00%	36	M7: Oxidation	440.7113	2	6.7	263	270	No
				LTELLK	R	Q	95.00%	32		716.4581	1	3.0	467	472	No
				NVQAEEMVEFSSGLK	R	G	95.00%	123	M7: Oxidation	842.4047	2	6.9	89	103	No
				NVQAEEMVEFSSGLK	R	G	95.00%	75		834.4069	2	6.4	89	103	No

				PAINVGLSVSR	R	V	95.00%	79		556.8278	2	4.5	406	416	No
				QGQYSPMAIEEQVAVIYAGVR	K	G	95.00%	118	M7: Oxidation	1163.0900	2	7.1	473	493	No
				QGQYSPMAIEEQVAVIYAGVR	K	G	95.00%	91	M7: Oxidation	775.7278	3	5.6	473	493	No
				QGQYSPMAIEEQVAVIYAGVR	K	G	95.00%	32		770.3907	3	-1.5	473	493	No
				QMSLLLR	R	R	95.00%	47	M2: Oxidation	438.7540	2	2.7	323	329	No
				RSTVAQLVK	K	R	95.00%	40		501.3099	2	1.2	253	261	No
				RTGAIVDVPVGEELLGR	K	V	95.00%	96		891.0071	2	7.9	133	149	No
				RTGAIVDVPVGEELLGR	K	V	95.00%	55		594.3388	3	4.7	133	149	No
				STVAQLVK	R	R	95.00%	65		423.2594	2	1.4	254	261	No
				TGAIVDVPVGEELLGR	R	V	95.00%	113		812.9535	2	4.8	134	149	No
				TGAIVDVPVGEELLGR	R	V	95.00%	86		542.3061	3	7.0	134	149	No
				TGTAEMSSILEER	K	I	95.00%	100	M6: Oxidation	720.3404	2	2.9	46	58	No
				TGTAEMSSILEER	K	I	95.00%	96		712.3450	2	5.7	46	58	No
				TSIAIDTIINQK	K	R	95.00%	62		1316.7550	1	9.3	219	230	No
				TSIAIDTIINQK	K	R	95.00%	104		658.8786	2	5.0	219	230	No
				TSIAIDTIINQK	K	R	95.00%	37		439.5878	3	3.7	219	230	No
				TSIAIDTIINQKR	K	F	95.00%	80		736.9296	2	5.1	219	231	No
				TSIAIDTIINQKR	K	F	95.00%	44		491.6219	3	4.3	219	231	No
				VGLKAPGIIPR	R	I	95.00%	45		560.8666	2	4.0	172	182	No
				VLSIGDGIAR	R	V	95.00%	80		500.7931	2	-0.8	74	83	No
				VVDALGNAIDGK	R	G	95.00%	63		1171.6390	1	5.7	150	161	No
				VVDALGNAIDGK	R	G	95.00%	100		586.3215	2	2.3	150	161	No
				VVDALGNAIDGKGPIGSK	R	T	95.00%	87		855.9807	2	8.3	150	167	No
501	IPI00440828; IPI00552360; IPI00604759	FAHD1	ISOFORM 2 OF FUMARYLACETOACETATE HYDROLASE DOMAIN-CONTAINING PROTEIN1.; ISOFORM 1 OF FUMARYLACETOACETATE HYDROLASE DOMAIN-CONTAINING PROTEIN1.; FUMARYLACETOACETATE HYDROLASE DOMAIN CONTAINING 1.	IITLEEGDIILTGTPK	K	G	95.00%	28		571.6649	3	5.7	179	194	No
				NLHHELELGVVMGK	R	R	95.00%	58	M12: Oxidation	796.4223	2	6.3	67	80	No
502	IPI00448095; IPI00797249; IPI00797917	DCXR	L-XYLULOSE REDUCTASE.; 26 KDA PROTEIN.; 26 KDA PROTEIN.	AVIQVSQIVAR	R	G	95.00%	41		592.3657	2	6.1	108	118	No
				GTVQALHATGAR	R	V	95.00%	75		591.3259	2	4.1	20	31	No
				SFEVNLR	R	A	95.00%	35		432.7351	2	5.2	103	109	No
				TQADLDSLVR	R	E	95.00%	53		559.2988	2	3.8	40	49	No
503	IPI00453474; IPI00473081	TNNI1	TROPONIN I, SLOW SKELETAL MUSCLE.; 22 KDA PROTEIN.	IPTLQTR	R	G	95.00%	31		414.7526	2	3.5	49	55	No
				NVEAMSGMEGR	K	K	95.00%	57	M5: Oxidation	598.7614	2	9.3	164	174	No
				NVEAMSGMEGR	K	K	95.00%	78	M5: Oxidation	606.7568	2	5.8	164	174	No
				NVEAMSGMEGR	K	K	95.00%	78	M5: Oxidation, M8: Oxidation	606.7568	2	5.8	164	174	No
				NVEAMSGMEGR	K	K	95.00%	51	M8: Oxidation	598.7598	2	6.5	164	174	No
				VEVVDEER	K	Y	95.00%	32		487.7468	2	6.5	73	80	No
				VEVVDEERYDIEAK	K	C	95.00%	54		847.4205	2	2.7	73	86	No
				VSADAMLR	R	A	95.00%	47	M6: Oxidation	439.7261	2	4.3	118	125	No
504	IPI00456626	TXLNB	BETA-TAXILIN.	AAAEELPVGASAGPQPR	R	N	95.00%	97		810.9262	2	6.1	657	673	No
				ALLDMIEEK	K	A	95.00%	32	M5: Oxidation	539.2824	2	6.1	415	423	No
				EANLLMQNLNK	K	L	95.00%	50	M6: Oxidation	652.3427	2	7.4	144	154	No
				EASVHPDISEELNR	K	Q	95.00%	40		798.3913	2	5.1	48	61	No
				EITSHFQSTLTDIQGQIEQQSER	K	N	95.00%	65		892.4431	3	8.1	245	267	No
				FEEFQSTLTK	R	S	95.00%	58		615.3088	2	3.5	367	376	No
				QLEDIINTYGSAASTAGK	R	E	95.00%	104		919.9653	2	4.9	62	79	No
				SIIDQYELR	K	E	95.00%	42		568.8050	2	6.0	284	292	No
				SNEVFATFK	K	Q	95.00%	35		521.7657	2	2.6	377	385	No
				YAELLDEHR	K	T	95.00%	35		573.2867	2	5.6	169	177	No
505	IPI00456965	COQ5	ISOFORM 1 OF UBIQUINONE BIOSYNTHESIS METHYLTRANSFERASE COQ5,MITOCHONDRIAL PRECURSOR.	EYQNEEDSLGGSR	K	V	95.00%	77		742.3240	2	6.7	154	166	No
				FLNYVQSQHQR	R	K	95.00%	65		710.3654	2	6.8	124	134	No
				FLNYVQSQHQR	R	K	95.00%	37		473.9118	3	4.6	124	134	No
				NVTHIDQALQEAHR	R	V	95.00%	74		816.4215	2	5.9	221	234	No
				NVTHIDQALQEAHR	R	V	95.00%	40		544.6164	3	4.9	221	234	No
				SYQYLVESIR	K	R	95.00%	36		629.3325	2	7.4	280	289	No
				VYQVFESVAK	K	K	95.00%	54		585.3170	2	4.8	68	77	No
506	IPI00465028; IPI00797687	TPI1	TRIOSEPHOSPHATE ISOMERASE 1 VARIANT.; ISOFORM 1 OF TRIOSEPHOSPHATE ISOMERASE.	ELASQPDVDGFLVGGASLKPEFVDIINAK	K	-	95.00%	60		1010.5410	3	7.9	257	285	No

				ELASQPDVDGFLVGGASLKPEFVDIINAK	K	-	95.00%	61		758.1583	4	8.6	257	285	No
				FFVGGNWK	K	M	95.00%	31		954.4905	1	7.2	7	14	No
				FFVGGNWK	K	M	95.00%	51		477.7483	2	5.4	7	14	No
				HVFGESDELIGQK	R	V	95.00%	95		729.8690	2	4.9	138	150	No
				HVFGESDELIGQK	R	V	95.00%	48		486.9159	3	6.2	138	150	No
				KFFVGGNWK	R	M	95.00%	31		541.7981	2	8.8	6	14	No
				KQSLGELIGTLNAAK	R	V	95.00%	103		771.9527	2	7.7	19	33	No
				KQSLGELIGTLNAAK	R	V	95.00%	51		514.9690	3	3.6	56	70	No
				LDEREAGITEK	K	V	95.00%	30		420.8871	3	1.5	132	142	No
				QSLGELIGTLNAAK	K	V	95.00%	105		707.9043	2	7.1	57	70	No
				QSLGELIGTLNAAK	K	V	95.00%	56		472.2721	3	7.0	20	33	No
				RHVFGESDELIGQK	R	V	95.00%	85		807.9217	2	7.1	100	113	No
				RHVFGESDELIGQK	R	V	95.00%	63		538.9501	3	6.5	100	113	No
				SNVSDAVAQSTR	K	I	95.00%	97		617.8070	2	2.9	232	243	No
				SNVSDAVAQSTR	K	I	95.00%	63		412.2077	3	4.0	232	243	No
				VIADNVKDWSK	K	V	95.00%	52		637.8459	2	7.4	150	160	No
				VIADNVKDWSK	K	V	95.00%	31		425.5641	3	1.4	150	160	No
				VTNGAFTGEISPGMIK	K	D	95.00%	86	M14: Oxidation	819.4188	2	5.3	70	85	No
				VTNGAFTGEISPGMIK	K	D	95.00%	88		811.4213	2	5.3	107	122	No
				VTNGAFTGEISPGMIK	K	D	95.00%	66		541.2840	3	6.2	107	122	No
				VVFEQTK	K	V	95.00%	31		850.4749	1	8.8	143	149	No
				VVFEQTK	K	V	95.00%	32		425.7394	2	4.1	180	186	No
				VVLAYEPVWAIGTGK	K	T	95.00%	105		801.9562	2	9.3	198	212	No
				VVLAYEPVWAIGTGK	K	T	95.00%	94		534.9726	3	7.8	161	175	No
507	IPI00465084; IPI00658057; IPI00793833	DES	DESMIN.; MUTANT DESMIN.; 47 KDA PROTEIN.	ADVDAATLAR	R	I	95.00%	67		501.7665	2	3.1	213	222	No
				DGEVVSEATQQQHEVL	R	-	95.00%	75		884.9257	2	4.5	455	470	No
				DNLLDDLQR	R	L	95.00%	60		551.2831	2	3.7	181	189	No
				EEAENNLAAFR	K	A	95.00%	40		632.3068	2	7.0	202	212	No
				ELQAQLQEQQVQVEMDMSKPDLTAALR	R	D	95.00%	96	M15: Oxidation, M17: Oxidation	1044.5270	3	9.7	249	275	No
				EYQDLLNVK	R	M	95.00%	49		1121.5950	1	9.6	387	395	Yes
				EYQDLLNVK	R	M	95.00%	65		561.2985	2	4.1	387	395	Yes
				FANYIEK	R	V	95.00%	29		442.7322	2	5.6	119	125	No
				FASEASGYQDNIAR	R	L	95.00%	105		764.8574	2	2.6	356	369	No
				FLEQQNAALAAEVNR	R	L	95.00%	95		837.4401	2	6.9	128	142	No
				FLEQQNAALAAEVNR	R	L	95.00%	46		558.6292	3	6.5	128	142	No
				IESLNEEIAFLK	R	K	95.00%	53		703.3870	2	5.8	229	240	No
				INLPIQTYSALNFR	R	E	95.00%	86		825.4600	2	6.5	416	429	No
				INLPIQTYSALNFR	R	E	95.00%	66		550.6426	3	6.4	416	429	No
				LQEEIQLKEEAENNLAAFR	K	A	95.00%	64		1123.0870	2	8.5	194	212	No
				LQEEIQLKEEAENNLAAFR	K	A	95.00%	64		749.0593	3	7.1	194	212	No
				MALDVEIATYR	K	K	95.00%	71	M1: Oxidation	649.3293	2	3.5	396	406	No
				NISEAEEWYK	K	S	95.00%	68		634.7955	2	2.6	288	297	No
				QVEVLTNQR	R	A	95.00%	34		543.7998	2	0.9	165	173	No
				RIESLNEEIAFLK	R	K	95.00%	83		781.4380	2	5.8	228	240	No
				RIESLNEEIAFLK	R	K	95.00%	62		521.2961	3	8.7	228	240	No
				RIESLNEEIAFLKK	R	V	95.00%	70		563.9922	3	4.2	228	241	No
				RIESLNEEIAFLKK	R	V	95.00%	27		423.2458	4	3.3	228	241	No
				TFGGAPGFPLGSPLSSPVFPR	R	A	95.00%	118		1044.5590	2	8.8	17	37	No
				TFGGAPGFPLGSPLSSPVFPR	R	A	95.00%	45		696.7084	3	8.4	17	37	No
				TNEKVELQELNDR	R	F	95.00%	84		794.4053	2	3.0	106	118	Yes
				TNEKVELQELNDR	R	F	95.00%	50		529.9399	3	3.9	106	118	Yes
				TSGGAGGLGSLR	R	A	95.00%	59		516.7781	2	4.4	59	70	No
				VAELYEEELR	R	E	95.00%	72		625.8213	2	6.2	151	160	No
				VDVERDNLLDDLQR	R	L	95.00%	48		850.4405	2	6.8	176	189	No
				VDVERDNLLDDLQR	R	L	95.00%	54		567.2953	3	5.0	176	189	No
				VELQELNDR	K	F	95.00%	43		558.2911	2	4.2	110	118	Yes
508	IPI00465179; IPI00743142	PFKM	CDNA FLJ44241 FIS, CLONE THYMU3008436, HIGHLY SIMILAR TO 6-PHOSPHOFRUCTOKINASE, MUSCLE TYPE.; ISOFORM 1 OF 6-PHOSPHOFRUCTOKINASE, MUSCLE TYPE.	AIAVLTSGGDAQGMNAAVR	K	A	95.00%	151	M14: Oxidation	909.4650	2	2.3	88	106	No
				AIAVLTSGGDAQGMNAAVR	K	A	95.00%	92	M14: Oxidation	606.6465	3	3.2	88	106	No
				AIAVLTSGGDAQGMNAAVR	K	A	95.00%	125		901.4681	2	3.0	88	106	No
				AIAVLTSGGDAQGMNAAVR	K	A	95.00%	70		601.3151	3	3.6	88	106	No
				ALVFQPVAELK	R	D	95.00%	52		1214.7250	1	7.8	788	798	No
				ALVFQPVAELK	R	D	95.00%	86		607.8635	2	3.4	788	798	No
				ALVFQPVAELKDQTDFEHR	R	I	95.00%	108		1122.0870	2	8.7	788	806	No
				ALVFQPVAELKDQTDFEHR	R	I	95.00%	47		748.3906	3	4.5	788	806	No

				ALVFQPVAELKDQTDFEHR	R	I	95.00%	45		561.5466	4	7.6	788	806	No
				AMNWMSGK	K	I	95.00%	38	M2: Oxidation, M5: Oxidation	478.7053	2	5.9	754	761	No
				DLQANVEHLVQK	R	M	95.00%	88		697.3791	2	4.6	675	686	No
				DLQANVEHLVQK	R	M	95.00%	45		465.2548	3	3.3	675	686	No
				EATWESVSMMLQLGGTVIGSAR	K	C	95.00%	39	M9: Oxidation, M10: Oxidation	785.7212	3	6.5	138	159	No
				GGTPSAFDR	R	I	95.00%	39		454.2186	2	2.2	373	381	No
				GQIEEAGWSYVGGWTGQGGSK	K	L	95.00%	156		1077.5080	2	8.5	517	537	No
				GQIEEAGWSYVGGWTGQGGSK	K	L	95.00%	97		718.6717	3	4.8	517	537	No
				IGLIQGNR	R	V	95.00%	62		435.7640	2	4.6	496	503	No
				IMEIVDAITTTAQSHQR	R	T	95.00%	135	M2: Oxidation	965.4959	2	7.0	256	272	No
				IMEIVDAITTTAQSHQR	R	T	95.00%	90	M2: Oxidation	643.9972	3	2.9	256	272	No
				IMEIVDAITTTAQSHQR	R	T	95.00%	125		957.4953	2	3.7	256	272	No
				IMEIVDAITTTAQSHQR	R	T	95.00%	41		638.6671	3	5.2	256	272	No
				KFDEALK	K	L	95.00%	42		425.7391	2	3.4	437	443	No
				KNVLGHMQQGGSPTPFDR	R	N	95.00%	80	M7: Oxidation	992.9891	2	2.0	727	744	No
				KNVLGHMQQGGSPTPFDR	R	N	95.00%	72	M7: Oxidation	662.3289	3	2.3	727	744	No
				KNVLGHMQQGGSPTPFDR	R	N	95.00%	75		984.9919	2	2.2	727	744	No
				KNVLGHMQQGGSPTPFDR	R	N	95.00%	57		656.9966	3	1.2	727	744	No
				KSFEQISANITK	K	F	95.00%	101		683.3738	2	1.4	547	558	No
				KSFEQISANITK	K	F	95.00%	51		455.9191	3	2.7	547	558	No
				LLAHVRPPVSK	K	S	95.00%	41		608.8809	2	0.7	458	468	No
				LLAHVRPPVSK	K	S	95.00%	34		406.2568	3	1.4	458	468	No
				LNIIIVAEGAIDK	R	N	95.00%	124		684.9136	2	6.6	328	340	No
				LNIIIVAEGAIDK	R	N	95.00%	66		456.9448	3	6.1	328	340	No
				LNIIIVAEGAIDKNGKPITSEDIK	R	N	95.00%	54		851.1550	3	5.6	328	351	No
				LNIIIVAEGAIDKNGKPITSEDIK	R	N	95.00%	23		638.6191	4	7.1	328	351	No
				NVLGHMQQGGSPTPFDR	K	N	95.00%	81	M6: Oxidation	928.9423	2	2.8	728	744	No
				NVLGHMQQGGSPTPFDR	K	N	95.00%	57	M6: Oxidation	619.6313	3	3.6	728	744	No
				NVLGHMQQGGSPTPFDR	K	N	95.00%	75		920.9449	2	2.9	728	744	No
				NVLGHMQQGGSPTPFDR	K	N	95.00%	46		614.2995	3	3.4	728	744	No
				RALVFQPVAELK	K	D	95.00%	56		685.9180	2	8.7	787	798	No
				RALVFQPVAELKDQTDFEHR	K	I	95.00%	42		800.4257	3	6.0	787	806	No
				RALVFQPVAELKDQTDFEHR	K	I	95.00%	50		600.5724	4	7.9	787	806	No
				SEWSDLLSDLQK	R	A	95.00%	94		710.8575	2	7.8	201	212	No
				SEWSDLLSDLQK	R	A	95.00%	52		474.2417	3	9.3	201	212	No
				SFEQISANITK	K	F	95.00%	44		1237.6490	1	4.5	548	558	No
				SFEQISANITK	K	F	95.00%	79		619.3275	2	3.5	548	558	No
				SFMNNWEVYK	R	L	95.00%	51	M3: Oxidation	667.2997	2	2.4	448	457	No
				SFMNNWEVYK	R	L	95.00%	55		659.3032	2	3.8	448	457	No
				SGSHTVAVMNVGAPAAGMNAAVR	K	S	95.00%	85	M18: Oxidation	1092.5400	2	3.1	469	491	No
				SGSHTVAVMNVGAPAAGMNAAVR	K	S	95.00%	47	M18: Oxidation	728.6955	3	2.6	469	491	No
				SGSHTVAVMNVGAPAAGMNAAVR	K	S	95.00%	118	M9: Oxidation, M18: Oxidation	1100.5360	2	1.6	469	491	No
				SGSHTVAVMNVGAPAAGMNAAVR	K	S	95.00%	60	M9: Oxidation, M18: Oxidation	734.0275	3	3.1	469	491	No
				SGSHTVAVMNVGAPAAGMNAAVR	K	S	95.00%	38	M9: Oxidation, M18: Oxidation	550.7718	4	1.7	469	491	No
				TFVLEVMGR	R	H	95.00%	66	M7: Oxidation	534.2839	2	3.7	273	281	No
				TFVLEVMGR	R	H	95.00%	33		526.2861	2	3.0	273	281	No
				VFFVHEGYQGLVDGGDHIK	R	E	95.00%	82		1059.0340	2	6.5	119	137	No
				VFFVHEGYQGLVDGGDHIK	R	E	95.00%	71		706.3580	3	5.9	119	137	No
				VFFVHEGYQGLVDGGDHIK	R	E	95.00%	54		530.0214	4	7.6	119	137	No
				VGIFTGAR	R	V	95.00%	65		410.7395	2	3.6	111	118	No
				VLVVHDGFEGLAK	R	G	95.00%	88		692.3884	2	3.8	504	516	No
				VLVVHDGFEGLAK	R	G	95.00%	56		461.9272	3	1.7	504	516	No
				VTVLGHVQR	R	G	95.00%	54		504.8035	2	3.6	364	372	No
				YEIDLDTSDHAHLEHITR	K	K	95.00%	127		1083.0260	2	7.9	826	843	No
				YEIDLDTSDHAHLEHITR	K	K	95.00%	67		722.3515	3	5.8	826	843	No
509	IPI00465248	ENO1	ISOFORM ALPHA-ENOLASE OF ALPHA-ENOLASE.	AAVPSGASTGIYEALELR	R	D	95.00%	58	S8: Phospho	942.9679	2	9.0	33	50	Yes
				AAVPSGASTGIYEALELR	R	D	95.00%	42	T9: Phospho	942.9656	2	6.5	33	50	Yes
				AAVPSGASTGIYEALELR	R	D	95.00%	60	Y12: Phospho	942.9658	2	6.8	33	50	Yes
				AAVPSGASTGIYEALELR	R	D	95.00%	162		902.9806	2	4.8	33	50	Yes
				AAVPSGASTGIYEALELR	R	D	95.00%	99		602.3227	3	4.4	33	50	Yes

				DATNVGDEGGFAPNILENK	K	E	95.00%	137		980.9750	2	8.6	203	221	No
				DATNVGDEGGFAPNILENK	K	E	95.00%	52		654.3183	3	7.0	203	221	No
				DATNVGDEGGFAPNILENKEGLELLK	K	T	95.00%	96		1372.2060	2	9.1	203	228	No
				DATNVGDEGGFAPNILENKEGLELLK	K	T	95.00%	68		915.1392	3	8.5	203	228	No
				FTASAGIQVVGDDLTVTNPK	K	R	95.00%	114		1017.0410	2	8.9	307	326	No
				FTASAGIQVVGDDLTVTNPK	K	R	95.00%	72		678.3605	3	5.0	307	326	No
				GNPTVEVDLFTSK	R	G	95.00%	84		703.8681	2	8.2	16	28	No
				HIADLAGNSEVILPVPAFNVINGGSHAGNK	R	L	95.00%	67		1004.5360	3	7.7	133	162	No
				IDKLMIEMDGTENK	K	S	95.00%	79	M5: Oxidation, M8: Oxidation	834.8981	2	3.4	90	103	No
				IDKLMIEMDGTENK	K	S	95.00%	58	M5: Oxidation, M8: Oxidation	556.9350	3	4.0	90	103	No
				IGAEVYHNLK	R	N	95.00%	60		572.3137	2	2.8	184	193	No
				LAMQEFMILPVGAANFR	K	E	95.00%	111	M3: Oxidation, M7: Oxidation	970.5013	2	9.0	163	179	No
				LAMQEFMILPVGAANFR	K	E	95.00%	49	M3: Oxidation, M7: Oxidation	647.3343	3	5.1	163	179	No
				LAQANGWGVMVSHR	K	S	95.00%	50	M10: Oxidation	771.3892	2	4.0	359	372	No
				LAQANGWGVMVSHR	K	S	95.00%	43	M10: Oxidation	514.5943	3	1.7	359	372	No
				LMIEMDGTENK	K	S	95.00%	74	M2: Oxidation, M5: Oxidation	656.7942	2	3.1	93	103	No
				SGKYDLDFK	R	S	95.00%	31		536.7712	2	2.7	254	262	No
				VNQIGSVTESLQACK	K	L	95.00%	98		788.9106	2	8.1	344	358	No
				VVIGMDVAASEFFR	K	S	95.00%	118	M5: Oxidation	778.8987	2	7.4	240	253	No
				VVIGMDVAASEFFR	K	S	95.00%	46	M5: Oxidation	519.6006	3	5.1	240	253	No
				YDLDFK	K	S	95.00%	44		400.6961	2	1.4	257	262	Yes
				YDLDFKSPDDPSR	K	Y	95.00%	38		777.8614	2	4.5	257	269	No
				YDLDFKSPDDPSR	K	Y	95.00%	50		518.9086	3	1.4	257	269	No
				YGKDATNVGDEGGFAPNILENKEGLELLK	K	T	95.00%	88		1031.1960	3	4.4	200	228	No
				YISPDQLADLYK	R	S	95.00%	82		713.3703	2	4.3	270	281	No
				YNQLLR	K	I	95.00%	30		403.7312	2	2.6	407	412	No
510	IPI00465256	AK3	GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL.	AVIMGAPGSGK	R	G	95.00%	60	M4: Oxidation	502.2700	2	7.3	10	20	No
				AYEDQTKPVLEYYQK	K	K	95.00%	64		937.9713	2	9.1	175	189	No
				AYEDQTKPVLEYYQK	K	K	95.00%	54		625.6452	3	1.1	175	189	No
				EDDKPETVIKR	R	L	95.00%	34		443.9075	3	3.9	162	172	No
				GTEIGVLAK	R	A	95.00%	57		444.2666	2	5.6	49	57	No
				GVLETFSGTETNK	K	I	95.00%	101		691.8481	2	5.8	191	203	No
				KGVLETFSGTETNK	K	I	95.00%	58		755.8987	2	9.3	190	203	No
				TLPQAEALDR	R	A	95.00%	50		557.3014	2	4.1	95	104	No
				TVGIDDLTGEPLIQR	K	E	95.00%	77		813.9469	2	9.4	147	161	No
				VYNIEFNPPK	R	T	95.00%	41		610.8252	2	9.0	137	146	No
511	IPI00465315	CYCS	CYTOCHROME C.	ADLIAYLK	R	K	95.00%	28		906.5385	1	9.2	93	100	No
				ADLIAYLK	R	K	95.00%	56		453.7712	2	4.8	93	100	No
				ADLIAYLKK	R	A	95.00%	48		517.8207	2	8.1	93	101	No
				GIIWGEDTLMEYLENPK	K	K	95.00%	66	M10: Oxidation	1012.4960	2	7.1	57	73	No
				GIIWGEDTLMEYLENPK	K	K	95.00%	80		1004.4940	2	2.9	57	73	No
				GIIWGEDTLMEYLENPKK	K	Y	95.00%	99	M10: Oxidation	1076.5460	2	9.4	57	74	No
				KTGQAPGYSYTAANK	R	N	95.00%	94		778.8951	2	7.4	40	54	No
				KTGQAPGYSYTAANK	R	N	95.00%	53		519.5981	3	5.1	40	54	No
				MIFVGIK	K	K	95.00%	33	M1: Oxidation	823.4828	1	9.1	81	87	No
				TGPNLHGLFGR	K	K	95.00%	91		584.8179	2	4.4	29	39	No
				TGQAPGYSYTAANK	K	N	95.00%	95		714.8478	2	8.3	41	54	No
512	IPI00465436	CAT	CATALASE.	ADVLTTGAGNPVGDK	K	L	95.00%	87		707.8640	2	1.6	24	38	No
				ADVLTTGAGNPVGDKLNVITVGPR	K	G	95.00%	77		788.7744	3	8.0	24	47	No
				AFYVNVLNEEQR	R	K	95.00%	92		741.3777	2	5.9	445	456	No
				DAQIFIQK	K	K	95.00%	38		962.5360	1	4.8	469	476	No
				DAQIFIQK	K	K	95.00%	50		481.7699	2	0.6	469	476	No
				DLFNAIATGK	R	Y	95.00%	45		1049.5720	1	7.9	264	273	No
				DLFNAIATGK	R	Y	95.00%	51		525.2875	2	3.7	264	273	No
				DPILFPSFIHSQK	R	R	95.00%	66		764.9194	2	9.4	157	169	No
				DPILFPSFIHSQK	R	R	95.00%	43		510.2801	3	5.4	157	169	No
				FNTANDDNVTQVR	R	A	95.00%	103		747.3555	2	3.1	432	444	No
				FSTVAGESGSADTVR	R	D	95.00%	98		742.3576	2	3.0	113	127	No
				FSTVAGESGSADTVRDPR	R	G	95.00%	46		617.9682	3	2.8	113	130	No

				GAGAFGYFEVTHDITK	K	Y	95.00%	101		856.9245	2	7.3	78	93	No
				GAGAFGYFEVTHDITK	K	Y	95.00%	35		571.6184	3	6.4	78	93	No
				GPLLVQDVVFTDEMAHFDR	R	E	95.00%	61	M14: Oxidation	735.7004	3	9.2	48	66	No
				GPLLVQDVVFTDEMAHFDRER	R	I	95.00%	45	M14: Oxidation	830.7493	3	9.4	48	68	No
				GPLLVQDVVFTDEMAHFDRER	R	I	95.00%	57	M14: Oxidation	623.3124	4	6.9	48	68	No
				LNVITVGPR	K	G	95.00%	60		484.7995	2	1.8	39	47	No
				LSQEDPDYGIR	R	D	95.00%	51		646.8121	2	3.1	253	263	No
				NAIHTFVQSGSHLAAR	K	E	95.00%	93		854.9543	2	7.2	507	522	No
				NAIHTFVQSGSHLAAR	K	E	95.00%	67		570.3040	3	4.6	507	522	No
				NFTEVHPDYGSHIQALLDK	K	Y	95.00%	37		728.7002	3	5.7	481	499	No
				NFTEVHPDYGSHIQALLDKYNAEKPK	K	N	95.00%	36		1005.5150	3	9.0	481	506	No
				NLSVEDAAR	K	L	95.00%	51		487.7501	2	1.8	244	252	No
				NPVNYFAEVEQIAFDPSNMPPGIEASPDK	R	M	95.00%	75	M19: Oxidation	1064.8430	3	9.9	321	349	No
				RFNTANDDNVTQVR	R	A	95.00%	55		825.4116	2	9.5	431	444	No
				VWPHKDYPLIPVGK	K	L	95.00%	37		550.3153	3	5.0	302	315	No
513	IPI00465439	ALDOA	FRUCTOSE-BISPHOSPHATE ALDOLASE A.	AAQEEYVK	K	R	95.00%	61		469.2400	2	9.8	323	330	No
				AAQEEYVKR	K	A	95.00%	76		547.2892	2	5.8	323	331	No
				ADDGRPFPQVIK	K	S	95.00%	53		671.8621	2	3.0	88	99	No
				ADDGRPFPQVIK	K	S	95.00%	57		448.2433	3	1.5	88	99	No
				ALANSLACQGK	R	Y	95.00%	64		538.2861	2	6.7	332	342	No
				ALQASALK	R	A	95.00%	69		401.2468	2	3.0	305	312	No
				ALSDHHIYLEGTLLK	K	P	95.00%	50		570.6486	3	4.1	216	230	No
				DGADFAK	K	W	95.00%	40		723.3379	1	8.9	141	147	No
				ELSDIAHR	K	I	95.00%	38		940.4908	1	5.9	15	22	No
				ELSDIAHR	K	I	95.00%	48		470.7505	2	8.5	15	22	No
				FSHEEIAMATVTALR	K	R	95.00%	117	M8: Oxidation	846.4308	2	6.5	244	258	No
				FSHEEIAMATVTALR	K	R	95.00%	57	M8: Oxidation	564.6208	3	2.4	244	258	No
				FSHEEIAMATVTALR	K	R	95.00%	111		838.4349	2	8.5	244	258	No
				FSHEEIAMATVTALR	K	R	95.00%	46		559.2904	3	4.6	244	258	No
				FSHEEIAMATVTALRR	K	T	95.00%	38	M8: Oxidation	924.4773	2	1.6	244	259	No
				FSHEEIAMATVTALRR	K	T	95.00%	31	M8: Oxidation	616.6549	3	2.8	244	259	No
				FSHEEIAMATVTALRR	K	T	95.00%	49	M8: Oxidation	462.7453	4	7.5	244	259	No
				FSHEEIAMATVTALRR	K	T	95.00%	51		916.4863	2	8.7	244	259	No
				FSHEEIAMATVTALRR	K	T	95.00%	32		458.7447	4	3.5	244	259	No
				GGVVGIKVDK	K	G	95.00%	43		971.5954	1	6.4	102	111	No
				GGVVGIKVDK	K	G	95.00%	32		486.2996	2	2.3	102	111	No
				GILAADESTGSIAK	K	R	95.00%	67	S11: Phospho	706.8398	2	2.9	29	42	No
				GILAADESTGSIAK	K	R	95.00%	61	S8: Phospho	706.8412	2	4.9	29	42	No
				GILAADESTGSIAK	K	R	95.00%	63	T9: Phospho	706.8402	2	3.5	29	42	No
				GILAADESTGSIAK	K	R	95.00%	65		1332.7130	1	9.0	29	42	No
				GILAADESTGSIAK	K	R	95.00%	107		666.8547	2	0.2	29	42	No
				GILAADESTGSIAKR	K	L	95.00%	68	S11: Phospho	784.8915	2	4.1	29	43	No
				GILAADESTGSIAKR	K	L	95.00%	66	S8: Phospho	784.8919	2	4.7	29	43	No
				GILAADESTGSIAKR	K	L	95.00%	56	T9: Phospho	784.8920	2	4.7	29	43	No
				GILAADESTGSIAKR	K	L	95.00%	116		744.9055	2	0.5	29	43	No
				GILAADESTGSIAKR	K	L	95.00%	48		496.9400	3	1.4	29	43	No
				GVVPLAGTNGETTTQGLDGLSER	K	C	95.00%	146		1136.5840	2	8.1	112	134	No
				GVVPLAGTNGETTTQGLDGLSER	K	C	95.00%	82		758.0576	3	6.6	112	134	No
				IGEHTPSALAIMENANVLAR	K	Y	95.00%	102	M12: Oxidation	1062.0600	2	9.7	154	173	No
				IGEHTPSALAIMENANVLAR	K	Y	95.00%	87	M12: Oxidation	708.3732	3	5.8	154	173	No
				IGEHTPSALAIMENANVLAR	K	Y	95.00%	132		1054.0620	2	9.3	154	173	No
				IGEHTPSALAIMENANVLAR	K	Y	95.00%	61		703.0423	3	6.8	154	173	No
				IVAPGK	R	G	95.00%	28		584.3799	1	4.6	23	28	No
				IVAPGKGILAADESTGSIAK	R	R	95.00%	105		949.5430	2	9.5	23	42	No
				IVAPGKGILAADESTGSIAK	R	R	95.00%	54		633.3616	3	4.7	23	42	No
				IVAPGKGILAADESTGSIAKR	R	L	95.00%	39		685.3953	3	4.4	23	43	No
				KDGADFAK	K	W	95.00%	32		426.2192	2	4.9	140	147	No
				KELSDIAHR	K	I	95.00%	64		534.7981	2	7.5	14	22	No
				LQSIGTENTEENR	R	R	95.00%	111		745.8605	2	3.0	44	56	No
				LQSIGTENTEENRR	R	F	95.00%	39		823.9040	2	-5.9	44	57	No
				LQSIGTENTEENRR	R	F	95.00%	53		549.6113	3	5.1	44	57	No
				PYQYPALTPEQK	M	K	95.00%	52		1434.7390	1	8.0	2	13	No
				PYQYPALTPEQK	M	K	95.00%	81		717.8690	2	2.0	2	13	No
				PYQYPALTPEQK	M	K	95.00%	49		478.9152	3	2.0	2	13	No
				PYQYPALTPEQKK	M	E	95.00%	70		781.9160	2	1.3	2	14	No
				PYQYPALTPEQKK	M	E	95.00%	47		521.6132	3	1.2	2	14	No

				QLLLTADDR	R	V	95.00%	44		1044.5760	1	6.5	61	69	No
				QLLLTADDR	R	V	95.00%	79		522.7914	2	5.6	61	69	No
				RLQSIGTENTEENRR	K	F	95.00%	65		901.9653	2	6.6	43	57	No
				RLQSIGTENTEENRR	K	F	95.00%	59		601.6415	3	-1.0	43	57	No
				RLQSIGTENTEENRR	K	F	95.00%	41		451.4850	4	3.3	43	57	No
				RTVPPAVTGITFLSGGQSEEEASINLNAINK	R	C	95.00%	71		1071.9070	3	9.4	259	289	No
				SKGGVVGIK	K	V	95.00%	38		422.7685	2	4.2	100	108	No
				SKGGVVGIKVDK	K	G	95.00%	28		593.8657	2	6.3	100	111	No
				TVPPAVTGITFLSGGQSEEEASINLNAINK	R	C	95.00%	91		1019.8730	3	9.1	260	289	No
				TVPPAVTGITFLSGGQSEEEASINLNAINK	R	C	95.00%	46		765.1548	4	7.1	260	289	No
				VDKGVVPLAGTNGETTTQGLDGLSER	K	C	95.00%	93		1307.6810	2	8.2	109	134	No
				VDKGVVPLAGTNGETTTQGLDGLSER	K	C	95.00%	83		872.1231	3	8.0	109	134	No
				VDKGVVPLAGTNGETTTQGLDGLSER	K	C	95.00%	43		654.3414	4	3.6	109	134	No
				VLAAVYK	K	A	95.00%	49		763.4747	1	3.8	209	215	No
				YTPSGQAGAAASESLFVSNHAY	K	-	95.00%	164		1114.5270	2	9.2	343	364	No
				YTPSGQAGAAASESLFVSNHAY	K	-	95.00%	81		743.3533	3	8.3	343	364	No
514	IPI00470359	TNNC1	TROPONIN C, SLOW SKELETAL AND CARDIAC MUSCLES.	AAVEQLTEEQK	K	N	95.00%	65		623.3236	2	5.3	7	17	No
				AAVEQLTEEQKNEFK	K	A	95.00%	94		882.4510	2	7.1	7	21	No
				AAVEQLTEEQKNEFK	K	A	95.00%	51		588.6341	3	2.9	7	21	No
				GKSEEELSDLFR	K	M	95.00%	84		705.3562	2	9.4	91	102	No
				GKSEEELSDLFR	K	M	95.00%	62		470.5713	3	5.0	91	102	No
				IDYDEFLEFMK	R	G	95.00%	78	M10: Oxidation	733.3392	2	9.7	148	158	No
				IMLQATGETITEDDIEELMK	K	D	95.00%	114	M2: Oxidation, M19: Oxidation	771.3757	3	9.7	119	138	No
				IMLQATGETITEDDIEELMKDGDK	K	N	95.00%	35	M2: Oxidation, M19: Oxidation	909.7646	3	6.7	119	142	No
				NADGYIDLDELK	K	I	95.00%	87		683.3354	2	6.6	107	118	No
				SEEELSDLFR	K	M	95.00%	36		612.7960	2	7.6	93	102	No
515	IPI00470535	CACNA2D1	DIHYDROPYRIDINE RECEPTOR ALPHA 2 SUBUNIT.	AKLEETITQAR	K	S	95.00%	48		630.3556	2	5.7	633	643	No
				AKLEETITQAR	K	S	95.00%	30		420.5690	3	-3.9	633	643	No
				FFGEIDPSLMR	R	H	95.00%	52	M10: Oxidation	664.3260	2	6.3	881	891	No
				FVVTDGGITR	R	V	95.00%	67		532.7923	2	2.4	740	749	No
				IIMLFTDGGEER	K	A	95.00%	54	M3: Oxidation	698.8475	2	6.3	357	368	No
				IKPVFIEDANFGR	R	Q	95.00%	65		753.4155	2	7.5	145	157	No
				IKPVFIEDANFGR	R	Q	95.00%	51		502.6116	3	4.9	145	157	No
				INTQEYLDVLGRPMVLAGDK	R	A	95.00%	51	M14: Oxidation	750.0648	3	6.1	421	440	No
				INTQEYLDVLGRPMVLAGDK	R	A	95.00%	41		744.7325	3	5.3	421	440	No
				MQEDLVTLAK	K	T	95.00%	41		574.3076	2	3.4	40	49	No
				NQLILGVMGVDVSLEDIKR	K	L	95.00%	41	M8: Oxidation	705.7256	3	6.0	481	499	No
				NREEDPSLLWQVFGSATGLAR	K	Y	95.00%	55		782.7402	3	8.8	196	216	No
				PIGVGIPTINLR	K	K	95.00%	48		625.3917	2	9.8	531	542	No
				SGPGAYESGIMVSK	K	A	95.00%	48	M11: Oxidation	699.8345	2	2.6	790	803	No
				TASGVNQLVDIYEK	K	Y	95.00%	94		768.9061	2	8.7	50	63	No
				TPNKIDLYDVR	R	R	95.00%	29		445.2445	3	4.5	229	239	No
				VFTFSVGQHNYDR	R	G	95.00%	63		785.3813	2	6.3	384	396	No
				YQDLYTVEPNNAR	K	Q	95.00%	55		791.8859	2	8.7	64	76	No
516	IPI00470631; IPI00746245	COQ9	ISOFORM 1 OF UBIQUINONE BIOSYNTHESIS PROTEIN COQ9, MITOCHONDRIALPRECURSOR.; 36 KDA PROTEIN.	AMLAAIYNTTELVMMQDSSPDFEDTWR	R	F	95.00%	45	M2: Oxidation, M14: Oxidation, M15: Oxidation	1061.8120	3	7.5	245	271	No
				LVQLGQAEK	K	R	95.00%	63		493.2902	2	4.1	167	175	No
				STGEALVQGLMGAAVTLK	K	N	95.00%	93	M11: Oxidation	881.4827	2	8.7	292	309	No
				STGEALVQGLMGAAVTLK	K	N	95.00%	75	M11: Oxidation	587.9913	3	9.1	292	309	No
				YTDQGGEEEEDYESEEQLQHR	R	I	95.00%	79		857.6894	3	5.0	82	102	No
517	IPI00470674	CYB5R1	NAD(P)H:QUINONE OXIDOREDUCTASE TYPE 3, POLYPEPTIDE A2.	DIILREDLEELQAR	K	Y	95.00%	56		856.9691	2	6.9	219	232	No
				DIILREDLEELQAR	K	Y	95.00%	60		571.6491	3	7.6	219	232	No
				EDLEELQAR	R	Y	95.00%	53		1102.5440	1	5.1	224	232	No

				EDLEELQAR	R	Y	95.00%	84		551.7763	2	6.0	224	232	No
				FALPTAHHTLGLPVGK	R	H	95.00%	38		829.9800	2	8.3	66	81	No
				FALPTAHHTLGLPVGK	R	H	95.00%	23		553.6548	3	6.3	66	81	No
				GFVTADMIR	K	E	95.00%	55	M7: Oxidation	513.2604	2	3.9	255	263	No
				GHFNIQPNKK	K	S	95.00%	42		591.8282	2	8.6	159	168	No
				GIQTSPVLLASLGVGLVTLLGLAVGSYLVR	M	R	95.00%	39		742.4526	4	7.2	2	31	No
				GPSGLLTYTGK	R	G	95.00%	34		1093.5980	1	8.0	148	158	No
				GPSGLLTYTGK	R	G	95.00%	64		547.3022	2	6.4	148	158	No
				HIYLSTR	K	I	95.00%	32		445.2510	2	5.3	82	88	No
				KLGMIAGGTGITPMLQLIR	K	A	95.00%	28	M4: Oxidation, M14: Oxidation	668.0508	3	8.5	178	196	No
				LGMIAGGTGITPMLQLIR	K	A	95.00%	109	M3: Oxidation	929.5253	2	6.9	179	196	No
				LGMIAGGTGITPMLQLIR	K	A	95.00%	124	M3: Oxidation, M13: Oxidation	937.5190	2	2.9	179	196	No
				LGMIAGGTGITPMLQLIR	K	A	95.00%	43	M3: Oxidation, M13: Oxidation	625.3518	3	7.9	179	196	No
				LGMIAGGTGITPMLQLIR	K	A	95.00%	111		921.5289	2	8.1	179	196	No
				LWFTLDHPPK	K	D	95.00%	32		418.5639	3	5.9	239	248	No
				MSQYLDSLK	K	V	95.00%	37	M1: Oxidation	1100.5360	1	5.7	131	139	No
				MSQYLDSLK	K	V	95.00%	32	M1: Oxidation	550.7718	2	5.3	131	139	No
				PYTPVTSDEDQGYVDLVIK	R	V	95.00%	85		713.6948	3	8.9	97	115	No
				RPQVTLLDPNEK	R	Y	95.00%	35		705.3956	2	5.6	35	46	No
				RPQVTLLDPNEK	R	Y	95.00%	27		470.6000	3	6.3	35	46	No
				VGDVVEFR	K	G	95.00%	36		920.4932	1	9.8	140	147	No
				VGDVVEFR	K	G	95.00%	66		460.7482	2	4.8	140	147	No
518	IPI00470829	IMMT	ISOFORM 3 OF MITOCHONDRIAL INNER MEMBRANE PROTEIN.	AVDEAADALLK	K	A	95.00%	37		1115.5960	1	1.2	255	265	No
				AVDEAADALLK	K	A	95.00%	47		558.3020	2	1.0	255	265	Yes
				ELDSITPEVLPGWK	R	G	95.00%	60		792.4234	2	4.1	340	353	Yes
				EVAGAKPHITAAEGK	K	L	95.00%	29		493.6058	3	3.3	284	298	No
				GIEQAVQSHAVAEEEAR	R	K	95.00%	104		912.4516	2	3.6	516	532	Yes
				GIEQAVQSHAVAEEEAR	R	K	95.00%	62		608.6362	3	2.3	516	532	Yes
				GMSVSDLADKLSTDDLNSLIAHAHR	K	R	95.00%	56	M2: Oxidation	894.7826	3	6.2	354	378	Yes
				GVYSEETLR	R	A	95.00%	49		527.2662	2	2.7	592	600	Yes
				KAHQLWLSVEALK	R	Y	95.00%	40		508.2989	3	4.2	533	545	Yes
				KAVDEAADALLK	R	A	95.00%	84		622.3502	2	2.1	254	265	Yes
				LFEMVLGPAAYNVPLPK	K	K	95.00%	75	M4: Oxidation	938.0121	2	3.9	85	101	Yes
				LFEMVLGPAAYNVPLPK	K	K	95.00%	50	M4: Oxidation	625.6768	3	3.0	85	101	Yes
				LHNMIVDLDNVVK	K	K	95.00%	75	M4: Oxidation	763.4110	2	6.2	299	311	Yes
				LHNMIVDLDNVVK	K	K	95.00%	35	M4: Oxidation	509.2776	3	8.0	299	311	Yes
				LHNMIVDLDNVVKK	K	V	95.00%	31	M4: Oxidation	551.9732	3	2.5	299	312	Yes
				LRGIEQAVQSHAVAEEEAR	R	K	95.00%	61		698.3663	3	4.4	514	532	Yes
				LRGIEQAVQSHAVAEEEAR	R	K	95.00%	52		524.0265	4	4.1	514	532	Yes
				LSEQELQFR	K	R	95.00%	65		575.3000	2	1.5	485	493	No
				LSQEQVDNFTLDINTAYAR	R	L	95.00%	124		1099.5470	2	6.0	495	513	Yes
				LSQEQVDNFTLDINTAYAR	R	L	95.00%	55		733.3662	3	4.6	495	513	Yes
				LSTDDLNSLIAHAHR	K	R	95.00%	35		416.4715	4	3.7	364	378	Yes
				QTASVTLQAIAAQNAAVQAVNAHSNILK	R	A	95.00%	83		944.8533	3	4.1	198	225	Yes
				QTASVTLQAIAAQNAAVQAVNAHSNILK	R	A	95.00%	45		708.8920	4	4.1	198	225	Yes
				SEFEQNLSEK	K	L	95.00%	39		605.7842	2	1.2	475	484	Yes
				TDHPEIGEGKPTPALSALAK	K	S	95.00%	44		678.0348	3	8.4	171	190	No
				TIPYSDKLFEMVLGPAAYNVPLPK	K	K	95.00%	34	M11: Oxidation	893.8137	3	5.6	78	101	Yes
				TSSAETPTIPLGSAVEAIK	K	A	95.00%	99		936.5066	2	4.7	550	568	Yes
				TSSAETPTIPLGSAVEAIK	K	A	95.00%	36		624.6743	3	5.7	550	568	No
				VAMIDETR	R	N	95.00%	45	M3: Oxidation	475.7369	2	4.4	613	620	Yes
				VQEQELKSEFEQNLSEK	R	L	95.00%	104		1033.0120	2	4.0	468	484	Yes
				VQEQELKSEFEQNLSEK	R	L	95.00%	73		689.0098	3	2.4	468	484	Yes
				VVSQYHELVVQAR	K	D	95.00%	96		764.4203	2	3.0	322	334	Yes
				VVSQYHELVVQAR	K	D	95.00%	49		509.9509	3	5.8	322	334	Yes
				YSTSGSSGLTTGK	R	I	95.00%	61		623.3045	2	3.9	33	45	Yes
519	IPI00472102; IPI00784154	HSPD1	61 KDA PROTEIN.; 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL PRECURSOR.	ALMLQGVDLLADAVAVTMGPK	R	G	95.00%	113	M3: Oxidation, M18: Oxidation	1073.0770	2	7.4	38	58	No
				ALMLQGVDLLADAVAVTMGPK	R	G	95.00%	101	M3: Oxidation, M18: Oxidation	715.7195	3	5.9	38	58	No

				ALMLQGVDLLADAVAVTMGPK	R	G	95.00%	84		705.0566	3	6.5	38	58	No
				DMAIATGGAVFGEEGLTLNLEDVQPHDLGK	K	V	95.00%	78	M2: Oxidation	1038.5180	3	8.9	317	346	No
				GANPVEIR	K	R	95.00%	48		428.2406	2	5.3	134	141	No
				GVMLAVDAVIAELKK	R	Q	95.00%	71	M3: Oxidation	786.9633	2	9.6	143	157	No
				GVMLAVDAVIAELKK	R	Q	95.00%	46	M3: Oxidation	524.9763	3	6.1	143	157	No
				GYISPYFINTSK	R	G	95.00%	71		695.3593	2	3.9	222	233	No
				IGIEIIKR	K	T	95.00%	46		471.3127	2	2.9	463	470	No
				IMQSSSEVGYDAMAGDFVNMVEK	K	G	95.00%	57	M2: Oxidation, M13: Oxidation, M20: Oxidation	852.7108	3	8.9	496	518	No
				IQEIIEQLDVTTSEYEK	R	E	95.00%	151		1019.5240	2	8.1	373	389	No
				IQEIIEQLDVTTSEYEKEK	R	L	95.00%	114		1148.0960	2	9.8	373	391	No
				IQEIIEQLDVTTSEYEKEK	R	L	95.00%	56		765.7300	3	6.0	373	391	No
				ISSIQSIVPALEIANAHR	K	K	95.00%	94		960.0488	2	9.5	251	268	No
				ISSIQSIVPALEIANAHR	K	K	95.00%	60		640.3668	3	6.9	253	270	No
				KISSIQSIVPALEIANAHR	K	K	95.00%	72		683.0656	3	7.1	252	270	No
				KISSIQSIVPALEIANAHR	K	K	95.00%	39		512.5516	4	7.9	252	270	No
				KPLVIIAEDVDGEALSTLVLNR	R	L	95.00%	163		1183.1800	2	7.9	269	290	No
				KPLVIIAEDVDGEALSTLVLNR	R	L	95.00%	29		789.1215	3	6.1	269	290	No
				KPLVIIAEDVDGEALSTLVLNR	R	L	95.00%	38		592.0934	4	6.7	271	292	No
				LKVGLQVVAVK	R	A	95.00%	36		577.3901	2	4.2	291	301	No
				LSDGVAVLK	K	V	95.00%	52		451.2741	2	4.9	399	407	No
				LVQDVANNTNEEAGDGTTTATVLAR	K	S	95.00%	182		1280.6400	2	9.1	97	121	No
				LVQDVANNTNEEAGDGTTTATVLAR	K	S	95.00%	77		854.0891	3	1.0	97	121	No
				NAGVEGSLIVEK	K	I	95.00%	75		608.3386	2	8.8	484	495	No
				NQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGK	K	V	95.00%	81	M6: Oxidation	899.9621	4	9.4	313	346	No
				RGVMLAVDAVIAELKK	R	Q	95.00%	70	M4: Oxidation	577.0123	3	9.5	142	157	No
				RIQEIIEQLDVTTSEYEKEK	K	L	95.00%	88		817.7660	3	8.3	372	391	No
				TALLDAAGVASLLTTAEVVVTEIPKEEK	R	D	95.00%	58		956.8735	3	8.0	527	554	No
				TALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGAMGGMGGGMGGGMF	R	-	95.00%	45	M32: Oxidation, M35: Oxidation, M38: Oxidation, M42: Oxidation, M46: Oxidation	1151.8060	4	9.1	529	575	No
				TLNDELEIIEGMKFDR	K	G	95.00%	70	M12: Oxidation	969.9865	2	8.6	206	221	No
				TLNDELEIIEGMKFDR	K	G	95.00%	56	M12: Oxidation	646.9933	3	8.2	208	223	No
				TVIIEQSWGSPK	R	V	95.00%	76		672.8665	2	6.4	61	72	No
				VGEVIVTK	K	D	95.00%	37		844.5228	1	9.8	347	354	No
				VGEVIVTK	K	D	95.00%	64		422.7628	2	3.8	347	354	No
				VGEVIVTKDDAMLLK	K	G	95.00%	66	M12: Oxidation	823.9568	2	1.0	345	359	No
				VGEVIVTKDDAMLLK	K	G	95.00%	45	M12: Oxidation	549.6431	3	5.9	347	361	No
				VGLQVVAVK	K	A	95.00%	32		912.5928	1	4.9	295	303	No
				VGLQVVAVK	K	A	95.00%	74		456.7991	2	2.3	293	301	No
				VTDALNATR	R	A	95.00%	49		480.7620	2	5.1	421	429	No
520	IPI00472442	PSMA1	ISOFORM LONG OF PROTEASOME SUBUNIT ALPHA TYPE 1.	IHQIEYAMEAVK	R	Q	95.00%	30	M8: Oxidation	724.3702	2	4.8	25	36	No
				ILHVDNHIGISIAGLTADAR	K	L	95.00%	30		522.2949	4	7.1	69	88	No
				LVSLIGSK	R	T	95.00%	27		816.5256	1	7.3	114	121	No
				NVSIGIVGK	K	D	95.00%	29		443.7744	2	5.2	215	223	No
				THAVLVALK	K	R	95.00%	22		476.3060	2	5.2	48	56	No
521	IPI00473011	HBB; HBD	HEMOGLOBIN SUBUNIT DELTA.	EFTPQMQAAYQK	K	V	95.00%	66	M6: Oxidation	729.3459	2	7.1	122	133	No
				EFTPQMQAAYQK	K	V	95.00%	57		721.3474	2	5.7	122	133	No
				FFESFGDLSSPDAVMGNPK	R	V	95.00%	103	M15: Oxidation	1030.9770	2	9.2	42	60	No
				FFESFGDLSSPDAVMGNPK	R	V	95.00%	48	M15: Oxidation	687.6533	3	8.1	42	60	No
				FFESFGDLSSPDAVMGNPK	R	V	95.00%	83		1022.9780	2	7.5	42	60	No
				FFESFGDLSSPDAVMGNPK	R	V	95.00%	59		682.3179	3	2.5	42	60	No
				KVLGAFSDGLAHLDNLK	K	G	95.00%	129		899.5036	2	7.2	67	83	Yes
				KVLGAFSDGLAHLDNLK	K	G	95.00%	81		600.0053	3	7.7	67	83	Yes
				KVLGAFSDGLAHLDNLK	K	G	95.00%	41		450.2552	4	6.0	67	83	Yes
				LHVDPENFR	K	L	95.00%	33		1126.5750	1	9.2	97	105	Yes
				LHVDPENFR	K	L	95.00%	56		563.7872	2	1.7	97	105	Yes
				LLVVYPWTQR	R	F	95.00%	31		1274.7390	1	9.8	32	41	Yes
				LLVVYPWTQR	R	F	95.00%	71		637.8707	2	5.7	32	41	Yes
				LLVVYPWTQR	R	F	95.00%	40		425.5841	3	8.3	32	41	Yes

				TAVNALWGK	K	V	95.00%	35		959.5367	1	5.5	10	18	No
				TAVNALWGK	K	V	95.00%	73		480.2740	2	9.2	10	18	No
				VHLTPEEK	M	T	95.00%	36		952.5192	1	9.2	2	9	No
				VHLTPEEK	M	T	95.00%	39		476.7600	2	1.8	2	9	No
				VLGAFSDGLAHLDNLK	K	G	95.00%	137		835.4454	2	-5.0	68	83	Yes
				VLGAFSDGLAHLDNLK	K	G	95.00%	66		557.3033	3	1.8	68	83	Yes
				VNVDAVGGEALGR	K	L	95.00%	105		628.8386	2	7.5	19	31	No
				VNVDAVGGEALGR	K	L	95.00%	35		419.5598	3	3.2	19	31	No
				VVAGVANALAHK	K	Y	95.00%	49		1149.6820	1	6.8	134	145	Yes
				VVAGVANALAHK	K	Y	95.00%	92		575.3436	2	4.4	134	145	Yes
				VVAGVANALAHKYH	K	-	95.00%	64		725.4076	2	7.5	134	147	Yes
522	IPI00477090; IPI00479708; IPI00549291; IPI00828205; IPI00829729; IPI00829768; IPI00829843; IPI00829854; IPI00829911	IGHM	IGHM PROTEIN.; IGHM PROTEIN.; IGHM PROTEIN.; IGHM PROTEIN.; IGHM PROTEIN.; IGHM PROTEIN.; IGHM PROTEIN.; IGHM PROTEIN.; IGHM PROTEIN.	DGFFGNPR	R	K	95.00%	33		455.2149	2	0.1	260	267	No
				GVALHRPDVYLLPPAR	K	E	95.00%	45		887.5185	2	9.2	462	477	No
				GVALHRPDVYLLPPAR	K	E	95.00%	40		592.0138	3	7.3	462	477	No
				NSLYLQMNSLR	K	A	95.00%	62	M7: Oxidation	677.8459	2	3.7	96	106	Yes
				NTLYLQMNSLR	K	A	95.00%	36	M7: Oxidation	684.8559	2	6.9	96	106	Yes
				QIQVSWLR	R	E	95.00%	39		515.2988	2	5.0	282	289	No
				QVGSGVTTDQVQAEAK	K	E	95.00%	105		809.4116	2	4.2	293	308	No
				VFAIPPSFASIFLTK	R	S	95.00%	26		819.4765	2	8.8	377	391	No
				VSVFVPPR	K	D	95.00%	49		450.7705	2	2.8	252	259	No
				YAATSQVLLPSK	K	D	95.00%	66		639.3611	2	2.9	218	229	No
				YVTSAPMPEPQAPGR	K	Y	95.00%	71	M7: Oxidation	808.8957	2	5.7	516	530	No
523	IPI00477131	SYPL2	ISOFORM 1 OF SYNAPTOPHYSIN-LIKE PROTEIN 2.	DVSSIIVAFGYPFR	K	L	95.00%	51		524.2853	3	8.4	72	85	No
				ETPWHGQGQGQDQDQDQDQGQGPSQESAAEQGAVEK	K	-	95.00%	41		963.4250	4	9.1	236	271	No
				LEEPLGFIK	R	V	95.00%	42		523.3037	2	5.7	31	39	No
524	IPI00375704; IPI00479306	PSMB5	HYPOTHETICAL PROTEIN DKFZP686I0180 (FRAGMENT).; PROTEASOME BETA 5 SUBUNIT.	ATAGAYIASQTVK	R	K	95.00%	34		640.8504	2	6.2	79	91	No
				GPGLYYVDSEGNR	R	I	95.00%	40		713.8405	2	9.0	170	182	No
				HGVIVAADSR	R	A	95.00%	33		512.7841	2	6.2	72	81	No
				LLANMVYQYK	K	G	95.00%	67	M5: Oxidation	629.8337	2	7.3	141	150	No
				RAIYQATYR	R	D	95.00%	31		571.3122	2	4.1	220	228	No
				RGPGLYYVDSEGNR	K	I	95.00%	42		528.2618	3	5.3	166	179	No
525	IPI00479877	ALDH9A1	ALDEHYDE DEHYDROGENASE 9A1.	ANDTTFGLAAGVFTR	R	D	95.00%	93		770.8959	2	5.1	436	450	No
				EILDKFTEEVVK	K	Q	95.00%	53		725.4003	2	5.9	323	334	No
				EVNLAVQNAK	K	A	95.00%	54		543.3033	2	3.0	74	83	No
				GIKPVTLELGGK	K	S	95.00%	68		606.3749	2	4.3	271	282	No
				GIKPVTLELGGK	K	S	95.00%	42		404.5857	3	3.8	271	282	No
				IGDPLLEDTR	K	M	95.00%	92		564.8020	2	5.2	341	350	No
				VSFTGSVPTGMK	K	I	95.00%	50	M11: Oxidation	613.8107	2	3.6	252	263	No
				VTIEYYSQLK	R	T	95.00%	69		622.3358	2	5.1	496	505	No
526	IPI00479905	NDUFB10	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 10.	AFDLIVDRPVTLVR	K	E	95.00%	45		807.4802	2	9.0	30	43	No
				AFDLIVDRPVTLVR	K	E	95.00%	58		538.6548	3	6.7	30	43	No
				DYKVDQEIINIMQDR	R	L	95.00%	63	M12: Oxidation	948.4691	2	6.8	89	103	No
				TPVQPNPIVYMMK	R	A	95.00%	57	M11: Oxidation, M12: Oxidation	775.3992	2	9.4	17	29	No
				VDQEIINIMQDR	K	L	95.00%	56	M9: Oxidation	745.3766	2	8.8	92	103	No
				YQDLGAYSSAR	R	K	95.00%	51		615.7955	2	6.2	137	147	No
527	IPI00513979	SEPW1	SELENOPROTEIN W.	KKLEDEFPGR	K	L	95.00%	29		609.8325	2	7.0	26	35	No
				KLEDEFPGR	K	L	95.00%	53		545.7827	2	3.6	27	35	No
				LEDEFPGR	K	L	95.00%	50		481.7351	2	4.1	28	35	No
528	IPI00549467	NIT2	NITRILASE FAMILY MEMBER 2.	AVDNQVYVATASPAR	R	D	95.00%	83		781.4092	2	8.4	196	210	No
				FAELAQIYAQR	R	G	95.00%	42		655.3531	2	6.0	158	168	No
				LALIQLQISSIK	R	S	95.00%	82		663.9279	2	8.8	6	17	No
529	IPI00003925; IPI00549885; IPI00798351	PDHB	ISOFORM 1 OF PYRUVATE DEHYDROGENASE E1 COMPONENT SUBUNIT BETA,MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF PYRUVATE DEHYDROGENASE E1 COMPONENT SUBUNIT BETA,MITOCHONDRIAL PRECURSOR.; 35 KDA PROTEIN.	DAINQGMDEELER	R	D	95.00%	67	M7: Oxidation	768.3429	2	8.5	19	31	No
				DAINQGMDEELERDEK	R	V	95.00%	44	M7: Oxidation	954.4210	2	2.4	37	52	No
				DFLIPIGK	K	A	95.00%	36		902.5400	1	5.2	220	227	No
				DFLIPIGK	K	A	95.00%	47		451.7743	2	6.0	202	209	No

				DIIFAIK	K	K	95.00%	35		410.2556	2	6.3	330	336	No
				DIIFAIKK	K	T	95.00%	36		474.3024	2	4.0	348	355	No
				ILEDNSIPQVK	K	D	95.00%	67		628.3513	2	3.8	337	347	No
				IMEGPAFNFLDAPAVR	R	V	95.00%	83	M2: Oxidation	882.4519	2	9.5	309	324	No
				IMEGPAFNFLDAPAVR	R	V	95.00%	40	M2: Oxidation	588.6358	3	7.1	291	306	No
				IMEGPAFNFLDAPAVR	R	V	95.00%	93		874.4545	2	9.6	309	324	No
				IMEGPAFNFLDAPAVR	R	V	95.00%	54		583.3027	3	4.7	309	324	No
				TIRPMDMETIEASVMK	R	T	95.00%	46	M5: Oxidation, M7: Oxidation, M15: Oxidation	950.4519	2	4.9	270	285	No
				TIRPMDMETIEASVMK	R	T	95.00%	55	M5: Oxidation, M7: Oxidation, M15: Oxidation	633.9725	3	8.0	252	267	No
				TIRPMDMETIEASVMK	R	T	95.00%	59		617.9770	3	7.1	270	285	No
				TYYMSGGLQPVPIVFR	K	G	95.00%	84	M4: Oxidation	922.4836	2	9.7	130	145	No
				VFLLGEEVAQYDGAYK	K	V	95.00%	103		901.4633	2	9.6	53	68	No
				VFLLGEEVAQYDGAYK	K	V	95.00%	78		601.3103	3	7.7	35	50	No
				VTGADVPMPYAK	R	I	95.00%	73	M8: Oxidation	632.8210	2	7.3	307	318	No
				VVSPWNSEDAK	K	G	95.00%	36		616.3054	2	5.7	174	184	No
530	IPI00550069; IPI00783491	RNH1	RIBONUCLEASE INHIBITOR.; RIBONUCLEASE/ANGIOGENIN INHIBITOR.	ELSLAGNELGDEGAR	K	L	95.00%	110		765.8784	2	5.7	288	302	No
				ELTVSNNDINEAGVR	K	V	95.00%	115		815.9097	2	4.9	174	188	No
				ESLKELSLAGNELGDEGAR	K	L	95.00%	49		663.3410	3	6.8	284	302	No
				VNPALAELNLR	R	S	95.00%	87		605.3575	2	9.6	54	64	No
531	IPI00550165	DHRS7B	DEHYDROGENASE/REDUCTASE (SDR FAMILY) MEMBER 7B.	SPVEVAQDVLAAVGK	R	K	95.00%	60		494.9490	3	9.8	268	282	No
				YGVMDTTTAQGR	R	S	95.00%	69	M4: Oxidation	658.3072	2	8.5	256	267	No
532	IPI00550239	H1F0	HISTONE H1.0.	LVTTGVLK	R	Q	95.00%	23		415.7752	2	8.7	75	82	No
				YSDMIVAAIQAEK	K	N	95.00%	63	M4: Oxidation	727.8704	2	8.8	28	40	No
533	IPI00551024	DAK	DIHYDROXYACETONE KINASE.	SPGADLLQVLTK	K	A	95.00%	70		621.3645	2	8.4	511	522	No
				VAPAEPQEAPDSTAAGGSASK	R	R	95.00%	63		970.9680	2	4.0	352	372	No
534	IPI00553177	SERPINA1	ALPHA-1-ANTITRYPSIN PRECURSOR.	AVLTIDEK	K	G	95.00%	38		888.5082	1	4.3	360	367	No
				AVLTIDEK	K	G	95.00%	39		444.7574	2	3.0	360	367	No
				DTEEEDFHVDQVTTVK	K	V	95.00%	110		946.4396	2	7.9	226	241	No
				DTEEEDFHVDQVTTVK	K	V	95.00%	34		631.2950	3	7.0	226	241	No
				ELDRDTVFALVNYIFFK	K	G	95.00%	76		1045.5590	2	6.4	199	215	No
				ELDRDTVFALVNYIFFK	K	G	95.00%	57		697.3733	3	4.0	199	215	No
				FLEDVKK	K	L	95.00%	30		439.7553	2	4.5	154	160	No
				FNKPFVFLMIEQNTK	K	S	95.00%	43	M9: Oxidation	936.4980	2	8.1	390	404	No
				FNKPFVFLMIEQNTK	K	S	95.00%	34	M9: Oxidation	624.6659	3	4.9	390	404	No
				GTEAAGAMFLEAIPMSIPPEVK	K	F	95.00%	72	M8: Oxidation, M15: Oxidation	1146.0800	2	9.3	368	389	No
				GTEAAGAMFLEAIPMSIPPEVK	K	F	95.00%	52	M8: Oxidation, M15: Oxidation	764.3874	3	6.9	368	389	No
				ITPNLAEFAFSLYR	K	Q	95.00%	82		821.4410	2	6.2	50	63	No
				ITPNLAEFAFSLYR	K	Q	95.00%	65		547.9627	3	5.1	50	63	No
				KLYHSEAFTVNFGDTEEAKK	K	Q	95.00%	58		772.0527	3	3.1	160	179	No
				LQHLENELTHDIITK	K	F	95.00%	96		902.4921	2	8.7	284	298	No
				LQHLENELTHDIITK	K	F	95.00%	68		601.9944	3	3.9	284	298	No
				LQHLENELTHDIITK	K	F	95.00%	35		451.7479	4	4.1	284	298	No
				LSITGTYDLK	K	S	95.00%	38		1110.6080	1	3.1	315	324	No
				LSITGTYDLK	K	S	95.00%	64		555.8079	2	2.6	315	324	No
				LSSWVLLMK	K	Y	95.00%	55	M8: Oxidation	546.8135	2	5.8	259	267	No
				LVDKFLEDVK	K	K	95.00%	56		603.3456	2	4.2	150	159	No
				LVDKFLEDVKK	K	L	95.00%	53		667.3939	2	4.9	150	160	No
				LVDKFLEDVKK	K	L	95.00%	38		445.2642	3	2.7	150	160	No
				LYHSEAFTVNFGDTEEAK	K	K	95.00%	107		1029.4820	2	4.9	161	178	No
				LYHSEAFTVNFGDTEEAK	K	K	95.00%	49		686.6575	3	5.6	161	178	No
				LYHSEAFTVNFGDTEEAKK	K	Q	95.00%	126		1093.5300	2	4.9	161	179	No
				LYHSEAFTVNFGDTEEAKK	K	Q	95.00%	64		729.3540	3	2.7	161	179	No
				LYHSEAFTVNFGDTEEAKK	K	Q	95.00%	48		547.2681	4	3.9	161	179	No
				SASLHLPK	R	L	95.00%	29		426.7522	2	2.7	307	314	No
				SVLGQLGITK	K	V	95.00%	32		1015.6240	1	8.8	325	334	No
				SVLGQLGITK	K	V	95.00%	71		508.3127	2	2.3	325	334	No
				TDTSHHDQDHPTFNK	K	I	95.00%	31		593.9319	3	6.4	35	49	No
				TLNQPDSQLQLTTGNGLFLSEGLK	R	L	95.00%	122		1287.6880	2	9.9	126	149	No
				TLNQPDSQLQLTTGNGLFLSEGLK	R	L	95.00%	52		858.7913	3	6.4	126	149	No

				VFSNGADLSGVTEEAPLK	K	L	95.00%	127		917.4723	2	7.2	335	352	No
535	IPI00554521	FTH1	FERRITIN HEAVY CHAIN.	IFLQDIK	R	K	95.00%	37		438.7653	2	3.6	81	87	No
				MGAPESGLAEYLFDK	K	H	95.00%	83	M1: Oxidation	822.3932	2	9.7	159	173	No
				NVNQSLLELHK	K	L	95.00%	63		647.8637	2	5.8	110	120	No
				NVNQSLLELHK	K	L	95.00%	31		432.2444	3	4.3	110	120	No
				QNYHQDSEAAINR	R	Q	95.00%	67		773.3620	2	7.6	11	23	No
				QNYHQDSEAAINR	R	Q	95.00%	63		515.9103	3	7.1	11	23	No
				YFLHQSHEEREHAEK	K	L	95.00%	45		647.3115	3	7.2	55	69	No
536	IPI00554701	UCRC	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.2 KDA PROTEIN.	AFDQGADAIYDHINEGK	R	L	95.00%	79		932.4378	2	8.7	35	51	No
				AFDQGADAIYDHINEGK	R	L	95.00%	55		621.9577	3	3.1	35	51	No
				LYSLLFR	K	R	95.00%	49		456.2756	2	8.8	10	16	No
537	IPI00444262; IPI00604620; IPI00827674	NCL	CDNA FLJ45706 FIS, CLONE FEBRA2028457, HIGHLY SIMILAR TO NUCLEOLIN.; ISOFORM 1 OF NUCLEOLIN.; ISOFORM 2 OF NUCLEOLIN.	EVFEDAAEIR	K	L	95.00%	44		589.7918	2	5.4	411	420	No
				FGYVDFESAEDLEK	K	A	95.00%	71		824.8788	2	7.0	349	362	No
				GFGFVDFNSEEDAK	K	A	95.00%	45		781.3513	2	8.7	504	517	No
				GIAYIEFK	K	T	95.00%	36		470.7637	2	5.4	430	437	No
				GLSEDTTEETLKESFDGSVR	K	A	95.00%	44		734.0173	3	4.7	471	490	No
				VTQDELKEVFEDAAEIR	K	L	95.00%	37		664.6744	3	7.4	297	313	No
538	IPI00604664	NDUFS1	NADH-UBIQUINONE OXIDOREDUCTASE 75 KDA SUBUNIT, MITOCHONDRIALPRECURSOR.	ALSEIAGMTLPYDTLDQVR	R	N	95.00%	112	M8: Oxidation	1055.0410	2	9.6	625	643	No
				ALSEIAGMTLPYDTLDQVR	R	N	95.00%	45	M8: Oxidation	703.6931	3	4.6	625	643	No
				AVEDKNIGPLVK	R	T	95.00%	52		641.8768	2	6.6	159	170	No
				DFYMTDSISR	K	A	95.00%	43	M4: Oxidation	625.7758	2	6.0	693	702	No
				DFYMTDSISR	K	A	95.00%	34		617.7772	2	4.1	693	702	No
				DVAAIAGGLVDAEALVALK	K	D	95.00%	139		898.5208	2	9.2	337	355	No
				FASEIAGVDDLGTTGR	R	G	95.00%	125		804.9034	2	7.3	185	200	No
				FAYDGLKR	R	Q	95.00%	42		485.2636	2	3.8	292	299	No
				FEAPLFNAR	R	I	95.00%	61		532.7828	2	4.6	409	417	No
				GLLTYTSWEDALSR	K	V	95.00%	123		806.4127	2	9.8	312	325	No
				GNDMQVGTYIEK	R	M	95.00%	65	M4: Oxidation	685.8210	2	5.7	201	212	No
				GWNILTNSEK	K	S	95.00%	52		581.3013	2	3.6	99	108	No
				IASQVAALDLGYKPGVEAIR	R	K	95.00%	98		1036.0870	2	5.7	519	538	No
				IASQVAALDLGYKPGVEAIR	R	K	95.00%	82		691.0619	3	7.2	519	538	No
				IASQVAALDLGYKPGVEAIRK	R	N	95.00%	66		733.7598	3	6.1	519	539	No
				IASQVAALDLGYKPGVEAIRK	R	N	95.00%	29		550.5708	4	4.3	519	539	No
				ILQDIASGSHPFSQVLK	K	E	95.00%	85		920.5068	2	4.8	451	467	No
				ILQDIASGSHPFSQVLK	K	E	95.00%	58		614.0071	3	4.7	451	467	No
				KPMVVLGSSALQR	K	N	95.00%	69	M3: Oxidation	701.3995	2	1.7	471	483	No
				KPMVVLGSSALQR	K	N	95.00%	54	M3: Oxidation	467.9353	3	1.0	471	483	No
				LEEVSPNLVR	R	Y	95.00%	56		578.3251	2	4.2	646	655	No
				LVNQQLLADPLVPPQLTIK	K	D	95.00%	86		1050.6330	2	6.5	674	692	No
				LVNQQLLADPLVPPQLTIK	K	D	95.00%	45		700.7578	3	6.6	674	692	No
				MHEDINEEWISDK	R	T	95.00%	73	M1: Oxidation	831.3620	2	2.6	277	289	No
				MHEDINEEWISDK	R	T	95.00%	45	M1: Oxidation	554.5779	3	3.7	277	289	No
				MHEDINEEWISDKTR	R	F	95.00%	39	M1: Oxidation	640.2955	3	5.3	277	291	No
				MTSGVTGDWK	R	V	95.00%	31	M1: Oxidation	549.2517	2	1.7	502	511	No
				NDGAAILAAVSSIAQK	R	I	95.00%	129		764.9252	2	5.9	484	499	No
				NDGAAILAAVSSIAQK	R	I	95.00%	98		510.2858	3	5.4	484	499	No
				NRLEEVSPNLVR	R	Y	95.00%	69		713.3972	2	3.7	644	655	No
				NRLEEVSPNLVR	R	Y	95.00%	30		475.9348	3	5.1	644	655	No
				VAGMLQSFQGK	R	D	95.00%	82	M4: Oxidation	591.3046	2	2.0	326	336	No
				VALIGSPVDLTYTYDHLGDSPK	K	I	95.00%	115		1181.1120	2	7.8	429	450	No
				VALIGSPVDLTYTYDHLGDSPK	K	I	95.00%	46		787.7412	3	4.2	429	450	No
				VAVTPPGLAR	K	E	95.00%	45		490.7996	2	2.0	608	617	No
				VGMQIPR	K	F	95.00%	40	M3: Oxidation	408.7258	2	4.3	56	62	No
539	IPI00641582	BAG3	BAG FAMILY MOLECULAR CHAPERONE REGULATOR 3.	ELLALDSVDPEGR	K	A	95.00%	90		707.3693	2	5.6	461	473	No
				FRTEAAAAAPQR	R	S	95.00%	35		644.8473	2	8.3	122	133	No
				VQGLEQAVDNFEGK	K	K	95.00%	104		767.3845	2	4.1	432	445	No
540	IPI00023048; IPI00642971	EEF1D	ELONGATION FACTOR 1-DELTA.; EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 DELTA ISOFORM 1.	ATAPQTQHVSPMR	R	Q	95.00%	36	M12: Oxidation	720.3621	2	6.8	490	502	No
				FYEQMNGPVAGASR	R	Q	95.00%	102	M5: Oxidation	771.8605	2	7.8	25	38	No
				GVVQELQQAISK	R	L	95.00%	78		650.3704	2	4.3	96	107	No
				IASLEVENQSLR	R	G	95.00%	93		679.8715	2	5.3	84	95	No
				LVPVGYGIR	K	K	95.00%	25		487.2987	2	6.1	599	607	No
				SIQLDGLVWGASK	R	L	95.00%	80		687.3795	2	6.0	220	232	No

				SLAGSSGPGASSGTSGDHGELVVR	K	I	95.00%	48		729.0236	3	3.1	60	83	No
541	IPI00644697	HEBP2	HEBP2 PROTEIN (FRAGMENT).	AEMTVFVR	R	S	95.00%	42	M3: Oxidation	484.7509	2	6.6	133	140	No
				VYYTAGYNSPVK	K	L	95.00%	57		681.3456	2	6.8	173	184	No
542	IPI00645016	S100A1	PROTEIN S100-A1.	ELLQTELSGFLDAQK	K	D	95.00%	122		846.4542	2	8.7	36	50	No
				ELLQTELSGFLDAQK	K	D	95.00%	73		564.6373	3	6.1	36	50	No
				ELLQTELSGFLDAQKDVDAVDK	K	V	95.00%	39		812.0911	3	9.0	36	57	No
				GSELETAMETLINVFHAHSGK	M	E	95.00%	39	M8: Oxidation	572.5368	4	9.2	2	22	No
543	IPI00645078	UBE1	UBIQUITIN-ACTIVATING ENZYME E1.	AAVATFLQSVQVPEFTPK	R	S	95.00%	71		967.0309	2	5.4	785	802	No
				AAVATFLQSVQVPEFTPK	R	S	95.00%	73		645.0237	3	6.1	785	802	No
				ALPAVQQNNLDEDLIR	R	K	95.00%	66		904.9880	2	9.6	369	384	No
				ALPAVQQNNLDEDLIRK	R	L	95.00%	117		969.0358	2	9.3	369	385	No
				ATLPSPDKLPGFK	K	M	95.00%	46		685.8920	2	5.5	831	843	No
				ATLPSPDKLPGFK	K	M	95.00%	40		457.5958	3	2.2	831	843	No
				AVTLHDQGTAQWADLSSQFYLR	K	E	95.00%	40		836.4208	3	6.0	98	119	No
				DEFEGLFK	R	Q	95.00%	32		492.7404	2	5.2	650	657	No
				GNVQVVIPFLTESYSSSQDPPEK	K	S	95.00%	37		841.0920	3	5.7	605	627	No
				IHVSDQELQSANASVDDSR	K	L	95.00%	63		690.9997	3	7.0	807	825	No
				IHVSDQELQSANASVDDSRLEELK	K	A	95.00%	84		895.1164	3	6.2	807	830	No
				IYDDDFFQNLDGVANALDNVDAR	R	M	95.00%	108		867.4079	3	6.7	559	581	No
				KPLLESGTLGTK	R	G	95.00%	50		622.3691	2	3.0	593	604	No
				LAGTQPLEVLEAVQR	R	S	95.00%	95		812.4617	2	5.1	679	693	No
				LAGTQPLEVLEAVQR	R	S	95.00%	65		541.9770	3	5.0	679	693	No
				LDQPMTEIVSR	R	V	95.00%	67	M5: Oxidation	652.8329	2	4.5	1011	1021	No
				LQTSSVLVSGLR	R	G	95.00%	69		630.3732	2	4.9	70	81	No
				NEEDAAELVALAQAVNAR	R	A	95.00%	128		942.4814	2	4.6	351	368	No
				NEEDAAELVALAQAVNAR	R	A	95.00%	62		628.6583	3	6.9	351	368	No
				NIILGGVK	K	A	95.00%	30		813.5253	1	6.6	90	97	No
				QFLDYFK	K	T	95.00%	45		480.7474	2	3.9	974	980	No
				QFLFRPWDVTK	R	L	95.00%	35		718.8942	2	7.9	516	526	No
				QPAENVNQYLTDPK	K	F	95.00%	79		808.9057	2	6.9	658	671	No
				SLVASLAEPDFVVTDFAK	K	F	95.00%	98		955.0093	2	7.9	305	322	No
				YDGQVAVFGSDLQEK	R	L	95.00%	99		828.4034	2	4.2	451	465	No
544	IPI00645194	ITGB1	INTEGRIN BETA 1 ISOFORM 1A PRECURSOR.	IGFGSFVEK	R	T	95.00%	51		492.2678	2	7.7	182	190	No
				LKPEDITQIQPQQLVLR	K	L	95.00%	75		1010.0900	2	5.5	106	122	No
				LKPEDITQIQPQQLVLR	K	L	95.00%	43		673.7283	3	4.3	106	122	No
				LSEGVTISYK	K	S	95.00%	30		548.8009	2	4.5	389	398	No
545	IPI00645836	ESD	PROTEIN.	AFSGYLGTDQSK	K	W	95.00%	56		637.3127	2	8.7	135	146	Yes
				AYDATHLVK	K	S	95.00%	41		509.2746	2	4.3	149	157	Yes
				SGYHQSASEHGLVVIAPDTSPR	K	G	95.00%	63		770.0551	3	7.6	13	34	Yes
546	IPI00654755	HBB	HEMOGLOBIN SUBUNIT BETA.	EFTPPVQAAYQK	K	V	95.00%	91		689.8578	2	5.1	122	133	No
				EFTPPVQAAYQK	K	V	95.00%	41		460.2432	3	9.6	122	133	No
				EFTPPVQAAYQKVVAGVANALAHK	K	Y	95.00%	37		837.1279	3	4.7	122	145	No
				EFTPPVQAAYQKVVAGVANALAHKYH	K	-	95.00%	31		703.1296	4	5.8	122	147	No
				FFESFGDLSTPDAVMGNPK	R	V	95.00%	130	M15: Oxidation	1037.9830	2	6.9	42	60	No
				FFESFGDLSTPDAVMGNPK	R	V	95.00%	101	M15: Oxidation	692.3245	3	7.1	42	60	No
				FFESFGDLSTPDAVMGNPK	R	V	95.00%	130		1029.9880	2	9.5	42	60	No
				FFESFGDLSTPDAVMGNPK	R	V	95.00%	77		686.9920	3	5.8	42	60	No
				FFESFGDLSTPDAVMGNPKVK	R	A	95.00%	60	M15: Oxidation	768.0440	3	4.2	42	62	No
				GTFATLSELHCDK	K	L	95.00%	87		711.3437	2	4.1	84	96	No
				KVLGAFSDGLAHLDNLK	K	G	95.00%	129		899.5036	2	7.2	67	83	Yes
				KVLGAFSDGLAHLDNLK	K	G	95.00%	81		600.0053	3	7.7	67	83	Yes
				KVLGAFSDGLAHLDNLK	K	G	95.00%	41		450.2552	4	6.0	67	83	Yes
				LHVDPENFR	K	L	95.00%	33		1126.5750	1	9.2	97	105	Yes
				LHVDPENFR	K	L	95.00%	56		563.7872	2	1.7	97	105	Yes
				LLGNVLVCVLAHHFGK	R	E	95.00%	64		573.9992	3	5.0	106	121	No
				LLGNVLVCVLAHHFGK	R	E	95.00%	41		430.7511	4	4.5	106	121	No
				LLVVYPWTQR	R	F	95.00%	31		1274.7390	1	9.8	32	41	Yes
				LLVVYPWTQR	R	F	95.00%	71		637.8707	2	5.7	32	41	Yes
				LLVVYPWTQR	R	F	95.00%	40		425.5841	3	8.3	32	41	Yes
				SAVTALWGK	K	V	95.00%	45		932.5253	1	5.1	10	18	No

				SAVTALWGK	K	V	95.00%	71		466.7651	2	2.0	10	18	No
				SAVTALWGKVNVDEVGGEALGR	K	L	95.00%	129		1114.5980	2	9.4	10	31	No
				SAVTALWGKVNVDEVGGEALGR	K	L	95.00%	68		743.3999	3	7.5	10	31	No
				SAVTALWGKVNVDEVGGEALGRLLVVYPWTQR	K	F	95.00%	47		871.7319	4	8.4	10	41	No
				SAVTALWGKVNVDEVGGEALGRLLVVYPWTQR	K	F	95.00%	24		697.5867	5	7.8	10	41	No
				VHLTPEEK	M	S	95.00%	36		952.5192	1	9.2	2	9	No
				VHLTPEEK	M	S	95.00%	39		476.7600	2	1.8	2	9	No
				VHLTPEEKSAVTALWGKVNVDEVGGEALGR	M	L	95.00%	57		791.1775	4	8.6	2	31	No
				VLGAFSDGLAHLDNLK	K	G	95.00%	137		835.4454	2	-5.0	68	83	Yes
				VLGAFSDGLAHLDNLK	K	G	95.00%	66		557.3033	3	1.8	68	83	Yes
				VNVDEVGGEALGR	K	L	95.00%	73		1314.6760	1	8.2	19	31	No
				VNVDEVGGEALGR	K	L	95.00%	115		657.8383	2	2.5	19	31	No
				VNVDEVGGEALGR	K	L	95.00%	79		438.8956	3	4.4	19	31	No
				VNVDEVGGEALGRLLVVYPWTQR	K	F	95.00%	38		857.4680	3	6.0	19	41	No
				VVAGVANALAHK	K	Y	95.00%	49		1149.6820	1	6.8	134	145	Yes
				VVAGVANALAHK	K	Y	95.00%	92		575.3436	2	4.4	134	145	Yes
				VVAGVANALAHKYH	K	-	95.00%	64		725.4076	2	7.5	134	147	Yes
547	IPI00719622; IPI00787692	LOC645899; LOC646195; RPS28	40S RIBOSOMAL PROTEIN S28.; 8 KDA PROTEIN.	EGDVLTLLESER	R	E	95.00%	66		680.8567	2	6.9	52	63	No
				VEFMDDTSR	R	S	95.00%	37	M4: Oxidation	558.2403	2	4.4	32	40	No
548	IPI00741097	GSTT1	GLUTATHIONE S-TRANSFERASE THETA-1.	GQHLSDAFAQVNPLK	K	K	95.00%	83		812.9329	2	8.0	38	52	No
				GQHLSDAFAQVNPLK	K	K	95.00%	34		542.2909	3	7.6	38	52	No
				GQHLSDAFAQVNPLKK	K	V	95.00%	46		584.9894	3	7.4	38	53	No
				QRVEAAVGEDLFQEAHEVILK	R	A	95.00%	30		596.0729	4	9.1	196	216	No
				VDEYLAWQHTTLR	R	R	95.00%	45		544.6153	3	7.3	95	107	No
549	IPI00031583; IPI00743314	VDP	HYPOTHETICAL PROTEIN DKFZP451D234.; GENERAL VESICULAR TRANSPORT FACTOR P115.	DSEQVAELKQELATLK	R	S	95.00%	73		901.4902	2	9.8	794	809	No
				DSEQVAELKQELATLK	R	S	95.00%	48		601.3275	3	6.4	783	798	No
				EQDDLLVLLADQDQK	K	I	95.00%	58		871.9487	2	4.5	916	930	No
				EVIRNDGVLLLQALTR	R	S	95.00%	37		604.0262	3	4.2	184	199	No
				GVMGGQSAGPQHTEAETIQK	R	L	95.00%	37	M3: Oxidation	681.3268	3	1.6	6	25	No
				IVAFENAFER	K	L	95.00%	57		598.3141	2	7.7	203	212	No
				LMDLLADSR	R	E	95.00%	31	M2: Oxidation	525.2731	2	7.8	171	179	No
				LQTEKQELLQK	K	T	95.00%	51		679.3907	2	3.1	811	821	No
				LREEIEELKR	R	N	95.00%	35		438.9197	3	3.9	735	744	No
				NDGVLLLQALTR	R	S	95.00%	74		656.8882	2	7.2	188	199	No
				NQELLQSQLTEK	R	D	95.00%	95		715.8821	2	5.0	745	756	No
				QSEDLGSQFTEIFIK	R	Q	95.00%	86		871.4423	2	6.8	109	123	No
				SQLNSQSVEITK	K	L	95.00%	61		667.3552	2	4.6	799	810	No
				SSQTSGTNEQSSAIVSAR	K	D	95.00%	99		905.4383	2	6.1	765	782	No
				SVEVQGETETIIATK	K	T	95.00%	64		802.9300	2	8.5	828	842	No
				TLEQHDNIVTHYK	K	N	95.00%	52		799.4094	2	8.4	644	656	No
550	IPI00745335	GPX4	GLUTATHIONE PEROXIDASE 4 ISOFORM C PRECURSOR.	DIDGHMVNLDK	K	Y	95.00%	37	M6: Oxidation	636.8033	2	7.2	85	95	No
				TEVNYTQLVDLHAR	K	Y	95.00%	35		553.6261	3	7.5	113	126	No
				YGPMEEPLVIEK	R	D	95.00%	60	M4: Oxidation	710.8615	2	8.1	217	228	No
551	IPI00745729	SELENBP1	SELENIUM BINDING PROTEIN 1.	DGLIPLEIR	K	F	95.00%	34		513.3059	2	4.0	252	260	No
				EGSVMLQVDVDTVK	R	G	95.00%	35	M5: Oxidation	768.3892	2	5.1	426	439	No
				GGFVLLDGETFEVK	K	G	95.00%	73		755.8995	2	7.8	167	180	No
				GGPVQVLEDEELK	K	S	95.00%	63		706.8714	2	5.3	364	376	No
				GGPVQVLEDEELKSQPEPLVVK	K	G	95.00%	72		797.4384	3	7.3	364	385	No
				HEIVQTLSLK	R	D	95.00%	65		584.3430	2	3.6	242	251	No
				HNVMISTEWAAPNVLR	R	D	95.00%	61	M4: Oxidation	927.4771	2	7.0	202	217	No
				IYVVDVGSEPR	R	A	95.00%	79		617.3302	2	3.8	110	120	No
				LNPNFLVDFGK	K	E	95.00%	69		632.3464	2	8.8	444	454	No
				LNPNFLVDFGKEPLGPALAHELR	K	Y	95.00%	84		849.8018	3	6.7	444	466	No
				LTGQLFLGGSIVK	R	G	95.00%	105		666.9019	2	4.9	351	363	No
				LVLPSLISSR	K	I	95.00%	72		542.8426	2	4.1	100	109	No
				NTGTEAPDYLATVDVDPK	R	S	95.00%	104		953.4652	2	7.4	41	58	No
				QFYPDLIR	K	E	95.00%	31		526.2844	2	3.0	418	425	No

				VAGGPQMIQLSLDGK	R	R	95.00%	33	M7: Oxidation	765.4089	2	6.5	389	403	No
				VAGGPQMIQLSLDGKR	R	L	95.00%	36	M7: Oxidation	843.4554	2	1.2	389	404	No
				VAGGPQMIQLSLDGKR	R	L	95.00%	39	M7: Oxidation	562.6410	3	3.7	389	404	No
552	IPI00745872	ALB	ISOFORM 1 OF SERUM ALBUMIN PRECURSOR.	AEFAEVSK	K	L	95.00%	45		880.4445	1	3.3	250	257	No
				AEFAEVSK	K	L	95.00%	57		440.7264	2	3.8	250	257	No
				AEFAEVSKLVTDLTK	K	V	95.00%	58		825.9559	2	5.0	250	264	No
				AEFAEVSKLVTDLTK	K	V	95.00%	48		550.9741	3	6.7	250	264	No
				AVMDDFAAFVEK	K	C	95.00%	95	M3: Oxidation	679.8226	2	5.2	570	581	No
				AVMDDFAAFVEK	K	C	95.00%	44	M3: Oxidation	453.5525	3	8.5	570	581	No
				AVMDDFAAFVEK	K	C	95.00%	76		671.8243	2	4.0	570	581	No
				DDNPNLPR	K	L	95.00%	45		940.4522	1	3.4	131	138	No
				DDNPNLPR	K	L	95.00%	53		470.7292	2	1.8	131	138	No
				DLGEENFK	K	A	95.00%	47		951.4467	1	4.5	37	44	No
				DLGEENFK	K	A	95.00%	37		476.2272	2	4.3	37	44	No
				DVFLGMFLYEYAR	K	R	95.00%	94	M6: Oxidation	820.4003	2	6.0	348	360	No
				DVFLGMFLYEYAR	K	R	95.00%	51	M6: Oxidation	547.2682	3	3.6	348	360	No
				FKDLGEENFK	R	A	95.00%	58		1226.6180	1	9.8	35	44	No
				FKDLGEENFK	R	A	95.00%	58		613.8035	2	-5.6	35	44	No
				FKDLGEENFK	R	A	95.00%	48		409.5415	3	2.5	35	44	No
				FQNALLVR	K	Y	95.00%	34		960.5679	1	5.0	427	434	No
				FQNALLVR	K	Y	95.00%	60		480.7861	2	1.2	427	434	No
				HPDYSVVLLLR	R	L	95.00%	70		656.3804	2	7.8	362	372	No
				HPDYSVVLLLR	R	L	95.00%	53		437.9212	3	4.0	362	372	No
				HPYFYAPELLFFAK	R	R	95.00%	62		871.9568	2	6.4	170	183	No
				HPYFYAPELLFFAK	R	R	95.00%	70		581.6390	3	3.9	170	183	No
				KLVAASQAALGL	K	-	95.00%	78		571.3533	2	3.7	598	609	No
				KQTALVELVK	K	H	95.00%	58		564.8547	2	1.9	549	558	No
				KVPQVSTPTLVEVSR	K	N	95.00%	111		820.4772	2	5.1	438	452	No
				KVPQVSTPTLVEVSR	K	N	95.00%	85		547.3200	3	3.7	438	452	No
				KYLYEIAR	K	R	95.00%	54		528.3001	2	3.2	161	168	No
				LDELRDEGK	K	A	95.00%	51		537.7772	2	3.1	206	214	No
				LVAASQAALGL	K	-	95.00%	37		1013.6050	1	5.4	599	609	No
				LVAASQAALGL	K	-	95.00%	102		507.3055	2	3.6	599	609	No
				LVNEVTEFAK	K	T	95.00%	40		1149.6250	1	8.3	66	75	No
				LVNEVTEFAK	K	T	95.00%	82		575.3112	2	-1.0	66	75	No
				LVTDLTK	K	V	95.00%	45		789.4758	1	4.3	258	264	No
				NYAEAK	K	D	95.00%	28		695.3401	1	5.4	342	347	No
				PLVEEPQNLIK	K	Q	95.00%	60		640.3707	2	5.5	403	413	No
				QNCELFEQLGEYK	K	F	95.00%	44		800.8742	2	5.5	414	426	No
				QTALVELVK	K	H	95.00%	29		1000.6110	1	6.4	550	558	No
				QTALVELVK	K	H	95.00%	82		500.8068	2	1.5	550	558	No
				RHPDYSVVLLLR	R	L	95.00%	61		734.4314	2	7.7	361	372	No
				RHPDYSVVLLLR	R	L	95.00%	94		489.9563	3	6.6	361	372	No
				RHPYFYAPELLFFAK	R	R	95.00%	79		950.0098	2	8.4	169	183	No
				RHPYFYAPELLFFAK	R	R	95.00%	79		633.6726	3	3.3	169	183	No
				RHPYFYAPELLFFAK	R	R	95.00%	54		475.5072	4	5.0	169	183	No
				RHPYFYAPELLFFAKR	R	Y	95.00%	42		514.5333	4	6.3	169	184	No
				SHCIAEVENDEMPADLPSLAADFVESK	K	D	95.00%	45	M12: Oxidation	978.4537	3	9.1	311	337	No
				SLHTLFGDK	K	L	95.00%	53		1017.5430	1	5.8	89	97	No
				SLHTLFGDK	K	L	95.00%	60		509.2738	2	2.8	89	97	No
				TYETTLEK	K	C	95.00%	44		492.7504	2	4.0	376	383	No
				VFDEFKPLVEEPQNLIK	K	Q	95.00%	106		1023.0590	2	6.9	397	413	No
				VFDEFKPLVEEPQNLIK	K	Q	95.00%	56		682.3737	3	4.4	397	413	No
				VPQVSTPTLVEVSR	K	N	95.00%	85		756.4295	2	5.2	439	452	No
				VPQVSTPTLVEVSR	K	N	95.00%	56		504.6211	3	2.9	439	452	No
				YLYEIAR	K	R	95.00%	31		927.4971	1	3.4	162	168	No
				YLYEIAR	K	R	95.00%	49		464.2514	2	1.1	162	168	No
553	IPI00746165	WDR1	ISOFORM 1 OF WD REPEAT PROTEIN 1.	AHDGGIYAISWSPDSTHLLSASGDK	K	T	95.00%	79		862.4228	3	9.7	232	256	No
				FATASADGQIYIYDGK	R	T	95.00%	56		860.4206	2	5.9	204	219	No
				FGAVFLWDSGSSVGEITGHNK	K	V	95.00%	45		736.7022	3	8.4	127	147	No
				IKDIAWTEDSKR	K	I	95.00%	34		731.3954	2	8.6	105	116	No
				LHHVSSLAWLDEHTLVTTSHDASVK	R	E	95.00%	35		696.6121	4	4.7	576	600	No
				LYSILGTTLKDEGK	R	L	95.00%	85		769.4307	2	3.7	471	484	No
				LYSILGTTLKDEGK	R	L	95.00%	30		513.2906	3	5.4	471	484	No
				NIDNPALADIYTEHAHQVVVAK	R	Y	95.00%	37		806.7560	3	4.5	44	65	No
				VFASLPQVER	K	G	95.00%	38		573.3218	2	3.4	8	17	No

				VVTVFSVADGYSENNVFYGHHAK	K	I	95.00%	54		847.4194	3	8.7	512	534	No
				VVTVFSVADGYSENNVFYGHHAK	K	I	95.00%	39		635.8149	4	6.2	512	534	No
				YAPSGFYIASGDVSGK	K	L	95.00%	119		809.8954	2	4.8	66	81	No
				YTSLMLR	R	D	95.00%	29	M5: Oxidation	450.2390	2	4.6	390	396	No
554	IPI00747355	PREP	PROLYL ENDOPEPTIDASE.	ELPDVLER	K	V	95.00%	48		970.5228	1	1.8	163	170	No
				ELPDVLER	K	V	95.00%	38		485.7661	2	3.5	163	170	No
				FIATLQYIVGR	K	S	95.00%	69		640.8765	2	6.5	652	662	No
				GIDASDYQTVQIFYPSK	K	D	95.00%	110		966.4810	2	7.7	429	445	No
				GMFYNSYPQQDGK	K	S	95.00%	45	M2: Oxidation	775.8336	2	0.6	184	196	No
				HMGGILAVANIR	R	G	95.00%	63	M2: Oxidation	634.3538	2	4.0	494	505	No
				HMGGILAVANIR	R	G	95.00%	58	M2: Oxidation	423.2377	3	2.2	494	505	No
				KQSNPLLIHVDTK	R	A	95.00%	52		746.9332	2	6.5	665	677	No
				KQSNPLLIHVDTK	R	A	95.00%	35		498.2895	3	2.5	665	677	No
				LIDNFEGEYDYVTNEGTVFTFK	K	T	95.00%	68		867.7477	3	9.2	282	303	No
				LPEADDIQYPSMLLLTADHDDR	K	V	95.00%	66	M12: Oxidation	848.7422	3	7.0	622	643	No
				MTELYDYPK	R	Y	95.00%	41	M1: Oxidation	588.2718	2	5.4	67	75	No
				NILQLHDLTTGALLK	K	T	95.00%	52		825.4893	2	7.0	359	373	No
				NILQLHDLTTGALLK	K	T	95.00%	30		550.6618	3	6.3	359	373	No
				TFPLDVGSIVGYSGQK	K	K	95.00%	92		834.4423	2	7.2	374	389	No
				TFPLDVGSIVGYSGQK	K	K	95.00%	50		556.6283	3	2.8	374	389	No
				VFLDPNILSDDGTVALR	R	G	95.00%	130		922.9985	2	7.1	112	128	No
				VFLDPNILSDDGTVALR	R	G	95.00%	76		615.6668	3	4.7	112	128	No
				VIEEVSDMFAFIAR	K	C	95.00%	46	M8: Oxidation	821.9170	2	6.9	689	702	No
				VINIDFRDPEESK	R	W	95.00%	41		781.4026	2	7.0	313	325	No
				VINIDFRDPEESKWK	R	V	95.00%	29		625.9948	3	4.2	313	327	No
				VLYVQDSLEGEAR	R	V	95.00%	71		739.8808	2	3.1	99	111	No
				WMGGAELSDDGR	K	Y	95.00%	34	M2: Oxidation	655.2803	2	3.4	234	245	No
				YFYFYNTGLQNQR	R	V	95.00%	67		857.4117	2	7.7	86	98	No
				YVLLSIR	R	E	95.00%	42		432.2730	2	3.3	246	252	No
555	IPI00759493	SUCLG1	SUCCINATE-COA LIGASE, GDP-FORMING, ALPHA SUBUNIT.	EKISALQSAGVVVSMSPAQLGTTIYK	K	E	95.00%	29	M15: Oxidation	898.8210	3	3.3	313	338	No
				GGQTHLGLPVFNTVK	K	E	95.00%	36		784.4412	2	9.3	91	105	No
				GGQTHLGLPVFNTVK	K	E	95.00%	29		523.2952	3	6.5	91	105	No
				IGIMPGHIHK	K	K	95.00%	34	M4: Oxidation	559.8155	2	7.6	183	192	No
				ISALQSAGVVVSMSPAQLGTTIYK	K	E	95.00%	74	M13: Oxidation	813.1135	3	9.6	315	338	No
				MGHAGAIIAGGK	R	G	95.00%	65	M1: Oxidation	549.7929	2	4.3	297	308	No
				QGTFHSQQALEYGTK	K	L	95.00%	44		847.9175	2	7.9	67	81	No
				QGTFHSQQALEYGTK	K	L	95.00%	36		565.6111	3	2.2	67	81	No
				RMGHAGAIIAGGK	R	G	95.00%	49	M2: Oxidation	418.8986	3	4.6	296	308	No
556	IPI00759542; IPI00759754	TTN	ISOFORM 8 OF TITIN.; ISOFORM 1 OF TITIN.	AGDTIVLNAISILGKPLPK	K	S	95.00%	26		640.7288	3	8.8	21443	21461	No
				ATSTAELLVQGEEEVPAKK	R	T	95.00%	34		667.3629	3	8.8	185	203	No
				TIVSTAQISESR	K	Q	95.00%	55		646.3512	2	6.9	206	217	No
				VGTGEPVETDNPVEAR	R	S	95.00%	57		835.4119	2	7.5	14221	14236	No
				VTGIPTPVVK	R	F	95.00%	21		505.8200	2	7.0	127	136	No
557	IPI00783128	FLNC	GAMMA FILAMIN VARIANT.	AEIAFEDR	K	K	95.00%	39		950.4654	1	7.4	2337	2344	No
				AEIAFEDR	K	K	95.00%	42		475.7347	2	3.3	2337	2344	No
				AEIAFEDRK	K	D	95.00%	39		539.7845	2	7.1	2337	2345	No
				AFGPGLEGGLVNK	R	A	95.00%	98		629.8481	2	6.8	1335	1347	No
				AGTNMMMVGVHGPK	K	T	95.00%	36	M5: Oxidation, M6: Oxidation, M7: Oxidation	739.3388	2	6.4	2643	2656	No
				AGTNMMMVGVHGPK	K	T	95.00%	39	M5: Oxidation, M6: Oxidation, M7: Oxidation	493.2277	3	4.9	2643	2656	No
				AKLDVQFAGTAK	K	G	95.00%	60		624.8552	2	5.8	880	891	No
				AKLDVQFAGTAK	K	G	95.00%	46		416.9054	3	4.2	880	891	No
				APLQVAVLGPTGVAEPVEVR	R	D	95.00%	124		1001.5790	2	7.7	1455	1474	No
				APLQVAVLGPTGVAEPVEVR	R	D	95.00%	61		668.0552	3	8.0	1455	1474	No
				ASGPGLNASGIPASLPVEFTIDAR	R	D	95.00%	39		780.7512	3	7.5	1524	1547	No
				ATIRPVFDPSK	K	V	95.00%	39		615.8511	2	7.8	1127	1137	No
				ATIRPVFDPSK	K	V	95.00%	38		410.9016	3	3.6	1127	1137	No
				AWGPGLETGQVGK	R	S	95.00%	89		650.3431	2	6.5	556	568	No
				DAGEGGLSLAVEGPSK	K	A	95.00%	123		743.8774	2	5.2	1866	1881	No
				DAGEGLLTVQILDPEGKPK	R	K	95.00%	102		990.5425	2	5.7	1548	1566	No
				DAGEGLLTVQILDPEGKPK	R	K	95.00%	49		660.6998	3	9.1	1548	1566	No
				DFEIIDNHDYSYTVK	R	Y	95.00%	104		929.9362	2	7.7	897	911	No

DLAEDAPWK	K	K	95.00%	35		522.7562	2	4.0	7	15	Yes
DNGDGTHTVHYTPATDGPYTVAVK	R	Y	95.00%	59		839.3979	3	3.4	1475	1498	No
DNGDGTYTVSYLPDMSGR	R	Y	95.00%	93	M15: Oxidation	982.4302	2	9.2	1572	1589	No
DTVEVALEDK	R	G	95.00%	55		1118.5630	1	3.8	402	411	No
DTVEVALEDK	R	G	95.00%	53		559.7844	2	2.4	402	411	No
DTVEVALEDKGDSTFR	R	C	95.00%	34		891.4362	2	4.8	402	417	No
DTVEVALEDKGDSTFR	R	C	95.00%	54		594.6267	3	4.8	402	417	No
EAGAGGLSIAVEGPSK	R	A	95.00%	113		721.8819	2	4.7	2321	2336	Yes
EKGDYILIVK	K	W	95.00%	29		589.3495	2	6.5	2680	2689	No
EVTTEFTVDAR	R	S	95.00%	45		1267.6280	1	8.3	1248	1258	No
EVTTEFTVDAR	R	S	95.00%	89		634.3160	2	5.6	1248	1258	No
FADKHVPGSPFTVK	K	V	95.00%	46		765.4158	2	7.9	2094	2107	No
FADKHVPGSPFTVK	K	V	95.00%	29		510.6121	3	5.7	2094	2107	No
FDDKHIPGSPFTAK	R	I	95.00%	38		520.6034	3	5.6	1912	1925	No
FNDEHIPDSPFVVPVASLSDDAR	K	R	95.00%	68		843.0810	3	6.7	2367	2389	No
FNDEHIPDSPFVVPVASLSDDARR	K	L	95.00%	33		895.1133	3	4.7	2367	2390	No
FNDEHIPDSPFVVPVASLSDDARR	K	L	95.00%	57		671.5864	4	3.9	2367	2390	No
FNGAHIPGSPFK	K	I	95.00%	39		636.3336	2	4.4	2462	2473	No
FVPQEMGPHTVAVK	R	Y	95.00%	38	M6: Oxidation	778.4025	2	1.8	2258	2271	No
GAGGQGQLDVR	R	M	95.00%	69		529.2767	2	6.0	972	982	No
GAGTGGLGLAIEGPSEAK	R	M	95.00%	122		792.9179	2	2.7	1357	1374	No
GAGTGGLGLAIEGPSEAK	R	M	95.00%	34		528.9495	3	5.9	1357	1374	No
GDYILIVK	K	W	95.00%	23		920.5538	1	8.7	2682	2689	No
GDYILIVK	K	W	95.00%	45		460.7792	2	5.2	2682	2689	No
GEVVRDFEIIDNHDYSYTVK	K	Y	95.00%	36		800.3948	3	7.2	892	911	No
GGLVGTPAPFSIDTK	K	G	95.00%	82		730.4005	2	9.0	1054	1068	No
GLSEGHTFQVAEFIVDTR	K	N	95.00%	66		669.3414	3	5.0	2030	2047	No
GPGLSQAFVGQK	R	N	95.00%	79		594.8259	2	5.1	2622	2633	No
GQHVPGSPFQFTVGPLGEGGAHK	R	V	95.00%	48		768.7294	3	8.7	2274	2296	No
GQHVPGSPFQFTVGPLGEGGAHK	R	V	95.00%	53		576.7983	4	7.5	2274	2296	No
GVAGVPAEFSIWTR	R	E	95.00%	62		745.4005	2	8.6	2307	2320	No
GVAGVPAEFSIWTR	R	E	95.00%	54		497.2699	3	9.1	2307	2320	No
HIGISFTPK	R	E	95.00%	43		999.5707	1	7.8	1980	1988	No
HIGISFTPK	R	E	95.00%	46		500.2882	2	5.7	1980	1988	No
HTIIISWGGVNVPK	K	S	95.00%	90		760.9391	2	7.5	718	731	No
HTIIISWGGVNVPK	K	S	95.00%	44		507.6274	3	4.9	718	731	No
IHALPTGDASK	R	C	95.00%	28		555.3066	2	8.8	1608	1618	No
ILVGPSEIGDASK	K	V	95.00%	82		643.3567	2	4.0	2011	2023	No
IPGNWFQMVSAQER	K	L	95.00%	78	M8: Oxidation	839.9113	2	8.1	2140	2153	No
IQIGQETVITVDAK	R	A	95.00%	104		757.9312	2	7.5	1638	1651	No
IQQNTFTR	K	W	95.00%	44		504.2695	2	3.8	17	24	Yes
ITESDLSQLTASIR	K	A	95.00%	88		767.4159	2	7.4	1949	1962	No
ITESDLSQLTASIR	K	A	95.00%	46		511.9456	3	5.7	1949	1962	No
LDVQFAGTAK	K	G	95.00%	69		525.2868	2	2.3	882	891	No
LENVSVALEFLER	K	E	95.00%	98		759.9173	2	6.5	77	89	No
LENVSVALEFLER	K	E	95.00%	74		506.9472	3	6.0	77	89	No
LEPGGGAEAQAVR	K	Y	95.00%	88		627.8296	2	5.6	995	1007	No
LGSFGSITR	R	Q	95.00%	48	S3: Phospho	509.2448	2	4.7	2211	2219	No
LGSFGSITR	R	Q	95.00%	65		469.2605	2	2.7	2211	2219	No
LIALLEVLSQK	R	R	95.00%	103		613.8940	2	6.3	50	60	Yes
LIALLEVLSQK	R	R	95.00%	43		409.5984	3	5.8	50	60	Yes
LIALLEVLSQKR	R	M	95.00%	80		691.9463	2	8.0	50	61	Yes
LIALLEVLSQKR	R	M	95.00%	60		461.6314	3	3.5	50	61	Yes
LLGWIQNK	R	V	95.00%	66		486.2895	2	3.5	145	152	No
LSGGHSLHETSTVLVETVTK	R	S	95.00%	126		1048.0630	2	6.6	2577	2596	No
LSGGHSLHETSTVLVETVTK	R	S	95.00%	85		699.0456	3	8.5	2577	2596	No
LSGGHSLHETSTVLVETVTK	R	S	95.00%	51		524.5341	4	4.5	2577	2596	No
LTVTSLQETGLK	R	V	95.00%	93		645.3739	2	6.2	2391	2402	No
NAGYGGLGLSIEGPSK	R	V	95.00%	82		760.3980	2	8.1	2048	2063	No
PNITDNKDGTITVR	R	Y	95.00%	52		515.2775	3	5.6	1792	1805	No
QQEGEASSQDMTAQVTSPSGK	R	V	95.00%	89	M11: Oxidation	1091.4920	2	8.5	2220	2240	No
QQEGEASSQDMTAQVTSPSGK	R	V	95.00%	69	M11: Oxidation	727.9937	3	3.9	2220	2240	No

				RDTVEVALEDK	R	G	95.00%	56		637.8364	2	4.3	401	411	No
				RDTVEVALEDKGDSTFR	R	C	95.00%	73		646.6600	3	3.7	401	417	No
				RLTVTSLQETGLK	R	V	95.00%	85		723.4264	2	8.3	2390	2402	No
				RLTVTSLQETGLK	R	V	95.00%	52		482.6197	3	7.3	2390	2402	No
				SLTATGGNHVTAR	R	V	95.00%	87		642.8409	2	6.2	1259	1271	No
				SPFEVNVGMALGDANK	R	V	95.00%	66	M9: Oxidation	832.9090	2	8.9	342	357	No
				SPFEVQVSPEAGVQK	R	V	95.00%	131		801.4181	2	6.9	539	553	No
				SPFVVNVAPPLDLSK	K	I	95.00%	88		791.9487	2	3.2	934	948	No
				TARPNITDNKDGTITVR	K	Y	95.00%	37		936.5098	2	9.4	1789	1805	No
				TARPNITDNKDGTITVR	K	Y	95.00%	52		624.6720	3	3.3	1789	1805	No
				TARPNITDNKDGTITVR	K	Y	95.00%	46		468.7553	4	1.8	1789	1805	No
				TDTYVTDNGDGTYR	K	V	95.00%	74		789.3439	2	5.0	1280	1293	No
				TGVEVGKPTHFTVLTK	R	G	95.00%	59		857.4876	2	7.7	860	875	No
				TGVEVGKPTHFTVLTK	R	G	95.00%	44		571.9916	3	2.8	860	875	No
				TGVEVGKPTHFTVLTK	R	G	95.00%	28		429.2467	4	5.3	860	875	No
				TSQLNVGTSTDVSLK	R	I	95.00%	86		775.4129	2	6.8	1934	1948	No
				TYAVSYVPK	R	V	95.00%	42		514.2799	2	5.3	315	323	No
				VAVGQEQAFSVNTR	K	G	95.00%	108		753.3917	2	2.9	958	971	No
				VAVGQEQAFSVNTR	K	G	95.00%	37		502.5977	3	4.3	958	971	No
				VDITYDGHPVPGSPFAVEGVLPPDPSK	K	V	95.00%	40		930.8109	3	6.4	1018	1044	No
				VEAAEIVEGEDSAYSVR	K	F	95.00%	149		912.4412	2	4.6	2241	2257	No
				VEAAEIVEGEDSAYSVR	K	F	95.00%	102		608.6295	3	3.6	2241	2257	No
				VEESTQVGGDPFPAVFGDFLGR	R	E	95.00%	118		1162.5730	2	7.8	2187	2208	No
				VEESTQVGGDPFPAVFGDFLGR	R	E	95.00%	71		775.3848	3	8.1	2187	2208	No
				VHVQPAVDTSGVK	R	V	95.00%	41		668.8706	2	8.1	1222	1234	No
				VHVQPAVDTSGVK	R	V	95.00%	57		446.2478	3	3.9	1222	1234	No
				VNQPASFAVQLNGAR	K	G	95.00%	90		786.4236	2	6.3	2403	2417	No
				VPQLPITNFNR	K	D	95.00%	48		649.8670	2	3.1	153	163	No
				VPVKDVVDPGK	R	V	95.00%	53		576.8375	2	3.5	1415	1425	No
				VPVKDVVDPGKVK	R	C	95.00%	44		690.4224	2	7.7	1415	1427	No
				VQYTAYEEGVHLVEVLYDEVAVPK	R	S	95.00%	39		917.4767	3	8.0	1294	1317	No
				VSGPGVEPHGVLR	K	E	95.00%	69		652.3611	2	1.5	1235	1247	No
				VSGPGVEPHGVLR	K	E	95.00%	42		435.2441	3	3.3	1235	1247	No
				VTVLFAGQNIER	K	S	95.00%	81		673.8776	2	3.0	330	341	No
				VTVLFAGQNIER	K	S	95.00%	37		449.5888	3	5.5	330	341	No
				VYGPGVEK	K	T	95.00%	43		424.7320	2	5.1	749	756	No
				VYNVTYTVK	R	E	95.00%	64		543.7976	2	3.5	2671	2679	No
				WGDESVPGSPFK	K	V	95.00%	64		653.3127	2	4.6	2690	2701	No
				YADQEVPR	K	S	95.00%	54		489.2416	2	6.3	1499	1506	No
				YDGNHIPGSPLQFYVDAINSR	K	H	95.00%	61		788.3928	3	8.7	1820	1840	No
				YGGDEIPYSPFR	K	I	95.00%	83		700.8336	2	7.6	1596	1607	No
				YGGPQHIVGSPFK	K	A	95.00%	93		693.8650	2	3.6	2557	2569	No
				YGGPQHIVGSPFK	K	A	95.00%	42		462.9139	3	6.5	2557	2569	No
				YRGQHVPGSPFQFTVGPLGEGGAHK	K	V	95.00%	49		656.5881	4	4.5	2272	2296	No
				YTAVQQGNMAVTVTYGGDPVPK	K	S	95.00%	50	M9: Oxidation	771.3857	3	7.9	912	933	No
				YVVTITWGGYAIPR	K	S	95.00%	65		798.4373	2	5.0	525	538	No
558	IPI00024913; IPI00218482; IPI00784162; IPI00784277; IPI00793677; IPI00794316; IPI00795385	C21orf33	ISOFORM LONG OF ES1 PROTEIN HOMOLOG, MITOCHONDRIAL PRECURSOR.; ISOFORM SHORT OF ES1 PROTEIN HOMOLOG, MITOCHONDRIAL PRECURSOR.; 25 KDA PROTEIN.; 28 KDA PROTEIN.; PROTEIN.; 24 KDA PROTEIN.; 23 KDA PROTEIN.	GGAEVQIFAPDVPQMHVIDHTK	R	G	95.00%	31	M15: Oxidation	802.4045	3	2.2	73	94	No
				GGAEVQIFAPDVPQMHVIDHTK	R	G	95.00%	36		797.0752	3	5.2	73	94	No
				GVEVTVGHEQEEGGK	R	W	95.00%	76		777.8788	2	6.2	189	203	No
				ITDLANLSAANHDAAIFPGGFGAAK	K	N	95.00%	68		814.7595	3	8.5	117	141	No
				NLSTFAVDGK	K	D	95.00%	45		526.2773	2	4.2	142	151	No
559	IPI00216704; IPI00237806; IPI00783228; IPI00784382	SPTB	ISOFORM 2 OF SPECTRIN BETA CHAIN, ERYTHROCYTE.; ISOFORM 3 OF SPECTRIN BETA CHAIN, ERYTHROCYTE.; ISOFORM 1 OF SPECTRIN BETA CHAIN, ERYTHROCYTE.; SPECTRIN BETA ISOFORM A.	AQEASVLLR	K	D	95.00%	35		493.7861	2	0.9	1263	1271	No
				DGLAFNALIHK	K	H	95.00%	35		599.8387	2	9.3	204	214	No

				DLAGIIAIQR	R	K	95.00%	59		535.3274	2	9.1	986	995	No
				DVSSVELLMK	R	Y	95.00%	28	M9: Oxidation	568.8022	2	8.1	1934	1943	No
				ELHLLGVQVQQFQDVATR	R	L	95.00%	50		694.3811	3	6.3	1844	1861	No
				FLDLLEPLGR	R	R	95.00%	59		586.8414	2	5.7	1460	1469	No
				HNLEHAFNVAER	R	Q	95.00%	36		479.5767	3	7.7	232	243	No
				LLSGEDVGQDEGATR	R	A	95.00%	70		773.8758	2	5.7	765	779	No
				LLTSQDVSYDEAR	K	N	95.00%	58		748.8711	2	7.3	1294	1306	No
				LMEADIAIQGDK	K	V	95.00%	37	M2: Oxidation	660.3325	2	4.0	572	583	No
				LVAEGNLYSDK	K	I	95.00%	33		604.8126	2	0.7	1234	1244	No
				TQLVDTADKFR	R	F	95.00%	32		647.3503	2	9.5	1897	1907	No
				VDNVNAFIER	R	L	95.00%	70		588.8088	2	7.2	1747	1756	No
				YFYTGAEILGLIDEK	R	H	95.00%	50		866.4523	2	6.9	1802	1816	No
560	IPI00787298	KIAA1881	SIMILAR TO PLASMA MEMBRANE ASSOCIATED PROTEIN, S3-12.	AKDAVSSGVASVVDVAK	R	G	95.00%	32		534.9666	3	8.6	88	104	Yes
				DAVSTGLTGAVNLAK	K	G	95.00%	75		708.8933	2	6.2	717	731	Yes
				DAVSTGLTGAVNVAK	K	G	95.00%	80		701.8852	2	6.0	420	434	Yes
				DAVSTGLTGAVNVAR	K	G	95.00%	89		715.8887	2	6.4	189	203	Yes
				DAVTTGVTGAVNVAK	K	G	95.00%	89		701.8838	2	3.9	1014	1028	Yes
				DTIYSGVTSAVNVAK	K	G	95.00%	106		762.9060	2	8.7	552	566	Yes
				DTMSTGLTGAANVAK	K	G	95.00%	57	M3: Oxidation	726.8597	2	7.6	486	500	Yes
				DTVFSGVTGAMSMAK	K	G	95.00%	70	M11: Oxidation, M13: Oxidation	767.3548	2	5.7	1047	1061	Yes
				DTVTTGLMGAVNVAK	K	G	95.00%	76	M8: Oxidation	746.8931	2	6.8	618	632	Yes
				DTVTTGLVGAVNVAK	K	G	95.00%	92		722.9084	2	5.3	519	533	Yes
				DTVTTGVMGAVNLAK	K	G	95.00%	53	M8: Oxidation	746.8915	2	4.7	156	170	No
				EAVSSGVTGAMDMAK	K	G	95.00%	83	M11: Oxidation, M13: Oxidation	743.3381	2	7.9	123	137	No
				GVVQGGLDTTR	K	S	95.00%	48		551.7995	2	4.8	105	115	Yes
				LDQGSGASAEDAAVQEER	R	D	95.00%	101		916.9216	2	4.9	1300	1317	Yes
				LGDLGPSFR	R	Q	95.00%	47		481.2621	2	5.7	1247	1255	Yes
				NTFGSGVTGAVNVAK	K	G	95.00%	115		711.3758	2	3.4	585	599	No
				VLSAEQGSYFVR	K	L	95.00%	59		678.3550	2	4.8	1235	1246	Yes
561	IPI00787362	LOC730839	SIMILAR TO HORNERIN.	GPYESGSGHSSGLGHR	R	E	95.00%	50		792.8666	2	6.2	1013	1028	No
				HGSGSGHSSSYGQHGSGSGWSSSSGR	R	H	95.00%	43		620.0169	4	9.4	1340	1365	No
				SSSRGPYESGSGHSSGLGHQESR	R	S	95.00%	51		587.2678	4	0.7	568	590	No
562	IPI00789324	JUP	JUP PROTEIN.	ALMGSPQLVAAVVR	R	T	95.00%	82	M3: Oxidation	714.4111	2	7.1	178	191	No
				LLNDEDPVVVTK	K	A	95.00%	47		671.3708	2	5.2	150	161	No
				LNYGIPAIVK	R	L	95.00%	35		544.3327	2	5.4	478	487	No
				NEGTATYAAAVLFR	R	I	95.00%	30		742.3882	2	9.5	638	651	No
				VSVELTNSLFK	R	H	95.00%	50		618.8497	2	6.2	664	674	No
563	IPI00792715	ENO2	37 KDA PROTEIN.	DGKYDLDFK	R	S	95.00%	44		1100.5370	1	9.5	161	169	No
				DGKYDLDFK	R	S	95.00%	51		550.7701	2	5.1	161	169	No
				MLELDGTENK	-	S	95.00%	45	M1: Oxidation	1165.5450	1	3.4	1	10	No
				YDLDFK	K	S	95.00%	31		400.6970	2	3.8	164	169	Yes
				YNQLMR	K	I	95.00%	41	M5: Oxidation	420.7076	2	4.2	314	319	Yes
564	IPI00793379		165 KDA PROTEIN.	APEILVR	R	L	95.00%	38		797.4920	1	4.3	153	159	No
				APVYSGSSPVSGYFVDFR	K	E	95.00%	100		967.9772	2	9.3	835	852	No
				APVYSGSSPVSGYFVDFR	K	E	95.00%	46		645.6537	3	8.8	835	852	No
				ATGIIEMVMDR	K	F	95.00%	43	M7: Oxidation, M9: Oxidation	634.3088	2	5.6	1069	1079	No
				ATLKDDRGQDVSILEIAGK	K	V	95.00%	35		677.0401	3	5.7	1200	1218	No
				AVNANGVGKPSDTSEPVLVEAR	R	P	95.00%	63		737.3895	3	5.0	889	910	No
				AVNAVGMSENSQESDVIK	K	V	95.00%	147	M7: Oxidation	947.4510	2	4.2	686	703	No
				AVNAVGMSENSQESDVIK	K	V	95.00%	39		939.4545	2	5.2	686	703	No
				DDEGLYTLR	K	I	95.00%	33		541.2656	2	6.0	348	356	No
				FKIETVGDHSK	R	L	95.00%	32		630.8362	2	4.6	956	966	No
				FKIETVGDHSK	R	L	95.00%	32		420.8917	3	0.5	956	966	No
				FLSELAHLEEDVHLAR	R	S	95.00%	77		939.9974	2	8.3	104	119	No
				FLSELAHLEEDVHLAR	R	S	95.00%	83		627.0004	3	7.6	104	119	No
				FLSELAHLEEDVHLAR	R	S	95.00%	37		470.5012	4	5.2	104	119	No
				FSGGSPILGYYLDKR	K	E	95.00%	92		836.9449	2	7.2	736	750	No
				FVVHGLTTGEQYIFR	R	V	95.00%	97		883.9735	2	9.1	669	683	No
				FVVHGLTTGEQYIFR	R	V	95.00%	75		589.6496	3	5.7	669	683	No
				FWLQAEHLSPDASYR	R	F	95.00%	124		910.4475	2	5.7	1034	1048	No
				FWLQAEHLSPDASYR	R	F	95.00%	73		607.3002	3	4.4	1034	1048	No
				GGVSDHSAFLFVR	R	D	95.00%	70		696.3592	2	2.5	361	373	No
				GGVSDHSAFLFVR	R	D	95.00%	56		464.5763	3	4.4	361	373	No

				GKDPLMYFIEK	R	S	95.00%	36	M6: Oxidation	678.8515	2	5.6	538	548	No
				GKDPLMYFIEK	R	S	95.00%	29	M6: Oxidation	452.9042	3	6.8	538	548	No
				GKDPLMYFIEK	R	S	95.00%	60		670.8530	2	4.1	538	548	No
				GQDVSILEIAGK	R	V	95.00%	92		615.3443	2	5.3	1207	1218	No
				GVTSEDSGKYSINIK	K	N	95.00%	87		799.4121	2	5.6	1405	1419	No
				HGEKIPDMAPPQQAK	K	P	95.00%	32	M8: Oxidation	554.9497	3	3.5	1436	1450	No
				HGEKIPDMAPPQQAKPK	K	L	95.00%	39	M8: Oxidation	629.9986	3	2.5	1436	1452	No
				HGEKIPDMAPPQQAKPK	K	L	95.00%	35	M8: Oxidation	472.7508	4	2.3	1436	1452	No
				HGLSEPSEITSPIQAQDVTVVPSAPGR	R	V	95.00%	73		924.8177	3	7.5	591	617	No
				HGLSEPSEITSPIQAQDVTVVPSAPGR	R	V	95.00%	33		693.8661	4	8.7	591	617	No
				IAAVNLAGIGEPSDPSEHFK	K	C	95.00%	77		684.6895	3	6.2	785	804	No
				IDVTVSVYK	K	H	95.00%	48		512.2917	2	2.8	1427	1435	No
				IESNYGVHTLEINR	R	A	95.00%	86		822.9254	2	5.1	205	218	No
				IESNYGVHTLEINR	R	A	95.00%	53		548.9517	3	3.0	205	218	No
				IPDMAPPQQAK	K	P	95.00%	49	M4: Oxidation	606.3115	2	4.6	1440	1450	No
				IPDMAPPQQAKPK	K	L	95.00%	58	M4: Oxidation	718.8844	2	2.5	1440	1452	No
				IPDMAPPQQAKPK	K	L	95.00%	40	M4: Oxidation	479.5919	3	1.8	1440	1452	No
				LIGGLPDVVTIMEGK	R	T	95.00%	64	M12: Oxidation	779.4380	2	7.5	1344	1358	No
				LIGGLPDVVTIMEGK	R	T	95.00%	34	M12: Oxidation	519.9611	3	7.1	1344	1358	No
				LIGGLPDVVTIMEGK	R	T	95.00%	40		771.4376	2	3.7	1344	1358	No
				LIPASASAAGQ	K	-	95.00%	30		985.5400	1	8.2	1453	1463	No
				LIPASASAAGQ	K	-	95.00%	51		493.2714	2	3.2	1453	1463	No
				LMALSNEIKNPTIPLK	R	S	95.00%	65	M2: Oxidation	899.5167	2	5.7	1004	1019	No
				LMALSNEIKNPTIPLK	R	S	95.00%	50	M2: Oxidation	600.0130	3	4.5	1004	1019	No
				NDQDIQLSEHFSVK	K	V	95.00%	81		830.4094	2	8.0	1379	1392	No
				NPTIPLKSELAYEIFDK	K	G	95.00%	63		989.5391	2	8.3	1013	1029	No
				NPTIPLKSELAYEIFDK	K	G	95.00%	32		660.0280	3	7.3	1013	1029	No
				NYVVLSWEPPTPR	R	G	95.00%	54		779.4136	2	8.1	525	537	No
				SELAYEIFDK	K	G	95.00%	75		607.8030	2	3.0	1020	1029	No
				SLDLSGQAFDEAFAEFQQFK	R	A	95.00%	86		760.0324	3	6.4	1315	1334	No
				SQSSLVLIGDAFK	K	T	95.00%	104		682.8791	2	5.7	1099	1111	No
				SYEEISDDER	K	F	95.00%	36		621.7623	2	3.4	946	955	No
				TSVVVQWDRPK	K	H	95.00%	56		657.8680	2	8.4	626	636	No
				TSVVVQWDRPK	K	H	95.00%	39		438.9125	3	3.4	626	636	No
				TVLEEAEFQR	K	K	95.00%	65		611.3124	2	4.4	1112	1121	No
				TVLEEAEFQRK	K	E	95.00%	57		675.3597	2	3.7	1112	1122	No
				VSDAVAALDPLDLR	R	R	95.00%	70		727.9003	2	5.0	471	484	No
				VSDAVAALDPLDLR	R	R	95.00%	48		485.6024	3	4.2	471	484	No
				VSDAVAALDPLDLRR	R	L	95.00%	62		537.6361	3	3.7	471	485	No
				WLKDDVLYETETLPNLER	K	G	95.00%	99		1117.5790	2	6.4	1163	1180	No
				WLKDDVLYETETLPNLER	K	G	95.00%	34		745.3889	3	7.3	1163	1180	No
				YAIQQMMEDK	K	L	95.00%	51	M6: Oxidation, M7: Oxidation	644.7850	2	5.3	129	138	No
				YAVFDLMEGK	R	S	95.00%	46	M7: Oxidation	594.7873	2	4.8	570	579	No
				YAVFDLMEGK	R	S	95.00%	43		586.7902	2	5.4	570	579	No
				YLLDEYASK	R	K	95.00%	43		551.2787	2	2.3	27	35	No
				YPVTGLFEGR	K	S	95.00%	65		569.7942	2	-8.0	442	451	No
				YQSLVAAYGEAK	R	R	95.00%	57		650.3359	2	4.1	89	100	No
				YTFEIFDGK	K	D	95.00%	38		560.2770	2	8.8	1301	1309	No
				YTFEIFDGKDNHQR	K	S	95.00%	75		885.4234	2	8.0	1301	1314	No
				YTFEIFDGKDNHQR	K	S	95.00%	31		443.2147	4	5.9	1301	1314	No
565	IPI00020599; IPI00793605	CALR	CALRETICULIN PRECURSOR.; 37 KDA PROTEIN.	EQFLDGDGWTSR	K	W	95.00%	71		705.8215	2	4.3	25	36	No
				FYALSASFEPFSNK	R	G	95.00%	33		804.3989	2	9.6	74	87	No
				FYGDEEKDKGLQTSQDAR	K	F	95.00%	49		696.3294	3	2.1	56	73	No
				KVHVIFNYK	K	G	95.00%	25		574.3373	2	3.4	143	151	No
566	IPI00794080		227 KDA PROTEIN.	ADIAESQVNK	R	L	95.00%	52		1074.5510	1	7.4	1939	1948	Yes
				ADIAESQVNK	R	L	95.00%	79		537.7779	2	4.4	1939	1948	Yes
				ADIAESQVNKLR	R	A	95.00%	34		448.5825	3	2.7	1939	1950	Yes
				AEDEEEINAELTAK	R	K	95.00%	117		781.3685	2	3.7	934	947	Yes
				AEDEEEINAELTAK	R	K	95.00%	68		521.2492	3	5.5	934	947	Yes
				AITDAAMMAEELK	K	K	95.00%	86	M7: Oxidation, M8: Oxidation	713.3404	2	8.6	1770	1782	Yes
				AITDAAMMAEELK	K	K	95.00%	45	M7: Oxidation, M8: Oxidation	475.8937	3	3.3	1770	1782	Yes
				AITDAAMMAEELKK	K	E	95.00%	102	M7: Oxidation	769.3866	2	3.0	1770	1783	Yes
				AITDAAMMAEELKK	K	E	95.00%	43	M7: Oxidation	513.2605	3	3.3	1770	1783	Yes
				AITDAAMMAEELKK	K	E	95.00%	83	M7: Oxidation	777.3852	2	4.5	1770	1783	Yes

AITDAAMMAEELKK	K	E	95.00%	52	M7: Oxidation	518.5913	3	1.7	1770	1783	Yes
AITDAAMMAEELKK	K	E	95.00%	83	M7: Oxidation, M8: Oxidation	777.3852	2	4.5	1770	1783	Yes
AITDAAMMAEELKK	K	E	95.00%	52	M7: Oxidation, M8: Oxidation	518.5913	3	1.7	1770	1783	Yes
AITDAAMMAEELKK	K	E	95.00%	97	M8: Oxidation	769.3875	2	4.2	1770	1783	Yes
AITDAAMMAEELKK	K	E	95.00%	48	M8: Oxidation	513.2620	3	6.3	1770	1783	Yes
AITDAAMMAEELKK	K	E	95.00%	64		761.3915	2	6.1	1770	1783	Yes
AITDAAMMAEELKK	K	E	95.00%	61		507.9294	3	4.5	1770	1783	Yes
AITDAAMMAEELKKEQDTSAHLER	K	M	95.00%	37	M7: Oxidation, M8: Oxidation	907.4404	3	6.9	1770	1793	Yes
ALQEAHQQALDDLQAEEDK	K	V	95.00%	48		718.0157	3	7.1	1006	1024	Yes
ANSEVAQWR	K	T	95.00%	51		1060.5270	1	9.1	1376	1384	Yes
ANSEVAQWR	K	T	95.00%	62		530.7650	2	4.5	1376	1384	Yes
ATLEQTER	R	A	95.00%	60		474.2459	2	4.3	1702	1709	No
DIDDLELTLAK	K	V	95.00%	51		1245.6700	1	9.1	961	971	Yes
DIDDLELTLAK	K	V	95.00%	99		623.3293	2	-5.9	961	971	Yes
DLEEATLQHEAMVAALR	R	K	95.00%	46		948.9764	2	-2.1	1185	1201	Yes
DLQHRLDEAEQLALK	K	G	95.00%	31		889.9805	2	7.2	1804	1818	Yes
DLQHRLDEAEQLALK	K	G	95.00%	48		593.6563	3	7.3	1804	1818	Yes
DPLNETVVGLYQK	K	S	95.00%	91		738.3958	2	6.1	607	619	Yes
DTQLHLDDALR	K	G	95.00%	86		648.8323	2	1.4	1664	1674	No
DTQLHLDDALR	K	G	95.00%	38		432.8916	3	3.3	1664	1674	No
EEQAEPDGTEVADK	R	T	95.00%	98		759.3368	2	3.3	371	384	No
ELEELSER	R	L	95.00%	49		1004.4910	1	0.9	1150	1157	No
ELEELSER	R	L	95.00%	42		502.7503	2	2.7	1150	1157	No
EMATMKEEFQK	K	T	95.00%	38	M2: Oxidation	694.3185	2	3.9	856	866	Yes
EMATMKEEFQK	K	T	95.00%	35	M2: Oxidation	702.3164	2	4.5	856	866	Yes
EMATMKEEFQK	K	T	95.00%	34	M2: Oxidation	468.5471	3	5.0	856	866	Yes
EMATMKEEFQK	K	T	95.00%	37	M2: Oxidation, M5: Oxidation	702.3176	2	6.3	856	866	Yes
EMATMKEEFQK	K	T	95.00%	35	M2: Oxidation, M5: Oxidation	468.5475	3	5.8	856	866	Yes
EMATMKEEFQK	K	T	95.00%	54		686.3251	2	9.8	856	866	Yes
ENQSILITGESGAGK	R	T	95.00%	118		752.3882	2	1.9	171	185	Yes
ENQSILITGESGAGK	R	T	95.00%	46		501.9288	3	3.5	171	185	Yes
EQDTSAHLER	K	M	95.00%	69		593.2841	2	8.6	1784	1793	Yes
ESIVSQLSR	K	S	95.00%	63		509.7831	2	5.0	1307	1315	No
EVTERAEDEEEINAELTAK	K	K	95.00%	123		1088.5220	2	4.6	929	947	Yes
EVTERAEDEEEINAELTAK	K	K	95.00%	64		726.0180	3	5.7	929	947	Yes
GSSFQTVSALFR	K	E	95.00%	99		650.3406	2	2.9	649	660	Yes
GSSFQTVSALFR	K	E	95.00%	47		433.8970	3	4.3	649	660	Yes
GTLEDQIISANPLLEAFGNAK	K	T	95.00%	33		734.3816	3	-7.3	215	235	No
HADSVAELGEQIDNLQR	K	V	95.00%	159		947.9762	2	9.8	1204	1220	Yes
HADSVAELGEQIDNLQR	K	V	95.00%	85		632.3179	3	6.4	1204	1220	Yes
IEELEEEIEAER	R	A	95.00%	103		744.8617	2	5.7	1123	1134	Yes
IEELEEEIEAER	R	A	95.00%	66		496.9096	3	4.0	1123	1134	Yes
IHFGTTGK	R	L	95.00%	46		860.4694	1	7.2	251	258	Yes
IHFGTTGK	R	L	95.00%	29		430.7379	2	5.7	251	258	Yes
IKELQAR	K	I	95.00%	29		429.2678	2	8.1	1116	1122	Yes
IKEVTERAEDEEEINAELTAK	K	K	95.00%	89		1209.1170	2	8.5	927	947	Yes
IKEVTERAEDEEEINAELTAK	K	K	95.00%	80		806.4133	3	8.1	927	947	Yes
IKEVTERAEDEEEINAELTAK	K	K	95.00%	50		605.0596	4	4.3	927	947	Yes
INQQLDTK	R	L	95.00%	52		480.2627	2	1.3	444	451	No
KAITDAAMMAEELKK	K	E	95.00%	98	M8: Oxidation	833.4359	2	4.9	1769	1783	Yes
KAITDAAMMAEELKK	K	E	95.00%	81	M8: Oxidation	555.9587	3	2.7	1769	1783	Yes
KAITDAAMMAEELKK	K	E	95.00%	35	M8: Oxidation	417.2235	4	8.8	1769	1783	Yes
KAITDAAMMAEELKK	K	E	95.00%	75	M8: Oxidation	841.4292	2	-0.1	1769	1783	Yes
KAITDAAMMAEELKK	K	E	95.00%	64	M8: Oxidation	561.2909	3	3.8	1769	1783	Yes
KAITDAAMMAEELKK	K	E	95.00%	75	M8: Oxidation, M9: Oxidation	841.4292	2	-0.1	1769	1783	Yes
KAITDAAMMAEELKK	K	E	95.00%	64	M8: Oxidation, M9: Oxidation	561.2909	3	3.8	1769	1783	Yes
KAITDAAMMAEELKK	K	E	95.00%	103	M9: Oxidation	833.4359	2	4.9	1769	1783	Yes
KAITDAAMMAEELKK	K	E	95.00%	63	M9: Oxidation	555.9584	3	2.3	1769	1783	Yes
KAITDAAMMAEELKK	K	E	95.00%	37	M9: Oxidation	417.2219	4	5.0	1769	1783	Yes
KAITDAAMMAEELKK	K	E	95.00%	104		825.4369	2	3.0	1769	1783	Yes
KAITDAAMMAEELKK	K	E	95.00%	87		550.6276	3	3.8	1769	1783	Yes
KDIDDLELTLAK	K	V	95.00%	109		687.3849	2	6.4	960	971	Yes
KDIDDLELTLAK	K	V	95.00%	46		458.5916	3	4.3	960	971	Yes

KGSSFQTVSALFR	K	E	95.00%	116		714.3909	2	6.5	648	660	Yes
KGSSFQTVSALFR	K	E	95.00%	57		476.5949	3	3.2	648	660	Yes
KHADSVAELGEQIDNLQR	K	V	95.00%	127		1012.0220	2	7.1	1203	1220	Yes
KHADSVAELGEQIDNLQR	K	V	95.00%	93		675.0148	3	3.8	1203	1220	Yes
KHADSVAELGEQIDNLQR	K	V	95.00%	66		506.5128	4	3.4	1203	1220	Yes
KKGSSFQTVSALFR	K	E	95.00%	66		778.4344	2	0.8	647	660	Yes
KKGSSFQTVSALFR	K	E	95.00%	49		519.2949	3	6.0	647	660	Yes
KKHADSVAELGEQIDNLQR	R	V	95.00%	89		717.7142	3	5.1	1202	1220	Yes
KKHADSVAELGEQIDNLQR	R	V	95.00%	53		538.5365	4	3.1	1202	1220	Yes
KLEGDLK	R	L	95.00%	39		401.7396	2	4.6	1062	1068	Yes
KRQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	89	M20: Oxidation	960.8171	3	8.9	147	170	Yes
KRQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	82		955.4839	3	7.2	147	170	Yes
LASADIETYLLEK	K	S	95.00%	129		733.3926	2	-1.2	259	271	Yes
LASADIETYLLEK	K	S	95.00%	66		489.2671	3	4.5	259	271	Yes
LDEAEQLALK	R	G	95.00%	51		1129.6220	1	9.6	1809	1818	Yes
LDEAEQLALK	R	G	95.00%	97		565.3107	2	2.5	1809	1818	Yes
LDEAEQLALKGGK	R	K	95.00%	66		686.3813	2	4.5	1809	1821	Yes
LDEAEQLALKGGK	R	K	95.00%	42		457.9226	3	2.6	1809	1821	Yes
LDEAEQLALKGGKK	R	Q	95.00%	81		750.4314	2	7.6	1809	1822	Yes
LDEAEQLALKGGKK	R	Q	95.00%	45		500.6212	3	2.9	1809	1822	Yes
LQDLVDK	R	L	95.00%	35		830.4684	1	7.0	1876	1882	Yes
LQDLVDK	R	L	95.00%	42		415.7369	2	4.1	1876	1882	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	49	M9: Oxidation	795.0505	3	7.6	486	503	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	35	M9: Oxidation	596.5412	4	9.8	486	503	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	43		789.7178	3	6.2	486	503	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	42		592.5402	4	6.1	486	503	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	68	M9: Oxidation	1256.1180	2	5.7	486	504	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	51	M9: Oxidation	837.7500	3	8.6	486	504	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	36		832.4160	3	5.8	486	504	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	42		499.8525	5	5.4	486	504	Yes
LTGAVMHYGNMK	K	F	95.00%	49	M11: Oxidation	669.3277	2	9.7	353	364	Yes
LTGAVMHYGNMK	K	F	95.00%	75	M6: Oxidation	669.3235	2	3.5	353	364	Yes
LTGAVMHYGNMK	K	F	95.00%	60	M6: Oxidation	677.3227	2	6.0	353	364	Yes
LTGAVMHYGNMK	K	F	95.00%	60	M6: Oxidation, M11: Oxidation	677.3227	2	6.0	353	364	Yes
LTGAVMHYGNMK	K	F	95.00%	54		661.3290	2	7.9	353	364	Yes
LYDQHLGK	K	S	95.00%	53		487.2609	2	3.1	560	567	Yes
MKGTLEDQIISANPLLEAFGNAK	K	T	95.00%	129	M1: Oxidation	1238.6360	2	-4.4	213	235	No
MKGTLEDQIISANPLLEAFGNAK	K	T	95.00%	107	M1: Oxidation	826.0911	3	-7.4	213	235	No
MKGTLEDQIISANPLLEAFGNAK	K	T	95.00%	96		1230.6560	2	9.0	213	235	No
NALAHALQSSR	K	H	95.00%	91		584.3190	2	5.8	1339	1349	Yes
NKDPLNETVVGLYQK	K	S	95.00%	115		859.4667	2	7.5	605	619	Yes
NKDPLNETVVGLYQK	K	S	95.00%	75		573.3107	3	2.1	605	619	Yes
QEAPPHIFSISDNAYQFMLTDR	R	E	95.00%	90	M18: Oxidation	866.0825	3	6.9	149	170	Yes
QEAPPHIFSISDNAYQFMLTDR	R	E	95.00%	38		860.7493	3	5.1	149	170	Yes
QKQREEQAEPDGTEVADK	K	T	95.00%	33		686.6686	3	7.7	367	384	No
QREEQAEPDGTEVADK	K	T	95.00%	104		901.4207	2	7.2	369	384	No
QREEQAEPDGTEVADK	K	T	95.00%	62		601.2809	3	3.6	369	384	No
RQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	106	M19: Oxidation	918.1165	3	6.7	148	170	Yes
RQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	114		912.7863	3	8.4	148	170	Yes
RQEAPPHIFSISDNAYQFMLTDRENQSILITGESGAGK	K	T	95.00%	70	M19: Oxidation	1060.0320	4	9.5	148	185	Yes
SAETEKEMATMK	K	E	95.00%	38	M11: Oxidation	686.3137	2	4.3	850	861	Yes
SAETEKEMATMK	K	E	95.00%	34	M11: Oxidation	457.8794	3	6.5	850	861	Yes
SAETEKEMATMK	K	E	95.00%	37	M8: Oxidation, M11: Oxidation	694.3143	2	8.8	850	861	Yes
SAETEKEMATMK	K	E	95.00%	36		678.3148	2	2.1	850	861	Yes
SAETEKEMATMK	K	E	95.00%	41		452.5479	3	6.8	850	861	Yes
SAETEKEMATMKEEFQK	K	T	95.00%	54	M11: Oxidation	1016.9680	2	4.0	850	866	Yes
SAETEKEMATMKEEFQK	K	T	95.00%	47	M11: Oxidation	678.3137	3	2.3	850	866	Yes
SAETEKEMATMKEEFQK	K	T	95.00%	67	M8: Oxidation	1016.9690	2	4.2	850	866	Yes
SAETEKEMATMKEEFQK	K	T	95.00%	72	M8: Oxidation	1024.9700	2	8.3	850	866	Yes
SAETEKEMATMKEEFQK	K	T	95.00%	49	M8: Oxidation	683.6454	3	2.4	850	866	Yes

				SAETEKEMATMKEEFQK	K	T	95.00%	72	M8: Oxidation, M11: Oxidation	1024.9700	2	8.3	850	866	Yes
				SAETEKEMATMKEEFQK	K	T	95.00%	49	M8: Oxidation, M11: Oxidation	683.6454	3	2.4	850	866	Yes
				SAETEKEMATMKEEFQK	K	T	95.00%	92		1008.9730	2	6.5	850	866	Yes
				SAETEKEMATMKEEFQK	K	T	95.00%	53		672.9824	3	2.8	850	866	Yes
				SLSTELFK	R	L	95.00%	34		924.5075	1	3.4	1488	1495	Yes
				SLSTELFK	R	L	95.00%	68		462.7583	2	4.8	1488	1495	Yes
				SSDTEMEVFGIAAPFLR	M	K	95.00%	40	M6: Oxidation	943.4534	2	-1.0	2	18	No
				TEELEEAK	R	K	95.00%	33		948.4558	1	3.3	1395	1402	Yes
				TEELEEAK	R	K	95.00%	39		474.7330	2	5.9	1395	1402	Yes
				TEELEEAKK	R	K	95.00%	40		538.7797	2	3.5	1395	1403	Yes
				TIHELEK	K	S	95.00%	31		435.2440	2	7.9	1534	1540	No
				TKYETDAIQR	R	T	95.00%	69		612.8171	2	3.2	1385	1394	Yes
				TKYETDAIQR	R	T	95.00%	55		408.8806	3	3.1	1385	1394	Yes
				TKYETDAIQRTEELEEAK	R	K	95.00%	74		1077.5420	2	8.6	1385	1402	Yes
				TKYETDAIQRTEELEEAK	R	K	95.00%	38		718.6949	3	5.7	1385	1402	Yes
				TKYETDAIQRTEELEEAK	R	K	95.00%	31		539.2729	4	5.3	1385	1402	Yes
				VGNEYVTK	K	G	95.00%	68		455.2394	2	3.0	407	414	Yes
				VKVGNEYVTK	R	G	95.00%	59		568.8224	2	4.7	405	414	Yes
				VLNASAIPEGQFIDSK	R	K	95.00%	115		844.9546	2	9.1	732	747	No
				VLNASAIPEGQFIDSK	R	K	95.00%	76		563.6365	3	4.6	732	747	No
				VLNASAIPEGQFIDSKK	R	A	95.00%	88		909.0018	2	8.1	732	748	No
				VLNASAIPEGQFIDSKK	R	A	95.00%	54		606.3343	3	3.4	732	748	No
				YETDAIQR	K	T	95.00%	34		498.2464	2	5.1	1387	1394	Yes
567	IPI00794464	CMYA1	CARDIOMYOPATHY-ASSOCIATED PROTEIN 1.	ALDTLKGDEEAGAEAPPKEEVVPGDVR	R	S	95.00%	41		931.4759	3	5.9	353	379	No
				AVPLAGEAAAPAQLQNTEK	K	Q	95.00%	51		939.9984	2	-2.1	1001	1019	No
				EQHLQVSQVPAGER	R	Q	95.00%	62		789.4128	2	8.9	643	656	No
				EQHLQVSQVPAGER	R	Q	95.00%	38		526.6096	3	5.9	643	656	No
				EQIVGGDVQGYR	R	W	95.00%	44		660.8344	2	4.6	502	513	No
				GISLEEGARPDVSATR	R	W	95.00%	35		829.4315	2	2.4	293	308	No
				KEELVSGELPR	R	I	95.00%	70		628.8508	2	6.8	819	829	No
				MATAEAQSLHQQVLNK	R	H	95.00%	32	M1: Oxidation	595.6419	3	7.6	1060	1075	No
				MQESQETAAEGTLR	R	T	95.00%	92	M1: Oxidation	783.8627	2	6.6	763	776	No
				QGPTPTATSNPIQDGLR	K	K	95.00%	53		876.9564	2	9.4	1078	1094	No
				RPDVDQQGLLVQEDPTGQLQLKPLR	R	L	95.00%	49		948.5266	3	9.2	837	861	No
				RPDVDQQGLLVQEDPTGQLQLKPLR	R	L	95.00%	47		711.6454	4	7.0	837	861	No
				VEIPSGQVSR	R	Q	95.00%	29		536.2977	2	7.1	686	695	No
				VIAGSIPAGSVHK	R	F	95.00%	50		618.3627	2	5.0	715	727	No
				WLFETQPLEMIHQR	R	E	95.00%	34	M10: Oxidation	615.3145	3	6.0	552	565	No
				WLFETRPLDAINQDPSQVR	R	V	95.00%	53		762.4000	3	7.2	271	289	No
568	IPI00794849	SLMAP	PROTEIN.	DEILLLHQAAAK	R	V	95.00%	100		661.3836	2	8.5	166	177	Yes
				ENVLLSSELQR	R	Q	95.00%	64		644.3555	2	9.6	263	273	No
569	IPI00797126	NACA	SIMILAR TO NASCENT POLYPEPTIDE ASSOCIATED COMPLEX ALPHA SUBUNIT.	EPSTQVATTLR	K	I	95.00%	37		601.8275	2	7.4	492	502	No
				IEDLSQQAQLAAAEK	K	F	95.00%	111		807.9264	2	6.7	838	852	No
				IEDLSQQAQLAAAEK	K	F	95.00%	60		538.9542	3	7.9	838	852	No
				IPVSPPLPDPEDLK	R	N	95.00%	43		758.9239	2	8.8	503	516	No
				KDPTVLPLVQAAPK	K	N	95.00%	31		738.9488	2	7.0	555	568	No
				KDPTVLPLVQAAPK	K	N	95.00%	40		492.9696	3	9.3	555	568	No
				NSPSFQSTSSSPEIPLSPEATLAKK	K	S	95.00%	43		868.4534	3	9.3	569	593	No
				SPASDTYIVFGEAK	K	I	95.00%	96		742.8740	2	8.6	824	837	No
				TISVDHSSTGASYPSQR	K	S	95.00%	92		896.9330	2	6.5	338	354	No
				TISVDHSSTGASYPSQR	K	S	95.00%	43		598.2903	3	4.8	338	354	No
				TNLNKVPSEVVPNPK	K	G	95.00%	25		545.9791	3	8.8	186	200	No
				VPSEVVPNPK	K	G	95.00%	36		533.3040	2	5.3	191	200	No
570	IPI00798211	TBCB	24 KDA PROTEIN.	AQASSIPVGSR	K	C	95.00%	32		536.7944	2	5.6	154	164	No
				YTISQEAYDQR	K	Q	95.00%	71		687.3265	2	8.3	107	117	No
571	IPI00815770	SNX3	ISOFORM 1 OF SORTING NEXIN-3.	KQGLEQFINK	R	V	95.00%	28		602.8434	2	8.2	119	128	No
				TNLPIFK	K	L	95.00%	44		416.7538	2	7.8	55	61	No
572	IPI00000335	HINT2	HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN 2.	AQQATPGGAAPTIFSR	K	I	95.00%	69		786.9176	2	8.8	43	58	No
				DVAPQAPVHFLVIPK	R	K	95.00%	29		815.9727	2	3.2	80	94	No
				ISQAEEEDQQLLGHLLLVAK	R	Q	95.00%	65		1117.6070	2	1.1	100	119	No
				ISQAEEEDQQLLGHLLLVAK	R	Q	95.00%	48		745.4102	3	5.2	100	119	No
573	IPI00000935	PLN	CARDIAC PHOSPHOLAMBAN.	ASTIEMPQQAR	R	Q	95.00%	55	M6: Oxidation	624.3107	2	6.5	15	25	No

				ASTIEMPQQAR	R	Q	95.00%	31	T3: Phospho, M6: Oxidation	664.2950	2	7.8	15	25	No
				RASTIEMPQQAR	R	Q	95.00%	47	S3: Phospho, M7: Oxidation	742.3473	2	9.3	14	25	No
574	IPI00001580	FYCO1	ISOFORM 1 OF FYVE AND COILED-COIL DOMAIN-CONTAINING PROTEIN 1.	AQSLQEAAHQELNTLK	R	F	95.00%	44		890.9711	2	8.4	989	1004	No
				LQAQVVDLQAK	R	M	95.00%	31		606.8572	2	9.3	788	798	No
575	IPI00001952	ENDOD1	ENDONUCLEASE DOMAIN-CONTAINING 1 PROTEIN PRECURSOR.	DRIPVYSAFR	R	A	95.00%	33		612.3365	2	9.4	73	82	No
				ILEVVNQIQDEER	K	M	95.00%	86		792.9211	2	6.9	282	294	No
				QALNTDYLDSDYQR	K	G	95.00%	101		851.3942	2	5.0	128	141	No
				STLLPPEASEGSSSFLGK	R	L	95.00%	72		903.9689	2	9.6	313	330	No
576	IPI00003091	PPP1R3A	ISOFORM 1 OF PROTEIN PHOSPHATASE 1 REGULATORY SUBUNIT 3A.	DLATLLSEHTAIPTR	R	A	95.00%	30		546.6390	3	9.1	561	575	No
				LDLQLGMLPTDK	K	T	95.00%	55	M7: Oxidation	680.3675	2	5.6	862	873	No
577	IPI00003348; IPI00012451; IPI00026268; IPI00639998; IPI00640462; IPI00640949	GNB1; GNB2; GNB4	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) SUBUNIT BETA 2.; GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA 4.; GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) SUBUNIT BETA 1.; GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), BETA POLYPEPTIDE 1.; GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), BETA POLYPEPTIDE 1.; GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), BETA POLYPEPTIDE 1.	LIIWDSYTTNK	K	V	95.00%	50		677.3631	2	9.5	79	89	No
				LLVSASQDGK	R	L	95.00%	46		509.2852	2	4.3	69	78	No
578	IPI00003420	MAPRE2	ISOFORM 1 OF MICROTUBULE-ASSOCIATED PROTEIN RP/EB FAMILY MEMBER 2.	FYDANYDGKEYDPVEAR	K	Q	95.00%	62		684.6441	3	8.8	157	173	No
				SDKDLETQVIQLNEQVHSLK	K	L	95.00%	47		775.4158	3	9.6	236	255	No
579	IPI00003921; IPI00218697; IPI00218698; IPI00218699; IPI00218700; IPI00218701; IPI00739613; IPI00791144	EPB41	ISOFORM 1 OF PROTEIN 4.1.; ISOFORM 2 OF PROTEIN 4.1.; ISOFORM 3 OF PROTEIN 4.1.; ISOFORM 4 OF PROTEIN 4.1.; ISOFORM 5 OF PROTEIN 4.1.; ISOFORM 6 OF PROTEIN 4.1.; EPB41 PROTEIN (FRAGMENT).; HYPOTHETICAL PROTEIN (FRAGMENT).	IRPGEQEQYESTIGFK	K	L	95.00%	48		627.9853	3	3.0	451	466	No
				SLDGAAAVDSADR	R	S	95.00%	43		624.2922	2	-8.2	542	554	No
				SPRPTSAPAITQGQVAEGGVLDASAK	R	K	95.00%	80		836.7759	3	2.4	555	580	No
580	IPI00004457	AOC3	MEMBRANE COPPER AMINE OXIDASE.	EALAIVFFGR	R	Q	95.00%	65		561.8235	2	7.0	123	132	No
				NLVTMTTAPR	R	G	95.00%	35	M5: Oxidation	560.2978	2	4.0	207	216	No
				SPVPPGPAPPLQFYPQGPR	K	F	95.00%	50		1001.5400	2	8.2	304	322	No
581	IPI00005202	PGRMC2	MEMBRANE-ASSOCIATED PROGESTERONE RECEPTOR COMPONENT 2.	DFSLEQLR	R	Q	95.00%	34		504.2665	2	8.8	126	133	No
				RGLGAGAGAGEESPATSLPR	R	M	95.00%	31		618.6600	3	9.2	102	121	No
582	IPI00005537	MRPL12	39S RIBOSOMAL PROTEIN L12, MITOCHONDRIAL PRECURSOR.	KLVESLPQEIK	K	A	95.00%	60		642.3860	2	5.1	163	173	No
				NYIQGINLVQAK	K	K	95.00%	48		680.8881	2	6.9	151	162	No
583	IPI00005614	SPTBN1	ISOFORM LONG OF SPECTRIN BETA CHAIN, BRAIN 1.	EVVAGSHELGQDYEHVTMLQER	R	F	95.00%	42	M18: Oxidation	848.4055	3	6.8	1718	1739	No
				LTTLELLEVR	R	R	95.00%	41		593.8621	2	9.6	2079	2088	No
584	IPI00005755	TCAP	TELETHONIN.	GLQEYQLPYQR	R	V	95.00%	46		697.8616	2	6.1	77	87	No
				VLPLPIFTPAK	R	M	95.00%	29		598.3806	2	6.4	88	98	No
585	IPI00005966	NDUFA12	13KDA DIFFERENTIATION-ASSOCIATED PROTEIN VARIANT (FRAGMENT).	FNVTGTPEQYVPYSTTR	K	K	95.00%	89		980.4860	2	9.5	116	132	No
				GLQQITGHGGLR	R	G	95.00%	50		618.8480	2	5.4	10	21	No
				GLQQITGHGGLR	R	G	95.00%	41		412.8996	3	1.4	10	21	No
				IQEWIPPSTPYK	K	-	95.00%	42		729.8925	2	9.3	135	146	No
586	IPI00006252; IPI00793201	SCYE1	MULTISYNTHETASE COMPLEX AUXILIARY COMPONENT P43.; 37 KDA PROTEIN.	ITFDAFPGEPDKELNPK	R	K	95.00%	61		959.4912	2	7.5	251	267	No
				KHPDADSLYVEEVDVGEIAPR	R	T	95.00%	44		585.5463	4	4.2	167	187	No

587	IPI00006721; IPI00107749; IPI00107750; IPI00107751; IPI00107752; IPI00107753; IPI00375149; IPI00375150; IPI00789199; IPI00797488	OPA1	ISOFORM 1 OF DYNAMIN-LIKE 120 KDA PROTEIN, MITOCHONDRIAL PRECURSOR.; ISOFORM 5 OF DYNAMIN-LIKE 120 KDA PROTEIN, MITOCHONDRIAL PRECURSOR.; OPTIC ATROPHY 1 ISOFORM 5.; OPTIC ATROPHY 1 ISOFORM 6.; ISOFORM 2 OF DYNAMIN-LIKE 120 KDA PROTEIN, MITOCHONDRIAL PRECURSOR.; OPTIC ATROPHY 1 ISOFORM 8.; ISOFORM 8 OF DYNAMIN-LIKE 120 KDA PROTEIN, MITOCHONDRIAL PRECURSOR.; OPTIC ATROPHY 1 ISOFORM 3.; ISOFORM 7 OF DYNAMIN-LIKE 120 KDA PROTEIN, MITOCHONDRIAL PRECURSOR.; ISOFORM 3 OF DYNAMIN-LIKE 120 KDA PROTEIN, MITOCHONDRIAL PRECURSOR.	AKNEILDEVISLSQVTPK	K	H	95.00%	90		992.5591	2	6.8	597	614	No
				AKNEILDEVISLSQVTPK	K	H	95.00%	37		662.0434	3	8.9	615	632	No
				ALGYFAVVTGK	K	G	95.00%	33		563.3211	2	3.0	495	505	No
				AVEVAWETLQEEFSR	K	F	95.00%	95		897.4462	2	7.6	669	683	No
				EFDLTKEEDLAALR	R	H	95.00%	42		550.6204	3	3.9	347	360	No
				ESVEQQADSFK	R	A	95.00%	36		634.2978	2	5.7	558	568	No
				GVEVDPSLIK	R	D	95.00%	32		528.8025	2	2.7	825	834	No
				IDQLQEELLHTQLK	K	Y	95.00%	41		569.9831	3	3.1	233	246	No
				MVLVDLPGVINTVTSGMAPDTK	R	E	95.00%	67	M1: Oxidation, M17: Oxidation	764.0671	3	7.9	412	433	No
588	IPI00006865	SEC22B	VESICLE-TRAFFICKING PROTEIN SEC22B.	IMVANIEEVLQR	R	G	95.00%	30	M2: Oxidation	715.8943	2	9.1	148	159	No
				NLGSINTELQDVQR	R	I	95.00%	90		793.9158	2	6.2	134	147	No
589	IPI00007755	RAB21	RAS-RELATED PROTEIN RAB-21.	MIETAQVDER	R	A	95.00%	55	M1: Oxidation	604.2883	2	4.9	180	189	No
				VNLAIWDTAGQER	R	F	95.00%	50		736.8826	2	5.1	68	80	No
590	IPI00008438; IPI00478810	RPS10	40S RIBOSOMAL PROTEIN S10.; RIBOSOMAL PROTEIN S10.	DYLHLPPEIVPATLR	R	R	95.00%	46		578.6611	3	4.8	81	95	No
				IAIYELLFK	R	E	95.00%	56		555.3367	2	3.9	9	17	No
591	IPI00009480; IPI00377080	COPS8	COP9 SIGNALOSOME COMPLEX SUBUNIT 8.; COP9 SIGNALOSOME SUBUNIT 8 ISOFORM 2.	FIPLSEPAPVPPIPNEQQLAR	K	L	95.00%	60		1157.1390	2	4.3	179	199	No
				KPVAGALDVSFNK	R	F	95.00%	51		673.3831	2	7.7	166	178	No
592	IPI00009747; IPI00792647	LSS	LANOSTEROL SYNTHASE.; 30 KDA PROTEIN.	EQTGLEAYALGLDTK	R	N	95.00%	96		804.9157	2	7.0	48	62	No
				ILGVGPDDPDLVR	R	A	95.00%	54		683.3760	2	4.6	163	175	No
				LSAAEDPLVQSLR	R	-	95.00%	66		699.8876	2	5.8	249	261	No
				LSAAEDPLVQSLR	R	Q	95.00%	76		699.8863	2	3.8	248	260	No
593	IPI00009960; IPI00554469	IMMT	ISOFORM 1 OF MITOCHONDRIAL INNER MEMBRANE PROTEIN.; ISOFORM 2 OF MITOCHONDRIAL INNER MEMBRANE PROTEIN.	AVDEAADALLK	K	A	95.00%	52		558.3036	2	3.9	276	286	Yes
				ELDSITPEVLPGWK	R	G	95.00%	59		792.4263	2	7.7	361	374	Yes
				ERPPEEVAAR	R	L	95.00%	43		577.3077	2	9.5	196	205	No
				FVNQLKGESR	K	R	95.00%	55		589.3227	2	3.9	709	718	No
				GIEQAVQSHAVAEEEAR	R	K	95.00%	97		912.4517	2	3.7	537	553	Yes
				GIEQAVQSHAVAEEEAR	R	K	95.00%	64		608.6378	3	4.9	537	553	Yes
				GMSVSDLADKLSTDDLNSLIAHAHR	K	R	95.00%	92	M2: Oxidation	894.7846	3	8.4	375	399	Yes
				GVYSEETLR	R	A	95.00%	49		527.2670	2	4.3	624	632	Yes
				KAHQLWLSVEALK	R	Y	95.00%	53		508.2982	3	3.0	554	566	Yes
				KAVDEAADALLK	R	A	95.00%	68		622.3519	2	4.7	286	297	Yes
				LFEMVLGPAAYNVPLPK	K	K	95.00%	73	M4: Oxidation	938.0167	2	8.7	85	101	Yes
				LFEMVLGPAAYNVPLPK	K	K	95.00%	54	M4: Oxidation	625.6777	3	4.4	85	101	Yes
				LHNMIVDLDNVVK	K	K	95.00%	74	M4: Oxidation	763.4112	2	6.4	320	332	Yes
				LHNMIVDLDNVVK	K	K	95.00%	34	M4: Oxidation	509.2755	3	4.1	320	332	Yes
				LHNMIVDLDNVVKK	K	V	95.00%	62	M4: Oxidation	551.9731	3	2.4	320	333	Yes
				LHNMIVDLDNVVKK	K	V	95.00%	43	M4: Oxidation	414.2306	4	-0.4	320	333	No
				LRGIEQAVQSHAVAEEEAR	R	K	95.00%	51		698.3668	3	5.1	535	553	Yes
				LRGIEQAVQSHAVAEEEAR	R	K	95.00%	45		524.0260	4	3.1	535	553	Yes
				LSQEQVDNFTLDINTAYAR	R	L	95.00%	129		1099.5500	2	8.9	516	534	Yes
				LSQEQVDNFTLDINTAYAR	R	L	95.00%	44		733.3675	3	6.3	516	534	Yes
				LSTDDLNSLIAHAHR	K	R	95.00%	37		416.4723	4	5.7	396	410	Yes
				QTASVTLQAIAAQNAAVQAVNAHSNILK	R	A	95.00%	94		944.8580	3	9.1	219	246	Yes
				QTASVTLQAIAAQNAAVQAVNAHSNILK	R	A	95.00%	60		708.8936	4	6.5	219	246	Yes
				SEFEQNLSEK	K	L	95.00%	43		605.7863	2	4.5	507	516	Yes

				TDHPEIGEGKPTPALSEEASSSSIR	K	E	95.00%	53		865.7602	3	4.2	160	184	No
				TIPYSDKLFEMVLGPAAYNVPLPK	K	K	95.00%	33	M11: Oxidation	893.8162	3	8.3	78	101	Yes
				TSSAETPTIPLGSAVEAIK	K	A	95.00%	106		936.5106	2	8.9	582	600	Yes
				VAMIDETR	R	N	95.00%	43	M3: Oxidation	475.7375	2	5.6	645	652	Yes
				VQEQELKSEFEQNLSEK	R	L	95.00%	102		1033.0150	2	6.7	489	505	Yes
				VQEQELKSEFEQNLSEK	R	L	95.00%	75		689.0117	3	5.2	500	516	Yes
				VVSQYHELVVQAR	K	D	95.00%	96		764.4218	2	5.0	343	355	Yes
				VVSQYHELVVQAR	K	D	95.00%	54		509.9495	3	3.0	343	355	Yes
				YSTSGSSGLTTGK	R	I	95.00%	40		623.3048	2	4.4	33	45	Yes
594	IPI00010154	GDI1	RAB GDP DISSOCIATION INHIBITOR ALPHA.	FDLGQDVIDFTGHALALYR	K	T	95.00%	64		717.7064	3	7.4	175	193	Yes
				FQLLEGPPESMGR	R	G	95.00%	74	M11: Oxidation	738.8660	2	5.6	56	68	No
				KFDLGQDVIDFTGHALALYR	R	T	95.00%	81		760.4036	3	5.6	174	193	No
				KFDLGQDVIDFTGHALALYR	R	T	95.00%	53		570.5549	4	6.0	174	193	No
				LSAIYGGTYMLNKPVDDIIMENGK	R	V	95.00%	42	M10: Oxidation, M20: Oxidation	892.1152	3	7.1	241	264	No
				MLLYTEVTR	K	Y	95.00%	37	M1: Oxidation	571.3029	2	4.6	90	98	Yes
				NPYYGGESSSITPLEELYKR	R	F	95.00%	36		768.3836	3	6.8	36	55	No
				SPYLYPLYGLGELPQGFAR	K	L	95.00%	116		1071.0660	2	7.8	222	240	Yes
				SPYLYPLYGLGELPQGFAR	K	L	95.00%	72		714.3803	3	8.3	222	240	Yes
				TFEGVDPQTTSMR	K	D	95.00%	34	M12: Oxidation	742.8456	2	9.5	157	169	No
				YIAIASTTVETTDPEKEVEPALELLEPIDQK	K	F	95.00%	53		1148.2700	3	6.5	349	379	No
595	IPI00010402	SH3BGRL3	HYPOTHETICAL PROTEIN.	IQYQLVDISQDNALR	R	D	95.00%	107		888.4692	2	0.7	166	180	No
				IQYQLVDISQDNALRDEMR	R	A	95.00%	40	M18: Oxidation	775.0551	3	6.2	166	184	No
596	IPI00010740	SFPQ	ISOFORM LONG OF SPLICING FACTOR, PROLINE-AND GLUTAMINE-RICH.	FATHAAALSVR	R	N	95.00%	44		572.3205	2	5.0	366	376	No
				FGQGGAGPVGGQGPR	R	G	95.00%	55		671.3400	2	4.1	667	681	No
597	IPI00010845	NDUFS8	NADH DEHYDROGENASE [UBIQUINONE] IRON-SULFUR PROTEIN 8, MITOCHONDRIALPRECURSOR.	GLGMTLSYLFR	R	E	95.00%	65	M4: Oxidation	637.3403	2	8.9	67	77	No
				TLLWTELFR	R	G	95.00%	70		589.8381	2	9.2	58	66	No
				YVNMQDPEMDMK	K	S	95.00%	53	M4: Oxidation, M9: Oxidation, M11: Oxidation	774.8116	2	8.6	38	49	No
598	IPI00011217	NDUFS4	NADH DEHYDROGENASE [UBIQUINONE] IRON-SULFUR PROTEIN 4, MITOCHONDRIALPRECURSOR.	LDITTLTGVPEEHIK	K	T	95.00%	60		555.9780	3	7.0	59	73	No
				SYGANFSWNKR	K	T	95.00%	45		665.3257	2	7.4	159	169	No
599	IPI00011253	RPS3	40S RIBOSOMAL PROTEIN S3.	DEILPTTPISEQK	K	G	95.00%	32		735.8957	2	9.5	215	227	No
				ELAEDGYSGVEVR	R	V	95.00%	80		712.3446	2	7.6	28	40	No
				KPLPDHVSIVEPK	K	D	95.00%	26		729.9247	2	6.4	202	214	No
600	IPI00011603	PSMD3	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 3.	AIQLEYSEAR	K	R	95.00%	60		590.3054	2	1.6	297	306	No
				AKPPPGGGEQEPPPPPAPQDVEMKEEAATGGGSTGEADGK	K	T	95.00%	37	M23: Oxidation	971.7069	4	2.6	15	54	No
				AVQGFFTSNNATR	K	D	95.00%	72		706.8515	2	2.1	116	128	No
				ELDTVTLEDIKEHVK	R	Q	95.00%	48		884.9757	2	5.7	66	80	No
				FNQVLDQFGEK	K	F	95.00%	64		662.8348	2	6.0	375	385	No
				HDADGQATLLNLLLR	R	N	95.00%	84		825.4578	2	6.0	242	256	No
				HDADGQATLLNLLLR	R	N	95.00%	69		550.6406	3	5.0	242	256	No
				LQLDSPEDAEFIVAK	K	A	95.00%	76		837.9393	2	6.9	426	440	No
				NYLHYSLYDQAEK	R	L	95.00%	69		822.3937	2	5.4	257	269	No
				SLMPYFLLTQAVR	R	T	95.00%	83	M3: Oxidation	777.9275	2	7.6	356	368	No
				SVFPEQANNNEWAR	K	Y	95.00%	52		831.3910	2	4.2	274	287	No
				VYEFLDKLDVVR	R	S	95.00%	48		748.4177	2	7.7	217	228	No
				VYEFLDKLDVVR	R	S	95.00%	61		499.2799	3	5.4	217	228	No
601	IPI00011654; IPI00645452	TUBB	TUBULIN BETA CHAIN.; TUBULIN, BETA POLYPEPTIDE.	AILVDLEPGTMDSVR	R	S	95.00%	70	M11: Oxidation	816.4242	2	5.5	63	77	No
				AILVDLEPGTMDSVR	R	S	95.00%	34	M11: Oxidation	544.6182	3	4.5	63	77	No
				ALTVPELTQQVFDAK	R	N	95.00%	63		830.4575	2	6.8	283	297	No
				ALTVPELTQQVFDAK	R	N	95.00%	63		553.9733	3	5.1	283	297	No
				EVDEQMLNVQNK	K	N	95.00%	79	M6: Oxidation	731.8483	2	2.7	325	336	Yes
				EVDEQMLNVQNK	K	N	95.00%	55		723.8522	2	4.6	325	336	Yes
				FPGQLNADLR	R	K	95.00%	59		565.8047	2	4.9	242	251	Yes
				FWEVISDEHGIDPTGTYHGDSDLQLDR	K	I	95.00%	83		1034.8160	3	7.8	20	46	No
				GHYTEGAELVDSVLDVVR	K	K	95.00%	168		980.0037	2	8.8	104	121	Yes
				GHYTEGAELVDSVLDVVR	K	K	95.00%	68		653.6696	3	5.5	104	121	Yes

				GHYTEGAELVDSVLDVVRK	K	E	95.00%	82		696.3701	3	8.4	104	122	Yes
				GHYTEGAELVDSVLDVVRK	K	E	95.00%	47		522.5282	4	5.8	104	122	Yes
				IMNTFSVVPSPK	R	V	95.00%	88	M2: Oxidation	668.3550	2	2.9	163	174	Yes
				ISEQFTAMFR	R	R	95.00%	76	M8: Oxidation	623.3034	2	4.2	381	390	Yes
				ISVYYNEATGGK	R	Y	95.00%	89		651.3244	2	2.5	47	58	No
				KLAVNMVPFPR	R	L	95.00%	56	M6: Oxidation	644.3694	2	4.7	252	262	Yes
				LAVNMVPFPR	K	L	95.00%	77	M5: Oxidation	580.3217	2	4.9	253	262	Yes
				LHFFMPGFAPLTSR	R	G	95.00%	43	M5: Oxidation	818.9237	2	5.1	263	276	Yes
				LHFFMPGFAPLTSR	R	G	95.00%	57	M5: Oxidation	546.2853	3	5.5	263	276	Yes
				MAVTFIGNSTAIQELFK	K	R	95.00%	114	M1: Oxidation	943.4987	2	8.5	363	379	No
				MAVTFIGNSTAIQELFK	K	R	95.00%	49	M1: Oxidation	629.3334	3	5.9	363	379	No
				MSMKEVDEQMLNVQNK	R	N	95.00%	67	M1: Oxidation, M3: Oxidation, M10: Oxidation	986.4527	2	7.6	321	336	Yes
				MSMKEVDEQMLNVQNK	R	N	95.00%	48	M1: Oxidation, M3: Oxidation, M10: Oxidation	657.9688	3	4.1	321	336	Yes
				NSSYFVEWIPNNVK	K	T	95.00%	53		848.9281	2	8.9	337	350	Yes
				SGPFGQIFRPDNFVFGQSGAGNNWAK	R	G	95.00%	81		933.4605	3	7.9	78	103	Yes
				YLTVAAVFR	R	G	95.00%	81		520.3027	2	3.3	310	318	Yes
602	IPI00012119; IPI00794413; IPI00795042	DCN	ISOFORM A OF DECORIN PRECURSOR.; 20 KDA PROTEIN.; 24 KDA PROTEIN.	DLPPDTTLLDLQNNK	K	I	95.00%	77		848.9458	2	4.5	78	92	No
				ITEIKDGDFK	K	N	95.00%	29		583.3117	2	4.0	93	102	No
				NLHALILVNNK	K	I	95.00%	64		624.8787	2	5.3	106	116	No
				NLHALILVNNK	K	I	95.00%	31		416.9210	3	3.5	106	116	No
				SSGIENGAFQGMK	K	K	95.00%	48	M12: Oxidation	671.3124	2	4.5	188	200	No
				VSPGAFTPLVK	K	L	95.00%	41		558.3291	2	3.4	120	130	No
603	IPI00012272	MYBPH	MYOSIN-BINDING PROTEIN H.	AVIDILVIEKPGPPSSIR	K	L	95.00%	38		952.5740	2	9.3	257	274	No
				AVIDILVIEKPGPPSSIR	K	L	95.00%	61		635.3834	3	6.3	257	274	No
				PMMVTQQTVR	R	N	95.00%	37	M2: Oxidation, M3: Oxidation	611.8046	2	7.2	124	133	No
				QVGETVNLQIPFQGK	R	P	95.00%	69		829.4541	2	5.3	187	201	No
				TGDQDSILFIR	R	S	95.00%	72		632.8326	2	2.8	224	234	No
				TGQWFTVLER	K	Y	95.00%	41		618.8270	2	6.7	310	319	No
				VPTAEPPGEVAVSESTR	K	E	95.00%	97		863.4422	2	6.2	24	40	No
				VSAVSSAGAGPPAMLDQPIHIR	R	E	95.00%	66	M14: Oxidation	730.7219	3	7.1	145	166	No
604	IPI00012493; IPI00794659	RPS20	40S RIBOSOMAL PROTEIN S20.; 16 KDA PROTEIN.	DTGKTPVEPEVAIHR	K	I	95.00%	48		550.2894	3	-8.1	5	19	No
				TPVEPEVAIHR	K	I	95.00%	51		416.5663	3	6.8	9	19	No
605	IPI00013297	PDAP1	28 KDA HEAT- AND ACID-STABLE PHOSPHOPROTEIN.	GVEGLIDIENPNR	K	V	95.00%	52		713.3766	2	8.0	76	88	No
				KVTQLDLDGPK	K	E	95.00%	65		607.3438	2	0.2	95	105	No
606	IPI00013452	EPRS	GLUTAMYL-PROLYL TRNA SYNTHETASE.	AYVDDTPAEQMK	K	A	95.00%	64	M11: Oxidation	692.3148	2	8.1	289	300	No
				DQDLEPGAPSMGAK	R	S	95.00%	42	M11: Oxidation	716.3312	2	8.2	1464	1477	No
607	IPI00013455; IPI00027172; IPI00217113	CLIP1	CLIP1 PROTEIN.; ISOFORM LONG OF CAP-GLY DOMAIN-CONTAINING LINKER PROTEIN 1.; ISOFORM SHORT OF CAP-GLY DOMAIN-CONTAINING LINKER PROTEIN 1.	GLGTETAEFAELK	K	T	95.00%	73		683.3517	2	3.8	648	660	No
				LMKVIK	K	E	95.00%	22	M2: Oxidation	747.4820	1	2.2	699	704	No
				LTNLQENLSEVSQVK	K	E	95.00%	100		851.4611	2	7.1	832	846	No
				TASESISNLSEAGSIK	K	K	95.00%	64		797.4072	2	5.9	191	206	No
608	IPI00013808	ACTN4	ALPHA-ACTININ-4.	FAIQDISVEETSAK	R	E	95.00%	89		769.3964	2	6.4	153	166	Yes
				KHEAFESDLAAHQDR	R	V	95.00%	58		585.2830	3	4.2	455	469	Yes
				KHEAFESDLAAHQDR	R	V	95.00%	40		439.2128	4	1.0	455	469	Yes
				LSNRPAFMPSEGK	R	M	95.00%	37	M8: Oxidation	725.3664	2	6.1	366	378	No
				LSNRPAFMPSEGK	R	M	95.00%	36	M8: Oxidation	483.9117	3	2.4	366	378	No
				MAPYQGPDAVPGALDYK	R	S	95.00%	53	M1: Oxidation	904.9390	2	9.4	883	899	No
				MLDAEDIVNTARPDEK	K	A	95.00%	35	M1: Oxidation	611.6326	3	6.5	240	255	No
				TINEVENQILTR	R	D	95.00%	61		715.3929	2	8.9	746	757	No
609	IPI00013917; IPI00456898	LOC440055; RPS12	40S RIBOSOMAL PROTEIN S12.; SIMILAR TO RIBOSOMAL PROTEIN S12.	DVIEEYFK	K	C	95.00%	28		1042.5190	1	9.0	122	129	No
				TALIHDGLAR	K	G	95.00%	38		533.8088	2	8.1	24	33	No
610	IPI00014230; IPI00794855	C1QBP	COMPLEMENT COMPONENT 1 Q SUBCOMPONENT-BINDING PROTEIN, MITOCHONDRIALPRECURSOR.; 25 KDA PROTEIN.	AFVDFLSDEIKEER	K	K	95.00%	66		849.4309	2	8.9	81	94	No
				AFVDFLSDEIKEER	K	K	95.00%	52		566.6209	3	4.9	81	94	No
				EVSFQSTGESEWK	R	D	95.00%	60		757.3485	2	5.3	208	220	No

611	IPI00014310	CUL1	CULLIN-1.	ESFESQFLADTER	K	F	95.00%	79		779.8610	2	7.4	230	242	No
				HLEIFHTEFQNLLDADKNEDLGR	K	M	95.00%	35		689.3485	4	7.8	299	321	No
				HQQLLGEVLTQLSSR	K	F	95.00%	44		570.3206	3	6.6	727	741	No
				LLETHIHNQGLAAIEK	K	C	95.00%	37		596.3368	3	7.4	339	354	No
				LLVLEDENANVDEVELKPDTLIK	K	L	95.00%	62		870.4778	3	9.6	648	670	No
				LVHQNSASDDAEASMISK	R	L	95.00%	43	M15: Oxidation	640.3015	3	3.8	474	491	No
612	IPI00014312; IPI00382458; IPI00382459	CUL3	ISOFORM 1 OF CULLIN-3.; ISOFORM 2 OF CULLIN-3.; ISOFORM 3 OF CULLIN-3.	ALVSEEGEGKNPVDYIQGLLDLK	K	S	95.00%	32		829.7768	3	6.6	327	349	No
				EDGSEVGVGGAQVTGSNTR	K	K	95.00%	75		910.4290	2	4.3	570	588	No
				GLTEQEVETILDK	K	A	95.00%	88		737.8904	2	5.8	378	390	No
				NNSGLSFEELYR	K	N	95.00%	54		714.8441	2	3.2	48	59	No
				SPEYLSLFIDDK	R	L	95.00%	56		713.8631	2	5.4	384	395	No
				YVNSIWDLLK	K	N	95.00%	33		625.8473	2	6.5	5	14	No
613	IPI00017030; IPI00402167; IPI00477329; IPI00760846; IPI00760925; IPI00828082	MYO18A; TIAF1	234 KDA PROTEIN.; 232 KDA PROTEIN.; 227 KDA PROTEIN.; ISOFORM 1 OF MYOSIN-XVIIIA.; ISOFORM 3 OF MYOSIN-XVIIIA.; ISOFORM 4 OF MYOSIN-XVIIIA.	NTGESASQLLDAETAER	R	L	95.00%	94		896.4300	2	8.9	1306	1322	No
				RFDSELSQAHEEAQR	R	E	95.00%	31		601.6205	3	2.0	1465	1479	No
614	IPI00017344	RAB5B	RAS-RELATED PROTEIN RAB-5B.	GAQAAIVVYDITNQETFAR	R	A	95.00%	54		689.6938	3	7.2	92	110	No
				LVLLGESAVGK	K	S	95.00%	50		543.3309	2	-2.9	23	33	No
615	IPI00017601	CP	CERULOPLASMIN PRECURSOR.	ALYLQYTDETFR	K	T	95.00%	53		760.3791	2	4.7	70	81	No
				GAYPLSIEPIGVR	K	F	95.00%	47		686.3911	2	7.8	469	481	No
				KAEEEHLGILGPQLHADVGDK	R	V	95.00%	33		752.7322	3	8.2	799	819	No
				KAEEEHLGILGPQLHADVGDKVK	R	I	95.00%	27		621.5887	4	2.3	799	821	No
				MFTTAPDQVDKEDEDFQESNK	R	M	95.00%	50	M1: Oxidation	830.6985	3	7.3	599	619	No
				NNEGTYYSPNYNPQSR	K	S	95.00%	76		952.4200	2	6.0	485	500	No
				PYTFHSHGITYYK	R	E	95.00%	40		807.3965	2	6.1	116	128	No
				QSEDSTFYLGER	R	T	95.00%	40		716.3265	2	4.1	721	732	No
				TTIEKPVWLGFLGPIIK	R	A	95.00%	36		638.0540	3	7.8	82	98	No
				VNKDDEEFIESNK	K	M	95.00%	70		783.8729	2	5.8	945	957	No
616	IPI00017672	NP	CDNA FLJ25678 FIS, CLONE TST04067, HIGHLY SIMILAR TO PURINE NUCLEOSIDEPHOSPHORYLASE.	DHINLPGFSGQNPLR	R	G	95.00%	32		555.6254	3	5.7	138	152	No
				LGADAVGMSTVPEVIVAR	K	H	95.00%	60	M8: Oxidation	900.9861	2	6.3	216	233	No
				VFGFSLITNK	R	V	95.00%	76		563.3239	2	8.0	239	248	No
617	IPI00018931	VPS35	VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN 35.	AELAELPLR	K	L	95.00%	41		506.2985	2	5.2	574	582	No
				ESPESEGPIYEGLIL	R	-	95.00%	55		816.9123	2	9.6	782	796	No
				ILVGTNLVR	R	L	95.00%	45		492.8166	2	4.8	218	226	No
				IPVDTYNNILTVLK	K	L	95.00%	86		801.9656	2	7.8	404	417	No
				IREDLPNLESSEETEQINK	K	H	95.00%	57		748.7075	3	3.3	750	768	No
				LFDIFSQQVATVIQSR	K	Q	95.00%	77		926.5087	2	6.8	324	339	No
				LSQLEGVNVER	R	Y	95.00%	53		622.3395	2	5.2	227	237	No
				NIIIALIDR	K	L	95.00%	46		520.8295	2	4.1	297	305	No
				SEDPDQQYLILNTAR	R	K	95.00%	85		881.9377	2	3.5	500	514	No
618	IPI00019345; IPI00640287	RAP1A	RAS-RELATED PROTEIN RAP-1A PRECURSOR.; RAP1A, MEMBER OF RAS ONCOGENE FAMILY.	LVVLGSGGVGK	K	S	95.00%	40		493.3103	2	8.2	6	16	No
				VKDTEDVPMILVGNK	R	C	95.00%	43	M9: Oxidation	837.4479	2	5.7	103	117	No
619	IPI00019580	PLG	PLASMINOGEN PRECURSOR.	EAQLPVIENK	K	V	95.00%	30		570.8193	2	3.6	718	727	No
				HSIFTPETNPR	R	A	95.00%	43		649.8320	2	5.3	513	523	No
				LSSPAVITDK	K	V	95.00%	33		515.7954	2	4.3	671	680	No
620	IPI00019591; IPI00639937	CFB	ISOFORM 1 OF COMPLEMENT FACTOR B PRECURSOR (FRAGMENT).; B-FACTOR, PROPERDIN.	VSEADSSNADWVTK	K	Q	95.00%	72		754.8509	2	4.7	324	337	No
				YGLVTYATYPK	R	I	95.00%	61		638.3394	2	6.6	309	319	No
621	IPI00019906; IPI00218019; IPI00795150	BSG	ISOFORM 2 OF BASIGIN PRECURSOR.; ISOFORM 1 OF BASIGIN PRECURSOR.; 46 KDA PROTEIN.	GGVVLKEDALPGQK	K	T	95.00%	66		705.9059	2	5.6	221	234	No
				RKPEDVLDDDDAGSAPLK	R	S	95.00%	59		647.6616	3	6.2	233	250	No
622	IPI00020416; IPI00640197	TPP2	TRIPEPTIDYL-PEPTIDASE 2.; TRIPEPTIDYL PEPTIDASE II.	AYDYLVQNTSFANK	K	L	95.00%	54		817.4042	2	8.8	507	520	No
				GTLTEAFPVLGGK	K	A	95.00%	29		645.3638	2	6.9	716	728	No
				LSTMETGTGLIR	R	A	95.00%	34	M4: Oxidation	647.8422	2	6.7	301	312	No
				VPITAVIAAK	R	V	95.00%	45		491.8203	2	2.7	629	638	No
623	IPI00020898	RPS6KA3	RIBOSOMAL PROTEIN S6 KINASE ALPHA-3.	DLKPENILLDEEGHIK	R	L	95.00%	79		621.6705	3	4.8	193	208	No

				DPTEEIEILLR	R	Y	95.00%	69		664.3643	2	7.3	459	469	No
				EASAVLFTITK	R	T	95.00%	45		590.3379	2	4.7	515	525	No
				GAMAATYSALNR	K	N	95.00%	33	M3: Oxidation	621.3026	2	2.2	701	712	No
				LGMPQFLSPEAQSLLR	K	M	95.00%	69	M3: Oxidation	901.9844	2	7.4	285	300	No
				NQSPVLEPVGR	R	S	95.00%	33		598.3307	2	8.4	713	723	No
				NSIQFTDGYEVK	R	E	95.00%	63		700.8415	2	3.8	414	425	No
624	IPI00020987	PRELP	PROLARGIN PRECURSOR.	LEHLYLNNNSIEK	R	I	95.00%	66		793.9192	2	8.0	313	325	No
				LENLLLLDLQHNR	K	L	95.00%	65		795.9589	2	8.2	194	206	No
				LENLLLLDLQHNR	K	L	95.00%	49		530.9753	3	8.4	194	206	No
				NLMQLNLAHNILR	K	K	95.00%	34	M3: Oxidation	522.6264	3	3.1	222	234	No
				NQLEEVPSALPR	K	N	95.00%	35		676.8674	2	7.0	160	171	No
				SFPNLAFIR	K	L	95.00%	44		532.8026	2	7.5	264	272	No
625	IPI00021439; IPI00021440	ACTB; ACTG1	ACTIN, CYTOPLASMIC 1.; ACTIN, CYTOPLASMIC 2.	AGFAGDDAPR	K	A	95.00%	57		976.4520	1	3.2	19	28	Yes
				AGFAGDDAPR	K	A	95.00%	90		488.7286	2	0.4	19	28	Yes
				AVFPSIVGR	R	P	95.00%	78		473.2801	2	0.1	29	37	Yes
				AVFPSIVGRPR	R	H	95.00%	77		599.8580	2	1.6	29	39	Yes
				AVFPSIVGRPR	R	H	95.00%	29		400.2415	3	2.1	29	39	Yes
				DLTDYLMK	R	I	95.00%	45	M7: Oxidation	1014.4920	1	9.3	184	191	Yes
				DLTDYLMK	R	I	95.00%	56	M7: Oxidation	507.7452	2	0.5	184	191	Yes
				DLTDYLMK	R	I	95.00%	44		499.7504	2	5.9	184	191	Yes
				DLYANTVLSGGTTMYPGIADR	K	M	95.00%	121	M14: Oxidation	1116.0480	2	9.6	292	312	No
				DLYANTVLSGGTTMYPGIADR	K	M	95.00%	80	M14: Oxidation	744.3667	3	8.3	292	312	No
				DSYVGDEAQSK	K	R	95.00%	85		599.7709	2	9.3	51	61	Yes
				DSYVGDEAQSKR	K	G	95.00%	65		677.8182	2	3.5	51	62	Yes
				DSYVGDEAQSKR	K	G	95.00%	36		452.2152	3	4.6	51	62	Yes
				EITALAPSTMK	K	I	95.00%	71	M10: Oxidation	1177.6180	1	3.4	316	326	Yes
				EITALAPSTMK	K	I	95.00%	91	M10: Oxidation	589.3099	2	-1.7	316	326	Yes
				EITALAPSTMK	K	I	95.00%	58		1161.6240	1	4.3	316	326	Yes
				EITALAPSTMK	K	I	95.00%	76		581.3145	2	1.8	316	326	Yes
				EITALAPSTMKIK	K	I	95.00%	36	M10: Oxidation	709.9036	2	4.5	316	328	Yes
				GILTLK	R	Y	95.00%	37		644.4368	1	3.0	63	68	Yes
				GYSFTTTAER	R	E	95.00%	46		566.7703	2	4.6	197	206	No
				HQGVMVGMGQK	R	D	95.00%	63	M5: Oxidation	594.2880	2	1.2	40	50	Yes
				HQGVMVGMGQK	R	D	95.00%	62	M5: Oxidation	602.2896	2	8.2	40	50	Yes
				HQGVMVGMGQK	R	D	95.00%	62	M5: Oxidation	401.8615	3	6.2	40	50	Yes
				HQGVMVGMGQK	R	D	95.00%	62	M5: Oxidation, M8: Oxidation	602.2896	2	8.2	40	50	Yes
				HQGVMVGMGQK	R	D	95.00%	62	M5: Oxidation, M8: Oxidation	401.8615	3	6.2	40	50	Yes
				HQGVMVGMGQK	R	D	95.00%	61	M8: Oxidation	594.2899	2	4.4	40	50	Yes
				HQGVMVGMGQK	R	D	95.00%	71		1171.5740	1	2.1	40	50	Yes
				HQGVMVGMGQK	R	D	95.00%	85		586.2923	2	4.3	40	50	Yes
				IIAPPERK	K	Y	95.00%	36		462.2889	2	2.3	329	336	Yes
				IKIIAPPER	K	K	95.00%	32		518.8319	2	3.8	327	335	Yes
				IKIIAPPERK	K	Y	95.00%	26		582.8785	2	1.9	327	336	Yes
				IWHHTFYNELR	K	V	95.00%	70		758.3789	2	0.2	85	95	Yes
				IWHHTFYNELR	K	V	95.00%	66		505.9227	3	1.9	85	95	Yes
				KDLYANTVLSGGTTMYPGIADR	R	M	95.00%	51	M15: Oxidation	787.0649	3	7.7	291	312	No
				LDLAGRDLTDYLMK	R	I	95.00%	34	M13: Oxidation	547.2877	3	6.4	178	191	Yes
				MQKEITALAPSTMK	R	I	95.00%	62	M1: Oxidation, M13: Oxidation	790.9117	2	8.0	313	326	Yes
				QEYDESGPSIVHR	K	K	95.00%	58		758.8572	2	2.2	360	372	No
				QEYDESGPSIVHR	K	K	95.00%	44		506.2405	3	1.8	360	372	No
				RGILTLK	K	Y	95.00%	40		400.7732	2	3.4	62	68	Yes
				SYELPDGQVITIGNER	K	F	95.00%	132		895.9526	2	2.7	239	254	Yes
				SYELPDGQVITIGNER	K	F	95.00%	73		597.6398	3	6.2	239	254	Yes
				TTGIVMDSGDGVTHTVPIYEGYALPHAILR	R	L	95.00%	50	M6: Oxidation	1067.2110	3	2.9	148	177	No
				VAPEEHPVLLTEAPLNPK	R	A	95.00%	56		652.0290	3	3.1	96	113	No
626	IPI00021842	APOE	APOLIPOPROTEIN E PRECURSOR.	AATVGSLAGQPLQER	R	A	95.00%	55		749.4104	2	6.9	210	224	No
				AKLEEQAQQIR	R	L	95.00%	69		657.3658	2	4.6	259	269	No
				DRLDEVKEQVAEVR	R	A	95.00%	53		843.4522	2	8.4	245	258	No
				LAVYQAGAR	R	E	95.00%	58		474.7698	2	5.5	177	185	No
				LGPLVEQGR	R	V	95.00%	25		484.7829	2	5.1	199	207	No
				SELEEQLTPVAEETR	K	A	95.00%	101		865.9294	2	3.4	94	108	No
				VQAAVGTSAAPVPSDNH	K	-	95.00%	98		810.9100	2	8.6	301	317	No
627	IPI00021854	APOA2	APOLIPOPROTEIN A-II PRECURSOR.	SKEQLTPLIK	K	K	95.00%	32		578.8543	2	5.5	68	77	No
				VKSPELQAEAK	K	S	95.00%	34		600.3372	2	2.3	52	62	No

628	IPI00022391	APCS	SERUM AMYLOID P-COMPONENT PRECURSOR.	QGYFVEAQPK	R	I	95.00%	35		583.7995	2	5.5	140	149	No
				VGEYSLYIGR	R	H	95.00%	51		578.8087	2	8.0	87	96	No
629	IPI00022418; IPI00339223; IPI00339225; IPI00339226; IPI00339227; IPI00339228; IPI00414283; IPI00470919; IPI00479723; IPI00642991	FN1	ISOFORM 1 OF FIBRONECTIN PRECURSOR.; ISOFORM 3 OF FIBRONECTIN PRECURSOR.; ISOFORM 5 OF FIBRONECTIN PRECURSOR.; ISOFORM 6 OF FIBRONECTIN PRECURSOR.; ISOFORM 7 OF FIBRONECTIN PRECURSOR.; ISOFORM 8 OF FIBRONECTIN PRECURSOR.; FIBRONECTIN 1 ISOFORM 4 PREPROPROTEIN.; FIBRONECTIN 1 ISOFORM 2 PREPROPROTEIN.; ISOFORM 10 OF FIBRONECTIN PRECURSOR.; FIBRONECTIN 1 ISOFORM 6 PREPROPROTEIN.	FTNIGPDTMR	R	V	95.00%	34	M9: Oxidation	584.2807	2	5.6	1275	1284	No
				RPGGEPSPEGTTGQSYNQYSQR	R	Y	95.00%	68		799.3711	3	4.6	2304	2325	No
				TEIDKPSQMQVTDVQDNSISVK	R	W	95.00%	59	M9: Oxidation	826.7457	3	7.4	1540	1561	No
630	IPI00022429	ORM1	ALPHA-1-ACID GLYCOPROTEIN 1 PRECURSOR.	TYMLAFDVNDEK	K	N	95.00%	50	M3: Oxidation	731.3362	2	5.1	127	138	No
				WFYIASAFR	K	N	95.00%	54		580.8023	2	6.5	43	51	No
				YVGGQEHFAHLLILR	R	D	95.00%	105		876.9857	2	4.8	109	123	No
				YVGGQEHFAHLLILR	R	D	95.00%	62		584.9928	3	4.3	109	123	No
631	IPI00022431	AHSG	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR.	HTFMGVVSLGSPSGEVSHPR	R	K	95.00%	74	M4: Oxidation	699.6807	3	3.6	318	337	No
				HTFMGVVSLGSPSGEVSHPR	R	K	95.00%	35	M4: Oxidation	525.0121	4	3.0	318	337	No
				HTLNQIDEVK	K	V	95.00%	42		598.8218	2	6.8	58	67	No
632	IPI00022432	TTR	TRANSTHYRETIN PRECURSOR.	AADDTWEPFASGK	K	T	95.00%	81		697.8201	2	6.8	56	68	No
				GSPAINVAVHVFR	R	K	95.00%	80		683.8871	2	5.0	42	54	No
				GSPAINVAVHVFR	R	K	95.00%	57		456.2613	3	6.5	42	54	No
				KAADDTWEPFASGK	R	T	95.00%	89		761.8702	2	9.6	55	68	No
				RYTIAALLSPYSYSTTAVVTNPKE	R	-	95.00%	34		882.4748	3	10.0	124	147	No
633	IPI00022488	HPX	HEMOPEXIN PRECURSOR.	GGYTLVSGYPK	K	R	95.00%	56		571.3003	2	2.9	333	343	No
				RLWWLDLK	R	S	95.00%	39		565.3339	2	6.6	379	386	No
				SGAQATWTELPWPHEK	K	V	95.00%	43		919.4512	2	3.7	387	402	No
				SGAQATWTELPWPHEK	K	V	95.00%	42		613.3062	3	8.3	387	402	No
634	IPI00022977	CKB	CREATINE KINASE B-TYPE.	DLFDPIIEDR	K	H	95.00%	34		616.8163	2	6.5	87	96	No
				DWPDAR	R	G	95.00%	44		759.3495	1	8.9	210	215	Yes
				GTGGVDTAAVGGVFDVSNADR	R	L	95.00%	121		982.9782	2	8.8	321	341	No
				LAVEALSSLDGDLAGR	K	Y	95.00%	104		793.9290	2	7.0	157	172	No
				LEQGQAIDDLMPAQK	R	-	95.00%	86	M11: Oxidation	836.9199	2	6.0	367	381	No
				LGFSEVELVQMVVDGVK	R	L	95.00%	106	M11: Oxidation	932.9942	2	4.0	342	358	No
				LGFSEVELVQMVVDGVK	R	L	95.00%	51	M11: Oxidation	622.3338	3	6.7	342	358	No
				LGFSEVELVQMVVDGVK	R	L	95.00%	97		924.9986	2	6.0	342	358	No
				PVSPLLLASGMAR	K	D	95.00%	77	M11: Oxidation	664.3789	2	6.9	197	209	Yes
				PVSPLLLASGMAR	K	D	95.00%	88		656.3820	2	7.7	197	209	Yes
				SMTEAEQQQLIDDHFLFDKPVSPLLLASGMAR	K	D	95.00%	74	M2: Oxidation, M30: Oxidation	1207.2750	3	8.8	178	209	No
				TFLVWVNEEDHLR	K	V	95.00%	79		829.4272	2	7.6	224	236	No
				TFLVWVNEEDHLR	K	V	95.00%	37		553.2868	3	6.5	224	236	No
				VLTPELYAELR	K	A	95.00%	46		652.3710	2	6.0	33	43	No
635	IPI00024067; IPI00455383	CLTC	ISOFORM 1 OF CLATHRIN HEAVY CHAIN 1.; ISOFORM 2 OF CLATHRIN HEAVY CHAIN 1.	LASTLVHLGEYQAAVDGAR	R	K	95.00%	38		657.6877	3	8.8	1227	1245	No
				LLLPWLEAR	K	I	95.00%	30		555.8422	2	8.0	857	865	No
				LLYNNVSNFGR	K	L	95.00%	34		648.8408	2	2.9	1216	1226	No
				RPISADSAIMNPASK	R	V	95.00%	55	M10: Oxidation	787.4070	2	3.4	64	78	No
				VANVELYYR	K	A	95.00%	51		563.7990	2	0.4	1398	1406	No
636	IPI00024107; IPI00218467; IPI00788661	SNCA	ISOFORM 1 OF ALPHA-SYNUCLEIN.; ISOFORM 2-4 OF ALPHA-SYNUCLEIN.; 12 KDA PROTEIN.	EGVVHGVATVAEK	K	T	95.00%	43		648.3549	2	4.6	46	58	No
				TKEGVLYVGSK	K	T	95.00%	35		590.8361	2	5.4	33	43	No
				TKEQVTNVGGAVVTGVTAVAQK	K	T	95.00%	44		719.7411	3	9.2	59	80	No
				TVEGAGSIAAATGFVKK	K	D	95.00%	41		803.9510	2	8.6	81	97	No
637	IPI00024266; IPI00639812	MGST3	MICROSOMAL GLUTATHIONE S-TRANSFERASE 3.; MICROSOMAL GLUTATHIONE S-TRANSFERASE 3.	IASGLGLAWIVGR	R	V	95.00%	102		656.8964	2	8.1	85	97	No
				VLYAYGYYTGEPSK	R	R	95.00%	84		805.8970	2	7.4	98	111	No
				VLYAYGYYTGEPSKR	R	S	95.00%	62		883.9486	2	7.9	98	112	No

638	IPI00024401	USP13	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 13.	GLQPGEEELPDISPPIVIPDDSKDR	R	L	95.00%	37		906.1336	3	6.0	618	642	No
				IGSENPSDVFR	R	F	95.00%	36		610.8040	2	7.4	464	474	No
639	IPI00024976	TOMM22	MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM22 HOMOLOG.	LQMEQQQQLQQR	K	Q	95.00%	63	M3: Oxidation	787.3981	2	8.0	106	117	No
				LWGLTEMFPER	R	V	95.00%	32	M7: Oxidation	697.8468	2	5.6	48	58	No
640	IPI00025156	STUB1	ISOFORM 1 OF STIP1 HOMOLOGY AND U BOX-CONTAINING PROTEIN 1.	LNFGDDIPSALR	R	I	95.00%	32		659.3497	2	8.4	129	140	No
				NPLVAVYYTNR	R	A	95.00%	62		655.3545	2	8.4	56	66	No
				SPLTQEQLIPNLAMK	R	E	95.00%	51	M14: Oxidation	849.9630	2	4.6	273	287	No
641	IPI00025341	BDH1	D-BETA-HYDROXYBUTYRATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.	SFLPLIR	K	R	95.00%	27		423.2694	2	7.1	178	184	No
				VVNISSMLGR	R	M	95.00%	37	M7: Oxidation	546.2962	2	-3.4	190	199	No
642	IPI00025717; IPI00477773	MTX2	METAXIN-2.; METAXIN 2 ISOFORM B.	GHSLSDGLEEVQK	K	A	95.00%	66		699.8503	2	4.5	86	98	No
				LGTQPYFFNK	R	Q	95.00%	31		607.8201	2	9.2	187	196	No
643	IPI00026260; IPI00604590; IPI00795292	NME1; NME1-NME2; NME2	NUCLEOSIDE DIPHOSPHATE KINASE B.; NME1-NME2 PROTEIN.; NME1-NME2 PROTEIN.	DRPFFPGLVK	K	Y	95.00%	29		588.3357	2	4.9	57	66	No
				GLVGEIIKR	R	F	95.00%	60		492.8172	2	6.0	19	27	Yes
				TFIAIKPDGVQR	R	G	95.00%	68		672.8903	2	6.4	7	18	No
				VMLGETNPADSKPGTIR	R	G	95.00%	54	M2: Oxidation	901.4668	2	7.6	89	105	Yes
				VMLGETNPADSKPGTIR	R	G	95.00%	48	M2: Oxidation	601.3131	3	6.4	89	105	No
644	IPI00027223	IDH1	ISOCITRATE DEHYDROGENASE [NADP] CYTOPLASMIC.	FKDIFQEIYDK	R	Q	95.00%	57		723.3737	2	5.2	223	233	No
				GQETSTNPIASIFAWTR	K	G	95.00%	79		939.9764	2	5.3	322	338	No
				ISGGSVVEMQGDEMTR	K	I	95.00%	74	M9: Oxidation, M14: Oxidation	864.3869	2	4.6	5	20	No
				LIFPYVELDLHSYDLGIENR	K	D	95.00%	56		802.7568	3	8.4	30	49	No
				LVSGWVKPIIIGR	R	H	95.00%	50		479.9723	3	4.4	120	132	No
				NILGGTVFR	R	E	95.00%	57		488.7877	2	9.7	101	109	Yes
				VEITYTPSDGTQK	K	V	95.00%	67		719.8637	2	8.9	152	164	No
				VTYLVHNFEEGGGVAMGMYNQDK	K	S	95.00%	64	M16: Oxidation, M18: Oxidation	864.3957	3	6.4	165	187	No
645	IPI00027342; IPI00552929; IPI00792495	CAP2	ADENYLYL CYCLASE-ASSOCIATED PROTEIN 2.; HYPOTHETICAL PROTEIN DKFZP686D0714.; CAP, ADENYLATE CYCLASE-ASSOCIATED PROTEIN, 2.	EMNDAATFYTNR	K	V	95.00%	29	M2: Oxidation	724.8145	2	6.7	158	169	No
				ILAGDVETHAEMVHSAFQAQR	R	A	95.00%	52	M12: Oxidation	776.0517	3	6.3	63	83	No
				IQEIQTFR	K	E	95.00%	36		517.7882	2	4.7	114	121	No
				SALFAQLNQGEAITK	R	G	95.00%	88		795.9328	2	5.3	258	272	No
646	IPI00027463	S100A6	PROTEIN S100-A6.	LMEDLDR	R	N	95.00%	30	M2: Oxidation	454.2160	2	5.0	56	62	No
				LQDAEIAR	K	L	95.00%	49		458.2500	2	2.4	48	55	No
647	IPI00027626	CCT6A	T-COMPLEX PROTEIN 1 SUBUNIT ZETA.	ALQFLEEVK	K	V	95.00%	48		538.8054	2	3.3	130	138	No
				AQLGVQAFADALLIIPK	R	V	95.00%	87		884.5286	2	6.6	433	449	No
				DGNVLLHEMQIQHPTASLIAK	K	V	95.00%	38	M9: Oxidation	777.7476	3	6.0	59	79	No
				GIDPFSLDALSK	K	E	95.00%	73		631.8395	2	6.1	296	307	No
				TEVNSGFFYK	K	S	95.00%	38		596.2905	2	3.9	242	251	No
				VATAQDDITGDGTTSNVLIIGELLK	K	Q	95.00%	70		848.7925	3	8.3	80	104	No
				VHAELADVLTEAVVDSILAIK	K	K	95.00%	156		1103.6320	2	10.0	160	180	No
				VHAELADVLTEAVVDSILAIK	K	K	95.00%	55		736.0867	3	5.1	160	180	No
				VLAQNSGFDLQETLVK	K	I	95.00%	112		881.4807	2	8.4	450	465	No
648	IPI00027701	ACADS	SHORT-CHAIN SPECIFIC ACYL-COA DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.	DSILGEPGMGFK	K	I	95.00%	38	M9: Oxidation	633.8084	2	3.8	251	262	No
				ELFPIAAQVDKEHLFPAAQVK	K	K	95.00%	44		784.4336	3	3.7	52	72	No
				GISAFLVPMPTPGLTLGK	K	K	95.00%	42	M9: Oxidation	908.0153	2	7.3	209	226	No
				IAMQTLDMGR	K	I	95.00%	70	M3: Oxidation, M8: Oxidation	584.2797	2	1.0	263	272	No
				IAMQTLDMGR	K	I	95.00%	43	M8: Oxidation	576.2825	2	1.5	263	272	No
				ITEIYEGTSEIQR	R	L	95.00%	102		769.8917	2	3.4	387	399	No
				ITEIYEGTSEIQR	R	L	95.00%	32		513.5945	3	-1.5	387	399	No
				LAASEAATAISHQAIQILGGMGYVTEMPAER	K	H	95.00%	78	M21: Oxidation, M27: Oxidation	805.4082	4	8.4	350	380	No
				LADMALALESAR	K	L	95.00%	68	M4: Oxidation	638.8361	2	5.7	314	325	No
				LQVIQFK	K	L	95.00%	36		438.2730	2	3.1	307	313	No
				LVIAGHLLR	R	S	95.00%	66		496.3265	2	3.4	400	408	No
				MAFGAPLTK	R	L	95.00%	39	M1: Oxidation	476.2541	2	3.1	298	306	No

649	IPI00028120; IPI00028614; IPI00619961; IPI00790118; IPI00827872	EPB42	ISOFORM LONG OF ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2.; EPB42 PROTEIN.; EPB42 PROTEIN.; 27 KDA PROTEIN.; ISOFORM SHORT OF ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2.	TQATFPISSLGDR	R	K	95.00%	45		696.8628	2	3.9	75	87	No
				TQATFPISSLGDRK	R	W	95.00%	34		760.9137	2	8.0	105	118	No
				VALTAQTGEQPSK	K	I	95.00%	60		665.3578	2	4.6	89	101	No
				VLGALLHFLK	R	E	95.00%	64		555.8602	2	7.5	244	253	No
				VLPTPQTQATQEGALLNK	R	R	95.00%	94		955.0309	2	7.5	227	244	No
				VVTTFASAQGTGGR	R	L	95.00%	72		676.3555	2	4.6	318	331	No
650	IPI00028883; IPI00642807	NDUFB8	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 8,MITOCHONDRIAL PRECURSOR.; NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUBCOMPLEX, 8, 19KDA.	QYPYNNLYLER	K	G	95.00%	42		736.8688	2	8.4	129	139	No
				YNMRVEDYEPYPDDGMGYGDYPK	K	L	95.00%	33	M3: Oxidation, M16: Oxidation	936.0545	3	6.7	24	46	No
651	IPI00029468	ACTR1A	ALPHA-CENTRACTIN.	AQYYLPDGSTIEIGPSR	K	F	95.00%	94		933.9746	2	9.4	239	255	No
				DQLQTFSEEHPVLLTEAPLNPR	K	K	95.00%	79		845.4432	3	9.7	97	118	No
				TLFSNIVLSGGSTLFK	R	G	95.00%	103		842.4764	2	7.6	293	308	No
				VMAGALEGDIFIGPK	R	A	95.00%	80	M2: Oxidation	767.4092	2	7.6	47	61	No
652	IPI00029739	CFH	ISOFORM 1 OF COMPLEMENT FACTOR H PRECURSOR.	EIMENYNIALR	R	W	95.00%	54	M3: Oxidation	691.3448	2	2.4	1172	1182	No
				RPYFPVAVGK	R	Y	95.00%	27		567.3273	2	-0.4	342	351	No
653	IPI00030154; IPI00479722; IPI00748256	PSME1	PROTEASOME ACTIVATOR COMPLEX SUBUNIT 1.; 29 KDA PROTEIN.; PROTEASOME ACTIVATOR SUBUNIT 1 ISOFORM 2.	APLDIPVPDPVK	K	E	95.00%	30		630.8684	2	6.6	59	70	No
				IEDGNNFGVAVQEK	R	V	95.00%	68		760.3782	2	6.0	142	155	No
				IVVLLQR	K	L	95.00%	42		420.7900	2	6.0	110	116	No
				QLVHELDEAEYR	R	D	95.00%	66		751.3752	2	9.2	199	210	No
654	IPI00030531; IPI00791574; IPI00794566	SLMAP	ISOFORM 3 OF SARCOLEMMAL MEMBRANE-ASSOCIATED PROTEIN.; ISOFORM 1 OF SARCOLEMMAL MEMBRANE-ASSOCIATED PROTEIN.; ISOFORM 2 OF SARCOLEMMAL MEMBRANE-ASSOCIATED PROTEIN.	DEILLLHQAAAK	R	V	95.00%	53		661.3827	2	7.1	565	576	Yes
				VASERDTDIASLQEELKK	K	V	95.00%	52		678.0284	3	6.4	577	594	No
655	IPI00030929; IPI00220278	MYL9	MYOSIN REGULATORY LIGHT CHAIN 9 ISOFORM B.; MYOSIN REGULATORY LIGHT CHAIN 2, SMOOTH MUSCLE ISOFORM.	EAFNMIDQNR	K	D	95.00%	34	M5: Oxidation	627.2878	2	7.5	36	45	Yes
				FTDEEVDEMYR	R	E	95.00%	54	M9: Oxidation	725.3025	2	8.9	80	90	No
656	IPI00031564	C7orf24	UNCHARACTERIZED PROTEIN C7ORF24.	SGMYVVIEVK	K	V	95.00%	28	M3: Oxidation	570.8076	2	8.6	102	111	No
				VSEEIEDIIK	K	K	95.00%	53		587.8187	2	7.5	172	181	No
657	IPI00032633	COQ6	UBIQUINONE BIOSYNTHESIS MONOOXYGENASE COQ6.	DLGSVSHLTGYETER	K	Q	95.00%	84		832.4050	2	5.5	402	416	No
				DLGSVSHLTGYETER	K	Q	95.00%	49		555.2714	3	3.4	402	416	No
				HNTALLAATDLLK	R	R	95.00%	83		690.9013	2	6.9	419	431	No
				HNTALLAATDLLKR	R	L	95.00%	90		512.9711	3	7.4	419	432	No
				ILLLEAGPK	K	K	95.00%	50		477.3075	2	3.6	65	73	No
				LYSTSASPLVLLR	R	T	95.00%	52		710.4183	2	5.4	433	445	No
				TWGLQATNAVSPLK	R	E	95.00%	94		743.4118	2	6.1	446	459	No
658	IPI00032957; IPI00450472	UBE2I	SUMO-CONJUGATING ENZYME UBC9.; UBIQUITIN-CONJUGATING ENZYME E2I.	KDHPFGFVAVPTK	R	N	95.00%	38		481.6016	3	6.5	18	30	No
				MLFKDDYPSSPPK	R	C	95.00%	56	M1: Oxidation	770.8789	2	9.1	62	74	No
659	IPI00037448; IPI00550682	GRHPR	GLYOXYLATE REDUCTASE/HYDROXYPYRUVATE REDUCTASE.; GRHPR PROTEIN (FRAGMENT).	GDVVNQDDLYQALASGK	R	I	95.00%	120		896.9472	2	8.2	246	262	No
				GEPMPSELKL	R	-	95.00%	33	M4: Oxidation	558.7873	2	4.9	319	328	No
				IAAAGLDVTSPEPLPTNHPLLTLK	K	N	95.00%	53		823.4714	3	8.8	263	286	No
				ILDAAGANLK	R	V	95.00%	52		493.2899	2	3.6	67	76	No
				LPEAIEEVK	R	N	95.00%	39		514.2911	2	6.5	126	134	No
				MKETAVFINISR	K	G	95.00%	77	M1: Oxidation	712.8883	2	8.1	234	245	No
				MKETAVFINISR	K	G	95.00%	36	M1: Oxidation	475.5924	3	3.0	234	245	No
				NTMSLLAANNLLAGLR	R	G	95.00%	88	M3: Oxidation	844.4705	2	9.8	303	318	No
				RLPEAIEEVK	R	N	95.00%	40		592.3406	2	3.9	125	134	No
				VISTMSVGIDHLALDEIK	K	K	95.00%	110	M5: Oxidation	979.0281	2	8.4	77	94	No
				VISTMSVGIDHLALDEIK	K	K	95.00%	32	M5: Oxidation	653.0189	3	4.7	77	94	No

660	IPI00042580; IPI00647123; IPI00797546	APOO	ISOFORM 1 OF APOLIPOPROTEIN O PRECURSOR.; 13 KDA PROTEIN.; ISOFORM 2 OF APOLIPOPROTEIN O PRECURSOR.	SQLEESISQLR	R	H	95.00%	63		645.3428	2	6.0	58	68	No
				VDELSLYSVPEGQSK	K	Y	95.00%	50		825.9233	2	9.8	37	51	No
661	IPI00045496	USP28	ISOFORM 1 OF UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 28.	ARQTFDRDGSEAGLIK	K	A	95.00%	38		882.4524	2	-4.2	785	800	No
				SISIMK	R	V	95.00%	26	M5: Oxidation	694.3846	1	5.2	861	866	No
662	IPI00065495; IPI00152070; IPI00736624	COQ10A	ISOFORM 1 OF PROTEIN COQ10 A, MITOCHONDRIAL PRECURSOR.; COQ10A PROTEIN.; ISOFORM 2 OF PROTEIN COQ10 A, MITOCHONDRIAL PRECURSOR.	FGPETAIPR	K	E	95.00%	33		494.2691	2	3.8	229	237	No
				LFNHLETIWR	K	F	95.00%	51		443.5795	3	8.5	166	175	No
663	IPI00105916	NOL3	ISOFORM 1 OF NUCLEOLAR PROTEIN 3.	LLLLVQGK	R	G	95.00%	49		442.3061	2	7.0	61	68	No
				LVETLQADSGLLLDALLAR	R	G	95.00%	51		671.0589	3	8.4	19	37	No
664	IPI00152692; IPI00829870	DTD1; HARS2	PROBABLE D-TYROSYL-TRNA(TYR) DEACYLASE 1.; HISTIDYL-TRNA SYNTHETASE 2.	ASVTVGGEQISAIGR	R	G	95.00%	52		722.8981	2	8.5	11	25	No
				SASSGAEGDVSSEREP	R	-	95.00%	71		782.8470	2	8.7	194	209	No
665	IPI00157790	KIAA0368	KIAA0368 PROTEIN.	HSVATAADLELK	R	S	95.00%	30		627.8422	2	5.7	446	457	No
				LGHAETDEQLQNIISK	R	F	95.00%	35		599.3132	3	2.7	195	210	No
				YLLLLAAGDPR	R	E	95.00%	38		601.3557	2	7.4	689	699	No
666	IPI00168620	ADPRHL1	ISOFORM 1 OF [PROTEIN ADP-RIBOSYLARGININE] HYDROLASE-LIKE PROTEIN 1.	AAMLLGSVGDALGYR	K	N	95.00%	78	M3: Oxidation	755.3950	2	5.7	6	20	No
				AAMLLGSVGDALGYR	K	N	95.00%	35	M3: Oxidation	503.9328	3	6.1	6	20	No
				AIFPDNYDAEER	K	E	95.00%	38		720.3291	2	4.2	245	256	No
				AIFPDNYDAEEREK	K	T	95.00%	71		848.8993	2	5.3	245	258	No
				GLYQDLEDKEK	K	L	95.00%	30		669.3377	2	6.3	328	338	No
				GLYQDLEDKEKLEDLGAALYR	K	L	95.00%	63		813.7575	3	6.5	328	348	No
				LEDLGAALYR	K	L	95.00%	84		560.8067	2	4.6	339	348	No
				WQFYLEER	K	K	95.00%	40		585.7852	2	3.4	228	235	No
667	IPI00171844	COPS4	COP9 SIGNALOSOME COMPLEX SUBUNIT 4.	AIQLSGAEQLEALK	K	A	95.00%	98		735.9176	2	7.1	33	46	No
				ASLLQNESTNEQLQIHYK	R	V	95.00%	41		706.0298	3	3.0	171	188	No
				ATTADGSSILDR	K	A	95.00%	43		603.8076	2	8.7	291	302	No
				AVIEHNLLSASK	R	L	95.00%	75		641.3619	2	-0.5	303	314	No
				LYLEDDDPVQAEAYINR	R	A	95.00%	94		1012.4900	2	5.2	154	170	No
				LYLEDDDPVQAEAYINR	R	A	95.00%	53		675.3305	3	7.2	154	170	No
				LYNNITFEELGALLEIPAAK	K	A	95.00%	108		1110.1120	2	8.6	315	334	No
				LYNNITFEELGALLEIPAAK	K	A	95.00%	89		740.4106	3	8.9	315	334	No
				MNGFIDQIDGIVHFETR	R	E	95.00%	63	M1: Oxidation	669.9955	3	5.4	348	364	No
				NAAQVLVGIPLETGQK	R	Q	95.00%	84		819.4721	2	8.3	122	137	No
				VISFEEQVASIR	R	Q	95.00%	80		689.3776	2	6.9	96	107	No
668	IPI00180408	MYH15	MYOSIN-15.	AEVAESQVNK	R	L	95.00%	43		537.7797	2	7.8	1922	1931	No
				LTGAIMHFGNMK	K	F	95.00%	62	M11: Oxidation	668.3378	2	9.1	364	375	Yes
				LTGAIMHFGNMK	K	F	95.00%	67	M6: Oxidation, M11: Oxidation	676.3319	2	4.2	364	375	Yes
				LTGAIMHFGNMK	K	F	95.00%	83		660.3402	2	9.1	364	375	Yes
				NLTEMEK	K	V	95.00%	32	M5: Oxidation	880.4110	1	2.6	1534	1540	No
669	IPI00215719	RPL18	60S RIBOSOMAL PROTEIN L18.	ILTFDQLALDSPK	K	G	95.00%	88		730.9065	2	3.3	120	132	No
				TAVVVGTITDDVR	K	V	95.00%	44		673.3737	2	5.1	79	91	No
670	IPI00215894; IPI00789376; IPI00797833	KNG1	ISOFORM LMW OF KININOGEN-1 PRECURSOR.; KNG1 PROTEIN.; KININOGEN 1.	IGEIKEETTSHLR	R	S	95.00%	33		756.9071	2	2.6	393	405	No
				IGEIKEETTSHLR	R	S	95.00%	57		504.9411	3	3.4	393	405	No
				YFIDFVAR	K	E	95.00%	29		515.7751	2	6.0	317	324	No
671	IPI00215979	BPGM	BISPHOSPHOGLYCERATE MUTASE.	AVGPHQFLGDQEAIQAAIK	R	K	95.00%	38		665.0271	3	7.4	228	246	No
				EQMALNHGEEQVR	R	L	95.00%	37	M3: Oxidation	778.8655	2	6.7	101	113	No
				HYGALIGLNR	R	E	95.00%	32		557.3148	2	4.2	91	100	No
				SESLKDVLER	R	L	95.00%	36		588.3204	2	4.8	155	164	No
672	IPI00216691	PFN1	PROFILIN-1.	DSLLQDGEFSMDLR	R	T	95.00%	93	M11: Oxidation	821.3791	2	4.4	76	89	No
				DSPSVWAAVPGK	K	T	95.00%	38		607.3177	2	4.8	27	38	No
				SSFYVNGLTLGGQK	R	C	95.00%	72		735.8907	2	9.7	57	70	No
				TFVNITPAEVGVLVGK	K	D	95.00%	54		822.4798	2	8.8	39	54	No
				TLVLLMGK	K	E	95.00%	27	M6: Oxidation	890.5456	1	7.7	109	116	No
				TLVLLMGK	K	E	95.00%	54	M6: Oxidation	445.7763	2	6.8	109	116	No

673	IPI00216697; IPI00297532; IPI00374973; IPI00646300; IPI00654646; IPI00744408; IPI00744846; IPI00744895; IPI00744986; IPI00745246; IPI00745348; IPI00747536; IPI00747552; IPI00748074; IPI00748330; IPI00748439; IPI00748895; IPI00749301	ANK1	ISOFORM ER1 OF ANKYRIN-1.; ISOFORM ER2 OF ANKYRIN-1.; ISOFORM ER3 OF ANKYRIN-1.; ISOFORM ER16 OF ANKYRIN-1.; ISOFORM ER5 OF ANKYRIN-1.; ISOFORM ER7 OF ANKYRIN-1.; ISOFORM ER10 OF ANKYRIN-1.; ISOFORM ER6 OF ANKYRIN-1.; ISOFORM ER9 OF ANKYRIN-1.; 207 KDA PROTEIN.; ISOFORM ER4 OF ANKYRIN-1.; ISOFORM ER11 OF ANKYRIN-1.; ISOFORM ER8 OF ANKYRIN-1.; ISOFORM ER15 OF ANKYRIN-1.; ISOFORM BR21 OF ANKYRIN-1.; ISOFORM ER14 OF ANKYRIN-1.; ISOFORM ER13 OF ANKYRIN-1.; ISOFORM ER12 OF ANKYRIN-1.	ELQFSVEDINR	R	I	95.00%	48		675.3449	2	8.8	1424	1434	No
				ISEILLDHGAPIQAK	R	T	95.00%	44		802.9553	2	0.8	287	301	No
				ISEILLDHGAPIQAK	R	T	95.00%	28		535.6401	3	2.0	287	301	No
				KGNTALHIAALAGQDEVVR	K	E	95.00%	45		655.0337	3	6.5	77	95	No
				LALQAQPVPDELVTK	K	L	95.00%	54		811.4681	2	7.2	1106	1120	Yes
				LDQVVESPAIPR	K	I	95.00%	47		662.3696	2	3.0	850	861	No
				SGLTPLHLVAQEGHVPVADVLIK	K	H	95.00%	37		798.4645	3	9.3	667	689	No
				TAAVLLQNDPNPDVLSK	R	T	95.00%	89		897.9919	2	8.8	188	204	No
				VVTDETSFVLVSDK	K	H	95.00%	53		769.9070	2	6.9	788	801	No
674	IPI00217960; IPI00396630	LOC730418; PRKACA	ISOFORM 2 OF CAMP-DEPENDENT PROTEIN KINASE, ALPHA-CATALYTIC SUBUNIT.; ISOFORM 1 OF CAMP-DEPENDENT PROTEIN KINASE, ALPHA-CATALYTIC SUBUNIT.	DLKPENLLIDQQGYIQVTDFGFAK	R	R	95.00%	52		918.1508	3	6.0	159	182	No
				DNSNLYMVMEYVPGGEMFSHLR	K	R	95.00%	47	M7: Oxidation, M9: Oxidation, M17: Oxidation	879.7251	3	6.8	105	126	No
				FPSHFSSDLKDLLR	R	N	95.00%	42		416.2234	4	3.1	250	263	No
				ILQAVNFPFLVK	R	L	95.00%	68		694.9253	2	8.7	87	98	No
				KVEAPFIPK	R	F	95.00%	54		514.8129	2	3.2	302	310	No
				KWESPAQNTAHLDQFER	K	I	95.00%	93		1029.0030	2	6.6	22	38	No
				KWESPAQNTAHLDQFER	K	I	95.00%	56		686.3353	3	3.0	22	38	No
				NLLQVDLTK	R	R	95.00%	56		1043.6190	1	8.4	264	272	No
				NLLQVDLTK	R	R	95.00%	40		522.3110	2	3.7	264	272	No
				VRFPSHFSSDLKDLLR	K	N	95.00%	36		639.6875	3	6.3	248	263	No
				VRFPSHFSSDLKDLLR	K	N	95.00%	47		480.0161	4	3.2	248	263	No
				WFATTDWIAIYQR	K	K	95.00%	57		835.9247	2	5.1	289	301	No
675	IPI00218465; IPI00759657	PLAA	PHOSPHOLIPASE A-2-ACTIVATING PROTEIN.; PHOSPHOLIPASE A2-ACTIVATING PROTEIN ISOFORM 2.	IGDVVGSSGANQQTSGK	K	V	95.00%	65		802.9037	2	7.2	377	393	No
				ILPEQGLMLTGSADK	K	T	95.00%	41	M8: Oxidation	794.9241	2	9.1	159	173	No
676	IPI00218728	PAFAH1B1	ISOFORM 1 OF PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB SUBUNITALPHA.	GHTDSVQDISFDHSGK	K	L	95.00%	31		577.2664	3	3.0	148	163	No
				LNEAKEEFTSGGPLGQK	K	R	95.00%	103		902.9658	2	8.5	72	88	No
				LNEAKEEFTSGGPLGQK	K	R	95.00%	36		602.3113	3	5.5	72	88	No
				TAPYVVTGSVDQTVK	K	V	95.00%	70		782.9196	2	5.8	391	405	No
677	IPI00218918	ANXA1	ANNEXIN A1.	ALTGHLEEVVLALLK	K	T	95.00%	104		803.4899	2	8.5	99	113	No
				ALTGHLEEVVLALLK	K	T	95.00%	55		535.9944	3	5.9	99	113	No
				GDRSEDFGVNEDLADSDAR	K	A	95.00%	46		689.9705	3	5.0	186	204	No
				GGPGSAVSPYPTFNPSSDVAALHK	K	A	95.00%	52		786.0644	3	8.6	30	53	No
				GLGTDEDTLIEILASR	K	T	95.00%	104		851.9543	2	8.2	129	144	No
				GVDEATIIDILTK	K	R	95.00%	75		694.3931	2	6.9	59	71	No
				SEDFGVNEDLADSDAR	R	A	95.00%	97		870.3769	2	5.7	189	204	No
				TPAQFDADELR	K	A	95.00%	71		631.8081	2	5.2	114	124	No
678	IPI00219291; IPI00220300; IPI00456013; IPI00719814	ATP5J2	ISOFORM 2 OF ATP SYNTHASE F CHAIN, MITOCHONDRIAL.; ISOFORM 1 OF ATP SYNTHASE F CHAIN, MITOCHONDRIAL.; ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F0 COMPLEX, SUBUNIT F2ISOFORM 2C.; ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F0 COMPLEX, SUBUNIT F2ISOFORM 2D.	DFSPSGIFGAFQR	R	E	95.00%	74		714.8558	2	8.7	34	46	No
				LGELPSWILMR	K	D	95.00%	61	M10: Oxidation	665.8696	2	9.0	23	33	No
679	IPI00219365	MSN	MOESIN.	APDFVFYAPR	K	L	95.00%	81		591.8027	2	2.3	264	273	Yes
				FYPEDVSEELIQDITQR	K	L	95.00%	58		694.6777	3	6.8	84	100	No
				GMLREDAVLEYLK	R	I	95.00%	31	M2: Oxidation	518.2779	3	8.7	181	193	No

				IAQDLEMYGVNYFSIK	K	N	95.00%	82	M7: Oxidation	953.9747	2	8.1	194	209	No
				IGFPWSEIR	K	N	95.00%	65		552.7990	2	5.2	238	246	Yes
				LFFLQVK	R	E	95.00%	40		447.7807	2	9.2	101	107	Yes
				QLFDQVVK	K	T	95.00%	42		488.7801	2	5.5	28	35	Yes
				RKPDTIEVQQMK	R	A	95.00%	37	M11: Oxidation	744.9012	2	6.6	295	306	Yes
				RKPDTIEVQQMK	R	A	95.00%	33	M11: Oxidation	496.9362	3	5.4	295	306	Yes
				TQEQLALEMAELTAR	K	I	95.00%	72	M9: Oxidation	860.4392	2	6.8	413	427	No
				VTTMDAELEFAIQPNTTGK	R	Q	95.00%	133	M4: Oxidation	1041.5160	2	8.1	9	27	Yes
680	IPI00219682; IPI00377081	STOM	ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN.; STOMATIN ISOFORM B.	EASMVITESPAALQLR	K	Y	95.00%	92	M4: Oxidation	866.4568	2	6.1	236	251	No
				LPDSFKDSPSK	R	G	95.00%	30		610.8157	2	5.8	15	25	No
				NSTIVFPLPIDMLQGIIGAK	K	H	95.00%	32	M12: Oxidation	715.0734	3	9.6	264	283	No
681	IPI00219772	NDUFB7	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 7.	EMVATQQEMMDAQLR	R	L	95.00%	77	M2: Oxidation, M9: Oxidation, M10: Oxidation	914.9050	2	7.7	38	52	No
				EREMVATQQEMMDAQLR	K	L	95.00%	55	M4: Oxidation, M11: Oxidation, M12: Oxidation	705.3222	3	9.1	36	52	No
682	IPI00220059	LOC727762; NDUFB4	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 4.	EYLLQYNDPNRR	R	G	95.00%	32		790.9011	2	7.6	46	57	No
				GLIENPALLR	R	W	95.00%	63		548.3329	2	4.7	58	67	No
683	IPI00220503; IPI00793544	DCTN2	DYNACTIN 2.; 42 KDA PROTEIN.	ENLATVEGNFASIDER	R	M	95.00%	141		882.9319	2	8.9	385	400	No
				LLGPDAAINLTDPDGALAK	K	R	95.00%	91		933.0141	2	9.6	162	180	No
				LLHEVQELTTEVEK	R	I	95.00%	85		834.4536	2	8.1	111	124	No
				LLLQLEATK	R	N	95.00%	41		514.8234	2	3.2	182	190	No
				TGYESGEYEMLGEGLGVK	R	E	95.00%	113	M10: Oxidation	967.9429	2	4.4	84	101	No
				VSALDLAVLDQVEAR	K	L	95.00%	89		799.9472	2	6.9	273	287	No
				YADLPGIAR	K	N	95.00%	38		488.2691	2	4.0	6	14	No
684	IPI00220834	XRCC5	ATP-DEPENDENT DNA HELICASE 2 SUBUNIT 2.	ANPQVGVAFPHIK	R	H	95.00%	46		689.3901	2	5.8	401	413	No
				HIEIFTDLSSR	R	F	95.00%	52		659.3478	2	5.6	131	141	No
				HLMLPDFDLLEDIESK	R	I	95.00%	85	M3: Oxidation	965.9846	2	7.1	82	97	No
				HLMLPDFDLLEDIESK	R	I	95.00%	38	M3: Oxidation	644.3265	3	8.5	82	97	No
				LTIGSNLSIR	R	I	95.00%	63		537.3196	2	-0.7	251	260	No
				TDTLEDLFPTTK	K	I	95.00%	57		690.8536	2	6.5	470	481	No
				YGSDIVPFSK	R	V	95.00%	41		556.7877	2	4.1	316	325	No
685	IPI00220991; IPI00333383; IPI00784156; IPI00784366; IPI00790702	AP2B1	HYPOTHETICAL PROTEIN DKFZP781K0743.; 105 KDA PROTEIN.; ISOFORM 1 OF AP-2 COMPLEX SUBUNIT BETA-1.; ISOFORM 2 OF AP-2 COMPLEX SUBUNIT BETA-1.; BETA ADAPTIN SUBUNIT.	LAPPLVTLLSGEPEVQYVALR	K	N	95.00%	42		755.7730	3	7.8	284	304	No
				MEPLNNLQVAVK	K	N	95.00%	32	M1: Oxidation	686.3740	2	7.0	813	824	No
686	IPI00255052; IPI00790752	NDUFB9	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 9.; NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT.	EAEEEFWYR	K	Q	95.00%	43		629.7769	2	6.4	66	74	No
				QHPQPYIFPDSPGGTSYER	R	Y	95.00%	53		726.0149	3	8.8	75	93	No
				QLQEETPPGGPLTEALPPAR	K	K	95.00%	74		1051.0570	2	5.8	139	158	No
687	IPI00289334; IPI00382696; IPI00477536; IPI00480131	FLNB	ISOFORM 1 OF FILAMIN-B.; ISOFORM 2 OF FILAMIN-B.; FILAMIN B.; 278 KDA PROTEIN.	DAGYGGISLAVEGPSK	R	V	95.00%	31		760.8905	2	8.7	2029	2044	No
				EAGAGGLSIAVEGPSK	R	A	95.00%	107		721.8835	2	6.9	2220	2235	Yes
				IQQNTFTR	K	W	95.00%	40		504.2716	2	7.9	17	24	Yes
				LIALLEVLSQK	R	R	95.00%	103		613.8940	2	6.3	50	60	Yes
				LIALLEVLSQK	R	R	95.00%	37		409.5990	3	7.2	50	60	Yes
				LIALLEVLSQKR	R	M	95.00%	74		691.9453	2	6.5	50	61	Yes
				LIALLEVLSQKR	R	M	95.00%	56		461.6335	3	8.0	50	61	Yes
				LLGWIQNK	R	I	95.00%	61		486.2915	2	7.5	145	152	No
				SPFTVGVAAPLDLSK	K	I	95.00%	75		751.4233	2	8.0	932	946	No
688	IPI00291136	COL6A1	COLLAGEN ALPHA-1(VI) CHAIN PRECURSOR.	GLEQLLVGGSHLK	K	E	95.00%	46		450.9336	3	7.7	136	148	No
				LLLFSDGNSQGATPAAIEK	R	A	95.00%	134		966.5156	2	7.9	939	957	No
				VAVVQYSGTGQQRPER	R	A	95.00%	36		592.3162	3	7.2	873	888	No
				VFSVAITPDHLEPR	K	L	95.00%	28		527.6233	3	6.6	186	199	No
				VPSYQALLR	R	G	95.00%	60		523.8066	2	5.2	1006	1014	No
689	IPI00291328; IPI00646556; IPI00793910	NDUFV2	NADH DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN 2, MITOCHONDRIALPRECURSOR.; 28 KDA PROTEIN.; 24-KDA SUBUNIT OF COMPLEX I.	AAAVLPVLDLAQR	K	Q	95.00%	83		668.9064	2	7.2	76	88	No
				DIEEIIDELK	K	A	95.00%	48		608.8222	2	4.1	200	209	No
				NSDSILEAIQK	R	K	95.00%	58		609.3267	2	6.3	144	154	No

690	IPI00291866; IPI00556459	SERPING1	PLASMA PROTEASE C1 INHIBITOR PRECURSOR.; SERINE/CYSTEINE PROTEINASE INHIBITOR CLADE G MEMBER 1 SPLICE VARIANT 2(FRAGMENT).	FQPTLLTLPR	K	I	95.00%	33		593.3569	2	5.1	391	400	No
				GVTSVSQIFHSPDLAIR	K	D	95.00%	79		913.9996	2	8.1	217	233	No
				GVTSVSQIFHSPDLAIR	K	D	95.00%	60		609.6672	3	5.0	217	233	No
				TNLESILSYPK	K	D	95.00%	46		632.8493	2	9.3	191	201	No
				VTTSQDMLSIMEK	K	L	95.00%	56	M7: Oxidation, M11: Oxidation	757.8637	2	7.4	403	415	No
691	IPI00292530	ITIH1	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H1 PRECURSOR.	EVAFDLEIPK	R	T	95.00%	47		580.8180	2	6.6	84	93	No
				FAHYVVTSQVVNTANEAR	R	E	95.00%	86		1003.5190	2	10.0	66	83	No
				IYEDHDATQQLQGFYSQVAK	R	P	95.00%	35		781.0484	3	8.3	458	477	No
692	IPI00294216; IPI00373875; IPI00746318	SGCD	DELTA-SARCOGLYCAN.; DELTA-SARCOGLYCAN ISOFORM 2.; DELTA-SARCOGLYCAN ISOFORM 1.	VLGAEGTVFPK	R	S	95.00%	44		559.3217	2	8.5	166	176	No
				VLTQLITGPK	K	A	95.00%	28		535.3367	2	3.0	121	130	No
693	IPI00297084	DDOST	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOSYLTRANSFERASEPRECURSOR.	GFELTFK	R	T	95.00%	31		421.2288	2	4.4	71	77	No
				LPDVYGVFQFK	K	V	95.00%	45		656.8543	2	4.9	381	391	No
				NTLLIAGLQAR	K	N	95.00%	80		585.3574	2	5.2	240	250	No
				SSLNPILFR	K	G	95.00%	53		523.8059	2	3.8	190	198	No
				TADDPSLSLIK	K	Y	95.00%	61		580.3167	2	3.6	78	88	No
				TAVIDHHNYDISDLGQHTLIVADTENLLK	K	A	95.00%	64		812.1748	4	9.8	154	182	No
				TLVLLDNLNVR	R	E	95.00%	69		635.3847	2	6.6	47	57	No
				WVPFDGDDIQLEFVR	K	I	95.00%	50		918.4614	2	9.8	345	359	No
				YSQTGNYELAVALSR	R	W	95.00%	105		836.4265	2	6.6	283	297	No
694	IPI00297626	STXBP3	SYNTAXIN-BINDING PROTEIN 3.	LLDDIKMLNKPK	K	D	95.00%	25	M7: Oxidation	722.4186	2	3.1	572	583	No
				VLLPVLLNK	R	N	95.00%	46		504.8477	2	5.3	389	397	No
695	IPI00298497	FGB	FIBRINOGEN BETA CHAIN PRECURSOR.	AHYGGFTVQNEANK	K	Y	95.00%	76		768.3720	2	7.8	354	367	No
				DNENVVNEYSSELEK	K	H	95.00%	98		884.9029	2	5.9	164	178	No
				EEAPSLRPAPPPISGGGYR	R	A	95.00%	36		651.0085	3	3.0	54	72	No
				HQLYIDETVNSNIPTNLR	K	V	95.00%	41		709.7038	3	5.7	179	196	No
				QGFGNVATNTDGK	K	N	95.00%	62		654.8182	2	7.6	301	313	No
696	IPI00298994; IPI00784273	TLN1	271 KDA PROTEIN.; TALIN-1.	ALSTDPAAPNLK	K	S	95.00%	31		599.3305	2	4.3	1333	1344	No
				AVASAAAALVLK	K	A	95.00%	41		542.8449	2	8.2	674	685	No
				GLAGAVSELLR	K	S	95.00%	58		543.3212	2	2.2	614	624	No
				GVGAAATAVTQALNELLQHVK	R	A	95.00%	32		697.7280	3	5.8	766	786	No
				LAQAAQSSVATITR	K	L	95.00%	77		708.8998	2	7.6	2056	2069	No
				TLAESALQLLYTAK	K	E	95.00%	49		761.4366	2	8.2	1767	1780	No
697	IPI00300502	MYOZ1	MYOZENIN-1.	GGAAGTAGVGETGSGDQAGGEGK	R	H	95.00%	80		945.9318	2	6.6	154	176	No
				GGAAGTAGVGETGSGDQAGGEGK	R	H	95.00%	33		630.9585	3	8.7	154	176	No
				LIMELTGGGQESSGLNLGKK	K	I	95.00%	28	M3: Oxidation	683.3657	3	5.6	18	37	No
698	IPI00302328	MYH6	MYOSIN-6.	ADIAESQVNK	R	L	95.00%	81		537.7761	2	1.1	1912	1921	Yes
				ADIAESQVNKLR	R	A	95.00%	34		448.5825	3	2.7	1912	1923	Yes
				AGLLGLLEEMR	K	D	95.00%	88	M10: Oxidation	609.3354	2	5.2	769	779	Yes
				AGLLGLLEEMR	K	D	95.00%	58	M10: Oxidation	406.5597	3	5.7	769	779	Yes
				AGLLGLLEEMR	K	D	95.00%	62		1201.6510	1	-9.1	769	779	Yes
				AGLLGLLEEMR	K	D	95.00%	94		601.3371	2	3.9	769	779	Yes
				AGLLGLLEEMRDER	K	L	95.00%	50	M10: Oxidation	809.4238	2	7.7	769	782	Yes
				AGLLGLLEEMRDER	K	L	95.00%	68	M10: Oxidation	539.9509	3	6.0	769	782	Yes
				AGLLGLLEEMRDER	K	L	95.00%	46		801.4236	2	4.3	769	782	Yes
				AGLLGLLEEMRDER	K	L	95.00%	54		534.6177	3	3.2	769	782	Yes
				AITDAAMMAEELK	K	K	95.00%	84	M7: Oxidation, M8: Oxidation	713.3408	2	9.2	1760	1772	Yes
				AITDAAMMAEELKK	K	E	95.00%	102	M7: Oxidation	769.3866	2	3.0	1760	1773	Yes
				AITDAAMMAEELKK	K	E	95.00%	44	M7: Oxidation	513.2606	3	3.4	1760	1773	Yes
				AITDAAMMAEELKK	K	E	95.00%	83	M7: Oxidation	777.3852	2	4.5	1760	1773	Yes
				AITDAAMMAEELKK	K	E	95.00%	48	M7: Oxidation	518.5920	3	3.1	1760	1773	Yes
				AITDAAMMAEELKK	K	E	95.00%	83	M7: Oxidation, M8: Oxidation	777.3852	2	4.5	1760	1773	Yes
				AITDAAMMAEELKK	K	E	95.00%	48	M7: Oxidation, M8: Oxidation	518.5920	3	3.1	1760	1773	Yes
				AITDAAMMAEELKK	K	E	95.00%	97	M8: Oxidation	769.3875	2	4.2	1760	1773	Yes
				AITDAAMMAEELKK	K	E	95.00%	52	M8: Oxidation	513.2598	3	1.9	1760	1773	Yes
				AITDAAMMAEELKK	K	E	95.00%	111		761.3883	2	1.9	1760	1773	Yes

AITDAAMMAEELKK	K	E	95.00%	77		507.9281	3	1.8	1760	1773	Yes
AITDAAMMAEELKKEQDTSAHLER	K	M	95.00%	37	M7: Oxidation, M8: Oxidation	907.4404	3	6.9	1760	1783	Yes
ALQEAHQQALDDLQVEEDKVNSLSK	K	S	95.00%	44		702.8600	4	5.4	1000	1024	No
ANDDLKENIAIVER	R	R	95.00%	120		800.4223	2	1.5	1665	1678	Yes
ANDDLKENIAIVER	R	R	95.00%	63		533.9522	3	4.1	1665	1678	Yes
ANDDLKENIAIVERR	R	N	95.00%	58		878.4757	2	4.6	1665	1679	Yes
ANDDLKENIAIVERR	R	N	95.00%	70		585.9875	3	6.6	1665	1679	Yes
ANDDLKENIAIVERR	R	N	95.00%	28		439.7414	4	3.9	1665	1679	Yes
ANSEVAQWR	K	T	95.00%	51		1060.5220	1	4.5	1366	1374	Yes
ANSEVAQWR	K	T	95.00%	66		530.7642	2	2.9	1366	1374	Yes
AQLEFNQIK	R	A	95.00%	43		1090.5980	1	7.5	1563	1571	Yes
AQLEFNQIK	R	A	95.00%	75		545.8004	2	2.8	1563	1571	Yes
AQLEFNQIKAEIER	R	K	95.00%	91		844.9600	2	8.7	1563	1576	Yes
AVVEQTER	R	S	95.00%	72		466.2471	2	1.7	1692	1699	Yes
DIDDLELTLAK	K	V	95.00%	54		1245.6670	1	7.2	955	965	Yes
DIDDLELTLAK	K	V	95.00%	99		623.3342	2	1.9	955	965	Yes
DLEEATLQHEATAAALR	R	K	95.00%	138		919.9714	2	5.4	1179	1195	Yes
DLEEATLQHEATAAALR	R	K	95.00%	67		613.6491	3	3.6	1179	1195	Yes
DLEEATLQHEATAAALRK	R	K	95.00%	119		984.0176	2	3.8	1179	1196	Yes
DLEEATLQHEATAAALRK	R	K	95.00%	75		656.3477	3	3.8	1179	1196	Yes
DLQHRLDEAEQIALK	K	G	95.00%	52		889.9805	2	7.1	1794	1808	Yes
DLQHRLDEAEQIALK	K	G	95.00%	58		593.6564	3	7.3	1794	1808	Yes
DTQIQLDDAVR	K	A	95.00%	55		1273.6480	1	6.6	1654	1664	Yes
DTQIQLDDAVR	K	A	95.00%	94		637.3256	2	3.5	1654	1664	Yes
EAEFQK	R	M	95.00%	32		751.3677	1	6.7	1170	1175	Yes
EALISQLTR	K	G	95.00%	46		1030.5930	1	2.7	1297	1305	Yes
EALISQLTR	K	G	95.00%	61		515.8003	2	2.8	1297	1305	Yes
EKSEFKLELDDVTSNMEQIIK	K	A	95.00%	79	M16: Oxidation	838.0959	3	9.1	1222	1242	Yes
EKSEFKLELDDVTSNMEQIIK	K	A	95.00%	33	M16: Oxidation	628.8243	4	9.7	1222	1242	Yes
EKSEFKLELDDVTSNMEQIIK	K	A	95.00%	84		832.7598	3	3.7	1222	1242	Yes
EKSEFKLELDDVTSNMEQIIK	K	A	95.00%	35		624.8219	4	3.9	1222	1242	Yes
ELEEISER	R	L	95.00%	49		1004.4910	1	0.9	1144	1151	Yes
ELEEISER	R	L	95.00%	42		502.7503	2	2.7	1144	1151	Yes
ELEEISERLEEAGGATSVQIEMNK	R	K	95.00%	82	M22: Oxidation	893.4395	3	7.5	1144	1167	Yes
ELEEISERLEEAGGATSVQIEMNK	R	K	95.00%	56	M22: Oxidation	670.3314	4	7.1	1144	1167	Yes
ELEEISERLEEAGGATSVQIEMNK	R	K	95.00%	69		888.1052	3	4.4	1144	1167	Yes
ELEEISERLEEAGGATSVQIEMNKK	R	R	95.00%	68	M22: Oxidation	936.1401	3	9.5	1144	1168	Yes
EMNERLEDEEEMNAELTAK	K	K	95.00%	70	M12: Oxidation	766.3376	3	2.6	923	941	Yes
EMNERLEDEEEMNAELTAK	K	K	95.00%	73	M2: Oxidation, M12: Oxidation	771.6697	3	3.2	923	941	Yes
ENIAIVER	K	R	95.00%	41		472.2679	2	7.1	1671	1678	Yes
ENQSILITGESGAGK	R	T	95.00%	118		752.3882	2	1.9	170	184	Yes
EQDTSAHLER	K	M	95.00%	69		593.2841	2	8.6	1774	1783	Yes
EQYEEETEAK	R	A	95.00%	47		628.2719	2	2.3	1347	1356	Yes
EQYEEETEAKAELQR	R	V	95.00%	104		926.9355	2	3.6	1347	1361	Yes
EQYEEETEAKAELQR	R	V	95.00%	39		618.2937	3	4.8	1347	1361	Yes
GSSFQTVSALHR	K	E	95.00%	78		645.3373	2	5.1	643	654	Yes
GSSFQTVSALHRENLNK	K	L	95.00%	60		944.4929	2	5.4	643	659	Yes
GTLEDQIIQANPALEAFGNAK	K	T	95.00%	143		1100.5760	2	8.4	215	235	Yes
GTLEDQIIQANPALEAFGNAK	K	T	95.00%	96		734.0500	3	4.2	215	235	Yes
HADSVAELGEQIDNLQR	K	V	95.00%	166		947.9739	2	7.4	1198	1214	Yes
HADSVAELGEQIDNLQR	K	V	95.00%	85		632.3179	3	6.4	1198	1214	Yes
HRLQNEIEDLMVDVER	K	S	95.00%	86	M11: Oxidation	671.3367	3	3.6	1421	1436	Yes
HRLQNEIEDLMVDVER	K	S	95.00%	79		998.5089	2	8.8	1421	1436	Yes
HRLQNEIEDLMVDVER	K	S	95.00%	88		666.0065	3	5.7	1421	1436	Yes
HRLQNEIEDLMVDVER	K	S	95.00%	34		499.7565	4	5.1	1421	1436	Yes
IEELEEELEAER	R	T	95.00%	103		744.8617	2	5.7	1117	1128	Yes
IEELEEELEAER	R	T	95.00%	67		496.9096	3	4.0	1117	1128	Yes
ILAEWK	K	Q	95.00%	33		759.4422	1	2.1	1454	1459	Yes
ILYGDFR	R	Q	95.00%	43		442.2399	2	4.6	715	721	Yes
INATLETK	R	Q	95.00%	52		445.2545	2	1.9	444	451	Yes
INATLETKQPR	R	Q	95.00%	51		635.8622	2	3.6	444	454	Yes
IQLEAK	K	V	95.00%	37		701.4219	1	2.9	915	920	Yes
KAITDAAMMAEELKK	K	E	95.00%	101	M8: Oxidation	833.4363	2	5.3	1759	1773	Yes

KAITDAAMMAEELKK	K	E	95.00%	81	M8: Oxidation	555.9587	3	2.7	1759	1773	Yes
KAITDAAMMAEELKK	K	E	95.00%	35	M8: Oxidation	417.2235	4	8.8	1759	1773	Yes
KAITDAAMMAEELKK	K	E	95.00%	80	M8: Oxidation	841.4315	2	2.7	1759	1773	Yes
KAITDAAMMAEELKK	K	E	95.00%	64	M8: Oxidation	561.2909	3	3.8	1759	1773	Yes
KAITDAAMMAEELKK	K	E	95.00%	80	M8: Oxidation, M9: Oxidation	841.4315	2	2.7	1759	1773	Yes
KAITDAAMMAEELKK	K	E	95.00%	64	M8: Oxidation, M9: Oxidation	561.2909	3	3.8	1759	1773	Yes
KAITDAAMMAEELKK	K	E	95.00%	103	M9: Oxidation	833.4359	2	4.9	1759	1773	Yes
KAITDAAMMAEELKK	K	E	95.00%	63	M9: Oxidation	555.9584	3	2.3	1759	1773	Yes
KAITDAAMMAEELKK	K	E	95.00%	107		825.4387	2	5.2	1759	1773	Yes
KAITDAAMMAEELKK	K	E	95.00%	92		550.6276	3	3.8	1759	1773	Yes
KAITDAAMMAEELKK	K	E	95.00%	42		413.2216	4	1.3	1759	1773	Yes
KDIDDLELTLAK	K	V	95.00%	109		687.3849	2	6.4	954	965	Yes
KDIDDLELTLAK	K	V	95.00%	44		458.5935	3	8.4	954	965	Yes
KGSSFQTVSALHR	K	E	95.00%	101		709.3837	2	3.0	642	654	Yes
KGSSFQTVSALHR	K	E	95.00%	69		473.2583	3	2.9	642	654	Yes
KHADSVAELGEQIDNLQR	K	V	95.00%	137		1012.0210	2	6.5	1197	1214	Yes
KHADSVAELGEQIDNLQR	K	V	95.00%	93		675.0148	3	3.8	1197	1214	Yes
KHADSVAELGEQIDNLQR	K	V	95.00%	66		506.5136	4	4.9	1197	1214	Yes
KKHADSVAELGEQIDNLQR	R	V	95.00%	89		717.7142	3	5.1	1196	1214	Yes
KKHADSVAELGEQIDNLQR	R	V	95.00%	53		538.5365	4	3.1	1196	1214	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	48	M10: Oxidation	565.5286	4	2.1	1618	1636	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	54	M3: Oxidation	753.7057	3	6.7	1618	1636	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	42	M3: Oxidation	565.5287	4	2.2	1618	1636	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	60	M3: Oxidation	759.0351	3	3.6	1618	1636	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	69	M3: Oxidation	569.5274	4	2.1	1618	1636	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	60	M3: Oxidation, M10: Oxidation	759.0351	3	3.6	1618	1636	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	69	M3: Oxidation, M10: Oxidation	569.5274	4	2.1	1618	1636	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	61		748.3721	3	4.1	1618	1636	Yes
KKMEGDLNEMEIQLSHANR	K	M	95.00%	69		561.5313	4	4.5	1618	1636	Yes
KLAEQELIETSER	R	V	95.00%	113		773.4159	2	7.4	1702	1714	Yes
KLAEQELIETSER	R	V	95.00%	66		515.9439	3	2.1	1702	1714	Yes
KLEGDLK	R	L	95.00%	39		401.7396	2	4.6	1056	1062	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	83	M2: Oxidation	711.0037	3	2.1	1619	1636	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	49	M2: Oxidation	533.5064	4	5.2	1619	1636	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	90	M2: Oxidation	1074.0030	2	6.0	1619	1636	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	58	M2: Oxidation	716.3366	3	3.8	1619	1636	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	46	M2: Oxidation	537.5038	4	2.6	1619	1636	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	90	M2: Oxidation, M9: Oxidation	1074.0030	2	6.0	1619	1636	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	58	M2: Oxidation, M9: Oxidation	716.3366	3	3.8	1619	1636	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	46	M2: Oxidation, M9: Oxidation	537.5038	4	2.6	1619	1636	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	52	M9: Oxidation	711.0025	3	0.3	1619	1636	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	37	M9: Oxidation	533.5066	4	5.5	1619	1636	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	107		1058.0130	2	9.9	1619	1636	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	87		705.6741	3	4.8	1619	1636	Yes
KMEGDLNEMEIQLSHANR	K	M	95.00%	46		529.5076	4	5.0	1619	1636	Yes
KVQHELDEAEER	R	A	95.00%	60		741.8669	2	4.8	1900	1911	Yes
KVQHELDEAEER	R	A	95.00%	62		494.9157	3	8.4	1900	1911	Yes
KVQHELDEAEERADIAESQVNK	R	L	95.00%	97		1269.6380	2	9.4	1900	1921	Yes
KVQHELDEAEERADIAESQVNK	R	L	95.00%	58		846.7584	3	6.3	1900	1921	Yes
KVQHELDEAEERADIAESQVNK	R	L	95.00%	67		635.3188	4	3.2	1900	1921	Yes
LAEKDEEMEQAKR	K	N	95.00%	50	M8: Oxidation	531.5968	3	9.8	1578	1590	Yes
LAEKDEEMEQAKR	K	N	95.00%	46		526.2601	3	0.3	1578	1590	Yes
LAEQELIETSER	K	V	95.00%	115		709.3655	2	3.9	1703	1714	Yes
LAEQELIETSER	K	V	95.00%	40		473.2461	3	3.4	1703	1714	Yes
LASADIETYLLEK	K	S	95.00%	129		733.3926	2	-1.2	259	271	Yes
LASADIETYLLEK	K	S	95.00%	66		489.2671	3	4.5	259	271	Yes
LDEAEQIALK	R	G	95.00%	50		1129.6190	1	7.2	1799	1808	Yes
LDEAEQIALK	R	G	95.00%	97		565.3107	2	2.5	1799	1808	Yes
LDEAEQIALKGGK	R	K	95.00%	66		686.3813	2	4.5	1799	1811	Yes
LDEAEQIALKGGK	R	K	95.00%	42		457.9226	3	2.6	1799	1811	Yes

LDEAEQIALKGGKK	R	Q	95.00%	81		750.4314	2	7.6	1799	1812	Yes
LDEAEQIALKGGKK	R	Q	95.00%	45		500.6212	3	2.9	1799	1812	Yes
LEDEEEMNAELTAK	R	K	95.00%	117	M7: Oxidation	819.3672	2	2.9	928	941	Yes
LEDEEEMNAELTAK	R	K	95.00%	124		811.3694	2	2.5	928	941	Yes
LEEAGGATSVQIEMNK	R	K	95.00%	146	M14: Oxidation	846.9111	2	1.7	1152	1167	Yes
LEEAGGATSVQIEMNK	R	K	95.00%	50	M14: Oxidation	564.9460	3	6.3	1152	1167	Yes
LEEAGGATSVQIEMNK	R	K	95.00%	132		838.9142	2	2.4	1152	1167	Yes
LEEAGGATSVQIEMNKK	R	R	95.00%	71	M14: Oxidation	910.9600	2	3.2	1152	1168	Yes
LELDDVTSNMEQIIK	K	A	95.00%	103	M10: Oxidation	882.4482	2	8.2	1228	1242	Yes
LELDDVTSNMEQIIK	K	A	95.00%	97		874.4501	2	7.5	1228	1242	Yes
LELDDVTSNMEQIIK	K	A	95.00%	72		583.3007	3	4.2	1228	1242	Yes
LEQQVDDLEGSLEQEK	K	K	95.00%	144		930.4526	2	5.2	1029	1044	Yes
LEQQVDDLEGSLEQEK	K	K	95.00%	113		620.6381	3	5.9	1029	1044	Yes
LEQQVDDLEGSLEQEKK	K	V	95.00%	116		994.5015	2	6.3	1029	1045	Yes
LEQQVDDLEGSLEQEKK	K	V	95.00%	69		663.3355	3	4.1	1029	1045	Yes
LKNAYEESLEHLETFK	K	R	95.00%	133		976.0031	2	8.7	1486	1501	Yes
LKNAYEESLEHLETFK	K	R	95.00%	75		651.0009	3	2.9	1486	1501	Yes
LKNAYEESLEHLETFK	K	R	95.00%	45		488.5031	4	3.9	1486	1501	Yes
LKNAYEESLEHLETFKR	K	E	95.00%	113		1054.0520	2	6.0	1486	1502	Yes
LKNAYEESLEHLETFKR	K	E	95.00%	59		703.0364	3	5.3	1486	1502	Yes
LKNAYEESLEHLETFKR	K	E	95.00%	53		527.5279	4	2.8	1486	1502	Yes
LLSSLDIDHNQYK	K	F	95.00%	105		773.4031	2	4.5	747	759	Yes
LLSSLDIDHNQYK	K	F	95.00%	34		515.9373	3	3.2	747	759	Yes
LQDLVDK	R	L	95.00%	35		830.4664	1	4.6	1866	1872	Yes
LQDLVDK	R	L	95.00%	32		415.7358	2	1.5	1866	1872	Yes
LQDLVDKLQLK	R	V	95.00%	85		656.8982	2	3.2	1866	1876	Yes
LQDLVDKLQLK	R	V	95.00%	64		438.2683	3	3.7	1866	1876	Yes
LQNEIEDLMVDVER	R	S	95.00%	122	M9: Oxidation	859.9222	2	5.5	1423	1436	Yes
LQNEIEDLMVDVER	R	S	95.00%	74	M9: Oxidation	573.6172	3	5.3	1423	1436	Yes
LQNEIEDLMVDVER	R	S	95.00%	109		851.9232	2	3.7	1423	1436	Yes
LQNEIEDLMVDVER	R	S	95.00%	79		568.2845	3	3.2	1423	1436	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	58	M9: Oxidation	795.0480	3	4.4	486	503	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	35	M9: Oxidation	596.5412	4	9.8	486	503	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	43		789.7178	3	6.2	486	503	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	42		592.5402	4	6.1	486	503	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	48	M9: Oxidation	837.7477	3	5.8	486	504	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	103		1248.1230	2	8.3	486	504	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	57		832.4158	3	5.6	486	504	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	42		499.8525	5	5.4	486	504	Yes
LTGAIMHYGNMK	K	F	95.00%	42	M11: Oxidation	676.3345	2	7.9	353	364	No
LTGAIMHYGNMK	K	F	95.00%	47		668.3338	2	3.2	353	364	No
LTQESIMDLENDK	K	L	95.00%	86	M7: Oxidation	776.3684	2	4.9	1063	1075	No
LTQESIMDLENDK	K	L	95.00%	58		768.3713	2	5.4	1063	1075	No
MEGDLNEMEIQLSHANR	K	M	95.00%	106	M1: Oxidation	1001.9560	2	4.1	1620	1636	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	68	M1: Oxidation	668.3069	3	4.4	1620	1636	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	88	M1: Oxidation	1009.9510	2	1.6	1620	1636	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	68	M1: Oxidation	673.6376	3	3.0	1620	1636	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	88	M1: Oxidation, M8: Oxidation	1009.9510	2	1.6	1620	1636	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	68	M1: Oxidation, M8: Oxidation	673.6376	3	3.0	1620	1636	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	83	M8: Oxidation	1001.9580	2	6.4	1620	1636	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	45	M8: Oxidation	668.3068	3	4.3	1620	1636	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	148		993.9626	2	8.0	1620	1636	Yes
MEGDLNEMEIQLSHANR	K	M	95.00%	83		662.9764	3	6.1	1620	1636	Yes
MFNWMVTR	K	I	95.00%	47	M1: Oxidation	550.7566	2	3.1	436	443	No
MFNWMVTR	K	I	95.00%	56	M1: Oxidation	558.7542	2	3.2	436	443	No
MFNWMVTR	K	I	95.00%	56	M1: Oxidation, M5: Oxidation	558.7542	2	3.2	436	443	No
MFNWMVTR	K	I	95.00%	54	M5: Oxidation	550.7580	2	5.5	436	443	No
MFNWMVTR	K	I	95.00%	35		1084.5120	1	4.2	436	443	No
MFNWMVTR	K	I	95.00%	52		542.7602	2	5.1	436	443	No
MVSLLQEK	K	N	95.00%	53	M1: Oxidation	963.5215	1	3.1	879	886	Yes
MVSLLQEK	K	N	95.00%	53	M1: Oxidation	482.2638	2	1.3	879	886	Yes
MVSLLQEK	K	N	95.00%	48		947.5253	1	1.7	879	886	Yes
MVSLLQEK	K	N	95.00%	55		474.2693	2	7.7	879	886	Yes
NALAHALQSAR	K	H	95.00%	47		1151.6330	1	4.3	1329	1339	Yes
NALAHALQSAR	K	H	95.00%	80		576.3195	2	2.2	1329	1339	Yes
NAYEESLEHLETFK	K	R	95.00%	112		855.4108	2	6.8	1488	1501	Yes
NAYEESLEHLETFK	K	R	95.00%	47		570.6091	3	5.5	1488	1501	Yes

NAYEESLEHLETFKR	K	E	95.00%	102		933.4626	2	7.5	1488	1502	Yes
NAYEESLEHLETFKR	K	E	95.00%	51		622.6431	3	5.5	1488	1502	Yes
NFDKILAEWK	R	Q	95.00%	40		632.3444	2	5.5	1450	1459	Yes
NFDKILAEWK	R	Q	95.00%	30		421.8982	3	4.0	1450	1459	Yes
NLTEEMAGLDEIIAK	K	L	95.00%	114	M6: Oxidation	831.9211	2	4.9	979	993	Yes
NLTEEMAGLDEIIAK	K	L	95.00%	71	M6: Oxidation	554.9494	3	3.8	979	993	Yes
NLTEEMAGLDEIIAK	K	L	95.00%	117		823.9225	2	3.6	979	993	Yes
NLTEEMAGLDEIIAK	K	L	95.00%	84		549.6174	3	3.1	979	993	Yes
NMEQTIK	K	D	95.00%	32	M2: Oxidation	440.2186	2	5.4	1787	1793	Yes
NMEQTIKDLQHR	K	L	95.00%	39	M2: Oxidation	764.8834	2	3.0	1787	1798	Yes
NNLLQAELEELR	R	A	95.00%	115		721.3893	2	3.9	1680	1691	Yes
NNLLQAELEELR	R	A	95.00%	96		481.2624	3	4.5	1680	1691	Yes
NNLLQAELEELRAVVEQTER	R	S	95.00%	72		785.4218	3	7.7	1680	1699	Yes
NWPWMK	K	L	95.00%	29		431.2093	2	3.1	828	833	Yes
QAEEAEEQANTNLSK	R	F	95.00%	109		831.3884	2	4.3	1883	1897	Yes
QAEEAEEQANTNLSK	R	F	95.00%	64		554.5937	3	2.1	1883	1897	Yes
QKYEESQSELESSQK	K	E	95.00%	99		900.4216	2	3.0	1460	1474	Yes
QKYEESQSELESSQK	K	E	95.00%	59		600.6168	3	2.6	1460	1474	Yes
RDLEEATLQHEATAAALR	R	K	95.00%	119		998.0237	2	6.8	1178	1195	Yes
RDLEEATLQHEATAAALR	R	K	95.00%	84		665.6832	3	3.9	1178	1195	Yes
RDLEEATLQHEATAAALR	R	K	95.00%	65		499.5138	4	2.9	1178	1195	Yes
RNNLLQAELEELR	R	A	95.00%	81		799.4423	2	6.6	1679	1691	Yes
RNNLLQAELEELR	R	A	95.00%	88		533.2958	3	3.4	1679	1691	Yes
RQAEEAEEQANTNLSK	K	F	95.00%	66		909.4342	2	-1.3	1882	1897	Yes
RQAEEAEEQANTNLSK	K	F	95.00%	46		606.6284	3	3.6	1882	1897	Yes
RSEAPPHIFSISDNAYQYMLTDR	K	E	95.00%	118	M19: Oxidation	909.7731	3	7.4	147	169	Yes
RSEAPPHIFSISDNAYQYMLTDR	K	E	95.00%	50	M19: Oxidation	682.5812	4	6.5	147	169	Yes
RSEAPPHIFSISDNAYQYMLTDR	K	E	95.00%	125		904.4421	3	8.1	147	169	Yes
RSEAPPHIFSISDNAYQYMLTDR	K	E	95.00%	45		678.5836	4	8.3	147	169	Yes
RSEAPPHIFSISDNAYQYMLTDRENQSILITGESGAGK	K	T	95.00%	56	M19: Oxidation	1053.7730	4	8.6	147	184	Yes
RSEAPPHIFSISDNAYQYMLTDRENQSILITGESGAGK	K	T	95.00%	77		1049.7750	4	9.3	147	184	Yes
SAETEKEMATMK	K	E	95.00%	40	M11: Oxidation	686.3135	2	4.0	844	855	Yes
SAETEKEMATMK	K	E	95.00%	34	M11: Oxidation	457.8794	3	6.5	844	855	Yes
SAETEKEMATMK	K	E	95.00%	37	M8: Oxidation, M11: Oxidation	694.3143	2	8.8	844	855	Yes
SAETEKEMATMK	K	E	95.00%	68		678.3158	2	3.6	844	855	Yes
SAETEKEMATMK	K	E	95.00%	41		452.5479	3	6.8	844	855	Yes
SAYLMGLNSADLLK	K	G	95.00%	89	M5: Oxidation	756.3945	2	2.0	385	398	Yes
SAYLMGLNSADLLK	K	G	95.00%	88		748.3988	2	4.4	385	398	Yes
SEAPPHIFSISDNAYQYMLTDR	R	E	95.00%	84	M18: Oxidation	857.7385	3	6.8	148	169	Yes
SEAPPHIFSISDNAYQYMLTDR	R	E	95.00%	78		852.4084	3	8.7	148	169	Yes
SEAPPHIFSISDNAYQYMLTDRENQSILITGESGAGK	R	T	95.00%	37	M18: Oxidation	1014.7450	4	6.5	148	184	Yes
SEFKLELDDVTSNMEQIIK	K	A	95.00%	113	M14: Oxidation	1128.0600	2	0.4	1224	1242	Yes
SEFKLELDDVTSNMEQIIK	K	A	95.00%	57	M14: Oxidation	752.3806	3	6.4	1224	1242	Yes
SEFKLELDDVTSNMEQIIK	K	A	95.00%	146		1120.0710	2	7.3	1224	1242	Yes
SEFKLELDDVTSNMEQIIK	K	A	95.00%	61		747.0488	3	6.1	1224	1242	Yes
SLQSLLKDTQIQLDDAVR	K	A	95.00%	54		681.7121	3	5.8	1647	1664	Yes
SLSTELFK	R	L	95.00%	34		924.5075	1	3.4	1478	1485	Yes
SLSTELFK	R	L	95.00%	65		462.7582	2	4.7	1478	1485	Yes
SNAAAAALDK	R	K	95.00%	32		466.2507	2	9.4	1437	1446	Yes
SNAAAAALDKK	R	Q	95.00%	81		530.2949	2	2.0	1437	1447	Yes
SRVIFQLK	K	A	95.00%	30		495.8115	2	5.2	272	279	Yes
TEELEEAK	R	K	95.00%	33		948.4558	1	3.3	1385	1392	Yes
TEELEEAK	R	K	95.00%	37		474.7331	2	6.0	1385	1392	Yes
TEELEEAKK	R	K	95.00%	40		538.7797	2	3.5	1385	1393	Yes
TKYETDAIQR	R	T	95.00%	69		612.8171	2	3.2	1375	1384	Yes
TKYETDAIQR	R	T	95.00%	48		408.8806	3	3.0	1375	1384	Yes
TKYETDAIQRTEELEEAK	R	K	95.00%	74		1077.5420	2	8.6	1375	1392	Yes
TKYETDAIQRTEELEEAK	R	K	95.00%	38		718.6949	3	5.7	1375	1392	Yes
TKYETDAIQRTEELEEAK	R	K	95.00%	31		539.2729	4	5.3	1375	1392	Yes
VGNEYVTK	K	G	95.00%	69		455.2391	2	2.3	407	414	Yes
VIFQLK	R	A	95.00%	31		747.4807	1	5.0	274	279	Yes

				VKEMNERLEDEEEMNAELTAK	K	K	95.00%	69	M14: Oxidation	842.0610	3	5.1	921	941	Yes
				VKEMNERLEDEEEMNAELTAK	K	K	95.00%	40	M14: Oxidation	631.7974	4	4.5	921	941	Yes
				VKEMNERLEDEEEMNAELTAK	K	K	95.00%	63	M4: Oxidation	842.0579	3	1.5	921	941	Yes
				VKEMNERLEDEEEMNAELTAK	K	K	95.00%	37	M4: Oxidation	635.7957	4	3.9	921	941	Yes
				VKEMNERLEDEEEMNAELTAK	K	K	95.00%	50	M4: Oxidation, M14: Oxidation	847.3940	3	6.7	921	941	Yes
				VKEMNERLEDEEEMNAELTAK	K	K	95.00%	37	M4: Oxidation, M14: Oxidation	635.7957	4	3.9	921	941	Yes
				VKEMNERLEDEEEMNAELTAK	K	K	95.00%	57		836.7292	3	5.0	921	941	Yes
				VKLEQQVDDLEGSLEQEK	K	K	95.00%	157		1044.0380	2	8.1	1027	1044	Yes
				VKLEQQVDDLEGSLEQEK	K	K	95.00%	68		696.3594	3	5.5	1027	1044	Yes
				VKLEQQVDDLEGSLEQEKK	K	V	95.00%	136		1108.0860	2	8.3	1027	1045	Yes
				VKLEQQVDDLEGSLEQEKK	K	V	95.00%	87		739.0583	3	6.1	1027	1045	Yes
				VKLEQQVDDLEGSLEQEKK	K	V	95.00%	47		554.5450	4	4.7	1027	1045	Yes
				VKNLTEEMAGLDEIIAK	K	L	95.00%	77	M8: Oxidation	945.5076	2	9.3	977	993	Yes
				VKNLTEEMAGLDEIIAK	K	L	95.00%	32	M8: Oxidation	630.6721	3	5.7	977	993	Yes
				VKNLTEEMAGLDEIIAK	K	L	95.00%	121		937.5083	2	7.4	977	993	Yes
				VKNLTEEMAGLDEIIAK	K	L	95.00%	54		625.3402	3	5.4	977	993	Yes
				VKVGNEYVTK	R	G	95.00%	59		568.8224	2	4.7	405	414	Yes
				VQHELDEAEER	K	A	95.00%	52		677.8201	2	6.2	1901	1911	Yes
				VQHELDEAEER	K	A	95.00%	35		452.2151	3	4.1	1901	1911	Yes
				VQHELDEAEERADIAESQVNK	K	L	95.00%	119		1205.5860	2	6.5	1901	1921	Yes
				VQHELDEAEERADIAESQVNK	K	L	95.00%	67		804.0601	3	6.6	1901	1921	Yes
				VQHELDEAEERADIAESQVNK	K	L	95.00%	61		603.2958	4	4.6	1901	1921	Yes
				VQLLHSQNTSLINQK	R	K	95.00%	119		861.9822	2	3.7	1715	1729	Yes
				VQLLHSQNTSLINQK	R	K	95.00%	59		574.9913	3	4.7	1715	1729	Yes
				VQLLHSQNTSLINQKK	R	K	95.00%	37		617.6885	3	2.4	1715	1730	Yes
				VVDSLQTSLDAETR	R	S	95.00%	138		767.3948	2	3.7	1595	1608	Yes
				VVDSLQTSLDAETR	R	S	95.00%	72		511.9321	3	2.9	1595	1608	Yes
				YEESQSELESSQK	K	E	95.00%	109		772.3451	2	3.9	1462	1474	Yes
				YETDAIQR	K	T	95.00%	31		498.2471	2	6.5	1377	1384	Yes
699	IPI00302927	CCT4	T-COMPLEX PROTEIN 1 SUBUNIT DELTA.	ALIAGGGAPEIELALR	R	L	95.00%	51		775.9566	2	9.3	420	435	No
				AYILNLVK	R	Q	95.00%	30		467.2939	2	2.7	281	288	No
				DALSDLALHFLNK	R	M	95.00%	93		728.8993	2	7.3	307	319	No
				DALSDLALHFLNK	R	M	95.00%	46		486.2662	3	2.0	307	319	No
				ETLLNSATTSLNSK	R	V	95.00%	85		739.8932	2	5.6	161	174	No
				GDVTITNDGATILK	K	Q	95.00%	75		709.3838	2	4.0	66	79	No
				GIHPTIISESFQK	K	A	95.00%	51		728.8967	2	3.7	127	139	No
				GIHPTIISESFQK	K	A	95.00%	30		486.2674	3	4.4	127	139	No
				MIQDGKGDVTITNDGATILK	K	Q	95.00%	63	M1: Oxidation	702.6992	3	3.0	60	79	No
				VIDPATATSVDLR	K	D	95.00%	86		679.3734	2	4.4	194	206	No
				VVSQYSSLLSPMSVNAVMK	K	V	95.00%	85	M12: Oxidation, M18: Oxidation	1036.5330	2	8.6	175	193	No
700	IPI00304273; IPI00784338	APOA4	APOLIPOPROTEIN A-IV PRECURSOR.; SIMILAR TO APOA4 PROTEIN.	ALVQQMEQLR	K	Q	95.00%	71		608.3315	2	2.6	317	326	No
				DKVNSFFSTFK	R	E	95.00%	49		660.3422	2	9.9	349	359	No
				LGEVNTYAGDLQK	K	K	95.00%	89		704.3623	2	3.4	66	78	No
				LGPHAGDVEGHLSFLEK	K	D	95.00%	59		903.4697	2	7.0	329	345	No
				LGPHAGDVEGHLSFLEK	K	D	95.00%	57		602.6468	3	3.3	329	345	No
				SELTQQLNALFQDK	K	L	95.00%	96		817.9296	2	7.5	52	65	No
				SLAELGGHLDQQVEEFR	K	R	95.00%	56		643.3254	3	4.7	288	304	No
				SLAELGGHLDQQVEEFRR	K	R	95.00%	41		695.3616	3	8.1	288	305	No
				SLAPYAQDTQEK	R	L	95.00%	46		675.8366	2	8.2	222	233	No
701	IPI00304417; IPI00304419; IPI00643978	IDH3B	ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT BETA, MITOCHONDRIAL PRECURSOR.; ISOFORM A OF ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT BETA,MITOCHONDRIAL PRECURSOR.; 42 KDA PROTEIN.	EQTEGEYSSLEHESAR	R	G	95.00%	85		926.4077	2	4.4	165	180	No
				EQTEGEYSSLEHESAR	R	G	95.00%	39		617.9403	3	3.1	165	180	No
				HLNLEYHSSMIADAVK	R	K	95.00%	81	M10: Oxidation	922.4601	2	6.1	335	350	No
				HLNLEYHSSMIADAVKK	R	V	95.00%	38	M10: Oxidation	493.7560	4	2.1	335	351	No
				HNNLDLVIIR	R	E	95.00%	85		603.8541	2	3.5	155	164	No
				HNNLDLVIIR	R	E	95.00%	35		402.9054	3	3.7	155	164	No
				KLDLFANVVHVK	R	S	95.00%	72		461.6127	3	4.5	135	146	No

				NIANPTAMLLSASNMLR	R	H	95.00%	108	M8: Oxidation, M15: Oxidation	924.9735	2	4.3	318	334	No
				NIANPTAMLLSASNMLR	R	H	95.00%	42	M8: Oxidation, M15: Oxidation	616.9856	3	5.4	318	334	No
702	IPI00073454; IPI00220613; IPI00304840	COL6A2	ISOFORM 2C2A' OF COLLAGEN ALPHA-2(VI) CHAIN PRECURSOR.; ISOFORM 2C2A OF COLLAGEN ALPHA-2(VI) CHAIN PRECURSOR.; ISOFORM 2C2 OF COLLAGEN ALPHA-2(VI) CHAIN PRECURSOR.	LFAVAPNQNLK	R	E	95.00%	54		607.8545	2	9.3	187	197	No
				NFVINVVNR	K	L	95.00%	41		537.8112	2	8.0	636	644	No
				NLEWIAGGTWTPSALK	K	F	95.00%	53		872.4635	2	6.8	693	708	No
				NLQGISSFR	K	R	95.00%	29		511.2783	2	5.7	121	129	No
703	IPI00305461; IPI00645038	ITIH2	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR.; INTER-ALPHA (GLOBULIN) INHIBITOR H2.	FLHVPDTFEGHFDGVPVISK	R	G	95.00%	32		561.0444	4	8.7	212	231	No
				IQPSGGTNINEALLR	K	A	95.00%	81		791.9394	2	9.8	369	383	No
				SSALDMENFR	R	T	95.00%	29	M6: Oxidation	593.2671	2	4.5	146	155	No
704	IPI00305692; IPI00642032	TXNL1	THIOREDOXIN-LIKE PROTEIN 1.; 37 KDA PROTEIN.	IDQYQGADAVGLEEK	R	I	95.00%	70		818.4000	2	3.3	88	102	No
				IFINLPR	K	S	95.00%	42		436.7747	2	6.6	196	202	No
				VGVKPVGSDPDFQPELSGAGSR	M	L	95.00%	38		733.7104	3	5.0	2	23	No
				VRIDQYQGADAVGLEEK	K	I	95.00%	47		630.9924	3	2.8	86	102	No
705	IPI00306280	DENR	DENSITY-REGULATED PROTEIN.	QEAGISEGQGTAGEEEEK	K	K	95.00%	79		924.9159	2	7.5	77	94	No
				QEAGISEGQGTAGEEEEKKK	K	Q	95.00%	54		702.3411	3	3.6	77	96	No
706	IPI00328415; IPI00446235	CYB5R3	ISOFORM 1 OF NADH-CYTOCHROME B5 REDUCTASE.; ISOFORM 2 OF NADH-CYTOCHROME B5 REDUCTASE.	DILLRPELEELR	K	N	95.00%	46		748.4330	2	6.3	215	226	No
				DILLRPELEELR	K	N	95.00%	34		499.2919	3	7.6	215	226	No
				FALPSPQHILGLPVGQHIYLSAR	R	I	95.00%	64		838.8115	3	8.0	62	84	No
				FKLWYTLDR	R	A	95.00%	30		621.3401	2	3.2	233	241	No
				GPSGLLVYQGK	R	G	95.00%	77		559.8184	2	7.0	144	154	No
				STPAITLESPDIK	R	Y	95.00%	48		686.3767	2	6.0	30	42	No
				STPAITLESPDIKYPLR	R	L	95.00%	51		634.3561	3	7.4	30	46	No
707	IPI00328650; IPI00411520; IPI00784009	C14orf159	ISOFORM 1 OF UPF0317 PROTEIN C14ORF159, MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF UPF0317 PROTEIN C14ORF159, MITOCHONDRIAL PRECURSOR.; 67 KDA PROTEIN.	APGDQAWTQALPSVIKEEK	R	M	95.00%	44		690.0351	3	8.6	552	570	No
				ELESMIGIDPGNR	R	G	95.00%	53	M5: Oxidation	723.8522	2	4.5	297	309	No
				EVAIIVDQR	K	A	95.00%	37		521.7982	2	-1.2	370	378	No
				FDHLVAIER	R	A	95.00%	63		550.3011	2	3.8	428	436	No
				HLVDPIDDLFLAAK	K	K	95.00%	55		783.9379	2	9.2	455	468	No
				HLVDPIDDLFLAAK	K	K	95.00%	65		522.9592	3	5.5	455	468	No
				IPEVHHISQDPLHYSIASVSASQK	R	I	95.00%	87		881.7938	3	4.8	271	294	No
				IPEVHHISQDPLHYSIASVSASQK	R	I	95.00%	56		661.5983	4	6.3	271	294	No
				IVEDAVEQGVLK	K	T	95.00%	121		650.3647	2	4.2	386	397	No
				KIPGISSTGVGDGGNELGMGK	K	V	95.00%	87	M19: Oxidation	995.5080	2	8.2	469	489	No
				KIPGISSTGVGDGGNELGMGK	K	V	95.00%	65	M19: Oxidation	664.0054	3	4.3	469	489	No
				LVDVTTAQV	K	-	95.00%	38		945.5317	1	6.3	608	616	No
				SGVSGIVGMEVDGLPFHNTHAEMIQK	R	L	95.00%	44	M9: Oxidation, M23: Oxidation	929.1207	3	6.2	582	607	No
708	IPI00329389; IPI00741742; IPI00790342	RPL6	60S RIBOSOMAL PROTEIN L6.; RIBOSOMAL PROTEIN L6.; DNA-BINDING PROTEIN TAXREB107.	AIPQLQGYLR	K	S	95.00%	53		579.8392	2	6.0	264	273	No
				QLASGLLLVTGPLVLNR	K	V	95.00%	49		882.5493	2	8.9	168	184	No
709	IPI00329646	PCBD2	PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE 2.	AAGWSELSER	K	D	95.00%	62		553.2709	2	5.6	49	58	No
				NQAILDLK	R	A	95.00%	48		457.7737	2	9.1	41	48	No
710	IPI00335085; IPI00783374	RNF123	ISOFORM 1 OF E3 UBIQUITIN-PROTEIN LIGASE RNF123.; ISOFORM 2 OF E3 UBIQUITIN-PROTEIN LIGASE RNF123.	AVLSVELDPVEGR	R	L	95.00%	80		692.3802	2	3.0	284	296	No
				FLLSNVLFDVLR	K	S	95.00%	80		718.4230	2	4.8	420	431	No
				FLSTAAVSLMTPR	R	R	95.00%	30	M10: Oxidation	705.3804	2	4.8	684	696	No
				FNQEEGVGDTHNSYAYDGNR	R	V	95.00%	42		758.3268	3	6.9	158	177	No
				IFSSSEHAPPAATSR	R	K	95.00%	38		779.3909	2	5.0	42	56	No

				MVGVSDDVNEYAMALR	K	D	95.00%	113	M1: Oxidation, M13: Oxidation	901.4151	2	6.8	769	784	No
				NYFGPVHSMEELPGYEETLTR	K	L	95.00%	40	M9: Oxidation	829.0557	3	7.0	879	899	No
711	IPI00337454; IPI00337455; IPI00477427; IPI00641544; IPI00747742	TNNT3	ISOFORM 1 OF TROPONIN T, FAST SKELETAL MUSCLE.; TROPONIN T3, SKELETAL, FAST ISOFORM 3.; ISOFORM 2 OF TROPONIN T, FAST SKELETAL MUSCLE.; ISOFORM 3 OF TROPONIN T, FAST SKELETAL MUSCLE.; HYPOTHETICAL PROTEIN DKFZP779M2348.	AKELWETLHQLEIDKFEFGEK	K	L	95.00%	63		864.1201	3	9.8	211	231	No
				AKELWETLHQLEIDKFEFGEK	K	L	95.00%	30		648.3402	4	7.0	211	231	No
				ALSSMGANYSSYLAK	K	A	95.00%	114	M5: Oxidation	789.8799	2	2.9	157	171	Yes
				ALSSMGANYSSYLAK	K	A	95.00%	92		781.8857	2	7.2	157	171	No
				DLMELQALIDSHFEAR	K	K	95.00%	91	M3: Oxidation	952.4731	2	8.3	78	93	No
				DLMELQALIDSHFEAR	K	K	95.00%	57	M3: Oxidation	635.3176	3	7.7	78	93	Yes
				DLMELQALIDSHFEAR	K	K	95.00%	42		629.9845	3	5.4	78	93	No
				ELWETLHQLEIDKFEFGEK	K	L	95.00%	80		1196.1040	2	5.1	213	231	No
				ELWETLHQLEIDKFEFGEK	K	L	95.00%	71		797.7391	3	5.9	213	231	No
				IPEGEKVDFDDIQK	K	K	95.00%	103		816.9144	2	5.2	59	72	Yes
				IPEGEKVDFDDIQK	K	K	95.00%	53		544.9445	3	3.4	59	72	Yes
				IPEGEKVDFDDIQKK	K	R	95.00%	79		880.9653	2	8.7	59	73	No
				IPEGEKVDFDDIQKK	K	R	95.00%	36		587.6431	3	3.5	59	73	No
				KALSSMGANYSSYLAK	K	A	95.00%	88	M6: Oxidation	853.9310	2	6.9	156	171	No
				KALSSMGANYSSYLAK	K	A	95.00%	44	M6: Oxidation	569.6223	3	5.3	156	171	No
				KEEEELVALK	K	E	95.00%	56		594.3326	2	4.1	95	104	Yes
				KKEEEELVALK	R	E	95.00%	79		658.3810	2	5.0	94	104	Yes
				KKEEEELVALK	R	E	95.00%	51		439.2556	3	2.7	94	104	Yes
				KPLNIDHLGEDK	R	L	95.00%	65		689.8745	2	5.7	195	206	Yes
				KPLNIDHLGEDKLR	R	D	95.00%	75		824.4702	2	8.5	195	208	No
				KPLNIDHLGEDKLR	R	D	95.00%	51		549.9805	3	4.4	195	208	Yes
				KPLNIDHLGEDKLR	R	D	95.00%	41		412.7375	4	4.7	195	208	Yes
				QKYDITTLR	R	S	95.00%	36		569.3199	2	4.4	235	243	No
				QNKDLMELQALIDSHFEAR	R	K	95.00%	58	M6: Oxidation	758.7186	3	9.3	75	93	No
				QNKDLMELQALIDSHFEAR	R	K	95.00%	41	M6: Oxidation	569.2879	4	4.1	75	93	No
				RKPLNIDHLGEDK	R	L	95.00%	57		767.9272	2	8.0	194	206	Yes
				RKPLNIDHLGEDK	R	L	95.00%	39		512.2853	3	3.8	194	206	Yes
				YDITTLR	K	S	95.00%	41		441.2411	2	1.1	237	243	No
712	IPI00375676	FTL	FERRITIN LIGHT POLYPEPTIDE VARIANT.	ALFQDIK	R	K	95.00%	37		417.7412	2	2.3	77	83	No
				KLNQALLDLHALGSAR	K	T	95.00%	40		430.7541	4	3.4	106	121	No
713	IPI00394809	APOOL	APOLIPOPROTEIN O-LIKE PRECURSOR.	LGSSSEIEVPAK	K	T	95.00%	42		608.8281	2	4.7	201	212	No
				TKSESTSGATQFMPDPK	K	L	95.00%	60	M13: Oxidation	914.4336	2	8.6	233	249	No
714	IPI00398162; IPI00478974; IPI00745227; IPI00786896	NRAP	ISOFORM 2 OF NEBULIN-RELATED-ANCHORING PROTEIN.; ISOFORM 3 OF NEBULIN-RELATED-ANCHORING PROTEIN.; ISOFORM 1 OF NEBULIN-RELATED-ANCHORING PROTEIN.; ISOFORM 4 OF NEBULIN-RELATED-ANCHORING PROTEIN.	FTTVVDSPDLVHAK	K	N	95.00%	43		764.9080	2	4.6	1429	1442	No
				GMAGPAIGAEGILTR	R	E	95.00%	71	M2: Oxidation	715.3831	2	7.6	274	288	No
				GSFPAMITPAYQIAK	K	R	95.00%	31	M6: Oxidation	805.9208	2	5.2	239	253	No
				LTIEALPFQAAR	K	A	95.00%	47		665.3845	2	6.1	1259	1270	No
				NNTFTSVYHTPLNLNVR	K	T	95.00%	58		664.0147	3	7.0	61	77	No
				YSSVTDTPQIVQAK	K	I	95.00%	52		768.9045	2	6.6	453	466	No
715	IPI00398837	CCDC88	COILED-COIL DOMAIN CONTAINING 88.	KLEAQNTEAARLSK	R	E	95.00%	35		779.9310	2	-0.8	754	767	No
				KLEVLEEEVR	R	A	95.00%	32		1243.6780	1	-9.9	1049	1058	No
716	IPI00399007; IPI00426051; IPI00829767	IGHG2	HYPOTHETICAL PROTEIN DKFZP686I04196 (FRAGMENT).; HYPOTHETICAL PROTEIN DKFZP686C15213.; PROTEIN.	DTLMISR	K	T	95.00%	53	M4: Oxidation	426.2194	2	1.4	266	272	Yes
				EPQVYTLPPSR	R	E	95.00%	48		643.8439	2	4.3	362	372	No
				EPQVYTLPPSREEMTK	R	N	95.00%	76	M14: Oxidation	960.9765	2	3.8	362	377	No
				GFYPSDIAVEWESNGQPENNYK	K	T	95.00%	81		1272.5700	2	0.0	388	409	Yes
				GFYPSDIAVEWESNGQPENNYK	K	T	95.00%	36		848.7162	3	0.5	388	409	Yes
				GLPAPIEK	K	T	95.00%	29		824.4943	1	7.2	297	304	No
				NSLYLQMNSLR	K	A	95.00%	62	M7: Oxidation	677.8459	2	3.7	97	107	Yes
				TTPPMLDSDGSFFLYSK	K	L	95.00%	84	M5: Oxidation	961.4572	2	9.0	410	426	No
				TTPPMLDSDGSFFLYSK	K	L	95.00%	55	M5: Oxidation	641.3073	3	8.9	363	379	No
				VVSVLTVVHQDWLNGK	R	E	95.00%	42		897.5079	2	9.3	319	334	No
				VVSVLTVVHQDWLNGK	R	E	95.00%	38		598.6681	3	-1.4	319	334	No
717	IPI00409750	OTUB1	ISOFORM 2 OF UBIQUITIN THIOESTERASE PROTEIN OTUB1.	FFEHFIEGGR	K	T	95.00%	32		413.5401	3	7.0	233	242	No

				LLTSGYLQR	R	E	95.00%	53		525.8049	2	6.7	221	229	No
718	IPI00411706; IPI00641040	ESD	S-FORMYLGLUTATHIONE HYDROLASE.; 28 KDA PROTEIN.	AFSGYLGTDQSK	K	W	95.00%	49		637.3118	2	7.3	158	169	Yes
				AYDATHLVK	K	S	95.00%	47		509.2753	2	5.6	172	180	Yes
				FAVYLPPK	K	A	95.00%	30		467.7772	2	6.9	3	10	No
				KAFSGYLGTDQSK	K	W	95.00%	57		701.3568	2	3.0	157	169	No
				SGYHQSASEHGLVVIAPDTSPR	K	G	95.00%	38		770.0561	3	9.0	36	57	Yes
				SYPGSQLDILIDQGK	K	D	95.00%	44		817.4315	2	6.9	181	195	No
719	IPI00418163	C4B	COMPLEMENT COMPONENT 4B PREPROPROTEIN.	ALEILQEEDLIDEDDIPVR	R	S	95.00%	106		1113.0740	2	8.9	757	775	Yes
				ASAGLLGAHAAAITAYALTLTK	K	A	95.00%	34		695.7328	3	5.7	1183	1204	Yes
				DFALLSLQVPLK	R	D	95.00%	54		672.4054	2	6.5	81	92	Yes
				DFALLSLQVPLKDAK	R	S	95.00%	43		553.3248	3	3.4	81	95	Yes
				EGAIHREELVYELNPLDHR	K	G	95.00%	42		764.0633	3	7.1	936	954	Yes
				EMSGSPASGIPVK	R	V	95.00%	29	M2: Oxidation	638.3207	2	6.4	392	404	No
				GLEEELQFSLGSK	R	I	95.00%	82		718.8721	2	6.1	1353	1365	Yes
				GPEVQLVAHSPWLK	R	D	95.00%	57		780.9374	2	8.2	105	118	Yes
				GSFEFPVGDAVSK	R	V	95.00%	59		670.3372	2	9.8	917	929	Yes
				GSSTWLTAFVLK	R	V	95.00%	39		655.3673	2	8.5	1073	1084	No
				HLVPGAPFLLQALVR	R	E	95.00%	56		544.3354	3	6.6	377	391	Yes
				LNMGITDLQGLR	K	L	95.00%	60	M3: Oxidation	673.8649	2	8.5	326	337	Yes
				PVAFSVVPTAATAVSLK	R	V	95.00%	55		829.4875	2	8.7	896	912	No
				TTNIQGINLLFSSR	R	R	95.00%	82		782.4342	2	7.1	124	137	Yes
				VGDTLNLNLR	R	A	95.00%	80		557.8180	2	5.4	485	494	Yes
				VLSLAQEQVGGSPEK	K	L	95.00%	102		771.4165	2	4.8	1085	1099	Yes
				VTASDPLDTLGSEGALSPGGVASLLR	R	L	95.00%	81		828.4452	3	8.4	980	1005	Yes
				YIYGKPVQGVAYVR	R	F	95.00%	31		806.9493	2	3.5	270	283	Yes
				YIYGKPVQGVAYVR	R	F	95.00%	42		538.3026	3	4.3	270	283	Yes
720	IPI00418495	CD36	PLATELET GLYCOPROTEIN 4.	QVVLEEGTIAFK	K	N	95.00%	70		667.3763	2	5.9	41	52	No
				SIYAVFESDVNLK	R	G	95.00%	40		742.8903	2	6.1	274	286	No
				TYLDIEPITGFTLQFAK	R	R	95.00%	92		979.0284	2	8.4	369	385	No
				TYLDIEPITGFTLQFAK	R	R	95.00%	60		653.0210	3	7.5	369	385	No
721	IPI00419266	NDUFA6	NADH DEHYDROGENASE (UBIQUINONE) 1 ALPHA SUBCOMPLEX, 6, 14KDA.	FFHETEAPRPK	R	D	95.00%	44		679.8535	2	9.8	132	142	No
				FFHETEAPRPK	R	D	95.00%	39		453.5696	3	5.4	132	142	No
				VVDLLVIK	R	G	95.00%	62		449.8047	2	4.1	104	111	No
722	IPI00419802	HIBCH	3-HYDROXYISOBUTYRYL-COENZYME A HYDROLASE ISOFORM 1.	AGIATHFVDSEK	R	L	95.00%	71		637.8248	2	2.9	210	221	No
				AGIATHFVDSEK	R	L	95.00%	33		425.5525	3	3.0	210	221	No
				AVLIDKDQSPK	R	W	95.00%	27		607.3472	2	5.7	348	358	No
				ENIASVLENYHTESK	K	I	95.00%	83		867.4280	2	7.8	238	252	No
				ENIASVLENYHTESK	K	I	95.00%	44		578.6201	3	5.8	238	252	No
				FLNALTLNMIR	K	Q	95.00%	49	M9: Oxidation	661.3718	2	4.2	56	66	No
				IAPVFFR	K	E	95.00%	36		425.2555	2	5.4	113	119	No
				KWEQDPETFLIIIK	K	G	95.00%	33		587.3296	3	5.4	74	87	No
				LAMLEEDLLALK	K	S	95.00%	80	M3: Oxidation	687.8871	2	7.8	222	233	No
				LGYFLALTGFR	K	L	95.00%	73		629.3586	2	7.8	191	201	No
				SLGSSDLKF	K	-	95.00%	54		477.2524	2	2.8	378	386	No
				TLQEVLTMEYR	K	L	95.00%	70	M8: Oxidation	699.8549	2	5.8	321	331	No
				WEQDPETFLIIIK	K	G	95.00%	50		816.4459	2	9.4	75	87	No
723	IPI00423460	IGHA1	HYPOTHETICAL PROTEIN DKFZP686G21220 (FRAGMENT).	DASGVTFTWTPSSGK	R	S	95.00%	82		770.8748	2	8.6	307	321	Yes
				QEPSQGTTTFAVTSILR	R	V	95.00%	120		918.4847	2	6.1	436	452	Yes
				QEPSQGTTTFAVTSILR	R	V	95.00%	64		612.6580	3	4.3	436	452	Yes
				TPLTATLSK	K	S	95.00%	33		931.5471	1	0.5	366	374	Yes
				TPLTATLSK	K	S	95.00%	43		466.2780	2	1.8	366	374	Yes
				WLQGSQELPR	R	E	95.00%	79		607.3225	2	3.4	417	426	No
724	IPI00452731	NDUFA7	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 7.	ALVSGKPAESSAVAATEK	K	K	95.00%	104		858.4708	2	9.2	75	92	No
				AVTPAPPIKR	K	W	95.00%	30		525.3322	2	8.8	94	103	No
				NWASGHDLQGK	R	L	95.00%	68		606.7948	2	4.5	13	23	No

725	IPI00453473	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4	HISTONE H4.	DNIQGITKPAIR	R	R	95.00%	52		663.3867	2	8.5	25	36	No
				DNIQGITKPAIR	R	R	95.00%	45		442.5918	3	4.2	25	36	No
				ISGLIYEETR	R	G	95.00%	35		590.8140	2	-1.1	47	56	No
				TVTAMDVVYALK	K	R	95.00%	32	M5: Oxidation	663.8581	2	7.9	81	92	No
				VFLENVIR	K	D	95.00%	46		495.2957	2	5.2	61	68	No
726	IPI00478003	A2M	ALPHA-2-MACROGLOBULIN PRECURSOR.	AAQVTIQSSGTFSSK	K	F	95.00%	33		756.3942	2	6.6	1275	1289	No
				AFQPFFVELTMPYSVIR	R	G	95.00%	55	M11: Oxidation	1031.0370	2	6.8	788	804	No
				AIGYLNTGYQR	K	Q	95.00%	55		628.3306	2	7.7	1004	1014	No
				ALLAYAFALAGNQDK	K	R	95.00%	62		783.4267	2	8.1	1148	1162	No
				ATVLNYLPK	K	C	95.00%	39		509.8035	2	5.3	812	820	No
				DTVIKPLLVEPEGLEK	K	E	95.00%	25		594.0131	3	6.9	897	912	No
				FEVQVTVPK	K	I	95.00%	32		523.8014	2	6.1	229	237	No
				GHFSISIPVK	K	S	95.00%	30		542.8158	2	7.5	522	531	No
				HYDGSYSTFGER	K	Y	95.00%	64		709.8071	2	6.1	1020	1031	No
				IAQWQSFQLEGGLK	R	Q	95.00%	57		802.9333	2	9.3	175	188	No
				KDTVIKPLLVEPEGLEK	R	E	95.00%	51		636.7081	3	1.3	896	912	No
				LHTEAQIQEEGTVVELTGR	K	Q	95.00%	42		704.0364	3	7.4	320	338	No
				LLIYAVLPTGDVIGDSAK	R	Y	95.00%	76		923.0302	2	8.1	540	557	No
				LLLQQVSLPELPGEYSMK	R	V	95.00%	69	M17: Oxidation	1031.0590	2	7.2	1298	1315	No
				LLLQQVSLPELPGEYSMK	R	V	95.00%	43	M17: Oxidation	687.7086	3	7.6	1298	1315	No
				LPPNVVEESAR	K	A	95.00%	74		605.8286	2	5.1	935	945	No
				MVSGFIPLKPTVK	K	M	95.00%	56	M1: Oxidation	716.9207	2	6.7	1385	1397	No
				NEDSLVFVQTDK	K	S	95.00%	78		697.8489	2	6.8	124	135	No
				NQGNTWLTAFVLK	R	T	95.00%	91		746.4082	2	8.4	1035	1047	No
				QFSFPLSSEPFQGSYK	K	V	95.00%	57		924.9518	2	8.1	189	204	No
				SASNMAIVDVK	R	M	95.00%	30	M5: Oxidation	575.7958	2	5.3	1374	1384	No
				SIYKPGQTVK	K	F	95.00%	26		560.8232	2	1.6	136	145	No
				SSGSLLNNAIK	R	G	95.00%	35		552.3080	2	1.8	1082	1092	No
				SSSNEEVMFLTVQVK	K	G	95.00%	65	M8: Oxidation	857.4288	2	7.6	94	108	No
				TEHPFTVEEFVLPK	R	F	95.00%	50		836.9387	2	6.5	215	228	No
				TEHPFTVEEFVLPK	R	F	95.00%	48		558.2943	3	5.1	215	228	No
				TEVSSNHVLIYLDK	R	V	95.00%	81		809.4353	2	8.7	1408	1421	No
				VDLSFSPSQSLPASHAHLR	K	V	95.00%	30		513.0192	4	0.8	568	586	No
				VGFYESDVMGR	R	G	95.00%	66	M9: Oxidation	638.2924	2	7.0	705	715	No
				VSVQLEASPAFLAVPVEK	R	E	95.00%	82		942.5347	2	7.1	824	841	No
				VSVQLEASPAFLAVPVEK	R	E	95.00%	37		628.6921	3	6.6	824	841	No
				VVSMDENFHPLNELIPLVYIQDPK	R	G	95.00%	36	M4: Oxidation	942.8257	3	8.0	148	171	No
				YGAATFTR	K	T	95.00%	31		443.7266	2	3.6	1264	1271	No
727	IPI00478292; IPI00744706; IPI00745092	SPTAN1	ISOFORM 1 OF SPECTRIN ALPHA CHAIN, BRAIN.; ISOFORM 3 OF SPECTRIN ALPHA CHAIN, BRAIN.; ISOFORM 2 OF SPECTRIN ALPHA CHAIN, BRAIN.	LGESQTLQQFSR	K	D	95.00%	37		697.3640	2	9.0	1535	1546	No
				SADESGQALLAAGHYASDEVR	K	E	95.00%	46		716.3452	3	9.2	419	439	No
728	IPI00478450	NDUFB11	ISOFORM 2 OF NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT11, MITOCHONDRIAL PRECURSOR.	RPPEPTTPWQEDPEPEDENLYEK	K	N	95.00%	57		932.7674	3	7.9	47	69	No
				TVVAPSAVAGK	R	R	95.00%	29		500.2977	2	3.7	36	46	No
729	IPI00478774	MYOM3	MYOMESIN-3.	APLTYSLEK	R	S	95.00%	31		511.2833	2	1.6	530	538	No
				ASELVVMGDHDAAR	K	R	95.00%	63	M7: Oxidation	743.8563	2	5.9	461	474	No
				FQWFFQR	R	A	95.00%	30		529.7693	2	9.0	1153	1159	No
				GNPITAYTIER	R	C	95.00%	55		617.8302	2	7.5	401	411	No
				GPPATLPPPAQVQAFR	R	D	95.00%	28		823.9620	2	8.7	597	612	No
				GPPATLPPPAQVQAFR	R	D	95.00%	38		549.6413	3	3.8	597	612	No
				IGALSATPLK	R	I	95.00%	32		485.8039	2	6.2	1223	1232	No

				ITISTDAFEDTVTIPSPPTNVHASEIR	K	E	95.00%	77		971.1697	3	8.4	487	513	No
				ITNNYGLLSLEIR	R	R	95.00%	37		753.4271	2	9.0	206	218	No
				LISGWNIDILER	K	G	95.00%	67		714.9013	2	6.7	1008	1019	No
				LSPAAELHLIFNNK	K	E	95.00%	66		783.9416	2	7.0	1031	1044	No
				NDQPVTFLDR	K	Y	95.00%	42		602.8049	2	4.7	1375	1384	No
				NQITLTLVDDDFDKLLR	K	K	95.00%	44		673.7003	3	4.2	1089	1105	No
				STFGPSVEFTSVLKPVFAR	R	E	95.00%	38		690.3799	3	8.1	265	283	No
				SVIGSGTWEAISSESPVR	K	S	95.00%	110		931.4777	2	9.7	539	556	No
				SVSEAGVGESSAATEPIR	R	V	95.00%	106		873.9338	2	5.0	675	692	No
				TEIAFLQTHR	R	L	95.00%	67		608.3321	2	6.2	111	120	No
				YGSETGQVTISVFK	K	H	95.00%	71		758.3959	2	9.6	1417	1430	No
730	IPI00550363; IPI00647915	CCDC19; TAGLN2	TRANSGELIN-2.; 24 KDA PROTEIN.	GASQAGMTGYGMPR	R	Q	95.00%	31	M7: Oxidation, M12: Oxidation	708.3117	2	7.6	183	196	No
				TLMNLGGLAVAR	R	D	95.00%	50	M3: Oxidation	616.3491	2	5.6	128	139	No
731	IPI00550991	SERPINA3	ISOFORM 1 OF ALPHA-1-ANTICHYMOTRYPSIN PRECURSOR.	ADLSGITGAR	K	N	95.00%	56		480.7620	2	4.8	366	375	No
				AVLDVFEEGTEASAATAVK	K	I	95.00%	123		954.4908	2	7.0	386	404	No
				EIGELYLPK	R	F	95.00%	31		531.3013	2	6.0	332	340	No
				FNRPFLMIIVPTDTQNIFFMSK	R	V	95.00%	48	M7: Oxidation, M20: Oxidation	897.8006	3	6.8	420	441	No
				ITLLSALVETR	K	T	95.00%	94		608.3726	2	4.8	405	415	No
				LYGSEAFATDFQDSAAAK	R	K	95.00%	106		946.4476	2	8.4	185	202	No
				NLAVSQVVHK	R	A	95.00%	34		547.8232	2	5.9	376	385	No
732	IPI00412545; IPI00554681	NDUFA5	HYPOTHETICAL PROTEIN DKFZP781K1356.; NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 5.	AGVLKK	M	T	95.00%	30		615.4246	1	8.2	2	7	No
				ILDVLEEIPK	K	N	95.00%	77		584.8496	2	7.0	31	40	No
				KLEDQLQGGQLEEVILQAEHELNLAR	K	K	95.00%	75		744.1538	4	9.1	67	92	No
				LWEPLVEEPPADQWK	K	W	95.00%	32		918.9692	2	7.1	99	113	No
733	IPI00555692; IPI00793199	ANXA4	ANXA4 PROTEIN.; ANNEXIN IV.	GLGTDEDAIISVLAYR	K	N	95.00%	104		846.9470	2	3.0	31	46	No
				ISQTYQQQYGR	R	S	95.00%	66		686.3430	2	9.2	126	136	No
734	IPI00555956	PSMB4	PROTEASOME SUBUNIT BETA TYPE 4 PRECURSOR.	FQIATVTEK	R	G	95.00%	33		518.7909	2	5.9	232	240	No
				TQNPMVTGTSVLGVK	R	F	95.00%	64	M5: Oxidation	774.4137	2	5.9	46	60	No
735	IPI00604707	DLAT	DIHYDROLIPOAMIDE S-ACETYLTRANSFERASE (E2 COMPONENT OF PYRUVATEDEHYDROGENASE COMPLEX) VARIANT.	DIDSFVPSK	K	V	95.00%	60		1007.5090	1	3.8	388	396	No
				DIDSFVPSK	K	V	95.00%	51		504.2588	2	4.7	388	396	Yes
				GIDLTQVK	K	G	95.00%	48		437.2569	2	1.3	369	376	Yes
				GVETIANDVVSLATK	K	A	95.00%	101		758.9186	2	4.6	533	547	No
				GVETIANDVVSLATK	K	A	95.00%	81		506.2808	3	2.7	533	547	Yes
				ILVAEGTR	K	D	95.00%	32		429.7583	2	4.5	148	155	No
				ISVNDFIIK	K	A	95.00%	43		524.8086	2	4.7	474	482	Yes
				KYLEKPITMLL	R	-	95.00%	44	M9: Oxidation	682.9013	2	6.0	637	647	No
				LQPHEFQGGTFTISNLGMFGIK	K	N	95.00%	78	M18: Oxidation	813.4189	3	9.6	553	574	No
				SKISVNDFIIK	R	A	95.00%	44		632.3729	2	5.2	472	482	No
				SKISVNDFIIK	R	A	95.00%	55		421.9170	3	3.0	472	482	No
				VPEANSSWMDTVIR	K	Q	95.00%	85	M9: Oxidation	810.8909	2	3.0	491	504	Yes
				VPLPSLSPTMQAGTIAR	K	W	95.00%	73	M10: Oxidation	877.9829	2	5.8	94	110	Yes
				VPLPSLSPTMQAGTIAR	K	W	95.00%	53	M10: Oxidation	585.6562	3	3.0	94	110	No
				VPLPSLSPTMQAGTIAR	K	W	95.00%	59		869.9849	2	5.3	94	110	No
				VVDGAVGAQWLAEFR	R	K	95.00%	82		809.4282	2	6.0	622	636	No
				YLEKPITMLL	K	-	95.00%	43	M8: Oxidation	618.8525	2	4.5	638	647	Yes
736	IPI00431645; IPI00478493; IPI00641737	HP	HP PROTEIN.; HP PROTEIN.; HAPTOGLOBIN PRECURSOR.	DIAPTLTLYVGK	K	K	95.00%	68		645.8724	2	4.4	91	102	No
				DIAPTLTLYVGKK	K	Q	95.00%	49		709.9203	2	4.7	91	103	No
				LRTEGDGVYTLNDKK	K	Q	95.00%	55		854.9391	2	-9.8	72	86	No
				TEGDGVYTLNDKK	R	Q	95.00%	62		720.3612	2	8.7	74	86	No
				TEGDGVYTLNNEK	R	Q	95.00%	81		720.3409	2	5.9	133	145	No
				VGYVSGWGR	R	N	95.00%	70		490.7521	2	1.1	153	161	No
				VTSIQDWVQK	K	T	95.00%	74		602.3250	2	4.0	267	276	No
				VVLHPNYSQVDIGLIK	K	L	95.00%	36		599.0131	3	6.5	111	126	No
737	IPI00645720	COQ7	20 KDA PROTEIN.	FNELMVTFR	K	V	95.00%	52	M5: Oxidation	586.7955	2	4.9	59	67	No
				TLMEEDPEKYEELLQLIK	R	K	95.00%	31	M3: Oxidation	746.3867	3	8.0	117	134	Yes
738	IPI00742696	GC	VITAMIN D-BINDING PROTEIN PRECURSOR.	AKLPDATPTELAK	K	L	95.00%	44		677.8860	2	4.2	428	440	No
				HLSLLTTLSNR	K	V	95.00%	56		627.8647	2	3.6	208	218	No
				LPDATPTELAK	K	L	95.00%	41		578.3193	2	3.7	430	440	No

				RTHLPEVFLSK	R	V	95.00%	46		442.9248	3	4.0	353	363	No
				THLPEVFLSK	R	V	95.00%	30		585.8326	2	4.2	354	363	No
				VPTADLEDVLPLAEDITNILSK	K	C	95.00%	91		1183.6440	2	3.8	243	264	No
				VPTADLEDVLPLAEDITNILSK	K	C	95.00%	44		789.4343	3	6.9	243	264	No
				YTFELSR	K	R	95.00%	28		458.2353	2	5.7	346	352	No
739	IPI00745471	SYNE1	OTTHUMP00000017444.	LETILK	R	H	95.00%	32		716.4601	1	5.8	6403	6408	No
				QSEADALAVLK	K	K	95.00%	28		572.8198	2	8.9	2008	2018	No
740	IPI00785200		HYPOTHETICAL PROTEIN.	LTVLSQPK	K	A	95.00%	26		443.2770	2	5.9	127	134	No
				SGTSASLAISGLR	K	S	95.00%	49		610.3409	2	7.6	87	99	No
741	IPI00792352	RAN	26 KDA PROTEIN.	FNVWDTAGQEK	K	F	95.00%	53		647.8120	2	7.3	81	91	No
				KYVATLGVEVHPLVFHTNR	K	G	95.00%	52		545.8069	4	2.8	58	76	No
				SNYNFEKPFLWLAR	K	K	95.00%	42		595.6465	3	6.5	173	186	No
742	IPI00000030; IPI00219543; IPI00219544	PPP2R5D	ISOFORM DELTA-1 OF SERINE/THREONINE-PROTEIN PHOSPHATASE 2A 56 KDAREGULATORY SUBUNIT DELTA ISOFORM.; ISOFORM DELTA-2 OF SERINE/THREONINE-PROTEIN PHOSPHATASE 2A 56 KDAREGULATORY SUBUNIT DELTA ISOFORM.; ISOFORM DELTA-3 OF SERINE/THREONINE-PROTEIN PHOSPHATASE 2A 56 KDAREGULATORY SUBUNIT DELTA ISOFORM.	ESSLTEPVIVGLLK	K	F	95.00%	41		742.9390	2	8.3	354	367	No
				FLESPDFQPNIAK	R	K	95.00%	56		753.3899	2	5.2	220	232	No
743	IPI00000146	NT5C1A	CYTOSOLIC 5'-NUCLEOTIDASE 1A.	EAIDEGIAAATIFSPSR	R	D	95.00%	85		874.4551	2	8.9	181	197	No
				EPGPGAETAAAPVWEEAK	R	I	95.00%	66		905.4434	2	7.0	14	31	No
				GFLEALGR	K	L	95.00%	54		431.7452	2	4.4	252	259	No
				IFYDNLAPK	K	K	95.00%	35		540.7931	2	4.9	32	40	No
				LINSINHYDLFIER	R	F	95.00%	94		873.9689	2	6.9	137	150	No
				LINSINHYDLFIER	R	F	95.00%	60		582.9813	3	5.9	137	150	No
				MDEEQQIYTEQGVEEYVR	R	Y	95.00%	72	M1: Oxidation	1131.5010	2	2.9	64	81	No
				VAFDGDAVLFSDESER	R	I	95.00%	87		878.9120	2	7.5	208	223	No
				YQLEHENEPFSPGPAFPFVK	R	A	95.00%	41		778.3854	3	7.0	82	101	No
744	IPI00000663; IPI00759655	MLYCD	ISOFORM MITOCHONDRIAL OF MALONYL-COA DECARBOXYLASE, MITOCHONDRIALPRECURSOR.; ISOFORM CYTOPLASMIC+PEROXISOMAL OF MALONYL-COA DECARBOXYLASE,MITOCHONDRIAL PRECURSOR.	GFGVDHGQVAEQSAGVLHLR	R	Q	95.00%	79		693.0281	3	5.1	94	113	No
				YFLEETGPNSTSYLGSK	R	I	95.00%	89		946.9576	2	8.2	456	472	No
745	IPI00000873; IPI00829641	VARS	VALYL-TRNA SYNTHETASE.; 140 KDA PROTEIN.	LSAAVTEAFVR	K	L	95.00%	96		582.3289	2	6.5	451	461	No
				SSAQDPQAVLGALGR	R	A	95.00%	88		735.3937	2	5.6	123	137	No
746	IPI00002270	C6orf211	UPF0364 PROTEIN C6ORF211.	IHEAIIQSPPIDYFDVFK	R	E	95.00%	35		711.3804	3	8.7	124	141	No
				LRNELQTDKPFIPLVEK	K	F	95.00%	42		680.7256	3	5.7	65	81	No
				LRNELQTDKPFIPLVEK	K	F	95.00%	37		510.7954	4	4.1	65	81	No
				NELQTDKPFIPLVEK	R	F	95.00%	32		590.9957	3	4.0	67	81	No
				TIEDLDENQLKDEFFK	R	L	95.00%	106		992.4890	2	7.5	168	183	No
				TIEDLDENQLKDEFFK	R	L	95.00%	40		661.9946	3	6.5	168	183	No
747	IPI00002311	SCRN3	SECERNIN-3.	ALNVIVDLLEK	K	Y	95.00%	57		613.8760	2	6.5	126	136	No
				EFDFAAAYSYLDTAK	K	M	95.00%	92		856.4025	2	6.7	218	232	No
748	IPI00002375	TMOD1	TROPOMODULIN-1.	FGYHFTQQGPR	K	L	95.00%	43		669.3275	2	5.9	315	325	No
				LEEVNLNNIR	K	N	95.00%	31		607.3303	2	-1.1	197	206	No
				YRDLDEDEILGALTEEELR	K	T	95.00%	36		760.3771	3	4.9	10	28	No
749	IPI00002519; IPI00220668	SHMT1	ISOFORM 1 OF SERINE HYDROXYMETHYLTRANSFERASE, CYTOSOLIC.; ISOFORM 2 OF SERINE HYDROXYMETHYLTRANSFERASE, CYTOSOLIC.	ALSEALTELGYK	R	I	95.00%	71		647.8520	2	5.1	337	348	No
				MLAQPLKDSDVEVYNIIK	K	K	95.00%	39	M1: Oxidation	698.0408	3	3.2	21	38	No
750	IPI00003918	RPL4	60S RIBOSOMAL PROTEIN L4.	APIRPDIVNFVHTNLR	K	K	95.00%	41		621.3549	3	4.7	30	45	No
				APIRPDIVNFVHTNLR	K	K	95.00%	34		466.2680	4	4.4	30	45	No
				EAVLLLK	K	K	95.00%	28		785.5170	1	4.1	166	172	No
				NIPGITLLNVSK	R	L	95.00%	42		634.8887	2	9.1	223	234	No
751	IPI00003944	DBT	LIPOAMIDE ACYLTRANSFERASE COMPONENT OF BRANCHED-CHAIN ALPHA-KETO ACIDDEHYDROGENASE COMPLEX, MITOCHONDRIAL PRECURSOR.	ASHNIGIAMDTEQGLIVPNVK	K	N	95.00%	50	M9: Oxidation	741.7243	3	5.7	340	360	No
				ILKEDILNYLEK	R	Q	95.00%	82		745.9345	2	9.3	200	211	No
				ILKEDILNYLEK	R	Q	95.00%	58		497.6243	3	6.6	200	211	No
				SYLENPAFMLLDLK	K	-	95.00%	94	M9: Oxidation	835.4366	2	8.4	469	482	No
752	IPI00004839	CRKL	CRK-LIKE PROTEIN.	IGDQEFDHLPALLEFYK	K	I	95.00%	39		679.0171	3	8.8	73	89	No

				IHYLDTTTLIEPAPR	K	Y	95.00%	47		580.6533	3	6.0	90	104	No
				TALALEVGDIVK	K	V	95.00%	79		614.8636	2	3.1	254	265	No
				TLYDFPGNDAEDLPFK	R	K	95.00%	47		921.4416	2	8.4	130	145	No
753	IPI00005198; IPI00641665	ILF2	INTERLEUKIN ENHANCER-BINDING FACTOR 2.; 12 KDA PROTEIN.	GTMTTGHNVADLVVILK	K	I	95.00%	34	M3: Oxidation	595.6626	3	7.8	111	127	No
				ILPTLEAVAALGNK	K	V	95.00%	81		705.4256	2	4.6	128	141	No
				VLQSALAAIR	K	H	95.00%	53		521.3259	2	1.6	197	206	No
754	IPI00005809	SDPR	SERUM DEPRIVATION-RESPONSE PROTEIN.	DNSQVNAVTVLTLLDK	R	L	95.00%	126		865.4781	2	8.5	49	64	No
				SDGDPVQPAVLQVHQTS	R	-	95.00%	61		889.4462	2	6.9	409	425	No
				VLIFQEENEIPASVFVK	K	Q	95.00%	65		981.5415	2	8.3	157	173	No
755	IPI00006114	SERPINF1	PIGMENT EPITHELIUM-DERIVED FACTOR PRECURSOR.	ALYYDLISSPDIHGTYK	R	E	95.00%	46		652.6686	3	7.5	107	123	No
				ELLDTVTAPQK	K	N	95.00%	41		607.8367	2	1.7	124	134	No
				LAAAVSNFGYDLYR	K	V	95.00%	83		780.4013	2	5.8	54	67	No
				LQSLFDSPDFSK	K	I	95.00%	59		692.3467	2	4.2	334	345	No
756	IPI00006451	NSF	VESICLE-FUSING ATPASE.	GSMAGSTGVHDTVVNQLLSK	R	I	95.00%	54	M3: Oxidation	673.0093	3	4.8	338	357	No
				LLDYVPIGPR	R	F	95.00%	48		571.8350	2	4.0	608	617	No
				NFSGAELEGLVR	K	A	95.00%	58		646.3387	2	3.9	435	446	No
				VLDDGELLVQQTK	R	N	95.00%	72		729.3975	2	1.1	517	529	No
757	IPI00006558; IPI00022824	SH3GLB1	ISOFORM 1 OF SH3 DOMAIN GRB2-LIKE PROTEIN B1.; ISOFORM 2 OF SH3 DOMAIN GRB2-LIKE PROTEIN B1.	ELIQTSALNFLTPLR	R	N	95.00%	66		858.4951	2	7.2	134	148	No
				GKVPITYLELLN	K	-	95.00%	42		680.4022	2	5.7	354	365	No
				LAADAGTFLSR	K	A	95.00%	66		561.3034	2	2.9	11	21	No
758	IPI00006957; IPI00339238	DHRS7	ISOFORM 1 OF DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER 7 PRECURSOR.; ISOFORM 2 OF DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER 7 PRECURSOR.	EKDILVLPLDLTDTGSHEAATK	K	A	95.00%	62		789.4268	3	8.0	102	123	No
				IDILVNNGGMSQR	R	S	95.00%	51	M10: Oxidation	716.8669	2	2.8	132	144	No
				LMLISMANDLK	R	E	95.00%	32	M2: Oxidation, M6: Oxidation	640.8368	2	5.0	272	282	No
759	IPI00007183; IPI00169267	ARL6IP2	HYPOTHETICAL PROTEIN ARL6IP2.; ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 6-INTERACTING PROTEIN 2.	NLVPLLLAPENLVEK	R	E	95.00%	53		831.5021	2	7.3	326	340	No
				SMLQATAEANNLAAVAGAR	K	D	95.00%	97	M2: Oxidation	937.9798	2	6.6	373	391	No
760	IPI00007675	DYNC1LI1	CYTOPLASMIC DYNEIN 1 LIGHT INTERMEDIATE CHAIN 1.	AGATSEGVLANFFNSLLSK	K	K	95.00%	110		963.5107	2	8.5	436	454	No
				IGILHENFQTLK	K	A	95.00%	38		471.6036	3	3.4	333	344	No
				SVSSNVASVSPIPAGSK	R	K	95.00%	43		793.9260	2	3.3	412	428	No
761	IPI00007682	ATP6V1A	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS ISOFORM.	ALDEYYDKHFTEFVPLR	R	T	95.00%	37		715.0278	3	8.3	460	476	No
				LAEMPADSGYPAYLGAR	R	L	95.00%	72	M4: Oxidation	899.4329	2	5.3	365	381	No
				VGSHITGGDIYGIVSENSLIK	R	H	95.00%	34		720.3862	3	3.6	143	163	No
762	IPI00008219	RAD23A	UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG A.	DQPQFQNMR	R	Q	95.00%	31	M8: Oxidation	590.2682	2	5.9	237	245	No
				EDKSPSEESAPTTSPESVSGSVPSSGSSGR	R	E	95.00%	57		974.7802	3	5.6	120	149	No
				ILSDDVPIRDYR	K	I	95.00%	34		487.9303	3	3.3	54	65	No
763	IPI00008223	RAD23B	UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG B.	IDIDPEETVK	K	A	95.00%	37		579.8004	2	2.7	15	24	No
				ILNDDTALKEYK	K	I	95.00%	46		711.8812	2	4.5	52	63	No
				NFVVVMVTK	K	P	95.00%	36	M6: Oxidation	526.7972	2	5.0	68	76	No
				NFVVVMVTKPK	K	A	95.00%	64	M6: Oxidation	639.3717	2	5.1	68	78	No
				QEKPAEKPAETPVATSPTATDSTSGDSSR	K	S	95.00%	70		982.4756	3	4.6	145	173	No
				QIIQQNPSLLPALLQQIGR	R	E	95.00%	116		1065.6340	2	9.5	290	308	No
				QIIQQNPSLLPALLQQIGR	R	E	95.00%	37		710.7578	3	8.3	290	308	No
764	IPI00009104	RUVBL2	RUVB-LIKE 2.	EVVHTVSLHEIDVINSR	K	T	95.00%	36		649.6846	3	4.3	237	253	No
				GLGLDDALEPR	R	Q	95.00%	71		578.3079	2	5.7	30	40	No
				LLIVSTTPYSEK	R	D	95.00%	41		675.8819	2	2.8	354	365	No
				TQGFLALFSGDTGEIK	R	S	95.00%	111		842.4376	2	4.6	254	269	No
765	IPI00009634	SQRDL	SULFIDE:QUINONE OXIDOREDUCTASE, MITOCHONDRIAL PRECURSOR.	EGNAIFTFPNTPVK	K	C	95.00%	50		767.9045	2	6.8	187	200	No
				TAAAVAAQSGILDR	K	T	95.00%	67		672.3722	2	6.2	345	358	No
				VGAENVAIVEPSER	K	H	95.00%	34		735.3868	2	3.9	66	79	No
				VILAEFDYK	R	A	95.00%	55		549.3003	2	4.0	388	396	No
				YADALQEIIQER	K	N	95.00%	78		724.8784	2	7.1	242	253	No

766	IPI00010314; IPI00442121; IPI00790373	ALAD	DELTA-AMINOLEVULINIC ACID DEHYDRATASE.; DELTA-AMINOLEVULINIC ACID DEHYDRATASE ISOFORM A.; DELTA-AMINOLEVULINIC ACID DEHYDRATASE ISOFORM B.	GSAADSEESPAIEAIHLLR	R	K	95.00%	42		656.0051	3	5.8	120	138	No
				LAEVALAYAK	R	A	95.00%	72		524.8085	2	4.5	159	168	No
767	IPI00010720	CCT5	T-COMPLEX PROTEIN 1 SUBUNIT EPSILON.	AVTIFIR	R	G	95.00%	49		410.2601	2	3.8	382	388	No
				DVDFELIK	R	V	95.00%	41		489.7633	2	4.0	203	210	No
				DVDFELIKVEGK	R	V	95.00%	68		696.3766	2	2.1	203	214	No
				HKLDVTSVEDYK	K	A	95.00%	43		717.3698	2	2.7	264	275	No
				HKLDVTSVEDYK	K	A	95.00%	43		478.5821	3	2.0	264	275	No
				ISDSVLVDIKDTEPLIQTAK	K	T	95.00%	61		729.0740	3	4.1	151	170	No
				LDVTSVEDYK	K	A	95.00%	52		584.7927	2	3.0	266	275	No
				LGFAGLVQEISFGTTK	K	D	95.00%	121		834.4616	2	8.6	353	368	No
				VAIEHLDKISDSVLVDIKDTEPLIQTAK	R	T	95.00%	42		773.4338	4	5.9	143	170	No
				WVGGPEIELIAIATGGR	R	I	95.00%	86		869.9829	2	4.9	324	340	No
768	IPI00012442	G3BP1	RAS GTPASE-ACTIVATING PROTEIN-BINDING PROTEIN 1.	LPNFGFVVFDDSEPVQK	K	V	95.00%	71		969.4919	2	5.5	377	393	No
				SSSPAPADIAQTVQEDLR	K	T	95.00%	84	S3: Phospho	982.9602	2	8.0	230	247	No
769	IPI00012578	KPNA4	IMPORTIN ALPHA-4 SUBUNIT.	DAQVVQVVLDGLSNILK	K	M	95.00%	129		906.0226	2	5.2	424	440	No
				DAQVVQVVLDGLSNILK	K	M	95.00%	107		604.3514	3	5.9	424	440	No
				EAAWAISNLTISGR	K	K	95.00%	92		744.9005	2	8.1	387	400	Yes
				IEQLQNHENEDIYK	K	L	95.00%	77		886.9291	2	2.8	462	475	No
				KLLSSDRNPPIDDLIK	R	S	95.00%	27		608.6829	3	5.2	97	112	Yes
				LLSSDRNPPIDDLIK	K	S	95.00%	55		848.4745	2	7.6	98	112	Yes
				NPPIDDLIK	R	S	95.00%	39		512.7897	2	3.3	104	112	Yes
770	IPI00013068	EIF3S6	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 6.	HLVFPLLEFLSVK	R	E	95.00%	31		771.4647	2	7.8	17	29	No
				HLVFPLLEFLSVK	R	E	95.00%	27		514.6440	3	4.3	17	29	No
				LGHVVMGNNAVSPYQQVIEK	K	T	95.00%	42	M6: Oxidation	733.7173	3	6.1	388	407	No
				LKETIDNNSVSSPLQSLQQR	R	T	95.00%	65		753.0674	3	3.4	192	211	No
				MLFDYLADK	R	H	95.00%	38	M1: Oxidation	566.2768	2	5.3	112	120	No
				NLYSDDIPHALR	K	E	95.00%	58		707.3620	2	2.4	60	71	No
				QLQAETEPIVK	K	M	95.00%	32		628.3506	2	2.7	83	93	No
				YLTTAVITNK	R	D	95.00%	31		562.3235	2	2.5	256	265	No
771	IPI00013122	CDC37	HSP90 CO-CHAPERONE CDC37.	DVQMLQDAISK	K	M	95.00%	56	M4: Oxidation	632.3189	2	3.5	313	323	No
				EGEEAGPGDPLLEAVPK	K	T	95.00%	95		854.4332	2	8.2	353	369	No
				LQAEAQQLR	R	K	95.00%	32		528.7958	2	3.2	84	92	No
				QYMEGFNDELEAFK	R	E	95.00%	70	M3: Oxidation	868.8839	2	7.0	247	260	No
				SMPWNVDTLSK	K	D	95.00%	32	M2: Oxidation	647.3140	2	4.0	111	121	No
				SMVNTKPEKTEEDSEEVR	K	E	95.00%	51	M2: Oxidation	708.6658	3	2.3	127	144	No
772	IPI00013219	ILK	INTEGRIN-LINKED PROTEIN KINASE.	EVPFADLSNMEIGMK	R	V	95.00%	64	M10: Oxidation, M14: Oxidation	856.9041	2	7.5	389	403	No
				FDMIVPILEK	K	M	95.00%	36	M3: Oxidation	610.8383	2	6.9	439	448	No
773	IPI00013466; IPI00783136	ASNA1	ARSA ARSENITE TRANSPORTER, ATP-BINDING, HOMOLOG 1 VARIANT.; ARSENICAL PUMP-DRIVING ATPASE.	LEETLPVIR	K	S	95.00%	51		535.3186	2	3.2	237	245	No
				LLNFPTIVER	R	G	95.00%	45		601.3542	2	4.9	176	185	No
774	IPI00015856; IPI00029820; IPI00658188; IPI00658215	DNPEP	HYPOTHETICAL PROTEIN DNPEP.; DNPEP PROTEIN (FRAGMENT).; 48 KDA PROTEIN.; 52 KDA PROTEIN.	GFFELFPSLSHNLLVD	K	-	95.00%	55		917.9819	2	9.7	363	378	No
				GTPEPGPLNAVDER	K	H	95.00%	48		726.3626	2	2.9	105	118	No
				LEQQLVHVERPILR	R	I	95.00%	38		577.3438	3	4.5	53	66	No
				YASNAVSEALIR	R	E	95.00%	69		647.3471	2	4.8	284	295	No
775	IPI00016249; IPI00554715	FXR1	ISOFORM 1 OF FRAGILE X MENTAL RETARDATION SYNDROME-RELATED PROTEIN 1.; ISOFORM 2 OF FRAGILE X MENTAL RETARDATION SYNDROME-RELATED PROTEIN 1.	EISEGDEVEVYSR	K	A	95.00%	66		756.3498	2	3.4	58	70	No
				GFLEFVEDFIQVPR	R	N	95.00%	83		848.4486	2	8.5	277	290	No
				GFLEFVEDFIQVPR	R	N	95.00%	58		565.9666	3	5.5	277	290	No
				KVPGVTAIELDEDTGTFR	R	I	95.00%	55		650.0095	3	5.0	246	263	No
776	IPI00016405	OCIAD1	OCIA DOMAIN CONTAINING 1 ISOFORM 1.	LENSPLGEALR	K	S	95.00%	56		599.8287	2	5.2	105	115	No
				SVPLAATSMLITQGLISK	R	G	95.00%	89	M9: Oxidation	923.5300	2	8.7	47	64	No

777	IPI00016458; IPI00029239	L2HGDH	ISOFORM 1 OF L-2-HYDROXYGLUTARATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR.; ISOFORM 2 OF L-2-HYDROXYGLUTARATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR.	HPSLSIGVLEK	R	E	95.00%	44		590.3430	2	3.5	71	81	No
				LASQNFSYGVTEMYK	K	A	95.00%	55	M13: Oxidation	877.4139	2	5.4	360	374	No
				LIVAVEQEEIPR	K	L	95.00%	50		698.3997	2	4.7	137	148	No
778	IPI00016610	PCBP1	POLY(RC)-BINDING PROTEIN 1.	AFAMIIDKLEEDINSSMTNSTAAS RPPVTLR	K	L	95.00%	65	M4: Oxidation, M17: Oxidation	853.4374	4	9.7	71	101	No
				ESTGAQVQVAGDMLPNSTER	R	A	95.00%	107	M13: Oxidation	1053.4940	2	1.6	125	144	No
				ESTGAQVQVAGDMLPNSTER	R	A	95.00%	52	M13: Oxidation	702.6662	3	2.6	125	144	No
				IANPVEGSSGR	K	Q	95.00%	61		543.7835	2	4.5	315	325	No
				IITLTGPTNAIFK	R	A	95.00%	72		694.9147	2	4.4	58	70	No
779	IPI00016801	GLUD1	GLUTAMATE DEHYDROGENASE 1, MITOCHONDRIAL PRECURSOR.	DDGSWEVIEGYR	R	A	95.00%	41		713.3223	2	5.6	125	136	No
				DSNYHLLMSVQESLER	R	K	95.00%	45	M8: Oxidation	968.9629	2	5.4	461	476	No
				GASIVEDKLVEDLR	R	T	95.00%	74		772.4263	2	7.4	77	90	No
				GFIGPGIDVPAPDMSTGER	K	E	95.00%	67	M14: Oxidation	966.4678	2	5.2	213	231	No
				HGGTIPIVPTAEFQDR	K	I	95.00%	77		869.4578	2	8.6	481	496	No
				IIAEGANGPTTPEADKIFLER	K	N	95.00%	64		748.0684	3	7.8	400	420	No
				MVEGFFDR	K	G	95.00%	35	M1: Oxidation	508.7298	2	0.7	69	76	Yes
				TAAYVNAIEK	R	V	95.00%	32		540.2919	2	2.0	536	545	No
				YNLGLDLR	K	T	95.00%	69		482.2693	2	4.5	528	535	No
				YSTDVSVDEVK	R	A	95.00%	54		621.3022	2	5.2	152	162	Yes
780	IPI00017184	EHD1	EH DOMAIN-CONTAINING PROTEIN 1.	ELVNNLGEIYQK	K	I	95.00%	66		710.3816	2	5.0	330	341	No
				LADVDKDGLLDDEEFALANHLIK	K	V	95.00%	62		852.1143	3	9.0	487	509	No
				LDISDEFSEVIK	K	A	95.00%	52		697.8617	2	7.2	194	205	No
				LFEAEEQDLFKDIQSLPR	K	N	95.00%	40		726.7123	3	5.9	270	287	No
				LNAFGNAFLNR	K	F	95.00%	49		618.8325	2	6.6	125	135	No
781	IPI00017763	NAP1L4	NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 4.	FYEEVHDLER	K	K	95.00%	51		668.8165	2	5.8	84	93	No
				GIPEFWFTIFR	K	N	95.00%	39		706.8764	2	5.8	158	168	No
				LDNVPHTPSSYIETLPK	R	A	95.00%	65		637.6700	3	4.0	45	61	No
				NVDMLSELVQEYDEPILK	R	H	95.00%	84	M4: Oxidation	1076.0370	2	5.8	169	186	No
				QVPNESFFNFFNPLK	K	G	95.00%	66		914.4649	2	8.3	283	297	No
				YAALYQPLFDK	K	R	95.00%	50		664.8522	2	5.6	95	105	No
782	IPI00017895; IPI00719611	GPD2	ISOFORM 1 OF GLYCEROL-3-PHOSPHATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR.; ISOFORM 2 OF GLYCEROL-3-PHOSPHATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR.	ANLLEIAPHLSAPLPIMLPVYK	R	W	95.00%	55	M17: Oxidation	806.1356	3	9.5	19	40	No
				GFITIVDVQR	K	V	95.00%	58		574.3298	2	3.5	641	650	No
				LAFLNVQAAEEALPR	R	I	95.00%	96		821.4572	2	6.1	558	572	No
				LAFLNVQAAEEALPR	R	I	95.00%	38		547.9736	3	5.1	432	446	No
				LVQDYGLESEVAQHLAATYGDK	R	A	95.00%	50		803.0706	3	7.4	483	504	No
				LVSEFPYIEAEVK	R	Y	95.00%	60		762.4073	2	4.6	526	538	No
				MNLAIALTAAR	R	Y	95.00%	69	M1: Oxidation	580.8309	2	6.6	102	112	No
				SEISLLPSDIDR	R	Y	95.00%	55		672.8583	2	5.7	616	627	No
				VIFFLPWQK	R	M	95.00%	48		589.3440	2	2.3	214	222	No
				YGAATANYMEVVSLLK	R	K	95.00%	90	M9: Oxidation	873.4491	2	6.9	239	254	No
783	IPI00018140; IPI00402183; IPI00402185	SYNCRIP	ISOFORM 1 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN Q.; ISOFORM 3 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN Q.; ISOFORM 5 OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN Q.	DLFEDELVPLFEK	R	A	95.00%	44		797.4117	2	6.4	172	184	No
				NLANTVTEEILEK	R	A	95.00%	64		737.3998	2	7.8	344	356	No
784	IPI00018813; IPI00743825	COPS2	ISOFORM 2 OF COP9 SIGNALOSOME COMPLEX SUBUNIT 2.; ISOFORM 1 OF COP9 SIGNALOSOME COMPLEX SUBUNIT 2.	AHTDFFEAFK	K	N	95.00%	32		606.7913	2	4.7	264	273	No
				AHTDFFEAFK	K	N	95.00%	37		404.8616	3	0.1	264	273	No
				ALYEQSLHIK	K	S	95.00%	37		601.3356	2	4.3	223	232	No
				IDQVNQLLELDHQK	R	R	95.00%	74		846.9583	2	9.8	412	425	No
				IDQVNQLLELDHQK	R	R	95.00%	34		564.9715	3	3.9	412	425	No
				IHIPFISK	R	E	95.00%	29		477.7944	2	3.3	379	386	No
				SGINPFDSQEAKPYK	K	N	95.00%	50		840.9175	2	2.2	299	313	No
				VLELEGEKGEWGFK	K	A	95.00%	32		540.9502	3	4.6	57	70	No

				WTNQLNSLNQAVVSK	K	L	95.00%	90		851.4548	2	5.6	437	451	No
				YLVLANMLMK	K	S	95.00%	39	M7: Oxidation, M9: Oxidation	614.3294	2	2.3	289	298	No
785	IPI00018873; IPI00337370	PBEF1	ISOFORM 1 OF NICOTINAMIDE PHOSPHORIBOSYLTRANSFERASE.; ISOFORM 2 OF NICOTINAMIDE PHOSPHORIBOSYLTRANSFERASE.	AVPEGFVIPR	K	G	95.00%	28		542.8148	2	5.6	118	127	No
				GTDTVAGLALIK	K	K	95.00%	48		579.8430	2	3.8	217	228	No
				GVSSQETAGIGASAHLVNFK	R	G	95.00%	102		987.0130	2	4.6	197	216	No
				GVSSQETAGIGASAHLVNFK	R	G	95.00%	33		658.3462	3	7.1	197	216	No
				STQAPLIIRPDSGNPLDTVLK	R	V	95.00%	34		745.7551	3	6.6	303	323	No
				TPAGNFVTLEEGKGDLEEYGQDLLHTVFK	R	N	95.00%	34		802.6589	4	8.5	435	463	No
				YLLETSGNLDGLEYK	K	L	95.00%	59		857.9370	2	7.0	175	189	No
786	IPI00018946	PANK4	PANTOTHENATE KINASE 4.	AVSAVLESDPYFGFEEAK	K	R	95.00%	104		979.9777	2	4.6	573	590	No
				DVYGGAHQTLGLSGNLIASSFGK	R	S	95.00%	48		764.7302	3	5.4	256	278	No
				FAIDIGGSLTK	R	L	95.00%	45		561.3175	2	5.7	37	47	No
				GEVQALFLR	K	H	95.00%	47		516.7983	2	4.4	346	354	No
				GLLAGNVFDWGAK	K	A	95.00%	62		674.3613	2	6.3	560	572	No
				QQPFAYGTLTVR	R	S	95.00%	34		690.8697	2	2.9	493	504	No
				VYFGGFFIR	R	G	95.00%	44		553.2980	2	4.2	319	327	No
787	IPI00018968; IPI00479845; IPI00604652; IPI00604676; IPI00646350	APPBP1	NEDD8-ACTIVATING ENZYME E1 REGULATORY SUBUNIT.; 60 KDA PROTEIN.; AMYLOID BETA PRECURSOR PROTEIN-BINDING PROTEIN 1 ISOFORM C.; AMYLOID BETA PRECURSOR PROTEIN-BINDING PROTEIN 1 ISOFORM B.; 61 KDA PROTEIN.	LLQSIGQAPESISEK	K	E	95.00%	76		800.4377	2	5.0	364	378	No
				YGAAEPHTIAAFLGGAAAQEVIK	R	I	95.00%	37		762.4091	3	8.2	485	507	No
788	IPI00019450; IPI00642416; IPI00646322; IPI00646813	TROVE2	ISOFORM LONG OF 60 KDA SS-A/RO RIBONUCLEOPROTEIN.; TROVE DOMAIN FAMILY, MEMBER 2.; TROVE DOMAIN FAMILY, MEMBER 2.; 60KD RO/SSA AUTOANTIGEN ISOFORM 1.	LGLENAEALIR	K	L	95.00%	67		599.8484	2	7.7	53	63	No
				TRDELEVIHLIEEHR	R	L	95.00%	45		473.0046	4	3.4	238	252	No
789	IPI00019912	HSD17B4	PEROXISOMAL MULTIFUNCTIONAL ENZYME TYPE 2.	GALVVVNDLGGDFK	R	G	95.00%	67		702.3835	2	4.0	33	46	No
				LGLLGLANSLAIEGR	K	K	95.00%	51		748.9506	2	8.7	169	183	No
				VVLVTGAGAGLGR	R	A	95.00%	55		585.3548	2	0.8	11	23	No
790	IPI00008943; IPI00019918; IPI00027599; IPI00155054	DDX19A; DDX19B	ISOFORM 1 OF ATP-DEPENDENT RNA HELICASE DDX19B.; ATP-DEPENDENT RNA HELICASE DDX19A.; ISOFORM 2 OF ATP-DEPENDENT RNA HELICASE DDX19B.; HYPOTHETICAL PROTEIN DKFZP686C21137.	EGHQVALLSGEMMVEQR	K	A	95.00%	38	M12: Oxidation, M13: Oxidation	649.3129	3	6.1	355	371	No
				LDTDDLDEIEK	R	I	95.00%	73		653.3099	2	4.1	465	475	No
				SNLVDNTNQVEVLQR	R	D	95.00%	91		864.9530	2	5.9	67	81	No
791	IPI00019927	PSMD7	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 7.	SVVALHNLINNK	R	I	95.00%	62		661.3876	2	6.3	268	279	No
				TFEHVTSEIGAEEAEEVGVEHLLR	K	D	95.00%	38		671.0861	4	5.6	154	177	No
				VVVHPLVLLSVVDHFNR	K	I	95.00%	65		648.3849	3	8.3	9	25	No
				VVVHPLVLLSVVDHFNR	K	I	95.00%	44		486.5382	4	3.3	9	25	No
792	IPI00020042; IPI00738042	LOC652826; PSMC4	ISOFORM 1 OF 26S PROTEASE REGULATORY SUBUNIT 6B.; SIMILAR TO 26S PROTEASE REGULATORY SUBUNIT 6B.	ADTLDPALLRPGR	R	L	95.00%	44		697.8945	2	3.7	314	326	No
				AQDEIPALSVSR	K	P	95.00%	56		643.3439	2	3.6	11	22	No
				EAVELPLTHFELYK	R	Q	95.00%	74		844.9546	2	6.8	179	192	No
				ELLKPNASVALHK	R	H	95.00%	32		473.9505	3	2.3	122	134	No
				ENAPAIIFIDEIDAIATK	K	R	95.00%	124		972.5264	2	5.9	256	273	No
				ENAPAIIFIDEIDAIATK	K	R	95.00%	63		648.6865	3	5.3	256	273	No
				ENAPAIIFIDEIDAIATKR	K	F	95.00%	45		700.7208	3	5.8	256	274	No
				ILLELLNQMDGFDQNVNVK	R	V	95.00%	119	M9: Oxidation	1110.0820	2	8.1	288	306	No
				ILLELLNQMDGFDQNVNVK	R	V	95.00%	77	M9: Oxidation	740.3908	3	8.4	288	306	No
				LIFSTITSK	R	M	95.00%	28		505.3025	2	3.7	343	351	No
				LQQELEFLEVQEEYIKDEQK	K	N	95.00%	70		846.7671	3	9.5	47	66	No
				MNLSEEVDLEDYVARPDK	K	I	95.00%	78	M1: Oxidation	1070.0100	2	9.7	352	369	No
				RLIFSTITSK	K	M	95.00%	29		583.3534	2	3.8	342	351	No
793	IPI00020672	BBS1; DPP3	ISOFORM 1 OF DIPEPTIDYL-PEPTIDASE 3.	LASVLGSEPSLDSEVTSK	R	L	95.00%	68		909.9782	2	8.2	216	233	No
				LVASAEQLLK	R	E	95.00%	38		536.3259	2	2.3	346	355	No

				VLLEAGEGLVTITPTTGSDGRPDAR	R	V	95.00%	64		842.4524	3	7.9	578	602	No
794	IPI00021728; IPI00176637; IPI00793912	EIF2S2; LOC728350	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 SUBUNIT 2.; SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR 2 SUBUNIT 2.; EIF2S2 PROTEIN.	DASDDLDDLNFFNQK	K	K	95.00%	101		878.8941	2	7.8	65	79	No
				EVEPEPTEDKDLEADEEDTR	K	K	95.00%	35		782.6791	3	4.6	43	62	No
				IFDIDEAEEGVK	K	D	95.00%	86		682.8367	2	5.0	88	99	No
				IFDIDEAEEGVK	K	I	95.00%	84		682.8367	2	4.9	88	99	No
795	IPI00021891; IPI00219713; IPI00411626	FGG	ISOFORM GAMMA-B OF FIBRINOGEN GAMMA CHAIN PRECURSOR.; ISOFORM GAMMA-A OF FIBRINOGEN GAMMA CHAIN PRECURSOR.; HYPOTHETICAL PROTEIN DKFZP779N0926.	AIQLTYNPDESSKPNMIDAATLK	K	S	95.00%	53	M16: Oxidation	846.0955	3	4.1	89	111	No
				IHLISTQSAIPYALR	K	V	95.00%	56		841.9891	2	6.5	259	273	No
				IHLISTQSAIPYALR	K	V	95.00%	37		561.6611	3	4.9	259	273	No
				VELEDWNGR	R	T	95.00%	42		559.2668	2	-1.9	274	282	No
				YEASILTHDSSIR	K	Y	95.00%	72		746.3784	2	3.1	122	134	No
				YLQEIYNSNNQK	R	I	95.00%	87		757.3701	2	2.4	135	146	No
796	IPI00021926	PSMC6	26S PROTEASE REGULATORY SUBUNIT S10B.	ALQSVGQIVGEVLK	K	Q	95.00%	82		720.9315	2	8.6	49	62	No
				EVIELPLTNPELFQR	R	V	95.00%	53		899.4997	2	9.1	147	161	No
797	IPI00022395	C9	COMPLEMENT COMPONENT C9 PRECURSOR.	AIEDYINEFSVR	R	K	95.00%	53		728.3620	2	2.9	497	508	No
				LSPIYNLVPVK	K	M	95.00%	25		621.8812	2	6.7	473	483	No
798	IPI00022538	GENX-3414	GENETHONIN-1.	EHVPSGQFPDTEAPATSETSNSR	R	S	95.00%	42		815.3746	3	4.6	113	135	No
				HSSWGDVGVGGSLK	R	A	95.00%	38		693.3492	2	6.6	209	222	No
				VAVMPAGSQQVSVR	R	F	95.00%	76	M4: Oxidation	722.8848	2	2.5	254	267	No
799	IPI00022648	EIF5	EUKARYOTIC TRANSLATION INITIATION FACTOR 5.	ALNRPPTYPTK	K	Y	95.00%	30		629.3538	2	3.3	45	55	No
				AMGPLVLTEVLFNEK	K	I	95.00%	94	M2: Oxidation	838.9568	2	7.4	274	288	No
				VLTLSDDLER	K	T	95.00%	47		580.8144	2	4.0	225	234	No
				VNILFDFVK	R	K	95.00%	45		547.8184	2	3.5	240	248	No
800	IPI00022694	PSMD4	ISOFORM RPN10A OF 26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 4.	IIAFVGSPVEDNEKDLVK	R	L	95.00%	61		987.0430	2	9.3	109	126	No
				VNVDIINFGEEEVNTEK	K	L	95.00%	96		974.9878	2	8.9	136	152	No
801	IPI00022895	A1BG	ALPHA-1B-GLYCOPROTEIN PRECURSOR.	LETPDFQLFK	R	N	95.00%	56		619.3314	2	6.4	53	62	No
				NGVAQEPVHLDSPAIK	K	H	95.00%	68		837.9479	2	3.8	63	78	No
				SGLSTGWTQLSK	R	L	95.00%	63		632.8325	2	2.6	95	106	No
				TPGAAANLELIFVGPQHAGNYR	R	C	95.00%	69		766.0706	3	5.4	448	469	No
802	IPI00023919; IPI00745502	PSMC5	26S PROTEASE REGULATORY SUBUNIT 8.; 45 KDA PROTEIN.	EHAPSIIFMDEIDSIGSSR	R	L	95.00%	36	M9: Oxidation	707.3438	3	8.9	240	258	No
				EVIELPVKHPELFEALGIAQPK	K	G	95.00%	57		819.8049	3	9.4	163	184	No
				GVLLYGPPGTGK	K	T	95.00%	39		579.8320	2	3.1	185	196	No
				IDILDSALLRPGR	R	I	95.00%	41		480.2862	3	3.1	298	310	No
				IEELQLIVNDK	K	S	95.00%	74		657.3721	2	3.3	28	38	No
				LLREELQLLQEQGSYVGEVVR	R	A	95.00%	74		820.1232	3	9.6	58	78	No
				RVHVTQEDFEMAVAK	R	V	95.00%	67	M11: Oxidation	592.6328	3	4.3	375	389	No
				TMLELLNQLDGFEATK	R	N	95.00%	74	M2: Oxidation	919.9715	2	7.6	272	287	No
				VPDSTYEMIGGLDK	K	Q	95.00%	46	M8: Oxidation	770.8659	2	2.1	143	156	No
803	IPI00024317	GCDH	ISOFORM LONG OF GLUTARYL-COA DEHYDROGENASE, MITOCHONDRIAL PRECURSOR.	AITGIQAFTASK	R	-	95.00%	31		604.3413	2	5.0	427	438	No
				EIISEMGELGVLGPTIK	R	G	95.00%	46	M6: Oxidation	901.4925	2	8.2	95	111	No
804	IPI00024403	CPNE3	COPINE-3.	DIVQFVPFR	R	Q	95.00%	43		560.8144	2	4.8	485	493	No
				GSITISAEEIKDNR	K	V	95.00%	50		766.8985	2	-1.9	126	139	No
				LYGPTNFSPIINHVAR	K	F	95.00%	40		600.3292	3	6.4	391	406	No
805	IPI00024580; IPI00789136; IPI00792499	MCCC1	METHYLCROTONOYL-COA CARBOXYLASE SUBUNIT ALPHA, MITOCHONDRIALPRECURSOR.; 48 KDA PROTEIN.; HYPOTHETICAL PROTEIN DKFZP686B20267.	IIEEAPAPGIK	K	S	95.00%	29		569.3317	2	3.0	247	257	No
				IYAEDPSNNFMPVAGPLVHLSTPR	R	A	95.00%	41	M11: Oxidation	881.1138	3	6.7	348	371	No
				SEQEFQEQLESAR	R	R	95.00%	49		790.8673	2	4.8	182	194	No
806	IPI00024623	ACADSB	SHORT/BRANCHED CHAIN SPECIFIC ACYL-COA DEHYDROGENASE, MITOCHONDRIALPRECURSOR.	GITSFLVDR	K	D	95.00%	36		504.2814	2	2.2	231	239	No
				LFDFQGLQHQVAHVATQLEAAR	R	L	95.00%	53		827.1069	3	8.4	326	347	No
				VPEANILGQIGHGYK	K	Y	95.00%	30		532.6262	3	5.2	270	284	No

				YYASEIAGQTTSK	K	C	95.00%	97		709.8476	2	4.9	372	384	No
807	IPI00024934	MUT	METHYLMALONYL-COA MUTASE, MITOCHONDRIAL PRECURSOR.	AAVQVLDDIEK	K	C	95.00%	51		600.8304	2	4.4	731	741	No
				IDSGSEVIVGVNK	R	Y	95.00%	70		658.8600	2	4.5	479	491	No
				IIADIFEYTAK	K	H	95.00%	51		642.3519	2	5.4	241	251	No
				ILFDGIPLEK	K	M	95.00%	45		572.8378	2	5.0	172	181	No
				LTGTIQNDILK	K	E	95.00%	61		608.3532	2	2.8	213	223	No
				NTQIIIQEESGIPK	R	V	95.00%	67		785.4326	2	5.3	407	420	No
808	IPI00026813; IPI00607601; IPI00607790	FNTA	PROTEIN FARNESYLTRANSFERASE/GERANYLGERANYLTRANSFERASE TYPE I ALPHASUBUNIT.; FARNESYLTRANSFERASE, CAAX BOX, ALPHA ISOFORM C.; FARNESYLTRANSFERASE, CAAX BOX, ALPHA ISOFORM B.	DPSQELEFIADILNQDAK	R	N	95.00%	103		1023.5150	2	9.5	181	198	No
				DPSQELEFIADILNQDAK	R	N	95.00%	49		682.6763	3	4.8	181	198	No
				EVQYTLEMIK	R	L	95.00%	52	M8: Oxidation	635.3271	2	4.8	259	268	No
				VLVEWLR	R	D	95.00%	36		457.7789	2	4.1	107	113	No
				YFVISNTTGYNDR	R	A	95.00%	51		775.3724	2	5.4	241	253	No
809	IPI00028091	ACTR3	ACTIN-LIKE PROTEIN 3.	AEPEDHYFLLTEPPLNTPENR	R	E	95.00%	43		828.0751	3	8.3	103	123	No
				DITYFIQQLLR	R	D	95.00%	71		705.3972	2	4.9	199	209	No
				DREVGIPPEQSLETAK	R	A	95.00%	68		884.9615	2	3.8	210	225	No
				FMEQVIFK	R	Y	95.00%	37	M2: Oxidation	529.2751	2	2.9	92	99	No
				GVDDLDFFIGDEAIEKPTYATK	K	W	95.00%	83		815.4085	3	9.1	54	75	No
810	IPI00028366	SETD7	HISTONE-LYSINE N-METHYLTRANSFERASE, H3 LYSINE-4 SPECIFIC SET7.	IAYVYPDER	K	T	95.00%	39		563.2847	2	3.0	144	152	No
				SGPEAPEWYQVELK	K	A	95.00%	59		816.9061	2	8.1	345	358	No
				VYVAESLISSAGEGLFSK	R	V	95.00%	113		928.9949	2	9.5	216	233	No
811	IPI00028369; IPI00784901; IPI00785171	KIAA1715	ISOFORM 1 OF PROTEIN LUNAPARK.; ISOFORM 3 OF PROTEIN LUNAPARK.; ISOFORM 2 OF PROTEIN LUNAPARK.	IVEYLVGDGPQNR	R	Y	95.00%	55		730.3856	2	6.0	259	271	No
				TVTPALSSNVLPR	R	H	95.00%	37		677.8928	2	6.1	211	223	No
812	IPI00029012	EIF3S10	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10.	FNVLQYVVPEVK	R	D	95.00%	40		717.9058	2	2.8	377	388	No
				LTSLVPFVDAFQLER	R	A	95.00%	30		867.9805	2	5.8	455	469	No
813	IPI00029643	ZAK	ISOFORM 2 OF MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE MLT.	EAEILSVLSHR	K	N	95.00%	67		627.3477	2	1.7	53	63	No
				EAEILSVLSHR	K	N	95.00%	44		418.5689	3	4.5	53	63	No
				LTEQSNTPLLLPLAAR	K	M	95.00%	81		869.0077	2	9.3	322	337	No
				NVVIAADGVLK	R	I	95.00%	41		549.8315	2	2.6	138	148	No
814	IPI00030320	DDX6	PROBABLE ATP-DEPENDENT RNA HELICASE DDX6.	GPVKPTGGPGGGGTQTQQQMNQLK	R	N	95.00%	64	M20: Oxidation	794.7391	3	7.5	23	46	No
				GVTQYYAYVTER	K	Q	95.00%	32		725.3594	2	6.6	308	319	No
815	IPI00031708; IPI00793664	FAH	FUMARYLACETOACETASE.; 33 KDA PROTEIN.	ASSVVVSGTPIR	R	R	95.00%	74		586.8364	2	0.8	163	174	No
				HLFTGPVLSK	K	H	95.00%	37		549.8199	2	0.6	48	57	No
				IGVAIGDQILDLSIIK	R	H	95.00%	83		834.5063	2	5.7	32	47	No
				LGEPIPISK	R	A	95.00%	25		477.2870	2	-1.1	212	220	No
				VFLQNLLSVSQAR	R	L	95.00%	86		737.9283	2	7.2	83	95	No
816	IPI00031812; IPI00385699; IPI00643351	YBX1	NUCLEASE SENSITIVE ELEMENT-BINDING PROTEIN 1.; 35 KDA PROTEIN.; PROTEIN.	EDGNEEDKENQGDETQGQQPPQR	R	R	95.00%	43		876.7128	3	6.9	257	279	No
				GAEAANVTGPGGVPVQGSK	K	Y	95.00%	122		848.4381	2	0.9	119	137	No
				RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	R	Q	95.00%	55	M14: Oxidation	810.6416	4	5.6	205	234	No
				SVGDGETVEFDVVEGEK	R	G	95.00%	118		898.4222	2	7.0	102	118	Yes
817	IPI00031820	FARSA	PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN.	LDAEPRPPPTQEAA	R	-	95.00%	32		746.3784	2	2.9	495	508	No
				SLQALGEVIEAELR	K	S	95.00%	112		764.4291	2	7.8	43	56	No
818	IPI00032179	SERPINC1	ANTITHROMBIN III VARIANT.	EQLQDMGLVDLFSPEK	K	S	95.00%	74	M6: Oxidation	932.9597	2	5.8	366	381	No
				EVPLNTIIFMGR	R	V	95.00%	58	M10: Oxidation	703.3842	2	6.5	447	458	No
				FRIEDGFSLK	R	E	95.00%	35		606.3278	2	4.3	356	365	No
				FRIEDGFSLK	R	E	95.00%	46		404.5536	3	2.0	356	365	No
				NDNDNIFLSPLSISTAFAMTK	K	L	95.00%	44	M19: Oxidation	1158.0760	2	9.2	104	124	No
				TSDQIHFFFAK	K	L	95.00%	53		670.8392	2	4.9	148	158	No
				VAEGTQVLELPFKGDDITMVLILPKPEK	R	S	95.00%	32	M19: Oxidation	1032.9120	3	9.8	296	323	No
819	IPI00033025; IPI00552502; IPI00816201	SEPT7	ISOFORM 1 OF SEPTIN-7.; CELL DIVISION CYCLE 10 ISOFORM 2.; ISOFORM 2 OF SEPTIN-7.	FEDYLNAESR	K	V	95.00%	49		622.2876	2	6.3	139	148	No
				VNIIPLIAK	K	A	95.00%	36		490.8316	2	4.4	188	196	No

820	IPI00043073; IPI00178745; IPI00298800; IPI00384414	GYPA	GLYCOPHORIN ERIK (STA) PRECURSOR.; GLYCOPHORIN MZ II-V.; GLYCOPHORIN A PRECURSOR.; GLYCOPHORIN ERIK I-IV PRECURSOR.	KSPSDVKPLPSPDTDVPLSSVEIENPETSDQ	K	-	95.00%	81		1103.2150	3	6.7	120	150	No
				SPSDVKPLPSPDTDVPLSSVEIENPETSDQ	K	-	95.00%	81		1060.5190	3	8.9	121	150	No
821	IPI00065491; IPI00748058	STAC3	ISOFORM 1 OF SH3 AND CYSTEINE-RICH DOMAIN-CONTAINING PROTEIN 3.; ISOFORM 2 OF SH3 AND CYSTEINE-RICH DOMAIN-CONTAINING PROTEIN 3.	EVLESPKPSFPAETR	K	Q	95.00%	42		843.9421	2	3.5	5	19	No
				ITVIDDSNEEWWR	K	G	95.00%	48		831.8998	2	9.3	274	286	No
				KVGLFPTDFLEEI	R	-	95.00%	52		754.4136	2	9.6	352	364	No
				NDPVFETLR	R	T	95.00%	42		545.7818	2	2.1	174	182	No
				VGFFPPNFIIR	K	V	95.00%	38		653.8730	2	5.2	293	303	No
				VGLFPTDFLEEI	K	-	95.00%	44		690.3630	2	5.9	353	364	No
822	IPI00075080; IPI00219941	OSBPL1A	ISOFORM B OF OXYSTEROL-BINDING PROTEIN-RELATED PROTEIN 1.; ISOFORM A OF OXYSTEROL-BINDING PROTEIN-RELATED PROTEIN 1.	ITMPVIFNEPLSFLQR	K	L	95.00%	30	M3: Oxidation	641.0193	3	8.5	51	66	No
				NDFSIWSILR	R	K	95.00%	66		625.8349	2	6.9	545	554	No
				NYFNLPDIY	R	-	95.00%	51		579.7809	2	5.8	942	950	No
				TGKPFNPLLGETYELVR	R	D	95.00%	46		645.3550	3	5.5	108	124	No
823	IPI00096066	SUCLG2	SUCCINYL-COA LIGASE [GDP-FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR.	EQIDIFEGIK	K	D	95.00%	32		596.3216	2	7.6	191	200	No
				ETYLAILMDR	R	S	95.00%	50	M8: Oxidation	620.8201	2	6.1	151	160	No
				FFVADTANEALEAAK	R	R	95.00%	72		798.9051	2	7.1	59	73	No
				ILNNSGLPITSAIDLEDAAK	K	K	95.00%	70		1028.0590	2	6.4	404	423	No
				ILNNSGLPITSAIDLEDAAKK	K	A	95.00%	37		728.4081	3	7.4	404	424	No
				INFDDNAEFR	K	Q	95.00%	58		620.7875	2	5.9	260	269	No
824	IPI00100247	TXNDC13	THIOREDOXIN DOMAIN-CONTAINING PROTEIN 13 PRECURSOR.	FFVTTLPAFFHAK	R	D	95.00%	54		509.2825	3	7.2	103	115	No
				VDVIQEPGLSGR	K	F	95.00%	48		635.3481	2	6.2	91	102	No
825	IPI00100292; IPI00168532; IPI00252412; IPI00744937; IPI00746278	NPEPL1; STX16	ISOFORM 1 OF PROBABLE AMINOPEPTIDASE NPEPL1.; ISOFORM 3 OF PROBABLE AMINOPEPTIDASE NPEPL1.; ISOFORM 2 OF PROBABLE AMINOPEPTIDASE NPEPL1.; 52 KDA PROTEIN.; 56 KDA PROTEIN.	ELGIIPTIIRDEELK	K	T	95.00%	43		870.0096	2	8.9	207	221	No
				ELGIIPTIIRDEELK	K	T	95.00%	38		580.3402	3	5.1	207	221	No
				HNSPSAAHFITR	R	L	95.00%	52		446.5641	3	3.8	86	97	No
826	IPI00101405; IPI00797614	FDPS	FARNESYL DIPHOSPHATE SYNTHASE.; FARNESYL PYROPHOSPHATE SYNTHETASE.	ATPEQYQILK	R	E	95.00%	42		595.8270	2	3.4	278	287	No
				VLTEDEMGHPEIGDAIAR	R	L	95.00%	76	M7: Oxidation	984.9779	2	7.1	27	44	No
827	IPI00105598	PSMD11	PROTEASOME 26S NON-ATPASE SUBUNIT 11 VARIANT (FRAGMENT).	AELRDDPIISTHLAK	R	L	95.00%	44		560.3112	3	2.8	311	325	No
				EQSILELGSLLAK	K	T	95.00%	65		700.9100	2	8.5	47	59	No
				IMLNTPEDVQALVSGK	K	L	95.00%	77	M2: Oxidation	865.9592	2	6.1	259	274	No
				LYDNLLEQNLIR	K	V	95.00%	52		752.4183	2	7.7	326	337	No
				TGQAAELGGLLK	K	Y	95.00%	69		579.3343	2	6.5	60	71	No
				VQIEHISSLIK	R	L	95.00%	70		633.8765	2	2.2	345	355	No
				VQIEHISSLIK	R	L	95.00%	34		422.9206	3	3.2	345	355	No
828	IPI00156689	VAT1	SYNAPTIC VESICLE MEMBRANE PROTEIN VAT-1 HOMOLOG.	GVDIVMDPLGGSDTAK	K	G	95.00%	88	M6: Oxidation	795.8921	2	4.8	256	271	No
				PAAPPAPGPGQLTLR	R	L	95.00%	44		721.9134	2	4.7	68	82	No
829	IPI00163230	COPS6	COP9 SIGNALOSOME COMPLEX SUBUNIT 6.	ASEAGEVPFNHEILR	K	E	95.00%	45		834.9256	2	5.2	244	258	No
				ASEAGEVPFNHEILR	K	E	95.00%	49		556.9528	3	4.8	244	258	No
				SQEGRPVQVIGALIGK	R	Q	95.00%	37		551.3243	3	4.6	60	75	No
830	IPI00164528	SNTA1	ALPHA-1-SYNTROPHIN.	GSVPYDAELSFALR	K	T	95.00%	82		762.8963	2	9.8	356	369	No
				HGVDTHLFSVESPQELAAWTR	R	Q	95.00%	72		794.0689	3	9.5	374	394	No
				VKDELQALLAATSTAGSQDIK	R	Q	95.00%	31		720.3954	3	6.7	275	295	No
831	IPI00165261; IPI00374338; IPI00794956	SCFD1	SEC1 FAMILY DOMAIN-CONTAINING PROTEIN 1.; VESICLE TRANSPORT-RELATED PROTEIN ISOFORM B.; VESICLE TRANSPORT-RELATED PROTEIN ISOFORM A VARIANT (FRAGMENT).	FGQDIISPLLSVK	R	E	95.00%	43		708.9147	2	7.9	51	63	No
				LIDLHTNVATAVLEHIK	R	A	95.00%	50		629.6995	3	6.5	331	347	No
				LIDLHTNVATAVLEHIK	R	A	95.00%	47		472.5262	4	5.7	331	347	No
				LTSAVSSLPELLEK	K	K	95.00%	53		743.9275	2	6.8	382	395	No
				SKLEDIANAALAASAVTQVAK	R	V	95.00%	37		691.0576	3	8.4	125	145	No
				SLLDIISDPDAGTPEDK	K	M	95.00%	93		893.4488	2	7.6	437	453	No

832	IPI00166866; IPI00386879	IGHA1	IGHA1 PROTEIN.; CDNA FLJ14473 FIS, CLONE MAMMA1001080, HIGHLY SIMILAR TO HOMO SAPIENSSNC73 PROTEIN (SNC73) MRNA.	DASGVTFTWTPSSGK	R	S	95.00%	68		770.8742	2	7.8	295	309	Yes
				NSLYLQMNSLR	K	V	95.00%	54	M7: Oxidation	677.8461	2	4.0	96	106	No
				QEPSQGTTTFAVTSILR	R	V	95.00%	99		918.4871	2	8.7	424	440	Yes
				QEPSQGTTTFAVTSILR	R	V	95.00%	59		612.6591	3	6.1	424	440	Yes
				TPLTATLSK	K	S	95.00%	32		931.5513	1	5.1	354	362	Yes
				TPLTATLSK	K	S	95.00%	42		466.2785	2	2.9	354	362	Yes
833	IPI00167515; IPI00745895	ZADH1	ISOFORM 1 OF ZINC-BINDING ALCOHOL DEHYDROGENASE DOMAIN-CONTAININGPROTEIN 1.; SIMILAR TO ZINC BINDING ALCOHOL DEHYDROGENASE, DOMAIN CONTAINING 1.	DKFEPGILQLSQWFK	K	E	95.00%	34		612.6656	3	6.2	224	238	No
				DVPYPPPLSPAIEAIQK	K	E	95.00%	32		918.0074	2	6.1	192	208	No
				GDFVTSFYWPWQTK	K	V	95.00%	47		881.4244	2	7.5	93	106	No
				MEEVYLPDNINEGQVQVR	R	T	95.00%	95	M1: Oxidation	1075.0250	2	8.4	25	42	No
				TLYLSVDPYMR	R	C	95.00%	36	M10: Oxidation	687.3463	2	5.2	43	53	No
834	IPI00168407	PDPR	HYPOTHETICAL PROTEIN DKFZP686J1643.	DSNLLLEDVTWK	K	Y	95.00%	39		716.8760	2	8.1	609	620	No
				INAGLNVIGIPSEIISPK	R	K	95.00%	30		918.0435	2	7.9	143	160	No
835	IPI00172450; IPI00172452; IPI00216378; IPI00296678; IPI00334344; IPI00336118; IPI00556423; IPI00646849	CAMK2G	ISOFORM 4 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II GAMMACHAIN.; CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II GAMMA ISOFORM 6.; CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II GAMMA ISOFORM 1.; CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II GAMMA ISOFORM 2.; ISOFORM 1 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II GAMMACHAIN.; CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II GAMMA ISOFORM 4.; ISOFORM 3 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II GAMMACHAIN.; CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE (CAM KINASE) II GAMMA.	AGAYDFPSPEWDTVTPEAK	K	N	95.00%	73		1040.9880	2	8.3	228	246	Yes
				DLKPENLLLASK	R	C	95.00%	48		670.8962	2	4.1	136	147	Yes
				DLKPENLLLASK	R	C	95.00%	41		447.5987	3	0.9	136	147	Yes
				FTDDYQLFEELGK	R	G	95.00%	70		802.8852	2	8.7	10	22	No
				FYFENLLSK	K	N	95.00%	45		580.8054	2	3.2	448	456	No
				NLINQMLTINPAK	K	R	95.00%	42	M6: Oxidation	743.4136	2	6.2	247	259	Yes
836	IPI00172636; IPI00430291; IPI00827573; IPI00827606; IPI00827625; IPI00827717; IPI00828081; IPI00828139; IPI00828178	CAMK2D	ISOFORM DELTA 6 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IIDELTA CHAIN.; ISOFORM DELTA 2 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IIDELTA CHAIN.; ISOFORM DELTA 10 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPEII DELTA CHAIN.; ISOFORM DELTA 7 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IIDELTA CHAIN.; ISOFORM DELTA 11 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPEII DELTA CHAIN.; ISOFORM DELTA 3 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IIDELTA CHAIN.; ISOFORM DELTA 4 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IIDELTA CHAIN.; ISOFORM DELTA 8 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IIDELTA CHAIN.; ISOFORM DELTA 9 OF CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IIDELTA CHAIN.	AGAYDFPSPEWDTVTPEAK	K	D	95.00%	73		1040.9880	2	8.3	228	246	Yes
				DLKPENLLLASK	R	S	95.00%	48		670.8962	2	4.1	136	147	No
				DLKPENLLLASK	R	S	95.00%	41		447.5987	3	0.9	136	147	No
				FTDEYQLFEELGK	R	G	95.00%	99		809.8925	2	7.9	10	22	No
				FYFENALSK	R	S	95.00%	42		559.7841	2	7.2	397	405	No
				LTQYMDGSGMPK	R	T	95.00%	46	M5: Oxidation, M10: Oxidation	680.3040	2	5.5	434	445	No

				VTEQLIEAINNGDFEAYTK	K	I	95.00%	102		1078.0420	2	9.6	353	371	No
837	IPI00179057; IPI00480142; IPI00643885; IPI00644450	CUL4B	ISOFORM 1 OF CULLIN-4B.; ISOFORM 2 OF CULLIN-4B.; 103 KDA PROTEIN.; 28 KDA PROTEIN.	SIFLFLDR	R	T	95.00%	30		505.7908	2	6.1	287	294	No
				TIDGILLLIER	K	E	95.00%	50		628.3891	2	5.9	328	338	No
838	IPI00179415; IPI00747748	PPP3CA	ISOFORM 1 OF SERINE/THREONINE-PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNITALPHA ISOFORM.; ISOFORM 2 OF SERINE/THREONINE-PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNITALPHA ISOFORM.	GLTPTGMLPSGVLSGGK	K	Q	95.00%	76	M7: Oxidation	794.4314	2	8.2	425	441	No
				IITEGASILR	R	Q	95.00%	55		536.8243	2	3.8	64	73	No
				LFEVGGSPANTR	K	Y	95.00%	69		624.3240	2	1.5	101	112	Yes
839	IPI00180675	TUBA1A	TUBULIN ALPHA-3 CHAIN.	AFVHWYVGEGMEEGEFSEAR	R	E	95.00%	47	M11: Oxidation	782.6827	3	8.1	403	422	Yes
				AVFVDLEPTVIDEVR	R	T	95.00%	84		851.4623	2	6.1	65	79	No
				AVFVDLEPTVIDEVR	R	T	95.00%	81		567.9778	3	6.8	65	79	Yes
				DVNAAIATIK	K	T	95.00%	36		1015.5870	1	7.7	327	336	No
				DVNAAIATIK	K	T	95.00%	73		508.2952	2	3.6	327	336	Yes
				EIIDLVLDR	K	I	95.00%	64		543.3175	2	5.7	113	121	Yes
				FDGALNVDLTEFQTNLVPYPR	R	I	95.00%	128		1205.1200	2	9.5	244	264	Yes
				FDGALNVDLTEFQTNLVPYPR	R	I	95.00%	64		803.7485	3	8.6	244	264	Yes
				IHFPLATYAPVISAEK	R	A	95.00%	94		878.9923	2	7.4	265	280	Yes
				IHFPLATYAPVISAEK	R	A	95.00%	78		586.3296	3	5.4	265	280	Yes
				LDHKFDLMYAK	R	R	95.00%	38	M8: Oxidation	698.8528	2	3.0	391	401	Yes
				LIGQIVSSITASLR	R	F	95.00%	102		729.4421	2	4.9	230	243	No
				NLDIERPTYTNLNR	R	L	95.00%	60		859.9495	2	4.9	216	229	Yes
				NLDIERPTYTNLNR	R	L	95.00%	50		573.6350	3	3.9	216	229	Yes
				QLFHPEQLITGK	R	E	95.00%	45		705.8943	2	4.2	85	96	Yes
				QLFHPEQLITGK	R	E	95.00%	40		470.9325	3	4.9	85	96	Yes
				QLFHPEQLITGKEDAANNYAR	R	G	95.00%	73		805.7444	3	5.1	85	105	Yes
				TIGGGDDSFNTFFSETGAGK	K	H	95.00%	105		1004.4600	2	8.9	41	60	No
				VGINYQPPTVVPGGDLAK	K	V	95.00%	84		912.9996	2	2.8	353	370	Yes
840	IPI00181231; IPI00783302	PTCD3	79 KDA PROTEIN.; PENTATRICOPEPTIDE REPEAT DOMAIN 3.	SELLNELMDSAK	R	V	95.00%	48	M8: Oxidation	683.3356	2	4.6	608	619	No
				VAVLQALASTVNR	K	D	95.00%	81		671.4022	2	8.4	68	80	No
				VEGTDVTGIEEVVIPK	K	K	95.00%	119		842.9621	2	9.0	46	61	No
841	IPI00185374; IPI00335069; IPI00787055	PSMD12	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 12.; SIMILAR TO PROTEASOME 26S NON-ATPASE SUBUNIT 12 ISOFORM 2.; SIMILAR TO 26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 12.	DPNNLLNDWSQK	K	L	95.00%	67		722.3518	2	6.1	420	431	No
				LAGIINFQR	R	P	95.00%	48		516.3056	2	3.0	409	417	No
				LAGIINFQRPK	R	D	95.00%	33		628.8805	2	4.1	409	419	No
				LFTTMELMR	K	W	95.00%	45	M5: Oxidation, M8: Oxidation	587.2888	2	4.2	308	316	No
				LNSLMSLVNK	K	T	95.00%	34	M5: Oxidation	567.8156	2	3.7	432	441	No
				LQEVIETLLSLEK	R	Q	95.00%	58		757.9434	2	6.9	40	52	No
				VEFILEQMR	R	L	95.00%	75	M8: Oxidation	590.8077	2	3.4	183	191	No
				WSTLVEDYGMELR	R	K	95.00%	82	M10: Oxidation	807.8840	2	7.8	317	329	No
842	IPI00216003	CUL5	CULLIN HOMOLOG 5.	AVVNDATIFK	K	L	95.00%	39		539.3030	2	3.3	432	441	No
				IHQALKEDILEFIK	K	Q	95.00%	58		566.3286	3	3.6	118	131	No
				ISNAQLQTELVEILK	K	N	95.00%	93		849.9925	2	7.6	786	800	No
				LATELPDAELRR	K	T	95.00%	31		461.9264	3	2.8	678	689	No
				QVLLYEPQVNSPK	R	D	95.00%	52		757.9156	2	0.9	703	715	No
				TLWSLVAFPK	R	L	95.00%	43		581.3409	2	5.8	690	699	No
				VFVSLPTELEDLIPEVEEFYKK	K	N	95.00%	41		875.4703	3	7.6	600	621	No
				VSEDLNQAFK	K	E	95.00%	49		575.7922	2	1.7	559	568	No
				YVEQLLTLFNR	K	F	95.00%	79		698.3899	2	6.0	397	407	No
843	IPI00216470	PIP5K2B	ISOFORM 1 OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE TYPE-2 BETA.	DVEFLAQLK	R	I	95.00%	57		531.7991	2	6.2	267	275	No
				FGIDDQDYQNSVTR	R	S	95.00%	77		829.3807	2	4.6	110	123	No
844	IPI00216694	PLS3	PLASTIN 3.	LSPEELLLR	K	W	95.00%	59		535.3174	2	1.0	267	275	No
				MINLSVPDTIDER	K	A	95.00%	44	M1: Oxidation	759.8835	2	7.6	169	181	No
845	IPI00216951	DARS	ASPARTYL-TRNA SYNTHETASE, CYTOPLASMIC.	ESIVDVEGVVR	K	K	95.00%	41		601.3300	2	7.7	111	121	No
				IYVISLAEPR	K	L	95.00%	35		580.8411	2	5.5	142	151	No
				LPLQLDDAVRPEAEGEEEGR	R	A	95.00%	34		741.7048	3	4.2	152	171	No

846	IPI00218015; IPI00329133	LDHD	ISOFORM 2 OF PROBABLE D-LACTATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR.; ISOFORM 1 OF PROBABLE D-LACTATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR.	AVLDPQGLMNPGK	K	V	95.00%	75	M9: Oxidation	678.3566	2	4.2	470	482	No
				DNVLNLEVVLPDGR	R	L	95.00%	70		776.9277	2	8.9	185	198	No
847	IPI00218971; IPI00788806; IPI00790255; IPI00794806	PPM2C	[PYRUVATE DEHYDROGENASE [LIPOAMIDE]]-PHOSPHATASE 1, MITOCHONDRIALPRECURSOR.; PYRUVATE DEHYDROGENASE PHOSPHATASE PRECURSOR.; 65 KDA PROTEIN.; 67 KDA PROTEIN.	HAVGNNEFGTVDHER	R	L	95.00%	56		561.2633	3	3.6	485	499	No
				MLSLPEELAR	K	M	95.00%	38	M1: Oxidation	587.8137	2	4.4	503	512	No
				MSSVFEDQNAATHLIR	K	H	95.00%	40	M1: Oxidation	612.2993	3	3.4	469	484	No
				VIESGPDQLNDNEYTK	R	F	95.00%	124		911.4344	2	5.6	368	383	No
848	IPI00219575; IPI00794082	BLMH	BLEOMYCIN HYDROLASE.; 32 KDA PROTEIN.	GEISATQDVMMEEIFR	K	V	95.00%	82	M10: Oxidation, M11: Oxidation	944.4323	2	5.2	27	42	No
				IGPITPLEFYR	K	E	95.00%	42		653.3694	2	7.8	245	255	No
				TLYNNQPIDFLK	K	K	95.00%	60		733.3904	2	2.5	298	309	No
849	IPI00219613; IPI00787827	PITRM1	ISOFORM 1 OF PRESEQUENCE PROTEASE, MITOCHONDRIAL PRECURSOR.; ISOFORM 2 OF PRESEQUENCE PROTEASE, MITOCHONDRIAL PRECURSOR.	EDTNNLFSVQFR	R	T	95.00%	44		735.3607	2	7.5	82	93	No
				MTAQELANGIPDSGHLYASIR	K	A	95.00%	45	M1: Oxidation	754.0452	3	7.3	706	726	No
850	IPI00220150	IDH3G	ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT GAMMA, MITOCHONDRIAL PRECURSOR.	AVLASMDNENMHTPDIGGQGTTSEAIQDVIR	K	H	95.00%	92	M6: Oxidation, M11: Oxidation	1101.5240	3	8.8	351	381	No
				ENTEGEYSSLEHESVAGVVESLK	R	I	95.00%	59		831.7319	3	6.9	168	190	No
				HKDIDILIVR	R	E	95.00%	46		407.9170	3	2.6	158	167	No
				HTVTMIPGDGIGPELMLHVK	R	S	95.00%	39	M5: Oxidation, M16: Oxidation	726.3787	3	4.8	55	74	No
851	IPI00220396	PHKG1	PFKFB2 PROTEIN.	DLKPENILLDDNMNIK	R	L	95.00%	62	M13: Oxidation	950.9925	2	4.2	153	168	No
				DLKPENILLDDNMNIK	R	L	95.00%	31	M13: Oxidation	634.3328	3	7.2	153	168	No
				LIDAYAFR	R	I	95.00%	51		484.7658	2	3.3	349	356	No
				VIDVTGGGSFSPEEVR	K	E	95.00%	107		824.9194	2	7.6	50	65	No
				YTAEEALAHPFFQQYLVEEVR	R	H	95.00%	83		847.4275	3	8.4	280	300	No
852	IPI00220637; IPI00514587	SARS	SERYL-TRNA SYNTHETASE, CYTOPLASMIC.; SERYL-TRNA SYNTHETASE.	EIGNLLHPSVPISNDEDVDNKVER	R	I	95.00%	82		897.1276	3	8.8	134	157	No
				LLIDEAILK	R	C	95.00%	36		514.3273	2	5.9	108	116	No
				VLDLDLFR	M	V	95.00%	62		495.7872	2	4.1	2	9	No
853	IPI00249656	LOC347273	HYPOTHETICAL PROTEIN LOC347273.	SVQIDLLK	K	L	95.00%	37		458.2825	2	6.1	67	74	No
				VASIVDSVQASQK	K	R	95.00%	63		666.3639	2	2.2	40	52	No
854	IPI00257508	DPYSL2	DIHYDROPYRIMIDINASE-RELATED PROTEIN 2.	DIGAIAQVHAENGDIIAEEQQR	R	I	95.00%	55		793.0644	3	1.1	190	211	No
				GSPLVVISQGK	R	I	95.00%	48		542.8240	2	3.0	441	451	No
				ILDLGITGPEGHVLSRPEEVEAEAVNR	R	A	95.00%	46		967.5173	3	8.3	212	238	No
				ILDLGITGPEGHVLSRPEEVEAEAVNR	R	A	95.00%	35		725.8868	4	4.1	212	238	No
				IVLEDGTLHVTEGSGR	K	Y	95.00%	82		841.9437	2	4.8	452	467	No
				IVLEDGTLHVTEGSGR	K	Y	95.00%	42		561.6316	3	4.6	452	467	No
				IVNDDQSFYADIYMEDGLIK	K	Q	95.00%	99	M14: Oxidation	1183.0590	2	7.9	24	43	No
				NLHQSGFSLSGAQIDDNIPR	R	R	95.00%	44		723.6973	3	3.4	533	552	No
				QIGENLIVPGGVK	K	T	95.00%	47		662.3886	2	4.2	44	56	No
855	IPI00291016	NDUFV3	NADH-UBIQUINONE OXIDOREDUCTASE FLAVOPROTEIN 3 ISOFORM A PRECURSOR.	GSPAPAVLAEEAR	K	A	95.00%	35		634.3391	2	4.5	305	317	No
				TLLQKPHVDITDPEKPHQPK	K	K	95.00%	29		581.0749	4	6.0	209	228	No
856	IPI00291262; IPI00400826; IPI00795633	CLU	CLUSTERIN PRECURSOR.; CLUSTERIN ISOFORM 1.; 52 KDA PROTEIN.	ASSIIDELFQDR	R	F	95.00%	86		697.3569	2	6.8	183	194	No
				ELDESLQVAER	R	L	95.00%	51		644.8249	2	2.7	326	336	No
				VTTVASHTSDSDVPSGVTEVVVK	R	L	95.00%	46		772.0686	3	5.5	386	408	No
857	IPI00291510	IMPDH2	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 2.	DKYPNLQVIGGNVVTAAQAK	K	N	95.00%	65		696.0538	3	7.7	292	311	No
				GKLPIVNEDDELVAIIAR	K	T	95.00%	43		655.7095	3	5.4	207	224	No
				KYEQGFITDPVVLSPK	K	D	95.00%	108		910.9993	2	5.8	109	124	No
				KYEQGFITDPVVLSPK	K	D	95.00%	29		607.6675	3	3.8	109	124	No
				LPIVNEDDELVAIIAR	K	T	95.00%	78		890.5043	2	8.4	209	224	No
				NLIDAGVDALR	K	V	95.00%	62		578.8222	2	3.3	312	322	No

				REDLVVAPAGITLK	K	E	95.00%	33		494.6306	3	4.6	182	195	No
				RFGVPVIADGGIQNVGHIAK	R	A	95.00%	52		683.3890	3	5.2	356	375	No
858	IPI00291972	RTN4IP1	ISOFORM 1 OF RETICULON-4-INTERACTING PROTEIN 1, MITOCHONDRIALPRECURSOR.	IKGEEFPLTLGR	K	D	95.00%	50		680.3893	2	5.1	110	121	No
				LGADDVIDYK	K	S	95.00%	37		554.7811	2	1.2	247	256	No
859	IPI00293307	ADFP	ADIPOPHILIN.	LPILNQPSTQIVANAK	R	G	95.00%	101		854.0024	2	9.6	94	109	No
				SQQTISQLHSTVHLIEFAR	K	K	95.00%	31		732.3962	3	7.1	246	264	No
				SVVSGSINTVLGSR	K	M	95.00%	84		688.3847	2	5.2	154	167	No
860	IPI00293616	DDX3Y	ATP-DEPENDENT RNA HELICASE DDX3Y.	HVINFDLPSDIEEYVHR	R	I	95.00%	63		695.0181	3	6.8	510	526	No
				LEQELFSGGNTGINFEK	R	Y	95.00%	63		941.9700	2	7.1	144	160	No
861	IPI00293655	DDX1	ATP-DEPENDENT RNA HELICASE DDX1.	DQLSVLENGVDIVVGTPGR	R	L	95.00%	58		984.5278	2	3.7	331	349	No
				DQLSVLENGVDIVVGTPGR	R	L	95.00%	36		656.6883	3	4.5	331	349	No
				EAQTSFLHLGYLPNQLFR	K	T	95.00%	31		712.0474	3	8.5	721	738	No
				ELLIIGGVAAR	R	D	95.00%	79		556.3480	2	3.5	320	330	No
				GHVDILAPTVQELAALEK	K	E	95.00%	74		952.5336	2	5.1	703	720	No
				GHVDILAPTVQELAALEK	K	E	95.00%	57		635.3604	3	8.3	703	720	No
				GIDIHGVPYVINVTLPDEK	R	Q	95.00%	37		693.7146	3	7.3	578	596	No
				TGAFSIPVIQIVYETLK	K	D	95.00%	43		940.0405	2	7.9	53	69	No
862	IPI00294158	BLVRA	BILIVERDIN REDUCTASE A PRECURSOR.	FGFPAFSGISR	R	L	95.00%	66		593.3119	2	8.6	162	172	No
				FGVVVVGVGR	K	A	95.00%	81		494.8038	2	5.5	9	18	No
				NPHPSSAFLNLIGFVSR	R	R	95.00%	61		619.3362	3	6.1	29	45	No
				SGSLENVPNVGVNK	K	N	95.00%	83		707.3730	2	3.1	235	248	No
863	IPI00295992; IPI00643435; IPI00646144	ATAD3A	ISOFORM 2 OF ATPASE FAMILY AAA DOMAIN-CONTAINING PROTEIN 3A.; ISOFORM 1 OF ATPASE FAMILY AAA DOMAIN-CONTAINING PROTEIN 3A.; ATPASE FAMILY, AAA DOMAIN CONTAINING 3A.	ATLNAFLYR	R	T	95.00%	49		534.7995	2	6.5	431	439	No
				GLLLFVDEADAFLR	R	K	95.00%	87		789.9370	2	8.1	405	418	No
				ITVLEALR	R	H	95.00%	52		457.7904	2	6.0	291	298	No
864	IPI00297982	EIF2S3	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 SUBUNIT 3.	IVSLFAEHNDLQYAAPGGLIGVGTK	K	I	95.00%	62		857.4665	3	8.6	318	342	No
				NEVLMVNIGSLSTGGR	K	V	95.00%	49	M5: Oxidation	831.9359	2	9.3	401	416	No
				VGQEIEVRPGIVSK	K	D	95.00%	46		755.9364	2	3.6	290	303	No
865	IPI00298887; IPI00306436; IPI00412752; IPI00784414	STAT3	88 KDA PROTEIN.; ISOFORM DEL-701 OF SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 3.; SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 3 ISOFORM 3.; ISOFORM 1 OF SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 3.	GLSIEQLTTLAEK	R	L	95.00%	95		701.8982	2	6.4	522	534	No
				LLQTAATAAQQGGQANHPTAAVVTEK	R	Q	95.00%	61		859.4565	3	4.2	115	140	No
				SIVSELAGLLSAMEYVQK	R	T	95.00%	54	M13: Oxidation	652.0171	3	7.6	219	236	No
866	IPI00299240; IPI00514837; IPI00642897	CACNA1S	VOLTAGE-DEPENDENT L-TYPE CALCIUM CHANNEL SUBUNIT ALPHA-1S.; CALCIUM CHANNEL, VOLTAGE-DEPENDENT, L TYPE, ALPHA 1S SUBUNIT.; CALCIUM CHANNEL, VOLTAGE-DEPENDENT, L TYPE, ALPHA 1S SUBUNIT.	LLDQVIPPIGDDEVTVGK	K	F	95.00%	47		954.5268	2	6.5	1505	1522	No
				TGGLFGQVDNFLER	R	T	95.00%	62		776.8970	2	6.4	1601	1614	No
867	IPI00299571; IPI00644989	PDIA6	ISOFORM 2 OF PROTEIN DISULFIDE-ISOMERASE A6 PRECURSOR.; ISOFORM 1 OF PROTEIN DISULFIDE-ISOMERASE A6 PRECURSOR.	ALDLFSDNAPPPELLEIINEDIAK	R	R	95.00%	62		879.8023	3	9.3	317	340	No
				GSFSEQGINEFLR	K	E	95.00%	72		742.3647	2	2.4	374	386	No
				GSTAPVGGGAFPTIVER	R	E	95.00%	102		808.4302	2	5.0	445	461	No
				LAAVDATVNQVLASR	K	Y	95.00%	121		764.4330	2	5.7	217	231	No
				NSYLEVLLK	R	L	95.00%	51		539.8149	2	6.5	366	374	No
				TGEAIVDAALSALR	R	Q	95.00%	95		693.8871	2	4.9	119	132	No
868	IPI00303120	TMEM143	TRANSMEMBRANE PROTEIN 143.	DTPLEGLEQLLPELK	K	V	95.00%	31		847.9717	2	8.0	256	270	No
				EALLAHSFLAR	K	R	95.00%	37		614.3490	2	4.2	368	378	No
				LLIQEFHSSPAEK	R	A	95.00%	46		749.9040	2	6.3	85	97	No
				LQALYDPINPDRETLDQPSLTDPQR	R	L	95.00%	73		965.8290	3	7.8	122	146	No
				SEVENWLLAK	R	S	95.00%	36		594.8203	2	5.3	396	405	No
				SFKDTPLEGLEQLLPELK	K	V	95.00%	38		686.3823	3	6.8	253	270	No
				STSNNSELLSALALR	R	A	95.00%	73		788.4269	2	7.4	346	360	No
869	IPI00303200	TMOD4	TROPOMODULIN-4.	EALLQYLEQQALEVK	R	E	95.00%	102		887.9922	2	9.8	66	80	No
				EALLQYLEQQALEVK	R	E	95.00%	71		592.3290	3	6.7	66	80	No
				ERDDLVPFTGEK	K	K	95.00%	55		703.3555	2	4.7	81	92	No

				FGYHFTQQGPR	R	A	95.00%	43		669.3275	2	5.9	315	325	No
				SGDPIANAVADMLR	R	E	95.00%	58	M12: Oxidation	723.3607	2	5.2	236	249	No
				YKPVPDEPPNPTNIEEILKR	K	V	95.00%	60		783.7595	3	7.3	170	189	No
				YKPVPDEPPNPTNIEEILKR	K	V	95.00%	35		588.0694	4	3.6	170	189	No
				YRDIDEDEILR	K	T	95.00%	44		718.8576	2	3.5	11	21	No
				YRDIDEDEILR	K	T	95.00%	55		479.5743	3	3.4	11	21	No
870	IPI00304803	GMPR	GMP REDUCTASE 1.	GDVENTILDILGGLR	K	S	95.00%	90		792.9401	2	7.7	299	313	No
				MTSILEAVPQVK	K	F	95.00%	63	M1: Oxidation	666.3705	2	6.6	113	124	No
				TVEVPYKGDVENTILDILGGLR	K	S	95.00%	59		801.1094	3	6.0	292	313	No
871	IPI00329600; IPI00641681	SCCPDH	PROBABLE SACCHAROPINE DEHYDROGENASE.; SACCHAROPINE DEHYDROGENASE.	GYSIPFMGSDVSVVR	K	R	95.00%	55	M7: Oxidation	815.4083	2	8.7	74	88	No
				NVSNLKPVPLIGPK	R	L	95.00%	47		738.4546	2	4.2	215	228	No
				SAIYGFGDQSNLR	K	K	95.00%	64		714.3539	2	5.6	199	211	No
872	IPI00329633	TARS	THREONYL-TRNA SYNTHETASE, CYTOPLASMIC.	GAYIYNALIEFIR	K	S	95.00%	49		771.9263	2	8.3	349	361	No
				IYGISFPDPK	R	M	95.00%	44		568.8062	2	4.6	297	306	No
873	IPI00329653; IPI00384529; IPI00807589; IPI00807621; IPI00807645	COBL	ISOFORM 5 OF PROTEIN CORDON-BLEU.; ISOFORM 1 OF PROTEIN CORDON-BLEU.; ISOFORM 2 OF PROTEIN CORDON-BLEU.; ISOFORM 3 OF PROTEIN CORDON-BLEU.; ISOFORM 4 OF PROTEIN CORDON-BLEU.	DNIAGEELELSK	R	S	95.00%	73		659.3334	2	3.8	200	211	No
				SLTLGPSLSLGSISGVSVK	R	S	95.00%	76		901.5266	2	9.9	276	294	No
				VSLGSQIDLQK	K	K	95.00%	65		594.3372	2	2.5	320	330	No
874	IPI00333619; IPI00394758	ALDH3A2	ISOFORM 1 OF FATTY ALDEHYDE DEHYDROGENASE.; ISOFORM 2 OF FATTY ALDEHYDE DEHYDROGENASE.	EFYGENIKESPDYER	K	I	95.00%	47		938.4245	2	0.5	267	281	No
				FDHIFYTGNTAVGK	R	I	95.00%	42		785.3921	2	3.9	178	191	No
				IAFGGETDEATR	K	Y	95.00%	64		633.8037	2	2.2	300	311	No
				NVDEAINFINER	K	E	95.00%	90		717.3589	2	5.3	344	355	No
				VMQEEIFGPILPIVPVK	K	N	95.00%	44	M2: Oxidation	963.0504	2	5.5	327	343	No
				VMQEEIFGPILPIVPVK	K	N	95.00%	26	M2: Oxidation	642.3692	3	4.9	327	343	No
				YIAPTVLTDVDPK	R	T	95.00%	52		716.3961	2	7.4	312	324	No
875	IPI00383947	KBTBD5	ISOFORM 1 OF KELCH REPEAT AND BTB DOMAIN-CONTAINING PROTEIN 5.	EIAYAAGATFLPVR	R	L	95.00%	70		739.9085	2	5.7	599	612	No
				ILPGILNDTLR	R	F	95.00%	32		612.8747	2	7.9	301	311	No
				WAPFEAFPQER	K	S	95.00%	34		689.3383	2	6.9	537	547	No
876	IPI00396485; IPI00472724	EEF1A1	ELONGATION FACTOR 1-ALPHA 1.; EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 ALPHA-LIKE 3.	EHALLAYTLGVK	R	Q	95.00%	74		657.8776	2	3.8	135	146	Yes
				EHALLAYTLGVK	R	Q	95.00%	44		438.9206	3	3.1	135	146	Yes
				IGGIGTVPVGR	K	V	95.00%	35		1025.6170	1	5.6	256	266	Yes
				IGGIGTVPVGR	K	V	95.00%	90		513.3107	2	2.6	256	266	Yes
				LPLQDVYK	R	I	95.00%	39		975.5573	1	5.8	248	255	Yes
				LPLQDVYK	R	I	95.00%	61		488.2806	2	1.8	248	255	Yes
				QLIVGVNK	K	M	95.00%	42		870.5441	1	3.1	147	154	Yes
				QLIVGVNK	K	M	95.00%	37		435.7753	2	1.6	147	154	Yes
				QTVAVGVIK	R	A	95.00%	38		914.5709	1	3.7	431	439	No
				QTVAVGVIK	R	A	95.00%	43		457.7881	2	0.9	431	439	No
				STTTGHLIYK	K	C	95.00%	53		560.8058	2	3.1	21	30	Yes
				THINIVVIGHVDSGK	K	S	95.00%	58		530.3015	3	4.8	6	20	Yes
				VETGVLKPGMVVTFAPVNVTTEVK	R	S	95.00%	39	M10: Oxidation	844.4707	3	6.8	267	290	No
				YYVTIIDAPGHR	K	D	95.00%	32		702.8706	2	4.1	85	96	No
				YYVTIIDAPGHR	K	D	95.00%	60		468.9156	3	2.6	85	96	No
877	IPI00399036; IPI00411639; IPI00413108; IPI00553164; IPI00790580	LOC388524; RPSA; RPSAP15; hCG_1984468	SIMILAR TO 40S RIBOSOMAL PROTEIN SA (P40) (34/67 KDA LAMININ RECEPTOR)(COLON CARCINOMA LAMININ-BINDING PROTEIN) (NEM/1CHD4) (MULTIDRUGRESISTANCE-ASSOCIATED PROTEIN MGR1-AG) ISOFORM 1.; LAMININ RECEPTOR-LIKE PROTEIN LAMRL5.; RIBOSOMAL PROTEIN SA.; 40S RIBOSOMAL PROTEIN SA.; 16 KDA PROTEIN.	AIVAIENPADVSVISSR	R	N	95.00%	116		870.9829	2	4.9	64	80	No
				FAAATGATPIAGR	K	F	95.00%	66		602.3301	2	2.9	90	102	Yes
				FLAAGTHLGGTNLDFQMEQYIYK	K	R	95.00%	44	M17: Oxidation	878.4366	3	8.9	18	40	No
				FTPGTFTNQIQAAFR	R	E	95.00%	67		849.9417	2	8.8	103	117	No
				KSDGIYIINLK	R	R	95.00%	47		632.3720	2	3.8	42	52	No
				SDGIYIINLK	K	R	95.00%	46		568.3248	2	4.5	43	52	No

878	IPI00413451	SERPINB6	HYPOTHETICAL PROTEIN DKFZP686I04222.	ELNMIIMLPDETTDLR	K	T	95.00%	67	M4: Oxidation, M7: Oxidation	968.4803	2	6.0	260	275	No
				GNTAAQMAQILSFNK	K	S	95.00%	105	M7: Oxidation	805.4084	2	5.1	80	94	No
				IAELLSPGSVDPLTR	K	L	95.00%	76		784.4459	2	9.0	179	193	No
				LVLVNAVYFR	R	G	95.00%	76		597.3601	2	6.4	194	203	No
				NLGMTDAFELGK	R	A	95.00%	57	M4: Oxidation	656.3213	2	7.0	321	332	No
				SGGGGDIHQGFQSLLTEVNK	K	T	95.00%	82		1022.5180	2	8.7	95	114	No
				SGGGGDIHQGFQSLLTEVNK	K	T	95.00%	60		682.0129	3	6.2	95	114	No
879	IPI00418497; IPI00656071	TIMM50	ISOFORM 2 OF IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM50,MITOCHONDRIAL PRECURSOR.; ISOFORM 1 OF IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM50,MITOCHONDRIAL PRECURSOR.	IPDEFDNDPILVQQLR	K	R	95.00%	96		956.5023	2	7.7	201	216	No
				TIALNGVEDVR	K	T	95.00%	65		593.8273	2	2.9	388	398	No
				VLLDLSAFLK	R	T	95.00%	51		559.8479	2	4.7	378	387	No
880	IPI00419237; IPI00789806	LAP3	ISOFORM 1 OF CYTOSOL AMINOPEPTIDASE.; ISOFORM 2 OF CYTOSOL AMINOPEPTIDASE.	EKEDDVPQFTSAGENFDK	K	L	95.00%	41		685.9792	3	3.4	44	61	No
				ETLNISGPPLK	R	A	95.00%	41		584.8354	2	4.3	69	79	No
				GITFDSGGISIK	K	A	95.00%	56		597.8251	2	4.4	283	294	No
				GSPNANEPPLVFVGK	K	G	95.00%	60		763.4098	2	6.8	268	282	No
				GVLFASGQNLAR	K	Q	95.00%	75		616.8442	2	4.4	189	200	No
				LFEASIETGDR	K	V	95.00%	69		619.3094	2	3.7	418	428	No
				TFYGLHQDFPSVVLVGLGK	R	K	95.00%	39		693.0483	3	8.1	85	103	No
				TLIEFLLR	R	F	95.00%	54		502.8130	2	3.6	506	513	No
881	IPI00419263; IPI00639841; IPI00827665	PECI	PEROXISOMAL 3,2-TRANS-ENOYL-COA ISOMERASE.; PEROXISOMAL 3,2-TRANS-ENOYL-COA ISOMERASE.; 22 KDA PROTEIN.	PGVFDLINK	K	A	95.00%	45		501.7858	2	1.2	47	55	No
				QNYVDLVSSLSPSLESSSQVEPGTDRK	R	S	95.00%	98		974.8245	3	8.4	74	100	No
				STGFETLVVTSEDGITK	K	I	95.00%	33		892.4596	2	8.1	101	117	No
				WDAWNALGSLPK	K	E	95.00%	63		679.3539	2	6.8	58	69	No
882	IPI00423426; IPI00423430	EPM2A	ISOFORM 1 OF LAFORIN.; ISOFORM 3 OF LAFORIN.	HTTDFYFNIAGHQAMHYSR	K	I	95.00%	48	M15: Oxidation	578.7660	4	4.4	141	159	No
				RPAVYIDEEALAR	K	A	95.00%	42		751.9065	2	5.5	300	312	No
				RPAVYIDEEALAR	K	A	95.00%	61		501.6059	3	3.5	300	312	No
883	IPI00427586; IPI00436355	PRKG1	CGMP-DEPENDENT PROTEIN KINASE 1, ALPHA ISOZYME.; CGMP-DEPENDENT PROTEIN KINASE 1, BETA ISOZYME.	DLKPENLILDHR	R	G	95.00%	35		488.2741	3	3.2	484	495	No
				LADVLEETHYENGEYIIR	K	Q	95.00%	42		722.0283	3	6.1	233	250	No
				LSDFNIIDTLGVGGFGR	K	V	95.00%	105		890.9719	2	6.9	372	388	No
				SVPTFQSLPEEILSK	K	L	95.00%	48		837.9568	2	6.2	233	247	No
884	IPI00444179; IPI00787636	LSDP5	LIPID STORAGE DROPLET PROTEIN 5.; LIPID STORAGE DROPLET PROTEIN 5.	LPFLQQPSETVVTSAK	K	D	95.00%	50		872.9868	2	9.9	104	119	No
				SVDALQTAFADAR	R	C	95.00%	73		682.8483	2	5.5	322	334	No
885	IPI00449049	PARP1	POLY [ADP-RIBOSE] POLYMERASE 1.	TTNFAGILSQGLR	R	I	95.00%	93		689.3828	2	6.1	866	878	No
				VVSEDFLQDVSASTK	R	S	95.00%	113		812.9142	2	8.3	453	467	No
886	IPI00465233; IPI00745266	EIF3S6IP	DJ1014D13.1 PROTEIN.; EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 6-INTERACTINGPROTEIN.	LAGFLDLTEQEFR	K	I	95.00%	81		769.9040	2	9.4	475	487	No
				VFSDEVQQQAQLSTIR	K	S	95.00%	94		924.9840	2	7.8	446	461	No
887	IPI00465430; IPI00644712	XRCC6	70 KDA PROTEIN.; ATP-DEPENDENT DNA HELICASE 2 SUBUNIT 1.	DSLIFLVDASK	R	A	95.00%	64		604.3366	2	6.5	36	46	No
				FDDPGLMLMGFKPLVLLK	R	K	95.00%	33	M7: Oxidation, M9: Oxidation	689.3774	3	4.4	340	357	No
				IISSDRDLLAVVFYGTEK	K	D	95.00%	46		676.0370	3	4.6	75	92	No
				ILELDQFK	R	G	95.00%	41		503.2873	2	4.4	116	123	No
				NIYVLQELDNPGAK	K	R	95.00%	76		787.4211	2	7.4	101	114	No
				SDSFENPVLQQHFR	R	N	95.00%	88		852.4143	2	3.9	475	488	No
				TFNTSTGGLLLPSDTKR	R	S	95.00%	41		603.3269	3	5.2	302	318	No
888	IPI00477616	PPP2R4	REGULATORY SUBUNIT PR 53 OF PROTEIN PHOSPHATASE 2A ISOFORM B.	FGSLLPIHPVTSG	K	-	95.00%	59		662.8722	2	7.6	361	373	No
				VDDQIAIVFK	R	V	95.00%	60		574.3264	2	7.3	224	233	No
889	IPI00479186	PKM2	ISOFORM M2 OF PYRUVATE KINASE ISOZYMES M1/M2.	APIIAVTR	R	N	95.00%	35		840.5320	1	1.4	448	455	Yes
				APIIAVTR	R	N	95.00%	62		420.7706	2	3.1	448	455	Yes
				DPVQEAWAEDVDLR	K	V	95.00%	97		821.8951	2	6.6	476	489	Yes
				DPVQEAWAEDVDLR	K	V	95.00%	65		548.2656	3	5.9	476	489	Yes
				EAEAAIYHLQLFEELR	R	R	95.00%	52		644.6713	3	6.0	384	399	No
				EAEAAIYHLQLFEELRR	R	L	95.00%	59		696.7051	3	5.7	384	400	No

FDEILEASDGIMVAR	R	G	95.00%	120	M12: Oxidation	841.4142	2	5.8	280	294	Yes
FGVEQDVDMVFASFIR	K	K	95.00%	121	M9: Oxidation	938.4593	2	8.4	231	246	Yes
FGVEQDVDMVFASFIR	K	K	95.00%	67	M9: Oxidation	625.9751	3	7.8	231	246	Yes
FGVEQDVDMVFASFIR	K	K	95.00%	135		930.4608	2	7.4	231	246	Yes
FGVEQDVDMVFASFIR	K	K	95.00%	63		620.6429	3	7.0	231	246	Yes
FGVEQDVDMVFASFIRK	K	A	95.00%	39	M9: Oxidation	668.6734	3	7.2	231	247	Yes
GADFLVTEVENGGSLGSK	K	K	95.00%	123		890.4465	2	4.8	189	206	Yes
GADFLVTEVENGGSLGSK	K	K	95.00%	62		593.9673	3	5.4	189	206	Yes
GADFLVTEVENGGSLGSKK	K	G	95.00%	101		954.4987	2	9.5	189	207	Yes
GADFLVTEVENGGSLGSKK	K	G	95.00%	57		636.6658	3	5.3	189	207	Yes
GDLGIEIPAEK	R	V	95.00%	48		1141.6160	1	4.6	295	305	Yes
GDLGIEIPAEK	R	V	95.00%	69		571.3098	2	0.9	295	305	Yes
GDVVIVLTGWRPGSGFTNTMR	K	V	95.00%	59	M20: Oxidation	760.3990	3	9.1	506	526	Yes
GDYPLEAVR	K	M	95.00%	48		1019.5200	1	3.7	368	376	Yes
GDYPLEAVR	K	M	95.00%	52		510.2629	2	1.7	368	376	Yes
GPEIR	K	T	95.00%	30		571.3227	1	4.0	116	120	Yes
GSGTAEVELK	K	K	95.00%	54		495.7619	2	5.2	126	135	Yes
GSGTAEVELKK	K	G	95.00%	53		559.8099	2	5.5	126	136	Yes
GVNLPGAAVDLPAVSEK	K	D	95.00%	125		818.9558	2	7.7	208	224	Yes
GVNLPGAAVDLPAVSEK	K	D	95.00%	59		546.3052	3	5.4	208	224	Yes
GVNLPGAAVDLPAVSEKDIQDLK	K	F	95.00%	92		1175.1470	2	7.8	208	230	Yes
GVNLPGAAVDLPAVSEKDIQDLK	K	F	95.00%	64		783.7662	3	6.9	208	230	Yes
IENHEGVR	K	R	95.00%	45		477.2463	2	4.5	271	278	Yes
ITLDNAYMEK	K	C	95.00%	50	M8: Oxidation	1213.5850	1	6.1	142	151	Yes
ITLDNAYMEK	K	C	95.00%	75	M8: Oxidation	607.2951	2	3.9	142	151	Yes
ITLDNAYMEK	K	C	95.00%	61		599.2980	2	4.5	142	151	Yes
IYVDDGLISLQVK	K	Q	95.00%	111		731.9161	2	5.8	174	186	Yes
IYVDDGLISLQVK	K	Q	95.00%	49		488.2799	3	5.6	174	186	Yes
KGDVVIVLTGWR	K	P	95.00%	84		671.9004	2	6.1	505	516	Yes
KGDVVIVLTGWR	K	P	95.00%	57		448.2683	3	3.2	505	516	Yes
KGDVVIVLTGWRPGSGFTNTMR	K	V	95.00%	41	M21: Oxidation	803.0960	3	7.0	505	526	Yes
KGDVVIVLTGWRPGSGFTNTMR	K	V	95.00%	42	M21: Oxidation	602.5722	4	4.1	505	526	Yes
KGVNLPGAAVDLPAVSEK	K	D	95.00%	145		883.0006	2	4.1	207	224	Yes
KGVNLPGAAVDLPAVSEK	K	D	95.00%	51		589.0039	3	5.6	207	224	Yes
KGVNLPGAAVDLPAVSEKDIQDLK	K	F	95.00%	90		1239.1940	2	7.4	207	230	Yes
KGVNLPGAAVDLPAVSEKDIQDLK	K	F	95.00%	96		826.4634	3	5.1	207	230	Yes
KGVNLPGAAVDLPAVSEKDIQDLK	K	F	95.00%	49		620.0998	4	5.6	207	230	Yes
LAPITSDPTEATAVGAVEASFK	R	C	95.00%	143		1088.0700	2	6.5	401	422	No
LAPITSDPTEATAVGAVEASFK	R	C	95.00%	61		725.7160	3	6.3	401	422	No
LDIDSPPITAR	R	N	95.00%	50		1197.6590	1	9.0	33	43	Yes
LDIDSPPITAR	R	N	95.00%	77		599.3289	2	1.5	33	43	Yes
LNFSHGTHEYHAETIK	R	N	95.00%	112		942.4594	2	3.6	74	89	Yes
LNFSHGTHEYHAETIK	R	N	95.00%	68		628.6415	3	2.5	74	89	Yes
MQHLIAR	R	E	95.00%	35	M1: Oxidation	442.7451	2	5.5	377	383	Yes
NTGIICTIGPASR	R	S	95.00%	57		651.8483	2	3.6	44	56	Yes
PGSGFTNTMR	R	V	95.00%	42	M9: Oxidation	542.2507	2	3.8	517	526	Yes
PVAVALDTK	R	G	95.00%	42		457.2727	2	1.8	107	115	Yes
PVAVALDTKGPEIR	R	T	95.00%	40		733.4247	2	2.4	107	120	Yes
PVAVALDTKGPEIR	R	T	95.00%	58		489.2866	3	4.2	107	120	Yes
QKGADFLVTEVENGGSLGSK	K	K	95.00%	112		1018.5240	2	5.3	187	206	Yes
QKGADFLVTEVENGGSLGSK	K	K	95.00%	69		679.3526	3	5.9	187	206	Yes
QKGADFLVTEVENGGSLGSKK	K	G	95.00%	41		722.0516	3	6.5	187	207	Yes
RFDEILEASDGIMVAR	R	G	95.00%	91	M13: Oxidation	919.4687	2	9.6	279	294	Yes
RFDEILEASDGIMVAR	R	G	95.00%	75	M13: Oxidation	613.3121	3	4.7	279	294	Yes
RFDEILEASDGIMVAR	R	G	95.00%	84		911.4675	2	5.6	279	294	Yes
RFDEILEASDGIMVAR	R	G	95.00%	55		607.9806	3	5.1	279	294	Yes
SVETLKEMIK	R	S	95.00%	49	M8: Oxidation	597.3270	2	0.8	57	66	Yes
TATESFASDPILYR	R	P	95.00%	89		785.8962	2	5.9	93	106	Yes
TATESFASDPILYRPVAVALDTK	R	G	95.00%	59		1233.1580	2	6.2	93	115	Yes
TATESFASDPILYRPVAVALDTK	R	G	95.00%	67		822.4424	3	7.7	93	115	Yes

				TATESFASDPILYRPVAVALDTKGPEIR	R	T	95.00%	61		1006.5450	3	7.8	93	120	Yes
				VFLAQK	K	M	95.00%	45		705.4304	1	0.5	306	311	Yes
				VLGEK	K	G	95.00%	34		545.3339	1	7.2	257	261	Yes
				VNFAMNVGK	R	A	95.00%	45	M5: Oxidation	995.5024	1	4.0	490	498	Yes
				VNFAMNVGK	R	A	95.00%	70	M5: Oxidation	498.2536	2	1.0	490	498	Yes
				VNFAMNVGK	R	A	95.00%	39		979.5096	1	6.2	490	498	Yes
				VNFAMNVGK	R	A	95.00%	69		490.2569	2	2.6	490	498	Yes
				VVEVGSK	K	I	95.00%	34		717.4197	1	7.1	167	173	Yes
890	IPI00479217; IPI00644079; IPI00644224	HNRPU	ISOFORM SHORT OF HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN U.; HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN U ISOFORM A.; HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN U.	EKPYFPIPEEYTFIQNVPLEDR	K	V	95.00%	67		908.7993	3	9.5	444	465	No
				NFILDQTNVSAAAQR	R	R	95.00%	61		824.4337	2	8.5	557	571	No
				YNILGTNTIMDK	K	M	95.00%	54	M10: Oxidation	699.8538	2	4.0	506	517	No
891	IPI00549672	PSMD13	HSPC027.	ETIEDVEEMLNNLPGVTSVHSR	K	F	95.00%	65	M9: Oxidation	829.0733	3	6.6	133	154	No
				LNIGDLQVTK	K	E	95.00%	71		550.8216	2	3.2	123	132	No
				LYENFISEFEHR	K	V	95.00%	68		792.3820	2	4.2	59	70	No
				LYENFISEFEHR	K	V	95.00%	52		528.5915	3	6.0	59	70	No
				VNPLSLVEIILHVVR	R	Q	95.00%	95		851.0170	2	-9.8	71	85	No
				VNPLSLVEIILHVVR	R	Q	95.00%	70		567.6888	3	4.7	71	85	No
				YYQTIGNHASYYK	K	D	95.00%	65		804.3787	2	0.1	162	174	No
892	IPI00550689	C22orf28	UPF0027 PROTEIN C22ORF28.	QIGNVAALPGIVHR	K	S	95.00%	35		482.2861	3	2.6	68	81	No
				SYNDELQFLEK	R	I	95.00%	32		693.3377	2	6.3	4	14	No
893	IPI00550852	DCTN4	DYNACTIN SUBUNIT 4.	ATSISTQLPDDPAK	R	T	95.00%	51		722.3715	2	1.1	87	100	No
				IQLVAVNYIPEVR	K	I	95.00%	69		757.4462	2	6.9	298	310	No
894	IPI00641829	ATP6V1G2; BAT1	BAT1 PROTEIN.	DFLLKPELLR	R	A	95.00%	27		415.2545	3	4.9	49	58	No
				GLAITFVSDENDAK	K	I	95.00%	109		740.3743	2	5.0	400	413	No
				ILVATNLFGR	R	G	95.00%	47		552.3348	2	3.7	355	364	No
895	IPI00643525	C4A	COMPLEMENT COMPONENT 4A.	ALEILQEEDLIDEDDIPVR	R	S	95.00%	127		1113.0730	2	8.6	757	775	Yes
				ALEILQEEDLIDEDDIPVR	R	S	95.00%	50		742.3814	3	4.2	757	775	No
				ASAGLLGAHAAAITAYALTLTK	K	A	95.00%	51		695.7311	3	3.3	1183	1204	Yes
				DFALLSLQVPLK	R	D	95.00%	54		672.4054	2	6.5	81	92	Yes
				DFALLSLQVPLKDAK	R	S	95.00%	38		829.4832	2	3.2	81	95	No
				DFALLSLQVPLKDAK	R	S	95.00%	43		553.3248	3	3.4	81	95	Yes
				DSSTWLTAFVLK	R	V	95.00%	57		684.3674	2	4.2	1073	1084	No
				EGAIHREELVYELNPLDHR	K	G	95.00%	42		764.0633	3	7.1	936	954	Yes
				GLEEELQFSLGSK	R	I	95.00%	82		718.8721	2	6.1	1353	1365	Yes
				GPEVQLVAHSPWLK	R	D	95.00%	57		780.9374	2	8.2	105	118	Yes
				GPEVQLVAHSPWLK	R	D	95.00%	37		520.9584	3	3.6	105	118	No
				GSFEFPVGDAVSK	R	V	95.00%	41		670.3350	2	6.5	917	929	Yes
				HLVPGAPFLLQALVR	R	E	95.00%	50		544.3339	3	3.7	377	391	Yes
				KYVLPNFEVK	K	I	95.00%	43		618.8559	2	3.8	235	244	No
				LNMGITDLQGLR	K	L	95.00%	68	M3: Oxidation	673.8609	2	2.6	326	337	Yes
				PVAFSVVPTAAAAVSLK	R	V	95.00%	56		814.4778	2	3.4	896	912	No
				TTNIQGINLLFSSR	R	R	95.00%	82		782.4342	2	7.1	124	137	Yes
				VGDTLNLNLR	R	A	95.00%	84		557.8171	2	3.6	485	494	Yes
				VLSLAQEQVGGSPEK	K	L	95.00%	102		771.4165	2	4.8	1085	1099	Yes
				VTASDPLDTLGSEGALSPGGVASLLR	R	L	95.00%	81		828.4452	3	8.4	980	1005	Yes
				YIYGKPVQGVAYVR	R	F	95.00%	48		806.9490	2	3.2	270	283	Yes
				YIYGKPVQGVAYVR	R	F	95.00%	42		538.3026	3	4.3	270	283	Yes
896	IPI00643920; IPI00788802; IPI00789310; IPI00792641; IPI00793119	TKT	TRANSKETOLASE.; TRANSKETOLASE VARIANT (FRAGMENT).; 37 KDA PROTEIN.; HYPOTHETICAL PROTEIN DKFZP686J13123.; 39 KDA PROTEIN.	SVPTSTVFYPSDGVATEK	R	A	95.00%	50		942.9709	2	5.8	439	456	No
				TSRPENAIIYNNNEDFQVGQAK	R	V	95.00%	52		836.7463	3	4.7	472	493	No
897	IPI00646909; IPI00791613	TUBA8	TUBULIN ALPHA-8 CHAIN.; 52 KDA PROTEIN.	AFVHWYVGEGMEEGEFSEAR	R	E	95.00%	47	M11: Oxidation	782.6827	3	8.1	403	422	Yes
				AVMIDLEPTVVDEVR	R	A	95.00%	92	M3: Oxidation	851.4486	2	9.4	65	79	No
				DVNVAIAAIK	K	T	95.00%	64		507.3054	2	3.3	327	336	No
				ESIDLVLDR	K	I	95.00%	54		530.2898	2	2.8	113	121	No
				FDGALNVDLTEFQTNLVPYPR	R	I	95.00%	128		1205.1200	2	9.5	244	264	Yes
				FDGALNVDLTEFQTNLVPYPR	R	I	95.00%	64		803.7485	3	8.6	244	264	Yes
				IHFPLVTYAPIISAEK	R	A	95.00%	29		900.0162	2	7.6	265	280	No
				IHFPLVTYAPIISAEK	R	A	95.00%	37		600.3455	3	5.5	265	280	No

				LDHKFDLMYAK	R	R	95.00%	38	M8: Oxidation	698.8528	2	3.0	391	401	Yes
				LISQIVSSITASLR	R	F	95.00%	98		744.4507	2	9.3	230	243	Yes
				LISQIVSSITASLR	R	F	95.00%	83		496.6353	3	7.1	230	243	Yes
				NLDIERPTYTNLNR	R	L	95.00%	60		859.9495	2	4.9	216	229	Yes
				NLDIERPTYTNLNR	R	L	95.00%	50		573.6350	3	3.9	216	229	Yes
				QLFHPEQLITGK	R	E	95.00%	45		705.8943	2	4.2	85	96	Yes
				QLFHPEQLITGK	R	E	95.00%	40		470.9325	3	4.9	85	96	Yes
				QLFHPEQLITGKEDAANNYAR	R	G	95.00%	73		805.7444	3	5.1	85	105	Yes
				VGINYQPPTVVPGGDLAK	K	V	95.00%	84		912.9996	2	2.8	353	370	Yes
898	IPI00647400	RNPEP	68 KDA PROTEIN.	GLSGTAVLDLR	R	C	95.00%	49		551.3199	2	4.5	58	68	No
				RPLHSAQAVDVASASNFR	R	A	95.00%	60		642.6740	3	6.2	15	32	No
				TYQLVYFLDK	K	I	95.00%	39		645.3484	2	8.4	493	502	Yes
899	IPI00654777	EIF3S5	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 5.	AYVSTLMGVPGR	K	T	95.00%	40	M7: Oxidation	633.8326	2	4.5	230	241	No
				FLMSLVNQVPK	R	I	95.00%	59	M3: Oxidation	646.3613	2	4.9	322	332	No
				IGVDLIMK	R	T	95.00%	37	M7: Oxidation	452.7639	2	2.2	262	269	No
				LHPVILASIVDSYER	R	R	95.00%	84		856.4800	2	8.1	109	123	No
				LHPVILASIVDSYER	R	R	95.00%	53		571.3217	3	6.6	109	123	No
				TMGVMFTPLTVK	R	Y	95.00%	56	M2: Oxidation, M5: Oxidation	678.8528	2	5.2	242	253	No
				VIGLSSDLQQVGGASAR	R	I	95.00%	127		829.4521	2	5.4	277	293	No
				VIGLSSDLQQVGGASAR	R	I	95.00%	32		553.3035	3	4.6	277	293	No
				VIGTLLGTVDK	R	H	95.00%	75		558.3405	2	4.7	131	141	No
900	IPI00742905	DHX9	ATP-DEPENDENT RNA HELICASE A.	ELDALDANDELTPLGR	R	I	95.00%	40		871.4413	2	7.8	838	853	No
				GMTLVTPLQLLLFASK	K	K	95.00%	62	M2: Oxidation	874.5107	2	5.8	1058	1073	No
901	IPI00743654	NEB	NEBULIN (FRAGMENT).	ENLGTGIPTTVTPEIER	K	V	95.00%	65		913.9867	2	8.4	2649	2665	Yes
				INAVQISEPLYR	K	D	95.00%	46		701.8939	2	7.6	116	127	No
				ITVVQDTPEILR	K	V	95.00%	69		692.3989	2	3.7	2561	2572	Yes
				NLTGLEVTPALLHVK	R	Y	95.00%	75		802.9806	2	9.9	2380	2394	No
				NLTGLEVTPALLHVK	R	Y	95.00%	25		535.6547	3	6.8	2380	2394	No
902	IPI00747849; IPI00816734	ATP1B1	ISOFORM 1 OF SODIUM/POTASSIUM-TRANSPORTING ATPASE SUBUNIT BETA-1.; ISOFORM 2 OF SODIUM/POTASSIUM-TRANSPORTING ATPASE SUBUNIT BETA-1.	SYEAYVLNIVR	K	F	95.00%	79		663.8609	2	6.3	97	107	No
				VAPPGLTQIPQIQK	R	T	95.00%	56		745.4439	2	3.7	72	85	No
				VAPPGLTQIPQIQK	R	T	95.00%	40		497.2994	3	5.4	72	85	No
903	IPI00791485	CORO6	ISOFORM 1 OF CORONIN-6.	NITEPIITLEGHSK	R	R	95.00%	58		776.4260	2	3.6	190	203	No
				RSQSASDAPLSQHTLETLLEEIK	R	A	95.00%	31		851.7847	3	8.8	492	514	No
				SQSASDAPLSQHTLETLLEEIK	R	A	95.00%	53		799.7498	3	7.7	493	514	No
				VGILSWHPTAR	R	N	95.00%	37		412.9016	3	3.1	205	215	No
904	IPI00007247; IPI00387103	PCCB	PROPIONYL-COA CARBOXYLASE BETA CHAIN, MITOCHONDRIAL PRECURSOR.; HYPOTHETICAL PROTEIN.	IQEGVESLAGYADIFLR	R	N	95.00%	67		940.9990	2	7.6	166	182	No
				SVTNEDVTQEELGGAK	K	T	95.00%	79		838.9051	2	2.6	233	248	No
905	IPI00008483	MAOA	AMINE OXIDASE [FLAVIN-CONTAINING] A.	ASIAGHMFDVVVIGGGISGLSAAK	K	L	95.00%	52	M7: Oxidation	758.4078	3	5.0	7	30	No
				YVINAIPPTLTAK	K	I	95.00%	35		700.9152	2	5.1	268	280	No
906	IPI00009771	LMNB2	LAMIN B2.	ALYESELADAR	K	R	95.00%	46		619.3103	2	5.1	94	104	No
				GLESDVAELR	R	A	95.00%	57		544.7859	2	4.7	172	181	No
907	IPI00010346	NLN	NEUROLYSIN, MITOCHONDRIAL PRECURSOR.	AELGALPDDFIDSLEK	K	T	95.00%	44		866.9410	2	5.4	218	233	No
				LVNTGLLTLR	R	Q	95.00%	62		550.3473	2	2.4	568	577	No
				NLNEDDTFLVFSK	K	A	95.00%	37		771.3822	2	5.1	205	217	No
908	IPI00011916	JTV1	MULTISYNTHETASE COMPLEX AUXILIARY COMPONENT P38.	FLFSLFGQK	R	H	95.00%	33		543.8077	2	8.1	216	224	No
				SYGPAPGAGHVQEESNLSLQALESR	R	Q	95.00%	48		866.4319	3	8.0	34	58	No
909	IPI00013881; IPI00026230; IPI00479191	HNRPH1; HNRPH2	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H.; HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H'.; HNRPH1 PROTEIN.	HTGPNSPDTANDGFVR	K	L	95.00%	35		842.8893	2	1.7	99	114	No
				STGEAFVQFASQEIAEK	R	A	95.00%	85		921.4566	2	7.2	151	167	No
910	IPI00019502	MYH9	MYOSIN-9.	LQVELDNVTGLLSQSDSK	K	S	95.00%	78		973.5170	2	9.2	1278	1295	No
				QLLQANPILEAFGNAK	R	T	95.00%	55		863.9838	2	6.0	210	225	No
911	IPI00019568; IPI00784409	F2	PROTHROMBIN PRECURSOR (FRAGMENT).; 70 KDA PROTEIN.	ELLESYIDGR	R	I	95.00%	48		597.8055	2	1.9	354	363	No
				TATSEYQTFFNPR	R	T	95.00%	41		781.3713	2	4.0	315	327	No
912	IPI00020567	ARHGAP1	RHO GTPASE-ACTIVATING PROTEIN 1.	ETVAYLQAHALTTEGIFR	R	R	95.00%	31		674.0256	3	5.2	265	282	No
				NPEQEPIPIVLR	K	E	95.00%	38		702.8992	2	3.7	253	264	No
913	IPI00021301; IPI00790886	ASPA	ASPARTOACYLASE.; 30 KDA PROTEIN.	IFDLENLGK	R	K	95.00%	43		524.7903	2	4.4	72	80	No

				YPVGIEVGPQPQGVLR	K	A	95.00%	60		854.9813	2	9.4	173	188	No
914	IPI00022371	HRG	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.	ADLFYDVEALDLESPK	R	N	95.00%	93		912.9537	2	4.7	220	235	No
				DGYLFQLLR	R	I	95.00%	42		562.8123	2	5.4	44	52	No
				DSPVLIDFFEDTER	K	Y	95.00%	99		841.9051	2	6.5	140	153	No
915	IPI00022697; IPI00794194; IPI00794224; IPI00797141	DRG2	DEVELOPMENTALLY-REGULATED GTP-BINDING PROTEIN 2.; 38 KDA PROTEIN.; 18 KDA PROTEIN.; 27 KDA PROTEIN.	GANIQLLDLPGIIEGAAQGK	K	G	95.00%	52		660.0422	3	6.6	108	127	No
				VALIGFPSVGK	R	S	95.00%	41		544.3328	2	5.6	65	75	No
916	IPI00023006	ACTC1	ACTIN, ALPHA CARDIAC MUSCLE 1.	AGFAGDDAPR	K	A	95.00%	57		976.4520	1	3.2	21	30	Yes
				AGFAGDDAPR	K	A	95.00%	90		488.7286	2	0.4	21	30	Yes
				AVFPSIVGR	R	P	95.00%	78		473.2805	2	1.0	31	39	Yes
				AVFPSIVGRPR	R	H	95.00%	72		599.8580	2	1.6	31	41	Yes
				DLTDYLMK	R	I	95.00%	42	M7: Oxidation	1014.4830	1	0.5	186	193	Yes
				DLTDYLMK	R	I	95.00%	56	M7: Oxidation	507.7452	2	0.5	186	193	Yes
				DLTDYLMK	R	I	95.00%	43		499.7490	2	3.1	186	193	Yes
				DLYANNVLSGGTTMYPGIADR	K	M	95.00%	116	M14: Oxidation	1122.5440	2	8.4	294	314	No
				DSYVGDEAQSK	K	R	95.00%	85		599.7688	2	5.8	53	63	Yes
				DSYVGDEAQSKR	K	G	95.00%	65		677.8182	2	3.5	53	64	Yes
				DSYVGDEAQSKR	K	G	95.00%	36		452.2152	3	4.6	53	64	Yes
				EITALAPSTMK	K	I	95.00%	71	M10: Oxidation	1177.6180	1	3.4	318	328	Yes
				EITALAPSTMK	K	I	95.00%	91	M10: Oxidation	589.3121	2	2.0	318	328	Yes
				EITALAPSTMK	K	I	95.00%	58		1161.6240	1	4.3	318	328	Yes
				EITALAPSTMK	K	I	95.00%	57		581.3137	2	0.3	318	328	Yes
				GILTLK	R	Y	95.00%	37		644.4368	1	3.0	65	70	Yes
				GYSFVTTAER	R	E	95.00%	42		1130.5520	1	3.3	199	208	Yes
				GYSFVTTAER	R	E	95.00%	80		565.7791	2	1.8	199	208	Yes
				HQGVMVGMGQK	R	D	95.00%	63	M5: Oxidation	594.2880	2	1.2	42	52	Yes
				HQGVMVGMGQK	R	D	95.00%	58	M5: Oxidation	602.2905	2	9.6	42	52	Yes
				HQGVMVGMGQK	R	D	95.00%	58	M5: Oxidation	401.8611	3	5.1	42	52	Yes
				HQGVMVGMGQK	R	D	95.00%	58	M5: Oxidation, M8: Oxidation	602.2905	2	9.6	42	52	Yes
				HQGVMVGMGQK	R	D	95.00%	58	M5: Oxidation, M8: Oxidation	401.8611	3	5.1	42	52	Yes
				HQGVMVGMGQK	R	D	95.00%	61	M8: Oxidation	594.2899	2	4.5	42	52	Yes
				HQGVMVGMGQK	R	D	95.00%	71		1171.5740	1	2.1	42	52	Yes
				HQGVMVGMGQK	R	D	95.00%	82		586.2905	2	1.3	42	52	Yes
				IIAPPERK	K	Y	95.00%	36		462.2889	2	2.3	331	338	Yes
				IKIIAPPER	K	K	95.00%	21		518.8315	2	2.9	329	337	Yes
				IKIIAPPERK	K	Y	95.00%	26		582.8785	2	1.9	329	338	Yes
				IWHHTFYNELR	K	V	95.00%	70		758.3789	2	0.2	87	97	Yes
				IWHHTFYNELR	K	V	95.00%	61		505.9238	3	4.1	87	97	Yes
				KDLYANNVLSGGTTMYPGIADR	R	M	95.00%	63	M15: Oxidation	791.3947	3	5.2	293	314	No
				MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	64	M1: Oxidation	1089.8870	3	6.0	121	149	Yes
				MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	87	M1: Oxidation	1095.2200	3	7.4	121	149	Yes
				MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	38	M1: Oxidation	821.6656	4	5.9	121	149	Yes
				MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	63	M1: Oxidation	1100.5530	3	8.7	121	149	Yes
				MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	87	M1: Oxidation, M5: Oxidation	1095.2200	3	7.4	121	149	Yes
				MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	38	M1: Oxidation, M5: Oxidation	821.6656	4	5.9	121	149	Yes
				MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	63	M1: Oxidation, M5: Oxidation	1100.5530	3	8.7	121	149	Yes
				MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	63	M1: Oxidation, M5: Oxidation, M14: Oxidation	1100.5530	3	8.7	121	149	Yes
				MTQIMFETFNVPAMYVAIQAVLSLYASGR	K	T	95.00%	91	M5: Oxidation	1089.8870	3	6.1	121	149	Yes
				QEYDEAGPSIVHR	K	K	95.00%	85		750.8606	2	3.3	362	374	Yes
				QEYDEAGPSIVHR	K	K	95.00%	63		500.9085	3	1.1	362	374	Yes
				QEYDEAGPSIVHRK	K	C	95.00%	64		814.9073	2	2.1	362	375	Yes
				QEYDEAGPSIVHRK	K	C	95.00%	36		543.6075	3	2.1	362	375	Yes
				RGILTLK	K	Y	95.00%	39		400.7726	2	1.9	64	70	Yes
				SYELPDGQVITIGNER	K	F	95.00%	132		895.9526	2	2.7	241	256	Yes
				SYELPDGQVITIGNER	K	F	95.00%	73		597.6398	3	6.2	241	256	Yes

				TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	R	L	95.00%	65	M29: Oxidation	1071.5500	3	9.3	150	179	Yes
				TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	R	L	95.00%	56	M29: Oxidation	643.3307	5	5.5	150	179	Yes
				TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	R	L	95.00%	72		1066.2180	3	9.2	150	179	Yes
				TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	R	L	95.00%	39		799.9139	4	7.0	150	179	Yes
				VAPEEHPTLLTEAPLNPK	R	A	95.00%	96		978.5319	2	5.7	98	115	Yes
				VAPEEHPTLLTEAPLNPK	R	A	95.00%	61		652.6883	3	2.4	98	115	Yes
				YPIEHGIITNWDDMEK	K	I	95.00%	35	M14: Oxidation	988.9588	2	1.6	71	86	Yes
917	IPI00024990	ALDH6A1	METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE [ACYLATING], MITOCHONDRIALPRECURSOR.	TLADAEGDVFR	K	G	95.00%	42		597.2964	2	3.8	130	140	No
				VNAGDQPGADLGPLITPQAK	R	E	95.00%	54		981.5238	2	4.9	345	364	No
918	IPI00025721	COPS3	COP9 SIGNALOSOME COMPLEX SUBUNIT 3.	AMDQEITVNPQFVQK	K	S	95.00%	85	M2: Oxidation	882.4391	2	3.6	392	406	No
				FIKPLSNAYHELAQVYSTNNPSELR	R	N	95.00%	93		964.5012	3	6.6	252	276	No
919	IPI00026516	OXCT1	SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE 1, MITOCHONDRIALPRECURSOR.	GLTAVSNNAGVDNFGLGLLLR	K	S	95.00%	127		1051.0840	2	9.1	84	104	No
				MVSSYVGENAEFER	R	Q	95.00%	75	M1: Oxidation	817.3655	2	4.1	111	124	No
				YGDLANWMIPGK	K	M	95.00%	41	M8: Oxidation	690.8390	2	5.7	407	418	No
920	IPI00026942	ERLIN2	SPFH2 PROTEIN (FRAGMENT).	IEVVNFLVPNAVYDIVK	R	N	95.00%	75		966.5549	2	9.0	89	105	No
				ISEIEDAAFLAR	K	E	95.00%	83		667.8566	2	7.2	242	253	No
921	IPI00027258; IPI00413058; IPI00413060	SYNPO	ISOFORM 2 OF SYNAPTOPODIN.; ISOFORM 1 OF SYNAPTOPODIN.; ISOFORM 3 OF SYNAPTOPODIN.	VASEEEEVPLVVYLK	K	E	95.00%	72		852.4618	2	3.0	17	31	No
				VTPNPDLLDLVQTADEK	K	R	95.00%	84		934.4933	2	7.1	389	405	No
922	IPI00027444	SERPINB1	LEUKOCYTE ELASTASE INHIBITOR.	FAYGYIEDLK	K	C	95.00%	32		609.8091	2	4.7	204	213	No
				TYGADLASVDFQHASEDAR	K	K	95.00%	57		684.9835	3	4.2	111	129	No
923	IPI00028635; IPI00383680; IPI00552307; IPI00552972; IPI00789816	RPN2	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 63 KDASUBUNIT PRECURSOR.; RIBOPHORIN II.; RIBOPHORIN II.; 56 KDA PROTEIN.; 71 KDA PROTEIN.	SIVEEIEDLVAR	R	L	95.00%	70		686.8747	2	6.7	54	65	No
				TGQEVVFVAEPDNK	K	N	95.00%	34		766.8908	2	9.1	318	331	No
924	IPI00029485	DCTN1	ISOFORM P150 OF DYNACTIN-1.	AFLQGGQEATDIALLLR	R	D	95.00%	81		908.5070	2	4.9	769	785	No
				KTSQLLETLNQLSTHTHVVDITR	R	T	95.00%	31		659.3638	4	3.8	1151	1173	No
				VDELTTDLEILKAEIEEK	R	G	95.00%	38		696.7084	3	6.2	332	349	No
925	IPI00031618; IPI00796836	DDI2; RSC1A1	PROTEIN DDI1 HOMOLOG 2.; 112 KDA PROTEIN.	EDVRPEEIADQELAEALQK	R	S	95.00%	39		728.3708	3	6.0	371	389	No
				LFSADPFDLEAQAK	R	I	95.00%	52		776.3930	2	5.5	192	205	No
926	IPI00166642	D2HGDH	ISOFORM 1 OF D-2-HYDROXYGLUTARATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR.	LYDIVTDLR	R	A	95.00%	54		554.3098	2	6.0	411	419	No
				YDLSLPVER	K	L	95.00%	34		546.2932	2	4.4	402	410	No
927	IPI00179291; IPI00645898; IPI00793375	XPNPEP1	ISOFORM 1 OF XAA-PRO AMINOPEPTIDASE 1.; X-PROLYL AMINOPEPTIDASE (AMINOPEPTIDASE P) 1, SOLUBLE.; CYTOSOLIC AMINOPEPTIDASE P.	GSLTFEPLTLVPIQTK	R	M	95.00%	67		872.5046	2	6.5	598	613	No
				TLSLDEVYLIDSGAQYK	R	D	95.00%	67		957.9949	2	6.1	448	464	No
928	IPI00215610	MPP1	55 KDA ERYTHROCYTE MEMBRANE PROTEIN.	HSSIFDQLDVVSYEEVVR	K	L	95.00%	34		708.0243	3	5.6	259	276	No
				IAILDIEPQTLK	K	I	95.00%	64		677.4078	2	6.0	375	386	No
929	IPI00215637	DDX3X	ATP-DEPENDENT RNA HELICASE DDX3X.	DLLDLLVEAK	K	Q	95.00%	56		564.8324	2	4.4	555	564	No
				SFLLDLLNATGK	R	D	95.00%	93		646.3701	2	4.5	429	440	No
				VGNLGLATSFFNER	R	N	95.00%	67		762.8974	2	3.8	535	548	No
930	IPI00218857; IPI00218858; IPI00220438	MAP2K3	ISOFORM 1 OF DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE3.; ISOFORM 2 OF DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE3.; ISOFORM 3 OF DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE3.	LLMDLDINMR	R	T	95.00%	42	M3: Oxidation, M9: Oxidation	633.3137	2	-3.1	112	121	No
				NMTIPEDILGEIAVSIVR	K	A	95.00%	70	M2: Oxidation	662.6968	3	8.4	163	180	No
931	IPI00220271	AKR1A1	ALCOHOL DEHYDROGENASE.	AWRDPDEPVLLEEPVVLALAEK	R	Y	95.00%	47		830.4546	3	7.7	219	240	No
				GLEVTAYSPLGSSDR	R	A	95.00%	56		776.3913	2	6.0	204	218	No
				GLVQALGLSNFNSR	K	Q	95.00%	78		738.4067	2	5.8	154	167	No
				MPLIGLGTWK	K	S	95.00%	37	M1: Oxidation	566.3171	2	2.3	14	23	No

932	IPI00221234; IPI00786942	ALDH7A1	SIMILAR TO ALDEHYDE DEHYDROGENASE FAMILY 7 MEMBER A1.; SIMILAR TO ANTIQUITIN.	GAPTTSLISVAVTK	K	I	95.00%	87		672.8939	2	4.4	219	232	No
				IQVLGSLVSLEMGK	K	I	95.00%	29	M12: Oxidation	745.4236	2	6.1	125	138	No
				VNLLSFTGSTQVGK	R	Q	95.00%	39		725.9026	2	4.6	267	280	No
933	IPI00291165; IPI00744711	PNPT1	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE 1, MITOCHONDRIAL PRECURSOR.; 86 KDA PROTEIN.	IVMEAIQQASVAK	K	K	95.00%	55	M3: Oxidation	702.3849	2	3.7	572	584	No
				YTQQIIQGIQQLVK	K	E	95.00%	96		830.4814	2	6.9	251	264	No
934	IPI00294578	TGM2	ISOFORM 1 OF PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE 2.	ALLVEPVINSYLLAER	R	D	95.00%	81		900.5243	2	7.5	565	580	No
				YLLNLNLEPFSEK	K	S	95.00%	37		790.4264	2	4.9	528	540	No
935	IPI00296283	MAPK12	MITOGEN-ACTIVATED PROTEIN KINASE 12.	DFASILTNASPLAVNLLEK	K	M	95.00%	60		1008.5570	2	2.0	272	290	No
				DFASILTNASPLAVNLLEK	K	M	95.00%	68		672.7105	3	7.0	272	290	No
				ILDFGLAR	K	Q	95.00%	54		452.7682	2	3.1	169	176	No
				VTGTPPAEFVQR	K	L	95.00%	34		651.3474	2	1.1	241	252	No
936	IPI00298237; IPI00554538; IPI00554617	TPP1	ISOFORM 1 OF TRIPEPTIDYL-PEPTIDASE 1 PRECURSOR.; ISOFORM 3 OF TRIPEPTIDYL-PEPTIDASE 1 PRECURSOR.; ISOFORM 2 OF TRIPEPTIDYL-PEPTIDASE 1 PRECURSOR.	ILSGRPPLGFLNPR	R	L	95.00%	23		512.9745	3	4.2	493	506	No
				LFGGNFAHQASVAR	R	V	95.00%	98		737.8855	2	5.2	246	259	No
				LFGGNFAHQASVAR	R	V	95.00%	34		492.2593	3	4.6	246	259	No
937	IPI00298520; IPI00514053	ARCN1	HYPOTHETICAL PROTEIN DKFZP686M09245.; COATOMER SUBUNIT DELTA.	LFTAESLIGLK	K	N	95.00%	46		596.3572	2	6.2	378	388	No
				NSNILEDLETLR	K	L	95.00%	71		708.8754	2	6.5	114	125	No
938	IPI00298971	VTN	VITRONECTIN PRECURSOR.	DVWGIEGPIDAAFTR	R	I	95.00%	66		823.9176	2	5.6	198	212	No
				FEDGVLDPDYPR	R	N	95.00%	43		711.8329	2	2.5	230	241	No
939	IPI00299063	STIM1	STROMAL INTERACTION MOLECULE 1 PRECURSOR.	ALDTVLFGPPLLTR	K	H	95.00%	61		756.9465	2	4.0	194	207	No
				QALSEVTAALR	K	E	95.00%	70		579.8298	2	3.0	414	424	No
940	IPI00301280	TMEM43	TRANSMEMBRANE PROTEIN 43.	SGDTLLLLHHGDFSAEEVFHR	K	E	95.00%	41		595.8020	4	6.8	279	299	No
				VSFSYAGLSGDDPDLGPAHVVTVIAR	R	Q	95.00%	70		881.7913	3	6.3	241	266	No
941	IPI00302329	MYH8	MYOSIN-8.	AAYLQSLNSADLLK	K	A	95.00%	105		753.9153	2	4.0	387	400	Yes
				AAYLQSLNSADLLK	K	A	95.00%	74		502.9464	3	4.4	387	400	Yes
				ADIAESQVNK	R	L	95.00%	81		537.7761	2	1.1	1913	1922	Yes
				AGLLGLLEEMR	K	D	95.00%	81	M10: Oxidation	609.3345	2	3.7	770	780	Yes
				AGLLGLLEEMR	K	D	95.00%	94		601.3371	2	3.9	770	780	Yes
				AGLLGLLEEMRDEK	K	L	95.00%	66	M10: Oxidation	795.4192	2	5.9	770	783	Yes
				AGLLGLLEEMRDEK	K	L	95.00%	47	M10: Oxidation	530.6141	3	3.5	770	783	Yes
				AGLLGLLEEMRDEK	K	L	95.00%	90		787.4214	2	5.6	770	783	Yes
				AGLLGLLEEMRDEK	K	L	95.00%	48		525.2841	3	6.6	770	783	Yes
				AITDAAMMAEELK	K	K	95.00%	84	M7: Oxidation, M8: Oxidation	713.3373	2	4.4	1761	1773	Yes
				AITDAAMMAEELKK	K	E	95.00%	88	M7: Oxidation	769.3863	2	2.6	1761	1774	Yes
				AITDAAMMAEELKK	K	E	95.00%	44	M7: Oxidation	513.2606	3	3.4	1761	1774	Yes
				AITDAAMMAEELKK	K	E	95.00%	83	M7: Oxidation	777.3834	2	2.2	1761	1774	Yes
				AITDAAMMAEELKK	K	E	95.00%	39	M7: Oxidation	518.5920	3	3.1	1761	1774	Yes
				AITDAAMMAEELKK	K	E	95.00%	83	M7: Oxidation, M8: Oxidation	777.3834	2	2.2	1761	1774	Yes
				AITDAAMMAEELKK	K	E	95.00%	39	M7: Oxidation, M8: Oxidation	518.5920	3	3.1	1761	1774	Yes
				AITDAAMMAEELKK	K	E	95.00%	90	M8: Oxidation	769.3892	2	6.4	1761	1774	Yes
				AITDAAMMAEELKK	K	E	95.00%	52	M8: Oxidation	513.2598	3	1.9	1761	1774	Yes
				AITDAAMMAEELKK	K	E	95.00%	111		761.3883	2	1.9	1761	1774	Yes
				AITDAAMMAEELKK	K	E	95.00%	77		507.9281	3	1.8	1761	1774	Yes
				ANSEVAQWR	K	T	95.00%	51		1060.5220	1	4.5	1367	1375	Yes
				ANSEVAQWR	K	T	95.00%	66		530.7642	2	2.9	1367	1375	Yes
				DIDDLELTLAK	K	V	95.00%	54		1245.6670	1	7.2	956	966	Yes
				DIDDLELTLAK	K	V	95.00%	99		623.3339	2	1.4	956	966	Yes
				DLEEATLQHEAMVAALR	R	K	95.00%	53		948.9759	2	-2.6	1180	1196	Yes
				DLQHRLDEAEQLALK	K	G	95.00%	52		889.9805	2	7.1	1795	1809	Yes
				DLQHRLDEAEQLALK	K	G	95.00%	58		593.6564	3	7.3	1795	1809	Yes
				EAEFQK	R	L	95.00%	31		751.3661	1	4.5	1171	1176	No
				EEQAEPDGTEVADK	R	A	95.00%	79		759.3370	2	3.5	373	386	Yes
				EEQAEPDGTEVADKAAYLQSLNSADLLK	R	A	95.00%	84		1002.4970	3	5.4	373	400	Yes
				ELEEISER	R	L	95.00%	48		1004.4960	1	6.0	1145	1152	Yes
				ELEEISER	R	L	95.00%	38		502.7501	2	2.4	1145	1152	Yes

ELTYQTEEDRK	K	N	95.00%	59		706.3409	2	2.4	1852	1862	Yes
EMATMKEEFQK	K	T	95.00%	41	M2: Oxidation	694.3182	2	3.5	851	861	Yes
EMATMKEEFQK	K	T	95.00%	45	M2: Oxidation	702.3162	2	4.3	851	861	Yes
EMATMKEEFQK	K	T	95.00%	32	M2: Oxidation	468.5458	3	2.2	851	861	Yes
EMATMKEEFQK	K	T	95.00%	45	M2: Oxidation, M5: Oxidation	702.3162	2	4.3	851	861	Yes
EMATMKEEFQK	K	T	95.00%	32	M2: Oxidation, M5: Oxidation	468.5458	3	2.2	851	861	Yes
EMATMKEEFQK	K	T	95.00%	48	M5: Oxidation	694.3182	2	3.5	851	861	No
EMATMKEEFQK	K	T	95.00%	56		686.3207	2	3.4	851	861	Yes
ENKNLQQEISDLTEQIAEGGK	R	Q	95.00%	56		782.0655	3	7.4	1504	1524	No
ENQSILITGESGAGK	R	T	95.00%	113		752.3880	2	1.7	173	187	Yes
GQTVQQVYNAVGALAK	K	A	95.00%	138		823.9529	2	7.0	417	432	Yes
GQTVQQVYNAVGALAK	K	A	95.00%	73		549.6364	3	4.2	417	432	Yes
GSSFQTVSALFR	K	E	95.00%	46		1299.6800	1	7.8	644	655	Yes
GSSFQTVSALFR	K	E	95.00%	88		650.3420	2	5.0	644	655	Yes
GSSFQTVSALFR	K	E	95.00%	40		433.8968	3	3.9	644	655	Yes
HADSMAELGEQIDNLQR	K	V	95.00%	47		963.9618	2	9.1	1199	1215	No
IAEKDEEIDQLK	K	R	95.00%	87		715.8757	2	3.8	1579	1590	Yes
IAEKDEEIDQLK	K	R	95.00%	45		477.5863	3	3.5	1579	1590	Yes
IAEKDEEIDQLKR	K	N	95.00%	95		793.9271	2	4.4	1579	1591	Yes
IAEKDEEIDQLKR	K	N	95.00%	74		529.6190	3	1.3	1579	1591	Yes
IAEQELLDASER	K	V	95.00%	84		687.3519	2	3.4	1704	1715	Yes
IEAQNKPFDAK	R	T	95.00%	33		630.8347	2	1.9	27	37	Yes
IKELQAR	K	I	95.00%	31		429.2654	2	2.3	1111	1117	Yes
IKEVTER	K	A	95.00%	35		437.7546	2	1.7	922	928	Yes
INQQLDTK	R	Q	95.00%	55		480.2638	2	3.6	446	453	Yes
IQLEAK	K	I	95.00%	37		701.4219	1	2.9	916	921	Yes
IQLELNQVK	R	S	95.00%	46		1084.6430	1	5.9	1564	1572	Yes
IQLELNQVK	R	S	95.00%	70		542.8231	2	1.5	1564	1572	Yes
KAITDAAMMAEELKK	K	E	95.00%	101	M8: Oxidation	833.4363	2	5.3	1760	1774	Yes
KAITDAAMMAEELKK	K	E	95.00%	69	M8: Oxidation	555.9593	3	3.8	1760	1774	Yes
KAITDAAMMAEELKK	K	E	95.00%	34	M8: Oxidation	417.2206	4	2.0	1760	1774	Yes
KAITDAAMMAEELKK	K	E	95.00%	80	M8: Oxidation	841.4315	2	2.7	1760	1774	Yes
KAITDAAMMAEELKK	K	E	95.00%	58	M8: Oxidation	561.2901	3	2.4	1760	1774	Yes
KAITDAAMMAEELKK	K	E	95.00%	80	M8: Oxidation, M9: Oxidation	841.4315	2	2.7	1760	1774	Yes
KAITDAAMMAEELKK	K	E	95.00%	58	M8: Oxidation, M9: Oxidation	561.2901	3	2.4	1760	1774	Yes
KAITDAAMMAEELKK	K	E	95.00%	73	M9: Oxidation	833.4340	2	2.6	1760	1774	Yes
KAITDAAMMAEELKK	K	E	95.00%	59	M9: Oxidation	555.9584	3	2.3	1760	1774	Yes
KAITDAAMMAEELKK	K	E	95.00%	107		825.4387	2	5.2	1760	1774	Yes
KAITDAAMMAEELKK	K	E	95.00%	92		550.6276	3	3.8	1760	1774	Yes
KAITDAAMMAEELKK	K	E	95.00%	42		413.2216	4	1.3	1760	1774	Yes
KDIDDLELTLAK	K	V	95.00%	93		687.3838	2	4.8	955	966	Yes
KDIDDLELTLAK	K	V	95.00%	43		458.5912	3	3.3	955	966	Yes
KGSSFQTVSALFR	K	E	95.00%	125		714.3884	2	3.1	643	655	Yes
KGSSFQTVSALFR	K	E	95.00%	56		476.5944	3	2.1	643	655	Yes
KIAEQELLDASER	R	V	95.00%	123		751.3984	2	1.7	1703	1715	Yes
KIAEQELLDASER	R	V	95.00%	62		501.2687	3	2.7	1703	1715	Yes
KKGSSFQTVSALFR	K	E	95.00%	46		519.2935	3	3.4	642	655	Yes
KKMEGDLNEMEIQLNHANR	K	L	95.00%	39	M10: Oxidation	762.7066	3	3.1	1619	1637	No
KKMEGDLNEMEIQLNHANR	K	L	95.00%	36	M10: Oxidation	572.2819	4	3.0	1619	1637	No
KKMEGDLNEMEIQLNHANR	K	L	95.00%	70	M3: Oxidation	762.7065	3	3.0	1619	1637	No
KKMEGDLNEMEIQLNHANR	K	L	95.00%	77	M3: Oxidation	572.2819	4	3.1	1619	1637	No
KKMEGDLNEMEIQLNHANR	K	L	95.00%	58	M3: Oxidation	768.0369	3	1.3	1619	1637	No
KKMEGDLNEMEIQLNHANR	K	L	95.00%	50	M3: Oxidation	576.2795	4	1.2	1619	1637	No
KKMEGDLNEMEIQLNHANR	K	L	95.00%	58	M3: Oxidation, M10: Oxidation	768.0369	3	1.3	1619	1637	No
KKMEGDLNEMEIQLNHANR	K	L	95.00%	50	M3: Oxidation, M10: Oxidation	576.2795	4	1.2	1619	1637	No
KKMEGDLNEMEIQLNHANR	K	L	95.00%	53		757.3764	3	4.9	1619	1637	No
KKMEGDLNEMEIQLNHANR	K	L	95.00%	60		568.2845	4	5.5	1619	1637	No
KLEGDLK	R	L	95.00%	37		401.7387	2	2.3	1057	1063	Yes
KLQHELEEAEER	R	A	95.00%	77		755.8810	2	2.5	1901	1912	Yes
KLQHELEEAEER	R	A	95.00%	59		504.2543	3	-2.0	1901	1912	Yes
KLQHELEEAEERADIAESQVNK	R	L	95.00%	93		1283.6470	2	4.3	1901	1922	Yes
KLQHELEEAEERADIAESQVNK	R	L	95.00%	43		856.1024	3	6.4	1901	1922	Yes

KLQHELEEAEERADIAESQVNK	R	L	95.00%	61		642.3271	4	3.9	1901	1922	Yes
KMEGDLNEMEIQLNHANR	K	L	95.00%	74	M2: Oxidation	720.0091	3	4.4	1620	1637	No
KMEGDLNEMEIQLNHANR	K	L	95.00%	50	M2: Oxidation	540.2582	4	3.3	1620	1637	No
KMEGDLNEMEIQLNHANR	K	L	95.00%	66	M2: Oxidation	1087.5070	2	4.4	1620	1637	No
KMEGDLNEMEIQLNHANR	K	L	95.00%	50	M2: Oxidation	725.3399	3	3.3	1620	1637	No
KMEGDLNEMEIQLNHANR	K	L	95.00%	50	M2: Oxidation	544.2559	4	1.3	1620	1637	No
KMEGDLNEMEIQLNHANR	K	L	95.00%	66	M2: Oxidation, M9: Oxidation	1087.5070	2	4.4	1620	1637	No
KMEGDLNEMEIQLNHANR	K	L	95.00%	50	M2: Oxidation, M9: Oxidation	725.3399	3	3.3	1620	1637	No
KMEGDLNEMEIQLNHANR	K	L	95.00%	50	M2: Oxidation, M9: Oxidation	544.2559	4	1.3	1620	1637	No
KMEGDLNEMEIQLNHANR	K	L	95.00%	69	M9: Oxidation	1079.5140	2	8.5	1620	1637	No
KMEGDLNEMEIQLNHANR	K	L	95.00%	67	M9: Oxidation	720.0086	3	3.7	1620	1637	No
KMEGDLNEMEIQLNHANR	K	L	95.00%	36	M9: Oxidation	540.2574	4	1.8	1620	1637	No
KMEGDLNEMEIQLNHANR	K	L	95.00%	113		1071.5160	2	8.2	1620	1637	No
KMEGDLNEMEIQLNHANR	K	L	95.00%	89		714.6783	3	5.6	1620	1637	No
KMEGDLNEMEIQLNHANR	K	L	95.00%	59		536.2598	4	4.0	1620	1637	No
KRQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	35	M20: Oxidation	960.8145	3	6.2	149	172	Yes
KRQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	97		955.4839	3	7.2	149	172	Yes
LAQIITR	K	T	95.00%	37		814.5181	1	3.6	784	790	No
LAQIITR	K	T	95.00%	59		407.7621	2	1.4	784	790	No
LASADIETYLLEK	K	S	95.00%	129		733.3953	2	2.4	261	273	Yes
LASADIETYLLEK	K	S	95.00%	64		489.2677	3	5.7	261	273	Yes
LDEAEQLALK	R	G	95.00%	43		1129.6160	1	4.8	1800	1809	Yes
LDEAEQLALK	R	G	95.00%	97		565.3106	2	2.4	1800	1809	Yes
LDEAEQLALKGGK	R	K	95.00%	53		686.3796	2	2.0	1800	1812	Yes
LEQQVDDLEGSLEQEK	K	K	95.00%	144		930.4526	2	5.2	1030	1045	Yes
LEQQVDDLEGSLEQEK	K	K	95.00%	96		620.6370	3	4.2	1030	1045	Yes
LEQQVDDLEGSLEQEKK	K	L	95.00%	112		994.5015	2	6.3	1030	1046	Yes
LEQQVDDLEGSLEQEKK	K	L	95.00%	54		663.3357	3	4.5	1030	1046	Yes
LINDLTAQR	R	A	95.00%	51		1043.5890	1	3.9	1272	1280	Yes
LINDLTAQR	R	A	95.00%	89		522.2970	2	1.1	1272	1280	Yes
LQDLVDK	R	L	95.00%	32		415.7358	2	1.5	1867	1873	Yes
LQDLVDKLQAK	R	V	95.00%	85		635.8749	2	3.7	1867	1877	Yes
LQDLVDKLQAK	R	V	95.00%	50		424.2519	3	2.1	1867	1877	Yes
LQHELEEAEER	K	A	95.00%	68		691.8333	2	2.6	1902	1912	Yes
LQHELEEAEER	K	A	95.00%	55		461.5579	3	2.0	1902	1912	Yes
LQHELEEAEERADIAESQVNK	K	L	95.00%	114		1219.6040	2	8.0	1902	1922	Yes
LQHELEEAEERADIAESQVNK	K	L	95.00%	59		813.4023	3	4.6	1902	1922	Yes
LQHELEEAEERADIAESQVNK	K	L	95.00%	50		610.3027	4	3.1	1902	1922	Yes
LQNEVEDLMLDVER	R	S	95.00%	122	M9: Oxidation	859.9222	2	5.5	1424	1437	No
LQNEVEDLMLDVER	R	S	95.00%	86	M9: Oxidation	573.6165	3	3.8	1424	1437	No
LQNEVEDLMLDVER	R	S	95.00%	115		851.9251	2	5.9	1424	1437	No
LQNEVEDLMLDVER	R	S	95.00%	75		568.2850	3	4.2	1424	1437	No
LQQFFNHHMFVLEQEEYK	K	K	95.00%	58	M9: Oxidation	795.0480	3	4.4	488	505	Yes
LQQFFNHHMFVLEQEEYK	K	K	95.00%	41		789.7194	3	8.3	488	505	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	48	M9: Oxidation	837.7477	3	5.8	488	506	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	103		1248.1230	2	8.3	488	506	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	57		832.4158	3	5.6	488	506	Yes
LQQFFNHHMFVLEQEEYKK	K	E	95.00%	35		499.8518	5	3.9	488	506	Yes
LTGAVMHYGNMK	K	F	95.00%	72	M11: Oxidation	669.3234	2	3.3	355	366	Yes
LTGAVMHYGNMK	K	F	95.00%	64	M6: Oxidation	669.3222	2	1.5	355	366	Yes
LTGAVMHYGNMK	K	F	95.00%	62	M6: Oxidation	677.3207	2	3.1	355	366	Yes
LTGAVMHYGNMK	K	F	95.00%	62	M6: Oxidation, M11: Oxidation	677.3207	2	3.1	355	366	Yes
LTGAVMHYGNMK	K	F	95.00%	61		661.3256	2	2.7	355	366	Yes
LYDQHLGK	K	S	95.00%	55		487.2609	2	3.1	555	562	Yes
MEGDLNEMEIQLNHANR	K	L	95.00%	108	M1: Oxidation	1015.4620	2	4.5	1621	1637	No
MEGDLNEMEIQLNHANR	K	L	95.00%	73	M1: Oxidation	677.3097	3	3.1	1621	1637	No
MEGDLNEMEIQLNHANR	K	L	95.00%	77	M1: Oxidation	1023.4590	2	4.2	1621	1637	No
MEGDLNEMEIQLNHANR	K	L	95.00%	71	M1: Oxidation	682.6416	3	3.5	1621	1637	No
MEGDLNEMEIQLNHANR	K	L	95.00%	77	M1: Oxidation, M8: Oxidation	1023.4590	2	4.2	1621	1637	No
MEGDLNEMEIQLNHANR	K	L	95.00%	71	M1: Oxidation, M8: Oxidation	682.6416	3	3.5	1621	1637	No
MEGDLNEMEIQLNHANR	K	L	95.00%	89	M8: Oxidation	1015.4640	2	6.8	1621	1637	No

MEGDLNEMEIQLNHANR	K	L	95.00%	45	M8: Oxidation	677.3091	3	2.3	1621	1637	No
MEGDLNEMEIQLNHANR	K	L	95.00%	124		1007.4680	2	8.1	1621	1637	No
MEGDLNEMEIQLNHANR	K	L	95.00%	77		671.9785	3	3.8	1621	1637	No
MFLWMVTR	K	I	95.00%	43	M1: Oxidation	550.2784	2	5.2	438	445	Yes
MFLWMVTR	K	I	95.00%	50	M1: Oxidation	558.2754	2	4.4	438	445	Yes
MFLWMVTR	K	I	95.00%	50	M1: Oxidation, M5: Oxidation	558.2754	2	4.4	438	445	Yes
MFLWMVTR	K	I	95.00%	50	M5: Oxidation	550.2784	2	5.2	438	445	Yes
MFLWMVTR	K	I	95.00%	41		542.2811	2	5.5	438	445	Yes
MQGTLEDQIISANPLLEAFGNAK	K	T	95.00%	129	M1: Oxidation	1238.6320	2	6.9	215	237	Yes
MQGTLEDQIISANPLLEAFGNAK	K	T	95.00%	101	M1: Oxidation	826.0912	3	7.5	215	237	Yes
MVTLLK	K	E	95.00%	37		704.4404	1	3.2	880	885	Yes
NALAHALQSSR	K	H	95.00%	52		1167.6270	1	3.0	1330	1340	Yes
NALAHALQSSR	K	H	95.00%	94		584.3176	2	3.3	1330	1340	Yes
NLQQEISDLTEQIAEGGK	K	Q	95.00%	159		987.0016	2	6.3	1507	1524	No
NLQQEISDLTEQIAEGGK	K	Q	95.00%	98		658.3360	3	4.8	1507	1524	No
NLTEEMAGLDETIAK	K	L	95.00%	121	M6: Oxidation	825.9019	2	3.6	980	994	Yes
NLTEEMAGLDETIAK	K	L	95.00%	66	M6: Oxidation	550.9374	3	4.0	980	994	Yes
NLTEEMAGLDETIAK	K	L	95.00%	131		817.9053	2	4.7	980	994	Yes
NLTEEMAGLDETIAK	K	L	95.00%	77		545.6058	3	4.2	980	994	Yes
NTQGILK	R	E	95.00%	33		773.4540	1	2.2	1648	1654	No
QEAPPHIFSISDNAYQFMLTDR	R	E	95.00%	103	M18: Oxidation	866.0826	3	7.0	151	172	Yes
QEAPPHIFSISDNAYQFMLTDR	R	E	95.00%	81		860.7453	3	0.4	151	172	Yes
QREEQAEPDGTEVADK	K	A	95.00%	94		901.4185	2	4.7	371	386	Yes
QREEQAEPDGTEVADK	K	A	95.00%	54		601.2800	3	2.1	371	386	Yes
QREEQAEPDGTEVADKAAYLQSLNSADLLK	K	A	95.00%	96		1097.2200	3	7.7	371	400	Yes
QRLQNEVEDLMLDVER	K	S	95.00%	64		663.0079	3	8.0	1422	1437	No
QVEQEKCEIQAALEEAEASLEHEEGK	K	I	95.00%	90		976.4582	3	0.4	1535	1560	No
RQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	104	M19: Oxidation	918.1191	3	9.7	150	172	Yes
RQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	34	M19: Oxidation	688.8396	4	7.2	150	172	Yes
RQEAPPHIFSISDNAYQFMLTDR	K	E	95.00%	111		912.7822	3	3.9	150	172	Yes
RQEAPPHIFSISDNAYQFMLTDRENQSILITGESGAGK	K	T	95.00%	66	M19: Oxidation	1060.0300	4	7.6	150	187	Yes
RVIQYFATIAVTGEK	K	K	95.00%	106		848.4809	2	6.2	193	207	Yes
RVIQYFATIAVTGEK	K	K	95.00%	71		565.9888	3	4.3	193	207	Yes
SAETEKEMATMK	K	E	95.00%	40	M11: Oxidation	686.3135	2	4.0	845	856	Yes
SAETEKEMATMK	K	E	95.00%	68		678.3158	2	3.6	845	856	Yes
SAETEKEMATMKEEFQK	K	T	95.00%	83	M11: Oxidation	1016.9680	2	4.0	845	861	Yes
SAETEKEMATMKEEFQK	K	T	95.00%	39	M11: Oxidation	678.3148	3	3.8	845	861	Yes
SAETEKEMATMKEEFQK	K	T	95.00%	75	M8: Oxidation	1016.9690	2	4.3	845	861	Yes
SAETEKEMATMKEEFQK	K	T	95.00%	33	M8: Oxidation	678.3148	3	3.8	845	861	No
SAETEKEMATMKEEFQK	K	T	95.00%	75	M8: Oxidation	1024.9670	2	5.5	845	861	Yes
SAETEKEMATMKEEFQK	K	T	95.00%	51	M8: Oxidation	683.6451	3	1.9	845	861	Yes
SAETEKEMATMKEEFQK	K	T	95.00%	75	M8: Oxidation, M11: Oxidation	1024.9670	2	5.5	845	861	Yes
SAETEKEMATMKEEFQK	K	T	95.00%	51	M8: Oxidation, M11: Oxidation	683.6451	3	1.9	845	861	Yes
SAETEKEMATMKEEFQK	K	T	95.00%	96		1008.9730	2	6.2	845	861	Yes
SAETEKEMATMKEEFQK	K	T	95.00%	47		672.9822	3	2.5	845	861	Yes
SANFQKPK	K	V	95.00%	43		460.2563	2	4.9	563	570	Yes
SLSTELFK	R	V	95.00%	34		924.5073	1	3.2	1479	1486	No
SLSTELFK	R	V	95.00%	65		462.7567	2	1.5	1479	1486	No
SYHIFYQITSNK	R	K	95.00%	87		750.8779	2	-0.5	285	296	Yes
SYHIFYQITSNK	R	K	95.00%	43		500.9233	3	3.7	285	296	Yes
TEELEEAKK	R	K	95.00%	37		538.7814	2	6.8	1386	1394	Yes
TKYETDAIQR	R	T	95.00%	69		612.8162	2	1.6	1376	1385	Yes
TKYETDAIQR	R	T	95.00%	46		408.8804	3	2.4	1376	1385	Yes
TKYETDAIQRTEELEEAK	R	K	95.00%	37		718.6936	3	3.9	1376	1393	Yes
TPGAMEHELVLHQLR	K	C	95.00%	65	M5: Oxidation	873.9549	2	3.3	683	697	Yes
TPGAMEHELVLHQLR	K	C	95.00%	71	M5: Oxidation	582.9729	3	3.9	683	697	Yes
TPGAMEHELVLHQLR	K	C	95.00%	35	M5: Oxidation	437.4808	4	2.1	683	697	Yes
TPGAMEHELVLHQLR	K	C	95.00%	109		865.9571	2	2.9	683	697	Yes
TPGAMEHELVLHQLR	K	C	95.00%	71		577.6407	3	3.0	683	697	Yes

				TPGAMEHELVLHQLR	K	C	95.00%	45		433.4824	4	2.8	683	697	Yes
				TSVFVAEPK	K	E	95.00%	36		977.5336	1	2.9	38	46	Yes
				TSVFVAEPK	K	E	95.00%	71		489.2706	2	2.6	38	46	Yes
				VGNEYVTK	K	G	95.00%	69		455.2391	2	2.3	409	416	Yes
				VIQYFATIAVTGEK	R	K	95.00%	132		770.4273	2	2.9	194	207	Yes
				VIQYFATIAVTGEK	R	K	95.00%	81		513.9551	3	4.8	194	207	Yes
				VKELTYQTEEDRK	R	N	95.00%	84		819.9244	2	4.2	1850	1862	Yes
				VKELTYQTEEDRK	R	N	95.00%	58		546.9517	3	3.3	1850	1862	Yes
				VKELTYQTEEDRK	R	N	95.00%	40		410.4650	4	1.6	1850	1862	Yes
				VKNLTEEMAGLDETIAK	K	L	95.00%	34	M8: Oxidation	626.6595	3	5.1	978	994	Yes
				VKNLTEEMAGLDETIAK	K	L	95.00%	136		931.4893	2	6.6	978	994	Yes
				VKNLTEEMAGLDETIAK	K	L	95.00%	61		621.3281	3	5.5	978	994	Yes
				VKVGNEYVTK	R	G	95.00%	53		568.8211	2	2.5	407	416	Yes
				VLNASAIPEGQFIDSK	K	K	95.00%	113		844.9516	2	5.5	727	742	Yes
				VLNASAIPEGQFIDSK	K	K	95.00%	70		563.6371	3	5.8	727	742	Yes
				VLNASAIPEGQFIDSKK	K	A	95.00%	87		909.0000	2	6.1	727	743	Yes
				VLNASAIPEGQFIDSKK	K	A	95.00%	51		606.3344	3	3.6	727	743	Yes
				VQLLHTQNTSLINTK	R	K	95.00%	111		855.4861	2	5.4	1716	1730	Yes
				VQLLHTQNTSLINTK	R	K	95.00%	74		570.6585	3	2.8	1716	1730	Yes
				VQLLHTQNTSLINTKK	R	K	95.00%	102		919.5307	2	1.9	1716	1731	Yes
				VQLLHTQNTSLINTKK	R	K	95.00%	62		613.3572	3	3.3	1716	1731	Yes
				VVETMQSTLDAEIR	R	S	95.00%	44	M5: Oxidation	804.4082	2	8.4	1596	1609	No
				VVETMQSTLDAEIR	R	S	95.00%	39		796.4103	2	7.9	1596	1609	No
				YKVLNASAIPEGQFIDSK	R	K	95.00%	50		660.6903	3	5.4	725	742	Yes
				YKVLNASAIPEGQFIDSKK	R	A	95.00%	78		703.3875	3	3.7	725	743	Yes
942	IPI00303335	NEB	NEBULIN.	ENLGTGIPTTVTPEIER	K	V	95.00%	56		913.9846	2	6.1	6218	6234	Yes
				ITVVQDTPEILR	K	V	95.00%	70		692.3977	2	1.9	6130	6141	Yes
				NQENFSSVLYK	R	E	95.00%	46		664.8309	2	4.1	6238	6248	No
943	IPI00304071	FLJ20920	HYPOTHETICAL PROTEIN FLJ20920.	DLVVAYGTTENSPVTFAHFPEDTVEQK	K	A	95.00%	36		998.8259	3	8.4	403	429	No
				GATLSHYNIVNNSNILGER	K	L	95.00%	36		691.3586	3	3.8	272	290	No
944	IPI00334190	STOML2	STOMATIN-LIKE PROTEIN 2.	APVPGTPDSLSSGSSR	K	D	95.00%	45		757.8771	2	0.9	322	337	No
				ILEPGLNILIPVLDR	R	I	95.00%	87		838.0195	2	9.0	58	72	No
945	IPI00375333	RRAD	GTP-BINDING PROTEIN RAD.	IFGGVEDGPEAEAAGHTYDR	R	S	95.00%	50		697.6555	3	4.2	110	129	No
				VLLLGAPGVGK	K	S	95.00%	43		512.3347	2	4.5	94	104	No
946	IPI00396370; IPI00719752; IPI00747447	EIF3S9	ISOFORM 1 OF EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9.; ISOFORM 2 OF EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9.; 99 KDA PROTEIN.	GTQGVVTNFEIFR	K	M	95.00%	41		734.3881	2	5.9	536	548	No
				GYIFLEYASPAHAVDAVK	K	N	95.00%	33		651.0084	3	6.6	231	248	No
947	IPI00410693; IPI00412714; IPI00470497; IPI00470498	SERBP1	ISOFORM 1 OF PLASMINOGEN ACTIVATOR INHIBITOR 1 RNA-BINDING PROTEIN.; ISOFORM 4 OF PLASMINOGEN ACTIVATOR INHIBITOR 1 RNA-BINDING PROTEIN.; ISOFORM 2 OF PLASMINOGEN ACTIVATOR INHIBITOR 1 RNA-BINDING PROTEIN.; ISOFORM 3 OF PLASMINOGEN ACTIVATOR INHIBITOR 1 RNA-BINDING PROTEIN.	FDQLFDDESDPFEVLK	R	A	95.00%	84		972.4589	2	9.4	17	32	No
				KPANDITSQLEINFGDLGR	R	P	95.00%	38		696.6995	3	4.9	340	358	No
948	IPI00465260	GARS	GARS PROTEIN.	LPFAAAQIGNSFR	K	N	95.00%	52		696.3793	2	5.1	319	331	No
				TVNVVQFEPSK	K	G	95.00%	55		624.3378	2	3.3	491	501	No
949	IPI00604624	NIF3L1	HYPOTHETICAL PROTEIN NIF3L1.	INIILSETDRDPLQVV	K	-	95.00%	42		913.0145	2	7.6	362	377	No
				VGIYSPHTAYDAAPQGVNNWLAK	R	G	95.00%	34		824.7531	3	5.1	121	143	No
950	IPI00642211	RNPEP	AMINOPEPTIDASE B.	ETFASTASQLHSNVVNYVQQIVAPK	K	G	95.00%	63		911.1458	3	6.3	632	656	No
				TYQLVYFLDK	K	I	95.00%	36		645.3459	2	4.5	540	549	Yes
951	IPI00748490; IPI00827636	AARSD1	ALANYL-TRANSFER RNA SYNTHETASE FAMILY PROTEIN.; ISOFORM 1 OF ALANYL-TRNA SYNTHETASE DOMAIN-CONTAINING PROTEIN 1.	GGGLFLLAGPPASVETLGPR	K	V	95.00%	36		955.0399	2	8.8	349	368	No
				TNLIFLSGNR	R	V	95.00%	34		567.8198	2	4.1	236	245	No
952	IPI00791835	ANK1	PROTEIN.	LALQAQPVPDELVTK	K	L	95.00%	52		811.4663	2	4.9	428	442	Yes
				LLGNQATFSPIVTVEPR	K	R	95.00%	66		921.5160	2	6.2	443	459	No
953	IPI00828062		ANTI-(ED-B) SCFV (FRAGMENT).	EVQLLESGGGLVQPGGSLR	-	L	95.00%	114		948.5184	2	5.1	1	19	No
				FSGSGSGTDFTLTISR	R	L	95.00%	82		816.9050	2	9.3	193	208	No
				NTLYLQMNSLR	K	A	95.00%	65	M7: Oxidation	684.8549	2	5.4	77	87	Yes
954	IPI00830047		PROTEIN.	AAPSVTLFPPSSEELQANK	K	A	95.00%	60		993.5208	2	7.7	5	23	No
				YAASSYLSLTPEQWK	K	S	95.00%	91		872.4412	2	8.6	66	80	No

---

[1] Proteins that share the same group of assigned peptides

[2] Indication of whether a peptide was assigned to more than one protein